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1 About these Instructions for Use

These Instructions for Use consist of three volumes:

1. Your MRI System
2. Operation in the Magnet Room
3. Operation at the MR console

This volume 3 of these Instructions for Use, "Operation at the MR console", contains information on how to operate the MR console, e.g. scanning of examinations, viewing and postprocessing of MR data.

This manual may contain descriptions regarding the features and functionalities that are not implemented on the current equipment shipped for Japan and/or the product(s) that is/are not currently sold in Japan due to limitations and restrictions under the applicable local laws and regulations in Japan.

Within these Instructions for Use, the most extensive configuration of the system is described, with the maximum number of options and accessories. Not every function described may be available on your system.
2 System startup and switch off

NOTICE
If your system has been upgraded to the current release, your hardware may differ from the systems described in this manual.
If this is the case please refer to the Instructions for Use originally delivered with your System for proper system startup and switch off. Even when this system is switched off some subsystems remain powered.

Powering and system startup must be performed by a Philips service representative. This includes final adjustments of hardware compensation and control settings.
Under normal circumstances it is not possible to switch off the system completely or partly. When not in use the system will switch into standby mode after approximately two hours of inactivity. Power consumption is then minimized.

WARNING
The system and all subsystems remain powered.
Danger of an electric shock.

It is only possible to shut down the computer as described in chapter “Computer shutdown” on page 17.

CAUTION
It is strongly recommended to keep the computer running permanently.
It is sufficient to exit the system software and to switch off the display without using Shutdown. When the computer is running the system will remain available for remote servicing and will run scheduled tasks (quality checks).

- It is only necessary to switch off the computer if a system hang up occurs.
- Never exit the system software while a background process (such as hard copy, DVD recording or Network) is still running.
- It is advisable to switch off the display unit on the Operator’s Console at night.

Switch off by Philips service representative
Please contact your local Philips service representative if a serious reason exists that requires the complete system to be switched off.
CAUTION
System switch off and opening the technical cabinets may only be done by or under guidance of Philips service.

CAUTION
Helium boil-off will occur when the system is completely switched off. The cryogen cooler will not work and the system may quench.

Computer start up
1. Switch on the computer in the operator’s console.
2. When the logon screen appears on the monitor press Ctrl+Alt+Delete keys on the keyboard. The logon dialog box is displayed.
3. Log in: Type in Username and Password and confirm by clicking |OK| or pressing the Return key. The system software will start.

NOTICE
After first logon a different password must be entered of at least seven characters.
Initial settings of username and password are "MRuser" and "Philips".

NOTICE
Verify that there is no (bootable) CD/DVD in your system.
The system may try to start up from the CD/DVD drive.

NOTICE
The user interface of the system does not provide direct visual feedback of the user that is currently signed-in.
The signed-in user can be revealed by pressing |Ctrl-Alt-Del|. The user name is displayed in the subsequent dialog box. Exit the dialog by pressing ‘Esc’ or click on |Cancel|.

Exit system software

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<th>4</th>
<th>5</th>
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<td>Examination</td>
<td>Review</td>
<td>Analysis</td>
<td>System</td>
<td>Help</td>
</tr>
</tbody>
</table>

Fig. 1: 5: System menu.
1. Select ‘Exit’ from the System menu.
   The Exit confirmation window is displayed: Confirm the request to exit, cancel/proceed.
2. Click |Proceed|.
   The ‘Stop’ status box is displayed until the software has been logged off.
   The Logon dialog box is then displayed.
   To start-up the system software again see chapter “System startup and switch off” on page 15.

**Computer shutdown**

The computer can be shut down directly or indirectly.

**System shutdown with start menu**

1. Press the Windows Start key on your keyboard.
2. Select ‘Shutdown’. The Shutdown window is displayed.
3. Click on one of the following options:

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<tr>
<th>Option</th>
<th>Description</th>
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<tr>
<td>Log Off</td>
<td>Exits the system software</td>
</tr>
<tr>
<td>Shutdown</td>
<td>Shuts down the System.</td>
</tr>
<tr>
<td>Restart</td>
<td>Restarts the system.</td>
</tr>
<tr>
<td>Cancel</td>
<td>Cancels the shutdown procedure.</td>
</tr>
</tbody>
</table>

**Computer shutdown from system Software**

1. Exit the system software as described.
   This will display the logon screen.
2. Press |Ctrl + Alt + Del buttons|.
   The logon dialog box is displayed
3. Click |Shutdown|.
   The dialog box ‘It is safe to turn off your computer’ is displayed.
3 Help and User Documentation

Both the Help information and the user documentation are available on the system. Furthermore there is an editable Help available for the ExamCards. The user documentation also includes a Technical Description, a DICOM Conformance Statement and other information.

Within the application software

From within the MR application software, the Help information and the user documentation can be viewed in the configured application language.

Context sensitive Help
1. Move the cursor on a field that you want more information about.
2. Press [F1] on your Keyboard.

If the selected field includes context sensitive information the related topic is displayed on your screen. If not available, the start page of the Help is displayed and you can search for a topic manually.

Help
The Help system is a compilation of information from the Instructions for Use (three volumes), the Technical Description and the parameter help.
1. Select ‘Help’ on the main menu bar.
2. Select ‘Help topics’. The Help is displayed. You can search through the help using the table of contents, the index or the word search.

User Documentation
The user documentation includes the Instructions for Use (three volumes), the Technical Description and the DICOM Conformance Statement.
1. Select ‘Help’ on the main menu bar.
2. Select ‘User Documentation’.
A browser window is opened where you can select the user documentation.

From the Windows Start menu
All provided documents can be accessed from the Windows start menu:
1. Press the Windows Start key.
2. Select ‘User documentation’ and 'index.html'.
3. Scroll to the required language and select the document you want to view:
• Help system
• Instructions for Use
• Technical Description
• DICOM Conformance Statement.
4 Operator-Patient Intercom

The Operator-Patient Intercom enables communication with the patient, it provides music to the patient and signals when the patient uses the nurse call.

![Operator-Patient intercom](image)

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<th>Description</th>
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<td>3</td>
<td>Talk volume</td>
</tr>
<tr>
<td>4</td>
<td>Music volume</td>
</tr>
<tr>
<td>5</td>
<td>Patient music on/off</td>
</tr>
<tr>
<td>6</td>
<td>Talk and Nurse call light ring</td>
</tr>
<tr>
<td>7</td>
<td>Listen on/off</td>
</tr>
<tr>
<td>8</td>
<td>Listen volume</td>
</tr>
</tbody>
</table>

*) Note that depending on your system configuration the intercom may not have an emergency stop button.

**Emergency Stop button**

This button has the same functionality as the emergency stop button on the UIM. Pressing the Emergency stop button will stop the tabletop movement. This can be reset using the Resume button.
**Talk volume +/- button**

Use this button to adjust the talk volume to the patient. The level is indicated on the LED bar next to the button.

**Music volume +/- button**

Use this button to adjust the music volume for the patient. The level is indicated on the LED bar next to the button.

**Patient music on/off Button**

Use this button to toggle the music for the patient on and off. The button icon lights up when music is turned on. Music is muted while the talk button is pressed.

**Talk and Nurse call light ring**

Press and hold this button to talk to the patient, releasing it will stop communication. Music is muted while the talk button is pressed.

When the pinch ball of the nurse call is pressed more than once within 4 seconds or for more than 1.5 seconds, a beep sounds and the light ring around the talk button flashes to attract the attention of the operator. Press the talk button to stop the beep and the flashing of the light ring.

**Listen on/off Button**

Use this button to toggle the listen function on and off. The button icon lights up when the listen function is turned on. The listen function is muted while the talk button is pressed.

**Listen volume +/- button**

Use this button to adjust the speaker volume of the intercom. The level is indicated on the LED bar next to the button.
5 Customizing your system

To display the Windows Taskbar and Start button press the Windows key on your keyboard.

Hospital administrator and user accounts

About accounts
The default user account "MRuser" can be used by different system operators, but does not provide a personified logging of the actions done by each operator.

Personified user accounts providing the logging of the actions done by each individual user may be required by legislation: for example HIPAA. Each of these individual users has the same permissions and rights as the default system user.

User accounts should be managed by the hospital administrator.
It is also possible to create multiple hospital administrator accounts.

Connect system to hospital Active Directory
Domain privileges are needed to connect the system to the hospital Active Directory.
► Logon as Hospital Admin.
► Configure DNS in Network and Sharing Center on the Windows Control Panel.
► Add the system to the Hospital Domain in System on the Windows Control Panel.

Change password Policies

► Click Windows Start and select MR System Management and System Management.

Create a new local user account
1. Logon with username HospitalAdmin (not case sensitive).
2. Password: ‘Hospital’ (case sensitive) at first logon. You have to replace and confirm the initial password ‘Hospital’ by another password of minimum 7 characters *. The system does not start, but a restricted Windows environment is opened.
3. Open the Windows start menu, select Systems Management and User Management (Operators) or User Management (Hospital Administrators).
   The MR User Manager panel for user accounts or administrator accounts is displayed.

4. Select User and Add Local user.

5. Enter a personal username, a full name, an account description and define and confirm a password of minimum 7 characters for the new user.

   *1 The Password policy can be changed by the Hospital Admin.

NOTICE
On first login the new user or administrator is forced to change the password (minimum 7 characters).

Create an Active Directory (AD) account
The system must be connected to Hospital Active Directory for creating an AD account.

► Select User and Add AD user.
► The Select User dialog appears. Enter username (Check names).
► Depending on the account type of the hospital admin (local or domain) a domain password is needed.

Edit an account
1. Open the **User Management (Operators)** or **User Management (Hospital Administrators)** panel.

2. Right-click on a user in the list and select **Properties** or select a user in the list and click on **User** and **Properties**.

3. Change the account as required:
   - Full name.
   - Account description.
   - Password.
   - Disable the user account.
   - Enable/disable blocking of the user account during a certain time when the wrong password is entered repeatedly (Blocking time and occurrence of wrong password to be set by the Service Engineer).
   - Delete the user account.

**Delete an account**

An account can be deleted in the **User Management (Operators)** or **User Management (Hospital Administrators)** panel.

- Right-click on a user in the list and select **Delete user** or select a user in a list and click on **User** and **Delete user**.

**NOTICE**

The system provides functionality to synchronize with customer Active Directory.

### Hospital/Institution name setting

The hospital or institution name can be changed:

1. Click the Windows **Start button** and select **MR User** and **MR System**. The MR System Properties window is displayed.

2. Select a name from the scroll list or enter a new name and click **Apply**.

**NOTICE**

A new name entered will be added to the scroll list.

3. Click **OK**, the system will warn you that changes will only take effect after reboot of your system.

After rebooting your system the hospital or institution name will have changed.
Language settings

The application software and the Windows operating system can be set to the following languages:

<table>
<thead>
<tr>
<th>Language</th>
<th>English</th>
<th>Danish</th>
<th>German</th>
</tr>
</thead>
<tbody>
<tr>
<td>Greek</td>
<td>Spanish</td>
<td>French</td>
<td></td>
</tr>
<tr>
<td>Italian</td>
<td>Japanese</td>
<td>Norwegian</td>
<td></td>
</tr>
<tr>
<td>Dutch</td>
<td>Russian</td>
<td>Swedish</td>
<td></td>
</tr>
<tr>
<td>Simplified Chinese (PRC)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Change the language setting

1. Select Start and Control panel.
2. Click on the Region and Language, the Region and Language dialogue is displayed.
3. Select the Keyboard and Language tab.

4. Select your language from the scroll list and click Apply.
5. Click the Change keyboards button and select your keyboard layout.
   If your keyboard layout is not present in the field click Add...:

Fig. 4: Region and Language dialogue.
• On the **Add Input Language** dialogue select the input language from the top scroll list and your keyboard layout.
• Confirm by clicking **OK**.

6. Confirm by clicking **OK**. The window closes.

7. For Greek and Russian ONLY:
   • select the Advanced tab.
   • from the scroll list select Greek or Russian.

8. Click **OK** on the **Region and Language** dialogue.
The system will warn you that changes will only take effect after you logoff (exit system application) and logon again.

**CAUTION**
The system will ask you to logoff. However, when clicking **Yes** it will REBOOT, not logoff.

9. Click **Yes** to reboot the system.
After reboot the language setting will have changed.
6 Keyboard and Mouse Interaction

The keyboard and the mouse are used to input information to the computer.

Mouse

The mouse has three buttons: a left, a middle and a right button. In these Instructions for Use, the following terms are used when referring to the use of the mouse:

• "Click" refers to a single click with the left button.
  "Double-click" refers to a double click with the left button.
• "Right-click" refers to a single click with the right button.
• "Drag" refers to moving the mouse while pressing down the left button.
• "Right-drag" refers to moving the mouse while pressing down the right button.
• Other mouse actions such as combinations of mouse buttons are described where applicable.

Keyboard

The keyboard is used to enter text such as patient data and annotations. At times, keyboard entry is disabled by the system. When this occurs, all new keystrokes are ignored and an audible signal is sounded. To rectify this, click on the window to make it active.

A keyboard overlay shows the functions of all function keys on your keyboard in the system application software.

![Keyboard overlay](image)

**Fig. 5: Keyboard overlay.**

Windows Start key

Pressing the Windows Start key opens the Windows Start menu with Windows functionality, but also dedicated MR functionality.

![Windows Start key](image)

**Fig. 6: Windows Start key.**

The Keyboard Function Keys

Help Topics... <F1>

To open the Help system.
New Examination... <F2>
To enter/select examination data (e.g. patient name, birth date, patient weight) in order to scan a new examination.
For more information, refer to chapter “Entering examination data” on page 197.

Open for Review... <F3>
To display the list of examinations in order to view the imaging series of an examination.

Administration <F4>
To open the Patient Administration panel in order to e.g. copy, transfer, delete and import examinations and/or images.
For more information, see chapter “Administration (Patient Database)” on page 357.

Refresh <F5>
To refresh the screen and to make the latest changes visible.

Manage Job Queue ... <F6>
To check the status of background processes. For more information, see chapter “Check status of background processes with the Job Queue” on page 364.

Autoview <F7>
To display the latest reconstructed image of the current scan.

Start Scan <F8>
To start the next scan or ExamCard.

Menu Bar <F10>
To immediately display the corresponding menu, e.g. the Examination menu when you are in scanning mode.

Stop Scan <F12>
To stop the current scan.
• Pressing |F12| (or clicking 'Stop Scan') ONCE will stop the scan immediately: all high power RF and Gradient output is terminated, including acoustic noise. The reconstruction commences if enough data is available.
• Pressing |F12| (or clicking 'Stop Scan') for the second time will stop the reconstruction.
• If tabletop movement is inititated by the TTS function, pressing |F12| (or clicking 'Stop Scan') will abort tabletop movement.

Play (Movie) <Pause>
• To play (or pause/stop) the current dataset as a movie.

**NOTICE**
To view a MultiMovie, link the viewports first and then click 'Play (movie)'.
A MultiMovie shows multiple imaging series in a movie in parallel. For information about linking, refer to chapter “Review toolbar” on page 93.

The Movie functionality is a generic functionality occurring in Graphical PlanScan and all Review and Analysis packages. For more information about movies, refer to chapter “On Toolbars” on page 55.
7 Terminology and Definitions

ExamCard

An ExamCard (EC) is the electronic version of a clinical MR examination procedure. It has to be defined once and can then be reused for following patients with similar examinations in order to simplify the daily routine. An ExamCard consists of ExamCard items (see chapter “ExamCard Items” on page 34):

- Scan protocols (e.g. survey, T1- and T2-weighted scans in different orientations)
- SmartLine processing steps

These are postprocessing presets which will automatically be performed as part of an ExamCard. See chapter “SmartLine Processing” on page 41 for more information.

NOTICE

In what follows, the term ExamCard item is used to refer to both, scan protocols and SmartLine processing steps, as components of an ExamCard.

Furthermore an ExamCard contains

- Geometry reuse
  - Scans within an ExamCard can share the same geometry settings. Planning one scan with a specific geometry means that all scans with this geometry will be planned automatically.
- Online information about the scans
  - A short description of the delivered scans is available including an example image.

ExamCards and scan protocols are indicated by the following icons:

- ExamCard
- Scan protocol

ExamCards and scan protocols can be accessed in the chapter “ExamCard Manager” on page 78 and in the chapter “List View or Thumbnail View” on page 69.

ExamCard Databases (EC databases)

ExamCards are available in three different EC databases. The table gives an overview:
### Terminology and Definitions

<table>
<thead>
<tr>
<th>EC Database</th>
<th>Database contents</th>
<th>Locked/Not locked</th>
</tr>
</thead>
<tbody>
<tr>
<td>Philips</td>
<td>Philips ExamCards and scan protocols</td>
<td>The Philips EC database is locked and cannot be modified or overwritten by the operator or the hospital administrator. ExamCards and scan protocols in this database can only be used for scanning.</td>
</tr>
<tr>
<td>Hospital</td>
<td>Hospital ExamCards and scan protocols</td>
<td>The Hospital EC database can be locked using password protection. If the database is locked, its content cannot be changed or overwritten. ExamCards and scan protocols in this database can always be used for scanning.</td>
</tr>
<tr>
<td>Other</td>
<td>Reserved for Import/Export of ExamCards and scan protocols</td>
<td>This database cannot be locked. ExamCards and scan protocols can always be stored in this database.</td>
</tr>
</tbody>
</table>

Some ExamCards are delivered for the different subanatomies in order to give an example. You can find these in the Philips database: folder ExampleCards.

Locking is indicated by means of a 'Lock' icon in the ExamCard database tabs:

![Lock Icons](image)

**Fig. 7:** The three tabs for the three ExamCard databases. In this example, the Philips and the Hospital database are locked, 'Other' is not.

#### To store ExamCards in the Hospital ExamCard database

Remove the "lock" first:

- Right-click in the EC database window.
- Click "Unlock ExamCards Database".

If the Hospital EC database is password protected, the user will be asked to enter the password.

Once the lock is removed, the 'Lock' icon is not longer shown in the Hospital tab and ExamCards can now be saved in the Hospital EC database.

- Drag and drop ExamCards into the Hospital ExamCard database to save them there.

### ExamCard Items

An ExamCard item (EC item)

- is part of the ExamCard.
- stands either for a scanning step (also referred to as "scan item") or a postprocessing step.
- corresponds to one single row.

**NOTICE**

The maximum number of ExamCard items is 125.
The display of the ExamCard items changes in real-time from planning to scanning and to scan completion:

- different status icons are used,
- prior to scanning EC items are displayed in gray, completed scan items are displayed in blue.

**Fig. 8:** Example of ExamCard showing EC items. On top: during planning, Bottom: partly scanned.

<table>
<thead>
<tr>
<th>Number</th>
<th>Object (More information can be found in the text below the table.)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>EC item number (appears only when scanning is completed)</td>
</tr>
<tr>
<td>2</td>
<td>Status information about the EC item</td>
</tr>
<tr>
<td>3</td>
<td>if applicable: Warning signs indicating that scan item will be executed in first level control mode is due to high SAR (Specific Absorption Rate), high PNS (Peripheral Nerve Stimulation) or high SED (Specific Energy Dose).</td>
</tr>
<tr>
<td>4</td>
<td>Properties of the EC item</td>
</tr>
<tr>
<td>5</td>
<td>Name of the EC item</td>
</tr>
<tr>
<td>6</td>
<td>Geometry name of the EC item</td>
</tr>
<tr>
<td>7</td>
<td>Geometry Link</td>
</tr>
<tr>
<td>8</td>
<td>Laterality: R(right), L(left), B(oth), blank - if not specified</td>
</tr>
<tr>
<td>9</td>
<td>Expand / Collapse button</td>
</tr>
<tr>
<td>10</td>
<td>EC Header Line with ExamCard icon, ExamCard name and the remaining ExamCard duration. This is the remaining scan time for the complete ExamCard.</td>
</tr>
<tr>
<td>11</td>
<td>Possibility to add a new scan item from the ExamCard databases.</td>
</tr>
</tbody>
</table>
**ExamCard Item Number**

The scanning and postprocessing steps will be numbered by two digits where the first digit increases for scanning steps and the second digit for the postprocessing steps. The ExamCard Item Number appears only when scanning is completed.

<table>
<thead>
<tr>
<th>Number</th>
<th>Serie characteristics</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.1.</td>
<td>Survey</td>
</tr>
<tr>
<td>2.1.</td>
<td>T2w/TSE</td>
</tr>
<tr>
<td>2.2.</td>
<td>PicturePlus image enhancement (postprocessing)</td>
</tr>
<tr>
<td>3.1.</td>
<td>DWI</td>
</tr>
<tr>
<td>3.2.</td>
<td>Diffusion postprocessing</td>
</tr>
</tbody>
</table>

**Tab. 1:** Example: ExamCard Item Number in an ExamCard

**Status information about the EC item**

Icons indicate the current status of planning and/or planning of an EC item.

<table>
<thead>
<tr>
<th>Button</th>
<th>Status of the EC Item</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>The item needs planning.</td>
</tr>
<tr>
<td></td>
<td>The item is being modified.</td>
</tr>
<tr>
<td></td>
<td>The item is ready to run as it has been fully planned.</td>
</tr>
<tr>
<td></td>
<td>The item contains a parameter conflict.</td>
</tr>
<tr>
<td></td>
<td>The item containing a parameter conflict is being modified.</td>
</tr>
<tr>
<td></td>
<td>The item awaits update.</td>
</tr>
<tr>
<td></td>
<td>The item awaits resources and will be started as soon as sufficient resources are available.</td>
</tr>
<tr>
<td></td>
<td>The item is being prepared for execution.</td>
</tr>
</tbody>
</table>
### Button Status of the EC item

<table>
<thead>
<tr>
<th>Button</th>
<th>Status of the EC item</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1.png" alt="Image" /></td>
<td>The item is in progress.</td>
</tr>
<tr>
<td><img src="image2.png" alt="Image" /></td>
<td>The acquisition of the item is completed, and the reconstruction is in progress.</td>
</tr>
<tr>
<td><img src="image3.png" alt="Image" /></td>
<td>The item is successfully completed.</td>
</tr>
<tr>
<td><img src="image4.png" alt="Image" /></td>
<td>The item is aborted, either by the operator or scanner or reconstruction fault.</td>
</tr>
<tr>
<td><img src="image5.png" alt="Image" /></td>
<td>The item is invalid and cannot be executed, e.g. because it originates from an older release.</td>
</tr>
</tbody>
</table>

### Properties of the scan item

The Properties column provides information in the following order on:

- High SAR (Specific Absorption Rate), high PNS (Peripheral Nerve Stimulation) or high SED (Specific Energy Dose) values
- User Start required / Manual start
- Breathholds
- Table movement

### Button Property Description

<table>
<thead>
<tr>
<th>Button</th>
<th>Property</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1.png" alt="Image" /></td>
<td>Warning</td>
<td>Operator attention is required due to high SAR, PNS or high SED.</td>
</tr>
<tr>
<td><img src="image2.png" alt="Image" /></td>
<td>User Start Required</td>
<td>User start is required. The scan will not start automatically.</td>
</tr>
<tr>
<td><img src="image3.png" alt="Image" /></td>
<td>Manual start</td>
<td>Scan stops after the preparation phase. Manual start is required.</td>
</tr>
<tr>
<td><img src="image4.png" alt="Image" /></td>
<td>Breathhold</td>
<td>Scan stops when breathhold commands are required.</td>
</tr>
<tr>
<td><img src="image5.png" alt="Image" /></td>
<td>Table movement</td>
<td>Operator action is required in order to perform table movement.</td>
</tr>
</tbody>
</table>
**Geometry Name (or GeoName)**

The GeoName is used to simplify planning:

Scans sharing the same geometry (same geometry name) by default have

- the same number of stacks,
- the same orientation,
- each stack with identical angulations and offcenters.

A blue border around the geometry field indicates that modification of the existing geometry name or new input is possible.

**Geometry Link (or GeoLink)**

The GeoLink between scans includes that scans with different geometry parameters are linked to each other. The linked protocols are combined within a geometrically linked group.

A GeoLink

- groups scans that will be planned at once within planning in Graphical PlanScan.
- includes scan alignment to all scans within the group (applied constantly when planning the GeoLink until it is switched off).
- includes that all scans within a geometrically linked group will get the same scan number.
- is only possible for scans of the same scan type.
- can be defined once only under a specified name. E.g. a scan being stopped or aborted being part of link "C", the remaining scans of this current link "C" have to be updated to another link name.

<table>
<thead>
<tr>
<th>Button</th>
<th>Property</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Geometry link.</td>
<td>The current item belongs to a geometrically linked group where 'X' is the group name [A ... Z]. .</td>
<td></td>
</tr>
</tbody>
</table>

Typical applications are examinations with a large Field-of-View in Feet-Head direction, such as MobiFlex and Whole Body imaging. These examinations have to be performed in multiple stations with table movement between the stations in order to cover the complete area.

**Laterality**

When applicable, the laterality ("R" for right, "L" for left, "B" for both, or blank if not specified). The parameter laterality is primarily used for paired anatomies such as knee, ankle, shoulder, elbow etc. The laterality value can be used by PACS systems.

**NOTICE**

It is recommended to store dedicated left and right ExamCards.
**Expand / Collapse button**

Clicking 'Expand' will expand an ExamCard item and show the corresponding SmartLine post-processing step.

![T2W_VISTA sag]

![T2W_VISTA sag]

**Fig. 9:** The effect of the Expand and Collapse buttons in ExamCards.

**Characteristics**

**Saving and retrieving of examinations AND ExamCards**

ExamCards are saved to and retrieved from the patient database with the examination.

- Saving an examination will also save the corresponding ExamCard
  - when saving into any patient database;
  - when exporting to devices such as DVD.
- Retrieving an examination will also retrieve an ExamCard
  - when retrieving from any patient database;
  - when importing from devices such as DVD.

**NOTICE**

ExamCards are not retrieved for datasets acquired with previous software releases.

**Automatic ExamCard backup**

- A backup of ExamCards is automatically generated and preserved for 3 hours. This can be especially helpful after crashes.
  - Simply reselect the examination and the ExamCard will be restored including planned geometry.
  - Double-click on the ExamCard to confirm.
Preparation of ExamCards

ExamCards can be created and edited without a current examination/case in any of the viewing slots. This facilitates the preparation of ExamCards without a patient who needs to be scanned. Preparing ExamCards in such a way is referred to as ExamCard Prep Mode.

Password Protection of the EC Hospital folder

In order to ensure consistency and to protect the quality of the ExamCards, the contents of the Hospital folder can only be modified by authorized users.

NOTICE

The default password for the ‘Password Protection of the EC Hospital folder’ is Philips.

Enable/Disable EC Hospital folder password protection

► Select the 'ExamCard Password Manager' via the Windows Start menu.
► Enter the current password. Press |Enter| or click ‘OK’.

The ExamCard Password Manager opens.

► Enable or disable the ‘(Hospital) Database locking’.
► Click ‘OK’ to confirm.

A message will be displayed notifying that database locking has successfully been enabled or disabled and that the changes will be activated after a reboot.

► Reboot the system.

Change the password

This can only be done when logged in as MRUSER.

► Select the 'ExamCard Password Manager' via the Windows Start menu.
► Enter the current password. Press |Enter| or click ‘OK’.
The ExamCard Password Manager opens.

- Enter the new password
  - in the field "New password’ and
  - in the field ‘Confirm password’.
- Click ‘OK’.

A message will be displayed notifying that the password has successfully been changed and that the new password will be activated after a reboot.

- Reboot the system.

**Reset the password**

This can be done by the hospital administrator or by Philips service engineers. When you are the hospital administrator, then follow the procedure below:

- Log in to the MR system as hospital administrator.
- Select the 'ExamCard Password Reset' application via the Windows Start menu.
- Click ‘Reset password’.

  The current password will be reset to the default password.

- A message will be displayed notifying that the default password will be activated after a reboot.

- Reboot the system.

**SmartLine Processing**

Once the 'Generate Series' function is used during the analysis with a postprocessing package,

- a new imaging series will be generated, and
- a postprocessing item will be added to the ExamCard.

  The performed operation will be part of the current ExamCard and in such a way will automatically be performed whenever the ExamCard is executed again.

SmartLine Processing applies for the following postprocessing packages:

- VolumeView
- MobiView
- Diffusion
- Diffusion registration
- Basic T1 Perfusion
- Neuro (T2*) Perfusion
- Picture Plus
- Image Algebra
• IViewBOLD (in this case, the IViewBOLD will only be launched with the correct paradigm)

NOTICE
The maximum number of SmartLine processing steps is 6.

Smart MPR
If a 3D scan is planned using SmartExam (e.g. VISTA Knee or 3D-TFE Brain) angulations can be stored relative to the volume in the Smart MPR.
This means that if this ExamCard is stored with the SmartLine MPR, every MPR will have the same orientation.

ExamCard Exchange
ExamCard Exchange is an internet-based service that enables fast and simple download of ExamCards from NetForum.
The ExamCard Exchange functionality provides ExamCard download at the touch of a button
• Philips updates of ExamCards
• Customer ExamCards
For information on how to import/export ExamCards and/or ExamCard databases, refer to chapter “Export/Import of ExamCards” on page 214.

Connect to NetForum
It is possible to connect to NetForum in two ways.

Directly from the scanner
• via a secure, fast and reliable connection
1. Press the Windows Start key or click the Windows Start button.
2. Select ‘Favorites’.

From any PC connected to the Internet
1. Connect to the Internet as usual.
2. Go to the website http://www.philips.com/netforum.

Different User Levels on NetForum
Much of the information on NetForum (www.philips.com/netforum) is accessible for any visitors of the site.
However, registration is required for:

- Downloading ExamCards - Viewing restricted content, for instance scan protocols, some application tips
- Online training modules on use of Philips MR scanners and packages, use of coils, use of EWS, MR safety.
- Submitting content
- Utilization services

**Register / login for ExamCard Exchange**

On a first time visit, it is necessary to register. When registration already has taken place, the login can be performed at once.

**To register**

1. Click [Register].
2. Enter your data.
   - On a first time visit, the web site will try to acquire the configuration of the MR scanner automatically. Clearly this is only possible if the website is accessed directly from the scanner.
     - The website server will build configuration data of the user and save it for later use.
     - If the information has been retrieved automatically, then the server will show a summary to the user and ask for confirmation.
     - If confirmed, the user will be taken to the next page. If not, the user is informed about possible consequences and taken to the manual configuration page.
   - If there is no access to the internet, a semi-automatic procedure is available. The user will be instructed to copy a configuration file from the scanner to the computer that does have access to the internet and where the configuration file can be uploaded to the scanner.

**To login**

1. Enter your User-ID.
2. Enter your Password.

**Download or upload protocols**

2. Select ‘Magnetic Resonance’ /’International’ or ‘USA’.
3. Login as registered user.
4. Click ‘ExamCard Sharing’ to access ExamCards for download.
NOTICE
Images being exported with the ExamCard may not contain any patient data.
This is the customer’s responsibility.

SmartExam
SmartExam is a tool that automates planning, scanning and processing in brain, knee, shoulder, breast, cervical and lumbar spine examinations. Automatic planning and scanning is realized by SmartPlan, automatic processing by SmartLine Processing.

The principle of SmartPlan
SmartPlan makes use of an algorithm that automatically detects some typical anatomic structures in a Smart survey, e.g. corpus callosum for brain examinations, but also symmetry aspects are taken into account.

These typical structures are recognized, stored and used as a reference for further automatic planning.

SmartPlan is available for head, knee, shoulder, breast, cervical and lumbar spine examinations. It is a tool that helps in automatically planning scans with respect to the geometry parameters ‘offcenter’ and ‘angulation’.

Geometry databases
SmartPlan makes use of geometry databases which specify the way of planning for each anatomy. These geometry databases are predefined with the most common way of planning and allow for the immediate use of SmartExam. If another way of planning is preferred, user-specified geometry databases can be created:

► Copy the Philips geometry database.
► Add planning samples to this database or remove samples.

NOTICE
For shoulder, breast, cervical and lumbar spine, all angulations in the Philips geometry databases are set to zero.
This is also referred to as ‘Snap-to-table’.

Prerequisites for SmartExam
There are several prerequisites for a Smart ExamCard.
Smart survey

- The Smart ExamCard has to start with a Smart survey. The Smart survey is a dedicated 3D survey scan covering the anatomic region completely. Parameters of the Smart survey cannot be changed.

SmartGeometries

- In a Smart ExamCard, only SmartGeometries can be planned automatically.
- Existing ‘normal’ geometries need to be
  - replaced with existing SmartGeometries
  - converted into SmartGeometries.

Refer to volume 2 of your Instructions for Use to find out which coils can be used and are supported for SmartExam.

SmartExam Spine

A SmartExam Spine examination requires additional features to cope with variations in planning procedures compared to head, knee and shoulder examinations.

Every spine examination is unique. It is not always known beforehand at which disc level the transverse scans need to be positioned. SmartExam Spine comes with a unique graphical user interface. A schematic drawing of the spine allows easy definition of the precise levels for each stack.

Often a high resolution scan is necessary to determine the precise locations at which the transverse stacks must be planned. A Philips-unique snapping mechanism is implemented: dragging a stack in the graphical planscan user interface from one disc level to another results in the stack snapping precisely to the new disc level. This snapping occurs according to the user preferred planning as learned during the training phase.

If necessary, all stacks can be freely manipulated to tweak and train SmartExam planning better. The graphical planscan user interface automatically differentiates between manual fine tuning of individual stacks and dropping stacks at different levels.

NOTICE

Severe pathology or metal might cause SmartExam Spine to fail.

SmartExam Breast

Different to other anatomies, Image Based (IB) Shimming is automatically performed as part of SmartExam Breast, based on the IB-Smart segmentation algorithm.

IB-Smart requires that a SmartBreast survey is performed. The SmartBreast survey is designed to acquire the entire volume of tissue placed in the breast coil. It is important to position the patient so that they are in the center of the chosen coil. As with other Smart Surveys, first 3D
images are acquired, then orthogonal reconstructions (including both left and right breasts) are created and automatically updated in the view ports upon completion of the SmartExam analysis.

Fig. 11: Smart Surveys with the orthogonal reconstructions.

To provide optimal shimming for the tissue of interest, IB-Smart uses the 3D volume acquired during the SmartBreast Survey: an automatic segmentation is performed that excludes the lungs, heart, arms and silicone if present.

Fig. 12: Segmentation of the breasts to exclude lungs, heart, arms and silicone.

Shimming is performed on the remaining breast and axillae, leading to a uniform flip angle in the areas of interest and uniform fat suppression. Optimal shimming is obtained by calculating a B0 map before shimming and making adjustments to the shim in order to optimize the B0 in the segmented area.

Fig. 13: B0 maps.

Once calculations are completed they are available to the system to be applied to any sequence in which IB-Smart is the enabled shim parameter.

NOTICE

In order to utilize the segmentation algorithm for the SPIR and SPAIR sequences, enable 'IB-Smart' via the 'Shim' parameter on the 'Contrast' tab.

A shim box will not be visualized, and the values calculated by IB-Smart will be used.
Additionally, if performing on a 3.0T system, RF shimming must be adaptive and therefore a B1 calibration scan is required.

A system with SmartBreast enabled is delivered with trained Smart Geometries. The Smart-Breast geometries are trained at 0 angle, covering the breasts:

- Cor_PH – centered right to left
- Sag_PH – centered foot to head according to the breast tissue
- Tra_PH – centered to just anterior to the subcutaneous adipose tissue and chest wall, midway right and left between the breasts.

![Planning example.](image)

If the provided Smart Geometries do not meet the user's individual needs, site specific geometries can be trained. For more information, refer to the section SmartExam: Workflow ‘Set up a Smart ExamCard’.

**Related parameters**

- Shim (values relevant for SmartExam Breast: IB-Volume, IB-Smart)
- RF Shim (values relevant for SmartExam Breast: IB-Volume, IB-Smart)
- Interactive F0

**Interactive Scanning**

**About Interactive Scanning**

Interactive Scanning is a tool to be used whenever planning is difficult, e.g. due to complex anatomy as in the heart, the pancreas or the parotids. It can be used to track spatial and temporal changes. Interactive Scanning means that specific scan parameters (geometry and a few contrast parameters) are changed while scanning whereas the effect is to be seen in real-time. In such a way the optimal slice plane can quickly be found e.g. in case of difficult anatomies.

Imaging parameters which can be modified interactively are:

- Orientation parameters as offcenters, angulations, slice orientation
- FOV and slice thickness
- Flip angle (in gradient echo techniques)
• Trigger delay
• TFE prepulse on/off and TFE prepulse delay time
• Viewing settings as windowing or display of mirrored, flipped or rotated images

The key to Interactive Scanning is that scan geometry can be stored and be re-used in the following scans.

**Interactive scans**

- Can be combined with:
  - Any scan technique like SE, FFE, TSE, GRASE or EPI
  - Respiratory and/or cardiac triggering
- Have the following constraints:
  - Single-slice
  - Single-phase
  - Not combinable with dynamic scan mode

**Interactive Modes**

Interactive Scanning can be performed in two different modes. Toggling between these modes is possible at any time during the interactive session.

**Continuous mode**

Also referred to as real-time mode.

The same slice is scanned repeatedly until a user action (e.g. a right click) instructs the scanner to use different scan parameters for the next image(s).

The ‘Image delay’ field (‘Scan parameters’ subwindow) defines the time between two images (relative to the time needed to scan a single image). Increasing this delay can be used to avoid high SAR or high temperature warnings and to increase SNR in TSE methods.

**Applications**

- Cardiac examinations
- Functional joint studies
  - Typically gradient echo scans.
  - TSE is not used due to saturation effects unless DRIVE is enabled.

**Single-image mode**

Means that only one single image is scanned after the user triggers the scanner, for example through a right-click.

**Applications**

E.g. for tracking a needle in a biopsy guidance. Typically TSE scans which provide high spatial resolution and are less sensitive for field inhomogeneities.
8 Introduction to the User Interface and General Information

**iPatient** provides patient-centric workflow: An intuitive interface allows users to adapt imaging to the patient in a consistent manner, aided by SmartExam, SmartSelect and user guidance.

This chapter gives an introduction to the user interface and describes generic functionality available throughout the complete user interface with respect to planning, scanning, reviewing and analysis.

For more information about:
- screen layout and the most important windows and menus, please refer to chapter “Screen Layout, Menus and Windows” on page 61.
- Review and Analysis packages, please refer to chapter “Review and Analysis Packages” on page 105.
- workflows, please refer to chapter “Workflows Scanning and Planning” on page 197.

**Viewports and Windows**

A **window** is a visual area containing some kind of user interface. The windows in the MRI user interface have a rectangular shape that can overlap with the area of other windows. They are used for multiple purposes, e.g. they may allow input to processes, or they are used to display notifications and error messages.

A **viewport** is a window dedicated to the display of images, e.g. MR slices, reformats or parameter maps.

**Viewport Buttons**

- Click any of the viewport buttons in the upper right corner of each viewport to:
  - Hide the Toolbar
  - Maximize or Minimize the View
  - Close the View.

**Typical Buttons**

Depending on the kind of window, several controls/buttons apply:

<table>
<thead>
<tr>
<th>Control/Button</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hide</td>
<td>Hides the window.</td>
</tr>
<tr>
<td>OK</td>
<td>Leaves the window/browser/editor with changes made, but without applying the current changes.</td>
</tr>
</tbody>
</table>
Introduction to the User Interface and General Information

The various controls

<table>
<thead>
<tr>
<th>Control/Button</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Apply</td>
<td>Leaves the window/browser/editor with changes made, and applies the current changes.</td>
</tr>
<tr>
<td>Proceed</td>
<td>Leaves the window/browser/editor: confirms a selected procedure and goes ahead.</td>
</tr>
<tr>
<td>Cancel</td>
<td>Leaves the window/browser/editor without any changes.</td>
</tr>
</tbody>
</table>

The |ESC| key on the keyboard can also be used to close windows similar to Cancel.

Switch between views

One view is always the “current view. If a series is displayed in that view, it is the "current series".

To select another view as current view

► Click on another view.

![Fig. 15: 3 views in a tiled view: the upper left one is the current one (with orange tab and orange border).](image)

The various controls

The MR User Interface has various controls especially set up to meet the specific requirements of each application. These controls are:

• the main menu bar with comprehensive menus to access essential functionality.

• the application-specific toolbars, e.g. for planning or reviewing. For easy and quick access, the most important functions can be performed via these toolbars.

• dedicated functionality on all panels on the system.

• various right mouse menus (context menus)
Right mouse menus are available throughout all applications to facilitate the use of the system and to offer various interaction possibilities.

- Simply right-click on any viewport/screen area to access the right mouse menu.

**Keyboard**

Keyboard functions can be used for several purposes, e.g. for scrolling through images by means of the arrow keys.

Most of the functions in planning, reviewing or postprocessing can be performed via all controls. It's purely a matter of taste which control is going to be used.

For more information about menu bar, toolbars and panels available, refer to chapter “Screen Layout” on page 61.

For more information about the keyboard functions, refer to chapter “Keyboard and Mouse Interaction” on page 29.

More information about the right mouse menus is available where applicable.

**Notifications and Alerts**

Standard notifications and error messages show up in the bottom row of windows.

Alerts or notifications that require user attention pop up in dedicated windows.

**Image Information**

Information about images and imaging series is given at different locations in the Review and Analysis packages.

**About Imaging Series**

Information about the imaging series can be displayed when hovering the cursor over the Thumbnail View:

![Image Information](image.png)

**Fig. 16:** Information about imaging series in tooltip.

**Image Information**

Image information in the upper left corner of every image appears when you open an imaging series in any of the Review or Analysis packages.

Every image is displayed with text information:
Fig. 17: Typical examples. The upper left image shows the format of the image information: see table below.

<table>
<thead>
<tr>
<th>Number</th>
<th>Representing</th>
<th>Possible values</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>scan number</td>
<td>1, 1 or 2, 1 or 3, 1 or 4, 1 where the first digit increases for scanning steps and the second digit for the postprocessing steps</td>
</tr>
<tr>
<td>2</td>
<td>slice number</td>
<td>mostly 2 numbers separated by a “/” where the first digit is the current slice number and the second digit the total number of slices in this series</td>
</tr>
<tr>
<td>3</td>
<td>scan technique</td>
<td>e.g. (T)SE - (Turbo) Spin Echo, FFE - Fast Field Echo, (B-)TFE - (Balanced) TFE</td>
</tr>
<tr>
<td>4</td>
<td>image type</td>
<td>e.g. M - Modulus, P - Phase, R - Real, I - Imaginary, SW_M,R,I,P - Susceptibility Weighted-M,R,I,P</td>
</tr>
</tbody>
</table>
| 5      | More               | • empty - if not applicable  
• Dt (dynamic time) - only applicable for dynamic imaging series  
• Td (Trigger delay) - only applicable for triggered imaging series  
• Ec1, Ec2 - only applicable for multi-echo imaging series |

Tab. 2: Format

Graphical information per viewport

By default, the following graphical information is given in every viewport:

- The fold-over indicator  
  that indicates the fold-over direction in which typically MR artifacts occur.

- The 3D coordinate system  
  that indicates the Head-Feet (H_F), the Anterior-Posterior (AP) and the Left-Right (LR) direction.

- If applicable a Link symbol  
  indicating that imaging series are linked.
Increasing/decreasing the amount of information

In ImageView, you can increase or decrease the amount of information by means of the button 'Image Information' which is available on the ImageView toolbar. For more information, refer to chapter “Toolbar” on page 107. The amount of information displayed cannot be changed in Review or Analysis packages other than ImageView.

Windowing, Zooming and Panning

Zoom, Pan, Window width and level

Zooming, panning and windowing are performed via direct mouse actions. Direct mouse actions must start in the current viewport. Mouse movement is not limited to this viewport but to the viewing area of the screen.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Mouse button(s) and movement</th>
<th>Movement and Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Window level (Brightness)</td>
<td>middle</td>
<td>• upwards = darker</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• downwards = brighter</td>
</tr>
<tr>
<td>Window width (Contrast)</td>
<td>middle</td>
<td>• to the right = less contrast</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• to the left = more contrast</td>
</tr>
<tr>
<td>Zoom</td>
<td>middle + right</td>
<td>• upwards = zooming in; Max. zoom factor of 8</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• downwards = zooming out; Min. zoom factor of 0.25</td>
</tr>
</tbody>
</table>
Scrolling through images

The way of scrolling through images depends on the view settings and the number of image attributes.

You can use the mouse or the arrow keys to scroll through images.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Mouse button(s) and movement</th>
<th>Movement and Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pan</td>
<td>middle + left</td>
<td>• to pan in all directions.</td>
</tr>
</tbody>
</table>

To scroll through...

Press the arrow keys Mouse movement Effect on image attribute

1st image attribute ▶ In the image viewport, drag to the left or to the right. Movement to the right increases (to the left decreases) the number of the image attribute.

2nd image attribute a Alternatively use the left and right arrow keys. Upwards movement increases (downwards decreases) the number of the image attribute.

3rd image attribute ▶ In the image viewport, drag up- or downwards. Movement right-upwards increases (left downwards decreases) the number of the image attribute.

Example: Scrolling in a scan with only one image attribute

The image dataset has only slices.

Through slices (or resulting) maps

▶ In the image (or map) viewport, drag to the left or to the right.
▶ Alternatively use the left and right arrow keys.

Example: Scrolling in a scan with two image attributes

The dataset consists of multiple dynamics with multiple slices. The first image attribute are the dynamics, the second one are the slices. First all slices for the first dynamic are displayed, then all slices for the second dynamic and so on.

Through dynamics

▶ In the image viewport, drag to the left or to the right.

Through slices

▶ In the image viewport, drag up- or downwards.
Generic functions for images

The functions listed below can be performed throughout the complete user interface. They are available via the right mouse menus of the image viewports.

In Right Mouse Menus

Interaction Mode

- can be used to define the left mouse usage for interaction with images.

By default, dragging (by means of left mouse button) is used for scrolling. However, depending on the preference of the user, this can be changed. The following options can be enabled:

<table>
<thead>
<tr>
<th>Possible setting</th>
<th>Corresponding icon</th>
<th>Description (left mouse)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Scroll (default)</td>
<td><img src="image" alt="Drag to scroll" /></td>
<td>Drag to scroll through the dataset.</td>
</tr>
<tr>
<td>Zoom</td>
<td><img src="image" alt="Drag to zoom" /></td>
<td>Drag to zoom.</td>
</tr>
<tr>
<td>Pan</td>
<td><img src="image" alt="Drag to pan" /></td>
<td>Drag to pan.</td>
</tr>
<tr>
<td>Gray Level</td>
<td><img src="image" alt="Drag to adjust the gray level" /></td>
<td>Drag to adjust the gray level.</td>
</tr>
</tbody>
</table>

In the Review and Analysis packages, more options might be available.

Reset Window (Viewing)

To reset images to original window level and width.

Reset Zoom / Pan (Viewing)

To reset images to original zoom and pan values.

On Toolbars

Play (Movie) <Pause>

- To play (or pause/stop) the current dataset as a movie.
NOTICE
To view a MultiMovie, link the viewports first and then click 'Play (movie)'.
A MultiMovie shows multiple imaging series in a movie in parallel. For information about linking, refer to chapter “Review toolbar” on page 93.

Movie ToolBox
• To adjust the movie settings.
  ► Select 'Movie ToolBox' from the Movie drop-down menu besides the icon.

Fig. 19: Movie ToolBox.

<table>
<thead>
<tr>
<th>Number</th>
<th>Purpose/ Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Click this button to toggle between Play, Pause and Stop movie mode.</td>
</tr>
<tr>
<td>2</td>
<td>Click this button, then scroll to the image to start the movie with and click 'Play Movie'.</td>
</tr>
<tr>
<td>3</td>
<td>Click this button, then scroll to the image to end the movie with and click 'Play Movie'.</td>
</tr>
</tbody>
</table>
| 4      | Select the type of movie from the drop-down menu:  
  • cyclic (loop): the images are displayed in the order 1 ... n, 1 ... n etc.  
  • bounce (yoyo): the images are displayed in the order 1 ... n, n ... 1, 1 ... n, etc. |
| 5      | Select type of image for the movie, e.g. slices or phases. |
| 6      | Adjust the movie speed by dragging the slider. |

Viewing
To adjust the viewing settings:

Orientation (Viewing)
To change the orientation of the images:
• Mirror, Flip,  
• Rotate clockwise, Rotate counterclockwise,  
• Reset orientation,  
• Display Images in Radiological View
Image Information (Viewing)
• To define the amount of displayed image information:

  • minimum: no text is displayed,
  • standard: scan, image number and the scan name are displayed,
  • maximum: also the offcenter values, the window values (width and level) and the caliper
    are displayed.

Interpolate (Viewing)
To interpolate the image(s).

Invert Gray Level (Viewing)
• To invert the images of the current dataset (change black and white in the grayscale).

Capture ...
To capture images and save them. Type of image and destination are to be defined in the 'Capt-
ure' pop-up window. Check according to your preferences:

  • 'Capture Selected Image' captures the current image.
  • 'Capture ImageView' captures the current image including orange border and ImageView
    tab.
  • 'Capture Full Screen' captures the full screen.
  • 'Capture Slices' captures all slices of the current imaging series.
  • 'As Displayed and Annotated' or 'As Acquired' allow to capture images with or without their
    window/zoom settings and annotations.
  • 'Save to External Folder' allows to save the data to an external folder.
    In this case, it is necessary to browse to this external folder.
  • 'Save to Patient Database' allows to save the data to the patient database.
  • In order to include the hospital name, check the eponymic option.

The function 'Capture ...' as part of Viewing is only available in Review and Analysis packages,
not in Graphical PlanScan.

Save Presentation State <Ctrl+S> (Viewing)
To save a special way of presenting images.

Reload Presentation State <Ctrl+R> (Viewing)
To reload a special way of presenting images.
Reset Window (Viewing)
To reset images to original window level and width.

Reset Zoom / Pan (Viewing)
To reset images to original zoom and pan values.

Generate Series and ExamCards
Once the 'Generate Series' function is used and a new imaging series generated, a postprocessing item will be added to the ExamCard. The performed operation will be part of the current ExamCard and in such a way will automatically be performed whenever the ExamCard is executed again.

For more information, see chapter “SmartLine Processing” on page 41.

ROIs
In MRI, a Region of Interest (ROI) is a selected subset of voxels within a dataset: contours need to be drawn to define the region of interest.

The ROI function is only applicable within some of the postprocessing packages, e.g. QFlow and iView BOLD.

In the following sections, the various ROI functions *Draw, Propagate, Edit, Rename and Delete* are described.

**NOTICE**
Not all of these ROI functions are not available in every package.

Draw a ROI

*-> Smoothed Polygon*
Click to start up the ROI definition.
Draw with the left mouse button (no dragging).
Click as often as needed to add new points and to define a smoothed polygon.
Control points are created / deleted by pressing |Shift| and clicking on a contour or point.
Double-click to end drawing and to confirm the shape.
Clicking |ESC|, the entire contour is cancelled.
Scaling of Imaging Series

Introduction to the User Interface and General Information

-> Ellipse

Click twice to define one axis of the ellipse, click once more to define the other axis of the ellipse.
The area of the shape and the intensity mean value will be displayed by default.
To move the shape, drag the center of the shape.
To modify the shape, drag the outer edge of the shape.

-> Freehand

Click to start up the ROI definition.
Draw with the left mouse button (no dragging).
Click to end drawing and to confirm the ROI.
The area of the shape and the intensity mean value will be displayed by default.

Delete and copy a ROI

1. Right-click on the ROI to open the ROI context menu.
2. Select any of the options:
   • Cut <Ctrl+x>
   • Copy <Ctrl+c>
   • Copy To All
   • Delete <Del>
   • Delete All

Rename a ROI

You can rename existing ROIs.

► Right-click on a ROI and select 'Rename'.
   • It is advised to rename the ROIs for easier identification (e.g. left breast, right breast, tumor, cyst). It might be helpful to add the slice number to the name so that navigation to the respective ROI is facilitated.
   • If multiple ROIs are renamed to the same name, automatically a numerical extension is added to this name, e.g. Hemisphere, and Hemisphere 2

Edit a ROI

• |Ctrl| in combination with the left mouse click, selects respectively deselects a ROI.
• |Shift| in combination with the left mouse click enter the ‘ROI Edit’ mode.

Scaling of Imaging Series

Imaging series are linearly scaled.
Scaling is unique per imaging series. As a consequence, the scaling will also be different in e.g.
• imaging series with and without fat suppression:
• pre- and post-contrast imaging series

NOTICE
To ensure the same scaling for pre- and post-contrast imaging series, these scans should be scanned in dynamic mode.

The ExamCard function 'Split Dynamics' can be used to ensure a similar scaling of all required scans.
9 Screen Layout, Menus and Windows

Screen Layout

Planning, scanning, reviewing and postprocessing can be done in one MRI environment. Screen areas are reserved for specific operations such as planning or reviewing.

Fig. 20: Screen layout in Plan mode (large image) and in Review mode (small image).

<table>
<thead>
<tr>
<th>Number</th>
<th>Item</th>
<th>Purpose/Description</th>
<th>More information</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Main menu bar</td>
<td>To access the corresponding menus with comprehensive functionality.</td>
<td>chapter “Main menu bar and corresponding menus” on page 62</td>
</tr>
<tr>
<td>2</td>
<td>Launch pad with one tab for scanning and two tabs for reviewing, the buttons 'Plan' and 'Review' and information about the current examination.</td>
<td>To switch between reviewing and scanning tabs and to switch between Plan and Review mode.</td>
<td>chapter “Launch Pad” on page 68</td>
</tr>
<tr>
<td>Number</td>
<td>Item</td>
<td>Purpose/Description</td>
<td>More information</td>
</tr>
<tr>
<td>--------</td>
<td>------</td>
<td>---------------------</td>
<td>------------------</td>
</tr>
<tr>
<td>3</td>
<td>List View</td>
<td>(Current ExamCard) or Thumbnail View (Pictorial Index)</td>
<td>To toggle between List View (Current ExamCard) and Thumbnail View (Pictorial Index) List View shows the items of the current ExamCard whereas Thumbnail View shows a representative image per series of all imaging series, e.g. scans, reformats.</td>
</tr>
<tr>
<td>4</td>
<td>Graphical PlanScan area with Planning toolbar.</td>
<td>To graphically plan the imaging series of an examination.</td>
<td>chapter “Graphical PlanScan area” on page 72</td>
</tr>
<tr>
<td>5</td>
<td>Patient Status (PS) area</td>
<td>To monitor scan progress and to monitor the status of the patient during the examination: physiology signals and e.g. SAR, SED and PNS.</td>
<td>chapter “Patient Status area” on page 77</td>
</tr>
<tr>
<td>6</td>
<td>Parameter Editor or ExamCard Manager</td>
<td>To access everything around parameters via the Scan Dashboard, the Parameter Groups tabs, and the Scan Assistance. To manage ExamCards in different views.</td>
<td>chapter “Parameter Editor” on page 79 chapter “ExamCard Manager” on page 78</td>
</tr>
<tr>
<td>7</td>
<td>Review toolbar</td>
<td>To enable/disable/adjust generic reviewing settings.</td>
<td>chapter “Review toolbar” on page 93</td>
</tr>
<tr>
<td>8</td>
<td>Reviewing area</td>
<td>Reserved for reviewing imaging series with a user-defined layout.</td>
<td>chapter “Reviewing area” on page 95</td>
</tr>
</tbody>
</table>

**Main menu bar and corresponding menus**

**Table:**

<table>
<thead>
<tr>
<th>1</th>
<th>Patients</th>
<th>Examination</th>
<th>Review</th>
<th>Analysis</th>
<th>System</th>
<th>Help</th>
</tr>
</thead>
</table>

**Fig. 21:** Main menu bar in Plan and Review mode. Menus or menu options that are not applicable will be grayed out.

The Main menu bar allows to access menus with comprehensive functionality:

1. Patients menu
2. Examination menu
3. Review menu
4. Analysis menu
5. System menu
6. Help menu

When function keys are part of a menu option, the indicated function key can be pressed instead of selecting a menu option, e.g. `<F2>` means that the function key F2 can be pressed instead of selecting the function 'New Examination' from the Patients menu.

**Patients menu**

This section describes the menu options that are available via the 'Patients' menu.

**New Examination... <F2>**
To enter/select examination data (e.g. patient name, birth date, patient weight) in order to scan a new examination.

For more information, refer to chapter “Entering examination data” on page 197.

**Open for Review... <F3>**
To display the list of examinations in order to view the imaging series of an examination.

... or <Patient Name>
To switch between reviewing and scanning (examination) tabs.
This is an alternative to the 3 buttons in the chapter “Launch Pad” on page 68.

Three menu options are available which represent the three patients slots available for scanning and viewing. They are displayed as:
- ... when this patient tab is not filled with an examination
- <patient name> when this patient tab is filled with an examination

**Administration <F4>**
To open the Patient Administration panel in order to e.g. copy, transfer, delete and import examinations and/or images.

For more information, see chapter “Administration (Patient Database)” on page 357.

**Close Exam...**
To close the current examination.

**Examination menu**

This section describes the menu options that are available via the 'Examination' menu.

**Autoview <F7>**
To display the latest reconstructed image of the current scan.
Reuse Scan Items (from Previous Examinations) ...

To display the list of examinations in order to select and consequently reuse scan items from a previous examination.

- Browse to the patient and the ExamCard to be reused.
- Drag this ExamCard into List View.

Fig. 22: Patient Database.

**NOTICE**

This function can be used to display the imaging parameters of previously scanned series.

Repeat Prescans

To repeat previously performed prescans for the current ExamCard.

SmartExam

To access SmartExam related functionality for the current examination. This menu entry opens a submenu with several SmartExam options:

- Show SmartGeometries
- Improve SmartGeometries with Current Planning ...
- Reset to SmartPlan
- Analyze SmartSurvey
- Stop offline analyzing

Enable Automatic Start Scan

To enable/disable the automatic start of a scan.

Enable Autopush to Workstation

To enable/disable the automatic transfer of an examination to a workstation, e.g. EWS, (if connected) upon completion.

Save ExamCard

To save the current ExamCard under a user defined name.
Adjust Ventilation in Bore ...
To increase or decrease the ventilation in the bore. For more information, see chapter “Adjust Ventilation in Bore” on page 226.
Depending on your system’s configuration, this menu option is available or not.

Choose Physiology Properties ...
- To select the physiology signal (e.g. VCG, PPU, Respiratory) for display and adjust the display settings.
  For more information, refer to chapter “Physiology Properties” on page 98.

Navigator Display ...
To enable/disable the display of navigator data.

Data Monitoring...
To monitor data transfer.

Review menu
The Review menu allows to access the reviewing packages that are available on your MRI system:
- ImageView
- VolumeView
- MobiView
For more information about these packages, refer to chapter “Review and Analysis Packages” on page 105.

NOTICE
Depending on the commercially available options on your MRI system, less packages could be available.

Analysis menu
The Analysis menu allows to access the postprocessing packages that are available on your MRI system:
- PicturePlus
- ImageAlgebra
- Diffusion Registration
- Diffusion
- Basic T1 Perfusion
• QFlow
• SpectroView
• NeuroPerfusion
• iViewBOLD
• FiberTrak

For more information about these packages, refer to chapter “Review and Analysis Packages” on page 105.

**NOTICE**

Depending on the commercially available options on your MRI system, less packages could be available.

**System menu**

This section describes the menu options that are available via the 'System' menu.

**Capture the Screen ... <Ctrl+P>**

• To make a screen capture and save it into a DICOM file with a default name.
  This function is available in the 'System' menu and on the Review toolbar.

**Manage Job Queue ... <F6>**

To check the status of background processes. For more information, see chapter “Check status of background processes with the Job Queue” on page 364.

**Print History**

To display the previously initiated printing job by means of the Job Queue, see chapter “Check status of background processes with the Job Queue” on page 364.

**Enable Autopush To DICOM Node**

To enable/disable the automatic transfer of an examination to a DICOM node (if connected) upon completion.

**Manage ExamCards ...**

To open the ExamCard Manager. For more information, refer to chapter “ExamCard Manager” on page 78.

**SmartExam Tools**

To modify SmartExam settings and/or the SmartGeometry database by means of the options:
SmartExam Tools: User Confirmation Mode

- toggles between user confirmation mode and automatic confirmation mode.

SmartExam Tools: No automatic Add Samples Dialog

- adjusts how newly planned samples are treated:

<table>
<thead>
<tr>
<th>'No automatic Add Samples Dialog'</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>If Checked</td>
<td>Samples will not automatically be added to a SmartGeometry. As a consequence, the user will be asked after a planning, if this planning has to be added to a SmartGeometry: “Improve SmartGeometries with current planning?”</td>
</tr>
<tr>
<td>If Unchecked</td>
<td>Samples will automatically be added to a SmartGeometry.</td>
</tr>
</tbody>
</table>

SmartExam Tools: SmartGeometry Database Editor ...

- Allows to view the existing SmartGeometries for all anatomic regions: the Philips prelearned ones and the user defined ones;
- Can be used to e.g. delete all samples of a user defined SmartGeometry.

NOTICE

Philips prelearned SmartGeometries are grayed out and cannot be deleted.

SmartExam Tools: Export SmartGeometry Database ...

- allows to export a SmartGeometry database to another device/directory.
- can only be done if the ExamCard window is empty (no current ExamCard) or if the current ExamCard does not contain any SmartGeometries.

SmartExam Tools: Import SmartGeometry Database ...

- allows to import a SmartGeometry database from another device/directory.
- can only be done if the ExamCard window is empty (no current ExamCard) or if the current ExamCard does not contain any SmartGeometries.

SPT ...

To access the System Performance Tool (SPT).

Feedback ...

To give customer feedback and report an issue to Philips.
For more information, see chapter “Customer Feedback” on page 383.

Exit
To exit the system software.

Help menu
This section describes the menu options that are available via the 'Help' menu.

User Documentation...
To access and open the User Documentation via the User Documentation window.

Help Topics... <F1>
To open the Help system.

About ...
To display system name, release number etc.

Launch Pad
The Launch Pad allows to switch between up to three examinations. For this purpose, three examination tabs are available, one for scanning/planning and reviewing, the other two only for reviewing. They can be filled with three different examinations which can be processed at the same time and easily be switched between.

Furthermore the Launch Pad allows to switch between Plan mode and Review mode for the examination currently being scanned.

![Launch Pad diagram]

**Fig. 23:** Launch Pad. 1 - Scanning Tab button. 2 - Reviewing Tab button. 3 - Registration ID, Date of Birth and Gender of current examination. 4 - Plan button. 5 - Review button. Note that the Plan and Review button are only available for the currently scanned patient (in the scanning tab).
Switch between Reviewing and Scanning/Planning Examination Tabs

To switch to the examination in another tab, click on any of the buttons representing these tabs:

<table>
<thead>
<tr>
<th>Button</th>
<th>Type of tab</th>
<th>To replace an examination in this tab, use:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Scanning</td>
<td>'New Examination' from the Patient menu</td>
</tr>
<tr>
<td></td>
<td></td>
<td>An empty tab is indicated by the button with black outline. The colored button represents a tab with an examination loaded.</td>
</tr>
<tr>
<td></td>
<td>Reviewing</td>
<td>'Open for Review' from the Patient menu</td>
</tr>
<tr>
<td></td>
<td></td>
<td>An empty tab is indicated by the button with black outline. The colored button represents a tab with an examination loaded.</td>
</tr>
</tbody>
</table>

Switch between Planning and Reviewing

When the scanning tab is selected, the buttons 'Plan' and 'Review' are available. They allow to switch between planning and reviewing for the current examination.

- Click the 'Review' button to switch to the reviewing environment.
  - The complete image area can be used for reviewing.
- Click the 'Plan' button to switch to the planning environment.
  - In planning mode, the image area is reduced to 3 view ports in the upper part of the screen.
  - In the lower part, the Parameter Editor with its components is displayed.

List View or Thumbnail View

You can toggle between the List View which displays the Current ExamCard AND the Thumbnail View (Pictorial Index) which displays thumbnails of all imaging series for the current examination.
**Thumbnail View**

The Thumbnail View (also referred to as Pictorial Index) is particularly useful in reviewing imaging series as it gives a preview of the imaging series. It shows one thumbnail (representative image per series) per imaging series, e.g. for scan protocols, reformats, if applicable.

The Thumbnail View is empty for a new examination.

At the bottom of the Thumbnail View, image information about the current imaging series is displayed. This information can be expanded or collapsed.

Hovering the cursor above the thumbnails also displays some of this information.

**List View**

The List View shows the ExamCard that is currently in use at the system for:

- planning (including automatic planning by means of SmartExam)
- scanning
- automatic processing (SmartLine processing).

For more information about SmartExam and SmartLine processing, see chapter “Terminology and Definitions” on page 33.

In order to start scanning, it is required to select an ExamCard and make it the current one.

**To make an ExamCard the current ExamCard,**

- simply drag and drop the required ExamCard from the (Single or Double) ExamCard Database View (see chapter “ExamCard Manager” on page 78) into the List View.

The ExamCard opens and automatically shows up with all its ExamCard items:
ExamCard Properties

This window can be opened by clicking the 'ExamCard Properties' button in the List View. It allows to define 'General' and 'Push Nodes' properties for all items of an ExamCard via the tabs 'General' and 'Push Nodes'.

![ExamCard Properties window.](image)

**Fig. 25:** ExamCard Properties window.

### General

The following properties can be set to any of the listed values:

- **Patient Position**: Supine, Prone, DecubRight, DecubLeft
- **Patient Orientation**: HeadFirst, FeetFirst
- **Laterality**: Left, Right, Unpaired, Both, Mixed
  The parameter Laterality is primarily used for paired anatomies such as knee, shoulder, ankle etc. The laterality value can be used by PACS systems.
  - Left or Right - to be used for left or right joint
  - Unpaired - to be used for unpaired anatomies, e.g. abdomen
  - Both - to be used when both joints are scanned within one scan
  - Mixed - to be used when both joints are scanned within one ExamCard, but in different scans
- **Anatomic region**: Abdomen, AcroMioClavicularJoint, Ankle joint, (DICOM standard values in alphabetical order)

**NOTICE**

The value of the parameter ‘Anatomic region’ is used by the SpectroView package in order to select the default basic processing script.

- **Table Usage**: Use, Ignore
- **Heart rate [bpm]**
• Align overlap [mm]
• GeoLink propagation: No, Yes
• Geometries: list of available geometries.
• Disengage Posterior Coil: No, Yes (this parameter is automatically set to 'Yes' or 'No' depending on the used coil/coil solution).
• Activate Manual Confirmation: No, Yes (when this parameter is enabled, a manual confirmation will be required if the posterior coil is going to be disengaged)

**Push nodes**
The setting of this parameter is persistent. This means that even after restarting the system, the setting will be the same.

When 'Push to workstation' is enabled, the examination will automatically be pushed to the selected push node.

**Graphical PlanScan area**

In a MRI examination, first survey images are performed. The consecutive scans are planned on these survey images (mostly orthogonal images in multiple orientations), in the Graphical PlanScan area.

Images from any other series can also be used for planning purposes. Furthermore you can plan on movies. This is especially helpful in Cardiac imaging.

[Image: Graphical PlanScan area: toolbar and viewports.]

**Fig. 26:** Graphical PlanScan area: toolbar and viewports.

In the Graphical PlanScan area, the Planning toolbar and the PlanScan Overlay are the essential tools.

**Initiate planning in the Graphical PlanScan area**

- Double-click on a scan protocol in the List View to initiate planning.
  
  Graphical PlanScan starts up with its planning toolbar and three view ports with images and overlay.
Load images into the three viewports of the Graphical PlanScan area

After completion of the survey images:
- drag the completed EC item (e.g. survey) from the List View into the Graphical PlanScan area.
  If the EC item consists of images of different orthogonal orientations (e.g. Multistack Survey), an image of each orientation will automatically be displayed in every viewport.

Planning toolbar

The planning toolbar is only available in Plan mode. It offers the following functions:

3 Point Planscan

- To enable/disable 3 Point Planscan.
  3 Point Planscan is a tool which helps to define an irregular plane. The plane is determined by the placement of three points on two or more images of different orientations.

Workflow

- Activate ‘3PPS’.
  The 3PPS specific toolbar is displayed instead of the normal planning toolbar.
- Place the three points on any of the three images selected in the planning view ports:
  - Click the icon for point 1 on the toolbar, then click in the image to define point 1.
  - Click the icon for point 2 on the toolbar, then click in the image to define point 2.
  - Click the icon for point 3 on the toolbar, then click in the image to define point 3.
- To restart or change the positioning of the points click |Off|.
- Click the icon |Compute plane| to perform the Three-point planscan.
- Click the icon |3PPS| again to return to normal planscan.
  The angulation from the 3 Point PlanScan are taken over and displayed.
- Proceed with routine planning.

Stack A, B, ... drop-down menu

- To switch between stacks during planning.

Add Current Geometry

- To add the current geometry to the geometry database for reuse.
Delete Current Geometry
• To delete the current geometry from the geometry database.

Display ...
To adjust the display of the imaging volume in planning mode.

Box Mode
• To display the imaging volume as box.

3D Mode
• To display the imaging volume in 3D mode.

All Mid Planes
• To enable/disable the display of all midplanes.

Hide/Show
To hide/show the display of the imaging stack, the imaging volume or the slab.

Hide/Show Stack
• To hide/show the current stack.

Hide/Show Volume
• To hide/show the current volume.

Hide/Show Slab
• To hide/show the current REST slab.
Scan Align
• To align scans, especially with table movement to cover long anatomical areas.

Play (Movie) <Pause>
• To play (or pause/stop) the current dataset as a movie.

NOTICE
To view a MultiMovie, link the viewports first and then click 'Play (movie)'.
A MultiMovie shows multiple imaging series in a movie in parallel. For information about linking, refer to chapter “Review toolbar” on page 93.

The Movie functionality is a generic functionality occurring in Graphical PlanScan and all Review and Analysis packages. For more information about movies, refer to chapter “On Toolbars” on page 55.

Settings
• To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

Viewing
The Viewing drop-down menu is a generic menu occurring in Graphical PlanScan and all Review and Analysis packages. For more information, please refer to chapter “On Toolbars” on page 55.

PlanScan Overlay
This PlanScan overlay includes the display of volume or the stack(s) of slices, and if applicable e.g. (REST) saturation slab, shim box or navigator.
It can be adjusted by means of the functions available on the toolbar, see chapter “Planning toolbar” on page 73.

Display Conventions

<table>
<thead>
<tr>
<th>Color</th>
<th>Item displayed</th>
</tr>
</thead>
<tbody>
<tr>
<td>yellow</td>
<td>center slice and outer slices of stack or volume that is to be planned, or cross-sections with these slices</td>
</tr>
<tr>
<td>red</td>
<td>every slice of stack or volume that is to be planned, or cross-sections with these slices</td>
</tr>
<tr>
<td>Color</td>
<td>Item displayed</td>
</tr>
<tr>
<td>-------</td>
<td>---------------------------------------------------</td>
</tr>
<tr>
<td>blue</td>
<td>saturation (REST) slabs</td>
</tr>
<tr>
<td>green</td>
<td>shim volume</td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td>white</td>
<td>navigator</td>
</tr>
</tbody>
</table>

**Fig. 27:** Examples of planscan overlay according to above conventions.

**NOTICE**
To see the slice intersections (as slices or as a box), the (survey) image must be perpendicular to the planned slices.
When the (survey) image is parallel to the planned slices, the box slice intersection is displayed.

**NOTICE**
All images on the screen must have been scanned with the same subanatomy and patient position (Head first/Feet first, supine/prone).
For workflow information on how to plan, refer to chapter “Plan the items of the ExamCard geometrically” on page 203.

**Exit Planscan**

- Click |Accept|.

  The status of the EC item being planned changes to ‘ready to run’.

  Another scan can be planned while execution of the scan(s) is in progress.

**NOTICE**

Clicking |Accept| accepts any changes made to parameters while clicking |Cancel| concedes that all changes made will be lost.

**Patient Status area**

In the Patient Status (PS) area, information about the currently running scan and ExamCard is available.

![Fig. 28: Patient Status area. 1 - Patient name, 2 - Reserved for physiology signal (if connected), 3 - Scan progress bar, 4 - Message line, 5 - ExamCard progress bar, 6 - Start Scan button, 7 - Date, time and thermometer if the room temperature is above 25°C (77°F), 8 - Autoview button, 9 - Status indication area, 10 - Stop Scan button.](image)

**Status Indication area**

The Status Indication area indicates the status of:

- SED (Specific Energy Dose),
- SAR (Specific Absorption Rate),
- PNS (Peripheral Nerve Stimulation).
ExamCard Manager

The ExamCard Manager is the starting point in every examination: it opens automatically after entering examination via ‘New Examination’ from the Patient menu. It can also be started from the System menu: ‘Manage ExamCards’.

The ExamCard Manager has two main functions:

- To select an ExamCard for the current examination in the scanning slot,
- To manage ExamCards (Copy, Edit, Delete ExamCards).

**Fig. 29:** ExamCard Manager including ExamCard Dashboard (dark gray area with buttons 2, 3, and 4).

1. Tabs to switch between the ExamCard databases: Philips, Hospital, Other, and to browse to ExamCards and scan protocols.

   For more information, refer to chapter “ExamCard Databases (EC databases)” on page 33.

2. ExamCard (EC) Database View.

   The figure shows the Single EC Database View. You can enable the Double EC Database View by means of button '3'.

3. Toggle button to switch between two ExamCard views:

   - Single EC Database View (where only one EC database is open)
   - Double EC Database View (where two EC database are displayed aside in order to manage ExamCards).

   The Double EC Database view allows inspection of the ExamCard databases in two different browsers at the same time. ExamCards can be easily dragged from one EC database to another one, either within one browser or from one browser to the other.

4. Button ‘Refresh ExamCards views’ to make the most recent changes to the ExamCard database visible, e.g. after importing ExamCards.

5. Button ‘Close’ to close the ExamCard Manager.
6 Scan Assistance with three tabs and a viewport. For more information, refer to chapter “Scan Assistance” on page 92.

Parameter Editor

The Parameter Editor consists of multiple components:

- **Dashboard** which displays information about the currently planned EC item (see chapter “Dashboard” on page 79),

- **Parameter Groups tabs** which allow to access all imaging parameters (see chapter “Parameter Groups tabs” on page 80),

- **Summary tab** which allows to modify the most important imaging parameters (see chapter “Summary tab” on page 81).

Fig. 30: Parameter Editor with: 1 - Dashboard, 2 - Parameter Groups tabs, 3 - Summary tab, 4 - Bottom line reserved for messages and alerts.

Via the Parameter Groups tabs, more tools/windows can be accessed:

- **Extended Parameter Editor** which allows to edit all imaging parameters (see chapter “Extended Parameter Editor” on page 82),

- **Coil Selection UI** which allows to change the automatic coil selection (see chapter “Coil Selection Tab” on page 88),

- **Conflicts page** which shows conflicting parameters (see chapter “Conflicts page” on page 91).

Dashboard

The Dashboard is a control panel housing instrumentation and controls for scanning operation. It shows the effects of the planned protocol on SAR, SED and PNS immediately during planning. In such a way, planning can be optimized for each patient individually.
Screen Layout, Menus and Windows

Fig. 31: Dashboard with information (e.g. Rel. SNR, TE, TR, PNS, SAR) about EC item and the control buttons: 1 - Undo and Redo (the previous action), 2 - Accept (planning), 3 - Reset (to initial values), 4 - Cancel (planning).

For more information about SAR (Specific Absorption Rate), SED (Specific Energy Dose) and PNS (Peripheral Nerve Stimulation), refer to the Safety chapter.

Parameter Groups tabs

The MR imaging parameters are divided into different parameter groups. Initially the 'Summary' group is displayed.

The Parameter Groups tabs allow to access the

- **Summary** parameter group:
  - Simply click the button 'Summary' to access this group.

- **Physiology** parameter group, if Wireless Physiology is connected:
  - Simply click the button 'Physiology' to access this group.

- **Extended parameter groups**:
  - Click the arrows button to expand/collapse the tabs and to show/hide the extended parameter groups.
  - Click any of the tabs to access one of the extended parameter groups.

<table>
<thead>
<tr>
<th>Button</th>
<th>Parameter group</th>
<th>More information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Summary</td>
<td>The most commonly used parameters for easy access</td>
<td>chapter “Summary tab” on page 81</td>
</tr>
<tr>
<td>Geometry</td>
<td>Geometry related parameters</td>
<td>chapter “Extended Parameter Editor” on page 82</td>
</tr>
<tr>
<td>Contrast</td>
<td>Contrast related parameters</td>
<td>chapter “Extended Parameter Editor” on page 82</td>
</tr>
<tr>
<td>Motion</td>
<td>Motion related parameters</td>
<td>chapter “Extended Parameter Editor” on page 82</td>
</tr>
<tr>
<td>Dyn/ang</td>
<td>Dynamic or angio related parameters</td>
<td>chapter “Extended Parameter Editor” on page 82</td>
</tr>
</tbody>
</table>

Fig. 32: Parameter Groups tabs. Upper row: Summary tab and arrows button to expand the parameter groups. Lower row: Summary tab, tabs for the extended parameter groups and the arrows button to collapse the extended parameter groups tabs.
### Summary tab

The Summary tab is meant to quickly check a scan protocol prior to execution. The most commonly used parameters are displayed:

1. Field of View (FOV) in all directions (selection, phase- and frequency-encoding direction) in millimetres,
2. Voxel size in all directions (selection, phase- and frequency-encoding direction) in millimetres,
3. Matrix size in all directions (selection, phase- and frequency-encoding direction) in number of voxels x number of voxels x number of slices,
4. Slice Gap (which can be enabled or disabled by checking the checkbox, and which can be adjusted by typing in a value) in millimetres,
5. Number of Signals Averaged (NSA),
6. Fat Saturation by means of SPIR (SPectral Inversion Recovery) (which can be enabled or disabled by checking the checkbox).

<table>
<thead>
<tr>
<th>Summary</th>
<th>Parameter group</th>
<th>More information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Postproc</td>
<td>Parameters to control automatic post-processing</td>
<td>chapter “Extended Parameter Editor” on page 82</td>
</tr>
<tr>
<td>Offc/ang</td>
<td>Offcenters and angulations of stacks, slabs and navigators</td>
<td>chapter “Extended Parameter Editor” on page 82</td>
</tr>
<tr>
<td>Coils</td>
<td>Coil selection parameters. (Opens the Coil Selection UI)</td>
<td>chapter “Coil Selection Tab” on page 88</td>
</tr>
<tr>
<td>Conflicts</td>
<td>No parameters, but occurring conflicts resulting from conflicting parameter settings</td>
<td>chapter “Conflicts page” on page 91</td>
</tr>
</tbody>
</table>

Fig. 33: Summary tab.
Extended Parameter Editor

The Extended Parameter Editor allows modification of the items of an ExamCard on parameter level.

To open the Extended Parameter Editor

1. Double-click on an ExamCard scan protocol in order to open it in the Parameter Editor. The Parameter Editor opens automatically for the current ExamCard item.
2. Click on the arrows besides the Summary tab to display the extended parameter group tabs.
3. Click on one of the tabs Geometry, Contrast, Motion, Dyn/Ang, Postproc, Offc/Ang to open the Extended Parameter Editor.

Fig. 34: Extended Parameter Editor. 1 - Parameters per group, 2 - Detailed information about the currently planned scan.

The selected parameter group is displayed on one or more pages. A scroll bar indicates if more parameters are available.

Besides the parameters with their current values, detailed information about the currently planned scan is given, see chapter “Display the ’Scan Information Page’” on page 85.

Navigation and Editing

Select a parameter for editing

► Click to select the parameter that has to be modified. The parameter will be highlighted.

Once a parameter group has been selected, you can scroll to another parameter as follows:

► Use the [Arrow down] or [Arrow up] to scroll within a parameter group.

Alternatively you can search for a parameter:

1. Type in the first letter of the required parameter’s name. The cursor jumps to the first parameter starting with this letter.
2. Repeat typing in the first letter of the required parameter’s name. The cursor jumps to the next parameter starting with this letter.

Example
- Required parameter: REST
  - Typing in "R", the cursor jumps to "Respiratory compensation".
  - Typing in "R" once more, the cursor jumps to "REST".

Modify the current imaging parameter
The current imaging parameter is the highlighted parameter (blue). There are different ways of how to change the value of the current imaging parameter:

1. Enter the value manually:
   - Click into the value field to make it current.
   - Click again to position the cursor in the value field.
   - Delete with the |Del| or |Backspace| key and enter the value with the keyboard.

2. Select the value from the drop-down menu (applicable for parameters with text values):
   - Click to open the drop-down menu,
   - and select the value; or select the value field, type in the first letter of the wanted value and press the |Enter| key when the right value is displayed.

3. Increase/decrease the parameter values (especially used for numerical values) with arrow keys and 'Arrow up'/'Arrow down' buttons as shown in the table:

<table>
<thead>
<tr>
<th>Effect</th>
<th>Keyboard arrow keys</th>
<th>Buttons</th>
</tr>
</thead>
<tbody>
<tr>
<td>To increase parameter value by one</td>
<td>Press -&gt; key.</td>
<td>Click the 'Arrow up' button.</td>
</tr>
<tr>
<td>To increase parameter value to highest possible value.</td>
<td>Press and hold</td>
<td>Shift</td>
</tr>
<tr>
<td>To decrease parameter value by one</td>
<td>Press &lt;- key.</td>
<td>Click the 'Arrow down' button.</td>
</tr>
<tr>
<td>To decrease parameter value to lowest possible value</td>
<td>Press and hold</td>
<td>Shift</td>
</tr>
</tbody>
</table>

Fig. 35: Left: selecting value from drop-down menu. Right: using 'arrow up/down' buttons to increase/decrease a numerical value.
**Restore original value**

Pressing |Shift|+|Enter| restores the original (preset or last stored) parameter value.

**'Undo' Function**

An 'Undo' function is available by means of pressing 'Ctrl' + 'Z' or by clicking the 'Undo' icon. The 'Undo' function doesn't work after having clicked 'Accept' (to accept the changes made).

**Display helptext for imaging parameter**

Press |F1| or select 'Help Topics' from the Help menu to display the information about the current imaging parameter.

**NOTICE**

Not all combinations of parameter values are possible.
This will be indicated by a conflict on the 'Conflict' page. To solve the conflict, refer to the 'Conflicts' tab and the 'Assistance'.

**Parameter benefits and trade-offs**

**NOTICE**

For information about all MR imaging parameters, refer to the Parameter Help.
Press |F1| or select 'Help Topics' from the Help menu.

The relationships between MR imaging parameters are complex. The table shows the effects of increasing or enabling a parameter (set to “Yes”) on scan time, resolution, signal-to-noise ratio (SNR) and artifact level for some parameters.

↓ lower, ↑ higher, = unchanged, * more information available in following table

<table>
<thead>
<tr>
<th>PARAMETER</th>
<th>Scan time</th>
<th>Resolution</th>
<th>SNR</th>
<th>Artifacts</th>
</tr>
</thead>
<tbody>
<tr>
<td>NSA</td>
<td>↑</td>
<td>=</td>
<td>↑</td>
<td>↓</td>
</tr>
<tr>
<td>REST</td>
<td>↑</td>
<td>=</td>
<td></td>
<td>↓</td>
</tr>
<tr>
<td>Voxel Size</td>
<td>↓</td>
<td>↓</td>
<td>↑</td>
<td>↓/↑</td>
</tr>
<tr>
<td>FOV (in combination with fixed matrix size) *</td>
<td>=</td>
<td>↓</td>
<td>↑</td>
<td>=</td>
</tr>
<tr>
<td>FOV (in combination with fixed voxel size) *</td>
<td>↑</td>
<td>=</td>
<td>↑</td>
<td>=</td>
</tr>
<tr>
<td>Rectangular FOV (%)</td>
<td>↑</td>
<td>=</td>
<td>↑</td>
<td>=</td>
</tr>
</tbody>
</table>
The effect of the parameter FOV can differ depending on the way of working: you can either adjust the matrix size or the voxel size. The table illustrates the effects.

<table>
<thead>
<tr>
<th>Way of working</th>
<th>FOV</th>
<th>Scan matrix</th>
<th>Pixel size</th>
<th>TE</th>
<th>TR</th>
<th>Scan time</th>
<th>SNR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Matrix size</td>
<td>↓</td>
<td>=</td>
<td>↓</td>
<td>↑ 1)</td>
<td>↑ 2)</td>
<td>↑</td>
<td>↓</td>
</tr>
<tr>
<td>Voxel size</td>
<td>↓</td>
<td>↓</td>
<td>=</td>
<td>=</td>
<td>=</td>
<td>↓</td>
<td>↓ 4)</td>
</tr>
</tbody>
</table>

Footnotes:
1. This is valid in case of TE = shortest.
   For TE = user defined, this could lead to a conflict
2. This is valid in case of TR = shortest.
3. This is caused by smaller voxels.
4. This is caused by the reduction of scan time.

Display the ‘Scan Information Page’
The ‘Scan Information Page’ (also referred to as Info Page) is automatically displayed in the Parameter Editor window when an extended parameter group is worked on. It is not available together with the ‘Summary’ tab. The Scan Information Page displays the most important scan characteristics of a planned EC item, e.g. total scan duration and Rel. SNR.
The Info Page displays generic scan characteristics which are displayed for every current EC item (e.g. total scan duration, Rel. SNR), but also dedicated scan characteristics such as Minimum TI, Number of Packages or Minimum Slice Gap which only apply for specific scan methods. The table below lists the generic scan characteristics applicable for every kind of scan.

<table>
<thead>
<tr>
<th>Item displayed</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total scan duration</td>
<td>Scan duration per current ExamCard item.</td>
</tr>
<tr>
<td>Rel. SNR</td>
<td>Relative Signal-to-Noise Ratio, more info see below.</td>
</tr>
<tr>
<td>ACQ matrix M x P</td>
<td>Acquisition matrix Measurement x Preparation direction.</td>
</tr>
<tr>
<td>ACQ voxel MPS (mm)</td>
<td>Acquisition voxel size in Measurement, Preparation and Slice selection direction in millimetres.</td>
</tr>
<tr>
<td>REC voxel MPS (mm)</td>
<td>Reconstruction voxel size in Measurement, Preparation and Slice selection direction in millimetres.</td>
</tr>
<tr>
<td>Scan percentage (%)</td>
<td>Current scan percentage considering all imaging parameters.</td>
</tr>
<tr>
<td>Actual WFS (pix) / BW (Hz)</td>
<td>Actual Water-Fat Shift in pixels and Bandwidth in Hertz.</td>
</tr>
<tr>
<td>SAR / head</td>
<td>Specific Absorption Rate / head in %. Depending on the anatomy scanned, the SAR could also be indicated as e.g. SAR/local torso or SAR/local extremities.</td>
</tr>
<tr>
<td>Whole body / level</td>
<td>Whole Body SAR in W/kg, and the level indicated as normal or first level controlled operating mode.</td>
</tr>
<tr>
<td>SED</td>
<td>Specific Energy Dose in kJ/kg.</td>
</tr>
<tr>
<td>B1+rms</td>
<td>Average RF deposition in the patient, also denoted as B1+RMS in uTesla.</td>
</tr>
<tr>
<td>Max B1+rms</td>
<td>Maximum Average RF deposition in the patient, also denoted as Max B1+RMS in uTesla.</td>
</tr>
<tr>
<td>PNS / level</td>
<td>Peripheral Nerve Stimulation, and the level indicated as normal or first level controlled operating mode.</td>
</tr>
</tbody>
</table>
**dB/dt**
The strength of the switching gradient used for imaging.

**Sound Pressure level (dB)**
Sound pressure level. The sound pressure level is given with respect to an internal acoustic reference level which can be understood as the standard system noise level. Accordingly, negative/positive values indicate that the actual sound pressure level is below/above this reference level.

More information on SAR, SED, B1, PNS and dB/dt can be found in IFU volume 1 and the Technical Description.

**Relative SNR**
The Relative SNR

- shows the effects on the SNR (Signal-to-Noise Ratio) when modifying parameters.
- is displayed as factor where a value of 1.0 is identical to the SNR of the original scan protocol.
- is not an absolute value, but relative to the SNR of the initial scan protocol.

It is important to realize that the Relative SNR is based on a relative calculation.

**Example**
If the original slice thickness is halved, the displayed Relative SNR will be 0.5 (relative to the original procedure).

If this procedure is saved and retrieved again, the Relative SNR will still be displayed as 0.5. Modifications are always relative to the starting point which is the original scan protocol.

**Parameters affecting the Relative SNR-calculation**
The SNR of a scan and in such a way the Relative SNR-calculation is affected by e.g.: NSA, TR, TE, Flip angle, inversion time, voxel size, slice thickness, halfscan, FOV, (RFOV, matrix size, scan percentage) and water-fat shift.

The **Reference Tissue** parameter is also included in the RSL-calculation, but it does not affect the SNR of the image. It can be set to e.g. white matter, muscle, liver, bone marrow and CSF. The T1- and T2-values of the tissues are taken into account to give a more realistic interpretation of the SNR changes.

E.g., in a Spin Echo sequence a relatively small change in TE will cause a more rapid loss of signal in liver tissue than in white brain matter. That is why it is advised to leave this parameter set to white matter in brain imaging.

**Actual phase percentage**
The actual phase percentage relates to the parameter ‘Phase percentage’ (motion page). This parameter determines the fraction of the number of requested phases that is acquired.

With ‘Number of phases’ set to 30 and a phase percentage of 67%, only 20 phases are acquired and reconstructed to 30 phases.
With retrospective TFE, TFE shots are continuously acquired, mapped and stretched to an average RR-interval and finally reconstructed to the requested number of phases.

Fig. 37: Actual phase percentage with retrospective TFE. 1: Acquisition (18 phases, 7 heartbeats), 2: Stretching to average RR-interval, 3: Reconstruction (24 phases, 75% phase percentage).

**Actual phase percentage with retrospective TFE.**

The number of 20 acquired phases can only be achieved if 20 TFE shots fit exactly into one cardiac cycle. Generally this is not the case, but the actual acquired number of phases is a fraction higher or lower.

When 20.5 phases are acquired and reconstructed to 30 phases, this leads to an actual phase percentage of \((20.5/30)\times100 = 68.3\%\)

- As long as the actual phase percentage is close to the requested phase percentage, the resulting image will be fine. The difference can increase when higher TFE-factors are used, and in that case you might need to tune the sequence (change number of phases, spatial resolution and/or SENSE factor) to avoid that the actual phase percentage is much lower than the requested phase percentage: this could lead to increased temporal blurring.

**Coil Selection Tab**

The MR system automatically detects the connected coils. By default it selects the best-suited coil and coil elements for optimum signal-to-noise ratio for the current stack and/or scan.

**About the automatic coil selection**

The automatic coil and coil element selection is based on a Coil Survey scan that is automatically performed during scan preparation.

The Coil Survey scan

- will be repeated whenever the patient is repositioned or after tabletop movement.
- does not appear as scan item in the ExamCard.

**The Coil Selection Tab**

- shows all configured coils;
- shows the connected coils;
- shows the automatic coil selection;
NOTICE
Since the Q-Body coil is a built-in coil, it is always displayed as connected coil.
By default this coil will never be selected as part of the automatic coil selection. For more information, refer to the workflow description ‘Freely select the coil elements’.

Layout of the Coil Selection Tab
► Click the ‘Coils’ tab.

The Coil Selection Tab opens:

Fig. 38: Layout of the Coil Selection Tab. 1 - Automatic coil selection in thumbnail view (image with coil name), 2 - toolbar of coil selection UI, 3 - Thumbnail view of all configured coil (images with names).

Toolbar of Coil Selection Tab
The toolbar of the Coil Selection Tab might be slightly different depending on the type of scan protocol being planned.

1 Checkbox ‘SmartSelect’: to enable/disable SmartSelect
   For more information about SmartSelect, click chapter “SmartSelect” on page 90.

2 Button ‘Navigators’: to customize the coil (element) selection per navigator
   ► Click ‘Navigators’ to display the current selection.
   ► Modify the current selection by enabling/disabling elements in the Coil Panel.

3 Button ‘Stacks’: to customize the coil (element) selection per stack
   ► Click ‘Stacks’ to display the current selection.
   ► Modify the current selection by enabling/disabling elements in the Coil Panel.

NOTICE
The buttons ‘Navigators’ and ‘Stacks’ are only available when a protocol with multiple stacks and/or multiple navigators is planned.
**Coil Thumbnail Display**

**Fig. 40:** Thumbnail of a detected coil.

1. **Name of the coil.**

2. Optional: Indication if this coil is proposed by the current **ExamCard** (when SmartSelect is ‘On’).

3. Optional: Indication if a **coil is disconnected**.
   - In case of user defined selection (when SmartSelect is 'Off'), this indicates that a required coil is not connected to the scanner.

4. Optional: Indication if a coil’s selection is **locked for editing**.
   - Although this coil is in the protocol or connected, its elements cannot be selected.

3. Optional: Indication of a conflict with the coil.

4. Checkbox to deselect/select a coil for scanning.
   - When the checkmark is off, no elements in this coil are selected; the coil is not used. When the checkmark is on, one or more elements of this coil are selected; the coil is (partially) used. The state of this icon also changes as a result of explicit element selection.

5. Thumbnail image of the coil

**SmartSelect**

SmartSelect can be enabled or disabled.

**When SmartSelect is enabled (default setting)**

- The MR system performs a Coil Reference scan during the scan preparation.
- Based upon the results of the Coil Reference scan, the MR system comes up with a suggestion which coils, coil elements or regions should be used for a specific examination.
- The selection as suggested by the MR system will be used throughout the examination and does not need to be changed by the operator.
• Coil elements can be excluded from this coil selection by the operator. For ease of use, the Graphical 3D Coil view automatically opens in this case.

NOTICE
In clinical routine MR examinations, it is advised to use SmartSelect for ease of use and optimal image quality.

When SmartSelect is disabled
• The operator can select any coil or any coil elements/regions.
• The MR system doesn’t come up with a suggestion which coils, coil elements or regions should be used for a specific examination.
• A Coil Reference scan will not be performed.

Workflows

Scan with automatic coil selection
No action is required when the scans are to be performed with the automatic coil selection. In this case, you can use the Coil Selection UI simply to inspect the automatic selection and then leave it again by clicking on another ExamCard tab.

Selection of the Q-Body coil
Since the Q-Body coil is a built-in coil, it is always displayed as connected coil. By default this coil will never be selected as part of the automatic coil selection.

When the Q-Body coil is to be used for scanning, follow the workflow procedure as described above. The Q-Body coil can only be selected or deselected as a total and not per element.

Conflicts page
1. Click the [Conflicts] tab (from the Parameter Groups tabs) to display the occurring conflicts resulting from the current parameter settings.
   The conflicting parameters are displayed.

   Fig. 41: Parameter Groups tabs.

2. Modify their settings to solve the conflict.
3. For advice how to solve the conflict best, click 'Assistance' in the Scan Assistance window, see chapter “Assistance” on page 92.
Scan Assistance

By clicking on the tabs, the Scan Assistance allows to switch between the display of:

- Info,
- Assistance,
- Autoview.

**Info**

The Info tab gives information about the current ExamCard or the current scan protocol. Two types of information are available according to the template information: 'Tips' and 'Info' where 'Info' describes the protocol or ExamCard and 'Tips' includes planning tips.

<table>
<thead>
<tr>
<th>Info</th>
<th>Assistance</th>
<th>Autoview</th>
</tr>
</thead>
<tbody>
<tr>
<td>T2W_TSE</td>
<td></td>
<td></td>
</tr>
<tr>
<td>![T2W_TSE Image]</td>
<td><img src="https://example.com" alt="T2W_TSE Info" /></td>
<td><img src="https://example.com" alt="T2W_TSE Assistance" /></td>
</tr>
</tbody>
</table>

Fig. 42: Info about the current scan protocol.

The 'Info' for ExamCards or scan protocols in the Hospital Database can be edited according to the changes made to the ExamCard.

**Edit the Info**

- Right-click on an ExamCard or a scan and select 'Edit'.
- Modify the info text.
- Deselect 'Edit' when completed.

**Assistance**

The Assistance tab gives tips on how to efficiently solve conflicts.
Fig. 43: Conflict: "Current parameter set is invalid. Click undo (if available) to reverse change or resolve conflict manually." Proposal for solution: “Select one of the following parameter adjustments: Undo last change. Change SENSE from Yes to No."

**AutoView**

AutoView is a tool that allows to monitor scanning and reconstruction. If enabled, the latest reconstructed image of the scan currently in progress is displayed here.

**Review toolbar**

The Review toolbar is only available in Review mode. It applies for all Review and Analysis packages available and offers generic review functions.

**To access Review mode**

- Click any of the Reviewing Tab buttons to switch to a reviewing tab.

OR

- Click the Scanning Tab button to switch to the scanning tab, and then click the ‘Review’ button.

  The Review toolbar will be displayed.

**The Functions on the Review toolbar**

**Tile All Views**

- To arrange all views in a tiled layout.

**Tab All Views**

- To arrange all views in a tabbed layout.
Link

- To apply a link between selected imaging series.

► Select multiple imaging series in multiple viewports:
  click on the first viewport, keep |Shift| or |Ctrl| pressed and click on the other viewports.
  - Click 'Link'.

► Select from the drop-down menu:
  - Scroll/Movie
    Scrolling through images occurs simultaneously with linked imaging series. All image
    views of linked series show images with identical slice positions or with slice positions as
    close to each other as possible. The same applies for movies of linked imaging series.
  - Zoom/Pan
    Zooming/panning occurs identically for linked imaging series.
  - Gray Level
    Gray level adjustments are automatically performed for all linked imaging series.
  - All
    Scroll/Movie, Zoom/Pan and Gray Level will be applied in the same way for linked imaging
    series.

A Link symbol is displayed in the upper right corner of the viewport when imaging series are
linked.

Unlink All

- To remove all links between selected views.

Add to Link

- To add the current imaging series to the current link.

  - Click 'Current Link' and select the link where you want to add a scan to.
  - Select one or multiple imaging series.
  - Click 'Add to Link'.

Remove from Link

- To remove the current imaging series from the current link.
**Capture the Screen ... <Ctrl>P>**
- To make a screen capture and save it into a DICOM file with a default name. This function is available in the 'System' menu and on the Review toolbar.

**Set Selected Viewer as Source for Cross-Reference**
- To select a viewer as source for cross-reference in order to display cross reference lines on the other viewers. This function works in close cooperation with the function 'Enable Stack display mode selection'.
  - Click the viewer that is supposed to be the source for cross-reference.
  - Click 'Set Selected Viewer as Source for Cross-Reference'.
  - Click 'Enable Stack display mode selection' and select any of the options for the cross-reference display.

**Enable Stack display mode selection**
- To enable the display of cross-reference lines on the viewers other than the source for cross-reference viewer. This function works in close cooperation with the function 'Set Selected Viewer as Source for Cross-Reference'.
  - Once a source for cross-reference is defined, click 'Enable Stack display mode selection'.
  - Select any of the options for the cross-reference display from the drop-down menu:
    - Box Mode
    - Slice Mode
    - 3D Mode.

**Package Manager**
- To open the Package Manager. The Package Manager is used to easily switch between examinations/views and to stop the execution of packages. For more information, refer to chapter “Package Manager” on page 96.

**Reviewing area**
All viewports are available for reviewing by means of the Review and/or Analysis packages and can be divided in as many view ports as required.
The Review toolbar and various controls of the Review and Analysis packages offer the most important functions. For more information, refer to chapter “Review toolbar” on page 93 and to chapter “Review and Analysis Packages” on page 105.

Select an examination

Select an examination from the list of examinations
1. Select 'Open for Review' from the 'Patient' menu.
   The list of available examinations with scans/reconstructions is displayed.
2. Select an examination from the list.
3. Click 'Proceed'.
   The selected examination becomes the current examination.

Select an examination by switching between the reviewing slots
► Click on another 'Reviewing Slot' button.

Package Manager

The Package Manager is used to easily switch between examinations/views and to stop the execution of packages.

Furthermore the Package Manager assists the user in avoiding performance degradation of the system. Performance degradation may occur when too many packages are opened or too many instances of a package are opened.

The system status is indicated on the Reviewing toolbar as part of the 'Package Manager' icon. The icon is:
• Green; at normal system performance.
• Yellow; when system performance may degrade.
   It is advised to close packages.
• Red; when the maximum number of packages is reached.
   The workflow cannot be continued.

Access the Package Manager
► Click the 'Package Manager' icon on the Reviewing toolbar.
Package Manager Screen Layout, Menus and Windows

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Fig. 44: Package Manager window with the Package Overview.

For every currently loaded package, the following items are displayed in columns:

- Patient Name,
- Package Name,
- Series Name,
- Usage:
  Estimated memory usage, rated with one, two or three stars. The more stars, the higher the memory usage.

The window always stays on top and can be closed by clicking [Hide].

Switch views

► Select the package to switch to by clicking on it.
  For ease of display, you can sort the packages by case, package, used data set or estimated memory usage by clicking in the header of the overview.
  ► Click 'Switch To'.

Stop packages

One or more packages can be stopped by the Package Manager:

► Select a package by clicking on the package line or select more packages simultaneously by using the [Ctrl] or [Shift] key on your keyboard.
  ► Click [Stop] or [Stop All].
  The selected package or packages are stopped and removed from the overview.

Warnings

In the Package Manager window, warnings are displayed when:

- System performance may degrade (yellow indicator);
  ‘System performance may degrade. Avoid this by closing packages.’
- Too many instances of packages are open (red indicator);
  'Maximum number of packages already active.'

In the latter case the Package Manager is displayed automatically.
Physiology Properties

When Wireless Physiology (more information in volume 2 of the Instructions for Use) is connected to the system, the physiology signals will be displayed in the Patient Status Area.

Adjust the display of the physiology signals

The display of the physiology signals can be changed in the Physiology Properties window. This window can be accessed in two ways:

- Select 'Choose Physiology Properties...' from the Examination menu.
- Right-click the physiology display in the Patient Status Area and select 'Choose Physiology Properties...'.

<table>
<thead>
<tr>
<th>Number</th>
<th>Function</th>
<th>Description/Purpose</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Display Gridlines</td>
<td>Check or uncheck to enable/disable the display of gridlines.</td>
</tr>
<tr>
<td>2</td>
<td>Hold Screen</td>
<td>Check or uncheck to hold/resume the screen.</td>
</tr>
</tbody>
</table>
### Settings window

- Click 'Settings'.

A window pops up with three tabs representing parameters in three tabs: Display, Stacks and Propagate.

#### Display settings

1. Click ‘Display’ to open the window as shown in the figure above.
The three image directions indicated by arrows are associated with image dimensions, also referred to as image attributes as slices, phases, types, echoes, dynamics, chemical shifts and also stacks.

The rows and columns of the viewport area are ordered in two directions: X and Y. If available, the Z direction is associated with a third dimension.

2. Select a display mode and assign image dimensions to the image directions.

**Display mode ‘1D’**
- Images are arranged along one dimension only. Actually all images are displayed in one row (X direction) which is wrapped to fill the entire screen. (Y and Z dimension are not used).
- With a data set containing multiple image dimensions, select another dimension for the X-direction if necessary.
- This mode can be used for all scans with one image dimension only, but is also suitable for scans with more dimensions.
- Sometimes this is referred to as ‘Stack View’.

**Display mode ‘1D nested’**
- All images of the data set are displayed along one dimension only in a nested sorting order, no matter how many dimensions are included. This requires a dialog to select the sorting priority for each dimension.
  - Click on an image dimension to make it current.
  - Click |Up| or |Down| to move it within the list of dimensions.
  - Click |Default| to restore the default settings.

**Display mode ‘2D’**
- Two imaging dimensions are shown in the viewport area, one along the X-direction, one along the Y-direction and in case of more than 2 dimensions as layers in the Z-direction.
- Sometimes this is referred to as ‘Matrix View’.

**Display mode ‘2D wrapped’**
- This mode is comparable to the 2D mode, however the X-dimension is wrapped so that all image in that direction are visible.
- This mode is typically used for image data sets with few images in one dimension (e.g. image type). This dimension is preferably displayed in the X-direction.

1. Click |Default| to restore the default settings.

**Stack settings**

1. Click ‘Stacks’ to specify how to display stacks and enable any of the stack display options.
   - Reverse stacks: to enable reverse stack order.
   - Merge stacks: by default ‘stacks’ represent one imaging dimension. When ‘Merge stacks’ is enabled, the multiple stacks of a multistack scan will be considered as one dimension. This means that e.g. using the Movie function all images are scrolled through, and not only the current stack.
• Stack slice order: to enable reverse slice order within stacks.
2. Click |Default| to restore the default settings.

**Propagate settings**
1. Click ‘Propagate’ to specify how view and window settings are propagated to preceding or following images.
2. Click |Default| to restore the default settings.
3. Click |Close| to leave the ‘Settings’ window.

**Smart Editor**
The Smart Editor
• is the essential tool in creating a Smart ExamCard.
• can be used to add a Smart survey to the current ExamCard.
• is to be used to assign existing SmartGeometries to scans or to create new SmartGeometries.
• indicates if the name of a SmartGeometry is known or unknown, unique or double.

⚠️ If the new name conflicts with existing SmartGeometry names, this will be indicated by an exclamation mark.

The SmartExam Editor can be accessed from the Examination menu via 'SmartExam' and 'Show SmartGeometries'.

Fig. 48: Smart Editor.

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Drop-down menu for the selection of the anatomic region</td>
</tr>
<tr>
<td>2</td>
<td>Enable/disable 'Add SmartSurvey to ExamCard' by checking</td>
</tr>
<tr>
<td>3</td>
<td>Name of the non-Smart geometry</td>
</tr>
<tr>
<td>4</td>
<td>Enable/disable SmartGeometry by checking</td>
</tr>
<tr>
<td>5</td>
<td>SmartGeometry name</td>
</tr>
<tr>
<td>6</td>
<td>Reserved for remarks like 'New Smart Geometry' or similar</td>
</tr>
</tbody>
</table>
For more information about SmartExam, refer to chapter “SmartExam” on page 44.
For more information about SmartExam workflows, refer to chapter “Validate a Smart Exam-Card” on page 220.

SmartGeometry Database Editor
The SmartGeometry Database Editor ... is new.

To open the SmartGeometry Database Editor
► Select 'SmartExam Tools' from the System menu.
► Select 'SmartGeometry Database Editor'.

More about SmartExam & EC
The ExamCard right mouse menu offers more possibilities concerning SmartExam.
► Right-click on the ExamCard window.
► Select 'SmartExam'.
► Select any of the options from the context menu.

Confirm vertebrae count
• is valid for spine only,
• confirms/changes labeling of the detected vertebrae.

Improve SmartGeometries with current planning
• allows to improve SmartGeometries with the current planning even if the SmartGeometry is already validated.
• allows to add samples of current planning even though scanning has not been performed.

Reset to SmartPlan
• resets the offcenter and angulation parameters of all geometries to the values of the SmartExam algorithm. Manual corrections are undone.
Importing ExamCards

When you import a Smart ExamCard with SmartGeometries which are unknown to the system, the new SmartGeometry will automatically be created. This will indicated by a message: "The new SmartGeometry has been created in the SmartGeometry database."
# 10 Review and Analysis Packages

The available postprocessing packages are listed in the tables below. These packages can be accessed via the 'Review' or 'Analysis' menu.

## Review packages

<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
<th>More information</th>
</tr>
</thead>
<tbody>
<tr>
<td>ImageView</td>
<td>To view images (incl. movies)</td>
<td>chapter “ImageView” on page 106</td>
</tr>
<tr>
<td>VolumeView</td>
<td>For the calculation of Minimum / Maximum Intensity Projections, MultiPlanar Reformats and for Surface Rendering</td>
<td>chapter “VolumeView” on page 113</td>
</tr>
<tr>
<td>MobiView</td>
<td>Fusing and viewing package for acquisitions in multiple stations, e.g. whole body, total spine, MRA.</td>
<td>chapter “MobiView” on page 121</td>
</tr>
</tbody>
</table>

## Analysis packages

<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
<th>More information</th>
</tr>
</thead>
<tbody>
<tr>
<td>PicturePlus</td>
<td>To enhance images</td>
<td>chapter “PicturePlus” on page 133</td>
</tr>
<tr>
<td>ImageAlgebra</td>
<td>To perform image arithmetics e.g. subtract images</td>
<td>chapter “ImageAlgebra” on page 136</td>
</tr>
<tr>
<td>QFlow</td>
<td>Quantitative Flow postprocessing package</td>
<td>chapter “QFlow package” on page 127</td>
</tr>
<tr>
<td>Diffusion registration</td>
<td>To correct for patient movement which occured during a dynamic scan</td>
<td>chapter “Diffusion Registration package” on page 141</td>
</tr>
<tr>
<td>Diffusion</td>
<td>To calculate parametric diffusion maps, e.g. ADC or FA maps</td>
<td>chapter “Diffusion package” on page 141</td>
</tr>
<tr>
<td>FiberTrak</td>
<td>To visualize diffusion tensor data in the form of white matter tracts</td>
<td>chapter “FiberTrak package” on page 147</td>
</tr>
<tr>
<td>IViewBold</td>
<td>Real-time and postprocessing package for BOLD imaging</td>
<td>chapter “IViewBOLD” on page 162</td>
</tr>
<tr>
<td>Neuro T2* Perfusion</td>
<td>To evaluate neuro T2* dynamic scans and generate numerical and graphical results and maps</td>
<td>chapter “Neuro T2* Perfusion package” on page 172</td>
</tr>
<tr>
<td>Basic T1 Perfusion</td>
<td>To evaluate T1 dynamic scans and generate numerical and graphical results and maps</td>
<td>chapter “Basic T1 Perfusion package” on page 181</td>
</tr>
<tr>
<td>Package</td>
<td>Description</td>
<td>More information</td>
</tr>
<tr>
<td>---------------</td>
<td>-----------------------------------------------------</td>
<td>----------------------------------------</td>
</tr>
<tr>
<td>SpectroView</td>
<td>Postprocessing package for MR Spectroscopy</td>
<td>chapter “SpectroView” on page 189</td>
</tr>
</tbody>
</table>

**ImageView**

The ImageView package is optimized for viewing images.

**Documentation**

The following paragraphs give the following information:
- Screen layout
- Toolbar
- Settings window
- More Functions within ImageView

For information about workflows, refer to chapter “ImageView: Workflows“ on page 279.

**User Interface**

**Screen layout**

The ImageView package has a default layout of 2x2 viewports with the ImageView toolbar.

![ImageView layout with one large viewport.](image)

Fig. 50: ImageView layout with one large viewport.
Toolbar

Add / Remove Row and Add / Remove Column
• To add a column (to the right) or to remove a column.

OR/AND
• To add a row (below) or to remove a row.

• These function only affect the layout, not the current image data set.
• Alternatively press |Ctrl| and
  – the |Arrow down| or the |Arrow up| keys to add/remove a row.
  – the |Arrow right| key or the |Arrow left| key to add/remove a column.

Standard Layouts
• To select any of the standard screen layouts:
  1x1, 1x2, 1x3, 2x2, 2x3, 2x4, 3x3, 3x4

Play (Movie) <Pause>
• To play (or pause/stop) the current dataset as a movie.

NOTICE
To view a MultiMovie, link the viewports first and then click 'Play (movie)'.
A MultiMovie shows multiple imaging series in a movie in parallel. For information about linking, refer to chapter “Review toolbar” on page 93.

The Movie functionality is a generic functionality occurring in Graphical PlanScan and all Review and Analysis packages. For more information about movies, refer to chapter “On Toolbars” on page 55.

Text Box
• To overlay a text box to the images.

OR
To overlay an arrow with text box to the images.

Select an option from the drop-down menu. The Text Box with and without arrow can also be enabled via 'Annotation' from the right-mouse menu for every image.

**Measurements**

To perform measurements on the imaging series and overlay them and the results to the images.

- Depending on the type of graphical object chosen, different numeric results are provided.
- Every graphical object is defined by one or more anchor points. The anchor points are visible upon creation and when the graphical object is 'current': simply click on a graphical object to make it current.
- Graphical objects can be modified in size or shape by dragging any of these anchor points. They can be moved to another location by dragging the object anywhere else.
- Dedicated right mouse menus offer more functionality such as the calculation and display of histograms and profiles.

**Fig. 51:** Examples of measurements (inverted display). 1 - line with the anchor points (a) and the transform possibilities. 2 - line with measurement (not current, no anchor points). 3 - Open Angle measurement with anchor points, 4 - Ellipse measurement with anchor points.

The available options for measurements are listed here:

- **Point**
  
  Click on an image to mark a point. The intensity value for this point will be displayed.

- **Line**
  
  Click and drag to draw a line. Release to stop drawing. The length of the line will be displayed. Press |Shift| while dragging to get an orthogonal line, either horizontal or vertical.
**-> Open Angle**
Click four times to define an open angle. The angle will be displayed.

**-> Ellipse**
Click twice to define one axis of the ellipse, click once more to define the other axis of the ellipse.
The area of the shape and the intensity mean value will be displayed by default.
To move the shape, drag the center of the shape.
To modify the shape, drag the outer edge of the shape.

**-> Rectangle**
Click twice to define one border of the rectangle (the width), click once more to define the length of the rectangle.
The area of the shape and the intensity mean value will be displayed by default.

**-> Smoothed Polygon**
Click to start up the ROI definition.
Draw with the left mouse button (no dragging).
Click as often as needed to add new points and to define a smoothed polygon.
Control points are created / deleted by pressing |Shift| and clicking on a contour or point.
Double-click to end drawing and to confirm the shape.
Clicking |ESC|, the entire contour is cancelled.

**-> Freehand**
Click to start up the ROI definition.
Draw with the left mouse button (no dragging).
Click to end drawing and to confirm the ROI.
The area of the shape and the intensity mean value will be displayed by default.

**-> Right Mouse Menus**
Right-click on any graphical object to have the following additional functionality available:

- Histogram (available for all measurements except 'Open Angle' and 'Point')
- Profile (available for the 'Line measurement')
Fig. 52: Inverted displays of: Left - Histogram (pixel frequency versus pixel value range, and right - Profile (pixel value versus pixels).

- Add Text
to add descriptive text to the graphical object
- Show Details
- Color
to edit the color settings of the graphical object:
- Properties
to display and edit the properties of the graphical object such as ...
- Cut |Ctrl|+X
- Copy |Ctrl|+C
to copy the current graphical object to the clipboard for reuse on another image
- if applicable: Paste |Ctrl|+V
to paste the graphical object from the clipboard to the current image
- Copy To All
to copy the current graphical object to all images in the imaging series
- Delete |Del|
to delete the current graphical object

**Lock Drawing Mode**

- To lock the drawing mode.
  This means that once drawing mode is enabled, it stays enabled and more contours can be more defined in one go for ease of use.

**Hide/Show All Graphic Objects**

- To enable/disable the display of all graphic objects including ROIs, annotations and lines.
Color LUT (Look-Up Table)

- To select the color look-up table for the maps:

When a color LUT is selected, a vertical color scale bar is shown alongside each image. The window width and level can be adjusted with all types of color LUT.

<table>
<thead>
<tr>
<th>Values:</th>
<th>GrayScale</th>
<th>Rainbow</th>
<th>Blue To Red</th>
</tr>
</thead>
<tbody>
<tr>
<td>Display</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Maximum</td>
<td>White</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Gray</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Minimum</td>
<td>Black</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Settings

- To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

- In ImageView, these are Display parameters (e.g. order of image attributes on screen), Stacks parameters (e.g. order of stacks) and Propagate parameters (how to propagate view and window settings).

Viewing

The Viewing drop-down menu is a generic menu occurring in Graphical PlanScan and all Review and Analysis packages. For more information, please refer to chapter “On Toolbars” on page 55.

More

- Click the arrow besides 'More'.
  - The 'More' menu opens.
- Click on any menu option to select it.

Time-Intensity Diagram (TID)

To calculate and display a Time-Intensity Diagram.
The calculation of a TID requires to define a Region-Of-Interest (ROI).

- Click on "Time Intensity Display".
- Select a type of ROI and draw the ROI as described below:
-> Smoothed Polygon

Click to start up the ROI definition.
Draw with the left mouse button (no dragging).
Click as often as needed to add new points and to define a smoothed polygon.
Control points are created / deleted by pressing [Shift] and clicking on a contour or point.
Double-click to end drawing and to confirm the shape.
Clicking [ESC], the entire contour is cancelled.

-> Freehand

Click to start up the ROI definition.
Draw with the left mouse button (no dragging).
Click to end drawing and to confirm the ROI.
The area of the shape and the intensity mean value will be displayed by default.
For both ROI's, the shape is automatically copied to all images of the (dynamic) series and the TID displayed.

Fig. 53: TID Display with numeric ROI data on the left, the TID on the right and the buttons 'Export as' and 'Close'. To export the TID, click the button 'Export as', browse to the desired folder and click 'Save'.

Delete All Graphics
To delete all graphics such as ROI's or lines.

Deselect All Images
To deselect all images.

More Functions within ImageView

Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

Keyboard functions
Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

Right mouse menus
They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.
Right-click on any image to access the right mouse menus.

**VolumeView**

The VolumeView package is to be used for the calculation of Minimum / Maximum Intensity Projections, MultiPlanar Reformats and for Surface Rendering.

**Documentation**

The following paragraphs give the following information:

- Suitable scans
- Screen layout
- Toolbar
- Generate Series window
- Navigation
- More Functions within VolumeView


**Suitable Scans**

The VolumeView package provides different render modes (algorithms) to calculate projections and / or reformats of the original data set.

The table below shows the algorithms available in VolumeView and the types of suitable scans.

<table>
<thead>
<tr>
<th>Render Mode</th>
<th>Suitable scans</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maximum Intensity Projection (MaxIP)</td>
<td>• 3D PCA scan</td>
</tr>
<tr>
<td></td>
<td>• 3D/M2D Inflow scan</td>
</tr>
<tr>
<td></td>
<td>• CE-MRA scans</td>
</tr>
<tr>
<td>Minimum Intensity Projection (MinIP)</td>
<td>• Black blood scan</td>
</tr>
<tr>
<td></td>
<td>• VENBOLD (PRESTO based) scans</td>
</tr>
<tr>
<td></td>
<td>• as slab MIP in Susceptibility weighted scan</td>
</tr>
<tr>
<td></td>
<td>• as slab MIP in M2D balanced-FFE</td>
</tr>
<tr>
<td>MultiPlanar Reformat MPR)</td>
<td>• 3D scan. Best results are achieved with thin slices and preferably isotropic voxels.</td>
</tr>
<tr>
<td>Surface Rendering (shaded or unshaded)</td>
<td>• 3D scan. Best results are achieved with thin slices and preferably isotropic voxels.</td>
</tr>
</tbody>
</table>
User Interface

Screen layout

The Volume View package has a default layout of one large and three small viewports.

Fig. 54: VolumeView screen layout.

1 VolumeView toolbar
2 3D view calculated in real-time, by default: a MaxIP
3 Orthogonal views that serve as reference views (from top to bottom: coronal, sagittal, transverse view).

Each of the views is overlaid by colored lines indicating the position of the shown slices. The slices in the 3D view are linked to the slices in the orthogonal views.

Toolbar

Layout

- To select another screen layout.
  - Click 'Layout' and select:
    - 1x1: Displaying calculated image over whole volume.
    - 2x2: Displaying transverse original and sagittal reference in upper row, coronal reference and whole volume in lower row
View

- To display any non-rotated orthogonal view, click the <View> button successively. Alternatively you can select any option from the <View> drop-down menu:
  - Transverse, Coronal or Sagittal
  - Rotate Left 90, Rotate Right 90
  - Rotate Top 90, Rotate Bottom 90

Render Mode

- To select the render mode.

  - Click 'Render Mode' and select:
    - MPR (Multiple Planar Reformat)
    - MinIP (Minimum Intensity Projection)
    - MaxIP (Maximum Intensity Projection) which is the default setting
    - Shaded Surface (Rendering)
    - Unshaded Surface (Rendering)

Thickness

- To adjust the thickness of the real-time calculated object in the preview.

  - Click 'Thickness' and select:
    - 1, 2, 3 or 4 slices in case of MPR
    - Maximum, Minimum, 50%, 20% or 10% in case of MaxIP or MinIP (where 100% refers to the complete imaging volume)
Display Clipbox

- To view the edges of the data set and to enable interaction to reduce the volume of interest.

  - Click 'Display Clipbox'.
  - Drag the sides of the Clipbox with |CTRL| being pressed to reduce the volume in all directions.

  Rotating the object enables viewing for the sides of the Clipbox from different angles.

Center point

- To define a center point used as reference for subsequent actions.

  - Click 'Center point' to enable point selection mode.
  - Click on the image to select the center of rotation.

  The images and the colored lines on the images will be updated according to this center point. The MIP can also rotate around this point.

Draw Contour

- To draw a contour and to go for a non-cubic volume. Select/enable:
  - Cut outside: After drawing, the area outside the border will be cut away (Default).
  - Cut inside: After drawing, the area inside the border will be cut away.
  - Polygon: Point-to-point drawing where the points are connected in a straight line. Double-click to close the contour (Default).
  - Bezier: Point-to-point drawing where the points are connected in a curved line. Double-click to close the contour.
  - Free: click and draw while keeping the mouse pressed.
  - AutoCut Mode: If enabled, cutting will automatically occur when drawing is complete (Default).

Undo

- To undo the last action.

  This function can be used to undo multiple actions.

Redo

- To redo the last action.

  This function can be used to redo multiple actions.
Generate Series

- To calculate a new imaging series with the newly generated images.

A 'Generate Series' window pops up. It allows to specify which images are to be generated in which manner.

Viewing

The Viewing drop-down menu is a generic menu occurring in Graphical PlanScan and all Review and Analysis packages. For more information, please refer to chapter “On Toolbars” on page 55.

More

- Click the arrow besides 'More'.
  - The 'More' menu opens.
  - Click on any menu option to select it.

Reset All

- Click 'Reset All' to reset the orientation and to delete already drawn contours.

Reference Image Type

- To select the reference image type.

Can be set to:

- Source/Reformat
- Full Volume

Generate Series window

Out of the original dataset, you can easily generate new imaging series consisting of MaxIP, MinIP or MPR images.

You can

- set up and save protocols for the calculation of MaxIP, MinIP or MPR
- select and reuse the saved protocols for any other dataset.
- edit existing protocols
- delete protocols.

The Generate Series window shows up after clicking 'Generate Series'. It allows for the specification of the newly generated imaging series with respect to stack, propagation and geometry parameters.
Fig. 55: Generate Series window in VolumeView

1. To select a protocol. 'Compose' allows to compose a new protocol.

2. To delete the current protocol.

3. To save the current protocol.

4. To enter a series name for the new imaging series.

5. To generate a new imaging series with the given name.

6. To switch between the 'Generate series' parameter subsets, click on any of the tabs: Stack, Propagation, Geometry.

7. To change respectively enable or disable the Stack, Propagation or Geometry parameters.

**Stack parameters in the Generate Series window**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Possible settings</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Orientation</td>
<td>• Sagittal</td>
<td>To define the orientation of the newly generated imaging series.</td>
</tr>
<tr>
<td></td>
<td>• Coronal</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Transverse</td>
<td></td>
</tr>
<tr>
<td>Stack Type</td>
<td>• Radial</td>
<td>To define the stack type of the newly generated imaging series, e.g. for MPR preferably parallel or for MaxIP and MinIP preferably radial.</td>
</tr>
<tr>
<td></td>
<td>• Parallel</td>
<td></td>
</tr>
<tr>
<td>Radial Axis</td>
<td>• RL</td>
<td>To define the radial of the newly generated imaging series if 'Stack Type' is set to radial.</td>
</tr>
<tr>
<td></td>
<td>• AP</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• FH</td>
<td></td>
</tr>
<tr>
<td>Nr. of projections</td>
<td>1 ...</td>
<td>To specify the number of projections of the newly generated imaging series.</td>
</tr>
</tbody>
</table>

- Can be entered numerically.
- or via mouse interaction in the orthogonal views: press <SHIFT> and drag the outer yellow projection lines.
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Possible settings</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Thickness [mm]</td>
<td>[mm]</td>
<td>To specify the thickness of each projection.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Can be entered numerically.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• or via mouse interaction in the orthogonal views</td>
</tr>
<tr>
<td>Gap [mm]</td>
<td>[mm]</td>
<td>To specify the gap between the projections.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Can be entered numerically.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• or via mouse interaction in the orthogonal views: drag the outer yellow projection lines.</td>
</tr>
<tr>
<td>Radial Angle [deg]</td>
<td>[deg]</td>
<td>To specify the radial angle between the projections if 'Stack Type' is set to radial.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Can be entered numerically.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• or via mouse interaction in the orthogonal views: drag the outer yellow projection lines.</td>
</tr>
<tr>
<td>Reconstruction Accu-</td>
<td></td>
<td>To specify the reconstruction accuracy:</td>
</tr>
<tr>
<td>racy</td>
<td></td>
<td>• Best: best quality, longer calculation time</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Fast: shortest calculation time, suboptimal quality</td>
</tr>
<tr>
<td>Generate Slices in Re-</td>
<td></td>
<td>To generate a new imaging series with the slices in reverse order.</td>
</tr>
<tr>
<td>verse Order</td>
<td>Disabled</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Enabled</td>
<td></td>
</tr>
</tbody>
</table>

**Propagation parameters in the Generate Series window**

The Propagation parameters define how the settings are propagated. If propagation is applied e.g. for Dynamics, the settings of the current dynamic will be propagated to the Preceding or Following dynamics:

- Dynamics (preceding, following)
- Phases (all phases or the current phase, if not checked)
- Stations (all stations or the current station, if not checked)
- b-values (all b-values or the current b-value, if not checked)
- Diff.(usion) directions (all diffusion directions or the current diffusion direction, if not checked)

Select 'Single Axis' for multiple stacks or multiple stations.

You can also enable/disable 'Generate Orthogonals'. If enabled, three orthogonal MaxIPs will be calculated additionally.

**Geometry parameters in the Generate Series window**
The Geometry parameters allow entering of the offcentre and angulation values numerically, but also definition if the angulation of the new series is relative to the Volume or relative to the Magnet.

Select 'Magnet' for multiple stations. This compensates for planning differences between stations and aligns the new imaging series.

**Navigation**

The 3D view and the orthogonal views can be used for navigation.

**Scrolling**

To scroll through the orthogonal views to any desired location, drag the colored lines.

You can scroll within the preview if the <Thickness> is less than Maximum. Right-click in the 3D view and select Push/Pull. Drag to navigate through the volume.

To scroll through multiple dynamics if available, drag to the left or to the right on any of the orthogonal views. Alternatively you can press the left and right arrow key.

**NOTICE**

For DWI scans, drag diagonally to scroll through b-values.

**Rotate in any direction**

To rotate the dataset in any direction, right-drag on the 3D preview.

To display any non-rotated orthogonal view, click the <View> button successively. Alternatively you can select any option from the <View> drop-down menu.

**More Functions within VolumeView**

Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

**Keyboard functions**

Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

**Right mouse menus**

They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.

- Right-click on any image to access the right mouse menus.
Next Station and Previous Station
To display another station, right-click on any of the small viewports and select <Next station> or <Previous station>.

Hide Lines, Show Lines, Show Outline and Show Slices
Right-click on orthogonal view to toggle the display.

MobiView
MobiView can be used to fuse multistation datasets being acquired as different stacks in Head-Feet direction.
Typically, MobiFlex (or MobiTrak) and Whole Body scans are viewed in this way.

WARNING
After applying the fusion operation, double-check whether the result of the fusion operation is correct. Always keep the original images.
Horizontal lines on the image indicate where the operation took place. Check for any artifacts that could indicate a fusion error, like cut-off objects or anatomy. The fused images must be of the same acquired plane. Be aware that the resolution at the edges of a station can be lower than in the center.

Documentation
The following paragraphs give the following information:
• About Fusing
• User Interface
  – Screen layout
  – Toolbar
  – More Functions within MobiView
For information about workflows, refer to the section chapter “MobiView Workflow” on page 283.

About Fusing
Fusing
• creates one image from multiple images acquired at several stations.
• executes the following tasks:
  – Zooming of the images.
  – Panning in the image directions.
Review and Analysis Packages

MobiView

– Propagating these view settings to all images in such a way that the different stations are aligned if being displayed in a column.
– Fusing the images and creating one image.
– Removing the overlapping area either smooth or with a hard-cut.

• includes that the fusing area is clearly indicated by markers on the fused images.

NOTICE
Unfuse the images in case of artifacts.
This is to make sure that previously present artifacts which have not been visible on screen prior to fusing are not mistakenly interpreted as pathologies.

User Interface

Screen layout
The MobiView package automatically comes up with a screen layout related to the number of stacks within the selected scan, e.g.

• If the scan contains of 3 stations, the default screen layout is 3 x 3.
• If the scan contains of 5 stations, the default screen layout is 5 x 5.
• Corresponding slices (same AP, RL offcenter values) are automatically combined within one view.

Image Info Display
The matrix information in the Image Info corresponds to the fused image.
E.g. the matrix is displayed as "252 / 3518 x 512r"

• where 252 represents the initially scanned resolution per station of 252 in FH direction
• where 3518 represents the resolution of the fused images in FH direction
• where 512r represents the resolution in LR direction (r=reconstructed).

Toolbar

Add / Remove Row and Add / Remove Column

• To add a column (to the right) or to remove a column.

OR/AND
• To add a row (below) or to remove a row.

• These function only affect the layout, not the current image data set.

• Alternatively press |Ctrl| and
  – the |Arrow down| or the |Arrow up| keys to add/remove a row.
  – the |Arrow right| key or the |Arrow left| key to add/remove a column.

**Play (Movie) <Pause>**

• To play (or pause/stop) the current dataset as a movie.

**NOTICE**

To view a MultiMovie, link the viewports first and then click 'Play (movie)'.

A MultiMovie shows multiple imaging series in a movie in parallel. For information about linking, refer to chapter “Review toolbar” on page 93.

**Movie ToolBox**

• To adjust the movie settings.

► Select 'Movie ToolBox' from the Movie drop-down menu besides the icon.

---

**Fig. 56: Movie ToolBox.**

<table>
<thead>
<tr>
<th>Number</th>
<th>Purpose/ Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Click this button to toggle between Play, Pause and Stop movie mode.</td>
</tr>
<tr>
<td>2</td>
<td>Click this button, then scroll to the image to start the movie with and click 'Play Movie'.</td>
</tr>
<tr>
<td>3</td>
<td>Click this button, then scroll to the image to end the movie with and click 'Play Movie'.</td>
</tr>
</tbody>
</table>
| 4      | Select the type of movie from the drop-down menu:  
  • cyclic (loop): the images are displayed in the order 1 ... n, 1 ... n etc.  
  • bounce (yoyo): the images are displayed in the order 1 ... n, n ... 1, 1 ... n, etc. |
| 5      | Select type of image for the movie, e.g. slices or phases. |
| 6      | Adjust the movie speed by dragging the slider. |
Toggle or Select the Running Attribute

- To toggle between running attributes or to select a running attribute, e.g. echoes, slices, dynamics, image types.

Windowing Options

- To change the windowing characteristics for the multiple stations.
  Possible values are:
  - None
    Each station is displayed with its own window settings: in each station the maximum intensity is displayed white and the minimum intensity black.
  - Automatic
    The stations are windowed automatically based on the intensity values of all stations together: the maximum intensity of all stations is displayed white, the minimum intensity of all current stations is displayed black.
  - MIP
    The maximum intensity values of the stations are upscaled and the lower intensity values of the stations are downscaled to achieve a Maximum Intensity Projection (MIP) effect in the images.

Fusing Mode

To fuse stacks from multiple stations in different ways:

Fuse Hardcut

- Hardcut Fusing Mode is to be used for scans without overlap between stacks. It is typically used in sagittal and coronal multiple station imaging series.
- First half of the overlapping area is 100% of the first image, other half is 100% of the other image.

Fuse Smooth

- Smooth Fusing Mode is to be used for scans with overlapping stacks. It is typically used in sagittal and coronal multiple station imaging series.
- A smooth transition between images is created by using a sinusoidal function.

Merge Series

- Merge Series is to be used for multiple station imaging series acquired in transverse orientation.
- When enabled, it allows to easily scroll through the complete set of transverse images acquired for the multiple stations.
- Merged imaging series stay merged when they are transferred to PACS.
Select No Fusing Mode

- 'No Fusing Mode' disables fusing.

Generate Series

- To calculate a new imaging series with the newly generated images.
A 'Generate Series' window pops up where the name of the new series can be entered.

Settings

- To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

Viewing

To adjust the viewing settings:

Orientation (Viewing)

To change the orientation of the images:
- Mirror, Flip,
- Rotate clockwise, Rotate counterclockwise,
- Reset orientation,
- Display Images in Radiological View

Image Information (Viewing)

- To define the amount of displayed image information:
  - minimum: no text is displayed,
  - standard: scan, image number and the scan name are displayed,
  - maximum: also the offcenter values, the window values (width and level) and the caliper are displayed.

Interpolate (Viewing)

To interpolate the image(s).

Invert Gray Level (Viewing)

- To invert the images of the current dataset (change black and white in the grayscale).
Capture ...

To capture images and save them. Type of image and destination are to be defined in the 'Capture' pop-up window. Check according to your preferences:

- 'Capture Selected Image' captures the current image.
- 'Capture ImageView' captures the current image including orange border and ImageView tab.
- 'Capture Full Screen' captures the full screen.
- 'Capture Slices' captures all slices of the current imaging series.
- 'As Displayed and Annotated' or 'As Acquired' allow to capture images with or without their window/zoom settings and annotations.
- 'Save to External Folder' allows to save the data to an external folder.
  In this case, it is necessary to browse to this external folder.
- 'Save to Patient Database' allows to save the data to the patient database.
- In order to include the hospital name, check the eponymic option.

The function 'Capture ...' as part of Viewing is only available in Review and Analysis packages, not in Graphical PlanScan.

Save Presentation State <Ctrl+S> (Viewing)

To save a special way of presenting images.

Reload Presentation State <Ctrl+R> (Viewing)

To reload a special way of presenting images.

Reset Window (Viewing)

To reset images to original window level and width.

Reset Zoom / Pan (Viewing)

To reset images to original zoom and pan values.

More Functions within MobiView

Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

Keyboard functions

Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

Right mouse menus

They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.
Right-click on any image to access the right mouse menus.

**Store Fused Images**
The fused images are stored in an image file.

## QFlow package

The Quantitative Flow postprocessing package calculates quantitative information as flow velocity or flow rate.

### Q-flow

**WARNING**
For Q-Flow measurements the field-of-view (FOV) must be positioned in the isocenter of the magnet to avoid misinterpretations due to incorrect Q-Flow calculations.

**WARNING**
The option to export the results to a file just gives the user a momentary snapshot of the results as displayed on screen.
The correctness of these values is inconclusive.

### Documentation

The following paragraphs give the following information:

- Suitable Scans
- User Interface
  - Screen layout
  - Toolbar
  - Navigation matrix
  - More Functions within QFlow
- Results

For information about workflows, refer to chapter “QFlow Analysis” on page 285.

### Suitable Scans

Suitable scans are Quantitative Flow scans which are triggered PCA scans containing at least PCA/Phase images and FFE/Modulus and optionally PCA/Modulus images.
Reliable results are achieved when the scan has been acquired perpendicular to the vessel(s) of interest.

**User Interface**

**Screen layout**

The QFlow package has a default layout of four viewports.

![QFlow screen layout.](image)

**Fig. 57:** QFlow screen layout.

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Toolbar</td>
</tr>
<tr>
<td>2</td>
<td>Reserved for graphical results</td>
</tr>
<tr>
<td>3</td>
<td>Reserved for numerical results (table)</td>
</tr>
<tr>
<td>4</td>
<td>large FFE/M image</td>
</tr>
<tr>
<td>5</td>
<td>large PCA/P image, optionally to be replaced by other image types</td>
</tr>
</tbody>
</table>

**Toolbar**

**Display/Hide FFE/M, PCA/M, PCA/P**

- From the drop-down menu, select any image type for display in the right lower viewport:
  - from left to right: FFE/M, PCA/M, PCA/P
  - PCA/P Color overlays the PCA/P color mask to the recently chosen image type.
Display/Hide PCA/P Color Images
- Click to enable/disable the overlay of the PCA/P Color image to the image in the right lower viewport.

Draw Selected Contour
- Click 'Draw Selected Contour' to draw a ROI:
  - Smoothed Polygon
  - Ellipse
  - Freehand
  - Single Click.

Enable / Disable Active Contours
- Click 'Enable / Disable Active Contours' to enable or disable automatic contour detection.
  By default, ‘Active Contours’ is disabled to allow for automatic contour detection and adaptation.

Play (Movie) <Pause>
- To play (or pause/stop) the current dataset as a movie.

NOTICE
To view a MultiMovie, link the viewports first and then click 'Play (movie)'.
A MultiMovie shows multiple imaging series in a movie in parallel. For information about linking, refer to chapter “Review toolbar” on page 93.

The Movie functionality is a generic functionality occurring in Graphical PlanScan and all Review and Analysis packages. For more information about movies, refer to chapter “On Toolbars” on page 55.

Settings
- To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

Viewing
The Viewing drop-down menu is a generic menu occurring in Graphical PlanScan and all Review and Analysis packages. For more information, please refer to chapter “On Toolbars” on page 55.
More

- Click the arrow besides 'More'.
  ⇒ The 'More' menu opens.
- Click on any menu option to select it.

Results Setup ...

- Click 'Results Setup ...' to set up the results screen.
  The 'Results Setup' window opens.
- Select the vessel to display the results for.
- Specify if the results are to be displayed inverted.
- Select the display type and the unit.

Export Results

- Click 'Export Results' to export the results and browse to an export destination.

Link Time Points

To link multiple time points, also for movie display.

More Functions within the QFlow package

Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

Keyboard functions

Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

Right mouse menus

They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.

- Right-click on any image to access the right mouse menus.

Results

Graphical results and numerical results are presented in the reserved viewports.

The display of numerical results cannot be changed. The display of the graphical results however can be displayed in different ways:

- Right-click on the graphical results and select the result to be presented:
  - Area
  - Maximum Velocity
• Minimum Velocity
• Mean Velocity
• Peak Velocity
• Nr Pixels (number of pixels)
• Flux
• Standard Deviation.

A detailed description follows:

**General Results**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heart Rate [bpm]</td>
<td>As derived from acquisition.</td>
</tr>
<tr>
<td>RR Interval [ms]</td>
<td>As derived from acquisition.</td>
</tr>
</tbody>
</table>

**Flow Analysis Results for each ROI (vessel contour)**

The results are available per slice, per phase and per vessel.

Positive flow is flow into the plane (maximum positive: displayed white), e.g. in Feet-to-Head direction and in Right-to-Left direction.

Negative flow is flow out of the plane (maximum negative: displayed black), e.g. in Head-to-Feet direction and in Left-to-Right direction.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trigger delay [ms]</td>
<td>Time between R-peak and acquisition of the specific slice.</td>
</tr>
<tr>
<td>Flux [ml/s]</td>
<td>Blood volume that passes the contour per second. This is the same as ‘mean velocity * area’. Note that this value is only calculated if the flow direction is perpendicular to the image.</td>
</tr>
<tr>
<td>Area [cm²]</td>
<td>Area of the pixels that are partially or fully included in the contour. To visualize this area, right-click in an image viewport and select ‘Filled graphics’.</td>
</tr>
<tr>
<td>Nr. of pixels</td>
<td>Pixels that are partially or fully included in the contour.</td>
</tr>
<tr>
<td>Mean velocity [cm/s]</td>
<td>Mean blood flow velocity.</td>
</tr>
<tr>
<td>Maximum velocity [cm/s]</td>
<td>Highest measured positive flow in the contour.</td>
</tr>
<tr>
<td>Minimum velocity [cm/s]</td>
<td>Highest measured negative flow in the contour.</td>
</tr>
<tr>
<td>Peak velocity [cm/s]</td>
<td>Either maximum velocity or minimum velocity, whichever has the highest absolute value.</td>
</tr>
<tr>
<td>Velocity Standard Deviation [cm/s]</td>
<td>Standard deviation of the mean velocity.</td>
</tr>
</tbody>
</table>
Flow Analysis Results for a collection of ROI’s

These results are only generated for multiphase scans.

**Temporal integral values of flux:**

<table>
<thead>
<tr>
<th>Result</th>
<th>Available units</th>
<th>Default unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Forward flow volume [ml]</td>
<td>• Amount of positive flow.</td>
<td></td>
</tr>
<tr>
<td>Backward flow volume [ml]</td>
<td>• Amount of negative flow.</td>
<td></td>
</tr>
<tr>
<td>Regurgitant fraction</td>
<td>• Fraction of backward to forward flow.</td>
<td></td>
</tr>
<tr>
<td>Stroke volume</td>
<td>• Absolute value of the difference between forward and backward flow.</td>
<td></td>
</tr>
<tr>
<td>Absolute stroke volume</td>
<td>• Absolute value of forward flow PLUS absolute value of backward flow.</td>
<td></td>
</tr>
<tr>
<td>Mean flux [ml/s]</td>
<td>• Stroke volume x heartbeat / 60</td>
<td></td>
</tr>
</tbody>
</table>

**Temporal integral values of mean velocity:**

<table>
<thead>
<tr>
<th>Result</th>
<th>Available units</th>
<th>Default unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stroke distance</td>
<td>• Netto distance the blood proceeds in the vessel in 1 RR-interval.</td>
<td></td>
</tr>
<tr>
<td>Mean velocity</td>
<td>• Stroke distance x heartbeat / 60</td>
<td></td>
</tr>
</tbody>
</table>

Note that the units for each result type can be chosen by the user. Available units are:

<table>
<thead>
<tr>
<th>Result</th>
<th>Available units</th>
<th>Default unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Area</td>
<td>mm$^2$, cm$^2$</td>
<td>cm$^2$</td>
</tr>
<tr>
<td>Velocity</td>
<td>mm/s, cm/s, m/s</td>
<td>cm/s</td>
</tr>
<tr>
<td>Flux</td>
<td>mm$^3$/s, ml/s, ml/min</td>
<td>ml/s</td>
</tr>
<tr>
<td>Volume</td>
<td>mm$^3$, ml, cc, cm$^3$</td>
<td>ml</td>
</tr>
<tr>
<td>Distance</td>
<td>cm, mm, m</td>
<td>cm</td>
</tr>
<tr>
<td>Time</td>
<td>ms, s</td>
<td>depends on length of series</td>
</tr>
</tbody>
</table>
PicturePlus

PicturePlus applies a filter that reduces the visibility of noise and artifacts, thereby enhancing the anatomical structures in the images. It uses an intelligent algorithm of smoothing and edge enhancement, e.g. background noise is smoothed while vessels are sharpened.

Documentation

The following paragraphs give the following information:

• Suitable Scans
• User Interface
• Workflow

For more information about workflows, refer to chapter “PicturePlus Workflow” on page 287.

Suitable Scans

PicturePlus can be used for most image types (incl. modulus, real, flow) and all processed images (MPR, MaxIP, MinIP, subtracted images). New imaging series containing the enhanced images can be easily generated and stored.

User Interface

Screen layout

PicturePlus has a default layout of one viewport showing the center slice of the current scan.

Toolbar

Presets drop-down menu

• To display the list of available PicturePlus presets and select one of them for further processing.

Edit Presets

➢ To open the PicturePlus presets Editor and to edit the presets.

Generate Series

• To calculate a new imaging series with the newly generated images.

A 'Generate Series' window pops up. It allows to specify which images are to be generated in which manner.
Settings

- To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

Viewing

The Viewing drop-down menu is a generic menu occurring in Graphical PlanScan and all Review and Analysis packages. For more information, please refer to chapter “On Toolbars” on page 55.

PicturePlus Presets Editor

Preferred combinations of edge enhancement and smoothing can be saved as PicturePlus presets.

Create and edit a PicturePlus preset

You can edit existing PicturePlus presets or create new presets.

- Click on the ‘Presets ...’ to open the Preset Editor.
  The Preset Editor opens. The available presets are displayed along with their names, smoothing and edge enhancement settings.
- Click on a preset to make it current
- To create a new preset, click on 'Add' (+).
  The new preset is a copy of the current preset.
  - Enter a new name for this preset.
  - Click on the ‘Smooth plus’/’minus’ buttons to increase or decrease smoothing.
  - Click on the ‘Edge plus’/’minus’ buttons to increase or decrease the edge enhancement.
  - Click on 'Update' to update the changes in the list of presets.
  - Click on 'Save' to save the preset.
  - To close the Preset Editor, click on 'Hide'.
Delete a PicturePlus preset

- Open the Preset Editor.
- Select the preset to be deleted.
- Click on the 'Delete' button to delete the current preset.

More Functions within PicturePlus

Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

Keyboard functions

Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

Right mouse menus

They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.

- Right-click on any image to access the right mouse menus.

Interaction Mode

- can be used to define the left mouse usage for interaction with images.

The table below lists the functions which are specific for this package. For information about the generic functions, see chapter “Generic functions for images” on page 55.
### Image Algebra

The Image Algebra package can be used to perform pixelwise image calculations, e.g. subtracting one dynamic scan from the consecutive dynamic scans. A preview is available which shows the resulting image for the current scan/scans. New imaging series can be easily generated and stored.

#### Documentation

The following paragraphs give the following information:

- Available Calculations
- User Interface
- Workflow

For information about workflows, refer to chapter “Image Algebra Workflow” on page 288.

#### Available Calculations

The package provides the possibility to perform different calculations for two e.g. (groups of) slices or dynamic scans, being referred to as A and B. It is possible to apply a weighting factor, depending on the type of calculation for A or for B.

**Addition of images**
- Result = A + B

**Subtraction of images**
- Result = B - A or
- Result = A - B

**Relative subtraction of images**
- Result = \((B - A) / (A + B) / 2\) * 100
- Result = \((A - B) / (A + B) / 2\) * 100

**Ratio calculations**
- Result = \((B / A)\) * 100
- Result = \((A / B)\) * 100

**Cumulation**
- Result = Sum of multiple echoes

**Magnetic Transfer Coefficient**
- Result = \((B - A) / B\) * 100
- Result = \((A - B) / A\) * 100
ASL subtraction
where ASL stands for Arterial Spin Labeling
- Result = B - A

Requirements for Image Algebra datasets
The components A and B can be images of one scan, but also images of different scans. In order to perform calculations with A and B, they have to have the same slice distance (slice thickness and slice gap), FOV and patient position.

User Interface

Screen layout
The Image Algebra package has a default layout of four viewports.

1 Toolbar
2 Sliders for weighting factor and for slice selection
3 Component A
4 Preview, calculated in real-time
5 Component B

Toolbar

Adjust B0 Threshold
- To adjust the B0 threshold and to enable (default) or disable the display of the threshold mask.

    Setting a threshold mask will exclude background pixels from the functional map calculations. All pixels with values below the mask value will be displayed blue. Only pixels with intensity above the mask value are used for the calculations, colored areas will be excluded from the calculation.

In Image Algebra, you can adjust the threshold values for the components A and/or B, and in such a way focus on specific anatomy.

- Click 'Threshold A' or 'Threshold B' to enable the display of the threshold mask.
- Right-drag up- and downwards to adjust the threshold.
Link Threshold for A and B

- To link the thresholds for A and B: adjusting 'Threshold A', 'Threshold B' will automatically be adjusted in the same way.

Select the Operation drop-down menu

- To select the required operation from the drop-down menu, e.g. addition, subtraction, relative subtraction, ratio calculations, cumulation, magnetic transfer coefficient calculation and ASL subtraction.

Generate Series

- To calculate a new imaging series with the newly generated images.

A 'Generate Series' window pops up. It allows to specify which images are to be generated in which manner.

Settings

- To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

Viewing

The Viewing drop-down menu is a generic menu occurring in Graphical PlanScan and all Review and Analysis packages. For more information, please refer to chapter “On Toolbars” on page 55.

Sliders

Fig. 61: Image Algebra sliders viewport.

1. Display of weighting factor for A (or possibly for B), in this case: 1.00

You can apply a weighting factor, and in such a way perform calculations with defined percentages of A or B.

2. Selection Icon: Toggle between single selection and range selection ("Switch to single selection" and "Switch to range selection")
3 Sliders for slice selection (depending on setting: either single slice selection or range selection)
Note that for a dynamic scan another slider for the dynamic scans is available.

4 Slider for weighting factor for A (range: from 0.0 to 2.0)

5 Display of link symbol if A and B are linked for image selection

More about the Sliders for Slice Selection

You can select either multiple images or a single image as A and/or B.

Single selection for a single image

► Click on the selection icon and ‘Switch to single selection’.
A single selection box is displayed on the bar representing the slices.
► Drag the box to the position of the required slice.

Fig. 62: Sliders: Single selection (S) with the single selection box (1): in the upper example, the first image is selected. In the lower example, the single selection box is dragged to another slice.

Range selection for multiple images

► Click on the selection icon and ‘Switch to range selection’
► Drag the anchor points at the outer edges of the range bar to select the range.
The selected slices will be indicated as slice number on top of the slider.

Fig. 63: Sliders: Range selection (R) with anchor points (1 and 2) at the outer edges of the range bar.

Example: Dynamic scan

With dynamic scans, a slider bar for A and B is available for the dynamic scans and another one for the slices.
Fig. 64: The figure shows the example of a subtraction (B-A): post-contrast scan minus pre-contrast scan. The components A and B consist of 60 dynamics and 30 slices each. The selected range for A is: dynamic 1, all slices (pre-contrast scan). The selected range for B is: dynamic 2 to 60, all slices. In this case, dynamic 1 will be subtracted from the dynamics 2 to 60 for all slices.

More Functions within Image Algebra

Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

Keyboard functions

Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

Right mouse menus

They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.

- Right-click on any image to access the right mouse menus.

Interaction Mode

- can be used to define the left mouse usage for interaction with images.

<table>
<thead>
<tr>
<th>Possible setting</th>
<th>Corresponding icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Scroll (default)</td>
<td><img src="image.png" alt="Icon" /></td>
<td>Drag to scroll through the dataset.</td>
</tr>
<tr>
<td>Threshold</td>
<td><img src="image.png" alt="Icon" /></td>
<td>Drag to adjust the B0 threshold.</td>
</tr>
</tbody>
</table>

Set As Mask (Defining)
Diffusion Registration package

The Diffusion Registration package is a postprocessing package. It can be used to correct for patient movement which occurred during a dynamic brain scan. In such a way, diffusion registration improves image quality in calculated diffusion images.

- Images of successive dynamic series are compared.
- Images are realigned to correct for motion.
- A new series with the corrected images is generated in the patient database.
- The processing step 'Diffusion Registration' is stored in the current ExamCard and will be performed automatically when the ExamCard is executed again.

It is recommended to execute this package on all brain diffusion data prior to any kind of post-processing, as it improves diffusion maps (resulting from the Diffusion postprocessing package) and the fiber tracking results (generated by the FiberTrak package).

For information about workflows, refer to chapter “Diffusion Registration Workflow” on page 289.

Diffusion package

The process of diffusion of water molecules through brain tissue can be measured using MRI with diffusion weighted scanning. The actual diffusion properties depend on the local tissue. Furthermore, the water diffusion can be anisotropic: fast diffusion in one direction and slow diffusion in other directions.

For ease of evaluation, the Diffusion package generates various parameteric maps related to diffusion weighted and diffusion tensor imaging. New imaging series can easily be generated and stored.

WARNING

For ADC measurements the field-of-view (FOV) must be positioned in the isocenter of the magnet to avoid misinterpretations due to incorrect ADC calculations.

Documentation

The following paragraphs give the following information:

- User Interface
- Parametric Maps
- Transfer of DWI iso and ADC images

For information about workflows, refer to chapter “Diffusion Workflow” on page 290.
User Interface

Screen layout
The Diffusion postprocessing package has a default layout of two large viewports.

Fig. 65: Screen layout of Diffusion postprocessing package.

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Toolbar</td>
</tr>
<tr>
<td>2</td>
<td>Center b0 slice with threshold mask (blue) overlaid</td>
</tr>
<tr>
<td>3</td>
<td>Corresponding map, calculated in real-time</td>
</tr>
</tbody>
</table>

Toolbar

Select b-values
- To select at least 2 b-values for processing.

Generate Series
- To calculate a new imaging series with the newly generated images.

A 'Generate Series' window pops up. It allows to specify which images are to be generated in which manner.

Possible maps are:
• DWI iso map, ADC map, eADC map, ADC iso map, eADC iso map, FA (greyscale) map and/or FA color map.

**Settings**

• To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

**Viewing**

The Viewing drop-down menu is a generic menu occurring in Graphical PlanScan and all Review and Analysis packages. For more information, please refer to chapter “On Toolbars” on page 55.

**More Functions within the Diffusion package**

Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

**Keyboard functions**

Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

**Right mouse menus**

They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.

• Right-click on any image to access the right mouse menus.

**Interaction Mode**

• can be used to define the left mouse usage for interaction with images.

The table below lists the functions which are specific for this package. For information about the generic functions, see chapter “Generic functions for images” on page 55.

<table>
<thead>
<tr>
<th>Possible setting</th>
<th>Corresponding icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>B0 Threshold</td>
<td>![B0 Threshold icon]</td>
<td>Drag to adjust the B0 threshold.</td>
</tr>
</tbody>
</table>
Adjust B0 Threshold

- To adjust the B0 threshold and to enable (default) or disable the display of the threshold mask.

Setting a threshold mask will exclude background pixels from the functional map calculations. All pixels with values below the mask value will be displayed blue. Only pixels with intensity above the mask value are used for the calculations, colored areas will be excluded from the calculation.

Fig. 66: Left: Adjusting the B0 Threshold. Right: FA color map calculated in real-time.

Parametric Maps

The results will be provided as parametric maps. The type of the map is indicated in the map’s scan type field.

1: ADC-map
2: eADC-map
3: FA-map
4: FA direction (color)-map

Fig. 67: Example of ADC and eADC map, FA and FA color map.

Scrolling through the maps shows which types of maps are available for the current scan (not all types of maps are suitable for every type of diffusion scan).

If an ADC iso and eADC iso map are available, directional ADC and eADC maps can also be generated (even though they are not available in the preview).
**DWI iso**

The DWI iso map is calculated by first finding the average ADC from all of the available gradient directions.

This average ADC is then used together with the b=0 image to create the DWI iso map. Since this uses all available directions, the SNR of the DWI iso map is improved especially with DTI scans.

- DWI iso images are identical to the isotropic images if 3 diffusion directions are scanned.
- The DWI iso images show a better image quality when the number of diffusion direction increases. The DWI iso images will have less noise. There is an increase in signal when more than 16 directions are acquired. Higher signal gives a sharper appearance.
- The option to create DWI iso images is not available for diffusion scans that are acquired with gradient overplus as the P_oblique, M_oblique and S_oblique directions are not saved in the database. The DWI iso option is also only available when 2 b values are selected, and when the lowest b value is less than or equal to 100.

![Fig. 68: DWI isotropic images acquired in 6 directions.](image)

![Fig. 69: DWI isotropic images acquired in 32 directions.](image)

**ADC and ADC iso**

The Apparent Diffusion Coefficient (ADC) identifies the average diffusion as measured by the diffusion imaging sequence.

The ADC is given in ‘mm$^2$/s’ and can be expected to have an order of magnitude of 0.6 to 1.0 x 10$^{-3}$ mm$^2$/s for a tissue like white matter.
The ADC can be obtained for each separate diffusion direction (identified as ‘ADC’) but also the average or isotropic ADC (ADC iso) can be obtained when enough non-collinear diffusion directions were acquired.

**NOTICE**
The values given by the map are multiplied by a factor of 1000 for display purposes. Thus, an ADC map ROI mean value of '900' is identical to an ADC of $0.9 \times 10^{-3}$ mm$^2$/s.

<table>
<thead>
<tr>
<th>Tissue characteristics</th>
<th>Signal DW images</th>
<th>Signal ADC maps</th>
<th>Signal eADC maps</th>
</tr>
</thead>
<tbody>
<tr>
<td>High ADC (rapid diffusion)</td>
<td>hypointense, more signal</td>
<td>High signal intensity</td>
<td>Low signal intensity</td>
</tr>
<tr>
<td></td>
<td>attenuation</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Low ADC (slow diffusion)</td>
<td>hyperintense, less signal</td>
<td>Low signal intensity</td>
<td>High signal intensity</td>
</tr>
<tr>
<td></td>
<td>attenuation</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Tab. 3: Signal in ADC and eADC maps

ADC maps provide anisotropic information and are available for each diffusion direction: S, M, P.

**eADC and eADC iso**
The exponential-ADC or eADC is used to show the diffusion weighting effect of a tissue. The eADC is calculated as $\exp(-b*ADC)$. In the eADC maps, CSF has very low signal so that subtle periventricular (e)ADC differences are more easily noticed.

**FA (Fractional Anisotropy) map**
Fractional anisotropy (FA) maps can be calculated from the DTI information. The FA values indicate the degree of anisotropy and range from 0 to 1. In case of no anisotropy (or normal isotropic diffusion, e.g. in grey matter tissue) the FA equals 0. For most white matter regions the FA value is much higher (for example, in the corpus callosum the FA value is around 0.6).

At least six different diffusion directions are needed to uniquely describe the diffusion pattern and to calculate the diffusion tensor matrix per pixel. From this calculation, the fractional anisotropy can be displayed in a FA map. High signal intensity corresponds to high fractional anisotropy and low signal intensity to low anisotropy.

Two different types of FA map are available: FA greyscale map (also referred to as FA map) and FA color map.

**FA (greyscale) map**
Directional information is not provided.

**FA Color map**
The color indicates the most important diffusion direction:
- Blue for FH-direction.
• Red for RL-direction.
• Green for AP-direction.

Transfer of DWI iso and ADC images

Diffusion data and interoperability
To enable easy transfer of the DWI iso and ADC images, it is possible to create separate DWI iso and ADC series with the Diffusion processing package.

The generated series can be recognized by a prefix in both the Thumbnail Viewer as well as in the Administration window: iso for DWI iso images and d for ADC map, enabling the user to easily select the iso and ADC series for transfer to a PACS or other network node.

FiberTrak package

The FiberTrak (FT) package enables visualization of the diffusion tensor data in the form of white matter tracts. In order to achieve FiberTrak results an algorithm is applied using specific settings. These fibertract settings include signal-threshold, FA values and curvature of the fiber-tract.

WARNING
When fibertract settings are changed to low values (meaning no signal threshold, very low FA, and very high curvature acceptance) the white matter tracts may include erroneous results.
This may consequently lead to misdiagnoses.
It is advised to use default settings whenever possible.

WARNING
With FiberTrak the resulting fibers depend strongly on the parameter settings in the package.
Low SNR in the DTI dataset can influence the results, leading to structures without anatomical relevance.

Documentation
The following paragraphs describe:
• Requirements for a FT dataset
• User Interface of the FiberTrak package

For more information about workflows, refer to chapter “Fiber Tracking Workflow” on page 291 and to chapter “FiberTrak: Advanced Workflows“ on page 293.
Requirements for a FT dataset

Diffusion tensor data with a minimum of 6 diffusion directions is used to calculate the preferred diffusion direction. This diffusion direction indicates the orientation of the local fibertracts. The FiberTrak package uses all this information to delineate the various fibertract bundles.

In order to provide good Fiber Tracking results, a certain minimum quality of data is needed. ExamCards and preset procedures may be used to generate such data.

Diffusion Tensor Imaging (DTI) scan

At least 6 diffusion directions are needed. This corresponds to the setting ‘low’ of the imaging parameter ‘DTI directional resolution’.

However, it is better to use the setting ‘medium’ which includes 15 diffusion directions. This provides a better rotationally invariant accuracy of fiber directions.

Typical scan characteristics

• Medium DTI (15 directions)
• Single-shot SE-EPI scan
• SENSE factor in the range of 1.5 to 3.0
• Isotropic data if possible

NOTICE

DTI data can be processed by means of the Fiber Trak package when being acquired with releases from Release 10 onwards.

Anatomical reference scan

In order to visualize the obtained tracts with respect to the anatomical and pathological features, any scan may be used as an anatomical reference. However, it is advised to use scans with a high through-plane resolution. For example, T1w 3D/TFE protocols can be used as they show a clear delineation of white and grey matter.

User Interface

Screen Layout

The FiberTrak package has a default layout of one large viewport and three small viewports.
Fig. 70: FiberTrak package layout with the 3D view on the left and the orthogonal views on the right hand side.

The large viewport contains the 3D view which is meant to display the dataset and the obtained fibers in a 3D manner. Rotating, panning and zooming this 3D view allows viewing of white matter tracts from all angles.

The orthogonal views serve as reference views (from top to bottom: coronal, sagittal, transverse view). Each of the views is overlaid by colored lines indicating the position of the shown slices. The slices in the 3D view are linked to the slices in the orthogonal views.

The image type being displayed in the 3D or the orthogonal viewports can be chosen freely, either FA, B0, Anatomical, ADC iso, eADC iso or DWI iso map. For more information, see chapter “Colors: Fibers and ROIs” on page 161.

Toolbar

Layout
- offers options:
  - to show or hide statistics (see chapter “Statistics: Fibers, ROIs and current voxel” on page 161)
  - to show or hide orthogonal views
  - to reset the layout to the default FiberTrak package layout.
Switch To View

- defines the orientation in which the large viewport (3D view) is viewed: either transverse, sagittal or coronal.

View Slices: Show Transverse, Show Sagittal, Show Coronal

- allows the display of a transverse, sagittal or coronal slice in the 3D view or display of the corresponding reference line in the non-rotated 3D view.

Track Single ROI Fibers

- Can be used to define a single ROI. Fibers will automatically be tracked for each single ROI. For more information, refer to chapter “Fiber Tracking Workflow” on page 291.

Define multiple ROIs

- Can be used to define multiple ROIs consecutively. To start the fiber calculation, select ‘Track Multiple ROI Fibers’.

Track Multiple ROI Fibers

- Can be used to track multiple fibers if multiple ROIs have been drawn. Only those fibers will be tracked which originate from all of the ROIs. For more information, refer to chapter “Fiber Tracking Workflow” on page 291.

Select ROI Type

- To select a ROI type.

- Click on the down arrow besides the icon to display the possible options.

  - Freehand ROI (default)
  - Seeded-2D ROI
  - Seeded-3D ROI
  - Single-Point ROI
2D Cross-section Tract Series
• Can be used to generate 2D cross-section tract series of the FiberTrak dataset. For more information, refer to chapter “Output Series” on page 293.

3D Projection Tract Series
• Can be used to generate 3D projection tract series of the FiberTrak dataset. For more information, refer to chapter “Output Series” on page 293.

Settings
• To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

The Settings icon serves to define the initial colors for ROIs, fibers and the default image type for the 3D view and the orthogonal view. See chapter “Colors: Fibers and ROIs” on page 161 for more information.

Viewing
The Viewing drop-down menu is a generic menu occurring in Graphical PlanScan and all Review and Analysis packages. For more information, please refer to chapter “On Toolbars” on page 55.

More
➢ Click the arrow besides 'More'.
⇒ The 'More' menu opens.
➢ Click on any menu option to select it.

Algorithm Settings
• enables determination of the algorithm for fiber calculation and the definition of Seeded-2D and -3D ROIs.
• is also available via the right mouse menu of the Fiber and ROI legend. See chapter “Algorithms: Fibers and Seeded ROIs” on page 159 for more information.

Save Statistics
• saves the 'statistics' concerning ROIs, fibers and the current voxel in the directory ‘E:/Export’. The file name includes patient and scan name. It is a tabulated file with the extension ‘.tsv’ which can be opened by packages like Microsoft Excel. For more information, see chapter “Statistics: Fibers, ROIs and current voxel” on page 161.
Fiber Legend

The fiber legend shows the list of fibers for the current dataset. The list of fibers contains the name of the fiber set (e.g. fiber01) and the color that is assigned to it. The checkmark indicates that the fiber is displayed.

Fiber display features

The legend can be used to modify many of the fiber display features. Right-click on the name of a fiber in the Fiber Legend to
• select all or no fibers,
• show or hide the current fiber,
• rename or delete the current fiber,
• change the color of the current fiber,
• modify the algorithm settings with respect to fibers, 2D and 3D seeded ROIs. See section chapter “Algorithms: Fibers and Seeded ROIs” on page 159 for more information.

Fiber Statistics

The legend can be extended to display statistical information on fibers, ROIs and the current voxel.

► Click on the arrows icon to open the Fiber Statistics window. Clicking on the mirrored arrow symbol closes the statistics window again. See chapter “Statistics: Fibers, ROIs and current voxel” on page 161 for more information.

ROI Legend

The ROI legend shows the list of ROIs for the current dataset with ROI names (ROI01, ROI02 etc.) and the color that is assigned to the ROI. The checkmark indicates that the ROI is displayed. Note that only displayed ROIs will be taken into account in the multiple ROI FiberTrak calculation.

ROI display features

The legend can be used to modify many of the ROI display features. Right-click on the name of a ROI in the ROI Legend to
• select all or no ROIs,
• show or hide the current ROI,
• rename or delete the current ROI,
• merge multiple ROIs into a single ROI,
• change the color of the current ROI,
• change the type of ROI into either ‘include’ (default) or ‘exclude’. The latter means that this ROI will be used to exclude tracts in the fibertract algorithm.

See chapter “ROIs” on page 156 for more information on ROIs.

See chapter “Algorithms: Fibers and Seeded ROIs” on page 159 for more information on algorithms.

**Navigation**

In this section, various navigation possibilities are described. The 3D view or the orthogonal views can be used for navigation.

Zooming, panning and windowing are performed as usual.

**Scroll through the dataset**

- Right-click on an image.
- Select ‘Scroll’.
  
  This is the default setting.
- Drag in the 3D view to scroll through the slices.

  OR:

  - Drag the colored lines (blue: FH-, green: AP- and red: RL-image position) on the orthogonal views to any desired location. The image in the 3D view will be updated to the current location.

**Rotate the dataset**

- Right-drag on the 3D view to rotate in any direction.

By default, all of the orthogonal planes will be displayed in the 3D view. The intersection of the shown slices is accentuated by a white line. Note that the display of the orthogonal planes can be enabled or disabled.

![Fig. 71: Rotated 3D views without and with transverse plane being displayed.](image)
View Slices: Show Transverse, Show Sagittal, Show Coronal

- allows the display of a transverse, sagittal or coronal slice in the 3D view or display of the corresponding reference line in the non-rotated 3D view.

Switch to an orthogonal view

- Select 'Switch To View' from the FiberTrak toolbar: either transverse, sagittal or coronal. The image in the 3D view will be replaced by either an orthogonal (non-angulated) transverse, sagittal or coronal view.

Modify display for 3D view and Orthogonal views

The image display in the 3D viewport and the orthogonal viewports can be chosen. FA coloring of the selected image type can be enabled or disabled to overlay FA colors to the current image.

- Click on the ‘Settings’ icon from the FiberTrak toolbar.

► Click on the ‘Settings’ icon from the FiberTrak toolbar.

► Select ‘3D Slices’ or ‘Ortho Slices’.

► Select either
  - FA
  - B0
  - Anatomical
  - ADC iso
  - eADC iso
  - DWI iso

► Select or deselect ‘FA coloring’ to switch FA coloring ON or OFF.

View cross-sections or projections

Within the orthogonal views, there are two ways to view the obtained fibertracts. Default is that the complete tract is projected on top of the selected slice: even when the tract is actually "behind" the viewed slice. The second option is called "cross section". With this view only the intersection between the tracts and the current slice in the orthogonal view is displayed.

► Right-click on any of the orthogonal viewports.

► Select 'View Fibers' and then either 'Projection' or 'Cross-Section'.

NOTICE

When reformatted output is generated with the ’2D-Cross section Tract series’ tool the "cross section" view is chosen, independent of the setting in the orthogonal view.
Adjust Opacity

• The opacity parameter allows to make the slices translucent to different extents in order to facilitate viewing of the fibers.

Right-click on the view, select 'Opacity' and then drag up and downwards to adjust the opacity.

More Functions within FiberTrak

Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

Keyboard functions

Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

Right mouse menus

They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.

► Right-click on any image to access the right mouse menus.

Interaction Mode

• can be used to define the left mouse usage for interaction with images.

The table below lists the functions which are specific for this package. For information about the generic functions, see chapter “Generic functions for images” on page 55.

<table>
<thead>
<tr>
<th>Possible setting</th>
<th>Corresponding icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Track Single ROI Fibers</td>
<td><img src="image" alt="Icon" /></td>
<td>The left mouse can be used to define a single ROI. Fibers will automatically be tracked for each single ROI.</td>
</tr>
<tr>
<td>Define Multiple ROIs</td>
<td><img src="image" alt="Icon" /></td>
<td>The left mouse can be used to define multiple ROIs consecutively. To start the fiber calculation, select 'Track Multiple ROI Fibers'.</td>
</tr>
<tr>
<td>Opacity</td>
<td><img src="image" alt="Icon" /></td>
<td>Drag to adjust the opacity.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>See section ‘Navigation’ for more information.</td>
</tr>
<tr>
<td>Threshold</td>
<td><img src="image" alt="Icon" /></td>
<td>Drag to adjust the b0 threshold.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>See section ‘Algorithms: Fibers and Seeded ROIs’ for more information.</td>
</tr>
</tbody>
</table>

Fiber Colors

• changes the colors of the displayed fibers.

• is also available via the Fibers and ROI Legend. See chapter “Colors: Fibers and ROIs” on page 161 for more information.
ROI Colors

- can be used to change ROI colors
- is also available via the Fibers and ROI Legend.

ROIs

Fibers can be calculated from either a single ROI or multiple ROIs. This section describes the
- available ROI Types
- available ROI Operations.

ROI Types

Different ROI types are available for optimum results.

Freehand ROI

The freehand ROI enables the drawing of an irregular ROI within a given slice. In case of multiple ROI fibertracking, it is advised to draw the ROI slightly larger than the given bundle. It is important to ensure that the whole bundle is included.

Seeded-2D ROI

The seeded-2D ROI can be used to identify regions with a single mouse click. These ROI's will be perpendicular to the tract at the place of the mouse click and are thus not in-plane but optimized to best delineate the local tract.

The plane of a 2D-seeded ROI's is made to be perpendicular to the local preferred diffusion direction. As an example, in the mid-sagittal plane the cortical spinal tract will show up with a blue FA color (feet-head direction). If - with a single mouse click - a 2D seeded ROI is drawn in this tract the final ROI will be transverse, and thus will not fall within the sagittal plane. In this manner the optimal ROI is generated to identify the tract.

The size of the seeded-2D ROI depends on the settings of the ROI algorithm. See chapter “Algorithms: Fibers and Seeded ROIs” on page 159 for more information on this algorithm and on how to change the settings.

Example for Middle Cerebellar Peduncle (MCP)

An example of using multiple seeded-2D ROIs is given below for the middle cerebellar peduncle (MCP).

- Set the interaction mode to ‘Multiple ROI’ and the ROI type to ‘Seeded 2D’.
- Create two seeded-2D ROIs, each by a single mouse click on the green areas with the white arrows.
- Perform fiber tracking by clicking on the ‘Track Multiple ROI Fibers’ icon.
Fig. 72: MCP Example

A  A coronal view is given at the height of the MCP. The two white arrows indicate the crossing of the MCP in this plane.

B  Two seeded-2D ROIs have been created in both (green) areas of the MCP.

C  The final result is shown in a transverse view. Note that the ROI's do not fall within the coronal plane, but are perpendicular to the MCP.

Seeded-3D ROI
The seeded-3D ROI uses the seeding algorithm to create a 3D region of interest. These regions are thus larger. This ROI type is best used in combination with single-ROI Fibertracking to identify a large number of starting points.

Single Point
The single-point algorithm can be used to identify "single" tracts. In combination with the "Track Single ROI Fibers" interaction mode it can be used to identify tracts in a fast manner:

► Keep the left mouse button pressed while dragging the mouse over the data in the 3D viewport.
  The tracts, originating from the current pixel, will be shown and updated in real-time.

ROI Operations
Most fiber bundles can be defined using 2 or 3 correctly placed ROI's. Within the FiberTrak package only the ROI's which are visible are used in the generation of fiber bundles. Special possibilities exist to manipulate ROI's to improve the obtained fibertracts.

Select the best suited ROI type
► Click on the ROI icon or select ‘ROI settings’ from the FiberTrak menu.
  ► Select either of the ROI types.

Hide, rename or delete a ROI
► Right-click on a ROI or on a ROI name in the ROI legend.
  ► Either select 'hide', 'rename' or 'delete' (or press [Delete] key). In case of renaming, a new name needs to be entered.

Change the ROI color
► Right-click on a ROI or on a ROI name in the ROI legend.
Review and Analysis Packages

FiberTrak package

- Select ‘Change Color’. The ‘Color Settings’ window will open.
- Select either ‘Fixed’ or ‘Directional’ where
  - Fixed stands for a fixed color to be used, e.g. red only
  - Directional stands for the standard color codes being used within diffusion weighted imaging: Blue for FH-direction, Red for RL-direction, Green for AP-direction.
- Select any color.
- Click ‘Okay’ to apply the changes. Clicking ‘Cancel’ leaves the window without any changes.

**Change the ROI ‘Include/Exclude’ type**

In some cases the obtained fibertracts may have too many extensions. For example, they include many more white matter tracts than of interest in a certain pathology. In this case it is useful to define a ROI to exclude certain tracts.

- Right-click on a ROI or on a ROI name in the ROI legend.
- Select ‘Type’.
- Select either ‘Include’ or ‘Exclude’.
  - Include: the ROI will be used as a criterion. The resulting fiber must pass through the given ROI.
  - Exclude: the resulting fibers must not pass through that ROI.

**Example**

![Fig. 73: Example of an Exclude ROI. A: The left and right inferior fronto-occipital (IFO) tracts are generated using two large ROIs. This IFO result (in purple) does also show two spurious tracts (see arrows). B: In order to remove these tracts, two ROIs were created and set to ‘exclude’ (orange and red ROI). With the total setup of four ROIs, the IFO will be generated as shown in orange.](image)

**Merge ROIs**

It is also possible to turn separately drawn ROIs into one single ROI with the ‘Merge’ function. Such a merged ROI is then considered as a single ROI by the FiberTrak package.

- Select multiple ROIs by clicking on their names in the ROI legend with |Ctrl| being pressed.
- Right-click on either of the selected ROIs.
- Select ‘Merge’ and the current ROIs will turn into a single ROI.
The colors of the individual ROIs will now be identical while the multiple entries in the legend will be reduced to a single entry.

![Image of ROIs](image.png)

**Fig. 74:** Example: Two ROIs were defined to identify one tract that includes both, the left and the right corticospinal tract. The upper ROI (yellow) consists of two individual manually drawn ROI’s which were merged so that the left and right motor tracts are defined as one.

**Modify ROI colors**

The ROI colors can be modified using the ROI right mouse menu.

**Algorithms: Fibers and Seeded ROIs**

This section describes the algorithms for fiber calculation and Seeded ROI definition together with the involved parameters. The results of the white matter tracts will depend on the applied algorithm settings. Also the setting of the (B0) threshold has an effect.

**Adjust Threshold**

The B0-threshold identifies which pixels will be used in the fibertracking process. If the value of that pixel in the non-diffusion-weighted image (or the b=0 image) is lower than the threshold value it is excluded from processing. Tracts may thus end at this position. Note that the b=0 image can be viewed via the ‘Settings’ button (selecting ‘B0’ image).

**Fibers**

**Starting points**

There are two processes to define white matter tracts: a single ROI approach and a multi-ROI algorithm. The main difference between the two approaches relates to the starting points from which fibers are displayed.

*In case of a single ROI*

Only the pixels within this single ROI will be used as starting points to find fiber bundles. Tracts will be displayed immediately and the ROI will not be saved or displayed.
With multiple ROIs

The ROIs are the criteria for newly created bundles. Only fiber tracts that pass through all defined and visible ROIs will be shown. Note that hidden ROIs will not be considered. In order to find all the bundles two sets of starting points are used: all pixels within the ROIs and pixels within and around obtained fibers.

End / Stop fibertracts

Each fibertract will be extended until one of the following criteria is no longer met.

Minimum FA

- As soon as the FA is smaller than the threshold value the tract will no longer be continued.

Maximum Angle Change

- When the tract has a too high curvature the tract will no longer be continued.

Minimum length

- Fibers shorter than this minimum length will be discarded.

NOTICE

For existing tracts, the settings can be changed by using the Fiber Legend right mouse menu ‘Fiber Algorithm’ and modify the settings for each specific tract.

Optimum Settings for FiberTrak algorithm

It is difficult to define the best settings for the fibertracking. They depend on the actual quality of the data, the curvature of the expected tracts, and many other qualities of the underlying data. For testing, one could change the chosen algorithm settings for a given tract by pressing the right-mouse-button on the fiber and change settings in the given window. Lowering the FA and enlarging the Angle options will yield more fibers. This should only be done as long as the resulting tracts are shown as a coherent fiberbundle. Erroneous fibers will be shown when these values are too low.

Seeded-2D and Seeded-3D ROI

The size of seeded ROIs also depends on the parameters

- Minimum FA
- Max. Angle Change [%]

NOTICE

For new tracts or new seeded ROIs, these settings can be changed via ‘Algorithm Settings’ from the FiberTrak menu.
NOTICE
For new seeded ROIs, the size of the ROIs depends on the parameters Minimum FA and Maximum Angle Change. These settings can be changed via the ‘Settings’ icon from the FiberTrak toolbar.

Colors: Fibers and ROIs
It is possible to change the colors of new or existing ROIs and fibers.

Define initial colors
The initial values will be used for every FiberTrak session.
• Click on the ‘Settings’ icon of the FiberTrak toolbar.

Change colors for current FT session
• Select ‘ROI Colors’ or ‘Fiber Colors’ either/or
  – from the right mouse menu of the Fiber legend or the ROI legend.
  – from the FiberTrak menu (item belonging to ‘ROI settings’).
See section ‘Change the ROI color’ for more information.

Statistics: Fibers, ROIs and current voxel
Statistical information concerning fibers, ROIs and the current voxel is provided in the Fiber Statistics window.
This window can be accessed in two different ways:
► Click on the arrows symbol within the fiber legend.
  Clicking on the mirrored arrow symbol closes the statistics window again.
OR:
► Select ‘Layout’ / ‘Show Statistics’ from the FiberTrak menu.
To display Fiber and ROI Statistics

► Click on either of the tabs.
  The current voxel statistics show the values of ADC, FA etc. for the voxel at the pointer’s position.

Results
The following results per fiber, ROI (each identified by name) or voxel are shown. Note that for various statistics the result is given as the average plus or minus its standard deviation.
FA value
• Average FA value for current fiber, ROI or voxel.

**ADC value**

• Average ADC value \([10^{-3} \text{ mm}^2/\text{s}]\) for current fiber, ROI or voxel.

**Voxels**

• Number of voxels included in current ROI or fiber where the voxel size is equal to the original reconstructed DTI dataset.

**Lines**

• Number of lines included in current fiber.

**Length [mm]**

• Length of current fiber.

**Coordinates [mm] (LPH)**

• Coordinates of current voxel with respect to the patient frame where L stands for Left, P for Posterior and H for Head. The LPH frame has the three axis in the Left-Right, Posterior-Anterior and Head-Feet direction respectively.

**Eigenvalues: primary, secondary, tertiary**

• The Eigenvalues \([10^{-3} \text{ mm}^2/\text{s}]\) are the apparent diffusion coefficients along the preferred diffusion direction (primary) and two slower diffusion directions (secondary and tertiary). The direction of these three principle diffusion directions (PDD) are given with respect to the LPH patient frame. The LPH frame has the three axis in the Left-Right, Posterior-Anterior and Head-Feet direction respectively.

**Save Statistics**

The statistics can be saved in a file for further processing. This can be done via ‘Save Statistics’ which is available

• in the FiberTrak menu.
• in the right mouse menu in the Fiber legend if the Fiber Statistics window is open.

This function saves the ‘statistics’ concerning ROIs, fibers and the current voxel in the directory ‘E:/Export’. The file name includes patient and scan name. It is a tabulated file with the extension ‘.tsv’ which can be opened by packages such as Microsoft Excel.

**IViewBOLD**

The IViewBOLD package can be used in two different ways since the package can be used in two modes:

1. The default mode is the **Real-time BOLD analysis**. The data will be analyzed as soon as BOLD scanning has started.
2. The other mode is the **Postprocessing mode** (for existing BOLD scans). In this case, the real-time data from active BOLD scans will be ignored and detailed processing and analysis can be done on existing datasets.
WARNING
Misinterpretation of the results of the IViewBold technique is possible due to several causes on the system for which operator attention and training is required.

Overlaying the resulting parameter maps from the BOLD analysis on anatomical images, is very helpful in finding the anatomical location of specific areas in the parameter maps. However the anatomical location of these areas should be verified using the source images from the dynamic scan at all times. This verification is required since various factors (like patient movement and differences in scan techniques) may disturb the geometrical correspondence between the overlaid parameter map and the anatomical image resulting in an under/over estimation of the activation area.

WARNING
For the interpretation of the displayed correlation values and its threshold, the user is referred to the literature. Interpretation is the sole responsibility of the interpreter.

Correlation of the functional images and their underlying anatomical images may be influenced by patient motion and therefore depends on the accuracy of fixation of the patient. The operator is responsible for the correspondence between the programmed paradigm and the actually applied paradigm.

WARNING
Attention is needed for operator instructions displayed on the viewing screen.

Documentation
The following paragraphs give the following information:
- User Interface
- Statistical Parametric Maps (SPMs): t-test map, Standard Deviation map, Statistical and viewing parameters
- Time-Intensity Diagram

For information about workflows, refer to chapter “BOLD imaging Workflow” on page 297, to chapter “BOLD imaging: Paradigm Handling” on page 299 and to chapter “BOLD imaging: Esys synchronization” on page 303.
User Interface

Screen layout

The IVViewBOLD package has a layout of up to four tile viewers, depending on the number of tasks performed.

In a tile viewer, the following items are displayed:

![Figure 75: Default screen layout of IVViewBOLD for a BOLD measurement running two tasks (represented in two tile viewers): a language and a motor task. These areas highlight Broca’s and the motor areas respectively.]

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Toolbar with control buttons for the parameters</td>
</tr>
<tr>
<td>2</td>
<td>SPM identification line with the statistic’s name, e.g. Left (t-test), Right (t-test, MC), STD - where MC stands for motion correction and STD for standard deviation</td>
</tr>
<tr>
<td>3</td>
<td>Images and/or SPMs in viewports</td>
</tr>
<tr>
<td>4</td>
<td>Dynamic task display: The Dynamic Task Display can be extended with the Time Intensity Diagram. See chapter “Calculate a TID” on page 299 for more information.</td>
</tr>
</tbody>
</table>

Toolbar

Besides many generic toolbar functions, the IVViewBOLD toolbar allows to create, edit and delete paradigm; and to change the viewing parameters of the Statistical Parametric Maps (SPMs). Real-time mode and Motion Correction can be enabled.
Paradigm
allows to: Select Paradigm, New Paradigm, Edit Paradigm.
See chapter “BOLD imaging: Paradigm Handling” on page 299 for more information.

(Real-Time) Mode
This function enables or disables Real-Time Mode.

NOTICE
When the IViewBOLD package is started, without a selected scan in the Thumbnail View, the package will start in real-time mode.
This is only possible for the acquisition context.

In real-time mode, a message is displayed indicating that the system is waiting for a new scan to start: "Waiting for new scan to start."

Motion
- allows to enable or disable Motion Correction.
- allows to save motion corrected series as new imaging series.

Motion Correction
- registers images with respect to the first dynamic.
- performs a rigid transformation of the volume.
- is enabled by default.
The use of Motion Correction is indicated by the abbreviation MC in the heading of a SPM view.

NOTICE
This option is not available if the loaded scan has been corrected already.

Save Motion Corrected Series
This function saves motion corrected series as new imaging series.
When this option is enabled, a complete registered series will be saved to the database the next time that the SPM’s are computed. Afterwards this option will be disabled again automatically.
Add View -> 'SPM name' (as defined in paradigm)
This function adds another tile viewer of the chosen SPM to the current layout.

Viewing
The Viewing drop-down menu is a generic menu occurring in Graphical PlanScan and all Review and Analysis packages. For more information, please refer to chapter “On Toolbars” on page 55.

Layout
• To select another screen layout.

Cluster (Size)
The SPMs provide a statistical view on whether the time intensity changes are corresponding to the applied paradigm. However, statistics do not provide an absolute answer, and it is possible that a pixel will have a high t-test value. Such spuriously activated pixels (called "false positives") can generally be found spread out over the image.

Clustering is used to identify with an even larger likelihood which areas are reacting to the applied paradigm assuming that neighboring pixels with high t-test values more robustly identify a main response.

Only pixels belonging to clusters of the entered size or larger are displayed.
A cluster is defined, after application of the threshold, as a group of pixels within a slice that are connected to each other in horizontal or vertical (not diagonal) direction. Positive and negative pixels are not considered part of one and the same cluster.

Threshold
For the ‘Standard Deviation’ statistic, only pixels with a value at or above the threshold value are displayed as part of the color overlay.
For the ‘t-test’ statistic, pixels with a value at or above the threshold value are displayed as part of the color overlay. Also pixels with a value at or below minus the threshold value are displayed if the ‘Negative Statistics’ option is checked.
Thresholds are always equal to or larger than zero.

Mask
The mask function excludes pixels from being displayed. Only pixels with intensity above the mask value are displayed. Masking is based on the pixel values of the first dynamic scan of the functional dataset.

Negative Statistics
If enabled, the negative statistics are displayed combined with the positive values in viewing the SPMs.
Generate Series

- To calculate a new imaging series with the newly generated images.

A 'Generate Series' window pops up where the name of the new series can be entered.

Settings

- To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

SPM Identification

This line indicates the type of SPM which is displayed in the tile viewer.

<table>
<thead>
<tr>
<th>SPM type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>(t-test, MC)</td>
<td>t-test statistical map calculated from a dynamic scan on which retrospective motion correction is applied</td>
</tr>
<tr>
<td>(t-test)</td>
<td>t-test statistical map</td>
</tr>
<tr>
<td>(STD, MC)</td>
<td>standard deviation map calculated from a dynamic scan on which retrospective motion correction is applied</td>
</tr>
<tr>
<td>(STD)</td>
<td>standard deviation map</td>
</tr>
</tbody>
</table>

More Functions within IViewBOLD

Adjust Blending and Threshold

This function allows to adjust the threshold and the blending (or transparency) with the mouse.

1. Right-click on a map.
2. Select 'Adjust Blending and Threshold'.
3. Drag up- and downwards to adjust the threshold.
4. Drag to the right or the left to adjust the blending.

Load anatomical reference images

You can load an anatomical scan as underlay by simply dragging it from the List View into the package.

- Only one anatomical underlay can be loaded into the package.
- You can hide the anatomical scan (per tile viewer).
NOTICE
Also MPRs (Multiple Planar Reformats) and Fiber Tracking results (2D Cross-section results only) can be used as underlay.

**SmartLine Processing**
When the paradigm is stored as part of an ExamCard and this ExamCard is executed again, the IViewBOLD package will automatically be launched with the correct paradigm: The paradigm choice is stored in the current ExamCard.

**Statistical Parametric Maps (SPMs)**
In order to assess the likelihood that certain brain areas show a signal correlation with the applied paradigm, statistical tests are performed for each voxel. This results in the Statistical Parametric Maps (SPMs).

![Statistical Parametric Maps](image)

**Fig. 78:** Statistical Parametric Maps.

The IViewBOLD package calculates the t-test map for each task and if required also the Standard Deviation map.
t-test map

Statistical Parametric Maps (SPM) are a statistical tool to assess the statistical significance of a priori models of brain activation. As every statistical tool, SPMs cannot provide certainty of localization of brain function.

The SPMs are based on the General Linear Model (GLM). The GLM assumes that time intensity pattern of a pixel can follow certain predefined patterns. These are for example:

1. a general offset (the "average" signal of brain tissue)
2. a linear signal change in time
3. a time pattern following the applied instructions (paradigm)

The contribution of all these different sources of temporal variance, either noise or real brain function (correlating with the paradigm), can be separated with the GLM. The significance of the paradigm time pattern can be assessed with a t-test SPM at each location in the brain.

The t-test identifies the certainty with which the third component (the paradigm) is needed to explain (part of) the time intensity changes.

With a perfect non-changing time-pattern it is unlikely that the third component is needed to explain the observed signal pattern of that pixel. However, if the signal pattern of a pixel closely follows the applied paradigm it is highly likely (high t-test value) that the applied paradigm correlates to such signal changes.

Standard Deviation map

The Standard Deviation indicates the range of variation of a pixel's intensity over time.

- A small SD indicates that the pixel's intensity over time is close to the average.
- Head motion will increase the SD, especially at the edges of the brain.

Statistical and viewing parameters

For each SPM, a number of parameters is defined.

- Smoothing (Width)
- Hemodynamic Delay
- Threshold
- Cluster (size)
- Map Color Range
- Negative Statistics
- Mask
Smoothing (Smoothing width)

- is used to prepare images for the statistical calculation and reduce the noise level.
- increases the statistical power at the cost of spatial resolution.
- means that the value of every pixel is replaced with a weighted average of a group of pixels around that pixel (also referred to as kernel).
  - This kernel is a square of 1x1, 3x3 up to 9x9 pixels.
  - The pixels in the kernel are weighted using a Gaussian distribution.
- is the Full-Width-Half-Maximum (FWHM) of the Gaussian curve given in pixel sizes.

A large width will cause a broad smoothing effect. Note that smoothing is only applied for the kernel. A large width thus requires a large kernel (see table below).

<table>
<thead>
<tr>
<th>Smoothing Width</th>
<th>Yields a Kernel Size of</th>
</tr>
</thead>
<tbody>
<tr>
<td>0 - 0.6</td>
<td>1 pixel</td>
</tr>
<tr>
<td>0.7 - 1.2</td>
<td>9 pixels (3x3)</td>
</tr>
<tr>
<td>1.3 - 1.9</td>
<td>25 pixels (5x5)</td>
</tr>
<tr>
<td>2.0 - 2.7</td>
<td>49 pixels (7x7)</td>
</tr>
<tr>
<td>2.8 - 3.4</td>
<td>81 pixels (9x9)</td>
</tr>
<tr>
<td>&gt;= 3.5</td>
<td>81 pixels (9x9, cut off)</td>
</tr>
</tbody>
</table>

Hemodynamic Delay

- accounts for the physiological delay of the hemodynamic response with respect to the start of the paradigm.
- shifts the task combination by the specified number of dynamics in the calculation of the SPM.

Cluster (Size)

The SPMs provide a statistical view on whether the time intensity changes are corresponding to the applied paradigm. However, statistics do not provide an absolute answer, and it is possible that a pixel will have a high t-test value. Such spuriously activated pixels (called "false positives") can generally be found spread out over the image.

Clustering is used to identify with an even larger likelihood which areas are reacting to the applied paradigm assuming that neighboring pixels with high t-test values more robustly identify a main response.

Only pixels belonging to clusters of the entered size or larger are displayed.

A cluster is defined, after application of the threshold, as a group of pixels within a slice that are connected to each other in horizontal or vertical (not diagonal) direction. Positive and negative pixels are not considered part of one and the same cluster.
Threshold

For the 'Standard Deviation' statistic, only pixels with a value at or above the threshold value are displayed as part of the color overlay.

For the 't-test' statistic, pixels with a value at or above the threshold value are displayed as part of the color overlay. Also pixels with a value at or below minus the threshold value are displayed if the 'Negative Statistics' option is checked.

Thresholds are always equal to or larger than zero.

Map Color Range

The displayed pixels of the SPMs are colored according to gradually changing colors.

Fig. 79: Color bar and color coding with positive or negative values. With this example, a color overlay will be displayed when the t-test is larger than 3.0. At the value of 5.0 the color will be bright yellow indicating a large correlation with the applied paradigm.

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Pixels at threshold level plus color range</td>
</tr>
<tr>
<td>2</td>
<td>Pixels at threshold level</td>
</tr>
<tr>
<td>3</td>
<td>Positive values</td>
</tr>
<tr>
<td>4</td>
<td>Negative values</td>
</tr>
<tr>
<td>5</td>
<td>Pixels at minus threshold level</td>
</tr>
<tr>
<td>6</td>
<td>Pixels at minus threshold level minus color range</td>
</tr>
</tbody>
</table>

Note that the threshold only forms one end of the color range in the paradigm. This can be changed in the viewers where the SPMs are displayed.
**Negative Statistics**
If enabled, the negative statistics are displayed combined with the positive values in viewing the SPMs.

**Mask**
The mask function excludes pixels from being displayed. Only pixels with intensity above the mask value are displayed. Masking is based on the pixel values of the first dynamic scan of the functional dataset.

**Time-Intensity Diagram (TID)**
The TID can be used to review the signal response over time. If the signal response was taken from a region of interest with a high statistical value, the response should closely follow the applied paradigm.

*Fig. 80:* TID result for a paradigm of single-thumb motion, based on 2 ROIs: an average signal response of about 3% is given. The signal plateau during activation is only reached after about 2 dynamics which is related to the physiological delay in the hemodynamic response of the brain.

The display of the TID can be changed via the TID right mouse menu. The following parameters can be enabled or disabled:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Autoscale</td>
<td>Automatic scales the graphs such the graph display makes optimum use of the space available. Either for horizontal and vertical axis.</td>
</tr>
<tr>
<td>Autoscale horizontal</td>
<td>Or for horizontal axis only.</td>
</tr>
<tr>
<td>Autoscale vertical</td>
<td>Or for vertical axis only.</td>
</tr>
<tr>
<td>Relative values</td>
<td>Enables or disables display of relative values.</td>
</tr>
<tr>
<td></td>
<td>Note that the baseline is defined as the mean value of the 10% lowest values over all measured timepoints within the ROI.</td>
</tr>
</tbody>
</table>

**Neuro T2* Perfusion package**
This postprocessing package is meant to evaluate dynamic T2* studies and generate numerical and graphical results and maps.

The NeuroPerfusion tool is able to measure Index and Negative Integral (NI) using a deconvolution between the time courses of tissue signal and an Arterial-Input-Function (AIF).
WARNING
The results of deconvolution perfusion analysis may under- or overestimate the true perfusion depending on various factors.

- Inaccurate definition of the AIF. The AIF may suffer from partial-volume effects, thus it does not represent a 100% blood signal. For this reason the AIF time course will not correctly represent a 100% blood signal.
- Patient motion. Patient motion during the scan may introduce irregularities in the definition of the AIF and individual tissue signal time courses, causing deviations from the correct Index and Negative Integral.
- Temporal resolution. The temporal resolution of the measurement may be too low, causing large errors on the blood flow/volume results.
- Poor bolus injection. If the contrast bolus is too slow, the Index and Negative Integral may be incorrectly calculated.

Documentation
The following paragraphs give the following information:

- User Interface
- Results

For information about workflows, refer to chapter “Neuro T2* Perfusion Workflow” on page 306.

User Interface

Screen layout
The Neuro T2* Perfusion package has a default layout of four viewports.
Fig. 81: Screen layout of T2* Analysis package.

1. Neuro T2* Perfusion toolbar
2. Numerical results
3. Original image (with threshold mask overlaid) in the middle of the imaging volume
4. Graphical results
5. In real-time calculated Parametric map

**Toolbar**

Adjust B0 Threshold
- To adjust the B0 threshold and to enable (default) or disable the display of the threshold mask.

Setting a threshold mask will exclude background pixels from the functional map calculations. All pixels with values below the mask value will be displayed blue. Only pixels with intensity above the mask value are used for the calculations, colored areas will be excluded from the calculation.
Apply Spatial Smoothing

- To spatially smooth the resulting maps.
  Possible settings are: None (no smoothing), Weak, Medium or Strong.
  Spatial smoothing smoothes the maps ONLY, not the original images. Spatial smoothing doesn’t have any effect on the numerical results.

Apply Temporal Smoothing

- To temporally smooth the resulting maps.
  Possible settings are: None (no smoothing), Weak, Medium or Strong.

Color LUT (Look-Up Table)

- To select the color look-up table for the maps:
  When a color LUT is selected, a vertical color scale bar is shown alongside each image.
  The window width and level can be adjusted with all types of color LUT.

<table>
<thead>
<tr>
<th>Values:</th>
<th>GrayScale</th>
<th>Rainbow</th>
<th>Blue To Red</th>
</tr>
</thead>
<tbody>
<tr>
<td>Display</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Maximum</td>
<td>White</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Gray</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Minimum</td>
<td>Black</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Fitting routine

- To select a fitting routine for the calculation of the maps.
  The initial Neuro Perfusion maps are based on automated fitting routines. Three different routines are available:

1. **Gamma Variate Fitting**
   This is the automated fitting routine that is used by default. It is based on a curve fit algorithm.

2. **Model free**
   The 'model-free' algorithm does not make any assumptions about the contrast agent bolus passage through the brain. Instead it uses numerical integration to calculate the Negative Integral and the MTT, then derives the other parameters from those values.

3. **Arterial Input Function (AIF)**
Using the AIF, another algorithm (deconvolution) is used that is based on the knowledge of the Arterial Input Function to calculate the perfusion values. As such the AIF method is an alternative to the default perfusion calculation.

With the AIF calculation the curvature of the intensity curve of an arterial vessel is used to calculate the perfusion maps. This AIF needs to be identified by the user.

**Draw ROI**

- Click to start up the ROI definition.
- Draw with the left mouse button (no dragging).
- Click to end drawing and to confirm the ROI.

**Generate Series**

- To calculate a new imaging series with the newly generated images.

A 'Generate Series' window pops up. It allows to specify which images are to be generated in which manner.

**Settings**

- To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

**Viewing**

To adjust the viewing settings:

**Orientation (Viewing)**

To change the orientation of the images:

- Mirror, Flip,
- Rotate clockwise, Rotate counterclockwise,
- Reset orientation,
- Display Images in Radiological View

**Image Information (Viewing)**

- To define the amount of displayed image information:
  - minimum: no text is displayed,
  - standard: scan, image number and the scan name are displayed,
  - maximum: also the offcenter values, the window values (width and level) and the caliper are displayed.
Interpolate (Viewing)
To interpolate the image(s).

Invert Gray Level (Viewing)
- To invert the images of the current dataset (change black and white in the grayscale).

Capture ...
To capture images and save them. Type of image and destination are to be defined in the 'Capture' pop-up window. Check according to your preferences:
- 'Capture Selected Image' captures the current image.
- 'Capture ImageView' captures the current image including orange border and ImageView tab.
- 'Capture Full Screen' captures the full screen.
- 'Capture Slices' captures all slices of the current imaging series.
- 'As Displayed and Annotated' or 'As Acquired' allow to capture images with or without their window/zoom settings and annotations.
- 'Save to External Folder' allows to save the data to an external folder. In this case, it is necessary to browse to this external folder.
- 'Save to Patient Database' allows to save the data to the patient database.
- In order to include the hospital name, check the eponymic option.

The function 'Capture …' as part of Viewing is only available in Review and Analysis packages, not in Graphical PlanScan.

Save Presentation State <Ctrl+S> (Viewing)
To save a special way of presenting images.

Reload Presentation State <Ctrl+R> (Viewing)
To reload a special way of presenting images.

Reset Window (Viewing)
To reset images to original window level and width.

Reset Zoom / Pan (Viewing)
To reset images to original zoom and pan values.

More Functions within the Perfusion packages
Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.
Keyboard functions
Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

Right mouse menus
They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.

► Right-click on any image to access the right mouse menus.

Interaction Mode
• can be used to define the left mouse usage for interaction with images.

The table below lists the functions which are specific for this package. For information about the generic functions, see chapter “Generic functions for images” on page 55.

<table>
<thead>
<tr>
<th>Possible setting</th>
<th>Corresponding icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Threshold</td>
<td>![Threshold Icon]</td>
<td>Dragging the left mouse adjusts the threshold.</td>
</tr>
<tr>
<td>Draw freehand ROI</td>
<td>![Freehand ROI Icon]</td>
<td>Dragging the left mouse, a freehand ROI can be drawn. Releasing the left mouse button, the freehand ROI will be closed and the interaction mode will be set to its default setting ‘Scroll’ again.</td>
</tr>
</tbody>
</table>

View
• To select the type of image to be displayed:
  – the Source Image or
  – the Subtracted Image.

Set as Subtraction Reference
• To select a dynamic other than the first one as subtraction reference.

For subtraction purposes, by default the first dynamic (precontrast) is selected as reference. A different dynamic can be used as reference via this function.

NOTICE
This function is applicable only to T1 Perfusion.

Set as Mask
Enabled / disabled.
Modify the Results Display
1. Right-click on the graph viewport.
2. Select one of the options (see table) to modify the display.

<table>
<thead>
<tr>
<th>Function</th>
<th>Possible values</th>
</tr>
</thead>
<tbody>
<tr>
<td>Autoscale</td>
<td>Enabled/Disabled: If enabled, the graph will be automatically scaled.</td>
</tr>
<tr>
<td>Intensity</td>
<td>Enabled/Disabled: If enabled, intensity will be displayed versus time as graph (TID).</td>
</tr>
<tr>
<td>Base-log Corrected</td>
<td>Enabled/Disabled: If enabled, the graph will be base-log corrected (practically a sort of inversion). The vertical axis (intensity) uses a logarithmic scale resulting in an optimized display of the graphs.</td>
</tr>
<tr>
<td>Deconvolution</td>
<td>Enabled/Disabled.</td>
</tr>
<tr>
<td>Follow Mouse</td>
<td>Enabled/Disabled: If enabled, results per pixel will be generated where the results originate from the current pointer position.</td>
</tr>
<tr>
<td>Current Slice Average</td>
<td>Enabled/Disabled: If enabled, the graph displays the current slice average.</td>
</tr>
<tr>
<td>AIF Average</td>
<td>Enabled/Disabled: If enabled, the graph displays the AIF average.</td>
</tr>
<tr>
<td>ROI Average</td>
<td>Enabled/Disabled: If enabled, the graph displays the ROI average.</td>
</tr>
</tbody>
</table>

Results of the Neuro T2* Perfusion package
The package calculates the following results:

Graphical and numerical results
- The graphical results present a **Time-Intensity Diagram** (intensity versus time).
  - In 'Follow Mouse' mode, the graph correlates to a specific pixel and shows the intensity value (intensity) over the time for this pixel.
- The results will be provided as **parametric maps** and in a **table of results**.
  - Scrolling through the maps, the type of the map is indicated in the map’s scan type field.
  - The used values can be found in the descriptions below in brackets.

![Example of Table of Results as shown on screen. The table contains one column per ROI.](image-url)
Review and Analysis Packages

NOTICE
You can drag the columns to change their order in the table.

NOTICE
The table of results will not be updated with a new ROI column when a new ROI is drawn in AIF mode.
Right-click on the AIF graphs and select 'Proceed'. Then the results will be recalculated.

The figure below gives an overview of the T2* Analysis results.

Fig. 84: Time Intensity Diagram with definitions of NI, T0, TTP, MTT.

Mean Transit Time [s] (MTT)
- The mean transit time of the bolus.

T0 - Time of Arrival [s] (T0)
- Arrival of the contrast agent, i.e. begin of the enhancement curve.
**Time to Peak [s] (TTP)**
- Time till contrast agent bolus reaches peak intensity.

**Negative Integral (NI)**
- Calculated area under the curve.

**Index (Index)**
- Defined as NI divided by the MTT.

**NOTICE**
Using the AIF function, also the Index and the Negative Integral will be displayed with units: Index [ml/100g/min] and Negative Integral [ml/100g].

The calculation is based on known delay-insensitive deconvolution techniques and results may be influenced by incorrect assumptions in such a model.

**Delay maps with AIF algorithm**
If the AIF algorithm has been chosen for processing, the ‘Generate Series’ window provides the possibility of enabling the calculation of a ‘Delay’ map. For each pixel, the delay map shows the time between the AIF peak contrast agent concentration, and the tissue peak contrast agent concentration. The time is measured in seconds, with accuracy defined by the TR of the acquisition sequence.

**Basic T1 Perfusion package**
This postprocessing package is meant to evaluate dynamic T1 studies and generate numerical and graphical results and maps.

**Documentation**
The following paragraphs give the following information:
- User Interface
- Results

For information about workflows, refer to chapter “Basic T1 Perfusion Workflow” on page 308.

**User Interface**

**Screen layout**
The Basic T1 Perfusion package has a default layout of four viewports.
Additional T1 Perfusion package

**Fig. 85:** Screen layout of Basic T1 Perfusion package.

<table>
<thead>
<tr>
<th>1</th>
<th>Basic T1 Perfusion toolbar</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Numerical results</td>
</tr>
<tr>
<td>3</td>
<td>Original image in the middle of the imaging volume</td>
</tr>
<tr>
<td>4</td>
<td>Graphical results</td>
</tr>
<tr>
<td>5</td>
<td>In real-time calculated Parametric map</td>
</tr>
</tbody>
</table>

**Toolbar**

- **Adjust B0 Threshold**
  - To adjust the B0 threshold and to enable (default) or disable the display of the threshold mask.
  
  Setting a threshold mask will exclude background pixels from the functional map calculations. All pixels with values below the mask value will be displayed blue. Only pixels with intensity above the mask value are used for the calculations, colored areas will be excluded from the calculation.

- **Apply Spatial Smoothing**
  - To spatially smooth the resulting maps.

  Possible settings are: None (no smoothing), Weak, Medium or Strong.

  Spatial smoothing smoothes the maps ONLY, not the original images. Spatial smoothing doesn’t have any effect on the numerical results.
Color LUT (Look-Up Table)

- To select the color look-up table for the maps:

When a color LUT is selected, a vertical color scale bar is shown alongside each image. The window width and level can be adjusted with all types of color LUT.

<table>
<thead>
<tr>
<th>Values:</th>
<th>GrayScale</th>
<th>Rainbow</th>
<th>Blue To Red</th>
</tr>
</thead>
<tbody>
<tr>
<td>Display</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Maximum</td>
<td>White</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Gray</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Minimum</td>
<td>Black</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Draw ROI

- Click to start up the ROI definition.
- Draw with the left mouse button (no dragging).
- Click to end drawing and to confirm the ROI.

Generate Series

- To calculate a new imaging series with the newly generated images.

A 'Generate Series' window pops up. It allows to specify which images are to be generated in which manner.

Settings

- To adjust settings in the 'Settings' window, in most packages: display, stacks and propagation settings.

Viewing

To adjust the viewing settings:

Orientation (Viewing)

To change the orientation of the images:

- Mirror, Flip,
- Rotate clockwise, Rotate counterclockwise,
- Reset orientation,
- Display Images in Radiological View
Image Information (Viewing)

- To define the amount of displayed image information:
  - minimum: no text is displayed,
  - standard: scan, image number and the scan name are displayed,
  - maximum: also the offcenter values, the window values (width and level) and the caliper are displayed.

Interpolate (Viewing)
To interpolate the image(s).

Invert Gray Level (Viewing)

- To invert the images of the current dataset (change black and white in the grayscale).

Capture ...
To capture images and save them. Type of image and destination are to be defined in the 'Capture' pop-up window. Check according to your preferences:

- 'Capture Selected Image' captures the current image.
- 'Capture ImageView' captures the current image including orange border and ImageView tab.
- 'Capture Full Screen' captures the full screen.
- 'Capture Slices' captures all slices of the current imaging series.
- 'As Displayed and Annotated' or 'As Acquired' allow to capture images with or without their window/zoom settings and annotations.
- 'Save to External Folder' allows to save the data to an external folder.
  In this case, it is necessary to browse to this external folder.
- 'Save to Patient Database' allows to save the data to the patient database.
- In order to include the hospital name, check the eponymic option.

The function 'Capture ...' as part of Viewing is only available in Review and Analysis packages, not in Graphical PlanScan.

Save Presentation State <Ctrl+S> (Viewing)
To save a special way of presenting images.

Reload Presentation State <Ctrl+R> (Viewing)
To reload a special way of presenting images.
Reset Window (Viewing)
To reset images to original window level and width.

Reset Zoom / Pan (Viewing)
To reset images to original zoom and pan values.

More Functions within the Perfusion packages
Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

Keyboard functions
Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

Right mouse menus
They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.
- Right-click on any image to access the right mouse menus.

Interaction Mode
- can be used to define the left mouse usage for interaction with images.

The table below lists the functions which are specific for this package. For information about the generic functions, see chapter “Generic functions for images” on page 55.

<table>
<thead>
<tr>
<th>Possible setting</th>
<th>Corresponding icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Threshold</td>
<td>![Threshold Icon]</td>
<td>Dragging the left mouse adjusts the threshold.</td>
</tr>
<tr>
<td>Draw freehand ROI</td>
<td>![Freehand ROI Icon]</td>
<td>Dragging the left mouse, a freehand ROI can be drawn. Releasing the left mouse button, the freehand ROI will be closed and the interaction mode will be set to its default setting ‘Scroll’ again.</td>
</tr>
</tbody>
</table>

View
- To select the type of image to be displayed:
  - the Source Image or
  - the Subtracted Image.

Set as Subtraction Reference
- To select a dynamic other than the first one as subtraction reference.
For subtraction purposes, by default the first dynamic (precontrast) is selected as reference. A different dynamic can be used as reference via this function.

**NOTICE**
This function is applicable only to T1 Perfusion.

**Set as Mask**
Enabled / disabled.

**Modify the Results Display**
1. Right-click on the graph viewport.
2. Select one of the options (see table) to modify the display.

<table>
<thead>
<tr>
<th>Function</th>
<th>Possible values</th>
</tr>
</thead>
<tbody>
<tr>
<td>Autoscale</td>
<td>Enabled/Disabled: If enabled, the graph will be automatically scaled.</td>
</tr>
<tr>
<td>Intensity</td>
<td>Enabled/Disabled: If enabled, intensity will be displayed versus time as graph (TID).</td>
</tr>
<tr>
<td>Base-log Corrected</td>
<td>Enabled/Disabled: If enabled, the graph will be base-log corrected (practically a sort of inversion). The vertical axis (intensity) uses a logarithmic scale resulting in an optimized display of the graphs.</td>
</tr>
<tr>
<td>Deconvolution</td>
<td>Enabled/Disabled.</td>
</tr>
<tr>
<td>Follow Mouse</td>
<td>Enabled/Disabled: If enabled, results per pixel will be generated where the results originate from the current pointer position.</td>
</tr>
<tr>
<td>Current Slice Average</td>
<td>Enabled/Disabled: If enabled, the graph displays the current slice average.</td>
</tr>
<tr>
<td>AIF Average</td>
<td>Enabled/Disabled: If enabled, the graph displays the AIF average.</td>
</tr>
<tr>
<td>ROI Average</td>
<td>Enabled/Disabled: If enabled, the graph displays the ROI average.</td>
</tr>
</tbody>
</table>

**Results of the Basic T1 Perfusion package**
The package calculates the following results:

**Graphical and numerical results**
- The graphical results present a **Time-Intensity Diagram** (intensity versus time).
  - In 'Follow Mouse' mode, the graph correlates to a specific pixel and shows the intensity value (intensity) over the time for this pixel.
- The results will be provided as **parametric maps** and in a **table of results**.
  - Scrolling through the maps, the type of the map is indicated in the map's scan type field.
  - The used values can be found in the descriptions below in brackets.
**Fig. 86:** Example of Table of Results as shown on screen.

The figure below gives an overview:

**Fig. 87:** Results.

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SI</td>
<td>Signal intensity</td>
</tr>
<tr>
<td>t</td>
<td>Time</td>
</tr>
<tr>
<td>S0</td>
<td>Initial intensity</td>
</tr>
<tr>
<td>S1</td>
<td>Peak intensity</td>
</tr>
<tr>
<td>T0</td>
<td>Time of Arrival (time of initial intensity)</td>
</tr>
<tr>
<td>T1</td>
<td>Time of peak intensity</td>
</tr>
<tr>
<td>WO</td>
<td>Wash-Out Rate</td>
</tr>
<tr>
<td>WI</td>
<td>Wash-In Rate</td>
</tr>
<tr>
<td>TTP</td>
<td>Time to Peak</td>
</tr>
<tr>
<td>BrevEnh</td>
<td>Brevity of Enhancement</td>
</tr>
<tr>
<td>Relative Enhancement [%] (RELENH)</td>
<td></td>
</tr>
</tbody>
</table>
Review and Analysis Packages  

Basic T1 Perfusion package

- The signal enhancement of a pixel of certain dynamic relative to that same pixel in the reference dynamic. The reference dynamic is normally the first, pre-contrast dynamic. The reference dynamic can be set to another dynamic via the right mouse menu function ‘Set as Subtraction Reference’.

\[
\text{Relative Enhancement} = \left[ \frac{I(D)}{I(D_{\text{ref}})} - 1 \right] \times 100
\]

**Fig. 88: Formula**

- where \(I(D)\) stands for pixel intensity of current dynamic and \(I(D_{\text{ref}})\) stands for pixel intensity of reference dynamic.

**Maximum Enhancement (MAXENH)**
- Difference between peak intensity \(S_1\) and \(S_0\).

**Maximum Relative Enhancement [%] (MAXRELENH)**
- Maximum of all relative enhancements over all dynamics.

**T0 - Time of Arrival [s] (T0)**
- Arrival of the contrast agent, i.e. begin of the enhancement curve.

**Time to Peak (TTP)**
- Time between T0 and the time of peak intensity (T1).

**Wash-In Rate [l/s] (WASHIN)**
- Maximum slope between T0 and time of peak intensity T1.

\[
\text{Wash-In} = \text{Maximum}\left[\frac{I(D) - I(D-1)}{T}\right]
\]

**Fig. 89: Formula**

**Wash-Out Rate [l/s] (WASHOUT)**
- Maximum slope between time of peak intensity T1 and the end of the measurement.

\[
\text{Wash-Out} = \text{ABS}\left(\text{Maximum}\left[\frac{I(D) - I(D-1)}{T}\right]\right)
\]

**Fig. 90: Formula**

**Brevity of Enhancement [s] (BREVENH)**
- Time between point of maximum wash in rate and maximum wash out rate.

**Area under the curve (AREACURV)**
- Sum of all intensities under the curve.
SpectroView

The SpectroView package is used to present spectroscopy data after processing. Single Voxel (SV) and Chemical Shift Imaging (CSI) datasets can be analyzed. SpectroView handles both time and frequency domain data presented in the following form possibilities.

- Graphs
  - Processed spectra
  - Fitted spectra
- Tables providing information on
  - Peak position including label
  - Amplitude
  - Ratios
- Metabolite images (in color overlay)
- Ratio images (in color overlay)
- Spectral grids on reference images
  - Display of user-selected subset from an array of spectra

Using the basic script tool, additional apodization and processing steps for time domain data can be performed.

Documentation

The following paragraphs give the following information:

- User Interface

For information about workflows, refer to the sections chapter “SpectroView Workflow” on page 309, chapter “SpectroView: Advanced Workflows” on page 317 and to chapter “SpectroView: Process Unsuppressed Water Data” on page 338.
User Interface

Screen Layout

Fig. 91: SpectroView layout: Left for Single Voxel (SV), right for Chemical Shift Imaging (CSI).

For wide screen consoles, the SpectroView package has a default layout of three small viewports for anatomical images and maps, one large viewport for the graph of the spectrum (spectra) and two tables.

The results table is shown below the graph.

In the viewport on the right hand side of the screen, the tabs allow to toggle between acquisition parameters, script parameters and status information.

The Status tab appears when an error has been detected after the last script has been run. It will be colored red and be brought to the front. It contains information about failing voxels where only the first 5 failing voxels are identified, followed by a "multiple errors occurred" message if more voxels failed.

The planscan images in the ‘Image Display Area’ are overlaid by the position and orientation of the single voxel or spectral grid.

SpectroView Toolbar

For easy and quick access, the most important functions can be performed via the SpectroView toolbar. Depending on the dataset (SV or CSI) being analyzed the toolbar is slightly different.

The table lists the icons used and gives an explanation:

<table>
<thead>
<tr>
<th>Corresponding icon</th>
<th>Menu item text</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Select Script</td>
<td>• Allows to select a script.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• chapter “Select a script” on page 310</td>
</tr>
<tr>
<td>Corresponding Icon</td>
<td>Menu item text</td>
<td>Description</td>
</tr>
<tr>
<td>--------------------</td>
<td>--------------------------</td>
<td>-----------------------------------------------------------------------------</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Run Script</td>
<td>• Allows to run a script.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• chapter “Run the Script” on page 312</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Edit Script</td>
<td>• Allows to edit a script.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• chapter “Scripts and script handling” on page 318</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Save Script</td>
<td>• Allows to save an edited script.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• chapter “Scripts and script handling” on page 318</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Delete Script</td>
<td>• Allows to delete a script.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• chapter “Scripts and script handling” on page 318</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Select Relevant Voxels</td>
<td>• Allows to select the voxels for result display.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• chapter “Select Relevant Voxels” on page 312</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Modify Layout</td>
<td>• Allows to modify the layout.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• chapter “Modify Layout” on page 315</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Graph Display Mode</td>
<td>• Allows to modify the display of the graph.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• chapter “Optimize spectrum display” on page 314</td>
</tr>
<tr>
<td>None</td>
<td>Select Slice</td>
<td>• Toggle between slices in multislice 2D- or 3D-SI datasets. Processing is performed on a slice by slice baseis.</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Store Processing Parame-</td>
<td>• Stores the processed FD (frequency domain) spectrum and the</td>
</tr>
<tr>
<td>ters</td>
<td>ters</td>
<td>corresponding script parameters and, in case of CSI, selected voxels to</td>
</tr>
<tr>
<td></td>
<td></td>
<td>the database. A new series name can be specified.</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Process Unsuppressed Wa-</td>
<td>• Allows to switch between the suppressed and unsuppressed data sets, if</td>
</tr>
<tr>
<td>ter Data</td>
<td>ter Data</td>
<td>a series contains unsuppressed water data.</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Expert Mode</td>
<td>• To make some advanced features appear, you need to activate</td>
</tr>
<tr>
<td></td>
<td></td>
<td>“Expert Mode”.</td>
</tr>
<tr>
<td><img src="image" alt="" /></td>
<td>Peak Editor</td>
<td>• Opens the peak editor. chapter “Customization using the Peak Editor” on page 336</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• chapter “Customization using the Peak Editor” on page 336</td>
</tr>
</tbody>
</table>
More

As part of the toolbar a More drop-down menu is available. It offers the following options:
- Delete Script
- Peak Editor
- Delete Series Preferences
- Enable CSV Output

More Functions within SpectroView

Right mouse menus and keyboard functions are available in order to facilitate the use of the postprocessing package and to offer various interaction possibilities.

Keyboard functions

Keyboard functions can be used in the same way as in other postprocessing packages, e.g. scrolling through images can be done by means of the arrow keys or the mouse.

Right mouse menus

They provide many of the functions which are also available via the menu, toolbar or which are used throughout all postprocessing packages.

► Right-click on any image to access the right mouse menus.

Right-mouse menus in SpectroView are described in this section. They are available for:
- Anatomical image (overlaid grid)
- Map
- Spectrum
  - Spectrum for CSI dataset
  - Spectrum for SVS dataset
  - Spectrum Display Options

<table>
<thead>
<tr>
<th>Available options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Show Grid</td>
<td>To show/hide the grid overlay per viewport.</td>
</tr>
<tr>
<td>Use for Underlay Image</td>
<td>To select a different anatomical underlay image.</td>
</tr>
<tr>
<td>Running Attribute</td>
<td>To select the running attribute if more attributes are present in the anatomical series.</td>
</tr>
</tbody>
</table>
Available options | Description
---|---
Select All Processed Voxels | To select all voxels that were processed with the last used script.
Settings | These options can be used in the same way as throughout the complete user interface.
Reset Window |  
Reset Zoom/Pan |  
Interpolate |  
Export Picture |  
Export Picture As |  

**Tab. 4: Anatomical image (overlaid grid)**

<table>
<thead>
<tr>
<th>Available options</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adjust blending and threshold</td>
<td>OFF</td>
<td>If selected, dragging the left-mouse up and down changes the threshold of the color overlay. Dragging the left-mouse left to right changes the opacity of the color overlay.</td>
</tr>
<tr>
<td>Show Grid</td>
<td></td>
<td>To show/hide the grid overlay per viewport.</td>
</tr>
<tr>
<td>Interpolate Maps</td>
<td></td>
<td>Allows to display map images calculated by SpectroView in non-interpolated mode (color reflects metabolite value or ratios for the corresponding voxel) or interpolated mode (colors/values are &quot;smoothed&quot; across voxel boundaries).</td>
</tr>
<tr>
<td>Display Map</td>
<td></td>
<td>Enables the display of maps.</td>
</tr>
</tbody>
</table>

Settings | These options can be used in the same way as throughout the Advanced Viewing Environment.

Reset Window |  
Reset Zoom/Pan |  
Interpolate |  
Export Picture |  
Export Picture As |  

**Tab. 5: Map**

**Spectrum**

Dependent on the selected dataset (SVS or CSI), different features are available. The tables below describe these features.

<table>
<thead>
<tr>
<th>Available options</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Show Annotation</td>
<td>OFF</td>
<td>Enables or disables the display of an abbreviated list of spectrum qualities in the upper left corner of the spectrum viewport.</td>
</tr>
<tr>
<td>Available options</td>
<td>Default</td>
<td>Description</td>
</tr>
<tr>
<td>-------------------------------------------</td>
<td>-----------------------</td>
<td>---------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>CSI Graph Annotation</td>
<td>NAA/Cr and Cho/Cr</td>
<td>Specifies which quantities are displayed in the upper right corner of each spectrum box. Choices include whatever metabolite map quantities are currently displayed in the middle and in right viewports as well as some standard peak area ratios: NAA/Cr, Cho/Cr, NAA/Cho, Cho/NAA, and (if applicable) Cho/Ct and (Cho+Cr)/Cit.</td>
</tr>
<tr>
<td>Spectrum Display Options</td>
<td></td>
<td>Allows to optimize the spectrum display. chapter “Optimize spectrum display” on page 314 for more information on the available options.</td>
</tr>
<tr>
<td>Subtract Baseline From Graph Display</td>
<td>OFF</td>
<td>Subtracts the fitted baselines from both the original and fitted spectrum.</td>
</tr>
<tr>
<td>Display Graph: x,y</td>
<td></td>
<td>To select the spectrum from voxel x,y for display only. Disabling the step switches back to the last used selection.</td>
</tr>
<tr>
<td>Display Time Domain Data for Voxel x,y</td>
<td>OFF</td>
<td>Allows inspection of the time-domain data within a pop-up window.</td>
</tr>
<tr>
<td>Graph Display Mode</td>
<td>Geometrical</td>
<td>Sets the type of display for selected spectra:</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Horizontal: displays spectra horizontally.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Stack displays spectra vertically.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Geometrical: displays spectra corresponding to the arrangement of voxels.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Compressed: displays spectra in a square or rectangle array with a minimum of blank entries.</td>
</tr>
<tr>
<td>Phase Mode</td>
<td>Modulus for CSI max. echo, Real for CSI half echo</td>
<td>Defines which part of the spectrum is displayed.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Real: real component.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Imaginary: imaginary component.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Phase: phase information.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Modulus: magnitude.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Power: modulus squared spectral signal.</td>
</tr>
<tr>
<td>Display Average</td>
<td>OFF</td>
<td>Computes and displays an average of all selected spectra in single voxel format, if enabled. The table of results will be updated to show the values of the average spectrum. Choosing this entry runs the script again for the selected set of voxels and then displays the average with fitted spectrum in single voxel format. Clicking this entry again returns to multi-voxel display, with only that spectra, that contributed to the average selected. Screen layout matches SVS layout.</td>
</tr>
<tr>
<td>Line Display</td>
<td>OFF</td>
<td>Active only for stack display. Enables or disables display of a vertical line that follows the position of the mouse, for comparing peak positions in different spectra.</td>
</tr>
<tr>
<td>Set Spectrum Limits</td>
<td>---</td>
<td>Specifies left/right values for X-axis and minimum/maximum for Y-axis.</td>
</tr>
</tbody>
</table>
### Available options

<table>
<thead>
<tr>
<th>Available options</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Display Full Width</td>
<td>OFF</td>
<td>Displays the full spectrum if enabled.</td>
</tr>
<tr>
<td>Display Full Height</td>
<td>---</td>
<td>Scales the spectrum amplitude so that the tallest peak fills the spectrum viewport.</td>
</tr>
<tr>
<td>Reset View</td>
<td>---</td>
<td>Restores default chemical shift limits and adjusts the spectrum amplitude to display its full height. Note: The default display range is defined in the selected script. An autoscale mechanism is used to zoom the spectrum to fill the entire spectrum display area.</td>
</tr>
</tbody>
</table>

**Tab. 6: Spectrum for CSI dataset**

The graph display mode is also accessible via the main toolbar. For more information on horizontal, vertical, geometrical and compressed display, refer to the section ‘Modify Layout.’

<table>
<thead>
<tr>
<th>Available options</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Show Annotation</td>
<td>OFF</td>
<td>See table above: ‘Spectrum for CSI dataset’.</td>
</tr>
<tr>
<td>Spectrum Display Options</td>
<td></td>
<td>See chapter “Optimize spectrum display” on page 314 for more information on the available options.</td>
</tr>
<tr>
<td>Subtract Baseline From Graph Display</td>
<td>OFF</td>
<td>See table above: ‘Spectrum for CSI dataset’.</td>
</tr>
<tr>
<td>Display Time Domain Data for Voxel x.y</td>
<td>OFF</td>
<td>Changes the X-Axis units to Hz or ppm.</td>
</tr>
<tr>
<td>X-axis Units</td>
<td>ppm</td>
<td></td>
</tr>
<tr>
<td>Phase Mode</td>
<td>Real for SVS</td>
<td>See table above: ‘Spectrum for CSI dataset’.</td>
</tr>
<tr>
<td>Difference Mode</td>
<td>OFF</td>
<td>Enables or disables the possibility of adding vertical lines which can serve as markers for comparison. Two nr’s for each line indicate peak position and amplitude. Dx and Dy represent the difference in position and the difference in amplitude between the selected points. The integral of the spectrum between 2 markers is displayed as well.</td>
</tr>
<tr>
<td>Set Spectrum Limits</td>
<td>---</td>
<td></td>
</tr>
<tr>
<td>Display Full Width</td>
<td>OFF</td>
<td>See table above: ‘Spectrum for CSI dataset’.</td>
</tr>
<tr>
<td>Display Full Height</td>
<td>---</td>
<td></td>
</tr>
<tr>
<td>Reset View</td>
<td>---</td>
<td></td>
</tr>
</tbody>
</table>

**Tab. 7: Spectrum for SVS dataset**

<table>
<thead>
<tr>
<th>Available options</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Show Spectrum</td>
<td>ON</td>
<td>Enables or disables the display of the original spectrum.</td>
</tr>
</tbody>
</table>
The Spectrum Display Options can be used to modify the display of the spectrum with respect to the graph and metabolite labels.

<table>
<thead>
<tr>
<th>Available options</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Show Metabolite Labels</td>
<td>ON</td>
<td>Enables or disables the display of the metabolite names in the spectrum.</td>
</tr>
<tr>
<td>Show Fitted Spectrum</td>
<td>ON</td>
<td>Enables or disables the display of the fitted spectrum.</td>
</tr>
<tr>
<td>Show Fitted Baseline</td>
<td>ON</td>
<td>Enables or disables the display of the fitted baseline.</td>
</tr>
<tr>
<td>Show Residual</td>
<td>OFF</td>
<td>Enables or disables the display of the difference spectrum.</td>
</tr>
</tbody>
</table>

**Tab. 8: Spectrum Display Options**
11 Workflows Scanning and Planning

Entering examination data

Enter examination data in two steps:

1. Enter or select the patient data. This can be done by:
   • Entering new patient data.
     For more information, see chapter “Entering ‘New Examination’ data” on page 197.
   • Entering Asian patient names.
     For more information, see chapter “Entering Asian patient names” on page 199.
   • Selecting existing patient data.
     For more information, see chapter “Select existing patient data” on page 201.
   • Selecting patient data from RIS.
     For more information, see chapter “Select patient data from RIS” on page 201.

2. Select an ExamCard.

Entering 'New Examination' data

1. From the main menu bar, select ‘Patients’ and then ‘New Examination...’.
2. Enter the examination data.
   Press the |Tab| key to proceed to the next data field or click to make a data field current.
   The active data field is identified by the pointer.
3. Click |Confirm and Proceed|.
   The highlighted examination becomes the current examination. The system switches to scan mode.
   Clicking |Enter|, the examination is added to the examination list and highlighted, but not made the current examination.
   This function can be used to enter examination data prior to the actual examination for preparation purposes.

Format of the Examination Data

• Patient name: max. 64 characters for Asian names, see next section.
• Registration ID: max. 64 characters.
• Date of birth: MM/DD/YYYY (A future date is not accepted).
  From this date, the patient’s age is calculated and displayed.
  – The format can be changed by Customer Support (Service) personnel into e.g. DD-MM-YYYY or DD-MMM-YYYY.
  – MM must be in the range of 1 to 12.
– DD must be in the range of 1 to 31.

**WARNING**
Verify that the birth date of the patient is filled-in correctly.
Sound levels may be unacceptable for patient of below 3 years of age and a warning is displayed.

- Gender: Male, Female or Phantom/Other.
- Exam name: maximum 10 characters.
- Accession number: numeric value
- Patient weight: maximum 3 digits, value not greater than 400 kg.

**WARNING**
Verify that the patient weight is filled-in correctly.
Incorrect weight leads to incorrect SAR values. SAR values are calculated based on patient weight.

**NOTICE**
Your system has been set for entering the patient weight in either kilograms or lbs.
Please contact Philips Customer Support (Service) to change the weight unit.

**NOTICE**
Enter the patient weight accurately in the correct unit to control power deposition to the patient.
Your system has been set for entering the patient weight in either kilograms or lbs. Please contact Philips Customer Support (Service) to change the weight unit. Patient weight conversion: 1 kg = 2.2 lbs; 1 lbs = 0.454 kg).

- Referring Physician: max. 30 characters
- Performing Physician: max. 30 characters
- Study Comments: maximum 30 characters
Entering Asian patient names

Your system can be set to enable entering patient names in Chinese, Japanese or Korean. This is done with the *Windows© Input Method Editor (IME)*.

Please refer to the Microsoft (MS) Windows help for more information.

When your system is set to Japanese or Simplified Chinese, entering patient names in the selected language is possible by default. For all other system languages the patient name language must be selected by changing the MS Windows input settings.

For Asian languages the 'Patient name' line consists of three fields:

- field 1 (left), name in Latin characters, maximum 64 characters.
- field 2, name in ideographic characters, maximum 30 characters.
- field 3, name written phonetically, maximum 30 characters.

Changing MS Windows input settings

Change the MS Windows input settings when your patient name language is different than your system language.

1. Press the |Windows| key on your keyboard to show the Windows task bar.
2. Select ‘Start’ -> ‘Control panel’.
3. Double-click the ‘Region and Language’ icon. The ‘Region and Language’ window is displayed.
4. Click 'Change keyboards...'.

**NOTICE**

Do not change the default input language.

5. In Installed services:
   
   Check your keyboard layout (Chinese, Japanese or Korean).

   If your keyboard layout is not present in the field click |Add...|:
   
   - On the ‘Add Input Language’ window select the input language from the top scroll list and your keyboard layout.
   
   - Confirm by clicking |OK|.

6. Confirm by clicking |OK| to close the window.
7. Click |OK| to close the 'Region and Language' window. 
   The IME is displayed on your screen. If the IME is not visible press the |Windows| key on your keyboard.
8. Select the patient name language on the IME.
9. From the main menu bar, select ‘Patients’ and then ‘New Examination...’.
10. Enter the patient name as described below.

**Entering Japanese patient names**
1. Field 1: Enter the patient name in Latin characters.
2. Field 2 and 3:
   - Open the IME (Input Method Editor) by right-click in the field and selecting |Open IME| or by shortcut |Alt|+|~|.
   - Enter the patient name.
   - Press the |Space Bar|, open the scroll list with the |arrow-down| key and select the correct writing by:
     - using the arrow keys and press |Enter|, or
     - right-click, select the correct writing with the cursor and press |Enter|.
3. Close the IME by right-click in a field and selecting |Close IME| or by shortcut |Alt|+|~|.

**Reconversion**
If an incorrect writing is chosen in field 2 or 3 it can be corrected:
- Highlight the name to be changed.
- Right-click in the field and select |Reconversion|.
- Select the new writing and press |Enter|.

**Entering Chinese names**
1. Field 1: Enter the patient name in Latin characters.
2. Field 2:
   - Open the IME (Input Method Editor) by right-click in the field and selecting |Open IME| or by shortcut |Alt|+|~|.
   - Enter the character(s).
   - Press the |Enter| key or |Space Bar| to confirm or press the |Arrow-back| key to open a list with proposed characters, select the correct character and confirm by pressing the |Enter| key.
3. Field 3: Enter the patient name phonetically in Pinyin.

**NOTICE**
To close the IME right-click in a field and select |Close IME| or shortcut |Alt|+|~|. 
NOTICE
When the IME is active click |Ctrl+Space Bar| or |shift| to switch between entering Latin or ideographic characters.

Entering Korean names
1. Field 1: Enter the patient name in Latin characters.
2. Field 2 and 3: Enter the patient name in Korean characters.

Select existing patient data
A patient whose data has already been entered into the database can be selected for scanning as follows:
1. From the main menu bar, select ‘Patients’ and then ‘New Examination...’.
2. Select a patient from the patient list
   • Clicking |Patient name| sorts the patient data in alphabetical order.
3. Click |Confirm and Proceed|.
   The selected examination becomes the current examination. The system switches to scan mode.

Select patient data from RIS
If the operators console (OC) is connected to the Radiology Information System (RIS), the data can be copied from the RIS to the OC.
1. From the main menu bar, select ‘Patients’ and then ‘New Examination...’.
2. Click 'More....' and 'RIS'.
   A new window (RIS) appears. It contains the patient’s worklist from the current day (today) and the following day (tomorrow).

NOTICE
Downloading the list can take up to a few minutes!

3. Click on a patient’s data to select.
   Only one patient at a time can be selected.
4. Click |Enter|.
   The patient entry will be transferred to the ‘New Examination’ window.
   This may be repeated until |Proceed| or |Cancel| have been clicked.
5. Click |Confirm and Proceed|. 
The patient entry will become the current examination. The RIS window will close. The system switches to scan mode.

| Cancel | can be used to close the ‘RIS’ window.

| Refresh | can be used to refresh the downloaded list from ‘RIS’.

After scanning has been ended the examination data can be marked by selecting the examination in Patient Administration and clicking:

- | Ready |, for examinations which have been completed successfully,
- | Incomplete |, for examinations which have not been completed (aborted).

A MPPS message is then sent to the RIS and the scan data also automatically stored to PACS. The MPPS (Modality Performed Procedure Step) informs a DICOM partner about what has been performed by tracking the acquisition status. A MPPS partner can for example be, a PACS or RIS.

**Combine Accession Numbers (RIS)**

The **Combine Accession Number** functionality is used to combine several studies of one patient, as scheduled on the RIS, into a single study. The rationale behind combining several study requests from RIS is based on reimbursement requirements. For example, there may be no reimbursement for a Total Neuro examination, but there is for an examination of the Spine and an examination of the HeadCNS. However, for the patient it is more convenient if the examination is performed in one go, as one examination.

When combined examinations are sent to PACS, the user has to split the examination data in the PACS to accommodate for the initial request of multiple examinations.

**Workflow**

1. In the RIS, two entries with different accession numbers are present for one patient, e.g. a Spine and a HeadCNS examination.
2. From the main menu bar, select ‘Patient’ and then ‘New Exam’.
3. Click |RIS|.
   A new window opens.
4. Select the examinations to be combined, and then click More....
   The **Worklist (RIS)** window opens.
5. When examinations are combined into one, a common examination name has to be chosen. To do so:
   Select the future common examination name from the **Procedure Setup Description** drop-down menu, in this case either: Spine or HeadCNS.
6. Perform the examination as usual.
7. After completion of the examination, select ‘Administration’ from the ‘Patient’ main menu or press |F4|.
8. Click the combined examination to make it the current examination.
Run an ExamCard

Select an ExamCard and make it the Current ExamCard

In the ExamCard Manager:

1. Select either the|Philips| or the|Hospital| database.

2. Browse to the required ExamCard:
   - Double-click on the required anatomy (first time: ExampleCards folder).
     The required anatomy folder opens, and the list of available subanatomies is displayed.
   - Double-click on the required subanatomy.
     The required subanatomy folder opens, and the list of available items (ExamCards and scan protocols) is displayed.

   ExamCards are indicated by the ExamCard icon: 📄

3. Drag and drop this ExamCard into the List View, OR hover over the ExamCard, click the green plus icon 🍃.
   In both cases, the ExamCard opens in the List View and expands so that all ExamCard items within this ExamCard are visible.

Start the ExamCard

1. Click|Start scan| to start the ExamCard.
   The survey procedure starts. The survey images will automatically be loaded into the viewports.

Plan the items of the ExamCard geometrically

1. Select suitable images for planning.
Scroll to the slice best suited for planning. Window, zoom and pan to optimize the display of anatomic structures needed for planning.

2. Double-click on an ExamCard item to enable planning.

The icon 'Being Modified' indicates the ExamCard item currently being planned or modified.

3. Move the volume, stack or slab:
   • Click on the circle in the center.
   • Drag in any direction.
     The values of the Offcenter parameters are automatically adapted.

4. Angle the volume, stack or slab:

   • Click on one of the outer squares on the mid slice.
   • Drag up- or downwards to change the angulation. The values of the Angulation parameters are automatically adapted.

5. Optional:
   • Drag the upper or lower yellow line to change the gap.
   • Press and hold [Shift], drag the upper or lower yellow line to change the number of slices.

6. Repeat the previous steps for all ExamCard geometries.

7. Click 'Accept' to accept the planning.
   Clicking 'Cancel' ends the planning session without applying the changes.

**Resume the ExamCard**

1. Click [Start scan] to resume the ExamCard.
   All of the items within the ExamCard will be performed now.

**Tabletop movement during scanning**

If an ExamCard issue requires tabletop movement for optimum isocenter positioning, a message will pop up asking if tabletop can be performed. If this is confirmed, another message will pop up indicating that the tabletop is moving automatically. In order to stop this automatic tabletop movement, click 'Stop'.
Manage ExamCards

- Select 'Manage ExamCards .' from the System menu to open this view.
- Enable the Double EC Database View by clicking the 'Toggle DB View' button.
- Browse to a folder or ExamCard in both windows.
- Drag an ExamCard from one EC folder to the other one.
- Optional: Double-click the ExamCard to edit its contents: the EC items (scan protocols, post-processing steps).

Create (and/or Edit) an ExamCard

NOTICE
The maximum number of ExamCard items is 125. The maximum number of inline postprocessing steps is 6.

Select scan protocols
1. From the main menu bar, select ‘System’ and then ‘Manage ExamCards’.
2. Select either the |Philips| or the |Hospital| database.

NOTICE
The database ‘Other’ is meant for importing and exporting.

3. Browse to the required scan protocol(s):
   - Double-click on the required anatomy.
     The folder opens, and the list of available subanatomies is displayed.
   - Double-click on the required subanatomy.
     The folder opens, and the list of available items (ExamCards and scan protocols) is displayed.
4. Click on the required scan protocol(s).
   Multiple selections are possible.
   - Scan protocols are indicated by the Scan Protocol icon:

5. Drag and drop the scan protocol(s) into List View,
   OR hover over the ExamCard, click the green plus icon ,
   OR double-click the scan protocol.
   In all cases, the scan protocol will be added to the current ExamCard in List View.

Fine-tune the ExamCard

Change the ExamCard name
- Click on the ExamCard Header.
- Right-click on the ExamCard Header and select 'Edit Name' from the context menu.
- Edit the current name or enter a new name.

Select and Deselect Items

<table>
<thead>
<tr>
<th>Selecting/Deselecting</th>
<th>Procedure</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Select one item</td>
<td>Click on the item’s name.</td>
<td>The border color of the selected item(s) will change.</td>
</tr>
<tr>
<td>Select multiple consecutive items</td>
<td>Hold</td>
<td>Shift</td>
</tr>
<tr>
<td>Select multiple individual items</td>
<td>Hold</td>
<td>Ctrl</td>
</tr>
<tr>
<td>Deselect</td>
<td>Hold</td>
<td>Ctrl</td>
</tr>
</tbody>
</table>

Fig. 94: Selected (lower row) and non-selected item upper row).

Duplicate, Copy, Cut, Paste, Delete and Move items
All these functions work on selected items only.
- Select an item first and then proceed as described below.
<table>
<thead>
<tr>
<th>Procedure</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Duplicate an item</strong></td>
<td>➤ Drag while keeping [Ctrl] pressed. The item is copied to the current ExamCard, thus generating a duplicate.</td>
</tr>
</tbody>
</table>
| **Copy an item** | ➤ Either:  
  • Press the combination of [Ctrl] and [C].  
  Or:  
  • Right-click on the EC window and select 'Copy' from the EC context menu. The item is copied to the clipboard. |
| **Cut an item** | ➤ Either:  
  • Press the combination of [Ctrl] and [X].  
  Or:  
  • Right-click on the EC window and select 'Cut' from the EC context menu. The item is removed from the current ExamCard and moved to the clipboard. |
| **Paste an item** | ➤ Either:  
  • Press the combination of [Ctrl] and [V].  
  Or:  
  • Right-click on the EC window and select 'Paste' from the EC context menu. The item is moved from the clipboard to the current ExamCard. It will be inserted after the currently selected item. |
| **Delete an item** | 1. Either:  
  • Right-click on the EC window and select 'Delete' from the EC context menu.  
  Or:  
  • Press the [Del] key. The item is deleted from the current ExamCard. Items can only be deleted if they are not yet executed (prepared, running, in reconstruction or similar). |
| **Move an item** | 1. Drag the item to the desired position. Items can only be moved if they are not yet executed (prepared, running, in reconstruction or similar). Otherwise a copy will be created. |
| **Print an item** | 1. Right-click on a sequence in the ExamCard editor.  
  2. Select 'Save Protocol to Text File'.  
  3. Open the text file with e.g. Notepad.  
  4. Print the text file. The scan protocol will be saved to a text file and can then easily be printed. |

**Assign a scan geometry to an item**

Initially a geometry named "Geo1" is assigned to a scan protocol when dragged into ExamCard.
ExamCard items with the same geometry name have the same slice orientation, the same off-centers and angulations.

1. Click on the ‘Geometry’ column to select it for editing.
2. Enter a Geometry name, edit the current name or select an existing geometry from the drop-down list.

For survey scans, the geometry name can be deleted. Doing so indicates that the scan does not need further planning and is ready to run.

**Propagate the coverage**

Scans sharing the same geometry (same geometry name) by default have

- the same number of stacks,
- the same orientation,
- each stack with identical angulations and offcenters.

Enabling ‘Propagate Coverage’, these scans do also share

- the FOV (including RFOV and fold-over direction)
- the slice coverage (volume in slice direction):
  - In 3D scans, the number of slices will be adapted.
  - In 2D scans, the slice thickness will never be touched, but only the FOV, the rectangular FOV and the fold-over direction.
  - In M2D and MS scans, it depends on the kind of scan from which the geometry has to be taken over. Refer to the table below for more informations.

The following parameters are affected by ‘Propagate Coverage’:

- Number of stacks and/or slices
- FOV in measurement, phase and slice direction
- Slice thickness and gap
- Fold-over direction and the amount of fold-over suppression
- Fat shift direction

**NOTICE**

When using ‘Propagate Coverage’, always be aware of the fact that the fold-over direction is taken over.

<table>
<thead>
<tr>
<th>Take over geometry</th>
<th>What happens?</th>
</tr>
</thead>
<tbody>
<tr>
<td>3D scan -&gt; M2D or MS</td>
<td>• The number of slices will be adapted such that the coverage of the M2D or MS scan is identical to the 3D scan.</td>
</tr>
</tbody>
</table>
Create (and/or Edit) an ExamCard Workflows Scanning and Planning

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Take over geometry | What happens?
--- | ---
M2D or MS -> M2D or MS | Number of slices
- The number of slices will always be taken over to guarantee comparable slices.

Slice thickness and slice gap
- If the slice thickness has initially been the same, it will stay the same and changes to this parameter will be taken over, i.e. increasing the slice thickness from 5 mm to 6 mm, all other scans will also increase from 5 mm to 6 mm - if their initial value has been 5 mm. The slice gap will be adapted also.
- If the slice thickness has initially NOT been the same, the slice thickness and the slice gap will be adapted to the new slice distance (distance between adjacent slice centers) where the thickness / gap ratio stays the same. I.e. changing the slice thickness from 5 mm to 4 mm, in a scan with initially 4 mm / 0.8 mm will change to 4.58 mm / 0.92 mm. This is done in such a way with respect to IR scans where typically a slice gap of 20% of the slice thickness is used.

Workflow
1. Select multiple ExamCard items with the same geometry name in order to propagate the coverage.
   To select multiple successive items, press |Shift| and click to select.
   To select multiple items, press |Ctrl| and click to select.
2. Right-click and select ‘Propagate Coverage’ from the context menu.
   A checkmark indicates that ‘Propagate Coverage’ is enabled.
3. Double-click one of the EC items (with ‘Propagate Coverage’ enabled) to open it for editing.
4. Change geometry parameters as needed.
5. Click ‘Accept’ to confirm planning.
6. Automatically all other EC items with ‘Propagate Coverage’ enabled will have the same coverage settings.

Link items (GeoLink)
For more information about GeoLink, refer to chapter “” on page 38.
1. Move the cursor over the ‘GeoLink’ column.
   The geometry field turns blue.
2. Click on the column to select it for editing.
3. Enter a letter representing the geometrically linked group, e.g. ‘X’.

Insert a user start / manual start prior to an item
1. Move the cursor over the ‘Characteristics’ column.
Blue borders appear around the geometry field.

2. Click on the column to select it for editing.
3. Click on the arrow symbol to display a drop-down menu.
4. Select 'User Start Required'.

To indicate the pause or the manual start (e.g. after an injection), the corresponding symbol appears in this column.

![Fig. 95: Inserting a user or manual start.](image)

You can also select 'Requires Manual Start |Ctrl|+|U|' from the right mouse menu, or press |Ctrl|+|U|.

**Group and Ungroup Items**

Main purpose of grouping scans is to make sure that a scan is not started before another one is planned. Group items cannot be modified after the scan has been started.

This is especially relevant for contrast uptake studies e.g. BolusTrak where the pre-contrast scan, the 2D real-time reconstructed scan and the post-contrast scan are typically grouped. In such a way, the subtraction results will be reliable due to identical pre- and post-contrast scans.

![Fig. 96: Grouped items within a MobiFlex ExamCard.](image)

**Workflow of Grouping**

1. Select multiple consecutive items.
   Instead of a border around every item, the group of items will be surrounded by one border only.

**Workflow of Ungrouping**

1. Click on the group to make it current.
   Instead of a border around the group, now every item will be surrounded by its own border.

**Split dynamics**

1. Click on the group to make it current.
2. Right-click on the ExamCard window.
   The context menu appears.
3. Select "Split".
   The current dynamic scan consisting of multiple dynamic series will be split up in single scans.
   The resulting ExamCard items cannot be ungrouped, but unsplit: right-click and select 'Unsplit'.

**Align scans**

1. Click ‘Scan Align’ on the planning toolbar in Graphical PlanScan.

**Scan Align**

- To align scans, especially with table movement to cover long anatomical areas.

This function is comparable to the imaging parameter ‘Stack Align’.

**Start the ExamCard**

1. Click |Start scan| to start the ExamCard.
   The survey procedure starts. The survey images will automatically be loaded into the viewports (when no geometry name was assigned to the survey scan).

**Plan the items of the ExamCard geometrically**

1. Select suitable images for planning.
Scroll to the slice best suited for planning. Window, zoom and pan to optimize the display of anatomic structures needed for planning.

2. Double-click on an ExamCard item to enable planning.

The icon 'Being Modified' indicates the ExamCard item currently being planned or modified.

3. Move the volume, stack or slab:
   • Click on the circle in the center.
   • Drag in any direction.
     The values of the Offcenter parameters are automatically adapted.

4. Angle the volume, stack or slab:
   • Click on one of the outer squares on the mid slice.
   • Drag up- or downwards to change the angulation. The values of the Angulation parameters are automatically adapted.

5. Optional:
   • Drag the upper or lower yellow line to change the gap.
   • Press and hold [Shift], drag the upper or lower yellow line to change the number of slices.

6. Repeat the previous steps for all ExamCard geometries.

7. Click 'Accept' to accept the planning.
   Clicking 'Cancel' ends the planning session without applying the changes.

Access the ExamCard properties

ExamCard Properties

Click on the ExamCard Properties button in the List View.

► Select either ‘General’ or ‘Push nodes’.
► For ‘General’: set the general ExamCard parameters to the appropriate value.
► For ‘Push nodes’: Select the push node for this ExamCard.

For more information about the ExamCard Properties, refer to chapter “ExamCard Properties” on page 71.
Enable or disable ‘Push to workstation’

► Right-click on the ExamCard header (name).
► Select ‘Enable Autopush to Workstation’.
   The checkmark indicates that the function is enabled.
► Optionally for the current ExamCard this function can also be enabled from the main menu bar 'Examination'.

After selecting the whole ExamCard, it is possible to deselect series. In general, pushing to a workstation is possible on ExamCard level, but also on scan level and postprocessing step level.

Resume the ExamCard

1. Click |Start scan| to resume the ExamCard.
   All of the items within the ExamCard will be performed now.
   When an item is finished, the scanner will automatically proceed with the next item in the list, if the item is planned and has the status ‘Ready to run’.

Save the ExamCard

1. Click on the ExamCard header to enable editing of the ExamCard’s name. Rename the ExamCard.
2. From the main menu bar, select 'System' and then 'Manage ExamCards'.
3. Browse to the anatomy / subanatomy folder where the ExamCard has to be saved in.
   • Double-click on the desired anatomy folder.
     The folder opens, and the list of available subanatomies is displayed.
   • Double-click on the desired subanatomy folder.
     The folder opens, and the list of preset procedures and ExamCards is displayed.
4. Select the current ExamCard by clicking on the header.
5. Drag the ExamCard into the open folder.
Alternatively:
   ► Right-click on the ExamCard in List View.
   ► Select 'Save ExamCard'.
     The ExamCard will automatically be saved in the folder 'Other'/'Saved'.

Save some items of the current ExamCard as a new ExamCard

1. Click on the ExamCard header to enable editing of the ExamCard’s name. Rename the ExamCard.
2. From the main menu bar, select 'System' and then 'Manage ExamCards'.
3. Browse to the anatomy / subanatomy folder where the ExamCard has to be saved in.
• Double-click on the desired anatomy folder.
  The folder opens, and the list of available subanatomies is displayed.
• Double-click on the desired subanatomy folder.
  The folder opens, and the list of preset procedures and ExamCards is displayed.

4. Select the several items of the ExamCard which have to be saved within a new ExamCard by clicking on them combined with pressing |Ctrl|.
   An orange frame marks the selected items.
5. Drag the ExamCard items as a new ExamCard into the open folder.

Export/Import of ExamCards

ExamCards can be exported/imported for several purposes:
1. Use/reuse of an EC or EC DB on another Philips MRI scanner.
2. Backup of the Hospital ExamCard database.
3. Availability of several EC DBs to switch between for scanning.

NOTICE
When an ExamCard or ExamCard database is to be reused on another Philips MRI scanner, always make sure that the configuration of the systems are identical. Otherwise the ExamCard(s) might not work or even provide lower quality than expected.

ExamCards can be exported/imported in two ways:
• Specific ExamCard(s), or
• The complete Hospital ExamCard database.

Export specific ExamCards

In order to export hospital ExamCards:
► Right-click on the ExamCard or ExamCards in the ExamCard database.
  (Multiple selection is possible in combination with the |Alt| or |Ctrl| key.
► Select ‘Export ExamCards...’.
► Select the directory/drive to be copied to.

Make sure that the releases are the same or newer for the system where you want to import an ExamCard to.
NOTICE
The function ‘Export to NetForum’ exports the selected ExamCard(s) to the FTP-destination E:\Export\ExamCards\*.NetForumExamCard.

Import ExamCards
In order to import ExamCards from a directory or drive,
2. Select ‘Import ExamCards...’.
3. Browse to the ExamCard which has to be imported.
4. Double-click on this ExamCard. The ExamCard will be copied into the Inbox in the ExamCards database.
5. Return to the ExamCard environment to proceed.
During import of ExamCards from the ExamCards database, geometry filtering takes place which removes the unused geometries from the ExamCard.

Export Hospital ExamCard Database
► Right-click on any of the tabs (Philips, Hospital, Other) in the ExamCards window.
► Select ‘Export ExamCard Database As ...’ from the right-mouse menu (context menu).
► Browse to the desired folder and enter a name which represents the current ExamCard database.

NOTICE
Do not use spaces or special characters in the file name.

► Click ‘Save’ to start the export procedure to the desired folder.
In the bottom row of the ExamCards window, the progress will be indicated: “Preparing for export of Database. Please wait.” “Export of Database completed.”
The ExamCard database is saved as Database Archive file in a zip file format.

Import Hospital ExamCard Database
Four slots are available for ExamCards databases. Slot 1 is reserved for the ‘Default Database’ which is the current Hospital EC database. It is greyed out and cannot be overwritten. The slots 2 to 4 can be filled with any ExamCard database. Initially these slots are empty and marked as “...”.
► Right-click on any of the tabs (Philips, Hospital, Other) in the ExamCards window.
► Select ‘Import ExamCard Database’ from the right-mouse menu.
Click on the slots where to import the database to.

Browse to the ExamCard database to be imported.

Click ‘Open’ to start the import procedure of the desired ExamCard database.

In the bottom row of the ExamCards window, the progress will be indicated: “Importing Database. Please wait.” and “Importing of Database completed.”

When importing of the database is completed, the slot will automatically be renamed to the name of the ExamCard Database. In order to switch to this database, you still need to select it by means of ‘Select Hospital ExamCard Database’.

Select Hospital ExamCard Database

- Right-click on any of the tabs (Philips, Hospital, Other) in the ExamCards window.
- Select ‘Select ExamCard Database’ from the right-mouse menu.
- Select the EC database you want to use by clicking on the corresponding slot.
  The ‘Hospital’ tab will be replaced by the selected ExamCard database.
- To return to your Hospital ExamCard database, select ‘Select ExamCard Database’ again and select ‘Default Database’ in the first slot.

Workflow ‘Add Postprocessing to ExamCard’

- Switch from the Thumbnail View to the List View.
- Start up the postprocessing package by performing one of the following actions:
  - Right-click on a suitable scan and select the postprocessing package from the right mouse menu.
    A tentative step will be visible in the ExamCard.
- Click on the ‘Generate series’ icon (while the ExamCard is running).
  The postprocessing step is added to the ExamCard.
- Close the package as usual.
- Save the ExamCard to the database.

The next time that this ExamCard will be performed, postprocessing steps will already be visible in the ExamCard.

Workflow ‘Perform Automated Processing’

- If no user interaction is required, the postprocessing step is carried out automatically as soon as the source images are available.
- If user interaction is required, double-clicking the processing step will open the package.
  This allows for customization of the parameters.
• A pause can be specified for a processing step in the ExamCard. A double-click will be necessary to open the package allowing for manual parameter adjustments.

**Workflow ‘Set up a Smart ExamCard’**

**Select an ExamCard**

1. Browse to the ExamCard that you want to make a Smart ExamCard.
2. Drag this ExamCard into the List View.

Alternatively drag scan protocols into the ExamCard window to create a new ExamCard.

**NOTICE**

For joint or extremity examinations, ensure that the ExamCard parameter ‘Laterality’ is set to left when scanning the left extremity and set to right when scanning the right extremity.

**Open the Smart Editor**

> From the Examination menu, select 'SmartExam' and then 'Show SmartGeometries'. The SmartExam Editor opens.

**Fig. 97:** Smart Editor.

<table>
<thead>
<tr>
<th>1</th>
<th>Drop-down menu for the selection of the anatomic region</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Enable/disable 'Add SmartSurvey to ExamCard' by checking</td>
</tr>
<tr>
<td>3</td>
<td>Name of the non-Smart geometry</td>
</tr>
<tr>
<td>4</td>
<td>Enable/disable SmartGeometry by checking</td>
</tr>
<tr>
<td>5</td>
<td>SmartGeometry name</td>
</tr>
<tr>
<td>6</td>
<td>Reserved for remarks like 'New Smart Geometry' or similar</td>
</tr>
</tbody>
</table>
Select the Anatomic Region
1. Click on the ‘anatomic region’ drop-down menu.
2. Select one of the anatomic regions:
   • Brain
   • Knee
   • Shoulder
   • Breast
   • Cervical spine
   • Lumbar spine

NOTICE
In case of ‘Cervical spine’ or ‘Lumbar spine’, one more column will be displayed in the Smart Editor window: the ‘Grid Snap’ column.
This ‘Grid Snap’ column only applies for spine acquisitions.

Add a SmartSurvey to the current ExamCard
A Smart ExamCard has to start with a SmartSurvey. This SmartSurvey is a dedicated 3D survey scan that covers the chosen anatomic region completely.
1. Make sure that ‘Add SmartSurvey to ExamCard’ is enabled.
   A check sign indicates that the function is enabled.
   A Smart survey scan will be added to the current ExamCard.

Convert an ExamCard geometry into a SmartGeometry
In order to convert a scan within an ExamCard into a smart scan, you can perform one of the following actions:
1. Create a new SmartGeometry
2. Assign an existing SmartGeometry to the scans
3. Convert an existing spine geometry into a SmartGeometry

<table>
<thead>
<tr>
<th>Create a new SmartGeometry</th>
<th>Assign existing SmartGeometries to scans</th>
<th>Convert spine geometries into SmartGeometries</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Enable 'Smart' by clicking on the 'Smart' entry field. A check sign indicates that the function is enabled.</td>
<td>1. Enable 'Smart' by clicking on the 'Smart' entry field. A check sign indicates that the function is enabled.</td>
<td>1. Enable 'Smart' by clicking on the 'Smart' entry field. A check sign indicates that the function is enabled.</td>
</tr>
</tbody>
</table>

1. **Enter a SmartGeometry** (in the field 'Replace with') by typing a new name. Alternatively, existing SmartGeometries can be assigned to scans.

1. Click on the 'Replace with' drop-down menu to display the existing SmartGeometries. 2. Select one of these SmartGeometries.

1. Set 'Grid Snap' to 'no' for the SmartGeometries where acquisition is always done for a the same range, e.g. in the sagittal spine.

2. Set 'Grid Snap' to 'yes' for the SmartGeometries where acquisition is done on different disc levels, e.g. the transverse spine.

► Click [Apply].

The Smart survey will be added to the current ExamCard. The geometries in the ExamCard window will be replaced.

**NOTICE**

Each SmartGeometry name should refer to a unique planning.
Use unique geometry names throughout all anatomic regions.

---

**Fig. 99:** Selecting an existing SmartGeometry from the 'Replace with' drop-down menu.
Fig. 100: Converting spine geometries into Smart spine geometries: In the upper image Smart is enabled with Grid Snap not yet defined. The message 'Set Grid Snap' is displayed as remark. In the lower image 'Grid Snap' is set to 'no' for the sagittal Smart spine geometry and to 'yes' for the transverse Smart spine geometry. Note the different Smart icons besides the new geometry name.

1 Smart icon: not level specific.
2 Smart icon: level specific.

Fig. 101: Example: After applying the changes, the geometries have been replaced by SmartGeometries and the SmartSurvey has been added to the ExamCard. Note that the T1w_TSE axial scan is level specific.

Validate a Smart ExamCard

A newly defined SmartGeometry has to be planned and executed several times before it will turn into a validated SmartGeometry and doesn’t require planning anymore. Proceed as follows:

► Start the Smart ExamCard that needs to be validated. The SmartSurvey and the reference scan will be executed automatically.
► When the SmartSurvey is completed, double-click on the EC items of the diagnostic scans to plan them.
► Plan as accurately as possible. Keep in mind that the planning will contribute to the SmartGeometry samples.
► As soon as planning is complete and confirmed, the diagnostic scans will be executed automatically.
► When scanning is finished, you can add the planned samples to the SmartGeometry database. To do so, click 'Proceed' in the pop-up window.
Optional: Replace the Non-Smart ExamCard by the new Smart ExamCard

- First open the ExamCard database.
- Then select 'Delete' to delete the old ExamCard. Click 'Proceed' to confirm.
- Rename the current Smart ExamCard to indicate that it is a Smart ExamCard.
- To save this new Smart ExamCard, drag it into the Hospital folder. This ExamCard can now be used for all similar examinations.

Workflow ‘Execute a Smart ExamCard’

A Smart ExamCard can contain Smart items in different states. Depending on the status of the Smart items, the workflow is different. This section describes:

- Smart icons indicating the status of Smart items
- Workflow ‘Smart items are in validating mode’
- Workflow ‘Smart items are validated’
- Parameters ‘Laterality’ and ‘Patient Position’
- Switch to User-Confirmation Mode

Smart icons indicating the status of Smart items

The states are indicated by Smart icons. Note that Philips delivers predefined SmartGeometries. These predefined SmartGeometries are locked and as a consequence cannot be modified or deleted. They allow immediate usage of SmartExam without the need of validating SmartGeometries.

<table>
<thead>
<tr>
<th>Icon</th>
<th>Status of the item</th>
<th>More about the status</th>
</tr>
</thead>
<tbody>
<tr>
<td>🌟</td>
<td>Smart item that is validated (enough planning examples).</td>
<td>Final status.</td>
</tr>
<tr>
<td>🌟</td>
<td>Smart item that is in validating mode (not enough planning examples).</td>
<td>Collect more planning examples to finalize the validating process.</td>
</tr>
<tr>
<td>🗒️</td>
<td>Locked SmartGeometry.</td>
<td>This Philips preset SmartGeometry cannot be deleted nor modified.</td>
</tr>
<tr>
<td>🔒</td>
<td>Locked level-specific (e.g. transverse spine) SmartGeometry.</td>
<td>This Philips preset SmartGeometry cannot be deleted nor modified.</td>
</tr>
</tbody>
</table>

NOTICE

Validated geometry databases for the SmartExam anatomic regions are provided with your system which can immediately be used.
Workflow ‘Smart items are in validating mode’

When the Smart items of the ExamCard are still in ‘validating mode’, the workflow is:
1. Select an ExamCard.
2. Start the ExamCard (to acquire survey images).
3. Plan the items of the ExamCard geometrically within the Graphical PlanScan OR fine-tune the suggested planning and confirm.
4. Resume the ExamCard.
5. When the ExamCard is finished, you are asked to add (or ‘not to add’) the samples to the SmartGeometry database.

Workflow ‘Smart items are validated’

When the Smart items of the ExamCard are ‘validated’, the workflow is:
1. Select an ExamCard.
2. Start the ExamCard (to acquire survey images).

The validated items will show up as ‘ready to run’ and all the items of the ExamCard are planned and will run automatically.
The Smart items in validating mode have to be planned.

Parameters ‘Laterality’ and ‘Patient Position’

Always ensure that the settings of the parameters ‘Laterality’ and ‘Patient Position’ correspond to the actual patient position. Otherwise SmartExam will detect inconsistencies between positioning and parameter settings, and will abort the scan.

This is especially true for knee and shoulder examinations.

**Laterality**

For knee and shoulder examinations, ensure that the ExamCard parameter ‘Laterality’ is set to left when scanning the left extremity and set to right when scanning the right extremity.

**Patient position**

For knee examinations, ensure that the knee is positioned supine when the parameter ‘Patient position’ is set to ‘supine’.

Be careful with heavy exo-rotation, since a ‘decub-right’ or ‘decub-left’ position might be detected instead of a ‘supine’ patient position.

**Switch to User-Confirmation Mode**

A validated Smart ExamCard will be executed automatically. However, it is possible to ask for user confirmation of the planning.
To do so, select 'SmartExam Tools' from the System menu, and enable 'User Confirmation Mode'.

With user confirmation enabled, the ExamCard will stop so that planning can be inspected and/or modified.
With user confirmation disabled, the system automatically confirms Smart planning.

**Workflow SmartExam Spine**

For SmartExam Spine acquisitions, two features have been introduced:

- Vertebrae labelling and
- (disc) Level specific scanning.

**Vertebrae labelling**

Vertebrae labelling has to be confirmed to allow level specific scanning.

1. Start the SmartExam Spine ExamCard.
2. When the SmartSurvey is finished, the vertebrae labelling window pops up.
3. When labelling is correct press |Proceed| to continue.
4. Adjustments can be made by clicking the ‘up’ or ‘down’ arrow
5. Check ‘Manual’ to continue with manual planning.
6. Click |Proceed| to continue.

![Vertebrae labelling window](image)

**Fig. 102:** Vertebrae labelling window.
1. Window 'Confirm Vertebrae Labelling'

2. Click 'Up' or 'Down' to fine-tune the vertebrae labelling. Check 'L6 present' if L6 exists in a patient.

3. Continue planning: Manual or Smart. This allows to switch from 'Smart' planning to 'Manual' planning or vice versa.

4. Click [Cancel] to quit without any changes.

5. Click [Proceed] to confirm the vertebrae labelling.

**Level specific scanning**

In all scans with a level specific Smart Geometry (if 'level specific' is enabled by means of a checkmark), another tab is available in the Parameter Editor: the 'smartstacks' tab.

![Fig. 103: Tabs in planning a level specific scan.](image)

Clicking on the 'smartstacks' tab, the level specific planscan user interface (UI) pops up.
1 Indication of the scan 'Geometry' (in this case: transverse)
2 Indication of the level 'Definition' (in this case: L5 - S1)
3 Schematic display of the upper spine (use scrollbar to scroll down or up) with
   • gray lines representing possible new stacks
   • red line representing defined stack
   • arrows up/down to shift the stacks up or down
4 Schematic display of the lower spine (use scrollbar to scroll up or down).
   • gray lines representing possible new stacks
   • red line representing defined stack
   • arrows up/down to shift the stacks up or down
5 Window with Guidance (in this case: Define the desired stack by selecting stacks in the schematic spine)

You can **define the disc levels to be scanned** beforehand or after scanning the high resolution sagittal scan. Both ways are described here:

**Workflow: Define the disc level(s) to be scanned beforehand**
1. In the Parameter Editor, click on the ‘smartstacks’ tab.
   The graphical planscan user interface pops up.
2. Use the scrollbar to scroll to the required disc level.
3. Click on a gray stack line to add a stack.
4. Click on a red stack line to remove this stack.
5. Click on the ‘Up’ or ‘Down’ arrow to shift the stacks up or down.
Workflow: Define the disc level(s) after scanning on the high resolution scan

1. Check the high resolution T2w sagittal scan.
2. In Planscan, drag the stacks to the desired scanning location.
3. The snapping mechanism (‘Grid Snap’) recognizes the levels automatically and snaps the transverse stacks to the required levels.
4. Resume the ExamCard.

NOTICE
During the validating phase, fine tuning adjustments can be made without snapping.

Adjust Ventilation in Bore

The MR system has a recommended ventilation level. This is a static level based on average scans and system specific conditions.
The system does not change the recommended ventilation level for e.g. high SAR scans, ambient temperature and patient weights, clothing and conditions. It is solely the responsibility of the operator to determine the level of ventilation for different scans and conditions together with the patient.

NOTICE
For interventional procedures it is advised to scan with patient ventilation switched off and in normal operating mode. Recommended room temperature is 18 - 22°C.

The ventilation in the bore can be adjusted from the UIM (see Instructions for Use volume 2), as well as from the console.

Workflow
1. Select 'Examination' and 'Adjust Ventilation in Bore...' from the System menu.
The Patient Ventilation Control is displayed.

![Patient Ventilation Control]

Fig. 105: Patient Ventilation Control with the text: Current patient ventilation level. Level 5 is recommended. Use the <= and => buttons above to modify the patient ventilation level. Refer to the Instructions For Use for information about patient ventilation. |Proceed|
2. This control displays the current ventilation level and the recommended level.

3. Manipulate the current level by clicking the plus and minus buttons.

4. Click 'Proceed' to close the window.
   Note that a Patient Ventilation Warning is displayed if the patient ventilation level is below the recommended level and a scan is started:

![Patient Ventilation Warning](image)

**Text displayed in warning dialog**

The patient ventilation is below the recommended level.
Press <Modify...> to modify the patient ventilation.
Refer to the Instructions For Use for information about patient ventilation.
Press <Proceed> to proceed with the current patient ventilation level
Press <Cancel> to cancel the scan.

The Patient Ventilation Warning requires a deliberate action by clicking one of the following buttons:

- **Modify...**
  The Patient Ventilation Control is displayed again to modify the ventilation to the recommended level.

- **Cancel**
  The scan is not started. The Patient Ventilation Warning disappears.

- **Proceed**
  The set ventilation level is accepted. The Patient Ventilation Warning disappears and a scan can be started.

**NOTICE**

Once Proceed is clicked and ventilation is below recommended level, the set level is accepted for the current scan and all subsequent scans of the current patient.
The Patient Ventilation Warning will not be displayed anymore for this patient.
With a new patient and ventilation set below recommended level, the Patient Ventilation Warning is displayed again when a scan is started.
Delayed reconstruction

In general, MRI scans are automatically reconstructed immediately after their acquisition. However the automatic reconstruction can be switched off, and a manual reconstruction can be performed instead.

Such a delayed reconstruction can be performed at anytime, and the reconstruction parameters can be defined according to the user’s personal preference. This offers the possibility to generate multiple imaging series with different reconstruction settings and compare them on completion.

Parameters that can be defined during the delayed reconstruction are e.g.:

- Uniformity,
- Recon voxel size,
- Reconstruction matrix,
- Preset window contrast,
- Multichannel images.

Delayed reconstruction is integrated in the ExamCard overview.

A prerequisite for delayed reconstruction is that raw data are saved during scanning.

Workflow

► Make sure that the parameter ‘Save raw data’ is enabled in the scan where delayed reconstruction is to be used.

This postproc parameter can be set to 'Yes' or 'No'. ‘Yes’ will save the raw data and allow for delayed reconstruction.

► After scan completion, right-click on the scan in the List View.

► Select 'Reconstruction' and 'Delayed Reconstruction' from the right-mouse menu.

A Delayed Reconstruction processing step is automatically added to the current ExamCard under the corresponding scan.
Delayed reconstruction Workflows Scanning and Planning

Fig. 107: Adding a Delayed Reconstruction processing step to the current ExamCard. 1: Scan to add delayed reconstruction to. 2: (Extract of) Right-mouse menu. 3: ‘Reconstruction’ option. 4: ‘Delayed reconstruction’ option. 5: Delayed Reconstruction processing step is added to the ExamCard.

- Rename the delayed recon processing step so that it can easily be identified.
- Double-click the delayed recon processing step.
  The Delayed Recon Parameter Editor opens with the subset of parameters available for delayed reconstruction.
- Edit the parameters as usual in the ExamCard environment.
  The user interface is identical to the ExamCard Parameter Editor.
- Click 'Accept' to confirm the parameters.
- To start the reconstruction, click the 'User Specified Pause' icon in the delayed recon processing step.
  Delayed reconstruction is performed as background process and doesn’t affect the performance of the system, e.g. the acquisition of further scans.

Fig. 108: Click 'User Specified Pause' icon to start the reconstruction. 1: click the icon first, 2: then click the empty space under the arrow.

Reuse of Delayed Reconstruction processing steps
Once a Delayed Reconstruction processing step is defined, it can easily be reused:
- Simply drag and drop it to another scan in the same ExamCard.
- Or right-click on the source to copy this step,
and then right-click on the destination scan to paste it.

It is recommended to rename copied processing steps immediately for ease of identification.

**NOTICE**

You can also copy/paste or drag/drop a delayed recon processing step to another ExamCard in the Hospital database.

### Arterial Spin Labeling (ASL)

Arterial Spin Labeling (ASL) is a method to obtain brain perfusion imaging without the use of contrast agent. ASL uses magnetically labeled blood water in the arterial blood stream as an endogenous trace.

The two major parts of ASL are labeling/control. Perfusion images are generated by subtracting the control images from the label images. Perfusion estimation relies on the signal changes (1%-2%).

Additionally it is possible to measure the perfusion at multiple time points after labeling, this is called multiphase ASL. In this case the same area is imaged multiple times after labeling (or control) and multiple perfusion images result.

### Applications

Typical applications are cerebral perfusion studies.

### Properties of an ASL scan

An ASL scan consists of the following parts:

1. saturating the imaged area (pre- and postsaturation)
2. labeling / control (inverting spins)
3. read-out, possibly repeated multiple times
4. repeating steps 1-3 to gain SNR

![ASL complete sequence](image)

**Fig. 109:** ASL complete sequence. 1: Presaturation, 2: Labeling / Control, 3: Postsaturation, 4: Read-out, TD1-TD4: Trigger Delay 1 - 4, Ph1-4: Phase 1 - 4, Phint: Phase Interval, CycDur: Cycle Duration.
Labeling
During labeling, the spins are inverted by a single hyperbolic secant RF pulse. During control, two RF pulses are used with the total power being equal to the RF pulse used during labeling. After labeling, the imaged area can be saturated again using a simple single RF pulse. The area which needs to be labeled is depicted by the white slab visible on screen when ASL is enabled.

Read-out
After a delay time in which the labeled spins perfuse into the brain, any imaging technique can be used. Usually, a fast technique such as single-shot EPI is used; this can be repeated multiple times using the same mechanism as used in multiphase cardiac imaging. This is controlled on the motion page by the parameter “Multiphase ASL”, where the number of phases and the phase interval can be specified. The total label or control experiment duration is controlled by the parameter “Cycle duration”.

Postprocessing
Evaluation of the scan can be done with the ‘Image Algebra’ package. New imaging series can be easily generated and stored. Analyses are stored in the current ExamCard and performed automatically when the ExamCard is executed again. For more information, see chapter on ExamCards, Inline Processing.

Workflow ASL

MultiSlice Single-Phase or MultiSlice MultiPhase ASL
1. Start a normal survey (and reference) scan.
2. Select a single-phase or a multiphase ASL protocol.
3. Plan the scan.

Fig. 110: Planning ASL scan. The white band is the label area, a thickness of 100 mm to 130 mm is recommended. A label gap of 20 mm to 25 mm is fine.

4. Start the ASL scan.
5. After completion, select the ASL scan and open the DynamicView / ImageAlgebra package.
6. Select the ‘ASL subtraction’ function to calculate ‘Labeled’ image type minus ‘Control’ image type.

Fig. 111: Select the algorithm from the drop-down menu, in this case ASL subtraction (Example of screen in English).

The images from the ASL sequence are automatically loaded in the corresponding viewports. All the phase and slice images are automatically loaded with their default viewing settings.

Fig. 112: Layout of ASL subtraction window (right) with Image Algebra control area for different scans (left).

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
</table>
| 1 | Image Algebra control area.  
   This control area looks slightly different a MultiSlice SinglePhase scan (see 1a) compared to a MultiSlice MultiPhase scan (see 1b). |
| 2 | Preview: Perfusion image = Label image (B) minus Control image (A) |
| 3 | Control image type = A |
| 4 | Label image type = B |
NOTICE
Do NOT change the setting of any of the corresponding sliders.
ASL subtraction comes up with the correct settings for weighting factor, slices and phases.

1. Click |Generate| to generate ASL-subtracted image series.
2. Select the newly generated series from the Thumbnail View to view the data.

Examples of ASL perfusion images

Fig. 113: Multiphase ASL scan (FFE-EPI/ Perfusion) where s stands for the slices and p for the phases.
Fig. 114: FE-EPI/Perfusion single-phase scan.

BolusTrak Workflow

BolusTrak is a contrast-enhanced MRA technique. It provides fluoroscopic information of the vessels. It needs to be combined with a CE-MRA scan. The BolusTrak functionality offers the possibility to track the bolus and immediately start the CE-MRA scan on bolus arrival. Part of the realization are real-time reconstruction and viewing.

1. Select a BolusTrak ExamCard.
2. Plan this ExamCard.
3. Start the ExamCard.
   Preparation-only scan or Pre-contrast scan will be performed.
   Then the ExamCard will pause.
4. Start the contrast agent injection as a bolus simultaneously with the 2D real-time reconstructed scan. |Resume| the ExamCard to do so.
5. Use the ‘Fast Next Scan’ functionality
   • to interrupt the 2D real-time reconstructed scan.
   • to start the post-contrast scan at bolus arrival in vessels of interest.
6. Postprocessing, e.g. subtraction of pre-contrast mask, Maximum Intensity Projection (MIP) or TID.

The total procedure can be run first without contrast agent (this will take only 1 minute) to make the patient familiar with the examination procedure.
Workflows MobiTrak and MobiFlex

MobiTrak and MobiFlex are CE-MRA techniques using moving table technique with slowly infused contrast agent.

Two acquisitions will be performed per station:
- pre-contrast (mask)
- post-contrast (contrast-enhanced)

The pre-contrast scan will be subtracted from the post-contrast scan to eliminate signal from background tissue.

MobiTrak and MobiFlex provide a large coverage in FH-direction as multiple overlapping stations in FH-direction will be scanned sequentially which have been planned as a single volume.

Applications
Peripheral vessels from abdominal aorta down to pedal arch.

Patient safety

NOTICE
Patient observation during table motion must never be neglected.

NOTICE
If patient safety is endangered during table top movement, the tabletop must be stopped immediately.
In a MobiTrak examination the tabletop will move over large distances. Extra attention must be paid to guarantee patient safety.

WARNING
Before starting a scan which initiates tabletop movement, always check that nothing can get caught or hit during tabletop movement.
Check patient, patient extremities, clothing, equipment and accessories. Guide cables and intravenous lines. This especially applies when Transmit/Receive coils are used, which are connected to the T/R socket below the left UIM.

All instructions listed below must be followed strictly:
- Use ankle, knee and arm support in a correct manner.
- Secure intravenous lines to avoid lines being caught during table movement.
• Connect patient alarm and hand it to the patient.
• Remove all RF coils from the tabletop before a MobiTrak/MobiFlex scan is started.

**Table movement**

It is important that all stacks are scanned in the isocenter of the magnet to avoid parts of the FOV getting cut off by the shutter. Therefore table movement between stacks is mandatory. It can be initiated by:

- |Proceed| on the operator’s console/keyboard.
- |Travel to scanplane| at the operator’s console.
- |Start scan| at the magnet.
- With the tumble switch at the magnet.

**NOTICE**

Table top movement can be stopped by pressing |Stop scan|.
Table top movement can be resumed by pressing |Proceed| or |Travel to scanplane| or |Start scan| again.

**Total table stroke is computed at the start of the scan**

The total travel distance for the tabletop to reach optimal positions for all scans and all stacks, is computed at the start of the ExamCard and displayed on the Scan safety message(s) screen. If the table can not move in far enough for one of the stacks to reach the position for optimal image quality, the scan will not start. The operator has to adjust the feet-head offcenter of stack A or reposition the patient.

**Workflow MobiTrak**

1. Patient preparation and patient and coil positioning
2. Transverse survey scan in three stacks
   - Table movement during stacks.
   - Automatically calculated MIPs.
3. Contrast bolus timing scan and test bolus injection
   - Dynamic coronal scan (for visualization of entire aorta) started together with the test bolus injection.
   - To be planned just before the abdominal aortic bifurcation. Use the |Reset| geometry function.
   - To determine the acquisition delay between the contrast injection and the second dynamic scan. It equals the contrast bolus arrival time just before the abdominal aortic bifurcation.
4. Perform MobiTrak scan first dynamic
   - Acquires pre-contrast images in three stacks with table movement.
   - To be used for subtraction.

5. Start of contrast agent infusion

6. MobiTrak scan second dynamic
   - To be started after the acquisition delay (see contrast bolus timing scan).
   - Acquires contrast-enhanced images in three stacks with table movement.

**NOTICE**
Always allow automatic table movement.
In this way, the scan will be started as soon as the table has reached the optimal position without prompting for an additional |Proceed|.

7. Postprocessing MobiFlex
   - **MIP calculation of the three stacks and combination of the MIPs.**

**NOTICE**
Undo subtraction can be done by means of a weighting factor of +1 after a subtraction having been performed with a weighting factor of -1.

**MobiTrak scan**
The MobiTrak scan has the following characteristics:
   - Two dynamic scans, each consisting of three stacks: Stack A: lower legs, Stack B: upper legs, Stack C: abdomen. Abdominal stack with breathhold commands.
   - To be planned on sagittal MIP’s of survey scan. Easiest is to align the stacks and define a stack overlap.
   - Scan time per stack: 20 s to 30 s. If scan time has to be reduced, reduce the number of slices and increase the slice thickness.

**Workflow MobiFlex**

**MobiFlex ExamCard**
The table summarizes the scans of a typical MobiFlex ExamCard with e.g. their item properties and their GeoLinks.
<table>
<thead>
<tr>
<th>Scan</th>
<th>EC Item properties</th>
<th>Geo Link</th>
<th>Part of anatomy</th>
<th>Comparable to</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td>A</td>
<td>Lower Legs</td>
<td>Scan 1, dyn=1</td>
</tr>
<tr>
<td>2</td>
<td></td>
<td>A</td>
<td>Upper Legs</td>
<td>Scan 2, dyn=1</td>
</tr>
<tr>
<td>3</td>
<td></td>
<td>A</td>
<td>Abdomen</td>
<td>Scan 3, dyn=1</td>
</tr>
<tr>
<td>4</td>
<td></td>
<td></td>
<td>BolusTrak scan</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>in order to</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>track the bolus</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>arrival</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td></td>
<td>A</td>
<td>Abdomen</td>
<td>Scan 3, dyn=2</td>
</tr>
<tr>
<td>6</td>
<td></td>
<td>A</td>
<td>Upper Legs</td>
<td>Scan 2, dyn=2</td>
</tr>
<tr>
<td>7</td>
<td></td>
<td>A</td>
<td>Lower Legs</td>
<td>Scan 1, dyn=2</td>
</tr>
</tbody>
</table>

**Workflow**

1. Patient preparation and patient and coil positioning
2. Setup or select a MobiFlex ExamCard including Geometrical Links.
   - 6 scans for 3 stations (8 scans for 4 stations on 3.0T) plus a BolusTrak scan.
     - All stations need to have the same GeoLink (same bookmark behind the sequence).
   - BolusTrak scan prior to post-contrast scans (injection enabled).
   - Abdominal stack with breathhold commands.
   - Manual start for post-contrast scans.

**NOTICE**

If you like to have pre-contrast source images, integrate your subtraction postprocessing (Image Algebra) into your ExamCard. Three types of images will be available.

To do so, disable the imaging parameter ‘Immediate subtraction’ in the sequence.

3. Perform the transverse survey scan in three stacks
   - Table movement during stacks.
   - Automatically calculated MIPs.
4. Fuse the automatically calculated MIPs with MobiView.

5. Plan the scans on fused sagittal MIP’s of the survey scan.
   - Use the |Scan Align| button of the ExamCards window to align the scans (comparable to ‘Stack Align’ function).
   - For shorter scan times, reduce the number of slices and increase the slice thickness.

6. Perform MobiFlex scans pre-contrast
   - Acquires pre-contrast images in three scans with table movement.
   - To be used for subtraction.

7. Perform the BolusTrak scan with the start of the contrast agent infusion.

8. Check the bolus arrival in the |Autoview| window.

9. Press 'Next Scan' upon arrival of the bolus in the abdominal aorta to abort the BolusTrak scan.
   - MobiFlex scans post-contrast are automatically started due to the ‘Fast next scan’ functionality.
   - Acquires contrast-enhanced images in three scans with table movement.

**NOTICE**
Always allow automatic table movement. In this way, the scan will be started as soon as the table has reached the optimal position without prompting for an additional |Proceed|.

10. Postprocessing MobiFlex:
    - MIP calculation of the three scans and combination of the MIPs.

**NOTICE**
Undo subtraction can be done by means of a weighting factor of +1 after a subtraction having been performed with a weighting factor of -1.

**Important: modifying the MobiFlex ExamCard**
If the MobiFlex ExamCard is modified such that the amount of data on a certain station increases too much, the message "This can lead to discontinuities between stations" might show up. This message indicates that discontinuities between stations could appear which might be visible in the fused images.

To solve this problem,
   - reduce the reconstruction matrix.
   - set the reconstruction mode from 'real-time' to 'immediate'.
Furthermore, a multiple station CE-Angio could be acquired with different resolutions at the different stations. In this case, different geometry corrections might be used which may result in slight displacements of vessels between the stations.

**Postprocessing MobiFlex**

**Calculate Multistation MIPs**

1. Select one of the pre- or post-contrast scans.
2. Click on the ‘Volume View’ button.
3. Select the left upper view port.
4. Select the 2nd dynamic (subtracted images).
5. Click on the ‘Generate series’ button in order to calculate a set of new images out of the original data set -> a new window pops up.
6. Click |Stack| to define orientation, stack type, projections, radial axis and angle, e.g. coronal orientation, radial, FH axis, 9 projections, 12 degrees.
7. Click |Propagation| and select propagations to "All stations" and "Single Axis".
8. Click |Geometry| with an "Angulation relative to: Magnet".
9. Click |Generate| to run the protocol.
10. View the resulting images.
11. Hardcopies can be performed in the usual way.

**Viewing these MIPs with MobiView**

Use the MobiView package to view these MIPs. The MobiView package is described in detail in the Total Body Imaging chapter.

Fusing multiple stations created by the MobiFlex/MobiTrak package could lead to a mismatch in the connection between the stations. The area of overlap is indicated by brackets in the MobiView application. In case of doubt, it is best to use the ‘hard cut’ fusing algorithm.

**Integration of BolusTrak with MobiTrak/MobiFlex**

With the availability of BolusTrak software, the bolus arrival time can be synchronized with the start of the 3D MobiTrak/MobiFlex scan.

**Prepare the following scans:**

1. 3D MobiTrak (no contrast)
2. 2D BolusTrak scan
3. 3D MobiTrak (contrast-enhanced)

**Set the parameters to the values as listed in the table below:**
Interactive Scanning Workflows

Interactive Scanning parameter

- Click the 'Geometry' tab to access the geometry parameter subset.
- Set the parameter 'Interactive Positioning' to 'Yes' to enable interactive scanning.

All geometries that exist in ExamCards or are entered before Interactive Scanning is started, show up in Interactive Scanning (even if all scans are deleted again before Interactive Scanning is started).

Tab. 9: Scan 1: 3D MobiTrak (no contrast)

<table>
<thead>
<tr>
<th>Parameter subset</th>
<th>Parameter</th>
<th>Required setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dyn/ang</td>
<td>CE profile order / stack</td>
<td>• Yes</td>
</tr>
<tr>
<td>Dyn/ang</td>
<td>Order for stack A,B,C</td>
<td>• low-high, low-high, low-high</td>
</tr>
<tr>
<td>Geometry</td>
<td>Stack scan order</td>
<td>• descending</td>
</tr>
<tr>
<td>Postproc</td>
<td>Reconstruction mode</td>
<td>• delayed</td>
</tr>
<tr>
<td>Postproc</td>
<td>Preparation phases</td>
<td>• full</td>
</tr>
</tbody>
</table>

Tab. 10: Scan 3: 3D MobiTrak (contrast-enhanced)

Due to the fact that the pre- and post-contrast scans are acquired in two separate scans, subtraction and MIP images of the subtracted scan are not automatically available, but have to be postprocessed by the operator after the delayed reconstruction of the pre-contrast scan is performed.

NOTICE

For successful subtraction it is important to keep all geometry offcenters identical for pre- and post-contrast scan.

Best way to ensure this is to plan the pre-contrast scan and use the copy scan function for the post-contrast scan.

Interactive Scanning Workflows
Workflow

► Start an interactive scan.
  During preparation the ‘Interactive viewer’ window pops up.
► Click |Scan pars...| in the ‘Interactive viewer’ window.
  The scan parameters window pops up.
► Change the scan parameters.
  The modified parameter settings will be used for the acquisition of the next image of the
  same scan.
► Click on |Rescan| to rescan the image or scan a new image with modified parameters.
► Store the geometry under a certain name or store an image in the patient database.
► Click |Next scan| to stop the interactive scan.
  The next scan in ListView will be started automatically and, if the ‘used geometry’ para-
  meter is set, will take over the previously stored geometry.

More about Interactive Scanning

► Right-click in the Interactive viewer window
  • To retrieve the current scan parameters and pass them to the scanner
  • To scan an image and display the new image in the current viewport.
In single mode a right-click is necessary while in continuous mode every change is applied im-
mediately.

Different ways of how to scan a new image

• By modifying the yellow intersection lines; Click/drag the offcenter and angulation handles
  of the yellow intersection line displaying intersections between images in different view-
  ports.
• By clicking |Tra|, |Sag|, or |Cor| to scan a transverse, sagittal, or coronal image through
  the offcenter of the current image.
• By clicking |Orthog. flip| to scan an image orthogonal to current one.
• By clicking |Tilt| and define the tilt ‘Angle’ to scan a tilted image.
• By clicking |Pull/push| and define the step size in the ‘Step’ field (in mm) to scan a parallel
  image.
• By clicking |Inplane transf| to scan a translated or rotated image.
  – Move the red cross to where the offcenter of the next image should be.
  – Rotate the cross to define the rotation for the next image.
• By using 3-point Planscan: Click |P1*| and defining the P1 point. Drag P1 for repositioning.
  – Click |P2*| and |P3*| to define P2 and P3 in a similar way.
– Click |Scan| to scan an image through P1, P2 and P3 with its offcenter in the centre of gravity of the triangle.

**Store geometry for later use**

► Click ‘geom’ |Store|.

All geometries will be stored in ExamCards. An asterisk after the name indicates that a geometry was already stored. If the slot was already filled it will be overwritten.

**Scan with stored geometry**

► Select a geometry.

**Store image**

► Click ‘image’ |Store| to store the current image with its geometry, window and view settings etc. (without graphical overlays) in interactive memory.

The image is also stored in the patient database (within current scan).

**Measure the distance between two points**

► Click |Distance|, define two points on the same or on different images.

**Display conventions**

**Radiol. view**

• Corresponds to looking towards the lower left front side of the patient:
  – Transverse image: "A" near the top,"L" on the right,
  – Sagittal image: "H" near the top, "P" on the right,
  – Coronal image: "H" near the top, "L" on the right.

**Ignore view**

• Results in a view "as close as possible" to the previous image.
  Useful when rotating an image plane to prevent a sudden ‘flip’ of the orientation.

**User defined view**

• Means that viewing directions and in-plane rotations can be redefined through the mirror and rotate buttons.

**Intersection mode button**

• Allows the user to toggle between three different modes:
  – Current image shown on other images (default mode). Each non-current image is overlaid with a yellow intersection line, indicating how the current image intersects the non-current image.
  – No intersection lines shown.
  – Non-current images shown on current image.
The current image is overlaid with at most three intersection lines in different colors indicating how the current image is intersected.

**Redefine the patient coordinate system with |Rotate view|**

- Used to redefine the AP and RL axes of the patient coordinate system, in case the patient does not lie exactly aligned with the L,P,H axes in the scanner.

With a transverse image in the current viewport:

- Click |Rotate view|.
  
  A red cross appears representing the (AP, RL) axis pair.
- Rotate the cross to define the new axes for the patient coordinate system.
- Right-click to store the orientation.
  
  The stored definition is used for scanning and displaying subsequent images.
- Click |Rotate view| again and right-click in the viewport to reset the coordinates to the original view.

**NOTICE**

Only if the current image is really transverse (with angulations \((0,0,0)\)), the patient related axes relate to the system axes by rotation around the FH axis only.

The effect is only visible in the orientation of the images displayed within the Interactive Viewer.

If these images are stored in the database and loaded outside the Interactive session, the redefined orientation is not used.

**‘Previous image’ and ‘Next image’**

In the current viewport up to 16 previous images can be retrieved even if these images were not stored. ‘Image’ |Previous| and ‘image’ |Next| are only active in ‘Single image’ mode.

**Hide the ‘Interactive viewer’ window**

For switching to another viewing context the interactive viewer window must be hidden by clicking the |Interactive| button. It can be mapped to the foreground by once again clicking the |Interactive| button.

Toggling Interactive switches back and forth between normal planning and interactive until |Next| or |Stop Scan| is pressed.

**NOTICE**

When applicable, warnings are displayed in the ‘Scanner Status’ window.
Interactive scanning on ERD

The Examination Room Display (ERD) is a 1280 x 1024 monitor, situated in the examination room. The monitor of the operator console (OC) has a 1920 x 1200 resolution. The ERD always displays a rectangular subwindow (1280 x 1024) of the OC monitor.

The ERD is equipped with a trackerball that supports the panning (movement) of the OC contents in the ERD-window. The following picture shows the relative sizes of OC and ERD.

During Interactive scanning, the 2nd, 3rd and 4th viewport are only partly displayed on the ERD. Additionally, in specific examinations (like biopsy guidance) it is required to display only the 1st viewport as a full-size image on the ERD.

Three different screen layouts can be selected to optimize the Interactive display.

- original layout, optimized for display on the OC,
- full-screen display of 1st viewport, optimized for ERD,
- original layout, optimized for display on ERD.

The following images indicate the layout as presented on the OC and on the ERD (red rectangle) if layout 2 or 3 are selected:
Tips and Hints

Complete visualization of a duct

To check if e.g. a duct is completely visualized in a slice, it is recommended to scan with a 90° flipped slice orientation. On the resulting slice, the duct can be seen in the third dimension making optimal planning possible.

Double-oblique planning

To define a view orthogonal to two other views, it is recommended to

- Push the first oblique to another viewport,
- Define the second oblique with 90° tilt on this first oblique,
- Push that to another viewport,
- Define the final view with 90° tilt on the second oblique,
- Check if the yellow intersection line is perpendicular on both orthogonal views.

Planning the Cardiac Views

Planning the cardiac views is complex because angulations in the 3 different directions could be necessary to visualize the different connections between chambers.

Important is to follow a systematic way to create the different views. Always plan perpendicular on the previous scan.

Useful tools to facilitate planning are:

- the Interactive Scanning Tool
• 3 Points PlanScan
• PlanAlign.

**Interactive Scanning Tool**

Interactive scanning (more information, see chapter “Interactive Scanning” on page 47 and chapter “Interactive Scanning Workflows” on page 241) is especially useful for cardiac imaging, because the required geometry angulations can be found in real time for the different cardiac views.

An interactive scan has to fulfils the following prerequisites:

• One slice only
• Scan mode 2D, M2D or MS
• Cardiac triggering possible
• One heart phase only
• No dynamic scan
• Any scan technique as SE, FFE, TFE, TSE, GRASE or EPI.

When the correct planes have been found and saved in the interactive scan:

• |Next scan| has to be clicked in order to start the next scan in List View which is the diagnostic scan (e.g. a breath-hold scan). The geometry parameters are automatically taken over.
• |Stop Scan| has to be clicked to plan the next scans with use geometry (the stored geometry parameters within interactive).

For cardiac applications, interactive scanning should be performed in continuous mode which is also referred to as real-time mode.

**NOTICE**

TSE is not used due to saturation effects using continuous mode.

**NOTICE**

3 Points PlanScan can also be used during interactive scanning.

**NOTICE**

Interactive scanning can be combined with SENSE. Use phase oversampling (Pos factor) to avoid SENSE backfolding.
3 Points Planscan (3PPS)

3 PPS is a tool which helps to define an irregular plane which is determined by the placement of three points on one or more images of different orientations. It can be used in any application, however it is especially useful in planning aortic arch and coronary arteries.

Workflow

- In the Planscan window, click |3PPS|.
  - The 3 PPS window is overlaid.
- Place the three points on any of the three images selected in the Planscan view port.
- To change the positioning of the points, click on |P1 or P2 or P3| and then click on the new position in Planscan.
- To restart click |Off|.
- Click |Compute plane| to perform the 3 Points Planscan.
- Click |3PPS| again to close the 3PPS window.
- The angulations from the 3 PPS are taken over and displayed. Proceed with routine planning.

PlanAlign

PlanAlign is developed for applications where double oblique scans are made with large angulations in e.g. cardiac scanning. It is a powerful tool to avoid in-plane rotation and to avoid SENSE artifacts. When switched to yes, any modification of the angulations will result in a recalculation of the angulations such that the resulting images show no in-plane angulation.

- Transverse scans are aligned such that the horizontal image direction (RL) is in a non-angled coronal plane.
- Sagittal scans are aligned such that the vertical image direction (FH) is in a non-angled coronal plane.
- Coronal scans are aligned such that the vertical image direction (FH) is in a non-angled sagittal plane.
- Double angulated coronal scans tending to sagittal are aligned like sagittal scans. This means that the scans are aligned such that the vertical image direction (FH) is in a non-angled coronal plane.

NOTICE

When the geometry has been planned using InterActive scanning, PlanAlign will be set to ‘No’.
Basic Views

Below a poster will illustrate how to obtain the different basic views.

▲ Start with a transverse image through the left ventricle.
▲ Define the RAO (Right Anterior Oblique) or VLA (Vertical Long Axis) view on the transverse image by selecting a line through apex and centre of mitral valve.
▲ Define an approximate Four Chamber or HLA (Horizontal Long Axis) view on the RAO by defining a line through the apex and centre of the mitral valve.
▲ Define the Short Axis view, three methods are available:
Place a line orthogonal to the (long axis) line through the apex and the centre of the mitral valve (this is the most accurate method).

Place a line parallel to the mitral valve (this method makes it easier to decide whether to include the basal slice/s during post-processing).

Place a line orthogonal to the septum (this is the best method for Right Ventricle view).

- From the Short Axis view, the true Four Chamber view can be defined by placing a line through the centre of the Left Ventricular Cavity and the inferior margin of the right ventricle.

**Outflow Tracts**

**Right Two Chamber (R2CH) view**
- can be derived from the true Four Chamber view.
- can be defined by placing a line through the tricuspid valve parallel to the septum.

**Left Two Chamber (L2CH) view**
- can be derived from the true Four Chamber view.
- can be defined by placing a line through the apex and the center of the mitral valve.

**Left Ventricular Outflow Tract (LVOT)**
- can be derived from the true Four Chamber view.
- An additional basal short axis scan can be defined which is used to plan the Left Ventricular Outflow Tract (LVOT) by placing a line through the Left Ventricle and Aorta.

**Right Ventricular Outflow Tract (RVOT)**
- is best planned on a transverse view that shows the pulmonary artery valves.

**Pulmonary valve**
- is planned on the RVOT by placing a line through the pulmonary valve seen already on the RVOT view.

**Tricuspid valve**
- is planned on the R2CH by placing a line through the tricuspid valves seen on the R2CH view.

**Mitral valve**
- is planned on the L2CH by placing a line through the mitral valves already seen on the L2CH view.

**Aortic valve**
- is planned on the LVOT by placing a line through the aortic valves already seen on the LVOT.
**Cardiac Anatomy**

Image sets (Black blood or white blood in 3 orientations: Sag, Cor, Tra).

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>Ascending aorta</td>
</tr>
<tr>
<td>Arch</td>
<td>Aortic arch</td>
</tr>
<tr>
<td>DA</td>
<td>Descending aorta</td>
</tr>
<tr>
<td>IVC</td>
<td>Inferior vena cava</td>
</tr>
<tr>
<td>LA</td>
<td>Left atrium</td>
</tr>
<tr>
<td>LB</td>
<td>Left bronchus</td>
</tr>
<tr>
<td>LPA</td>
<td>Left pulmonary artery</td>
</tr>
<tr>
<td>LPV</td>
<td>Left pulmonary vein</td>
</tr>
<tr>
<td>LSPV</td>
<td>Left superior pulmonary vein</td>
</tr>
<tr>
<td>LV</td>
<td>Left ventricle</td>
</tr>
<tr>
<td>MPA</td>
<td>Main pulmonary artery</td>
</tr>
<tr>
<td>PA</td>
<td>Pulmonary artery</td>
</tr>
<tr>
<td>RA</td>
<td>Right atrium</td>
</tr>
<tr>
<td>RB</td>
<td>Right bronchus</td>
</tr>
<tr>
<td>RPA</td>
<td>Right pulmonary artery</td>
</tr>
<tr>
<td>RPV</td>
<td>Right pulmonary vein</td>
</tr>
<tr>
<td>RV</td>
<td>Right ventricle</td>
</tr>
<tr>
<td>SVC</td>
<td>Superior vena cava</td>
</tr>
</tbody>
</table>

**Tab. 11:** List of Abbreviations

**Cardiac Function**

Cine scans are typically used to study wall motion and ventricular function. A variety of scan methods are available for cine scans. However, balanced FFE is the preferred method for breath-hold cine scans.

**Stress-Test (Physical or Dobutamine)**

The workflow as presented here is based on the standardized acquisition guidelines by the SCMR (Society for Cardio-vascular Magnetic Resonance). More information can be found on the website of the SCMR: www.scmr.org
The intention of this section is only to give an illustration of how the workflow may look like in clinical practice. Philips Healthcare cannot take liability for dose regimen, infusion schemes etc.

Coronary artery disease can result in inducible ischemia. One of the first signs for myocardial ischemia is myocardial wall motion abnormality that occurs much earlier than ECG changes or anginal pain. Cine scans acquired under stress conditions can therefore help to identify these inducible ischemic areas.

The left ventricle is divided into 17 segments following the standards suggested by the American Society of Echocardiography. For all the segments the wall motion is classified as normal, hypokinetic, akinetic or dyskinetic.

![Diagram of heart segments](image)

**Fig. 118:** Segmentation of the left ventricle according to the standards of the American Society of Echocardiography in the views: SA - Short Axis, 4CH - Four Chamber, LA - Long Axis.

<table>
<thead>
<tr>
<th>Label</th>
<th>Heart segment</th>
<th>Label</th>
<th>Heart segment</th>
<th>Label</th>
<th>Heart segment</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>basal anterior</td>
<td>7</td>
<td>mid anterior</td>
<td>13</td>
<td>apical anterior</td>
</tr>
<tr>
<td>2</td>
<td>basal anteroseptal</td>
<td>8</td>
<td>mid anteroseptal</td>
<td>14</td>
<td>apical septal</td>
</tr>
<tr>
<td>3</td>
<td>basal inferoseptal</td>
<td>9</td>
<td>mid inferoseptal</td>
<td>15</td>
<td>apical inferior</td>
</tr>
<tr>
<td>4</td>
<td>basal inferior</td>
<td>10</td>
<td>mid inferior</td>
<td>16</td>
<td>apical lateral</td>
</tr>
<tr>
<td>5</td>
<td>basal inferolateral</td>
<td>11</td>
<td>mid inferolateral</td>
<td>17</td>
<td>apex</td>
</tr>
<tr>
<td>6</td>
<td>basal anterolateral</td>
<td>12</td>
<td>mid anterolateral</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Tab. 12:** Labeling of Heart Segments

**Workflow**

All 17 segments can be covered using a combination of three SA slices, a 4CH slice and a L2CH slice.

<table>
<thead>
<tr>
<th>Step</th>
<th>Scan / Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Survey scan</td>
</tr>
<tr>
<td>2</td>
<td>L2CH- and 4CH-scans</td>
</tr>
<tr>
<td>3</td>
<td>Three-slice SA scan</td>
</tr>
<tr>
<td>4</td>
<td>Dobutamine infusion</td>
</tr>
<tr>
<td>5</td>
<td>Three-slice SA-, L2CH- and 4CH-scans</td>
</tr>
<tr>
<td>6</td>
<td>Dobutamine infusion</td>
</tr>
</tbody>
</table>
Tab. 13: Workflow Overview

**Workflow Step-by-Step**

- Perform the survey scan.
- Plan and perform the L2CH- and 4CH-scans following the approach as described in the section Planning the cardiac views.
- Plan the three-slice SA scan on the 4CH view such that the most apical slice covers segments 13-16, the mid slice covers segments 7-12 and the most basal slice covers segments 1-6.
  - Set the number of slices to five for planning purposes only.
  - Select an end-systolic image.
  - Position the slices: first one on apex, fifth through mitral valve.
  - Set the number of slices back to three: leaving the slice position and slice gap unchanged, these three slices now cover the desired cardiac segments.
- Perform this scan.
- Start the Dobutamine infusion to stress the patient’s heart.
- Repeat the Three-slice SA-, the 4-CH- and the L2CH-scans after 3 min. of infusion.
- Increase the Dobutamine infusion rate to reach the next stress level.
- Repeat the Three-slice SA-, the 4-CH- and the L2CH-scans after 3 min. of infusion.
- Repeat the two previous steps for each stress level.
- If at the maximum stress level the sub-maximum age-predicted heart rate (\(= 0.85 \times (220 - \text{age})\)) is not reached, give atropine and repeat the three scans again.

<table>
<thead>
<tr>
<th>Step</th>
<th>Scan / Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>7</td>
<td>Three-slice SA-, L2CH- and 4CH-scans</td>
</tr>
<tr>
<td>8</td>
<td>Next stress levels: Repeat the steps 7 and 8 for each stress level.</td>
</tr>
</tbody>
</table>
NOTICE
The patient’s cardiac frequency will most likely vary depending on the stress level.
For each stress level the cardiac frequency should be adjusted.
When the TFE shot mode is set to ‘default’ this change in heart rate will not lead to a change in breath-hold duration or number of phases.
Make sure that the cine scans tolerate a certain variation in heart rate. This can be achieved by setting the R-R window range to 25%, 35%.

Myocardial Perfusion (Temporal Enhancement)
The workflow as presented here is based on the standardized acquisition guidelines by the SCMR (Society for Cardio-vascular Magnetic Resonance). More information can be found on the website of the SCMR: www.scmr.org
The intention of this section is only to give an illustration of how the workflow for myocardial perfusion may look like in clinical practice. Philips Healthcare cannot take liability for dose regimens, infusion schemes etc.

About Myocardial Perfusion
MRI can be used to analyze myocardial perfusion using first pass contrast passage enabling the detection of perfusion abnormalities.
To perform good quality perfusion scans with a high temporal resolution, dynamic slices have to be acquired as quickly as possible. In order to carefully study the contrast uptake all dynamic scans belonging to one slice should be performed at the same moment within the cardiac cycle. That is the reason that cardiac perfusion scans are cardiac triggered.
Obvious compromises have to be made regarding the image quality, or more specific, spatial resolution. The aim is now to find the right balance between the number of slices, the spatial resolution and the temporal resolution.
Following the standards suggested by the American Society of Echocardiography the left ventricle can be divided into 17 segments.
A three-slice approach as presented in the Cookbook is sufficient to cover 16 out of those 17 segments: the highest possible spatial resolution is chosen where three slices fit in a single heart beat. The number of dynamic scans and thus the number of R-R intervals determine the total scan time.
The aim of perfusion scanning is to identify inducible ischemia areas which often (in the presence of coronary artery stenoses) only occurs under stress conditions. Therefore the perfusion scan should be done both in rest and during stress, such as pharmacological vasodilatation. This can be achieved using e.g. adenosine or dipyridamole.
Workflow

Survey scan
First a survey scan is performed after which a 4CH view and a L2CH view is performed under rest conditions as described in the section Planning the cardiac views. The three-slice SA scan is planned such that each slice covers six segments of the left ventricle (See “Stress perfusion" workflow below for more information about slice positioning).

Stress perfusion
The next step is first to perform the stress perfusion. Stress is done first to have the best image quality for the most important scan since there is no enhancement yet due to earlier contrast injections. The perfusion scan is planned exactly the same as the three-slice SA scan to cover 16 out of the 17 segments. Foldover-artifacts have to be avoided. Therefore it is advised to first run the scan without contrast to make sure that no backfolding is present. This is especially important in the case that a (b)TFE SENSE scan is used. If necessary the FOV has to be increased. During the test scan also the breath-hold instruction can be practiced with the patient. Although adenosine mainly acts as a vasodilator also the heart rate increases. Therefore the scan should be defined such that it will run with higher heart rates. The simplest choice available is reducing the in-plane resolution. Decreasing the matrix size ensures that all three slices still fit into the R-R interval.

Adenosine infusion
After the test scan the infusion of adenosine is started to stress the patient’s heart. In the Cookbook an infusion rate of 140 ig/kg/min is suggested for maximum six minutes. During stress examinations monitoring of the patient is mandatory. Among blood pressure, pulse oximetry and symptoms also the heart rhythm is monitored.

Contrast injection
The best results for contrast uptake curves are obtained when a short compact bolus injection is used. The Cookbook suggests a Gd-DTPA contrast dosage 0.05 mmol/kg body weight applied with an injection rate of 4 ml/s. A saline flush of 20 ml with the same injection rate is necessary to facilitate a compact bolus passage.

Performing perfusion scan
The perfusion scan is started 4 minutes after the start of the adenosine infusion.
When the perfusion scan is running and the first images appear in the autoview window the contrast injection is started.
Carefully the contrast arrival is monitored and at the desired moment a breath-hold instruction is given. The breath-hold command is needed to ease postprocessing afterwards. Ask the patient to hold their breath as long as possible when the contrast agent is to arrive in the right ventricle which in most of the patients happens roundabout after twice inhaling and exhaling. If the patient cannot hold breath anymore, let him/her breathe once and then hold breath again. Alternatively, let the patient breathe shallowly after he/she cannot hold breath anymore.
Fig. 120: Perfusion sequence

1. Start scan
2. Injection contrast
3. Breath-hold command
4. End scan
A. Contrast arrival RV (right ventricle)
B. Contrast arrival LV (left ventricle)
C. Enhancement myocardium

Fig. 121: Example of myocardial perfusion scans at rest and at adenosine stress.

Fifteen minutes after termination of the adenosine infusion the heart has recovered from the applied stress. Then the perfusion scan can be repeated during rest.

Image analysis and postprocessing

After excluding the left ventricular cavity and the pericardium, the myocardium is divided into 6 equiangular segments per slice following the standards suggested by the American Society of Echocardiography. Postprocessing can be performed on the ViewForum (EWS) systems.
Late Enhancement (Spatial Enhancement)

The following paragraphs describe the late enhancement technique and workflow. It comprises these chapters:

- About Late Enhancement
- Workflow
- Phase Sensitive Inversion Recovery (PSIR)

The intention of this section is only to give an illustration of how the workflow for viability examinations using late contrast enhancement looks like in clinical practice. Philips Healthcare cannot take liability for dose regimen, infusion schemes etc.

Different MRI techniques can be used to visualize injured myocardium.

- Cine scans are used to look at wall thickness.
- Low doses dobutamine stress examinations have the potential in differentiating between viable myocardium (stunned and hibernating) and non-viable myocardium.
- Only the late contrast enhancement scans have the potential of visualizing the transmural extend of an infarction.

About Late Enhancement

Damaged cells take up contrast agent while in viable myocardium the contrast agent stays extracellular. The contrast washout for damaged cells evolves much slower than the washout of the extracellular contrast only. After a while the contrast concentration for viable myocardium is much lower than for injured myocardium. And thus the T1 relaxation rates evolve at different rates. An inversion pulse is then applied and the inversion time is chosen such that the normal myocardium appears black, maximizing the contrast between normal (black) and injured (white) myocardium.

Fig. 122: Example of late enhancement scans.
Workflow Scan and Planning

Late Enhancement (Spatial Enhancement)

Fig. 123: The inversion pulse is used to cancel out any signal from the myocardium. Infarcted areas where still contrast is visible show high signal intensities. a - Enhanced myocardium curve, b - (unenhanced) myocardium.

**Workflow**

Prior to performing the viability scan it is necessary to wait until the contrast agent has cleared from the (non-damaged) myocardium. This usually takes 10 minutes. During this time any kind of other scans can be performed, such as series of cine scans. 10 minutes after the (last) contrast injection the late enhancement scans can be performed.

**Late Enhancement sequence**

This sequence is a single-phase multishot TFE scan that utilizes a single 180°-inversion prepulse.

- The shots should be acquired in mid-diastole to keep the cardiac motion as small as reasonable.
- The inversion delay time to cancel the normal myocardium is patient dependent and cannot be calculated on beforehand. It also depends on the time after the contrast injection. A longer time after injection results in a slower T1 relaxation and less contrast in the (non-damaged) myocardium. Longer inversion times should be used. Usually the inversion time varies in a range of 200 to 300 ms.

There are three ways to find out the patient specific inversion time:

1. Use a “Look-Locker” sequence which is a cine scan that utilizes a single inversion pulse applied once every heart beat immediately after the R-peak. T1 relaxation is made visible over the individual cardiac phases.
2. By trial and error: Start with a TI of 200 ms, then increase the TI using small steps of 20 or 30 ms.
3. Change the inversion delay in real-time during an interactive scan. Make sure that the scan is running in continuous mode. The inversion time depends on the steady state that is reached over multiple heartbeats.

Remember that the inversion time found is valid only for a small period of time. Due to the washout of the contrast media from the myocardium the T1 relaxation rate decreases slowly over time.
Fig. 124: ‘Look-Locker’ technique to quickly find the zero crossing point of the myocardium within a breath-hold.

**Tips and hints**

Depending on the parameter settings, specific effects could occur:

<table>
<thead>
<tr>
<th>Effect / Appearance</th>
<th>Cause</th>
<th>Measure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Speckled appearance of the myocardium: appears as suppressed myocardium interspersed with white spots.</td>
<td>It occurs if the Ti is very close to the optimal inversion delay.</td>
<td>Increase the Ti by just 10 ms to attain optimal suppression.</td>
</tr>
<tr>
<td>Dark signal at the endocardial boundary</td>
<td>It is caused by a slightly shorter effective Ti of the tissue at the blood-myocardial interface (especially with large voxels).</td>
<td>Increase the Ti to obtain uniform suppression of the myocardium.</td>
</tr>
<tr>
<td>Insufficient suppression / lack of contrast of myocardium over a broad range of Ti</td>
<td>This indicates that the contrast has either washed out (i.e. the scanning is done much later, e.g. more than 30-min. after injection) or insufficient amount of Gd-DTPA was injected.</td>
<td>It may be helpful to check if the entire double dose of Gd-DTPA was given (check for leaks etc.).</td>
</tr>
<tr>
<td>The blood-pool appears too dark</td>
<td>The Ti is too short.</td>
<td>Increase its value to allow sufficient recovery.</td>
</tr>
<tr>
<td>Less contrast between blood-pool and injured myocardium</td>
<td>The Ti is too long.</td>
<td>Decrease its value.</td>
</tr>
<tr>
<td>SNR is too low</td>
<td>Due to the inversion prepulse, the SNR will be relatively low, especially if the heart rate is high and magnetization cannot recover completely before the next TFE shot is acquired (in the next RR-interval).</td>
<td>To increase SNR, the TFE shot interval can be set to ‘user defined’ and then to 2 beats to allow for more recovery, but the scan will take longer.</td>
</tr>
</tbody>
</table>

**Tab. 14:** Effects, causes and measures

**Phase Sensitive Inversion Recovery (PSIR)**

The PSIR (“AutoViability”) IR-TFE sequence can be used for late enhancement assessment. The advantage of this technique is that it is less sensitive to suboptimal inversion delays.

**PSIR is a 2 heart-beat sequence**

PSIR needs 2 cardiac cycles (per inversion prepulse).
• It is more robust against variations in heart rate, and the SNR and CNR will both be better compared to a single heart-beat technique.
• It is intrinsically slower than single heart-beat techniques.
• The loss in imaging speed can be compensated for by using SENSE.

In the PSIR sequence, the second heartbeat is used for determination of the phase. The inversion pulse is given only once every two heartbeats, so that the acquisition in the second heartbeat has had more time for relaxation (so that the magnetization of all tissues should be positive again), and can be used as a reference.

**PSIR provides Corrected Real Images**

The “CR” image type (Corrected Real) is the desired final phase corrected image.

**NOTICE**

PSIR and imaging parameters: not all can be combined, others are mandatory.
Halfscan and partial echo cannot be used with PSIR.
SENSE can be used with PSIR.
CLEAR is mandatory with PSIR.

**Related parameters**

• TFE prepulse (no, saturate, invert)
• PSIR (no, yes)
• Flip angle (default: 5°)

The flip angle parameter “Flip angle (deg)” specifies the flip angle of the 2nd TFE shot in the 2nd heart beat, which is typically taken smaller than the flip angle in the 1st heart beat (to prevent saturation).

**Tips & Tricks**

**MR cardiac analysis on the EWS**

PSIR datasets can be analyzed by means of the 'Spatial Enhancement' application in the Cardiac Explorer.

They cannot be analyzed by means of the 'Spatial Enhancement' application on the EWS, since they contain CR-images. Analysis can only be performed on the IR-M images, even if the image contrast is suboptimal due to incorrect inversion delay time.

**Work-around**

• Use 'Split image types' in Review Case to separate the CR-images from the IR/M images.
• Load the IR/M images in the 'Spatial Enhancement' application.
For optimal contrast in the IR/M image, use IR_TFE_LL_2beats to determine the optimal inversion delay time for the PSIR sequence prior to scanning PSIR.

**Optimal inversion delay time**

PSIR uses two RR intervals per inversion pulse. Compared to enhancement techniques which use a single RR interval per inversion pulse, a longer TI should be used for PSIR (because there is more time for relaxation). It’s always better to use an inversion delay time which is a bit too long (with positive myocardium). This will result in optimal contrast between normal and scarred myocardium. This is less important for PSIR scans, where a too short TI still results in optimal contrast between the normal and scarred myocardium in the CR-image.

**2D vs 3D**

PSIR can be used for 2D and 3D, but for practical reasons, PSIR is mainly useful for 2D imaging. This is mainly because of breathhold times.

**Navigator echo technique and PSIR**

When using navigators with PSIR, the following happens with respect to the acceptance of RR intervals.

- If the first RR interval is accepted, also the second one will be accepted.
- If the first RR interval is rejected, also the second one will be rejected.

**Coronary Angiography**

MRI of the coronary arteries, with the advent of the MotionTrak method is now feasible in a clinical setting.

This chapter will introduce the various aspects needed to perform a successful coronary examination. Covered here will be the utilization of MR methods, scan parameters, a recommended clinical scan procedure and angulation techniques.

**About Coronary Angiography**

Coronary scans can be made with a variety of techniques:

Balanced TFE is the most frequently used method because it is fast due to the very short TR’s that are used and it gives a nice strong signal from blood. Other methods include TFE and Black Blood TSE.

Breath holding could be used for respiratory motion reduction, but the total breath-hold time available is not sufficient to achieve good quality images. Another problem for breath-hold approaches is the high risk of unwanted movement of the diaphragm during breath holding.
The best way to acquire high-resolution images is to correct for any respiratory motion using navigators. Navigators correct for sub-millimeter motion and allow for longer scan times, more data acquisition and thus a higher spatial resolution. In the past these scans could easily exceed 10 minutes of scanning, but good results can be obtained in scans that last for a more practical 3 to 5 minutes of effective scan time.

There are two different approaches: the whole heart approach and the targeted approach where typically one scan is needed to catch the right coronary artery (RCA) in one scan, and a second scan is needed to catch the left coronary artery (LCA) and circumflex (LCX) together.

**Remark**

The most frequently made mistake is to determine the spatial resolution of coronary scan from the voxel size only (FOV and scan matrix), totally ignoring the influences of respiratory motion to the resolution. In other words, decreasing the acquisition resolution from 0.7 mm to 0.5 mm does not improve the resolution if the total amount of respiratory blurring is more than 0.7 mm. Try not to focus too much on the voxel size alone. Focussing on patient comfort is more important, reducing the risk of patient motion gives much better results!

**Workflow**

The best results are achieved when the patient is not moving at all since very small vessels are to be imaged. The slightest movement of the patient during scanning results in blurred images. It is therefore important to make sure that the patient lays very comfortable inside the magnet. Music through the head phones can help to create a more relaxed atmosphere. Explain to the patient the importance of keeping still during the whole examination.

**Procedure**

This procedure describes the targeted approach for the coronary arteries and the whole heart examination.

**Multistack survey**

- can best be performed in a breath hold (expiration).
  
  This allows for better planning of the navigator beam that is used for respiratory gating and motion tracking.

**High Temp Cine scan**

- is a b-FFE cine scan with a sufficient number of phases (40 or more) to allow the precise determination of the trigger delay and shot duration.

  - Position the scan in transverse orientation through the left and right ventricle. The idea is that this scan shows the motion of RCA and thus the precise moment that diastole starts and early systole begins.

  - Acquire this scan in free breathe as breath-hold might affect the patient’s heart rate. It is important to define the precise start of diastole during free breathe since the actual coronary scan is acquired in free breathe too (navigator).
Coronary survey (only needed for the targeted approach)

- is a high-resolution survey scan that covers the whole heart and that is needed for planning of the coronary scans.
- utilizes SENSE b-TFE to speed up the image acquisition.
- uses a navigator for respiratory gating and motion tracking. Position the navigator on the right hemi diaphragm.
- uses a trigger delay set to mid-diastole (if higher heart rates result in conflicting parameters, the trigger delay could also be set to longest).

Fig. 125: Coronal image that shows the main pulmonary artery: position the stack such that the first slice is located halfway the pulmonary artery, including as much of the heart as possible.

While this scan is running, the precise trigger delay and shot duration can now be determined from the previous high temp cine scan:

- Browse through the phases and find out at what moment diastole starts. This should be the trigger delay for the coronary scan.
- Browse through the phases to find the precise moment that the right coronary artery starts moving again at early systole. The difference between this moment and the previously mentioned trigger delay is the acquisition duration. The acquisition duration is displayed on the info page and can be controlled by changing the TFE factor.
- Alternatively, the TFE shot duration can be set in milliseconds directly on the 'Contrast' tab. The TFE factor is automatically calculated and displayed on the info page.
Fig. 126: Browse through the phases of the high temp cine scan to find out the precise moments where the coronary motion starts and stops.

Coronary scan

<table>
<thead>
<tr>
<th>Coronary scan</th>
<th>Approach</th>
</tr>
</thead>
<tbody>
<tr>
<td>Whole Heart Coronary scan</td>
<td>for whole heart approach</td>
</tr>
<tr>
<td>Right Coronary scan (RCA)</td>
<td>for targeted approach</td>
</tr>
</tbody>
</table>

Tab. 15: Use one of these coronary scans

- Enter the trigger delay as found using the High Temp Cine scan.
- Adjust the TFE factor or the TFE shot duration on the 'Contrast' tab.

When the images of the previous scan (coronary survey) are loaded into the main planning viewport, three-points-planscan can be used to position the stack of slices such that they cover the whole right coronary artery at once. To avoid any risk of respiratory ghosting artifacts over the image select a feet-head fold-over direction.

For the whole heart approach, the examination would be finished by now. For the targeted approach, another scan for the LCA could be necessary.
Fig. 127: Place the first point at the origin of the RCA, the second point more lateral at the most apical position and the third point at the most distal, inferior position.

**Left coronary artery (LM, LAD and LCX) scan - for targeted approach**

- The left main (LM), left anterior descending (LAD) and the left circumflex (LCX) can be acquired in a single 3D volume.
- Use three-points-planscan to position the stack.
- Fold-over direction should be set to LR to avoid any risk of respiratory ghosting artifacts.

Fig. 128: Place the first point at the origin of the LM, the second point more distal in the LAD and the third point at the LCX.
Technical background

The coronary scans make use of the ‘3D-K-space shutter’ which saves 20% of the scan-time and increases signal to noise. The technique utilizes a radial profile order, which means that the outer corners of 3D K-space are not acquired during acquisition resulting in improved image quality. As a result of this radial profile order, each individual TFE shot starts at the center of 3D K-space (low-high profile order). Because of this REST and SPAIR or SPIR pulses become more effective. Therefore it is also allowed to select fold-over suppression with only 1 NSA (implicit use of REST slabs).

A SPAIR or SPIR fat suppression pulse is used to enhance the contrast between the coronary artery and the surrounding epicardial fat.

A T2Prep pulse is used to further enhance the contrast between the coronary arteries and the myocardium. The T2Prep pulse is a non-selective pre-pulse that suppresses tissues with short T2 relaxation’s using a train of refocusing pulses over a short period of time. Both the number of refocusing pulses (1, 2 or 4) and the period of time (echo time) can be adjusted for the T2Prep pulse.

It is recommended to use volume shim, which is done selectively over a volume that can be freely chosen, but is restricted to a minimum value. Large transitions as air/tissue boundaries should be excluded from the selected volume and also areas where large homogeneity variations occur. When ‘ShimAlign’ is set to ‘yes’, any modification of the stack off-centers and angulations will result in a recalculation of the shim volume such that the shim volume will be aligned to the stack:

- Off-centers are adjusted such that the volume will be inside the stack.
- Angulations will be equal to the stack.
- The volume will be slightly thicker than the stack allowing easier selection in planscan mode.

Sequence description

In order to eliminate the contribution of fat signal into the navigator beam a second SPIR pulse is implemented to suppress the fat in the navigator beam. This results in a steady navigator signal. The excitation of the navigator is moved close to the acquisition train to ensure a minimum amount of residual motion. The order of pulses is:

- T2 prep pulse
- SPIR for navigator
- Navigator
- SPIR for image acquisition
- Implicit REST for fold-over suppression
- Acquisition train (Balanced TFE, TFE or TFE-EPI)
Workflow MultiNuclei (MN) MR Spectroscopy

Proton resonances are not always uniquely identifiable as the MRS fingerprints of different molecules may overlap. Thus spectroscopy of other nuclei is also interesting for biochemical or clinical research. Some compounds that are not readily identified in in-vivo proton spectra, are easily identified in $^{31}$P or $^{13}$C spectra.

Besides Proton spectroscopy, Phosphorous spectroscopy is the most commonly used one. Molecules that are examined in Phosphorous Spectroscopy are:

- Phosphorous ($^{31}$P);
- Adenosine triphosphate (ATP);
- Phospho-creatine (PCr);
- Inorganic phosphate (Pi);
- Phospho-monoesters;
- Phospho-diesters.

Pulse sequences and MRS protocols

Six main scan types are available for $^{31}$P Spectroscopy:

- No localization: ‘Pulse and Acquire’
- Single voxel, localized with ISIS (Image Selected In-vivo Spectroscopy; FID based volume selection method)
Workflows Scanning and Planning

• Single voxel parameter series
• Double voxel (an extension of ISIS that acquires data from two aligned voxels, using a 16-step localization cycle).
• One dimensional Spectroscopic Imaging (typically with two dimensions of spatial localization to define a bar).
• Two dimensional Spectroscopic Imaging (typically with slice selection, i.e. one dimension of spatial localization).

The scan setup is very flexible: phase encoding and spatial localization dimensions can be specified independently (the ‘FID volume sel changes’ parameter may need to be set to user defined). However, more extensive spatial localization requires a longer TR to stay below SAR limits. The minimum TR for Single Voxel ISIS in the brain is 5000 ms. Slice selected 2DSI requires fewer pulses, and hence TR can be reduced to ~4000 ms.

$^{31}$P imaging protocols and ExamCards are provided for the most common anatomical areas.

Planning

For accurate planning, make use of the marker in the Phosphorous coil which is buried at the center of the coil.

Localize the marker in the phosphorous coil

1. Acquire images in all three orthogonal directions with the Q-Body coil.

![Fig. 130: Localization of the marker. The red arrows indicate the position of the marker.](image)

2. Position the volume of interest at the same level as the marker in the coil.
   • This will provide the best SNR.
   • The penetration depth of the coil is ± half the diameter of the coil.

Acquiring Data

Once planning is completed and 'Start Scan' has been pressed, the following steps are executed:

• Manual adjustment of coil tuning and matching.
• Preparation phases/steps of other nucleus measurement (shimming, $F_0$ determination etc.; this can be skipped for repeated scans of the same voxel).

• Measurement.

**Manual tuning and matching**

An MRI coil is part of a tuned circuit, and for maximum performance, its resonance frequency should equal that of the nuclei of interest: 51.73 MHz for $^{31}$P at 3.0T. Moreover, to minimize the amount of reflected power, its impedance should be 50 ohms. Because the presence of a patient "loads the coil" and greatly changes the characteristics of the tuned circuit, long flexible rods attached to variable capacitors are used to optimize coil sensitivity for a particular anatomy.

**Fig. 131:** Tuning (left) and Matching (right).

In manual tuning mode, low power RF is swept through the resonance frequency, and reflected power is monitored as a function of frequency:

**Fig. 132:** Manual Tuning window. 1 - Buttons with functions like 'Autoscale', 'Show grid' and 'Show dots'. 2 - tuning signal presented as intensity versus frequency [kHz], 3 - signal types, 4 - numeric display of minimum and maximum values.

• The rod that is attached closer to the center of the coil adjusts the tuning - the frequency at which the tuned circuit resonates. Turning it will move the 'V' on the display left or right. When adjusted properly, it should be centered at zero frequency offset.
• The rod that is attached closer to the cable adjusts the matching - the impedance of the loaded coil. Turning it adjusts the sharpness and depth of the ‘V’. When adjusted properly, the ‘V’ should be as sharp as possible, and the reflected power minimized at zero offset frequency.

**Tips and hints for coil tuning and matching**

- Click on ‘Display on Magnet’ in the monitoring window to display the manual tuning window on the magnet-mounted screen.
- For better visualization of the ‘V’, turn on the ‘Autoscale’ and ‘Grid’ display options.

Coil response on resonance is characterized by a quality factor $Q$. SNR is proportional to $Q^{1/2}$. Patient loading lowers $Q$, but correct tuning and matching can minimize the drop. The system calculates $Q$ after manual tuning and before each subsequent scan. $Q$ can be inspected in Logging Application UI (only accessible when logged in as service user).

- From the Windows Start menu, select MR System Management > Diagnostics > Logging Application UI.
- Enter ‘coil q:’ (without quotes) in the free text box and click on ‘Search’.

Some typical loaded $Q$ values with the P-140 coil at 3.0T are:

<table>
<thead>
<tr>
<th>Anatomy</th>
<th>$Q$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Calf muscle</td>
<td>40 ... 60</td>
</tr>
<tr>
<td>Liver</td>
<td>35 ... 50</td>
</tr>
<tr>
<td>Brain (coil at the back on the head)</td>
<td>65 ... 95</td>
</tr>
<tr>
<td>Disk A positioned 1 cm away from the coil</td>
<td>35 ... 37</td>
</tr>
</tbody>
</table>

**NOTICE**

Make sure that the cables are connected to the MN box.

Loose cable connections at the MN box will give noise on the tuning/matching curve with a low power response and will finally result in bad spectra.
Preparation of other nucleus measurement

The preparation steps $F_0$ determination, power optimization, and shimming are actually performed on the proton signal from the selected voxel or VOI. The only user-selectable step is the shimming, with three choices for the higher order shimming (HOS) parameter when planning the scan:

<table>
<thead>
<tr>
<th>Type of HOS</th>
<th>Way of working</th>
<th>Advantages</th>
<th>Disadvantages</th>
</tr>
</thead>
</table>
| HOS = NO    | launches iterative shim which seeks to maximize peak height by cycling through adjustment of the static currents supplied to the X, Y, and Z gradients. | • A monitor window display for a visual assessment of the shim prior to the acquisition.  | • Very slow.  
|             |                                                                                 | • Less sensitive to motion.                                               | • Can be less accurate when local minima in field inhomogeneity are present. |
| HOS = First | uses a fast pencil beam projection method to set the first-order shim currents.                           |                                                                                    |                                                                                |
| HOS = Second | uses a fast pencil beam projection method to set both, the first- and second-order shim currents (this choice is available only if second-order shim hardware is present and operational). | • Fast.  
|             |                                                                                 | • Employs the five second-order shims ($Z_2$, $X_2-Y_2$, $XY$, $XZ$ and $XZ$) for better homogeneity over large voxels. | • No visible display of shim quality prior to scanning.  
|             |                                                                                 |                                                                                | • Possibly more sensitive to motion. |

Tab. 16: Table title
**Measurement**

For single voxel acquisitions, a spectrum monitor window displays an update of the averaged signal, once dummy shots are completed. Note that for ISIS, an accurate assessment of the localized spectrum is available only after every eighth shot (i.e., after excitation 8n, with n=1,2,...).

A spectrum monitoring window also appears for 1D Spectroscopic Imaging, but it displays the collected signal from the entire volume, and is therefore not a real representation of the final results. No spectrum monitoring is available for 2DSI.

**Processing with SpectroView**

This section gives some tips and hints for a phosphorous measurement being processed with SpectroView.

**Basic processing**

Once a time-domain spectroscopy dataset is selected, a Basic processing script is executed automatically to generate a frequency domain spectrum for display.

Different basic scripts are available, for both single voxel and CSI data, and optimized for various anatomic regions. If none is specified, a pop-up will be presented to allow selection of the anatomic region, before the basic script is executed.

**Single Voxels**

Once time-domain processing is complete, or after choosing a spectrum from the Pictorial Index, select a script from the drop-down menu in the SpectroView toolbar. All the scripts which are relevant for the selected anatomy will be available.

Either run the appropriate script as it is or edit the script.

**Select peaks**

The list of in vivo metabolites from which to choose includes ATP, PCR, Pi (inorganic phosphate), PME (phosphomonoesters), PDE (phosphodiesters), and "dnt" ("dinucleotide" - a small peak near the a-ATP doublet that has been variously labeled in the literature).

Default choices for each script and possible changes are detailed in the following table.

<table>
<thead>
<tr>
<th>Script</th>
<th>Default metabolites</th>
<th>Changes to consider</th>
</tr>
</thead>
<tbody>
<tr>
<td>31PMuscle_sv</td>
<td>PCR, ATP, Pi</td>
<td>Add PDE if the spectrum is proton decoupled. Add dnt if the SNR is good.</td>
</tr>
<tr>
<td>31PLiver_sv</td>
<td>ATP, Pi, PME, PDE</td>
<td>PCR shouldn’t appear in liver spectra, but it usually does a contaminant from surrounding muscle - if so, add it. Add dnt if the SNR is good.</td>
</tr>
</tbody>
</table>
### Script

<table>
<thead>
<tr>
<th>Script</th>
<th>Default metabolites</th>
<th>Changes to consider</th>
</tr>
</thead>
<tbody>
<tr>
<td>31P_Brain_sv</td>
<td>PCR, ATP, Pi, PME, PDE</td>
<td>Add dnt if the SNR is good.</td>
</tr>
</tbody>
</table>

In the 31P_Phantoms_sv script, there are three entries for the three 31P phantoms:

- 'Disk A' = phosphoric acid (singlet at 2.86 ppm relative to PCr)
- 'Disk B' = hypophosphorous acid (triplet centered at 13.53 ppm, $J_{PH} = 549$ Hz)
- 'Sphere B' = methylphosphonic acid (quarted centered at 32.5 ppm, $J_{PH} = 17.2$ Hz)

### Peak Fitting

Some modifications to consider are as follows:

- The default Gaussian character is 50%. However, if Gaussian or Gaussian-to-Lorentzian apodization has been applied to the data in the time domain, a better choice would be ~90%.

- The number of baseline terms characterizes the flexibility of the baseline function during the fitting process - more terms allow for more wiggle. For spectra without underlying broad components - like those from muscle - the number of baseline terms should be small (0-2). For brain spectra, more terms (7-9) may be needed to fit the broad phospholipid hump centered roughly on the PDE peak.

- If the SpectroView fit is to be used for pH information, Lock Relative Frequency should be OFF to let the fitted Pi and PCr chemical shifts vary independently. However, unless the SNR is very good, these extra degrees of freedom can impair the robustness of the fit. More reliable results can be obtained with Lock Relative Frequency = ON. (For pH measurements, right-mouse-click in the graph area to turn on Difference Mode, then move the vertical line cursors to the Pi and PCr peaks for a display of their chemical shift difference.)

- If peaks are not located correctly during the fitting routine, a manual peak assignment can be performed. This function is also used to center the PCr-peak to 0 ppm.

### 2D CSI Data

If processing 2D CSI data, enable ‘Voxel selection’ by clicking on the corresponding icon.
Select all voxels of interest to be proceeded.

Possible scripts are:
- 31PMuscle_csi
- 31PLiver_csi
- 31PBrain_csi
- 31P_Phantoms_csi

These are nearly identical to the single voxel scripts. Additionally, metabolite and/or ratio maps can be generated.

To specify a ratio map, choose a numerator from the left column and a denominator from the right column. All metabolites selected for maps must also be chosen for fitting on the ‘Select Peaks’ page.

Examples of 3.0T with the P-140 Coil

2DSI of calf muscle

Fig. 135: Calf muscle spectral results.
**Brain Single Voxel**

**Fig. 137:** Brain pulse acquired results. Resolved phosphomonoesters and phosphodiesters: PE = phosphorylethanolamine, PC = phosphorylcholine, Pi = inorganic phosphate, GPE = glycerophosphorylethanolamine, GPC = glycerophosphorylcholine, PCr = Phosphocreatine, γATP = gamma ATP, αATP = alpha ATP, βATP = beta ATP.
Brain 2DSI

Fig. 138: Brain 2DSI results. Upper row: planning. Lower row: spectra from two voxels.

Liver Single Voxel

Fig. 139: Liver SV spectral results.
Liver 2DSI

Fig. 140: Liver 2DSI spectral results.

31P Liver Metabolite Maps

Fig. 141: 31P Liver Metabolite maps.
12 Workflows Review and Analysis packages

This chapter describes the various workflows for the Review and Analysis packages. For information about the user interface and if applicable about suitable scans and results of these packages, refer to chapter “Review and Analysis Packages” on page 105.

Start up a Review or Analysis package

▷ In Review mode:

- Select the imaging series first and then the Review or Analysis package. You can select multiple scans.
  - To select multiple successive imaging series, press |Shift| and click to select.
  - To select multiple imaging series, press |Ctrl| and click to select.

There are different ways of how to start up a Review or Analysis package.

1. Right-click on an imaging series in Thumbnail View and select the required package from the context menu.
2. Click on an imaging series in Thumbnail View and select the required package from the 'Review' or 'Analysis' menu.
4. Drag an imaging series from List or Thumbnail View into the reviewing area. The default package (ImageView) opens automatically.

NOTICE

Only those Review or Analysis packages are displayed in the pop-up or 'Review' or 'Analysis' menu which apply to the current scan. The other packages are either not in the list or they are grayed out.

The selected and thus the current view is indicated by an orange tab and border.

ImageView: Workflows

For information

- about generic image functions, see chapter “Generic functions for images” on page 55.
- about ImageView and the ImageView toolbar, see chapter “ImageView” on page 106.
Start up ImageView

Preferred workflow

▷ In Review mode:
  ▷ Drag an imaging series from List or Thumbnail View into any viewport of the reviewing area.

The ImageView package opens.

Typical ImageView workflows

• **Windowing, zooming and panning**: see chapter “Windowing, Zooming and Panning” on page 53.
• **Scrolling**: see chapter “Scrolling through images” on page 54.
• **Changing the layout**: see chapter “” on page 107.
• **Reviewing PlanScan**: see chapter “” on page 95.
• **Comparing imaging series**: see chapter “” on page 94.
• **Performing measurements**: see chapter “” on page 108.
• **Playing a movie**: see chapter “” on page 107.

VolumeView: MaxIP and MinIP

Start up VolumeView

1. Right-click on a suitable scan in the Thumbnail View.
   A context menu appears.
2. Click ‘VolumeView’.
   The VolumeView package opens.

Optional: Select the Image Type

▷ Drag to the left or to the right on the orthogonal views to select another image type, e.g. in a PCA imaging series PCA/M or FFE/M images.

Select the Render Mode

For Maximum Intensity Projection (MaxIP)

▷ This step can be skipped, since MaxIP is the default setting.
For Minimum Intensity Projection
- Click ‘Render Mode’ and select MinIP from the drop-down menu.

Define the volume to be reconstructed
You can define the volume of interest in several ways, e.g. using the clipbox function or drawing a contour.
The most common way of drawing a contour is described here.
1. Click ‘Draw Contour’ to define the volume of interest.
   - Default settings are: Free, Cut Outside, AutoCut Mode Enabled.
2. For Free:
   - click once to start drawing,
   - move the mouse to define the contour,
   - click once more to close the contour.

Calculate the result images as new imaging series
- Click ‘Generate Series’ to calculate a new imaging series out of the original data set.
  A new window pops up.
- Click |Stack| to define orientation, stack type (e.g. radial for a Single- and Multi-Station MaxIP or parallel for a slab MinIP), projections, radial axis and angle.
- Enter a series name and click ‘Generate’ to generate new imaging series.

VolumeView: MPR

Start up VolumeView
1. Right-click on a suitable scan in the Thumbnail View.
   A context menu appears.
2. Click ‘VolumeView’.
   The VolumeView package opens.

Select the Render Mode

For Multiple Planar Reformats
- Click ‘Render Mode’ and select MPR from the drop-down menu.
Calculate the result images as new imaging series

► Click ‘Generate Series’ to calculate a new imaging series out of the original data set. A new window pops up.
► Click |Stack| to define orientation, stack type, projections, radial axis and angle.
► Enter a series name and click 'Generate' to generate new imaging series.

VolumeView: Surface Rendering

NOTICE
Only one object can be rendered at a time.

Start up VolumeView
1. Right-click on a suitable scan in the Thumbnail View.
   A context menu appears.
2. Click ‘VolumeView’.
   The VolumeView package opens.

Select the Render Mode
► Click ‘Render Mode’.
► Select ‘Shaded Surface Rendering’ (surface rendering with use of light source)
   OR
► Select ‘Unshaded Surface Rendering’ (surface rendering without use of light source)

Define the volume
If necessary, define the volume to be reconstructed.
MobiView Workflow

NOTICE
If the scans which have to be fused don’t have GeoLinks (e.g. due to scan aborts), select multiple scans to overcome this problem: in this case, fusing will be done for these multiple scans.

Start up MobiView
1. Right-click on a suitable scan in the Thumbnail View.
   A context menu appears.
2. Click ‘MobiView’.
   The MobiView package opens.

Fuse the coronal or sagittal imaging series

NOTICE
It is recommended to window and level each station prior to fusing.

1. Select 'Fuse Hardcut' OR 'Smooth Fuse' from the toolbar.
2. Check whether the result of the fusion operation is correct.
   Fused images can be windowed and zoomed in the usual way as other images.

NOTICE
The fusing area is indicated by markers on the multistation images.

Merge the transverse imaging series

NOTICE
It is recommended to window and level each station prior to fusing.
1. Select ‘Merge Series’ from the toolbar.
2. Check whether the result of the fusion operation is correct.
   Merged images can be windowed and zoomed in the usual way as other images.

**NOTICE**
The fusing area is indicated by markers on the multistation images.

### Save the fused images to database

1. Click ‘Generate Series’ to save the fused images to database.
2. Click ‘Yes’ to confirm.
   - Each time the ‘Generate Series’ button is clicked, the fused data is stored as a new series.
   - The name of this new series is derived from its original name extended with a "m".
   - The saved images will be marked as derived images, i.e. not originally scanned images.
   - The fusing area indication is saved with the images.

### Workflow for Multi-Station imaging series with Multiple Image Types

With multiple stations and multiple image types, fusing automatically occurs for one image type, e.g. Modulus or InPhase image.
In order to also fuse the second image type, proceed as follows:

**For coronal or sagittal multi-station imaging series**
- Select your imaging series and start up MobiView.
- Select the first image type (e.g. InPhase image).

- Fuse the images (either Smooth or Hardcut) and store the resulting fused image.
- Select the second image type (e.g. Water image).
- Fuse the images and store the resulting fused image.

**For transverse multi-station imaging series**
- Select your imaging series and start up MobiView.
- Select the first image type (e.g. InPhase image).

- Merge the images and store the resulting merged image.
- Select the second image type (e.g. Water image).
QFlow Analysis

Start up the QFlow package

1. Right-click on a suitable scan in the Thumbnail View.
   A context menu appears.
2. Click ‘QFlow’.
   The QFlow package opens.

Prepare the environment for drawing a ROI

Select the end diastolic FFE/M image:
- Drag to scroll through the images.

The end diastolic FFE/M image shows the largest diameter which is best for the automatic contour detection.

Define the vessel contour

Select the type of ROI

Active Contours algorithm
- ’Active Contours’ is disabled by default to allow for automatic contour detection and adaptation.

Draw a ROI

For Smoothed Polygon, Ellipse, Freehand:
- Click 'Draw Selected Contour'.
- Click once in the image viewport to start drawing a ROI.
- Move the mouse to define the contour.
- Double-click to close the contour.

The drawn contour will be adapted to the closest automatically detected contour if ’Active Contours’ is enabled.

For Single Click ROI:
- Click once within the vessel.

The contour detection algorithm will automatically come up with the vessel contour.

Merge the images and store the resulting merged image.
Propagate the ROI to the other images

- Right-click on the ROI and select ‘Propagate All’ to propagate the ROI to all images.

NOTICE
Repeat the steps of drawing a ROI and propagating the ROI if more ROIs for several vessels have to be drawn.

Check the ROIs on all images

- Use the movie function to check the ROIs on the images.

Show the results

A graphical chart and the numerical results (in a table) are automatically displayed in the upper viewports.

- Click ‘Results Setup ...’.
  The ‘Results Setup’ window opens.
- Click to select any of the display options as:
  - Select the vessel to display the results for.
  - Define if the results are to be displayed inverted.
  - Select the result type.
  - Select the unit.
- Right-click on the image to open a pop-up menu offering the possibilities:
  - Window (settings): No copy, Copy to right, Copy to all
  - Interpolate
  - Filled graphics
  - Display analysis graphics
- Right-click on the image and select an image type for display.
- Scroll through the numerical results by means of the vertical scroll bar on the right side.
- Right-click on the graphical chart and select an item for display:
  - Area
  - Maximum velocity
  - Minimum velocity
  - Mean velocity
  - Peak velocity
  - Nr. of pixels
• Flux
• Standard deviation

► Click on the graphical chart to navigate through images.
  In the lower viewports the corresponding image will be displayed indicated by a vertical line on the graphs.

Export and print the results

1. Click the 'Export results' button from the 'More' drop-down menu.
2. Select an ‘Export’ destination.
3. Click |Okay| to confirm.
4. Hardcopies can be performed in the usual way.

NOTICE
The results are exported as CSV (Comma Separated Values) file.
This file type has to be opened via Microsoft Excel in order to present the results.

PicturePlus Workflow

Start up PicturePlus

1. Right-click on a suitable scan in the Thumbnail View.
   A context menu appears.
2. Click ‘PicturePlus’.
   PicturePlus opens.

Enhance Images

It is possible to define the degree of smoothing and edge enhancement:

► To change edge enhancement, right-drag horizontally.
  Movement to the right increases and movement to the left decreases edge enhancement.

► To change smoothing, right-drag vertically.
  Downward movement decreases smoothing. Upward movement increases smoothing.

► To select one of the PicturePlus presets,
  • click in the ‘Presets’ field
  • select a preset from the drop-down menu and
  • click ‘Apply’.
Generate a new imaging series

► Click ‘Generate series’.

A new imaging series will be generated within the current examination.

Image Algebra Workflow

Start up Image Algebra

You can perform Image Algebra either on two different scans or on a single dynamic scan. This requires the selection of one or two scans when starting up the package.

1. Select the scan(s):

   A context menu appears.
   • To perform Image Algebra with a single dynamic scan, right-click on this scan in the Thumbnail View.
   • To perform Image Algebra with different scans, press and hold [Shift] and then click in the Thumbnail View to select the two scans.

2. Select ‘ImageAlgebra’.

   The ImageAlgebra package opens.

Select the type of operation

► Click on the field ‘Select the operation’ to display the drop-down menu with the available algorithms.

► Click to select the required algorithm.

Select the images for processing (A and B)

► Click on the selection (toggle) icon and ‘Switch to single selection’ or ‘Switch to range selection’.

► Select the images for A and B by dragging the slider.

Apply a weighting factor

► Define the weighting factor by clicking on the slider and dragging.

   The image in the preview will be updated in real-time.

![Slider for the weighting factor.](image-url)
Adjust the threshold values

- Click on either of the threshold buttons.
- Drag up- and downwards to adjust the threshold.

Generate a new imaging series

- Click ‘Generate series’.
  A new imaging series will be generated within the current examination.

Diffusion Registration Workflow

1. Right-click on a suitable diffusion dataset in the Thumbnail View.
   A context menu appears.

2. Click ‘Diffusion Registration’.
   The diffusion registration is performed as a background process.
   The start of this background process is indicated on screen: ‘The registration has been submitted’.

3. From the main menu bar, select 'System' and then 'Manage Job Queues' to check the status of the package.

4. The new imaging series appears automatically in the Thumbnail View when the diffusion registration process is finished.
   The new imaging series can be recognized by the prefix ‘Reg’.

5. View the new imaging series with the ‘ImageView’ package.

6. Compare the diffusion registered images with the original images in movie mode to get an impression on the effects of the diffusion registration package.

NOTICE

When the diffusion registration package is part of an ExamCard, it will be performed as a background function without notifying the user.
Diffusion Workflow

Start up the Diffusion package

1. Right-click on a suitable diffusion dataset (at least two different b-values) in the Thumbnail View.
   A context menu appears.

   NOTICE
   Use a registered dataset if available.

2. Click ‘Diffusion’.
   The Diffusion package opens, and the center slice with a corresponding map will be shown.

Navigate through images

Through slices (or resulting) maps

- In the image (or map) viewport, drag to the left or to the right.
- Alternatively use the left and right arrow keys.

Adjust the B0 Threshold

By default, the 'Adjust Threshold' function is automatically enabled: the threshold mask is laid over the original image.

Setting a threshold mask will exclude background pixels from the functional map calculations.

1. Right-drag up- and downwards to adjust the threshold.

Fig. 143: A diffusion map (FA map) without diffusion registration (left) and with diffusion registration (right).
Select b-values
1. Click ‘Select b-values’.
2. Select at least two b-values which are to be processed.
3. Click |Okay| to confirm the selection.

Generate a new imaging series
1. Click ‘Generate series’.
2. Select the map type to be calculated:
   DWI iso map, ADC map, eADC map, ADC iso map, eADC iso map, FA (greyscale) map and/or
   FA color map.
3. Define a unique name for the new series in the entry field.
4. Click |Okay| to confirm and to start the calculation.

Fiber Tracking Workflow

Start up FiberTrak
1. Right-click on any DTI dataset in the Thumbnail View.
   A context menu appears.
2. Click ‘FiberTrak’.
   The FiberTrak package opens.

Load anatomical data
1. Drag the required anatomical dataset into the package from the Thumbnail View.

Navigate through the data
There are various ways to navigate through the data. It is important to identify the structures of
interest prior to tracking fibers and to display them in the 3D view in such a way that ROIs can
easily be drawn. The most important navigation tools are:

Scroll through the dataset
   ▶ Right-click on an image.
   ▶ Select ‘Scroll’.
      This is the default setting.
   ▶ Drag in the 3D view to scroll through the slices.
      OR:
Drag the colored lines (blue: FH-, green: AP- and red: RL-image position) on the orthogonal views to any desired location. The image in the 3D view will be updated to the current location.

**Rotate the dataset**
- Right-drag on the 3D view to rotate in any direction.

See chapter “Tips for Fiber Tracking” on page 295 for an example concerning the IFO.

**Track fibers**
Either single ROI or multiple ROI Fiber Tracking can be performed. Single ROI Fiber Tracking is fast in delineating fibertracts, but may be less accurate. Multiple ROI Fiber Tracking is the method of choice for a more accurate determination of the complete fibertract bundle.

For more information, see chapter “Algorithms: Fibers and Seeded ROIs” on page 159.

1. Click ‘Track Single ROI Fibers’ on the toolbar.
2. Draw a freehand ROI (default ROI type) manually. The fibers originating from this ROI will be shown immediately.
   This can be done repeatedly.
   OR
3. Click ‘Define multiple ROIs’ on the toolbar.
4. Draw multiple freehand ROIs (default ROI type) manually which should all include the requested fiber.
5. Click ‘Track Multiple ROI Fibers’ (toolbar or via right-click on image) when all ROI’s are drawn. Tracts will be generated if they comply to the criterion that they pass through all ROIs.

**Generate result series**
- On the FiberTrak toolbar,
1. select either/or
   - ‘2D Cross-section Tract Series’
   - ‘3D Projection Tract Series’.
2. Specify the series:
   - In case of 2D Cross-section Tract Series: select orientation, slice range and the number of frames.
   - In case of 3D Projection Tract Series: define the number of frames and store viewpoints.
     See section ‘Output Series’ for more information.
3. Click ‘Generate’ to start the calculation.
The resulting color images can be sent to PACS or general archive.

**View FiberTrak results in movie mode**

- In ImageView,
  1. Click the ‘Movie’ icon to view the generated FiberTrak series in movie mode.
  2. Right-click when the movie is running to export such movies to a user defined network drive or USB device.

**FiberTrak: Advanced Workflows**

This section provides more information about the FiberTrak package in order to achieve best results and to optimally handle the package:

- ROIs
- Algorithms: Fibers and Seeded ROIs
- Colors: Fibers and ROIs
- Statistics: Fibers, ROIs and current voxel
- Output Series
- Tips for Fiber Tracking

**Output Series**

The FiberTrak package can generate output series of the FiberTrak dataset. It is possible to render 2D cross-section or 3D projection tract series.

**2D Cross-section Tract Series**

The ‘2D Cross-Section Tract Series’ will show slices of the dataset where the intersection of fibers is shown. Note that the coloring of the orthogonal view is used for the slices.

**3D Projection Tract Series**

In some cases, a 3D rotating, zooming and moving view of the resulting tracts is needed to view the interaction of tracts and pathology. The ‘3D Projection Tract Series’ are made by defining a script consisting of multiple viewpoints. The series is generated from smooth transitions between these viewpoints.

**Creating and viewing of 2D Cross-section Tract Series**

1. Click ‘2D Cross-section Tract Series’ on the FiberTrak toolbar.

The window to define 2D Cross-section tract series will open.

![Fig. 144: Window to define 2D Cross-section tract series.](image)
2. Define the orientation of the resulting series by selecting / deselecting either: coronal, sagittal or transverse.

3. Define the slices to be included in the calculation of the tract series:
   - Click on the selection icon to toggle between ‘range selection’ (where multiple images can be chosen) and ‘single selection’ (where only one slice can be chosen).
   - Select the slice or the slice range by clicking on the slider besides the icon and by dragging. The selected slice(s) will be indicated as slice number on top of the slider and as red lines or red box on the orthogonal views.

Fig. 145: Example: The upper row shows a single selection of slice 1. The lower row shows a range selection of slices 2 to 64.

4. Define the number of frames
   - either by selecting ‘1 per slice’ where one frame will be calculated per slice.
   - or by setting a number of frames where interpolation will occur between slices in order to reach the required number of frames.

5. Click |Generate| to generate the output series.
   Clicking |Close| closes the window without generating output series.

6. Define the image resolution (128, 256, 512 or 1024) of the 2D tract series and enter a series name.

7. Click |OK| to confirm.
   The output series will be generated.

**Creating and viewing of 3D Projection Tract Series**

3D Projection Tract Series are created by defining multiple viewpoints to a script (list of stored viewpoints). These viewpoints can also be deleted or updated within the script.

1. Click ‘3D Projection Tract Series’ on the FiberTrak toolbar.
   The window to define 3D Projection tract series will open.

2. Navigate through the FiberTrak dataset to display the data at the first desired viewpoint.
   Note that all elements of navigation can be used to define each view in the script. E.g. transparancy can be differently between views so that it appears that a slice is slowly disappearing.

3. Click on the ‘Add’ icon to add this viewpoint to the script. This view will be saved as ‘view0 (start)’.

4. Navigate through the FiberTrak dataset to display the data at the next desired viewpoint.

5. Define the number of frames between the previous and the current viewpoint, e.g. 20.

6. Repeat the steps 3 to 5 as often as required.

7. Click |Preview| to check if the viewpoints have been chosen correctly.
If necessary,

8. Select a viewpoint by simply clicking on it. Navigate to a different view and click |Update| to change this viewpoint.

9. Click |Generate| to generate the output series. Clicking |Close| closes the window without generating output series.

10. Define the image resolution (512 or 1024) of the 3D tract series and enter a series name.

11. Click |OK| to confirm.

The output series will be generated.

**Script Editor '3D Projection Tract Series'**

The script editor offers several options concerning the administration of these scripts, e.g. scripts can be stored, deleted or a preview can be generated. The following table summarizes the possibilities.

<table>
<thead>
<tr>
<th>Icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="File" /></td>
<td>A new script will be created. All of the entry fields within the '3D Projection Tract Series' will be cleared in order to enter new values and to save new views.</td>
</tr>
<tr>
<td><img src="image" alt="Save" /></td>
<td>The current script will be stored. It will be necessary to enter a name for this script.</td>
</tr>
<tr>
<td><img src="image" alt="Delete" /></td>
<td>The current script will be deleted.</td>
</tr>
<tr>
<td><img src="image" alt="Play" /></td>
<td>The current script will be shown as a preview.</td>
</tr>
<tr>
<td><img src="image" alt="Pause" /></td>
<td>The preview will be stopped.</td>
</tr>
<tr>
<td><img src="image" alt="Update" /></td>
<td>The current viewpoint will be updated to the actual navigation settings.</td>
</tr>
</tbody>
</table>

**Tips for Fiber Tracking**

**Drawing ROIs in Multiple ROI Fibertracking**

When a fiber is to be identified using two ROIs it is important that the ROIs are created in the correct fashion. One example is given below:
In order to identify the "inferior fronto-occipital fasciculus" (IFO), two (coronal) ROIs have to be defined in the frontal and occipital lobe respectively. It is advised to overlay FA colors to the anatomical background to guide the drawing of ROIs. The given delineation (yellow line) is clearly drawn in a "wide" manner: the combination of the two ROI’s will identify the tract.

**Quick Fiber Search**

In some cases it is convenient to perform a quick search for tracts first, after which the accurate delineation can take place. One way to do this is to combine ‘Single ROI Fiber Tracking’ with a freehand ROI. Drawing a ROI anywhere in the images will quickly identify the tracts in this area.

**Combine fMRI results with the FiberTrak results**

It is possible to combine fMRI results with the FiberTrak package. In order to do so the fMRI results should have been saved from within the IViewBOLD package into a separate series. These series can simply be loaded into the FiberTrak package and viewed as the "anatomic."
BOLD imaging Workflow

Patient preparation and positioning

BOLD imaging demands for optimum patient cooperation.

► Instruct the patient carefully about what to expect and about the paradigms he/she has to perform. It might be helpful to train the patient already outside of the scanner.

► Tell the patient what he/she has to do, e.g. "Move the right thumb", and practice.

► Tell him/her also what is not desired, e.g. "Do not move the whole hand or even the arm" as this might give a stimulus correlated activation which may influence the functional result.

► With visual stimulations, ensure that the patient can see the required information on screen by means of a mirror on the coil.

► Position the patient as usual.

Start up IViewBOLD

Real-time BOLD analysis

1. Start a BOLD imaging ExamCard.
   In general, a survey and a reference scan are performed.

2. Select 'IViewBOLD' from the Analysis menu (without selecting a thumbnail dataset).
   In real-time mode, a message is displayed indicating that the system is waiting for a new scan to start: "Waiting for new scan to start."
   The IViewBOLD package opens with the last-used paradigm.

NOTICE

When the IViewBOLD package is started, without a selected scan in the pictorial index, the package will start in real-time mode.

This is only possible for the acquisition context.

3. Optional: Select a paradigm if the current paradigm is not the correct one (or edit the current paradigm or generate a new paradigm).

4. Instruct the patient and start the BOLD scan.

5. View the SPMs in real-time.

Postprocessing (existing BOLD scans)

1. Right-click on a suitable BOLD dataset (minimum of 6 dynamics) in the Thumbnail View.
   A context menu appears.
2. Click ‘IViewBOLD’.

3. The IViewBOLD package opens with the last-used paradigm.

4. Optional: Select a paradigm if the current paradigm is not the correct one (or edit the current paradigm or generate a new paradigm).

5. Click ‘Compute’ to calculate the Statistical Parametric Maps (SPMs).
   In the info line, the message appears: ‘Analyzing scan. X dynamics processed. ... Ready.’

**NOTICE**
In real-time mode, the computation is performed automatically.

6. View the SPMs.

**View the SPMs**
Statistical Parametric Maps (SPMs) are computed using the General Linear Model (GLM) and represent the results of statistical tests (e.g. t-tests), computed at every voxel in the images. These t-tests will show a larger value when it is even more likely that the signal changes ‘follow’ the applied paradigm.

**Modify the results display**
1. Click on the up/down arrows besides the toolbar icons to increase or decrease the values of 'Cluster Size', 'Threshold', 'Mask' or manually enter a value.
2. Click ‘Negative Statistics’ to enable or disable this function.

![Fig. 148: Icons from left to right: Cluster size, Threshold, Mask, Negative Statistics.](image)

3. To change the color range: mid-drag while pressing the |Ctrl| key.
   Horizontal movement increases or decreases the color range, vertical movement shifts the range. The SPM and the tile viewer will automatically be refreshed.

**Load anatomical reference images**
1. Drag the required anatomical dataset from the pictorial index into the package.

**NOTICE**
MultiPlanar Reformats and Fiber Tracking results (2D cross-section) can be used as an underlay.
Enable or disable Motion correction
1. Enable or disable ‘Motion correction’ from the ‘IViewBOLD’ menu.
2. Click ‘Compute’ to recalculate the maps.

Adjust Blending and Threshold
1. Right-click on a map.
2. Select ‘Adjust Blending and Threshold’.
3. Drag up- and downwards to adjust the threshold.
4. Drag to the right or the left to adjust the blending.

Save results
1. Right-click on a map.
2. Select ‘Save results’.
3. Select either ‘Statistics’ or ‘Color Overlay’.
   A new series will be generated.
   The new series can be viewed with ImageView.

Calculate a TID
1. Click ‘Show Time Intensity Curve’ to open the TID window.
2. Click ‘ROI type’ and select the ROI type:
   • Freehand (for any kind of shape),
   • Bezier (for paraboloid or sinusoid shape of ROI),
   • Ellipsoid (for circular or any kind of ellipsoid ROI)
3. Click ‘Draw ROI’.
   • Click once to start drawing.
   • Drag to define the contour.
   • Click to close the contour.
4. Click ‘Compute’ to calculate the TID.
5. Right-click on the graph display to access the right mouse menu and change the graph display.

For more information, chapter “Time-Intensity Diagram (TID)” on page 172.

BOLD imaging: Paradigm Handling
This paragraph describes how to handle paradigms in the IViewBOLD package:
• Select a paradigm
• Set up a new paradigm
• Edit a paradigm (starting up with the current paradigm)
• Paradigm Editor
• Delete a paradigm

Select a paradigm

► Select ‘Select Paradigm’ from the IViewBOLD toolbar.
   A list of the available paradigms is displayed.
► Select the desired paradigm.
► Click |Ok| to apply the selected paradigm.
   Clicking |Cancel| closes the dialog box without applying the changes made.

NOTICE
The ‘Select paradigm’ option is disabled when a calculation is running.

Delete a paradigm

1. Select ‘IViewBOLD’ on the toolbar.
2. Select ‘Select Paradigm’.
   A list of the available paradigms is displayed.
3. Select the paradigm that has to be deleted.
4. Click |Delete|.
   A prompt appears:
   ‘Are you sure you want to permanently delete the selected paradigm?’
5. Click |Yes| to delete the paradigm.
   Clicking |No|, no paradigm is deleted.
   The list of paradigms will be updated.

Set up a new paradigm

► Select ‘New Paradigm’ from the IViewBOLD toolbar.
   The paradigm editor opens with an empty (paradigm editor) dialog box.
► Create a paradigm according to the tasks performed and save this paradigm under a new name.

See chapter “Paradigm Editor” on page 301 for more information.
Edit a paradigm

- Select 'Edit Paradigm' from the IViewBOLD toolbar. The paradigm editor opens and displays the settings of the current paradigm.
- Edit the settings of the chosen paradigm.
- After editing, |OK| can be used to apply this paradigm.
  Or |Save| can be used to save the changes for later usage.

For more information, see chapter “Paradigm Editor” on page 301.

Paradigm Editor

The paradigm editor allows to define and edit paradigms. The figure shows the layout of the paradigm editor.

![Paradigm Editor Layout](image)

Fig. 149: Definition of a language-speech paradigm using the paradigm editor: generation of words during the first 10 dynamics, rest during the 10 next dynamics. Note that "Paradigm Repetition Length" equals 20 to include both 10 dynamics of activation, and 10 dynamics of rest.

Paradigm Name

- Enter a paradigm name.

  The name should reflect the general identity of the BOLD examination.

Paradigm Repetition Length

- Specify the paradigm repetition length, either numerically or by using the up- and down arrows.

  The paradigm repetition length is defined by the number of dynamics which are to be performed repeatedly, e.g. the paradigm repetition length is 20 in an experiment of 10 activation dynamics alternating with 10 rest dynamics.

**NOTICE**

In the above example, the ‘Paradigm Repetition Length’ is set to 20 and the language task (active) is defined as dynamics 1 to 10. This automatically results in dynamic 11 to 20 being the dynamics in rest.
**SPMs**

- Enter a SPM name, e.g. ‘visual’.
- Drag the left mouse on the grid to mark or unmark the dynamic scans with brain activation (the dynamics where a stimulus is presented or a task has to be performed).

Only 50 dynamics are visible simultaneously. To view more dynamics, a scrollbar can be used. See chapter “Statistical Parametric Maps (SPMs)” on page 168 for more information on the statistics.

**NOTICE**

Dynamics in rest may not be marked as task, because all inactive dynamics are considered as reference in the SPM calculation.

If however this would be the case, an error message would be displayed in the bottom line: ‘Task 1 has all dynamics defined as active’.

**Icons**

- Click on the up/down arrows to increase or decrease the values or manually enter a value.

![Fig. 150: Icons](image)

<table>
<thead>
<tr>
<th>Icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Smoothing</td>
</tr>
<tr>
<td>2</td>
<td>Hemodynamic Delay</td>
</tr>
<tr>
<td>3</td>
<td>Cluster Size</td>
</tr>
<tr>
<td>4</td>
<td>Threshold</td>
</tr>
<tr>
<td>5</td>
<td>Map Color Range</td>
</tr>
<tr>
<td>6</td>
<td>Negative Statistics</td>
</tr>
</tbody>
</table>

See chapter “Statistical and viewing parameters” on page 169 for more information.

**Standard Deviation**

- Click on the check box to enable or disable the calculation of the standard deviation map. By default, the calculation of the standard deviation map is disabled.
Save the paradigm

- Click |Save| to save the paradigm.
  The paradigm is only saved, but not applied in this case.

In case of saving a paradigm without changing its name, a window pops up: "Confirm file replace: Paradigm already exists. Do you want to replace it?"

Click |Yes| to confirm file replacement.

Asterisk

An asterisk behind the name of the current paradigm indicates that the original paradigm has been edited (but has not been saved).

NOTICE

The Info line at the bottom of the window indicates if a paradigm is valid or not and gives hints on how to correct a problem.

- Click |Ok| to apply the paradigm and to leave the paradigm editor.
  Clicking |Cancel| closes the dialog box without applying the changes made.

BOLD imaging: Esys synchronization

This chapter describes the basic functionality of the Esys Synchronization Protocol (ESP). This synchronization will assure that the Esys will initialize, start paradigms etc., all automatically, started from instructions sent by the scanner. ESP will also update the operator behind the scanner console of the status of the Esys. This means that the operator will no longer need to perform any activity on the Esys itself during standard clinical BOLD imaging, when the ESP is used.

Workflow

1. Turn the Esys on.
2. Enter the patient and examination data at the scanner’s console.
   The patient name and session number will be sent to the Esys when the first fMRI BOLD scan is performed. This creates a new unique Esys session linked to this patient name.
3. Prepare the patient and position him/her in the scanner with the required Esys devices:
   - keyboard with buttons needed for paradigm interaction
   - a display attached to the head coil
   - the dedicated Eloquence headset
4. Select and start a BOLD ExamCard with IViewBOLD as inline processing step.
   The surveys and reference scans are performed.
5. Plan the anatomical scans and resume the ExamCard.

The ExamCard is executed. When the BOLD scan is started, the paradigm name and the specific timings of the BOLD experiment are sent to the Eloquence. Then the instructions of the paradigm are started at the Esys.

6. Let the patient confirm by pressing the ‘Okay’ button that he/she understood the instructions.

- Automatically, the information that the Eloquence and the patient are ready is sent to the scanner. The IViewBOLD package and the ExamCards info bar display an appropriate message.
- When the preparation of the BOLD scan is finished, a pop-up window appears to start the BOLD scan.

7. Click |Proceed| to start the BOLD scan.

- The FBI box creates an RF-trigger which identifies the exact beginning of the paradigm.
- When the scan is finished, an ‘end’ message is sent to the Esys, and the Esys will get ready for the next paradigm.
- The IViewBOLD package is launched automatically with the correct paradigm.

8. Proceed with the IViewBOLD analysis.

**Add IViewBOLD SmartLine processing to ExamCard**

In general, postprocessing steps can be added to the ExamCard as SmartLine processing steps which are executed automatically as part of the ExamCard.

This chapter describes how to add an IViewBOLD processing step to a BOLD ExamCard.

**Workflow**

1. Select a preferred BOLD ExamCard or preset procedure.

**NOTICE**

Do not yet start the scan.
2. Start IViewBOLD.
3. Select or create a paradigm with a name that exactly matches the name of the paradigm on the Esys (including language). For example, if you want to start the "Cognitive" paradigm, using the run name "N-Back" with the language set to "Italiano", a paradigm must be started/created with the following name: "Cognitive+N-Back+Italiano".

**NOTICE**
The paradigm name, run name and language must be separated by + characters.

4. Make sure that all the settings for analysis are set correctly. Note that the information on timing (e.g. how many dynamics for a certain block etc) will be sent to the Esys, and this will influence the actual paradigm run.
5. Start the BOLD scan.
6. Close the IViewBOLD package when the scan is finished.
   Now there is a newly created processing step with the name of the desired paradigm, and linked to the performed BOLD scan.
7. Save the ExamCard.
   The next time that this ExamCard is executed, the IViewBOLD package and the Esys will start automatically.

**NOTICE**
Not only the entire ExamCard will be saved, but also the processing step itself (with a specific paradigm name).

In this way, various processing steps can be saved and attached to BOLD scans at any time. Each processing step will be linked to a specific paradigm and run so that the processing steps basically determine which paradigm is chosen.

**NOTICE**
Make sure that the correct paradigm name is used with the notation "Paradigm+ Run+Language" where the three components exactly match the paradigm name on the Esys.

**More about the synchronization**
- In case of a scan abort initiated by the operator, the paradigm-run will automatically be stopped.
• If the Eloquence doesn’t know the paradigm name (e.g. due to a typo), the Eloquence will respond with a message "Paradigm is not available, cannot proceed". In this case, the sequence can be stopped or continued.

• If the paradigm cannot be run because of timing problems, the Eloquence will respond with a message "Paradigm available, but cannot proceed". In this case, the sequence can be stopped or continued. In this case the synchronization of the paradigm will very likely be incorrect. Reasons for timing problems might be a conflict between paradigm repetition length (in ms) and a TR which has been set to a too large value.

**Protocol requirements**

In order to assure correct synchronization, the following prerequisites must be met:

• The parameter ‘Synch. ext. device’ must be set to ‘Yes’ and the first RF trigger must be set to the dynamic ‘1’.

• A manual start is needed.

• The parameter ‘Real-time reconstruction’ must be enabled to allow for the presentation of pre-scan calibrations and presentation of instructions to the patient.

**Neuro T2* Perfusion Workflow**

**Start up the Neuro T2* Perfusion package**

1. Right-click on a suitable neurological perfusion data set in the Thumbnail View.
   
   A context menu appears.

2. Select ‘Neuro T2* Perfusion’.
   
   The package opens.

Moving the cursor over either the original image or the map, the curve and the numerical results originating from the current pixel will be shown.

**Navigate through images**

**Through dynamics**

- In the image viewport, drag to the left or to the right.

**Through slices**

- In the image viewport, drag up- or downwards.

**Through maps**

1. In the map viewport, drag to the left or to the right.
Adjust the threshold

By default, the 'Adjust Threshold' function is automatically enabled: the threshold mask is laid over the original image.

Setting a threshold mask will exclude background pixels from the functional map calculations.

1. Right-drag up- and downwards to adjust the threshold.

Calculation of the perfusion results using the AIF

1. Select 'Arterial Input Function' from the 'Select Algorithm' drop-down menu.
   
   A red square shows up in the image viewport. This red square spans the size of 7 by 7 voxels. In the right viewport the dynamic curves of these 7x7 voxels are shown.
2. Move the red square to the arterial vessel from which the AIF is supposed to be derived.
3. Click on the individual graphs if they are to be included in the definition of the AIF.
   
   The selected graphs will be green.
4. Right-click on the graphs and press 'Proceed' to confirm.
   
   Now the AIF is identified and the resulting maps will be shown.

Generate results

Results per pixel

In order to generate results per pixel, you have to select a pixel. This can easily be done by pointing at a pixel on the original image or the map. Prerequisite is that the pointer is in the 'Follow Mouse' mode.

1. Right-click on the curve view port.
2. Click to enable 'Follow Mouse'.
3. Move the pointer over the image or the map.
   
   Results will be updated with every move of the pointer.

Results per ROI

1. Right-click on one of the image viewports and set the Interaction mode to 'Draw ROI'.
2. Drag the left mouse over the image to draw a ROI.
   
   Release the left mouse button to close the ROI.
3. Right-click on the graph and select 'ROI average'.

You can draw up to 5 ROIs on any desired slice. Scroll through the slices between drawing if necessary.

- When 5 ROIs are drawn, the function 'Draw ROI' is automatically disabled.
• The 5 ROIs are initially called ROI A, ROI B, ROI C, ROI D and ROI E. The names are given in a random order.

**Generate a new imaging series**
► Click ‘Generate series’.
A new imaging series will be generated within the current examination.
Note that several output choices are provided in the ‘Generate’ box.

**Basic T1 Perfusion Workflow**

**Start up the Basic T1 Perfusion package**
1. Right-click on a suitable perfusion data set in the Thumbnail View.
   A context menu appears.
2. Select ‘Basic T1 Perfusion’.
   The package opens.
Moving the cursor over either the original image or the map, the curve and the numerical results originating from the current pixel will be shown.

**Navigate through images**

**Through dynamics**
► In the image viewport, drag to the left or to the right.

**Through slices**
► In the image viewport, drag up- or downwards.

**Through maps**
1. In the map viewport, drag to the left or to the right.

**Adjust the threshold**
By default, the 'Adjust Threshold' function is automatically enabled: the threshold mask is laid over the original image.
Setting a threshold mask will exclude background pixels from the functional map calculations.
1. Right-drag up- and downwards to adjust the threshold.
Generate results

Results per pixel
In order to generate results per pixel, you have to select a pixel. This can easily be done by pointing at a pixel on the original image or the map. Prerequisite is that the pointer is in the ‘Follow Mouse’ mode.
1. Right-click on the curve view port.
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Results per ROI
1. Right-click on one of the image viewports and set the Interaction mode to ‘Draw ROI’.
2. Drag the left mouse over the image to draw a ROI.
   Release the left mouse button to close the ROI.
3. Right-click on the graph and select ‘ROI average’.
You can draw up to 5 ROIs on any desired slice. Scroll through the slices between drawing if necessary.
- When 5 ROIs are drawn, the function ‘Draw ROI’ is automatically disabled.
- The 5 ROIs are initially called ROI A, ROI B, ROI C, ROI D and ROI E. The names are given in a random order.

Generate a new imaging series
- Click ‘Generate series’.
  A new imaging series will be generated within the current examination.

SpectroView Workflow
The table summarizes the workflow for processing of spectral data:

<table>
<thead>
<tr>
<th>Step</th>
<th>Single Voxel Spectroscopy (SVS)</th>
<th>Chemical Shift Imaging (CSI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>• Start up SpectroView</td>
<td>• Start up SpectroView</td>
</tr>
<tr>
<td>2</td>
<td>• Select a script</td>
<td>• Select a script</td>
</tr>
<tr>
<td>3</td>
<td></td>
<td>• Select relevant voxels</td>
</tr>
<tr>
<td>4</td>
<td>• Run the script</td>
<td>• Run the script</td>
</tr>
<tr>
<td></td>
<td>• If necessary: zooming and panning.</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>• Optimize the spectrum display</td>
<td>• Optimize the spectrum display</td>
</tr>
</tbody>
</table>
Start up SpectroView

- Right-click on a suitable spectroscopic dataset in the Thumbnail View.
  A context menu appears with several selection possibilities.
- Click on the ‘SpectroView’ icon.
  The SpectroView package opens.

Alternatively:
- Double-click on a spectroscopic dataset OR
- Drag a spectroscopic dataset into the viewports.

NOTICE
If ‘Anatomic Region’ is specified on ExamCard level, the corresponding Basic script is automatically executed for processing time domain data.

NOTICE
If no ‘Anatomic Region’ is specified on ExamCard level, a pop-up is displayed, indicating that a ‘brain’ processing script is executed.
After processing, a new Basic script can be selected.

NOTICE
If voxels fail, there will be a pop-up after all voxels have been processed, that gives information about the error(s).
More information is found in the ‘Status’-tab.

Select a script

A script is a set of processing steps that are performed to analyze and display a spectrum (or set of spectra).
The possibilities within a script are different depending on the type of the selected dataset.

<table>
<thead>
<tr>
<th>Type of dataset</th>
<th>Icon</th>
<th>Possibilities</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time Domain dataset</td>
<td><img src="image" alt="Icon" /></td>
<td>The script will allow for pre-processing steps via a 'basic processing' script.</td>
</tr>
</tbody>
</table>

For more information on scripts

- See chapter “Scripts and script handling” on page 318.
- See chapter “Processing steps” on page 320.

**Default processing script**

When you open a spectroscopic dataset in SpectroView, the system automatically comes up with a default script, dependent on the selected dataset. This default script is indicated as ‘current script’ in the toolbar.

**NOTICE**

This default script depends on the setting of the general imaging parameter ‘Anatomical Region’.

**NOTICE**

In case of a time domain dataset, this is the BasicProcessing script.

**Workflow ‘Select script’**

1. Click on the ‘Select Script’ icon on the toolbar.
   
   The ‘Script Selection’ window opens showing the list of available scripts.
   
   By default, only those scripts are displayed which are compatible with the currently selected dataset. To display also the scripts which are not compatible with the current dataset, disable one of the filters ‘Nucleus’, ‘Anatomy’, ‘Field’ and/or ‘TE’.

2. To select a script, double-click it, or click once and then click [OK].
Run the Script

1. Click on the ‘Run Script’ icon on the toolbar. Alternatively click [Run] within the script editor.

Zoom, Pan and Window for SpectroView

If necessary, zooming and panning can be performed now.

To zoom the spectrum,

- press middle and right mouse simultaneously. Move the mouse up and down to increase or decrease the displayed peak heights. Move the mouse left and right to increase or decrease the displayed chemical shift range.

To pan the spectrum,

- press middle and left mouse simultaneously. Move the mouse to pan the spectrum.

To change color range and threshold of color overlays,

- Press <CTRL> and middle mouse simultaneously to change the color settings. OR
- Select "adjust blending and threshold" from the image viewport menu to adjust threshold or opacity of the color overlay. If selected, dragging the left-mouse up and down changes the threshold of the color overlay. Dragging the left-mouse left to right changes the opacity of the color overlay.

This is only relevant for CSI data where metabolite maps are generated:

Select Relevant Voxels

NOTICE
This operation is only valid for CSI data sets or for dynamic single voxel data sets.
There are two possibilities of how to select relevant voxels, either by clicking on voxels or by drawing a ROI.

**In both cases:**

1. Click on the ‘Voxel selection’ icon in the toolbar.
   The drop-down menu opens.
2. Select one of the possibilities:
   - Select Individual Voxels
   - Select Voxels by Drawing

In voxel selection mode, the left mouse behaviour in the spectral grid is changed.

**In case of ‘Select Voxels by Drawing’**

1. Draw a freehand ROI by holding the left mouse and selecting a region over which you want to investigate. The voxels are automatically included based on the ROI drawn

**In case of ‘Select Individual Voxels’**

1. Click on a voxel to select it.

The corresponding spectrum and the table of results will be displayed. The screen layout matches the SVS screen layout. (Note that the table of results will only be shown if a script has been run before).

A new single click will select a new voxel and deselect the previously selected voxel. The spectrum and the table of results will be displayed again.

**Multivoxel Selection Mechanisms**

1. Click to select another voxel while simultaneously pressing <CTRL>.
   
   <CTRL> + left mouse click will select any unselected voxel and deselect any selected voxel. The other voxel will be selected additionally to the previously selected one. The spectra from the selected voxels are displayed.

2. Click to select one voxel, click once more to select another voxel while simultaneously pressing <Shift>.

   The two points define a box. All voxels in this box will be selected. The spectra from the selected voxels are displayed.
NOTICE
Voxel select can be chosen before a script is run to choose which voxels get processed. If no voxels are chosen before processing, a default grid of 5x5 voxels in the PRESS volume is displayed after processing.

Voxel color description
To facilitate further processing, the voxels are overlaid by a colored grid to indicate their current processing state:
- Blue outline: Voxels have been included in processing steps.
- Yellow shaded voxels: Voxel is currently displayed.
- Red outline: Voxel failed processing.
Right-clicking in the image display viewport and selecting "select all processed voxels", the previously processed voxels will be reselected.

NOTICE
Following the initial script generation, additional voxels can be added to the original processing as long as the script has not been changed.

Fig. 154: Example of voxel colors.

Optimize spectrum display
The spectrum display can be modified for any single spectrum display: SVS, one voxel CSI or one average of CSI.
1. Right-click on the spectrum display area to access the 'spectrum display' context menu. This menu offers possibilities as e. g.
   - show or hide list of spectrum data
   - show or hide spectrum and/or metabolite labels
• show fitted spectrum and/or fitted baseline
• select spectrum component for display (e.g. modulus, real)

2. Access the spectrum viewport context menu for multi-voxel display, via a right mouse click on the spectrum grid area. This menu offers possibilities as e.g.
• show or hide list of spectrum data
• specify quantities to be displayed
• set spectrum limits
• define type of display for spectra
• select spectrum component for display (e.g. modulus, real)

See section chapter “User Interface” on page 190, for more information on both menus.

Modify Layout

1. Click on the Layout icon to change the screen layout and select an option:

The resulting layout will be:

As layout requirements are different for SVS and CSI-cases, either one of the icons is grayed out, depending on the scan that is currently selected in SpectroView.

• the default screen layout with three image viewports at the top of the screen, a graph display area and a result display area.

• a screen with spectra only. The graph display area will be enlarged to fill the entire screen.

• a screen with a table of results only. The result display area will be enlarged to fill the entire screen.

• a screen with spectra on the image.

In case of CSI

1. Select the type of display from an array of selected spectra.
2. Click on either of the following icons:

• Horizontal display: The graphs are displayed horizontally. This is a multiple graph area mode.

• Stack display: The graphs are displayed vertically in one box with no dividing lines. This is a multiple graph area mode.
Spacing between spectra in stack display mode can be changed as follows: Press <Shift> and simultaneously, press both middle and right mouse icons. Moving the mouse upwards increases the space between spectra; moving the mouse downwards decreases the spacing between spectra. This does not affect the spectra themselves and is not applicable in other CSI display modes.

- **Geometrical display (default layout):** The graphs are displayed in viewports being structured in the same layout as in the CSI grid. Voxels that are not selected in the CSI grid have an empty corresponding graph.

- **Compressed display:** The graphs are displayed compactly, one by one in a square or rectangular array with a minimum of blank entries.

**Create screen captures**

There are different possibilities to create screen captures. These are listed below:

- Select ‘Screen Capture’ or ‘Screen Capture as’ from the Tools menu.
- Select ‘Print Screen’ via the corresponding icon on the general toolbar.
- Select ‘Export Picture’ to store the current viewport with overlays included as a *.png file in the E:\export directory.

**Storage and export of data**

There are three different data formats with respect to storage of data:

1. **DICOM-data (that is stored in the database)** For single voxel, entry x.1 = time domain data, entry x.2 to x.n are processed spectra. For CSI, x.1 is time-domain data, x.2 is image series. Each time a processing script is performed, the results can be stored via the toolbar option ‘Store Processing Parameters’. A new entry is added to the database.

2. **Export of spar/sdat** This export functionality is available in research tools only: If a spectroscopy dataset is selected for export in the DBIMEXP-research tool, spar/sdat data is exported to E:\export. In case of CSI series, par-rec data of the corresponding spectroscopic images is also exported.

3. **Output to a spreadsheet application**
   - Create a file named csvoutput.txt in E:\export. (empty file, it is used as a flag to tell SpectroV to enable CSV output.)
   - Only if enabled: Each time you run a script, the following files are placed in the G:\site \spectro folder:
     - [name].Fdd.csv - the Frequency Domain Data from the BasicProcessing Script
     - [name]Baseline.csv - the fitted baseline data
     - [name]Fitted.csv - the fitted peak data
BY default this is disabled to prevent unnecessary pollution of the export directory. This function can be enabled via the toolbar function 'More'/'Enable CSV Output'. When the package gets closed the functionality is disabled by default.

NOTICE

In case of running BasicProcessing Script, the only files created are "Fdd.csv" and "Script.txt".

These files use the naming scheme:

patient name-DICOM Study ID-DICOM Series ID-Date-Time-filename.ext

- patient name = the patient name with all the illegal filename characters and whitespace removed
- DICOM Study ID
- DICOM Series ID
- Date = the date of the script run
- Time = the time of the script run

The ".csv" files can be opened directly in Microsoft Excel and contain headers identifying each column. The data will contain X, Y, Z and T (time for dynamics) voxel coordinate columns (voxels are 4-dimensional objects).

- For single slice data sets, the Zcoord column will always be "1"
- For non-dynamic data sets, the Tcoord column will always be "1"
- For single voxel data sets, the coordinates will always be (1,1,1,t).
- In CSI data sets, the voxel with coordinate (-1,1,1,t) is the "average voxel", it contains the average of all the currently selected voxels.
- Spectrum values in these files are expressed in PPM

A maximum of 20 datasets can be present in the folder. If more than 20 sets are in the folder, SpectroView deletes the oldest set, as determined by the timestamp in the filename.

SpectroView: Advanced Workflows

This section provides more information about the SpectroView package in order to achieve best results and to optimally handle the package.

It covers:

- User Interface
- Scripts and script handling
• Processing steps
• Customization using the Peak Editor
• Series Preferences Database

Scripts and script handling
A script is a set of (pre-)processing steps that are performed to analyze and display a spectrum (or set of spectra). There are two different types of scripts:

• Basic Processing Scripts
  A Basic Processing Script defines the pre-processing steps that can be enabled or disabled.

• Fitting Scripts
  A Fitting Script defines the processing steps that can be enabled or disabled for the fitting process.
  – chapter “Processing steps” on page 320 for more information about the (pre-) processing steps.

Scripts can be selected from a list, modified and then saved with changes.

The following paragraphs describe the script handling how to edit and save a script and how to delete a script.

Edit Script
It is possible to define user defined scripts. This can be done by editing an existing script:

1. Click on the ‘Edit Script’ icon in the toolbar.

The script editor displays
• the name of the current script
• a description of the script and its purpose
• anatomy, nucleus, echo time and supported field strengths
• a list with all possible processing steps, each with a checkbox to allow the user to enable or to disable the corresponding step.

2. Select a nucleus: $^1$H, $^{31}$P or $^{13}$C. In such a way, you can make a $^{31}$P script out of a $^1$H script.
3. Set the Echo time property to ‘short’ or ‘long’ (longer than 75 ms).
4. Click in the Field Strength checkboxes to specify whether this script is tuned for a specific field strength or a range of field strengths.

**NOTICE**
The properties ‘Nucleus, Echo Time and Supported Field Strengths’ are only used to drive the Script Selection Dialog filtering.
Changes to these properties do not impart any automated tuning to an existing script.

5. Click on the checkbox of a processing step to enable or disable the step for the script.
The enabled step will be highlighted. Once a step is highlighted, a page of parameters associated with the step will be displayed.
6. Set the parameters to the desired values. Chapter “Processing steps” on page 320 for more information on the processing steps and corresponding parameters. Chapter “Scripts and script handling” on page 318 for more information on the scripts.

**NOTICE**
Edited scripts are renamed using the following format: <unnamed>date-time.

7. Click [Cancel] to close the dialog box without applying the changes made.
Clicking [Run] applies the script immediately and exits the script editor.
Clicking [OK] can be used when a script has not been saved yet. It closes the dialog box and stores the edited script temporarily until another script or spectroscopic data set is selected. The edited script can still be run or edited later. This is an useful option in order to judge the quality of a script prior to saving.
8. Save Script
The script is only saved, but not applied in this case.
• Click the ‘SaveScript’ icon in the toolbar to save the script.
• Enter a name (when editing a Philips supplied script) and optionally a script description.

**Delete Script**
• Click ‘Delete Script’ on the SpectroView toolbar to delete the current script.
Processing steps

This section describes the processing steps which can be performed within a basic processing script and/or fitting script.

Once a processing step is enabled, a page of parameters associated with the step will be displayed in the Script Editor.

![Processing steps in Basic Processing Script for Single Voxel Imaging.](image1)

![Processing steps in Peak Fitting script.](image2)

<table>
<thead>
<tr>
<th></th>
<th>General properties</th>
<th></th>
<th>Processing steps</th>
<th></th>
<th>Reserved for parameters belonging to the selected and thus highlighted processing step</th>
</tr>
</thead>
</table>
## Available pre-processing steps in Basic Processing Script

<table>
<thead>
<tr>
<th>For Single-Voxel Spectroscopy</th>
<th>For Chemical Shift Imaging</th>
</tr>
</thead>
<tbody>
<tr>
<td>• Dual Volume Decode</td>
<td>• Residual Water Subtraction</td>
</tr>
<tr>
<td>• Residual Water Subtraction</td>
<td>• Residual Water Subtraction</td>
</tr>
<tr>
<td>• Time Domain Signal Shifting</td>
<td>• Time Domain Signal Shifting</td>
</tr>
<tr>
<td>• Apodization Filtering</td>
<td>• Apodization Filtering</td>
</tr>
<tr>
<td>• Zero-Fill and FT</td>
<td>• Zero-Fill and FT</td>
</tr>
<tr>
<td>• Spectrum Phase Adjustment</td>
<td>• Spectrum Phase Adjustment</td>
</tr>
<tr>
<td>• Shift Peak Frequency</td>
<td>• Shift Peak Frequency</td>
</tr>
<tr>
<td>• Graph Display</td>
<td>• Graph Display</td>
</tr>
<tr>
<td></td>
<td>• Integration Ranges for Maps</td>
</tr>
</tbody>
</table>

## Available processing steps in Peak Fitting Script

<table>
<thead>
<tr>
<th>For Single-Voxel Spectroscopy</th>
<th>For Chemical Shift Imaging</th>
</tr>
</thead>
<tbody>
<tr>
<td>• Dual Volume Decode</td>
<td>• Spectrum Phase Adjustment</td>
</tr>
<tr>
<td>• Spectrum Phase Adjustment</td>
<td>• Spectrum Phase Adjustment</td>
</tr>
<tr>
<td>• Initial Baseline Subtraction</td>
<td>• Initial Baseline Subtraction</td>
</tr>
<tr>
<td>• Shift Peak Frequency</td>
<td>• Shift Peak Frequency</td>
</tr>
<tr>
<td>• Select Peaks</td>
<td>• Select Peaks</td>
</tr>
<tr>
<td>• Peak Fitting</td>
<td>• Peak Fitting</td>
</tr>
<tr>
<td>• Results Table</td>
<td>• Results Table</td>
</tr>
<tr>
<td>• Graph Display</td>
<td>• Graph Display</td>
</tr>
<tr>
<td></td>
<td>• Generate Maps</td>
</tr>
<tr>
<td></td>
<td>• Correct for DSA Filter</td>
</tr>
</tbody>
</table>

## Dual Volume Decode

- is used to decode the (A+B) and (A-B) encoding used in Dual Volume acquisitions. There are no adjustable parameters for this script step.
- appears at the top of all single voxel BasicProcessing scripts and at the top of all single voxel Peak Fitting scripts.
Residual Water Subtraction

- removes residual water signal by applying a high pass filter over which data points are combined and subtracted from the original signal.
- gives the possibility to adjust the high pass filter by means of a slider.

Typical application

If the water suppression applied during acquisition is imperfect, the residual water peak can at times interfere with the metabolite peaks of interest. One way to minimize its effect is to apply a high pass filter in the time domain (D. Marion, M. Ikura, and A. Bax, "Improved Solvent Suppression in One- and Two-Dimensional NMR Spectra by Convolution of Time-Domain Data," J. Magn. Reson. 84, 425-430, 1989). Because water is at or near resonance, a high pass filter will selectively remove the low frequency water signal.

High Pass Filter

The filter works by first smoothing the input time-domain signal using Gaussian convolution. Each point is replaced by the average over a Gaussian-weighted window of points with a user adjustable width. The smoothed version of the input signal is then subtracted from the original signal to leave only the higher frequency "wiggles."

Slider values

The slider defines the width in points (specifically the FWHM) of the Gaussian-weighted window of time-domain points.

Narrow window - broad filter

Only a few neighboring points are averaged together to replace each input point. Only the highest frequency wiggles are smoothed away. When this function is subtracted from the original, only the highest frequency wiggles remain: a broad filter has been applied in the frequency domain.

Wide window - narrow filter

Many points are averaged together, resulting in a very smooth function. When this is subtracted from the original, only frequencies very close to resonance will be affected: a narrow filter had been applied in the frequency domain.

Time Domain Signal Shifting

- Can be used to shift the time domain signal to either remove spurious signals or to align spectra. It will not be applied with standard acquisitions.
- Can be done with
  - Shift with zero padding
    
    This is a function to shift a time domain signal with an integer number of sample points by inserting zeroes. The point index for each point is changed by the parameter shift. The shift can be negative. Points that fall outside the array will be lost. If shift is greater...
than the total number of points N the result will be all zeroes. Typical use of the function is to remove spurious signals at the beginning of a FID that can cause baseline distortions in the spectrum.

- Cyclically shift
  This is a function to shift a time domain an integer number of sample points. The point index for each point is changed by the parameter shift. The shift can be negative. Points that fall outside the array will be appended at the other end. If shift is greater than the total number of points N, the result will be identical to a cyclic shift with parameter <shift> = (<shift> - k *N) points where k is any integer number. Typical use of the function is to align spectra.

Note that the default shift is zero.

**Apodization Filtering**

- improves the signal-to-noise in a dataset by partially filtering out the noise in a MRS signal prior to Fourier transform (FT): before the Fourier transform (FFT) there is a decaying signal in a constant background of noise. This means that the signal to noise in the first points of the signal is better than in the last points of the signal. A weighting function can be applied to emphasize the points with good signal to noise. The best weighting function is one that follows the decay of the signal. Because the peak areas should not be changed, the function must not change the data point of the FID corresponding to time zero. The intensity of this point before FFT is proportional to the total of the peak areas.

- allows to choose more than one filter if requested.

- The choice of filters includes the following:

<table>
<thead>
<tr>
<th>Available Filters</th>
<th>Description of Filter</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gaussian Multiplication</td>
<td>• Applied to transform a Lorentzian line shape to a more compact Gaussian shape (the foot of a Gaussian is smaller than Lorentzian shape, thus overlap of peaks is reduced).&lt;br&gt;  • This can only be positive apodization.  • It causes a line broadening effect.</td>
</tr>
<tr>
<td>Exponential Multiplication</td>
<td>• Applies a decaying exponential to increase the apparent SNR at the cost of a reduction in resolution.  • Can be applied as an apodization or negative (for cancellation of T₂ decay).  • Use of a positive value gives a an effect equal to ‘Lorentzian line broadening’.</td>
</tr>
<tr>
<td>Convolution Difference</td>
<td>• Can be used as a method for broad line suppression.  • The signal is multiplied with an exponential filter as in the exponential multiplication function. The result of this operation is subtracted from the original filter.  • The difference is then scaled.</td>
</tr>
</tbody>
</table>
### Available Filters

<table>
<thead>
<tr>
<th>Available Filters</th>
<th>Description of Filter</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lorentzian-to-Gaussian</td>
<td>• To change a line shape that is naturally Lorentzian, to a Gaussian line shape (if this is preferred for analysis or presentation)</td>
</tr>
<tr>
<td></td>
<td>• The signal is first multiplied with a Lorentz window with a negative line width parameter. Then the signal is filtered with a Gaussian function.</td>
</tr>
<tr>
<td>Broad Line Suppression</td>
<td>• Multiplies the time domain signal with a function that has low intensity in the first few data points and is unity for all other points.</td>
</tr>
<tr>
<td></td>
<td>• Filters out broad line components</td>
</tr>
<tr>
<td>Sine Window</td>
<td>• Applies a filter for suppressing artifacts in spectroscopic images.</td>
</tr>
<tr>
<td></td>
<td>• Usually not applied to the time domain of chemical shift data, but on the spatially encoding dimensions in a one or two-dimensional spectroscopic imaging</td>
</tr>
<tr>
<td>Sine Squared Window</td>
<td>• This is the squared sine function. It is equivalent to 1/2 times a sine function of double width plus a lift of 1/2.</td>
</tr>
<tr>
<td></td>
<td>• This is known as the Hanning window.</td>
</tr>
</tbody>
</table>

It is often easier to use the exponential multiply and Gaussian multiply functions rather than the LG function. Performing the function in two steps allows more flexibility. It is therefore the most commonly used form of apodization filtering.

Use the Exponential multiplication with a negative line broadening value to get a line sharpening (or de-convolution of the Lorentzian line shape). Combine this with a gaussian multiplication with a positive line broadening value. This positive line broadening must exceed the (negative) EM line sharpening value to have a noise filtering effect.

An example that should work for most proton spectra:

- Gaussian +3Hz, Exponential -1.5 Hz

This will result in an effective line broadening of 1.5 [Hz].

### Related parameters

This section describes all related parameters of this script step, for all selectable filters.

**Symmetry point**

- is a value between 0.0 and 100.0 % giving the relative position of the echo top in the FID.
- is the point where the filter function should have the value one and should correspond with time point zero.
  - For a half echo FID (echo acquisition = half) it is at the start of the FID: the symmetry point = 0%.
  - For a full or symmetric echo (echo acquisition = symmetric) the echo top position will be in the middle at 50 %.
  - For maximum echo (echo acquisition = maximum) the position of the echo top will be somewhere between 0 and 50 %.

The symmetry point can either be selected at "echo max": the echo top position is automatically defined, or at "xxx%", to manually specify the echo top position.
Gaussian mult [Hz], Exp mult [Hz]
- sets the line broadening values for the respective filters.

Line broadening [Hz]
- appears when the Convolution Difference (CD) filter is selected. The purpose of the CD filter is to selectively remove broad underlying features in the spectrum, leaving only sharp lines.
- is the estimated line width of the broad component. Broad peaks decay quickly in the time domain; hence the CD filter has a small value at the echo center (as defined by the symmetry point). Away from the echo center, it climbs quickly to a value of unity. As a result, broad signal components are suppressed, whereas narrow components (which decay slowly in the time domain) are only slightly affected.
- The filter function is defined as follows:
  \[ W_i = 1 - SC \exp\left(-\frac{N}{|i/N - SP|} \frac{\pi LB}{2 BW}\right) \]
  where
  \( W_i = \) weighting factor for time point \( i \)
  \( i = \) time point index
  \( N = \) number of acquired time-domain points
  \( SP = \) symmetry point of filter
  \( SC = \) scale factor (0.0 < SC < 1.0)
  \( LB = \) line width of the broad component
  \( BW = \) bandwidth

Scale factor
- appears when the Convolution Difference (CD) filter is selected. The purpose of the CD filter is to selectively remove broad underlying features in the spectrum, leaving only sharp lines.
- controls how completely the broad component is minimized. Allowed values for \( SC \) lie between zero and one.

Peak width [Hz]
- appears when the Lorentz-Gauss Multiply (LGM) filter is selected. The purpose of the LGM filter is to convert Lorentzian lineshapes to Gaussian lineshapes to improve resolution. (Lorentzian lines have broader "tails" than Gaussian lines with the same full width at half-maximum).
- should be set to the line width for which the user desires the filter to work best.

Suppression factor
- appears when the Broad Line Suppression (BLS) filter is selected. The purpose of the BLS filter is to selectively remove broad underlying features in the spectrum, leaving only sharp lines.
- controls how completely the broad component is minimized.

Cut-off frequency
• appears when the Broad Line Suppression (BLS) filter is selected. The purpose of the BLS filter is to selectively remove broad underlying features in the spectrum, leaving only sharp lines. (As such, it is similar to the Convolution Difference filter.)

• is the estimated dividing line in Hz that separates the width of broad components from the width of narrow components. Broad peaks decay quickly in the time domain; hence the BLS filter has a small value at the echo center (as defined by the symmetry point). Away from the echo center, it climbs quickly to a value of unity. As a result, broad signal components are suppressed, whereas narrow components (which decay slowly in the time domain) are only slightly affected.

• The filter function is defined as follows:

\[ Wi = \frac{1}{1 + SF \exp\left(-N |i/N - SP| \pi Fc / (2 BW) \right)} \]

where

- \( Wi \) = weighting factor for time point \( i \)
- \( i \) = time point index
- \( N \) = number of acquired time-domain points
- \( SP \) = symmetry point of filter
- \( SF \) = suppression factor
- \( Fc \) = cut-off line width between broad and narrow features
- \( BW \) = bandwidth

**Final points to zero**

• allows the user to zero out a selected number of points at the end of the time-domain signal -- the ultimate filter. Choosing 200, for example, will set the last 200 time-domain signal points equal to zero.

**Multiple filters: workflow**

1. Define first set of filter parameters.
2. At the top of the parameter panel, set ‘Number of Filters’ from ‘1’ to ‘2’.
3. At the top of the parameter panel, set ‘Edit Filter’ to ‘2’.
4. All the parameters should be "reset" and you can now set them for ‘Filter 2’.
5. To change the parameters for ‘Filter 1’, change ‘Edit Filter’ to ‘1’.
6. For only 1 filter, change ‘Number of Filters’ to ‘1’.

Note that the order of filter selection doesn’t matter as they are all multiplication filters.

**Zero-Fill and FT**

**FT**

• This processing step cannot be disabled, FT is always performed. To view time domain signals, select right mouse menu item ‘Display time domain signal for voxel x,x’.
DC correction

- Enables or disables the use of DC correction (to remove DC offset). A DC offset can be caused by hardware imperfections, or by the presence of a non-relaxed low-frequency signal (typically water), and will be presented as a spike.

- The window width is defined as a percentage of the total acquisition window, and is selectable between 1 and 15%.

Zero-Fill

- Is used to increase the number of points in a spectrum to a user defined value. The apparent digital resolution of the spectrum will be increased by increasing the digital number of points.

More about zerofill

The acquisition time should be set to record the FID or echo until well past the point where the signal disappeared into the noise. Rather than recording a signal with nothing in it but noise, some additional resolution may be obtained by zero filling.

Doubling the signal length by appending zeros will actually add information present in the imaginary part of the complex points to the absorption spectrum. Zero filling more than a factor two will just interpolate the spectrum without adding any more real definition.

**Fig. 157:** Zero filling results in interpolation in the frequency domain. The black line is a two peak spectrum with a low resolution. Zero filling the data to double the amount of points reveals two resolved peaks (gray line). The dashed thin grey line shows the smoothing effect of further zero filling. The resolution can improve significantly and a zero filled spectrum will look better.

Zerofill the spectral transform to

- defines the total number of points in the spectrum (= acquired number of points + zerofilled number of points)
  - Recommended value: twice as high as the acquired nr of points.
  - If zerofilling is not required, the number selected should be equal to the acquired number of points.
Spectrum Phase Adjustment

- Allows the user to correct the phase of the spectrum using both zero-order (global) and first-order (linear) terms.
- Both auto phasing and manual phasing can be selected.

Although any spectrum can be adjusted, this capability is most relevant for (a) non-proton spectra or (b) proton spectra acquired without an unsuppressed reference scan.

Autozeroth (global) term

- Zero order phase correction; being used if there are small delays between the transmit and reception of the signal in which the phase error has an influence on all peaks.
- Correction on a voxel-by-voxel basis.

Autofirst (linear) term

- First order phase correction in the case of phase differences which are present over various resonance frequencies.
- Correction on a voxel-by-voxel basis.

Manual Phase Adjustment

If enabled,

- the selection of the above options is disabled.
- the script will stop once phase adjustment is required, popping up a separate window in which both global and linear phase correction can be manually adjusted by the user:

![Image of Manual Phase Adjustment window]

**Fig. 158:** Window ‘Manual Phase Adjustment’: Sliders are just to interactively change the phase. Radio buttons are available for fine adjustments: the step size is reduced. Once phasing is completed, press ‘Next Step’ to resume the execution of the Basic Processing script.
Provide phase values below

- allows you to program exact values into the script itself. The default values shown here represent the values specified during the last Manual Phase Adjustment, as supplied by the Series Preferences database. As in Manual Adjustment, these values are applied to all selected voxels. Clinically, this option is probably not useful, but for experiments requiring you to process the same dataset using the same parameters more often – this improves workflow.

Integration Ranges for Maps

- allows the upper and lower bounds of a peak to be selected (in ppm) to which the estimated metabolite map is created

Initial Baseline Subtraction

Distortion of the spectral baseline caused by broad line resonances or missing data points can be corrected for visual presentation with the function ‘Initial Baseline Subtraction’.

‘Initial Baseline Subtraction’ is used to remove large distortions from the spectral baseline as they might confound later processing steps.

In this initial step, the ci variables are adjusted quickly and without knowledge of peak positions. As such, this step is omitted by default for short-TE brain spectra – the simple-minded algorithm does not distinguish well between broad peaks and true baseline variation.”

‘Baseline estimation occurs again during the fitting process, where it is done more accurately.

‘Baseline Polynomial Terms’ parameter

The baseline is modeled as a function of position x across the analysis range (e.g. 4.5 ppm to 0.0 ppm) with x defined from -1.0 to 1.0. The baseline is assumed to be a polynomial of x; for example:

\[ c_3 x^3 + c_2 x^2 + c_1 x + c_0. \]

Using a slider, the user can choose the degree of the polynomial - the highest power of x to be considered and in such a way the number of terms. The ci variables are adjusted for the best fit - quickly and without knowledge of peak choices here in this step - and later with more care during the peak fitting process.

Select Peaks

The next step for processing is to select and/or deselect the peaks that need to be fitted and quantitated.

‘Metabolites’ parameters

A list of metabolite peak names is provided in which the user can select or deselect the peaks of choice.

Note that the default ON/OFF settings for peak selection are defined by the target anatomy and TE as conveyed by the choice of the script.
Peak Fitting

An iterative nonlinear least-squares technique is used to fit spectra as the sum of a set of peaks (each modeled as a linear combination of a Gaussian and a Lorentzian function) plus a baseline (modeled as a polynomial function of position). In particular, an algorithm developed by Marquardt and Levenberg is used that efficiently searches for the best fit. This fitting process generates a list of optimized peak heights, widths, positions, and areas.

Definitions

Brief definitions are as follows:

Iterative

The fitted spectrum is not calculated in one shot. Rather, the initial estimate of the fitted spectrum is refined over a series of steps (typically 6 to 10).

Nonlinear

Some of the variables in the fitted spectrum are not simply scaling factors (like the variables that describe the baseline), but rather are incorporated within the model functions used for the fit. An example is the set of peak width variables, these appear in the expressions for Gaussian and Lorentzian line shapes in complicated ways.

Least-squares fit

The least-squares fit minimizes the sum over the analysis range of \((p_i - f_i)^2\), where

- \(p_i\) is the value of the initial spectrum at point \(i\)
- \(f_i\) is the value of the fitted spectrum at point \(i\).

Parameters

Analysis Range parameter

These parameters refer to the range of chemical shifts (expressed in ppm) which has to be considered while fitting the spectrum. The start and end value of this range can be entered as left and right analysis limit.

The default range is 4.35 ppm to 0.0 ppm.

Display Range parameters

These parameters refer to the default range of chemical shifts (in ppm) to be displayed after the script is run. The initial choice is from 4.0 to 0.0 ppm. These limits can be modified using the context menu (activated with a right-mouse click) in the spectrum viewport.

Gaussian Percentage parameter

This parameter defines the percentage of Gaussian character of the fitted peak lineshapes. The default value is 85%, based on trial-and-error adjustment of proton brain spectra. In general, metabolite peaks for in vivo proton spectroscopy are more Gaussian in nature than Lorentzian. An example of both lineshapes is presented in figure.

<table>
<thead>
<tr>
<th>Gaussian Percentage</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>0 %</td>
<td>Pure Lorentzian line.</td>
</tr>
</tbody>
</table>
**Gaussian Percentage**

<table>
<thead>
<tr>
<th>Percentage</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>100%</td>
<td>Pure Gaussian line.</td>
</tr>
</tbody>
</table>

![Gaussian vs Lorentzian Lineshape](image)

Fig. 159: Lorentzian (shaded area) versus Gaussian (black line) lineshape. The two peaks shown have the same integral area.

The Gaussian line is broader near the resonance frequency but trails off to zero more rapidly than the Lorentz line.

**Baseline Terms parameter**

This parameter specifies how many polynomial terms are used to model the baseline during the peak fitting process. A similar parameter is used in the ‘Initial Baseline subtraction’ step. Both functions correct for distortions of the spectrum baseline.

However, the initial baseline subtraction is to remove large variations in the baseline so that automatic peak assignment is more likely to succeed. It is done quickly without any prior knowledge where the peaks are. It’s too crude a technique for short TE spectra, because it can’t readily distinguish between broad J-coupled (or lipid) peaks and rolls in the baseline. It is much better at long TE where the difference between peak and baseline is more obvious.

During the actual fitting process, the baseline (or the “residual baseline,” if it has been trimmed in the residual baseline subtraction step) needs to be included as part of the overall spectrum fit. Otherwise the peaks will not be modeled properly. The baseline function should be flexible enough to follow the baseline, but not so flexible that it interferes with fitting the peaks themselves. As noted above, the Baseline Terms slider controls this flexibility by specifying the number of polynomials terms used during the fitting process.

**Phase Parameter**

Either the real spectrum or the modulus spectrum can be used in the fitting process. “Real” is the default for single-voxel acquisitions, and “Modulus” is the default for CSI. However, if the CSI echo acquisition type was set to hal echo instead of maximum, this phase parameter should be changed to “Real.”

**Lock Relative Frequency parameter**

When this fitting parameter is enabled, the number of free variables used to model the positions of N peaks is reduced from N to one. It makes use of the fact that peak positions are usually not independent of each other. For example, if the NAA peak position is known, one expects creatine to be 1.01 ppm away, choline to be 1.20 ppm away, etc. Reducing the number of free variables typically makes for a more robust fit.

<table>
<thead>
<tr>
<th>Lock Relative Frequency</th>
<th>Effects</th>
</tr>
</thead>
<tbody>
<tr>
<td>ON</td>
<td>• More robust fit.</td>
</tr>
<tr>
<td></td>
<td>• Less chance of peak functions moving away from their initial positions to fit baseline features.</td>
</tr>
</tbody>
</table>
Lock Relative Frequency  

<table>
<thead>
<tr>
<th>Effects</th>
</tr>
</thead>
<tbody>
<tr>
<td>OFF</td>
</tr>
<tr>
<td>• Better fine control of the fitting. If peak positions are free to move a little bit, then J-coupled lineshapes and moderately misshapen singlet peaks can be modeled more precisely.</td>
</tr>
<tr>
<td>• Safer in general, when spectrum quality is high (i.e. minimal baseline variation, minimal peak shape distortion and good SNR).</td>
</tr>
</tbody>
</table>

Lock Widths parameter

This feature is similar to locking relative peak frequencies and is intended primarily for long TE spectra. It is well known that the linewidths of NAA, Creatine and Choline are inherently similar. They should widen together when the shim is bad and narrow together when the shim is good. Based on this knowledge it is possible to replace three separately adjustable widths with one overall width parameter.

<table>
<thead>
<tr>
<th>Effects</th>
</tr>
</thead>
<tbody>
<tr>
<td>ON</td>
</tr>
<tr>
<td>• Useful when the SNR is low and peak shapes are distorted by noise in the spectrum.</td>
</tr>
<tr>
<td>• Ignores any possible differences between peak widths.</td>
</tr>
<tr>
<td>• The peak area ratio value is not likely to be distorted by baseline noise on peak shapes.</td>
</tr>
<tr>
<td>• All resulting peak area ratios will equal the corresponding peak height ratios.</td>
</tr>
<tr>
<td>OFF</td>
</tr>
<tr>
<td>• Better fine control of the fitting.</td>
</tr>
</tbody>
</table>

Parameter(s)  

<table>
<thead>
<tr>
<th>How to change the parameter value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Left analysis limit</td>
</tr>
<tr>
<td>Enter value in data entry box. Default: 4.2 ppm.</td>
</tr>
<tr>
<td>Right analysis limit</td>
</tr>
<tr>
<td>Enter value in data entry box. Default: 0.0 ppm.</td>
</tr>
<tr>
<td>Left display limits</td>
</tr>
<tr>
<td>Determines which part of the spectrum is displayed initially.</td>
</tr>
<tr>
<td>Right display limits</td>
</tr>
<tr>
<td>Determines which part of the spectrum is displayed initially.</td>
</tr>
<tr>
<td>Baseline terms</td>
</tr>
<tr>
<td>Slider to change the number of baseline polynomials. Maximum: 15, Default: 9.</td>
</tr>
<tr>
<td>Gaussian percentage</td>
</tr>
<tr>
<td>Slider to change this percentage. Default: 85%.</td>
</tr>
<tr>
<td>Phase</td>
</tr>
<tr>
<td>Real / Modulus</td>
</tr>
<tr>
<td>Determines phase aspect during peak fitting</td>
</tr>
<tr>
<td>Lock relative frequency</td>
</tr>
<tr>
<td>Click in checkbox to select or deselect. Default: ON.</td>
</tr>
<tr>
<td>Lock widths</td>
</tr>
<tr>
<td>Click in checkbox to select or deselect. Default: OFF.</td>
</tr>
</tbody>
</table>

Tab. 17: Parameters for processing step ’Peak Fitting’

Peak Editor

The Peak Editor makes it possible to add peaks into the peak fitting table. This peak will show up in the ’Edit script’ environment. chapter “Customization using the Peak Editor” on page 336 for more information.
Shift Peak Frequency

If peaks are not located correctly during the fitting routine, a manual assignment of peak positions can be performed. If peaks are assigned to their correct value, it will improve the fitting of the lesser, more difficult peaks.

- You can select “Specify shift interactively” to manually assign a ppm-position to a selected peak.
- You can deselect "Specify shift interactively", you have to specify the frequency shift value in ppm in the supplied textbox.

The default values shown in the textbox will represent the values specified during the last interactive Shift Peak Frequency, as supplied by the Series Preferences database.

Workflow

If ‘Shift Peak Frequency’ is enabled, the execution of the script is stopped, and a pop-up window allows the user to manually assign a ppm-position to a selected peak. Once completed all steps, the processing script is resumed.

The workflow is the same for SVS and CSI, but in SVS there is no "reference voxel" (step 2):

1. From the "Peak" ComboBox, select the peak to shift.
2. If CSI, select the reference voxel from the "Ref Voxel" ComboBox. Refer to the graphs in the graph area to find a voxel that has a good spectrum that can be used to set the shift.
3. A graph of the reference voxel is displayed and the cursor is labeled with the selected peak and positioned at a point determined by the "Peak Fitting" algorithm. The annotation in the graph describes the X and Y coordinates of the peak, as located by "Peak Fitting".
4. Examine the X coordinate and verify that it is located on the correct PPM value.
5. If it IS on the correct X PPM value, go to step 8
6. If it IS NOT on the correct X PPM value, use the mouse to move the cursor to the correct value. Click on the "Re-Process" button.
7. The pop-up will close, the "Peak Fitting" step will be repeated, the pop-up will return and the graph will now show the corrected result. If the X PPM value is not correct, go back to step 4. If the X PPM value is correct, continue with step 8.
8. Click on the ‘Next Step’ button to continue processing.

NOTICE

User definition of peaks is mainly important for multi-nuclei spectroscopy, where ppm-positions are usually assigned/changed for PCr.

In general, this step is not required for proton spectroscopy.
Results Table

You may specify up to 4 different denominators (or none at all), including unsuppressed water which will be provided in the Results Table ratio calculations. The Results Table will contain the height and area ratios for each denominator. Your selection of denominators is determined by the peaks specified in the Select Peaks script step.

All Peak Fitting scripts have been defined with Cr as a single ratio, to provide backward compatibility with R2.5. When running older user-defined scripts, which don’t have a Results Table step, we assume the same single Cr ratio to provide backward compatibility.

Correct for DSA Filter

NOTICE

This processing step is only available for datasets acquired prior to R2.

The processing step is disabled in all Philips Scripts.

This processing step

• is available for CSI data sets only and is only applicable if a DSA filter was applied during reconstruction.

• corrects for the intensity distorting effects of the DSA filter used by the reconstructor.

The DSA filter is a method to reduce residual water signals during reconstruction. The DSA filter works by shifting all FIDs over n points and subtracting these from the originals. The signals with zero frequency (water frequency) will then be nulled. The other frequencies are also attenuated except for an optimum frequency. Depending on the selected optimum frequency, the appearance of spectra, extracted from a CSI data set will be different as different weighting is applied to the various points in the spectrum. This will also have an influence on peak fitting and the results.

Fig. 160: Effect of DSA filter with different optimum frequency on the appearance of a spectrum.

In the figure above, the upper row shows a spectrum from a CSI data set with DSA filter optimized for NAA and lactate. The lower row shows the same spectrum with DSA filter optimized for choline and creatine.
The DSA filter does a good job of removing large residual water peaks, and hence it is applied by default during reconstruction. The DSA filter correction step in the script does not change the appearance of spectra. Instead, when enabled, it compensates for the frequency-dependent effect of the filter. It corrects the reported values of peak heights, peak areas, peak height ratios, and peak area ratios. It also corrects how these quantities are displayed in metabolite maps and ratio maps.

**Generate Maps**

This step is used to generate maps based on individual metabolites or ratios between metabolites.

### Individual metabolite maps

Once a metabolite has been selected a choice can be made whether to generate metabolite maps.

- based on the fitted area where fitted area is based on FWHM
- or
- based on the fitted height where fitted height is based on the overall intensity of the peak.

### Ratio Maps

To create a ratio map, select a single metabolite in both the numerator and denominator. Multiple selections of metabolites in both/either the numerator or denominator can also be utilized for grouped ratios.

### To add or remove a map

- Select the metabolites of interest (maps) in either one or both columns. Then click ‘Add’ or ‘Remove’.

![Fig. 161: Example: Window ‘Generate Maps’](image-url)
Graph Display

This function enables or disables the display of graphs with the spectral results. It also configures the layout. It allows to define the following:

- Display mode: geometrical, compressed, horizontal or stack
- Layout: default, full-screen graph or full-screen table
- Spectrum display options: enables/disables display of spectrum, fitted baseline, fitted spectrum, residual or metabolite labels
- Spectrum limits: Override X and Y range
- Show annotation: enabled or disabled.

These functions are only available via the graph right-mouse menu.

Customization using the Peak Editor

The Peak Fitting algorithms in SpectroView use a database of known peaks with attributes to drive the fitting, display and calculation results.

Commonly accepted peak definitions (known as PDPs or Philips Defined Peaks) are provided by default and may not be modified or deleted.

Users may add their own peak definitions to the database and may edit them or delete them. This can be done by means of the Peak Editor.

This section describes the Peak Editor and the following issues:

Start up the Peak Editor (PE)

1. Select ‘Peak Editor’ from the SpectroView toolbar.

The Peak Editor opens.

Fig. 162: Peak Editor layout.

1. Peak database filter combo box: Nucleus
2. Peak database filter combo box: (Magnetic) Field
3. Peak database filter combo box: Anatomy
4 Peak database filter combo box: Echo time Te
5 List of peaks
6 Control box: Apply
7 Control box: Store
8 Control box: Cancel

Peak database filter combo boxes
When a dataset is loaded, appropriate peaks are selected from the peak database according to the nucleus, field strength, anatomy and Te of this dataset. These filters are set to the values found in the currently loaded dataset. However, these filters may be changed at any time.

Table of peaks
The table shows all peaks which are part of the database.

Control buttons

Cancel
- exits the Peak Editor and discards all changes made in the current instance of the dialog. Changes made in previous instances of the dialog (by using the Apply button) remain in effect.

Apply
- applies changes to the database and exits the Peak Editor, but does not save the database to disk. The peak changes are immediately available for the next script run, but if you exit SpectroViewing without doing a Store, all applied changes will be discarded.

Store
- saves the updated database to disk and exits the Peak Editor. Once changes are saved to disk, they will be permanent, even across software updates.

Peak attributes
The table below lists the peak attributes which are supported in the peak database.

Add a new peak

Series Preferences Database
The Series Preferences Database facilitates the workflow for those series that do not have the proper anatomy settings included. Whenever loading such a series, it is necessary to specify the correct anatomy (e.g. brain or prostate).

SpectroView maintains a database containing “preferences” for the last series (approximately last 100 series) that were processed. For each series, the following information is captured:
- Anatomy
- Expert Mode On/Off
- Shift Peak Frequency Reference Voxel
• Shift Peak Frequency Shift Value
• Shift Peak Frequency Reference Peak
• Shift Peak Frequency Graph Cursor Position
• Shift Peak Frequency Graph X and Y Axis Scaling
• Manual Phase Adjust Reference Voxel
• Manual Phase Adjust Pivot Point
• Manual Phase Adjust Zeroth Order Correction
• Manual Phase Adjust First Order Correction
• Manual Phase Adjust Graph Phase Real/Imaginary/Modulus
• Manual Phase Adjust Graph X and Y Axis Scaling

When a series is reloaded, these preferences are also reloaded and applied to the ScriptEditor, interactive dialogs, etc.

Since it is possible you might make a mistake during processing (like selecting the wrong anatomy), you can clear all the preferences for the current series by clicking on the “Delete Series Preferences” menu item or button.

SpectroView: Process Unsuppressed Water Data

An exciting feature of SpectroView is the ability to visualize and fit the unsuppressed water signal. The benefits are as follows:

• The width of the water peak is a straightforward measure of shim quality.
• Artifacts are often easier to see (and interpret) in an unsuppressed water spectrum than in a normal suppressed spectrum.
• Most important, the size of the unsuppressed water peak is a useful denominator for peak area ratio (or height ratio) calculations. Moreover, if the water concentration is known for the tissue of interest, absolute metabolite concentrations can be estimated.

Workflow

1. Start up SpectroView with a suitable dataset. The dataset loads.

2. Click the ‘Process Unsuppressed Water Data’ icon to start the analysis.

   The icon remains highlighted. The dataset reloads, now with the unsuppressed water data information.
3. Select a basic processing script which is optimized for unsuppressed brain water. Make sure that the following parameters are set as follows:

- Residual Water Subtraction: Off
- Spectrum Phase Adjustment: On, and set to Auto Zeroth Order
- Use the same apodization filter settings for water and for metabolites

**Fig. 164:** Example: Script parameters of basic processing script for unsuppressed water analysis.

**NOTICE**

If you start off with Unsuppressed Water in SpectroView, it might be necessary that you create a new script with settings as described above.
4. Run this script. 
Figure shows the resulting spectrum.

5. Select a water-fitting script for the brain.

<table>
<thead>
<tr>
<th>Name: Water-fitting script</th>
</tr>
</thead>
<tbody>
<tr>
<td>Description: Based on Basic Processing (1H SV)</td>
</tr>
<tr>
<td>Anatomy: Brain</td>
</tr>
<tr>
<td>Nucleus: 1H</td>
</tr>
<tr>
<td>Echo time: Short</td>
</tr>
</tbody>
</table>

Select Peaks

<table>
<thead>
<tr>
<th>Ac</th>
<th>Cho</th>
<th>Cr</th>
<th>Cr2</th>
<th>Glx</th>
<th>H2O</th>
<th>Lac</th>
<th>lip</th>
<th>ml</th>
<th>NAA</th>
</tr>
</thead>
</table>

Fig. 165: Unsuppressed water, auto-phased and undistorted by “residual” water subtraction.

Fig. 166: Water-fitting script for the brain: Dual Volume Decode = off, Spectrum Phase Adjustment = off, Initial Baseline Subtraction = off, Shift Peak Frequency = off, Select Peaks = on, Peak Fitting = on, Results Table = off, Graph Display = on.

NOTICE

If you start off with Unsuppressed Water in SpectroView, it might be necessary that you create a brain water-fitting script.

In this case, start up with the standard water-fitting script and change its anatomy to ‘Brain’.

6. Run this script. Figure shows the result.
After analysis of the unsuppressed water is done, return to the usual water-suppressed spectrum by clicking off the "Process Unsuppressed Water Data" icon.

8. Select a generalized brain-fitting script to display metabolite ratios with respect to unsuppressed water.

**NOTICE**

If you start off with Unsuppressed Water in SpectroView, it might be necessary that you create a new generalized brain-fitting script.

![Generalized brain-fitting script](image)

**Fig. 168**: Generalized brain-fitting script, processing step: Results Table. In this example, NAA has been selected as "Denominator #3" as well.

9. Run this script. Figure shows the results.
Fig. 169: Results: Metabolite ratios with respect to unsuppressed water.

A table is also displayed providing the ratios in numeric values.

Make sure that ‘Unsupp. H₂O’ is selected as one of the denominators on the Results Table script page.

**Truncate Graph Peak**

When processing unsuppressed water data, the resulting spectra often looks like this:

Fig. 170: The overwhelming water peak causes smaller peaks and ripples to be scaled down to a flat line.

To overcome this situation, you can use the option ‘Truncate Graph Peak’ from the graph right-
mouse menu. This option only appears when “Expert Mode” is enabled, since careless use can
cause misleading results. Once activated, we see:

Fig. 171: Now the details of the “noise” surrounding the water peak can be visualized.
13 Printing

Printing can be performed as

- **Print Image**
  The purpose of this function is to compose a printout with multiple images of different series with a customizable layout.

- **Print Series**
  The purpose of this function is to compose a printout with multiple images of one or more series (maximum of 6 series) with layouts that have previously been predefined and set up.

The function **Print History** from the **System** menu allows to manage the printing jobs in the same way as the function **Manage Job Queue** manage all other types of jobs. Furthermore **Print History** enables you to easily redo a printing job by clicking 'Retry Jobs'.

User Interface

Printing in Overall Toolbars and Menus

Printing functions are available in toolbars and right mouse menus:
1. in the right mouse menu of the Thumbnail View;
2. in the Printing drop-down menu of the ImageView toolbar;
3. in the right mouse menu of ImageView.

<table>
<thead>
<tr>
<th>Icon</th>
<th>Function</th>
<th>Shortcut</th>
<th>Description</th>
<th>Available in</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Add Series To Print Setup icon" /></td>
<td>Add Series To Print Setup</td>
<td>Ctrl+Shift +S</td>
<td>To add series to the Print Setup. This function opens the window <strong>Print Setup (S)</strong> where (S) stands for series, if this window is not in use.</td>
<td>right mouse menu of the Thumbnail View</td>
</tr>
<tr>
<td><img src="image" alt="Add Image To Print Setup icon" /></td>
<td>Add Image To Print Setup</td>
<td>Ctrl+Shift +I</td>
<td>To add images to the Print Setup. This function opens the window <strong>Print Setup (I)</strong> where (I) stands for image, if this window is not in use.</td>
<td>Printing drop-down menu of ImageView toolbar</td>
</tr>
</tbody>
</table>

Tab. 18: Available Print functions
Print Setup

Print Setup allows

- setting up the printout with respect to output device, format and layout;
- adding ROIs, annotations and lines to the printout;
- creating and editing print presets.

Print Setup is available for Print Image and for Print Series.
It opens automatically in a dedicated window when images or series are added to it:

- **Add Series To Print Setup** opens the Print Setup(S) window where S stands for series.
  When Multiple Series (A|B or A|B|C) is enabled, this is indicated in the toolbar tab as Print Setup(MS).

- **Add Image To Print Setup** opens the Print Setup(I) window where I stands for image.

Print Setup Toolbars

The toolbars for Print Setup(S) and Print Setup(MS) are the same whereas the toolbar for Print Setup(I) is slightly different.

<table>
<thead>
<tr>
<th>Number</th>
<th>Icon</th>
<th>Function (and Shortcut)</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td><img src="image" alt="Print Preview" /></td>
<td>Print Preview (Ctrl + Shift + Q)</td>
<td>To display the Print Preview.</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>- This function can be used to verify the correct setup of the printout prior to printing.</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>- The function Print Settings which is available in the Print Setup(S) and Print Setup(I) windows determines the printout and the Print Preview.</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>- Example of preview and output on paper, see chapter “” on page 346.</td>
</tr>
<tr>
<td>Number</td>
<td>Icon</td>
<td>Function (and Shortcut)</td>
<td>Description</td>
</tr>
<tr>
<td>--------</td>
<td>------</td>
<td>-------------------------</td>
<td>-------------</td>
</tr>
<tr>
<td>2</td>
<td><img src="image" alt="Print (Ctrl + Shift + P)" /></td>
<td>Print (Ctrl + Shift + P)</td>
<td>To print the printout according to the settings as defined by means of Print Setup and Print Settings.</td>
</tr>
<tr>
<td>3</td>
<td><img src="image" alt="Default drop-down menu" /></td>
<td>Select Preset (initially 'Default')</td>
<td>To select any of the available presets so that the print setup is ready for printing with the selected preset values or settings.</td>
</tr>
<tr>
<td>4</td>
<td><img src="image" alt="Print Settings" /></td>
<td>Print Settings</td>
<td>To adjust print settings such as layout, annotation and format.</td>
</tr>
<tr>
<td>5</td>
<td><img src="image" alt="Multiple Series 2" /></td>
<td>Multiple Series 2</td>
<td>To enable Multiple Series printout for 2 series and to allow for this series to be loaded for printing. When Multiple Series printout is enabled, the toolbar of the Print Setup is displayed as Print Setup(MS).</td>
</tr>
<tr>
<td>6</td>
<td><img src="image" alt="Multiple Series 3" /></td>
<td>Multiple Series 3</td>
<td>To enable Multiple Series printout for 3 to 6 series and to allow for these series to be loaded for printing. When Multiple Series printout is enabled, the toolbar of the Print Setup is displayed as Print Setup(MS).</td>
</tr>
<tr>
<td>7</td>
<td><img src="image" alt="Load Protocol" /></td>
<td>Load Protocol</td>
<td>To load a printout protocol for Multiple Series that has previously been saved.</td>
</tr>
</tbody>
</table>
| 8      | ![More drop-down menu](image) | More functions | More provides the functions: Save Layout  
*Only available for Print Image: Enable Move Image Mode*  
When enabled, images can be moved to other locations in the Print Setup(I).  
*Only available for Print Image: Delete the current Page*  
To delete all images from the current page to be able to newly set up the printout.  
This function needs to be used in order to remove empty pages.  
Delete All Graphics  
To scroll through pages in Print Setup(I). |
| 9      | ![Scroll](image) | Scroll | To scroll through pages in Print Setup(I). |

Others  
Please refer to chapter “Toolbar” on page 107 for information about the other icons available on the Print Setup toolbars.
Print Setup Right Mouse Menus

Print Setup right mouse menus are slightly different for Print Image and Print Series. They provide many of the functions which are also available via the Print Setup toolbar or which are used throughout all postprocessing packages. These are the functions available:

<table>
<thead>
<tr>
<th>Available in Print Setup ...</th>
<th>(I)</th>
<th>(S)</th>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yes</td>
<td>Only for Print Setup(MS)</td>
<td>Split Vertical</td>
<td>To split a cell in Print Series(I) to allow for an even more flexible layout.</td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>Only for Print Setup(MS)</td>
<td>Split Horizontal</td>
<td>To split a page in Print Series(MS) to allow for more series to be put on the Print medium.</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>Yes</td>
<td>Propagation Scope</td>
<td>To adjust how view/window settings are propagated to the other images.</td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>Yes</td>
<td>Remove Image</td>
<td>To remove the current image from the printout.</td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>Yes</td>
<td>Remove Page</td>
<td>To remove the current page from the printout.</td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>Yes</td>
<td>Reset Window</td>
<td>To reset the window settings to the initial ones.</td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>Yes</td>
<td>Reset Zoom/Pan</td>
<td>To reset the viewing settings to the initial ones.</td>
<td></td>
</tr>
</tbody>
</table>

Print Settings

The Print Settings are part of Print Setup, and as such accessible via the Print Setup(I) and Print Setup(S) toolbars.

For Print Image and for Print Series, Print Settings allows
- to adjust the layout of the printout.
• to enable or disable the display of various forms of annotation on the printout.
• to select printer, film size, number of copies and number of pages.

For **Print Series**, additional functionality is available which allows:
• to create, edit or delete protocols for the Print procedure.
• to enable, disable or edit the display of planscan images on the printout.
• to specify image range and way of sorting on the printout.

**Print Protocol Area**
The Print Protocol Area is only available for Print Series. The following controls are available here:
• Drop-down for the Print protocols:
  either select an existing print protocol or enter a name for a new protocol.
  ![](image)

  • Delete icon to delete the currently selected Print protocol.
  ![](image)

  • Save icon to save the current settings as a Print protocol.
  ![](image)

**NOTICE**
Print protocols can be set up for up to six series within one printing job.
Parameter Area with Tabs

1. Layout, Annotations, Parameter Settings

2. Parameter Area with Tabs

Fig. 175: Parameter Area with: 1 - tabs, 2 - Different parameters for editing depending on the tab selection.

NOTICE

In Print Series, more tabs are available than in Print Image.

This is caused by the fact that Print Series offers more functionality with respect to the creation of Print protocols.

Layout Tab

The Layout tab is available for Print Series and Print Image, however with slight differences.

Fig. 176: Layout tab: Print Series (left) versus Print Image (right). See table for more information.

<table>
<thead>
<tr>
<th>Number</th>
<th>Function</th>
<th>Possible Values</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Number of Rows</td>
<td>• up to 8 rows</td>
<td>This parameter specifies the number of rows on the printout(s).</td>
</tr>
<tr>
<td>2</td>
<td>Number of Columns</td>
<td>• up to 8 columns</td>
<td>This parameter specifies the number of columns on the printout(s).</td>
</tr>
<tr>
<td>3</td>
<td>Film Layout</td>
<td>• All film layouts ever created and saved</td>
<td>Any layout can be selected for Print Image.</td>
</tr>
<tr>
<td>4</td>
<td>Separator Lines</td>
<td>• Checked</td>
<td>The display of separator lines can be enabled/disabled.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Unchecked</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>Patient Description</td>
<td>• Checked</td>
<td>The display of the patient description can be enabled/disabled.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Unchecked</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>Patient Name</td>
<td>• Checked</td>
<td>The display of the patient name can be enabled/disabled.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Unchecked</td>
<td></td>
</tr>
</tbody>
</table>
### Number | Function | Possible Values | Description
--- | --- | --- | ---
7 | Patient ID | • Checked  
|  |  | • Unchecked  | The display of the patient ID can be enabled/disabled.

**Tab. 19: Layout tab**

**Annotations Tab**

The Annotations tab is available for Print Series and Print Image, however with slight differences.

**Fig. 177:** Annotations tab: Print Series (left) versus Print Image (right). See table for more information.

### Number | Function | Possible Values | Description
--- | --- | --- | ---
1 | Image Text | • Checked  
|  |  | • Unchecked  | The display of Image Text can be enabled/disabled.

2 | Caliper | • Checked  
|  |  | • Unchecked  | The display of the Caliper can be enabled/disabled.

3 | Fold-over Indicator | • Checked  
|  |  | • Unchecked  | The display of the Fold-over Indicator can be enabled/disabled.

4 | Orientation Annotator | • Checked  
|  |  | • Unchecked  | The display of the Orientation Annotator can be enabled/disabled.

5 | ROIs and lines | • Checked  
|  |  | • Unchecked  | The display of ROIs and lines can be enabled/disabled.

6 | Series Info | • Checked  
|  |  | • Unchecked  | The display of Series Info can be enabled/disabled.

7 | Location of Series Info | • Once at start  
|  |  | • Every page  | If enabled, the location of the Series info can be selected.

**Tab. 20: Annotations tab**

**Printer Settings Tab**

The Printer Settings tab is available for Print Series and Print Image, however with slight differences.
### Number | Function | Possible Values | Description
--- | --- | --- | ---
1 | Printer | • Any printer available | Any configured printer can be used as output device and selected in this drop-down menu.
2 | Film Size | • Any film size available | Any film size for the printout can be selected in this drop-down menu.
3 | Number of Copies | • 1 to 100 | The Number of Copies can be increased or decreased by clicking the +/- buttons.
4 | Color | • Checked<br>• Unchecked | Depending on the printer connected, a color printout can be enabled/disabled.
5 | Print to File | • Checked<br>• Unchecked | Print to File can be enabled/disabled. Note that this function can only be selected when a printer is configured (even though it doesn’t require a printer).
6 | Number of Pages Warning | • Checked<br>• Unchecked | This parameter enables/disables if a message will be displayed indicating the total number of pages.
7 | Page Range | • All<br>• User Defined: From ... To ... | This parameter specifies which pages of the Print Setup will be printed.

### Tab. 21: Printer Settings tab

**Planscan Tab**

The Planscan tab is available for Print Series only.
Fig. 179: Planscan tab: available for Print Series only.

<table>
<thead>
<tr>
<th>Number</th>
<th>Function</th>
<th>Possible Values</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Planscan Image</td>
<td>• Checked</td>
<td>The display of the Planscan Image can be enabled/disabled.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Unchecked</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Inset Planscan</td>
<td>• Checked</td>
<td>The display of the Inset Planscan can be enabled/disabled.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Unchecked</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Location of Planscan Image</td>
<td>• Once at start • Once at end • Repeated at the start of each film • Repeated at the end of each film</td>
<td>This parameter specifies the location of the Planscan Image on the film(s).</td>
</tr>
<tr>
<td>4</td>
<td>Which Planscan Image</td>
<td>• A • B • C • All</td>
<td>This parameter specifies which Planscan Image will be used.</td>
</tr>
<tr>
<td>5</td>
<td>Planscan Display</td>
<td>• Lines • Box</td>
<td>This parameter specifies how the Planscan will be displayed.</td>
</tr>
<tr>
<td>6</td>
<td>Inset Planscan</td>
<td>![Icons](upper or lower left or right corner)</td>
<td>This parameter (icons only) specifies the location of the Inset Planscan.</td>
</tr>
<tr>
<td>7</td>
<td>Which Inset Planscan image</td>
<td>• A • B • C</td>
<td>This parameter specifies which Inset Planscan image will be used.</td>
</tr>
</tbody>
</table>

Tab. 22: Planscan tab

Images Tab

The Images tab is available for Print Series only.
Fig. 180: Images tab: available in Print Series only. The number of slider bars displayed as "Range" depend on the types of images in the series.

<table>
<thead>
<tr>
<th>Number</th>
<th>Function</th>
<th>Possible Values</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Descending Slice Order</td>
<td>• Checked</td>
<td>If enabled, descending slice order will be used for printing.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Unchecked</td>
<td>If disabled, ascending slice order will be used.</td>
</tr>
<tr>
<td>2</td>
<td>New Film Every</td>
<td>• None</td>
<td>This parameter specifies when a new film will be started.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• to be defined</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Every Nth Image</td>
<td>• Any number</td>
<td>Click +/- to increase/decrease n.</td>
</tr>
<tr>
<td>4</td>
<td>Sorting Dimensions</td>
<td>• Order of attributes, such as:</td>
<td>The parameter affects the order of images on the printing output.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>slice, dynamics, image types.</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Attributes can be moved up or</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>down by means of the eponymous</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>buttons.</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>Range (here Slice/Echoes)</td>
<td>• There is a slider per attrib-</td>
<td>Drag the slider to define start and end slice or echo.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ute, e.g. a slider for slices,</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>another one for echoes. The</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>attributes depend on the type of</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>the scan. Other options besides</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>slices and echoes are e.g. image</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>types, dynamics.</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>Range Start/End</td>
<td>• Pressed</td>
<td>To select the first image, click on this image and then click 'Start'.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Not pressed</td>
<td>To select the last image, click on this image and then click 'End'.</td>
</tr>
</tbody>
</table>

Tab. 23: Images tab
Control Area

For an image of the Control area, figure 174 on page 347.
  ▶ Click |Apply| to apply the changes.
  ▶ Click |OK| to save the changes without applying.
  ▶ Clicking |Cancel| closes the window without applying the changes made.

Workflows

Create Predefined Layout for Print Image

  ► Right-click on an image in ImageView and select Add Image To Print Setup.

  The window Print Setup(I) opens with its default layout.

  ► First change the layout:
    • To resize a cell, drag the lines up- or downwards or to the left or right.
    • To create multiple cells out of one, right-click on this cell and select 'Split Horizontal' or 'Split Vertical'.

  You can undo ONE action when dragging images or resizing cells.

  ► Click Print Settings in order to create/edit a predefined layout for Print Image.
    • Click the Layout tab and edit according to your preferences.
    • Click the Annotations tab and edit according to your preferences.
    • Click the Printer Settings tab and edit according to your preferences.

  ► Click |OK| to save these settings with the selected layout.

Available layouts are displayed as icon showing their rows/columns.

Fig. 181: Example of Print Image Layouts.

Create Protocol for Print Series

  ► Select 'Add Series To Print Setup'
    • in the right-mouse menu of the Thumbnail View,
    • in the Printing drop-down menu of the ImageView toolbar.

  The window 'Print Setup(S)' opens with its default layout.
First change the layout:
- Select another layout or add/remove columns and/or rows.
- To print multiple series, click one of the 'Multiple Series' buttons (A|B or A|B|C).

The Print Setup(S) will then be renamed to Print Setup (MS) and the printing area will be split in two or three parts, every part meant for one series.

Click 'Print Settings' in order to create/edit a protocol for Print Series.
- Click the 'Planscan' tab and edit according to your preferences.
- Click the 'Layout' tab and edit according to your preferences.
- Click the 'Images' tab and edit according to your preferences.
- Click the 'Annotations' tab and edit according to your preferences.
- Click the 'Printer Settings' tab and edit according to your preferences.

Enter a name for the protocol, and click |Save| to save these settings as protocol.

Print Image

Right-click on an image in ImageView and select Add Image To Print Setup.

The window Print Setup(I) opens with its default layout.

Click Tiled View to display the windows ImageView and Print Setup(I) besides each other.

In ImageView, select more images that have to be placed on the printout.

Click Add Image To Print Setup for every image needed.

Repeat the last two steps as often as required.

Optional: In order to select multiple images, hold |Ctrl| while clicking on the images. Then select Add Image To Print Setup.

Images of the multiple selection are indicated by a blue selection icon.
Fig. 182: ImageView and Print Setup(I) windows besides each other. Multiple images are selected in ImageView indicated by the blue selection icon. The right-mouse menu is open showing the option 'Add Image To Print Setup'.

- Optional: right-click on any cell and select any of the available options to e.g. remove an image or reset view/window settings.
- Optional: to resize a cell, drag the lines up- or downwards or to the left or right.
- Optional: to create multiple cells out of one, right-click and select 'Split Horizontal' or 'Split Vertical'.
- Optional: select Enable Image Move Mode from the More drop-down menu (toolbar) and drag the images to other positions.
  You can undo ONE action when dragging images or resizing cells.

**NOTICE**
If there is an image in the target cell already, this image will be lost if another image is dragged to this location.

- In order to select a preset for Print Image, click Print Settings, and select one of the available layouts.

- To move images from one cell to another, in Print Setup(I) click and drag this image to the new location.
Click **Print Preview** to verify everything is set up as needed.

Click **Print** to initiate printing.

### Print Series

- Right-click and select **Add Series To Print Setup:**
  - in the right-mouse menu of the Thumbnail View,
  - in the Printing drop-down menu of the ImageView toolbar.

The window **Print Setup(S)** opens with its default layout.

- Click the **Print Preset** drop-down menu and select a Print protocol.
  For information on how to set up such a print protocol, refer to chapter “Create Protocol for Print Series” on page 353.

- Optional: right-click on any cell and select any of the available options to remove an image or reset view/window settings.

- Click **Print Preview** to verify everything is set up as needed.

- Click **Print** to initiate printing.
14 Administration (Patient Database)

The ‘Administration’ area provides the functions:

- Display of databases from storage devices connected to the computer system.
- Manipulation of these databases where patient folders or scans can be copied to other destinations or deleted.

Network

The network facility can be used to exchange images and data with other systems (RIS, PACS).

Start up Administration

- Select ‘Administration’ from the ‘Patient’ main menu or press F4.
  This will open the main window of Administration.

Workflow ‘Storage and transfer of patient data’

1. **Step 1:** Select the source database or device.
2. **Step 2:** Select the data (examinations/series/images).
3. **Step 3:** Select the destination database or device.
4. **Step 4:** Check the status of background processes with the Job Queue.

The figure shows where these steps can be performed in the Administration window.

Fig. 183: Administration window. The numbers 1 to 4 indicate the workflow order as listed above.
NOTICE
In case the transfer is interrupted due to network failure, it may be needed to logout or restart the computer.
Afterwards the "failed" job in the queue must be reselected and submitted again.

Select the source database or device
The current source database or device is indicated in the source selector field. By default, the source device is defined as ‘Local Patient Database’.
1. Click on the arrow in the source selector field.
2. Select the source database or device from the drop-down menu.
   The content of the selected database or device will be listed.

<table>
<thead>
<tr>
<th>Icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1" alt="Local Patient Database (default setting)" /></td>
<td>Local Patient Database (default setting)</td>
</tr>
<tr>
<td><img src="image2" alt="MOD" /></td>
<td>MOD</td>
</tr>
<tr>
<td><img src="image3" alt="DVD" /></td>
<td>DVD</td>
</tr>
<tr>
<td><img src="image4" alt="Queue DVD" /></td>
<td>Queue DVD</td>
</tr>
<tr>
<td><img src="image5" alt="DICOM Network Node" /></td>
<td>DICOM Network Node</td>
</tr>
<tr>
<td><img src="image6" alt="PACS (Archive)" /></td>
<td>PACS (Archive)</td>
</tr>
<tr>
<td><img src="image7" alt="Disk files" /></td>
<td>Disk files</td>
</tr>
</tbody>
</table>

Select data from source database

Select examinations
1. Click on an examination to select it.
   You can select multiple examinations:
• Hold |Ctrl| and select multiple single examinations, or
• Hold |Shift| and click on two examinations successively to select these two examinations AND the examinations which are between them in the list.

2. Continue
• either with ‘Select destination database or device’ chapter “Select destination database or device” on page 360
• or with ‘Select series’:

Select series
To display the series within an examination,
1. click on the folder icon of an examination or double-click on an examination.
   The list of series for the current examination is displayed.

![Folder icon in list of examinations.](image1)

**Fig. 184:** Folder icon in list of examinations.

![List of series for the current examination.](image2)

**Fig. 185:** List of series for the current examination.

**NOTICE**
About 1300 items can be listed.
If a list contains too many items, a message "List contains too many items to be displayed at once" is displayed. Use the ‘Filter ...’ option to find other selections.

2. Click on a series to select it.
3. Continue
   • either with ‘Select destination database or device’ chapter “Select destination database or device” on page 360
   • or with ‘Select images (or an image range)’:

Select images (or an image range)
It is possible to select a subset of images.
NOTICE
This function cannot be used with PACS as destination.

1. Click the |Scan| button to open the ‘Select image range’ window.
   The ‘Select image range’ window opens.

   ![Scan button](image)

   Fig. 186: Scan button.

2. Select the required image type (e.g. SE/M, FFE/M, FFE/P).
3. For the selected image type, define

<table>
<thead>
<tr>
<th>Range</th>
<th>Step (size)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Slice</td>
<td>e.g. 5-15</td>
</tr>
<tr>
<td>Echo</td>
<td>e.g. 1</td>
</tr>
<tr>
<td>Phase</td>
<td>e.g. 1</td>
</tr>
<tr>
<td>Dynamic scan</td>
<td>e.g. 1</td>
</tr>
<tr>
<td>Chemical shift</td>
<td>e.g. 0</td>
</tr>
<tr>
<td>Gradient orientation</td>
<td>e.g. 1</td>
</tr>
<tr>
<td>Diffusion BValues</td>
<td>e.g. 1</td>
</tr>
</tbody>
</table>

   **Functions within ‘Select image range’ window:**

<table>
<thead>
<tr>
<th>Button / Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reset</td>
<td>To deselect: all ranges are reset to their default ranges.</td>
</tr>
<tr>
<td>Invert</td>
<td>To invert selection: selected image types are deselected and vice versa.</td>
</tr>
<tr>
<td>Cancel</td>
<td>To exit this window without selection.</td>
</tr>
<tr>
<td>Delete</td>
<td>To delete all selected images.</td>
</tr>
<tr>
<td>Keep</td>
<td>To keep all selected image and delete the rest.</td>
</tr>
<tr>
<td>Select</td>
<td>To confirm selection and exit this window.</td>
</tr>
</tbody>
</table>

**Select destination database or device**

When the source data selection is complete, select the destination database or device.

1. Click on any of the applicable destination devices.
Grayed-out devices are currently not available, or are not allowed to be used, i.e. a PACS only accepts complete scans/series.

1. Local Patient Database (default setting)
2. Queue DVD
   - Allows to suppress patient data.
   - Allows to select Enhanced or Classic Dicom.
   - Classic Dicom is recommended for multivendor applications.
   - Allows to export scans to a number of different research formats.
3. DICOM Network Node
4. PACS (Archive)
5. Disk files
   - Allows to suppress patient data.
   - Allows to select Enhanced or Classic Dicom.
   - Classic Dicom is recommended for multivendor applications.
   - Allows to export scans to a number of different research formats.
6. Queue Manager
7. Delete
   1. Click |Delete| to delete the selected source data. This command works on local database, local disk file or Queue DVD only.
   2. If applicable, answer the questions in the pop-up dialogue boxes and click |Proceed|.
NOTICE
You can only suppress patient data (and/or enter an alternative patient name) when you copy an examination or series to Queue DVD or disk files.
Patient data cannot be suppressed when you copy an examination or series to other locations or burn them to DVD.

Export to Disk Files
▷ Destination device is selected as 'Disk Files'.
▷ Click on one of the tabs to select the type of export:
• Dicom Export
• Non Dicom Export

Dicom Export
Output: Exported Dicom data can be imported at other MR consoles or any Dicom Viewers.
▷ Select the source data for export, e.g. a single or multiple examinations, a single or multiple imaging series.
▷ Browse to the destination device and folder.
▷ Select the output format by checking one of the options: Enhanced Dicom or Classic Dicom.
▷ Enable the suppression of patient data by checking this option.
If done so, you can enter an alternative patient name.
▷ Click 'Proceed' to export data.

Non Dicom Export
Output: exported non-dicom data is provided in the different research formats.
• XML-REC:
This format is generally used for Philips PRIDE and home-built packages based on IDL or MATLAB.
• NIfTI:
This format is generally used for fMRI analysis packages like SPM, BrainVoyager and FSL.
• SPAR-SDAT:
  This format is generally used for spectroscopy packages like jMRUI and LCMODEL.
  ► Select the source data for export, e.g. a single or multiple imaging series.
  ► Browse to the destination device and folder.
  ► Enter an Export file name or check 'Use Scan Name' to use the name of the scan as file name.
  ► Select the export type by checking.
    Note that by default all possible export types are selected for export.
  ► Click 'Proceed' to export data.

Fig. 190: FileExport 'Non Dicom Export' with 1 - Destination (folder) to browse to, 2 - Specification of Export File Name, 3 - Check boxes for the selection of the Export Type.

Export of image and video data

**WARNING**
To limit the output size, Export2Office uses storage formats with lossy compression. This compression can result in loss of detail.

**DICOM Export: Series Split functionality**

Imaging series with multiple dimensions (such as echoes, dynamics, or b-values) can be split into multiple series during DICOM export. This allows for an image sorting order based on the series number and is especially useful for those PACS/Workstations that cannot sort on these dimensions.

Each new series can easily be identified since its series number is derived from the series number of the original dataset.

Splitting is done in case of

• MultiEcho scans (resulting in a series per echo)
• Dynamic scans (resulting in a series per dynamic)
• Diffusion scans (resulting in a series per b-value)
• conventional DICOM MR images
• SC (Secondary Capture) images, e.g. screen grabs
• Private images (imaging protocols, ExamCards)

With the Series Split functionality, the presentation states will not be exported.
During import on the MR console, the new split series will be merged into one series again.

NOTICE
For automatic Series Split functionality you need a special configured network node.
The network nodes can be configured according to your needs together with your Customer Support Organization.

Check status of background processes with the Job Queue

The status of background processes (including image transfer) can be viewed using the tool ‘Job Queue’.

To open the Job Queue
1. Select ‘Manage Job Queue’ from the ‘System’ menu or from the ‘Administration’ window.

A list of jobs with the job name, patient name, status, priority and submit time is displayed in the Job Queue window.

Fig. 191: Job Queue window.
### More functions within Administration

Modify display of the list of examinations

For each storage device it can be specified which data columns are displayed or hidden in the Administration window:

**Data columns to be hidden or displayed are:**

<table>
<thead>
<tr>
<th>Number</th>
<th>Drop-down or button</th>
<th>Possible values</th>
<th>Description</th>
</tr>
</thead>
</table>
| 1      | Queue name          | • All queues (default)  
• Image transfer  
• MIP,  
• MPR,  
• Postprocessing  
• RIS | • to select which queues are displayed in the Job Queue window |
| 2      | Queue status        | • Disabled  
• Enabled | • to dis/enable background jobs; - to disable/enable one of the queues |
| 3      | Priority            | • Normal  
• Rush | • to set the priority: higher priority with |Rush| |
| 4      | Delete failed jobs  | - | • to delete failed jobs from the queue |
| 5      | Delete finished jobs| - | • to delete finished jobs from the queue |
| 6      | Delete              | - | • to delete the current job from the queue |
| 7      | Job status / Queue status | - | • displays the information concerning the current job |
| 8      | Suspend             | - | • to stop the current job, but keep it in the queue |
| 9      | Resume              | - | • to resume the selected (suspended) job |
| 10     | Retry (jobs)        | | • to retry a previously failed job |
| 11     | Stop                | - | • to stop the current job |
|        | Hide                | - | • to hide the Job Queue window |
• Date of birth
• Exam date
• Exam name
• Patient name
• Registration ID
• Sex

1. Right-click in the (blue) header of the patient list to display the Show/Hide columns dialog window.
2. Select the data to be hidden in the ‘Show’ list and click |Hide|.
3. Select the data to be displayed in the `Hide' list and click |Show|.
4. Click |Proceed|.

Refresh
• Click |Refresh| to update the display of the examinations window.
  – This does not change the selection state. Opened exams will stay open.

Deselect All and Select All
• Click |Select All| to select the entire list.
• Click |Deselect All| to deselect all files.

Manipulate a selected patient list
• Click |Filter ...| to display the ‘Filter …’ menu.

It allows selective display of parts of the patient list according to the selection criteria. The following find criteria can be entered:

<table>
<thead>
<tr>
<th>Find criterion</th>
<th>To be entered as</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patient name</td>
<td>String including wild cards *</td>
</tr>
<tr>
<td>Registration ID</td>
<td>String including wild cards *</td>
</tr>
<tr>
<td>Date of birth</td>
<td>Date in the current date format.</td>
</tr>
<tr>
<td>Exam name</td>
<td>String including wild cards *</td>
</tr>
<tr>
<td>Exam date</td>
<td>Date in the current date format. Specified as interval from ... to ...</td>
</tr>
<tr>
<td>Exam status</td>
<td>‘Ready’ or ‘Not Ready’: to find patients which are (not) ready according to the RIS.</td>
</tr>
</tbody>
</table>

Functions to be used within this menu:

<table>
<thead>
<tr>
<th>Button / Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Clear</td>
<td>To clear all search fields.</td>
</tr>
<tr>
<td>Cancel</td>
<td>To exit this window without taking filter settings into account.</td>
</tr>
<tr>
<td>Display all</td>
<td>To display the contents of the storagedevice and exit this window.</td>
</tr>
<tr>
<td>Button / Function</td>
<td>Description</td>
</tr>
<tr>
<td>-------------------</td>
<td>-------------</td>
</tr>
<tr>
<td>Apply filter</td>
<td>To apply the filter settings without exiting this window.</td>
</tr>
<tr>
<td>Proceed</td>
<td>To apply the filter settings and exit this window.</td>
</tr>
</tbody>
</table>

**Sorting order**

- Click one of the following buttons in the Main Menu bar to present the contents in a different order:
  - Patient name
  - Date of birth
  - Registration ID
  - Exam Name
  - Exam Date
  - Sex
  - Origin
  - Exam ready.

**Modify examination data**

Patient examination data of local and retrieved examinations can be modified.

1. Select the examination whose examination data have to be modified.
2. Click Modify.
3. Enable Presentation mode.
4. Modify the examination data, e.g. delete existing data, enter new data.
5. Click Proceed to confirm.

An asterisk in front of the patient name indicates a modified examination.

**WARNING**

Examinations modified in presentation mode are not longer compatible with the original RIS entry.

They should not be archived, but be stored on DVD.

There is a risk of mixing patients’ data if this function is not used carefully.

**More about storage devices**

The following storage devices can be available on the system. They can easily be recognized by their icons.
### NOTICE
Contact your local Customer Support Organization for setup.

<table>
<thead>
<tr>
<th>Icon</th>
<th>Storage device</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Folder" /></td>
<td>Local Patient Database</td>
</tr>
<tr>
<td><img src="image" alt="Folder" /></td>
<td>• containing the patient examination list</td>
</tr>
<tr>
<td><img src="image" alt="CD" /></td>
<td>DVD</td>
</tr>
<tr>
<td><img src="image" alt="Folder" /></td>
<td>• contents of the currently assigned (DICOM) DVD.</td>
</tr>
<tr>
<td><img src="image" alt="Folder" /></td>
<td>• DICOM media.</td>
</tr>
<tr>
<td><img src="image" alt="Queue" /></td>
<td>Queue DVD</td>
</tr>
<tr>
<td><img src="image" alt="Folder" /></td>
<td>• content of the selected Queue (DICOM) DVD slots.</td>
</tr>
<tr>
<td><img src="image" alt="Network" /></td>
<td>There are 5 Queue DVD slots available.</td>
</tr>
<tr>
<td><img src="image" alt="Network" /></td>
<td>chapter “More about data transfer to DVD” on page 370</td>
</tr>
<tr>
<td><img src="image" alt="Network" /></td>
<td>DICOM Network Node</td>
</tr>
<tr>
<td><img src="image" alt="Folder" /></td>
<td>• contents of the currently configured DICOM network node.</td>
</tr>
<tr>
<td><img src="image" alt="Network" /></td>
<td>Remote (DICOM) patient databases. Accessible via drop-down menu in the</td>
</tr>
<tr>
<td><img src="image" alt="Network" /></td>
<td>PACS</td>
</tr>
<tr>
<td><img src="image" alt="Folder" /></td>
<td>• contents of the currently assigned PACS</td>
</tr>
<tr>
<td><img src="image" alt="Network" /></td>
<td>Remote (DICOM) patient databases. Accessible via drop-down menu in the</td>
</tr>
<tr>
<td><img src="image" alt="Network" /></td>
<td>Disk files (Local DICOM directory)</td>
</tr>
<tr>
<td><img src="image" alt="Folder" /></td>
<td>By default, files are written to E:\DICOM. It is also possible to browse to a different destination folder, create a new folder or copy to a PC via a network connection.</td>
</tr>
</tbody>
</table>

### Database capacity indicator bar
In the upper right corner, a blue bar is available which indicates how much space of the current database/device is used.

The bar color changes to red when 80% or more are used.

### NOTICE
With DVD the indicator shows 100% always, multi session for DVD discs is not supported.
Retrieving data from PACS
During retrieval of data from a PACS, the scanner allows to delete data from the patient just being retrieved. Please check the QueueManager for completion of the job before taking new actions within administration.

Autopush to Workstation
If a DICOM node, e.g. EWS (Extended MR WorkSpace) is connected to the MR console, examinations can automatically be transferred to this DICOM node, to facilitate the workflow. All examinations are then available on the DICOM node where they can be viewed and postprocessed directly.

To enable automatic transfer, proceed as follows:
1. From the 'Examination' menu, select 'Autopush to Workstation' to enable the autopush function.

Since this is a persistent setting, this action has to be done only once.

Automatically push scans to a network node
You have to perform two steps in order to automatically push scans to a network node.
1. Enable the 'Push to workstation' function for the ExamCards/protocols. Every time these ExamCards/protocols are executed, the resulting scans will automatically be pushed to the network node.
2. Select the network node (push node) to which these ExamCards/scans have to be pushed.

Enable 'Push to Workstation'
1. Right-click on the protocol(s)/ExamCard and select 'Push to workstation'.
2. Save the ExamCard to ensure re-use of the settings.

Fig. 192: Right-mouse menu in ExamCard environment. The 'Push to workstation' function is enabled.

NOTICE
Push to workstation has to be set once per ExamCard.

Select the workstation
1. Click the ‘ExamCard Properties’ button in the List View.
2. Click the ‘Push Nodes’ tab.

![ExamCard Properties](image)

### Fig. 193: ‘General’ EC parameters and ‘Push Nodes’ tab.

3. Select the push nodes by setting the parameter to ‘Yes’.

The above-mentioned steps have to be repeated each time the system is started and only have effect on the ExamCards / scans that have "Push to workstation" enabled.

**DICOM**

Please refer to the ‘DICOM Conformance Statement’.

**NOTICE**

Prior to examination transfer to PACS, make sure that the examination is not in use in the viewing and/or scanning environment.

Otherwise it (or parts of it) could be locked and not be transferred. In this case, a message appears describing the cause of the problem.

---

**More about data transfer to DVD**

A DVD provides high-capacity storage of images.

**NOTICE**

The DVD recorder is compatible with Philips DVD+RW 4-speed media only.

**NOTICE**

Only perform one action at the time with DVD storage: writing a DVD, storage to Queue DVD or browsing a Queue DVD slot.
General
The DVD writer is a consumer product. The lifetime of consumer products in general is less than the lifetime of medical products. Of course lifetime also depends on the usage.
If writing to DVD is unsuccessful, please retry with a new DVD+RW 4x before contacting a Philips representative.

NOTICE
The quality of a DVD will decrease over time.
For long-term storage it is advised to use an approved medical archiving solution (e.g. PACS).

Queue DVD
A Queue DVD is a storage directory for data before it is written to a DVD.
There are five Queue DVD slots available to compile patient data for multiple DVD’s.

Refreshing of the information on Queue DVD
- Click the [Refresh] button for a complete rewrite of the directory. This may take several minutes. Click [Cancel] to cancel the operation.
- Select ‘QDVDx’ from the pull-down menu for a fast refresh.

Copy to DVD
It is also possible to write directly to a DVD by clicking the button [Copy to DVD] while you are in local database control.
This function can be used to quickly provide a patient with a copy of the exam or for Philips Service or Application Support services.

DICOM viewer
On every DVD a DICOM viewer will be installed. This viewer enables viewing of images on every PC running Windows XP.
In Windows Explorer, the DICOM viewer can be started by double-clicking on ‘pmsdview.exe’.
This viewer is not intended for clinical and/or diagnostic purposes.

To read data from a DVD
- ensure that the DVD is placed in the DVD reader and not in the DVD burner.

About DVDs
- Use Philips 4-speed DVD+RW media (medical grade) only. Other types are not supported.
- Please handle DVDs according to the manufacturer’s instructions. Realize that DVDs are vulnerable and need to be handled with care.
- Do not use adhesive labels on the DVD. These labels may cause unbalance to the DVD and the adhesive can damage the surface.
- For labeling only use special pens available for writing on DVDs.
• Remove fingerprints on DVDs according to the manufactures instructions at www.philips.com (consumer products).

• The DVD content is optimized for backup of the patient image data. Next to image data it also contains the "presentation states" (Window width, level, pan and zoom settings, ROIs, annotations, lines) and private objects for MRS. Basic DICOM viewers might not be able to handle these presentation states or private objects or enhanced DICOM objects.

• A DVD can contain about 30000 to 40000 images. In case of large datasets this limit can be reached for one patient. Divide the examination by opening the examination in ‘Administration’ and selectively write scans to DVD.

**NOTICE**

Take extra care when modifying the patient data in combination with storage on DVD.

The same image data with the original patient data and the modified patient data cannot be stored on the same DVD.

**Procedure**

1. Select the local patient database.
2. Select the data to be transferred.
3. Select one of the five Queue DVD slots.

![Queue DVD slots](image)

Fig. 194: Queue DVD slots.

4. Start the transfer by clicking on the |Export selection to Queue DVD| button.
5. Answer the questions in the pop-up dialogue boxes and click |Proceed|.

The above steps can be repeated until the selection is completed.

6. Select ‘Queue DVD’ in the top-left corner of the Administration window.
7. Start the transfer to DVD by clicking on the |Copy all to DVD| button. The DVD is automatically ejected when the writing session has finished.

If writing to DVD was succesfull, the data is automatically removed from the Queue DVD slot.
NOTICE
During a writing session the status can be displayed by pressing the |Windows| key to display the Windows task bar and selecting the application tab ‘Burn DVD’.

NOTICE
The DVD content is automatically verified after the writing session.
A window is displayed to indicate the result (when the host is not being rebooted).

NOTICE
It is recommended to check to contents of the DVD after writing.
Check images randomly using the viewer on the DVD.

NOTICE
Copy data to DVD is only available as a single session.
It is not possible to copy additional data to an existing DVD (no multi session).
15 Using USB storage devices

NOTICE
Using USB devices might be disabled by your system administrator.
Using USB storage devices can be enabled by the Hospital Admin.

USB storage devices (flash drives, hard drives) are recognized by the system and can be used for exchanging data. The operating system automatically assigns a drive letter to the device.

CAUTION
Do not remove the USB storage device without using the "Safely Remove Hardware" option. Removing the device without using this option can corrupt the data on the USB memory device.

NOTICE
The USB storage device may contain confidential information.
Take appropriate measures to protect this information. It is not possible to prevent the transfer of data to removable media.

Enable USB Devices (by Hospital Admin)
► Logon as Hospital Admin.
► Click on the Windows Start Button and select MR System Management followed by System Management and Enable or Disable Removable Media.

By clicking Yes, the access to removable media will be enabled for MrUsers, Click No to disable access to removable media for MrUsers.

► Click Yes to enable or No to disable the use of USB devices.
Using "Safely Remove Hardware" option
1. Close all applications that access the USB storage device.
2. Select ‘system’ -> ‘show taskbar’ or press the |windows| key on your keyboard to show the Windows taskbar.
3. Left click once on the ‘Safely Remove Hardware’ icon in the notification area of the taskbar and select ‘Safely remove USB Mass Storage Device - Drive (<drive letter>:)’.
4. You can safely remove your USB storage device when the ‘Safe To Remove Hardware’ message appears.

USB Hard Drives

CAUTION
Connecting a USB-powered external hard drive may cause the USB ports of the host computer to stop working. All USB connected devices will not work anymore.

The hard drive may consume too much power causing the host computer to shut down the USB ports because of safety reasons.

When this occurs the USB ports can be reactivated by:
1. Disconnect the USB hard drive.
2. Shut down the host computer and remove the power for 10 seconds.
3. Reconnect the power and start up the host computer.
   The USB ports are reactivated.

The problem can be prevented by using an external USB drive with an external power connection or using an external drive with a data USB cable and a power-to-USB cable.

*When using a power-to-USB cable:*
  ▶ First connect both USB cables to the computer.
  ▶ Connect the power-to-USB cable to the external device.
  ▶ Connect the USB data cable to the device.
16 Miscellaneous Chapters

Remote Desktop

This section describes the Remote Desktop application of your system.

Remote Desktop enables remote support or assistance on your system. This functionality enables remote users to access your system:

• ViewOnly: remote viewing of the system desktop.
• TakeOver: remote control of the system desktop.

In a ‘Single Session’ (ViewOnly or TakeOver) you allow the remote user to view your system or control your system for one session only. After a session is stopped or after a log-off or reboot of your system the remote connection has to be re-enabled by the local user.

In ‘Fixed Duration’ (TakeOver) you allow the remote user to control your system for a limited time period, from 1 to 60 hours. The remote user can access your system independently for the complete duration of the session by using a password protected connection. This password is set at the connection start up.

When a reboot of the system is necessary, it can be done by the remote user. After starting a Fixed Duration session the assistance of the local user is not required.

A Fixed Duration session may be used to service your system during the time that it is not used.

WARNING
Fixed duration session shall only be performed with appropriate safety, security and privacy measures taken according to hospital policies.

Every session can be stopped at all times by the local user. The remote connection is then closed and has to be re-enabled by the local user if necessary. This also applies to a Fixed Duration session.

NOTICE
When starting a Remote Desktop session a dialog box appears displaying a warning text. The session cannot be started before the local user agrees by clicking the [I agree] button.

WARNING
During a single TakeOver session, the local user must stay at the system console and monitor the activities performed by the remote user.
WARNING
The local user must be present at the console at all times during scanning of a patient in a Remote Desktop session.

WARNING
The local user is responsible for ensuring the safe and secure use of the system and for the safety of his patient. It is possible to terminate a session at all times using the |Stop| button on the screen.

WARNING
Only expert users are allowed to run a TakeOver session.

WARNING
During a TakeOver Fixed Duration session where the local user is not present, the local user has to verify that no person is present in the examination room. Take appropriate measures to inform people that a TakeOver session is running.
Remember that scanning is only possible when the door of the examination room is closed.

Workflow
Contact Philips customer support in case of a system failure or problem. The service engineer may want to view your system desktop while you are scanning or access it to remotely service your system.

NOTICE
It is advised to keep contact on the phone for the complete length of the session.

1. Click the Windows |Start| button, go to |MR user| and select |Enable Remote Desktop| to start the Remote Desktop application. A dialog box appears displaying the following text:

   **Enable Remote Desktop Session**
   A Remote Desktop session has been requested.
   If you accept this Remote Desktop request, you confirm that you know that this is an authorized Remote Desktop session.
   You further confirm that you are the responsible local operator for the system during this Remote Desktop session and have been fully informed about the possible consequences regarding Safety, Security and Privacy arising from permitting remote operation of the system, including those discussed in the system’s "instructions for use".
During a single windows Take Over session, you must stay at the system console and monitor the activities performed by the remote user. You can end the Remote Desktop session any time by pressing the “STOP” button on your screen. As the operator of the system, you are responsible for the safe and secure use of the system. Note that certain private information, including electronic Protected Health Information (ePHI) about patients, will become accessible to the remote operator. Be sure to stay within your institution’s policy regarding disclosure of confidential information to third parties.

2. If in doubt about the message click |Exit Session| to cancel. Click |I agree| to confirm. An ‘Enable Remote session’ box appears on the screen.

3. Select:
   (a) |Single Windows Session| or
   (b) |Fixed Duration| and the amount of time (1 to max. 60 hours) you allow the remote user to access your system, and click |OK|.

The application is active and a ‘VNC’ icon is displayed in the tray of your Windows taskbar.

- Single Windows Session
  A red Stop button appears on the screen. With this button you can stop the session. The button always stays on top and can be placed anywhere on the screen.

- Fixed Duration
  A dialog box appears on the screen with a |Stop| button and fields to enter/confirm a password.

**NOTICE**
The password has to be entered by the remote user.

4. Inform the service engineer that the application is active.
   The service engineer will start up the remote connection and a ‘VNC server acceptance’ box appears on the screen.
User (anonymous) is requesting remote access to your computer.
If you do nothing within the next 16 seconds then the request will be denied.

5. Click:
   • Approve to confirm a TakeOver session or
   • View-only to confirm a ViewOnly session.

When the Remote connection is active the background color of the ‘VNC’ icon in the tray of your Windows taskbar changes from white to black.

For a Fixed Duration the service engineer has to enter a password. After the password has been confirmed the box minimizes to the |Stop| button. With this button you can stop the session. The button always stays on top and can be placed anywhere on the screen. The remaining session time is displayed in the header of the button.

**NOTICE**
Error messages may appear on the screen when the password is not entered correctly.
These messages are for the remote user only.

**Stopping a session**
The local user can stop a Remote Desktop session at all times:
   • Click the red |Stop| button to stop the session. A confirmation box appears on the screen: ‘Are you sure you want to stop the remote session’.
   • Click |OK| to confirm. The session is stopped.

When finishing a Single Windows Session the local user as well as the remote user can close the session.

**NOTICE**
The start/stop of every Remote Desktop session is logged by your system.
The Remote Service Network logs who has been the remote user.

**Remote Software Installation (RSI)**
The Remote Software Installation application (RSI) detects software updates or fixes which are uploaded to your system and ready to install.
This application is started automatically at logon of your system.
When new updates or fixes are available, a flashing RSI icon will appear in the tray of your Windows taskbar. The taskbar is shown automatically. Hide the taskbar again by clicking on an arbitrary application.

1. Click on the RSI icon. The MR software Installation dialog appears.

   In the Installation dialog the following is listed:
   - Updates and fixes list.
     - ‘Name’, name of the update or fix.
     - ‘Application notes’, name of the Application Notes, if available.
     - ‘Patient data deleted?’, the value is ‘yes’ when patient data is deleted before installation of the update or fix.
     - ‘Installation time’, displays the estimated installation time of the update or fix.
     - ‘Status’, displays the status of the update or fix (ready for installation, or installed).
   - Buttons.
     - ‘Open Application Notes’, to view the application Notes.
     - ‘Install All’, to install all listed updates and fixes.
     - ‘Close’, to close the installation dialog.

   ![RSI dialog](image)

   **NOTICE**

   The ‘Install All’ button is not available to operators.

   Installation of updates and fixes can only be performed by the hospital administrator or MR service engineers.

   **NOTICE**

   The operator should inform the hospital administrator or MR service engineers when updates or fixes are available.
NOTICE
A Warning is displayed in the dialog when patient data will be deleted at installing of updates and fixes: ‘Patient database will be deleted. Archive the patient database before installation’.

2. Click on the row of the update of fix of which information is needed.
3. Click the ‘Open Release Notes’ or ‘Open Application Notes’ button to open the required document.

NOTICE
A warning is displayed when no row is selected.

Installation
Installation of updates and fixes can only be done by the hospital administrator or MR service engineers.

1. Logon as hospital administrator.

NOTICE
If necessary contact your local Philips service representative for logon details.

2. Double-click on the |RSI| icon. The MR software Installation dialog appears.
3. Click the ‘Install All’ button. The installation procedure of all updates and fixes will be started.
   When patient data is going to be deleted a confirmation dialog is displayed: ‘The Patient data will be deleted. Has the patient data been archived?’
4. Click ‘Yes’ to install the updates and fixes or ‘No’ to cancel the installation, the RSI application is then closed.
   The installation starts with creating a backup of the MR application software and site specific configurations. When the backup is successful the updates and fixes will be installed.
   After installations the system has to be rebooted and a dialog will appear.
5. Confirm to reboot the system or cancel.
After successful installation all updates and fixes will be deleted and the status is set to ‘Installed’.
The Release and Application Notes remain on the system and in the RSI dialog.
NOTICE
Please contact your local Philips service representative if an installation was unsuccessful.
A system restore may be required.

Customer Feedback
Problems found while working with the system can be described using the Customer Feedback tool, also called FPR (Field Problem Report) Utility.
The problem reports can be read out by your Philips service engineer.

NOTICE
Please inform your local Philips service representative in case you submitted a problem report on the system.

Prepare DICOM images
If DICOM images are to be included, these images need to be prepared first.
► Clean the 'Disk Files' partition first:
  • Select ‘Administration’ from the ‘Patient’ main menu or press |F4|.
  • Select 'Disk Files' as source database or device.
  • Click 'Select All'.
  • Click 'Delete' to clean the 'Disk Files' partition.

► Select the images you want to include and choose the destination:
  • Select ‘Administration’ from the ‘Patient’ main menu or press |F4|.
  • Select 'Local Patient Database' as source database or device.
  • Select the images to be included.
  • Select 'Disk Files' as destination.
  • Optional: Enable 'Suppress Patient Data'.
  • Press 'Proceed' to confirm.
   The selected images will be combined in a zip file on the Disk Files partition.

Submitting a FPR
1. Click |System| in the main menu and select 'Report Issue to Philips...'.
   The Customer Feedback window opens.
2. Select the |Submit FPR| tab, if it’s not active. The table below shows the data fields within the |Submit FPR| tab.
• 'Hospital Name' and 'System ref number' cannot be changed.
• Enter 'Occurrence date/time' when the problem occurred or select drop-down for calendar.
• Enter your name as 'Submitter'.
• Give a short description of the error case in the field 'Error Description'.
• Describe which actions have been done just before the error occurred in the field 'Actions prior to error'.

3. Check the box ‘Include DICOM images’ if you want to include the prepared images (see workflow 'Prepare DICOM images') with the problem report.

NOTICE
An error message is displayed if no DICOM images can be selected, because they have not been prepared.
In this case, follow the directions given to include DICOM images.

4. Click |Proceed| to submit the FPR.

<table>
<thead>
<tr>
<th>Field</th>
<th>Data</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hospital Name</td>
<td>Cannot be changed.</td>
</tr>
<tr>
<td>System ref number</td>
<td>Cannot be changed.</td>
</tr>
<tr>
<td>Occurrence date/time</td>
<td>Enter date and time when the problem occurred or select drop down for calendar.</td>
</tr>
<tr>
<td>Submitter</td>
<td>Enter your name.</td>
</tr>
<tr>
<td>Error Description</td>
<td>Give a short description of the error case.</td>
</tr>
<tr>
<td>Actions prior to error</td>
<td>Describe which actions have been done just before the error occurred.</td>
</tr>
</tbody>
</table>

Tab. 24: Overview of Data for the FPR Utility
17 Artifacts

Artifacts can occur in MRI for a number of reasons, degrading the image quality and sometimes hindering diagnosis. They may be caused by technical problems and data handling or by physiological effects from the patient. Since most artifacts can be reduced, it is important to recognize them, and to know what can be done to prevent them.

This includes methods of correcting or mitigating such artifacts (e.g. changing bandwidth, gradient moment nulling, pre-saturation, B0 and RF shimming, etc.).

Artifacts on high field strengths

Dielectric shading effect

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Hypo- or hyperintense areas.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>Non-uniform RF distribution in the body, caused by changes of the RF wave due to the electrical properties of tissue.</td>
</tr>
<tr>
<td></td>
<td>This physical phenomenon is more pronounced at 3.0T since the RF wavelength at 3.0T (approximately 25 cm) approaches the size of the body, resulting in a standing wave.</td>
</tr>
<tr>
<td>Countermeasures</td>
<td>• MultiTransmit technology addresses this problem at the source, no additional countermeasures have to be taken.</td>
</tr>
<tr>
<td></td>
<td>• On 3.0T systems without MultiTransmit technology, dielectric shading effects can occur depending on the patient, particularly in body imaging. To avoid these effects, it is advised to used Body tuned CLEAR - a specific B1 filter that is designed to overcome receive inhomogeneities in body imaging.</td>
</tr>
</tbody>
</table>

![Fig. 197: Left: Dielectric shading effect on 3.0T system without MultiTransmit. Right: Same patient scanned with MultiTransmit. No dielectric shading.](image-url)
Fig. 198: Formation of dielectric shading on 3.0T system using single transmission (no MultiTransmit). Without MultiTransmit, a standing wave (2) could be generated since the wavelength of the RF-wave (1) at 3.0T lies in the same range as the size of the body: 20 cm to 25 cm.

Fig. 199: MultiTransmit technology is designed to avoid the occurrence of dielectric effects. With MultiTransmit, simultaneous parallel RF transmission fully addresses the dielectric shading effect.

**Motion artifacts**

Patient motion is the largest physiological effect that causes artifacts. Motion during the acquisition results in inconsistencies in phase and amplitude, which lead to blurring and ghosting. These artifacts appear in the phase encoding direction, independent of the direction of the motion. The different motion artifacts and their remedies are shown below.

**Cardiac motion artifact**

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Blurring and ghosting.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>Signal variation during data collection due to movement of the heart.</td>
</tr>
<tr>
<td>Countermeasures</td>
<td>• Cardiac Synchronization.</td>
</tr>
<tr>
<td></td>
<td>• Triggering in combination with Flow Compensation and REST provides maximum artifact reduction.</td>
</tr>
</tbody>
</table>
Motion artifacts

Preset Procedures

Cardiac Synchronization is used in all heart and thorax procedures to suppress these artifacts.

Fig. 200: T-spine image without cardiac triggering.

**Artifact caused by breathing**

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Blurring and ghosting.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>Signal variation during data collection due to movement of the chest and the abdominal wall.</td>
</tr>
<tr>
<td>Countermeasures</td>
<td>Respiratory Compensation techniques:</td>
</tr>
<tr>
<td></td>
<td>• Respiratory Triggering: for TSE and TFE scans with a long TR (1800 ms ... 2500 ms).</td>
</tr>
<tr>
<td></td>
<td>• Breathhold techniques: to be used in FFE- and TFE.</td>
</tr>
<tr>
<td></td>
<td>• PEAR to be used in SE, FFE and IR.</td>
</tr>
<tr>
<td>Navigator echo technique</td>
<td></td>
</tr>
</tbody>
</table>

**Related topics**

- Respiratory Triggering.
- Breathhold techniques.
- PEAR.
- SMART.

**Respiratory compensation**

- is the recommended method for abdominal scans.
- is of minor importance in the thorax area. Most artifacts are caused by cardiac motion.
- should be combined with Cardiac Synchronization in lung imaging.
- is not necessary in the pelvic area, but improves SE images.
Artifact due to blood flow

Artifact appearance
Repeated ghost signal in the phase encoding direction or unwanted high blood signal.

Caused by
Flowing blood due to a misregistration effect of blood flowing within or through the image plane, because of the difference in time between the preparation and read-out gradient.

Countermeasures
- REST and Shared REST: especially useful when applying two parallel REST slabs in transverse imaging to saturate the signal of blood flowing through plane. Blood will appear as a signal void instead of high signal intensity.
- REST in combination with Flow Compensation (FC) for optimum results.
- REST in Inflow MRA to suppress venous or arterial flow.
- Cardiac Synchronization in MRA to get rid of pulsation artifacts of vessels.

Related topics
- REST (Regional Saturation Technique).

Fig. 201: Transverse abdomen, left: without RC, right: with RC.

Fig. 202: Transverse scan of abdomen, left: without REST and FC, right: with REST and FC.
**CSF pulsation artifact**

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Ghost artifacts superimposed in the image.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>Signal variations during data collection due to pulsatile CSF flow.</td>
</tr>
<tr>
<td>Countermeasures</td>
<td>• Flow Compensation has proved to be very useful in sagittal spine images and axial liver images.</td>
</tr>
<tr>
<td></td>
<td>• Cardiac Triggering is an additional option if Flow Compensation is applied and there are still flow artifacts.</td>
</tr>
<tr>
<td></td>
<td>• Inherently compensated: b-FFE (balanced FFE).</td>
</tr>
<tr>
<td>Related topics</td>
<td>• Flow Compensation.</td>
</tr>
<tr>
<td></td>
<td>• Cardiac Triggering.</td>
</tr>
<tr>
<td></td>
<td>• b-FFE.</td>
</tr>
</tbody>
</table>

Fig. 203: C-spine, left: without FC, right: with FC.

**Flow void artifact**

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Black hole like artifacts in axial and sagittal T2W TSE scans with a high TSE-factor.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>Fast flowing CSF.</td>
</tr>
<tr>
<td>Countermeasures</td>
<td>• Increasing the TSE-factor (minimize echo spacing) so that the scans are less sensitive to flow.</td>
</tr>
<tr>
<td></td>
<td>• Flow Compensation.</td>
</tr>
<tr>
<td></td>
<td>• Cardiac Triggering.</td>
</tr>
<tr>
<td></td>
<td>• Use of b-FFE (balanced FFE).</td>
</tr>
<tr>
<td></td>
<td>• Performing a 3D TSE multichunk instead of a MS TSE scan.</td>
</tr>
<tr>
<td>Related topics</td>
<td>• Flow Compensation.</td>
</tr>
<tr>
<td></td>
<td>• Cardiac Triggering.</td>
</tr>
</tbody>
</table>
Chemical shift artifacts

Water-Fat shift

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Hypo- and hyperintense lines between tissue boundaries</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• in frequency encoding direction for non-EPI/GRASE scans</td>
</tr>
<tr>
<td></td>
<td>• in phase encoding direction for EPI/GRASE scans.</td>
</tr>
</tbody>
</table>

| Caused by | Resonance frequency difference between water and fat resulting in displacement between water and fat by a number of pixels. The hypointense lines are originated by empty voxels and hyperintense lines by superimposed signals. |

| Countermeasures | • Set the parameter WFS (Water-Fat Shift) to a user defined value. Note that using a smaller WFS decreases the artifact at the cost of SNR. |
|                | • Change the Fat-Shift direction. |

| Related topics | • Water-Fat Shift. |
|               | • Fat-Shift Direction. |

Fig. 204: Transverse TSE spine with flow voids.

Fig. 205: From left to right: WFS on phantom. Small WFS. Large WFS.
**NOTICE**
The chemical shift artifact increases with the field strength.

**Water-Fat dephasing**

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Signal dephasing in voxels containing both water and fat showing up as black lines around anatomic structures.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Caused by</strong></td>
<td>• Resonance frequency differences between water and fat AND</td>
</tr>
<tr>
<td></td>
<td>• Use of an ‘out of phase TE’ (water and fat signals are out of phase).</td>
</tr>
<tr>
<td><strong>Countermeasures</strong></td>
<td>• Choose an ‘in phase echo time’ (field strength dependent). See table below.</td>
</tr>
<tr>
<td><strong>Related topics</strong></td>
<td>• Water-Fat Shift.</td>
</tr>
<tr>
<td></td>
<td>• Fat Shift Direction.</td>
</tr>
</tbody>
</table>

![Fig. 206: Left: water and fat are in phase, right: water and fat are out of phase.](image)

**In phase TE’s and out of phase TE’s**

<table>
<thead>
<tr>
<th>In phase TE [ms]</th>
<th>1.0T</th>
<th>1.5T</th>
<th>3.0T</th>
</tr>
</thead>
<tbody>
<tr>
<td>6.9</td>
<td>4.6</td>
<td>2.3</td>
<td></td>
</tr>
<tr>
<td>13.8</td>
<td>9.2</td>
<td>4.6</td>
<td></td>
</tr>
<tr>
<td>20.7</td>
<td>13.8</td>
<td>6.9</td>
<td></td>
</tr>
<tr>
<td>27.6</td>
<td>18.4</td>
<td>9.2</td>
<td></td>
</tr>
<tr>
<td></td>
<td>23.0</td>
<td>11.5</td>
<td></td>
</tr>
</tbody>
</table>

| Water and fat are in phase when the TE is a multiple of ... [ms] | 6.9 | 4.6 | 2.3 |
Aliasing artifacts

Aliasing artifacts are also referred to as fold-over artifact.

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Tissue outside the FOV which is folded back into the image, most commonly occurring in fold-over direction (phase encoding direction).</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>The spins within the FOV acquire a maximum phase shift of n x 360°. Spins just outside the FOV have a phase shift of more than one cycle. This results in misregistration of those spins.</td>
</tr>
<tr>
<td>Countermeasures</td>
<td>• Fold-over suppression: Signal from outside the FOV is suppressed.</td>
</tr>
<tr>
<td></td>
<td>• Increase RFOV so there is no tissue outside the FOV.</td>
</tr>
<tr>
<td></td>
<td>• Change the fold-over direction if possible so there is no tissue to fold back. This also depends on other artifacts that might occur.</td>
</tr>
<tr>
<td></td>
<td>• Use REST slabs to saturate tissue outside the FOV.</td>
</tr>
<tr>
<td>Related topics</td>
<td>• Fold-over suppression.</td>
</tr>
<tr>
<td></td>
<td>• REST.</td>
</tr>
<tr>
<td></td>
<td>• RFOV.</td>
</tr>
<tr>
<td></td>
<td>• SENSE.</td>
</tr>
</tbody>
</table>
Magnetic material artifacts

Artifact appearance | Signal loss around ferromagnetic material or metallic material.
--- | ---
Caused by | • Magnetic field distortions by ferromagnetic metal implants such as hip prostheses, surgical wires and clips, and also some eye cosmetics and small metallic particles.  
• Eddy currents induced in non-ferromagnetic metallic material by switching gradients.
Countermeasures | • Remove any kind of ferromagnetic and metallic material.

Susceptibility artifacts

Artifact appearance | Signal dephasing resulting in misregistration at interfaces of tissues with different magnetic susceptibility.  
| in FFE- and EPI-scans.
--- | ---
Caused by | • Different magnetic susceptibility (different local magnetic fields). For example, at interfaces between air and tissue, inhomogeneities are induced.
Countermeasures | • Larger matrix size or smaller FOV (smaller pixels).  
• Shorter TE.  
• A smaller WFS value and control of Fat Shift Direction.  
• Full acquisition (scan percentage 100%).
Related topics | • FFE and EPI.  
• Fat Shift direction.
Ringing (Gibbs) artifacts

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Ring like or linear truncation artifact, also called Gibbs artifact.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>Reduced acquisition. The artifacts are induced by high contrast transitions, and are particularly common with scan percentages below 80%.</td>
</tr>
</tbody>
</table>
| Countermeasures     | • Ringing filtering: Pre-reconstruction filter which also smooths the image.  
                        • Higher ‘Scan Percentage’ value. |
| Related topics      | • Scan Percentage. |

Zebra stripe artifact

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Zebra stripes.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>REST saturation pulse interfering with the data acquisition in 3D-TSE scans.</td>
</tr>
</tbody>
</table>
| Countermeasures     | • Change the number of REST slabs.  
                        • Decrease the TSE factor.  
                        • Use an even number of ‘true’ NSA. |

NOTICE
This artifact does not occur anymore in TSE scans with more than 1 ‘true’ NSA.
MRA inflow artifacts

Venetian blind artifact

| Artifact appearance | Dark bands (signal decrease) at the end of a volume in the MIP’s (Maximum Intensity Projection) of a multichunk 3D Inflow MRA-technique. The larger the volume, the more prominent this effect. |
| Caused by | Saturation effects. |
| Countermeasures | • TONE.  
• CHARM. The artifact doesn’t occur anymore with CHARM being introduced with Release 9. |
| Related topics | • TONE.  
• CHARM. |

Fig. 210: Left and right: MIP oblique Multichunk scan.

Staircase artifact

| Artifact appearance | Staircase in the MIPs of an M2D Inflow technique. |
| Caused by | Saturation effects. |
| Countermeasures | • Use a slice gap with a negative value. Normally an overlap of 25% - 30% is sufficient. |
Fat suppression artifact

Artifact appearance
Fat is not completely suppressed using the SPIR-, SPAIR- or ProSet-technique.

Caused by

• locally distorted magnetic field (B0): water could partially be suppressed instead of fat.

and/or

• locally distorted RF field (B1): the flip angle used for the SPIR- and ProSet-pulse could slightly vary over the FOV.

Countermeasures

• There are several ways for complete fat suppression. See following list.

Related topics

• STIR.
• SPIR.
• SPAIR.
• ProSet.
• Shimming.

NOTICE

SPAIR, SPIR and ProSet are critical with regard to the magnetic field homogeneity.

Countermeasures

Patient preparation

• Remove all metal (also dentures, dental devices) from the patient.
• Ask the patient to remove eye make-up (often containing metallic particles).
• Make sure the patient has been to the toilet, because high signal intensities (e.g. full bladder) may disturb the autoshim.

Positioning

• Ensure that the area of interest is as close as possible to the isocenter (less than 80 mm in any direction).
• Always move the table whenever ‘travel to scan plane’ is prompted.
• Avoid placing two objects (knees, ankles) in one FOV.
• Do not use sandbags inside or near the FOV, because they may enlarge susceptibility effects.
In some cases, the use of pads made out of special material (e.g. satpads®) may help. Note that by putting the pad between surface coil and patient, the SNR may adversely be affected (larger coil-patient distance).

**Parameter settings**
- Adjust the FOV to the anatomy of interest.
- Use volume shimming and select the area that needs to be fat suppressed.

**Alternative**
Do not use spectral fat suppression on anatomies that suffer from large susceptibility effects (neck, cervical spine, thoracic spine). Use STIR instead.

**STIR-sequence**
- IR or IR-TSE with a short TI.
- Providing good fat suppression.
- Not useful in combination with contrast agents since they will suppress all tissues with a short T1 including contrast enhanced tissues.

**Quadrupole artifact**

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Signal intensity variations with SPIR, especially in abdomen and pelvis.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>Eddy currents in the patient. This results in B1 disturbance from left to right and from anterior to posterior.</td>
</tr>
<tr>
<td>Countermeasures</td>
<td>STIR or SPAIR instead of SPIR.</td>
</tr>
<tr>
<td>Related topics</td>
<td>• STIR.</td>
</tr>
<tr>
<td></td>
<td>• SPIR.</td>
</tr>
<tr>
<td></td>
<td>• ProSet.</td>
</tr>
<tr>
<td></td>
<td>• Shimming.</td>
</tr>
</tbody>
</table>

Fig. 211: Left: Coronal oblique. Right: transverse.

**NOTICE**
Both, SPIR and ProSet are very critical with regard to the magnetic field homogeneity.
## Multiple stack artifact

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Black line artifacts in a multistack scan where slices of the different stacks overlap or cross over.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>When the stacks are measured in one package, the measurement is done in an interleaved manner. Interference between the different slices occurs which results in signal loss.</td>
</tr>
</tbody>
</table>
| Countermeasures     | • Planning the stacks in different packages (Parameter ‘Stacks as packages’).  
                     • Changing the position or angulation of the stacks such that they do not overlap. |
| Related topics      | • Stacks.                                                                                       |

**Fig. 212:** A: Planscan of B. B: Transverse spine image with multistack artifact.

## REST artifact

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Signal distortion in the region where the REST has been applied.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>Two free REST slabs which intersect each other.</td>
</tr>
<tr>
<td>Countermeasures</td>
<td>Applying the REST slabs such that they do not overlap.</td>
</tr>
<tr>
<td>Related topics</td>
<td>REST.</td>
</tr>
</tbody>
</table>

**Fig. 213:** REST artifact.
SENSE Artifacts

Intrinsic backfolding

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Backfolding in the center of the image or the 3D volume:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• in-plane (fold-over direction) in M2D and MS scan mode,</td>
</tr>
<tr>
<td></td>
<td>• also in slice direction in 3D scan mode</td>
</tr>
</tbody>
</table>

| Caused by            | FOV, RFOV or 3D volume have been planned too small. Special attention has to be given to double-oblique cardiac scans. |

| Countermeasures      | Enlarge FOV, RFOV or 3D volume. Increase the flexible fold-over suppression area. |

Fig. 214: Left: 3D - intrinsic backfolding in slice direction. Right: MS - intrinsic backfolding in plane.

Fig. 215: Left and right: The ear folds back in MS scan.

Intrinsic backfolding of artifacts

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Fold-over of ghost artifacts from just outside the FOV.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>FOV, RFOV or 3D volume have been planned slightly too small.</td>
</tr>
</tbody>
</table>
Artifacts MR Spectroscopy Artifacts

| Countermeasures | Enlarge FOV, RFOV or 3D volume. Increase the flexible fold-over suppression area. |

Cut-line artifacts

| Artifact appearance | Dark area separated from a bright area by a cut-line. |
| Caused by | The coil elements move during the scan due to breathing. |
| Countermeasures | Right mouse: repeat prescans. |

Single-shot sequences and Fat Shift Direction

| Artifact appearance | Susceptibility related artifact in single-shot EPI sequences with SENSE, fold-over direction AP and fat shift direction A(nterior): |
| | • E.g. high signal at the border of the frontal sinus. |
| | • Especially in b0 images in diffusion weighted scans. Less pronounced in high-b images which in turn might result in low signal in the calculated ADC-map. |
| Caused by | Fat shift direction set to A(nterior) in these scans. |
| Countermeasures | Set the ‘Fat shift direction’ to ‘P(osterior)’ in all cases. |
| Related topics | SENSE. |
| | Fat shift direction. |

Fig. 216: Upper row: Fat Shift Direction = Anterior. Lower row: Fat Shift Direction = Posterior.

MR Spectroscopy Artifacts

Like MR-imaging, MR-spectroscopy techniques can suffer from artifacts. Some of these artifacts are hard to recognize, but can completely alter the outcome of the spectrum. It is important to recognize the artifacts and to know how to avoid them.
## Truncation at the end of the signal

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Artifacts presented as sinc wriggles around the peaks appear in the spectrum. The wriggles are mainly seen around the residual water peak.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>Signal sampling is stopped before the signals have decayed to (close to) zero resulting in abrupt signal intensity changes which cannot be handled well by the Fourier transform.</td>
</tr>
</tbody>
</table>
| Countermeasure / Solution | Re-acquisition with increased Tacq is the best solution, but time is not always available to do so. For signal to decay completely to zero, the Tacq should be at least 5 x $T_2^*$ relaxation time. Increase Tacq by:  
  - Increased number of sampled with equal bandwidth.  
  - Reduce bandwidth with equal number of samples.  
  If re-acquisition is not an option, filtering of the time domain signal is used to influence the signal such that abrupt signal intensity changes are removed. Note that linewidth increases by applying filters. |

![Time domain signal](image1)

![Spectrum after Fourier transform](image2)

**Fig. 217:** Time-domain signal (A) that is cut off before signal has decayed, and the resulting spectrum (B). The baseline is distorted by sinc wriggles.

![Time domain signal](image3)

![Spectrum after Fourier transform](image4)

**Fig. 218:** Same time domain signal (A), with additional Gaussian filtering applied (6Hz). No truncation artifacts in resulting spectrum (B), at the cost of spectral resolution.
Truncation with maximum echo sampling

<table>
<thead>
<tr>
<th>Artifact appearance</th>
<th>Artifacts presented as sinc wriggles appear around the baseline of the spectrum.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caused by</td>
<td>If maximum echo signal sampling is used and signal sampling only starts close to the echo top position, abrupt signal intensity changes which cannot be handled well by the Fourier transform will occur at the start of signal sampling. This will mainly happen if maximum echo is used with short TE.</td>
</tr>
<tr>
<td>Countermeasure / Solution</td>
<td>Asymmetric filtering is applied with the symmetry point set to the echo top position.</td>
</tr>
</tbody>
</table>

Saturation

| Artifact appearance | Saturation effects in the spectrum. |

Fig. 219: Image examples in healthy volunteer: SVS TE 144 ms. Different Tacq’s.

Fig. 220: A: Unfiltered signal versus B: filtered signal (asymmetric filter) where TD is the time domain signal and Sp the spectrum: truncation effect is seen in the unfiltered time domain signal, resulting in wriggles in the baseline of the spectrum whereas the artifacts are minimized when applying an asymmetric filter.
Caused by

Incomplete $T_1$ relaxation.

To maximally measure the metabolite signals, full $T_1$-relaxation is required before the next excitation is performed.

Saturation effects are seen if $T_1$-relaxation is not complete. The amount of saturation is different for the various metabolites and saturation effects will affect the values found during peak fitting.

Even though the saturation effect is not hindering spectral quality, it is mentioned in the artifact section, as it something to be aware of.

Countermeasure / Solution

To allow full $T_1$-relaxation, the TR used should be $\geq 5 \times T_1$ of the metabolite of interest.

As $T_1$-relaxation times of metabolites are long, scan times would increase tremendously.

Fig. 221: Brain spectra (inverted) from a healthy volunteer. The Cho/Cr ratio is changed from 1.69 (1000 ms) to 1.44 (4000 ms).

**NOTICE**

If full $T_1$-relaxation is not achieved within the TR chosen, it is important to acquire some startup acquisitions.

These shots are used to place the spin system into steady state.

**Frequency drift**

Artifact appearance

Increased linewidths. Peaks smear out.

Caused by

Frequency drift.

As part of the preparation phases, $\alpha_0$ determination is performed. During the long spectroscopy scan, this $\alpha_0$ frequency could change slightly,

Countermeasure / Solution

• Save each FID separately, correct for the drift in post-processing.
**Artifacts MR Spectroscopy Artifacts**

**Fig. 222:** As the frequency of the peak slightly changes over time, the resultant spectrum will show up as a broader peak with reduced amplitude. Blue lines (B): measured signal in each respective excitation, Red lines (R): resultant spectrum.

**Ghosting**

**Artifact appearance**

Distorted spectra in row of voxels with equal phase encoding gradient.

For CSI: even in two directions as phase encodings is done in two directions.

**Caused by**

(Pulsatile) through-plane flow:

Like in MR imaging, (pulsatile) through-plane flow can cause ghosting in the phase encoding directions in spectroscopic imaging.

**Countermeasure / Solution**

To reduce the signal intensity of through-plane flow, parallel REST slabs can be positioned above and below the stack of CSI-slices.

**Baseline distortions**

**Artifact appearance**

Baseline distortions, mainly seen in short TE spectra.

**Caused by**

Signals of fast relaxing macromolecules and/or signals of unsuppressed water which are still present in the first few points in the time domain signal.

These baseline distortions hamper good fitting and quantification.

**Countermeasure / Solution**

- In time-domain: take out the first points of the FID with shift with zero padding.
- In frequency-domain: fit polynomial spline.

It is caused in the first few points in the time-domain signal, where signals of fast-relaxing macromolecules and/or signals of non-suppressed water are still present.

These baseline distortions hamper good fitting and quantification.
DC-Offset

Artifact appearance  Spike signal in the spectrum at zero frequency.

Caused by  Time domain signal decay to a constant, but not to zero.

Countermeasure / Solution  
- Phase cycling, to cancel the effect in subsequent measurements.
- Subtract the last 10% of the FID.

Incomplete water suppression

Artifact appearance  Wriggle artifacts around the (residual) water peak.

Caused by  Incomplete water suppression: residual water signal from outside of the volume of interest gives rise to stimulated echoes, causing artifacts.

Countermeasure / Solution  
- Phase cycling (is already implemented in preset procedures).
- REST slabs around the VOI to suppress non-suppressed water.
- Longer duration of the spoiler gradients.

Residual signals

Artifact appearance  Signals around -2ppm and +10ppm in corrected spectra.

Caused by  Presence of high fat signal in the reference measurement.

Countermeasure / Solution  Reprocess without use of reference measurement.
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