8 MR SpectroView

The MR SpectroView package is used to analyze and present spectroscopy data after processing. The package can be used for the evaluation of Single Voxel and Multi Voxel (Chemical Shift Imaging CSI) data. It 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
  - SNR (Signal-to-Noise Ratio)
  - Height
  - Peak Area
  - FWHM (Full Width Half Maximum)
  - Area Ratio
- Metabolite images (in color overlay), optional with quality indicator and mini spectra (Multi Voxel)
- Ratio images (in color overlay), optional with quality indicator and mini spectra (Multi Voxel)
- Spectral grids on reference images
  - Display of user-selected subset from an array of spectra

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Indications for Use

MR SpectroView is a task-guided application for the post-processing and visualization of Proton Magnetic Resonance Spectroscopy (MRS) imaging, providing hydrogen single and multi-voxel spectra, metabolite maps, and/or ratio maps. Refer to section “Specify Metabolites” on page 117 for details on how to properly select metabolites and metabolite ratios for anatomies such as Brain, Breast, Liver, Muscle and Prostate.

User Interface

Screen layout

The MR SpectroView package has a default layout of a viewport displaying the spectrum with metabolite information and reference views.

Reference Views

Reference views display information according to the type of spectroscopy analysis: single voxel or multiple voxels.

Reference view	Content of viewport with SVS data	Content of viewport with CSI data
Top	Planning • by default: Axial Feet (A) • by default with quality indicator and mini spectra	Planning • by default: Axial Feet (A), • by default with quality indicator and mini spectra
Middle	Planning Coronal Front (C) • by default with quality indicator and mini spectra	Metabolite map • by default without quality indicator and mini spectra
Bottom	Planning Sagittal Left (S) • by default with quality indicator and mini spectra	Metabolite map • by default without quality indicator and mini spectra
For all	The voxel is displayed as a cube in orthogonal reference views.	A grid is displayed on all viewports with the selected voxels highlighted.
	For more information about quality indicator and mini spectra, refer to section “More Functions within the MR SpectroView package” on page 113	

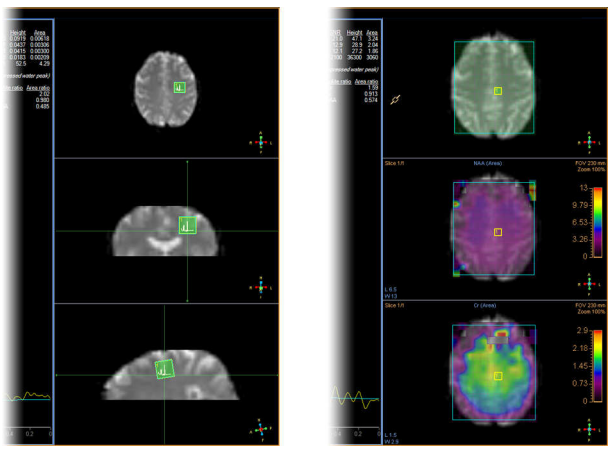

Fig. 43: Reference view layout for single voxel analysis (left) and multiple voxel analysis (right)

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Reference Box

NOTICE

The reference box in the reference views represents the PRESS box (Point Resolved Spectroscopy) as stored in the volume localization sequence. Only voxels with their center located inside the box are processed and displayed. If the volume localization sequence is not present, all spectroscopy grid slices are displayed.

The reference box is color-coded as follows:

- Green: unprocessed.
- Light green: processing in progress.
- Cyan: processed.

Quality Indicator

The quality of a spectrum is based on the following properties:

- Field homogeneity of the magnetic field
- Signal-to-noise ratio (SNR)

Full Width Half Maximum

The field homogeneity is specified by the Full Width Half Maximum (FWHM) of the unsuppressed water peak as present in the water reference frame.

If the water reference frame is not present, the FWHM is derived from the water peak in the clinical spectrum (if the clinical spectrum is fitted for the water peak).

If the water peak is not present in the clinical spectrum, or if it is not fitted, the highest peak is used (excluding the fat peak).

The FWHM assessment is based on the following values:

FWHM H_2O [ppm]	Quality of Homogeneity
≤ 0.10	Good
0.10 < FWHM H_2O ≤ 0.16	Moderate
> 0.16	Poor

Tab. 2: FWHM H_2O Quality Indicator

FWHM Other Peaks [ppm]	Quality of Homogeneity
≤ 0.07	Good
0.07 < FWHM ≤ 0.14	Moderate
> 0.14	Poor

Tab. 3: FWHM Other Peaks Quality Indicator

For prostate, the FWHM assessment is based on the following values:

FWHM Other Peaks [ppm]	Quality of Homogeneity
≤ 0.4	Good
0.4 < FWHM ≤ 0.6	Moderate
> 0.6	Poor

Tab. 4: FWHM Citrate Quality Indicator

The formula used for calculating ppm (parts per million) is as follows:

- Delta f (at half max) / fres * 10^6.

Signal-to-Noise Ratio

The signal-to-noise ratio (SNR) is defined in the frequency domain (FD) as the height of the largest metabolite peak divided by the root-mean-square (rms) amplitude (¼ SD) of the noise in a signal- and artifact-free part of the spectrum.

SNR is based on the highest peak, excluding the water and lipid peak.

The SNR assessment is based on the following values:

FWHM Other Peaks [ppm]	Quality of Homogeneity
> 10	Good
5 < SNR < 10	Moderate
< 5	Poor

Tab. 5: SNR Quality Indicator

The quality indicator supports an assessment of the quality of the spectrum, based on the homogeneity and the signal-to-noise ratio on a voxel by voxel basis.

It supports an assessment of whether the quality of the spectrum of a voxel is clinically acceptable based on FWHM and SNR, and as a consequence, it indicates the confidence level of results derived from the spectrum.

The assessed quality of the spectrum is indicated using colors: green, orange and red. The colors indicate that the quality of the spectrum is good, moderate, or poor based on the described characteristics.

The colors represent the following combination of FWHM and SNR:

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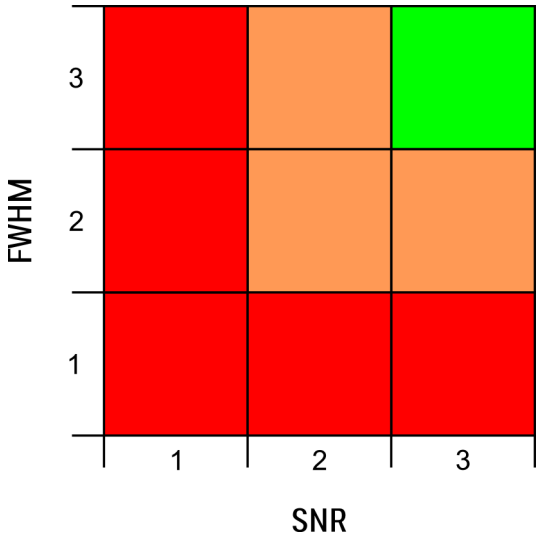

Fig. 44: FWHM / SNR Quality Indicator

1	Poor
2	Moderate
3	Good

Task Guidance

Similar to all packages on the IntelliSpace portal, also the MR SpectroView package provides a Task Guidance panel in the left part of the screen. The task guidance panel provides the following steps:

- Select the Anatomy
- Adjust Phase
- Specify Metabolites
- Save Graphs and Maps

The Workflow section later in these Instructions for Use is based on this Task Guidance. For details, see section “Workflow” on page 115.

NOTICE

Follow the steps of the Task Guidance to make optimal use of the MR SpectroView function.

More Functions within the MR SpectroView package

In IntelliSpace Portal MR packages, the most important functions can be performed via the Task Guidance and the toolbar. However there are more functions which you can access via the right mouse menus.

For more information, see section “Right mouse menus” on page 12.

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Additional right mouse functions with MR SpectroView

In addition to the standard right mouse functions, MR SpectroView provides the following package-specific functions in the right mouse menu:

Function	Description
Show Actual Spectrum	Displays the line representing raw data (yellow line)
Show Fitted Spectrum	Displays the smoothed line representing processed data for the selected metabolites (light blue line)
Show Fitted Baseline	Displays the baseline of the fitted spectrum (pink line)
Real	Displays the data in the analysis graph using real spectrum components
Modulus	Displays the data in the analysis graph using the magnitude values of the spectrum

Tab. 6: Analysis graph

Function	Description
Show Grid (Right click outside the grid, if displayed)	Displays the spectroscopy grid (voxel) - can be displayed per viewport
Align View to Grid (Right click the grid)	Aligns the view to the same plane as the grid
Show Quality Indicator (Right click the grid)	Applies a color-coded background color per voxel to indicate the quality of the spectrum from the voxel Quality is indicated as: • green representing good quality; • orange representing intermediate quality; • red representing poor quality. The quality assessment is based on the line width of the unsuppressed water peak and signal-to-noise ratio of the highest metabolite peak, in most cases in brain examinations this will be NAA or creatine.
Show Mini Spectra (Right click the grid)	Displays a spectra icon in the voxel as a miniature representation of the actual analysis results

Tab. 7: Reference views - Single voxel

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Function	Description
Show Grid (Right click outside the grid, if displayed)	Displays the spectroscopy grid - can be displayed per viewport
Align View to Grid (Right click the grid, only in the anatomical (upper) view)	Aligns the view to the same plane as the grid
Show Quality Indicator (Right click the grid)	Applies a color-coded background color to each voxel in the grid to indicate the quality of the spectrum from the voxel More information, see table 'Reference views - Single voxels'.
Show Mini Spectra (Right click the grid)	Displays a spectra icon in each voxel in the grid as a miniature representation of the actual analysis results
Smoothen (Right click outside the grid, only in the map views)	Smooths the color scale gradients in the metabolite map
Color Scale (Right click outside the grid, only in the map views)	Displays the color scale on the right side of the metabolite map
Orient to Grid Plane (Right click the grid, only in the anatomical (upper) view)	Aligns orientation of the underlying anatomy to the grid plane.
Orient to Grid Rows (Right click the grid, only in the anatomical (upper) view)	Aligns orientation of the underlying anatomy to the grid rows.
Orient to Grid Columns (Right click the grid, only in the anatomical (upper) view)	Aligns orientation of the underlying anatomy to the grid column.

Tab. 8: Reference views - Multiple voxels

Workflow

Launch the MR SpectroView package

▷ In the 'Directory' tab of the activity bar:

1. Select a suitable spectroscopy series and a suitable imaging series.

NOTICE

Ensure that *all* series that are required for analysis are selected. For example, a spectroscopy series also requires an anatomical series for reference. If you do not select all the required series, the application cannot be launched.

⇨ When you make a selection of multiple series and start an analysis package, only the selected series are displayed in the series browser. To add a series to an analysis after the analysis package has been started, right-click the series in the **Directory** and click **Add to running application**.

2. Click 'MR SpectroView'.

   The MR SpectroView package opens.

Select the Anatomy

When you open a spectroscopic dataset in SpectroView, the system automatically comes up with a default set of processing steps that are performed to analyse and display a spectrum (or set of spectra). This default set of processing steps depends on the selected spectroscopic dataset and on the examined anatomy.

In order to make sure that the correct processing steps will be performed on your dataset, select the anatomy (if the displayed option is not correct):

- Brain,
- Breast,
- Liver,
- Muscle,
- Prostate.

NOTICE

For frequency domain data loaded into SpectroView, the Task Guidance steps are grayed out.

SpectroView transforms time domain data into frequency domain data. Of course frequency domain data can be viewed.

Select a voxel for analysis

1. Zoom and pan the reference views to optimally display the voxels of interest:
2. Optional: enable/disable the display of the grid:
   - Right-click outside the grid and check/uncheck 'Show Grid'.
3. Optional: enable/disable the display of mini spectra and quality indicator:

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- Right-click inside the grid and check/uncheck 'Show Mini Spectra' and 'Show Quality Indicator'.

4. Once the display is optimal, select a voxel by clicking on it.

   The corresponding spectrum is displayed in the analysis graph viewport.

Adjust Phase

Spectrum Phase Adjustment

- Allows the user to correct the phase of the spectrum using zero-order (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.
  - Corrections are performed on 3x3 voxels in the center of the grid and propagated to all other voxels.
- Both auto phasing and manual phasing can be selected.

  Although any spectrum can be adjusted, this capability is most relevant for proton spectra acquired without an unsuppressed reference scan.

Automatic phase adjustment is performed by default.

When automatic adjustment is not optimal, you can manually adjust the phase to make sure that the major peaks are as symmetric as possible and closer to the baseline.

Manual Phase Adjustment

1. Drag the upper slider to interactively change the zero-order phase correction.
   Drag the lower slider to finetune the zero-order phase correction.
2. Alternatively enter the degrees directly instead of dragging the sliders.
   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.
3. Click **Apply** to apply the changes and see the effects on the spectrum.

   Clicking **Cancel** doesn't apply the changes, but resets the phase to the previous settings.

Specify Metabolites

The selected metabolites are used for peak fitting and labeling. Metabolite maps and ratio maps can be calculated accordingly.

1. If you want to add/delete metabolites, use the drop-down menu and choose the desired ones.
2. Proceed similarly for the maps.
3. Click on the ... button to add a metabolite/ratio map.

The following metabolites and metabolite maps can be selected for the anatomies:

Abbreviation	Name of Metabolite	Brain	Breast	Liver	Muscle	Prostate
Ac	Acetate	**x**	-	-	-	-
Cho	Choline	**x**	**x**	**x**	-	**x**
Cit	Citrate	-	-	-	-	x as Cit, Cit140, Cit38
Cr	Creatine	**x**	-	-	**x**	**x**
Cr2	Creatine	**x**	-	-	**x**	-
Glx	Glutamate and Glutamine	**x**	-	-	-	-
Lac	Lactate	**x**	-	-	-	-
lip	Lipid	**x**	**x**	**x**	**x** as lip1, lip2, lip3, lip4, lip5	**x**
mI	myo-Inositol	**x**	-	-	-	-
NAA	N-acetylaspartate	**x**	-	-	-	-
sI	scyllo-Inositol	**x**	-	-	-	-
TMA	Trimethylamine	-	--	-	**x**	-
H2O	Water	-	-	**x**	-	-
Pa	Polyamine (spermine)	-	-	-	-	**x**

Tab. 9: Metabolites

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NOTICE

Water is only selectable for liver. Unsuppressed water reference measurements (if available) are automatically processed for the anatomies.

Abbreviation	Brain	Breast	Liver	Muscle	Prostate
Cho	**x**	**x**	**x**	-	**x**
Cho/Cit140	-	-	-	-	**x**
Cho/Cr	**x**	-	-	-	-
Cho/NAA	**x**	-	-	-	-
Cit140	-	-	-	-	**x**
Cr	**x**	-	-	**x**	-
H2O	-	-	**x**	-	-

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Abbreviation	Brain	Breast	Liver	Muscle	Prostate
lip	-	-	**x** as lip and lip H_2O	**x** as lip1, lip2	-
NAA	**x**	-	-	-	-
NAA/Cr	**x**	-	-	-	-
TMA	-	-	-	**x**	-

Tab. 10: Metabolite and Ratio Maps

The table above displays the default metabolite and ratio maps. You can create other metabolite and ratio maps as desired.

Save Graphs and Maps

1. To save the graphs and metabolite maps as a new series, click Save **Graphs and Maps**.

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