14 MR Advanced Diffusion Analysis

Introduction

Philips Medical Systems' MR Advanced Diffusion Analysis application is post-processing software to be used as an advanced visualization application of diffusion MRI medical images. The Advanced Diffusion application is intended to perform image viewing, process and analysis of MRI Diffusion Weighted Images (DWI).

The Advanced Diffusion application can display images acquired at different b-values, where the b-value is a factor that reflects the strength and timing of the gradients used to generate diffusion-weighted images. The Advanced Diffusion application provides advanced supportive analysis and visualization tools of diffusion MRI images and parametric maps, which can be used by the physician for further analysis. The physician retains the ultimate responsibility for making the final diagnosis.

The Advanced Diffusion application is launched from Philips Medical Systems’ Advanced Visualization Workspace (AVW) environment.

Key Features

The MR Advanced Diffusion Analysis application has the following key features:

1. Support visualization and processing of isotropic diffusion-weighted MRI data.
2. Calculate and display a computed Diffusion Weighted Image (cDWI) at a b-value of choice.
3. Support input image registration in a pre-processing step.
4. Present a default analysis model based on the available original DWI images and provide a selection of alternative available models.
5. Provide diffusion analysis models, as well as parametric maps of Perfusion fraction (f), Pseudo Diffusion coefficient (D*), Diffusion coefficient (D) and Kurtosis (K).
6. Provide a ‘Goodness of fit’ map, 'Goodness of fit’ value, and fitted curve showing the fitting quality of the selected model.
7. Display parameter values from user defined ROI’s (Regions of Interest).
8. Display the ROI results in tabular and graphical formats.
9. Support export of the parametric maps as grayscale or RGB images for visualization in other viewers or PACS systems.

Indications for Use

The Advanced Visualization Workspace MR Advanced Diffusion Analysis application can be used to perform image viewing, process and analyze MRI Diffusion Weighted Images (DWI). The Advanced Diffusion application supports any oncology and neurology conditions for which diffusion and/or perfusion analysis are indicated as part of patient management.

Intended Users

The Advanced Visualization Workspace MR Advanced Diffusion Analysis application is intended to be used by adequately trained and qualified medical professionals, including but not limited to physicians and medical technicians. The main clinicians or medical and para-medical professionals who use the Philips Advanced Visualization Workspace Advanced Diffusion Analysis application are listed below:

- Radiologists in the radiology department/clinic
- 3D technologists in the radiology department

Other clinicians/roles using the Philips Advanced Visualization Workspace are listed below:

- Oncologists and oncology technologists
- Neurologists
- Referring Physicians

Intended Patient Population

The intended patient population covers all patients who are indicated for neurological or oncological diseases with DWI scans as part of their MR imaging examinations

Benefits

When used as specified in the Intended Use under the circumstances and conditions as specified in the Indications for Use, the application assists the user with interpreting the clinical image data on par with the state of the art, thus realizing a positive impact on diagnosis or patient management.

Contraindications

None.

Limitations for Use

Rx Only

CAUTION

In the United States, Federal law restricts this device to sale, distribution and use by or on the order of a physician.

NOTICE

When using a virtualization solution, images should be reviewed by a responsible physician to ensure appropriate clinical image quality.

Using Compute DW Image (cDWI) Mode

1. In the **Patient Directory**, select the study (an Isotropic Diffusion weighted image) that you want to investigate.
2. Click **MR Advanced Diffusion** in the **Review** panel of the Advanced Visualization Workspace client to start the application.

⇨ When the application starts, the selected mode is the one that was last used.

NOTICE

Ensure that all studies belong to the same patient before launching the Advanced Diffusion application. The application displays a warning message whenever data from multiple studies is combined.

3. In the task guidance panel, select **Compute DW image**.

⇨ A 2x1 viewport layout is displayed:

- The left image shows the source data (input image).
- The right image shows the cDWI calculated for a selected b value for the selected model.

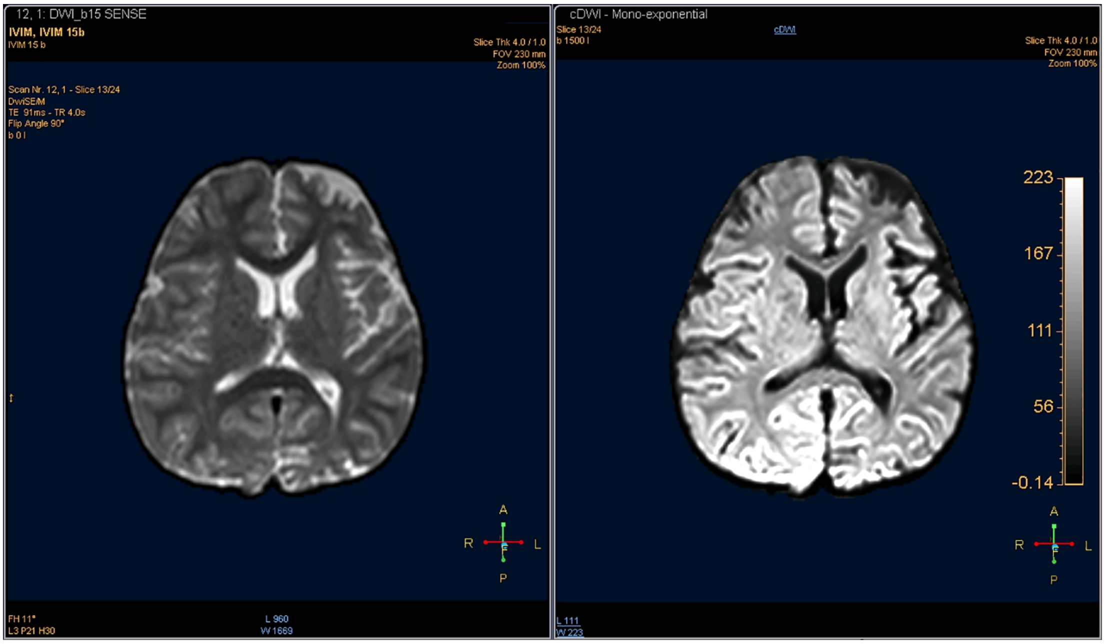


Fig. 79: cDWI Mode in Advanced Diffusion

⇨ The application selects the **Mono-exponential** diffusion model by default.

⚠ **WARNING**

Image quality (compression annotation) to be displayed on all the viewers images where lossy compression is used.

4. If you want to use an alternative diffusion model, select a model from the drop-down list in the task guidance panel, **Select Model**.

   Depending on the number of b values that are available in the study, you can use the following diffusion models with cDWI mode:

   - **Mono-exponential**: This model is based on two b values.
   - **Simplified IVIM**: This model requires at least three b values.
   - **Bi-exponential**: This model requires at least four b values.

⇨ The list displays diffusion models that are appropriate for the available b values in the study.

5. To change the b values used for the analysis, do the following:
   - Click **Edit input b-values** in the task guidance panel.
   - In the **Select B-values** dialog box, select the b values to be used and click **Apply**.

⇨ The cDWI image is recalculated using the selected b values.

NOTICE

Depending on the selected diffusion model, some b values in the **Edit input b-values** dialog box may be grayed out, in which case their setting cannot be changed. Additionally, the minimum number of b values required for the selected diffusion model is always maintained. For example, if four b values are required for the selected model, you cannot clear further selections if only four b values remain selected.

NOTICE

The user may adjust the thresholds for including and excluding b values from analysis models. For more information, see section "Setting B-Value Thresholds" on page 339.

6. Select a b value to calculate by dragging the b value slider in the task guidance panel, **Select b-value for computation**.

⇨ The computed cDWI is displayed in the right image. The slider moves in increments of 100. Specific values can be entered directly in the box by the user.

⇨ By default, the application automatically adjusts the window width and window level for the calculated b value. However, you can change this behavior using the **Control WW/WL adaptation** function.

7. To use ADC-based segmentation to view the CDWI image, select the **Control WW/WL adaptation** check box and, if desired, set the threshold (the default value is 600).

⇨ The application adjusts the WW and WL settings such that pixels below the threshold ADC are intensified as you select higher b values, while pixels above the threshold ADC reduce in intensity as you select higher b values.

8. To apply a mask to hide unwanted pixels in the calculation, set the mask from task guidance or via the context menu by right-clicking the image.
9. To generate a series for the cDWI image, click **Generate series** in the task guidance panel.

⇨ The generated series and images can be opened in MultiModality Viewer or sent to a PACS. The file name of the generated series contains details of the mode name (cDWI), the applicable diffusion model, and registration indication (if applicable). Independent of the series name, full information is available in the DICOM tag.

Using Analyse Diffusion Signal Mode

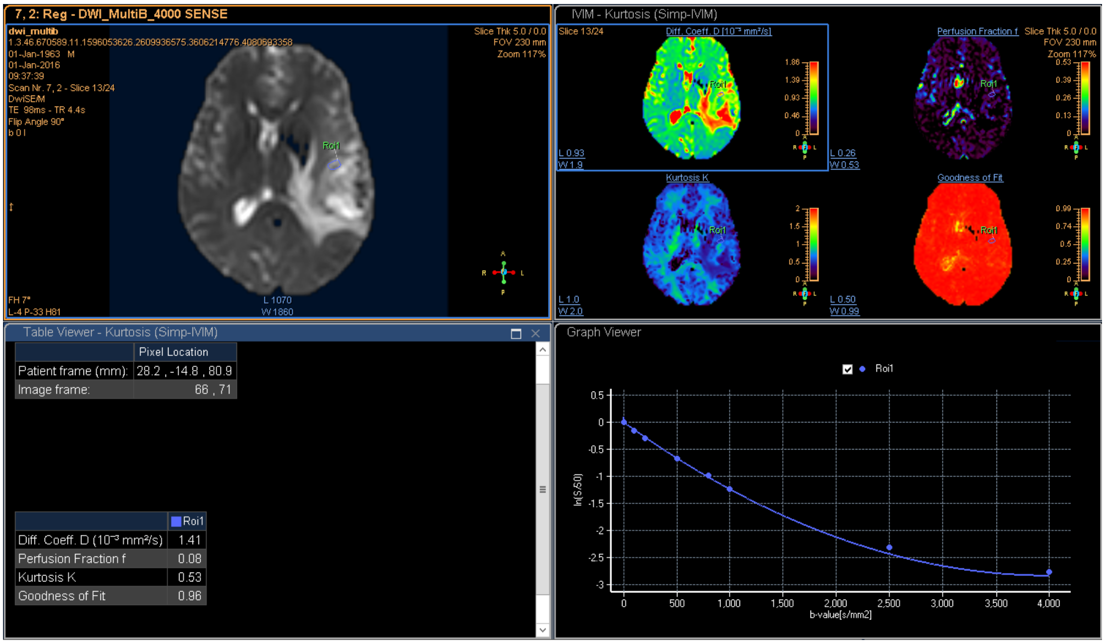
1. In the task guidance panel, select **Analyse Diffusion Signal**.

⇨ A 2x2 viewport layout is displayed:

- The upper-left viewport displays the DWI image used as input. Scrolling vertically displays anatomical slices and scrolling horizontally displays the acquired b values.
- The upper-right viewport displays parametric maps. The type of maps that are displayed depends on the selected diffusion model. To change the displayed maps view in the upper-right viewport (from all selected parametric maps to one parametric map), into presentation of only one parametric map, double click one of the parametric maps. To change the displayed map, click the title of the map viewport and select a different map.
- The lower-left viewport displays results in the **Table Viewer**.
- The lower-right viewport displays the **Graph viewer**.

WARNING

Image quality (compression annotation) to be displayed on all of the viewers images where lossy compression is used.



	Pixel Location
Patient frame (mm):	28.2 , -14.8 , 80.9
Image frame:	66 , 71

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Diff. Coeff. D (10^{-3} mm²/s)	1.41
Perfusion Fraction f	0.08
Kurtosis K	0.53
Goodness of Fit	0.96

Fig. 80: IVIM analysis in MR Advanced Diffusion

⇨ For any given set of b values, the application presents a default diffusion model.

2. The user may choose an alternative diffusion model from the drop-down list in the task guidance panel as suggested by the application. The alternative models in the drop-down list depend on the number and range of the b values which were acquired for the study, **Select Model**.

   The following diffusion models are available in the Analyse Diffusion Signal mode:

   - **Mono-exponential**: This model is based on at least two b values and generates diffusion coefficient map comparable to routine ADC map.
   - **Simplified IVIM**: This model is based on at least three b values and creates diffusion coefficient map and perfusion fraction map.
   - **Bi-Exponential**: This model is based on at least four b values and creates diffusion coefficient map, perfusion fraction map and pseudo diffusion coefficient map.
   - **Kurtosis (Mono-exponential)**: This model requires at least three b values and creates diffusion coefficient map and kurtosis map.
   - **Kurtosis (Simp-IVIM)**: This model is based on at least four b values and creates diffusion coefficient map, perfusion fraction map and Kurtosis map.

⇨ The models that are suggested by the application are also affected by default thresholds for the applicable b value range (the IVIM threshold and the Kurtosis threshold), these thresholds may be manually adjusted by the user.

⇨ The list displays only diffusion models that are appropriate for the available b values in the study.

3. To change the b values used for the analysis, do the following:

   - Click **Edit input b-values** in the task guidance panel, **Select Model**.
   - In the **Edit input b-values** dialog box, select the b values to be used.

⇨ The output parameters are recalculated using the selected b values.

NOTICE

Depending on the selected diffusion model, some b values in the **Edit input b-values** dialog box may be grayed out, in which case their setting cannot be changed. Additionally, the minimum number of b values required for the selected diffusion model is always maintained. For example, if four b values are required for the selected model, you cannot clear further selections if only four b values remain selected.

NOTICE

The user can adjust the thresholds for including and excluding b values from analysis models. For more information, see section “Setting B-Value Thresholds” on page 339.

4. Select the parametric maps that you want to generate in the task guidance panel, **Select Maps**.

NOTICE

The parametric maps that are available depend on the selected diffusion model.

5. To apply a mask to hide unwanted pixels in the calculation, set the threshold of the mask from the task guidance or the context menu by right-clicking a map.
6. To view real-time values of pixels in the maps, use **Follow Mouse**.

⇨ When this option is enabled and you move the pointer over an image, the pixel value at the mouse pointer position is indicated in the table viewer, and the graph viewer displays a curve of the signal intensities of the pixel across the b values.

7. To draw an ROI, click the ROI tool in the task guidance panel, **Measure ROIs**.

   You can draw up to ten ROIs across different slices in the study.

⇨ The application calculates the average value of the output parameters inside the ROI and displays the value in the **Table Viewer**. The color of the ROI corresponds to the color of the curve in the **Graph Viewer**.

⇨ Click the top of a column in the **Table Viewer** to display the slice containing the corresponding ROI in the input DWI image.

⇨ Click a curve in the **Graph Viewer** to highlight the corresponding b values.

NOTICE

If you change the mode at any time (to **Compute DW image**) any ROIs that you have created are removed.

Before changing the mode, bookmark your progress in the current mode if you want to return to it later.

⇨ The generated series and images can be opened in MultiModality Viewer or sent to a PACS system. The file name of the generated series contains details of the parametric map name, the diffusion model, RGB indication (if applicable), and registration indication (if applicable). Independent of the series name, full information is available in the DICOM tag.

Register Data While Saving

Once enabled, this function performs registration when generating actual maps. In such a way image quality will most likely improve in the maps.

NOTICE

If the input data is unregistered, there can be a mismatch between the previewed and generated maps as the generated maps are calculated after registering the input.

Generate Series

You can generate a new imaging series containing the results as defined in the previously described workflow.

1. To generate a standard DICOM-compatible series, select **Generate Series** using the Secondary Capture option from the drop-down list, and then click the button.
2. Enter the name of the new imaging series in the **Name** box.
3. To generate a series as RGB images (high resolution color maps), select **Generate Series** using the Secondary Capture RGB option.

Measurement Type Selection

To change the type of measurement for all parametric maps, right-click the results summary table and select an option.

- **Region Parameters (Factory default)**: The application calculates T1 parameters using the time intensity curve for the drawn ROI and displays the values in the Table Viewer.
- **Mean Voxel Parameters**: The application calculates the mean of all the voxels inside the ROI of the output parameters and displays the values in the Table Viewer.

  The table heading is updated based on the selected type.

Show ROI Statistics

You can right-click the results summary table and choose to show ROI voxel statistics (or) select from the **More** menu.

An additional numerical results table is displayed as a floating window and displays Maximum, Minimum, Median, Average and Standard deviation of the quantitative parameters for the ROI voxels within the parametric maps.

When the number of columns in the Table Viewer exceeds thr default width, or number of rows exceeds default height, the auto scroll is visible to allow the user to scroll to see all the columns and rows.

To export table results:

1. Select **Copy to Clipboard** an open either Microsoft Word or Excel and paste the contents from your clipboard into the application.
2. Select secondary capture. A dialog box is displayed allowing you to select a file name, file format, and destination. You can save the series in DICOM format, or in non-DICOM format. If you select a non-DICOM format, you should additionally select a file system destination for exporting the table results.

Setting B-Value Thresholds

For advanced workflows, users can adjust the b-value threshold settings. The two b-value threshold values described below control the availability of the different models.

- **Simplified IVIM Threshold**
  - This threshold is applicable to the models that use Simplified IVIM: a) Simplified IVIM and b) Kurtosis (simplified-IVIM).
  - Any b-value between 0 and this threshold is eliminated from the data for processing. The default value of the simplified IVIM threshold is 100 mm2/s.
- **Kurtosis Threshold**
  - This threshold is applicable to the models that support Kurtosis analysis: a) Kurtosis (mono exp) and b) Kurtosis (simplified-IVIM).
  - The dataset should contain diffusion-weighted images at this b-value threshold or above, for processing. The default value of the Kurtosis threshold is 800 mm2/s.

The below table summarizes the conditions (to be satisfied by a dataset) under which the suitable models become active.

Model	Diffusion Parameters (output)	Conditions and Recommendations
Mono-exponential	D	**Required** Minimum number of b-values: 2 **Recommended** IVIM threshold (Default 100) ≤ b-values < Kurtosis threshold (Default 800)

Model	Diffusion Parameters (output)	Conditions and Recommendations
Simplified IVIM	D, f	**Required** • Minimum number of b-values: 3 • b-value = 0 is present • Excluded: 0 < b-values < IVIM threshold (Default 100) **Recommended** b-values < Kurtosis threshold (Default 800)
Bi-exponential	D, f, D*	**Required** Minimum number of b-values: 4 **Recommended** • b-value = 0 is present • At least 1 b-value in the range 0 < b < IVIM threshold (Default 100) • b-values < Kurtosis threshold (Default 800)
Kurtosis + Mono exponential	D, K	**Required** • Minimum number of b-values: 3 • At least 1 b-value ≥ Kurtosis threshold (Default 800) **Recommended** b-values ≥ IVIM threshold (Default 100)
Kurtosis + Simplified IVIM	D, K, f	**Required** • Minimum number of b-values: 4 • b-value = 0 is present • Excluded: 0 < b-values < IVIM threshold (Default 100) • At least 1 b-value ≥ Kurtosis threshold (Default 800)

To set threshold values:

1. To adjust the b-value threshold settings, click **Model Threshold editing from the More menu.**.
2. To set the **Simplified IVIM** threshold, enter a value in the corresponding box.

⇨ B values above this threshold will be included when the **Simplified IVIM** model is selected.

3. To set the **Kurtosis** threshold, enter a value in the corresponding box. Note that the Kurtosis threshold cannot be set below 600 mm^2/s.

⇨ B values above this threshold will be included when one of the kurtosis models is selected.

4. Click **Apply** to confirm your settings and close the dialog box.

NOTICE

Changes to the thresholds are not stored and will revert to default values the next time that the application is launched.

Measurement Accuracy

Based on an in-house verification, the model fitting errors measured by maximum normalized root mean square are shown below.

Model	Mean±SD (%)
Mono-exponential	9 ± 1.55
Simplified IVIM	7 ± 1.52
Bi-exponential	6 ± 1.12
Kurtosis (Mono-exponential)	0.6 ± 0.15
Kurtosis (Simplified IVIM)	2.32 ± 0.09