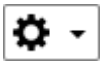
Item	Description
3	**OPTIONS** • **Switch between simple and advanced modes** (requires the OncoQuant license) In simple mode, any measurement can be deposited and compared over time. It is not possible to compute sum of statistics, nor flagging lesions as target/non-target lesions. To enable these functionalities, select **(Show morphological tools)**. To disable these functionalities, select **(Hide Morphological tool)**. • **Sort Findings** Sort findings by ID, location, Target type (Advanced Mode only) or Anatomy (Advanced Mode only). Sorting can be performed ascending or descending order. • **Display options** ○ Show/hide RAS coordinates and/or series number/slice location. ○ Show/hide relative comparison (%) and/or absolute comparison (multiple dates only) ○ Dates: Show/hide specific dates when multiple dates are displayed in Summary Table columns. ○ Volumes: Show/hide specific modality when measurements have been performed on multiple modalities (e.g. show only measurements performed on MR series). • **Flag / Unflag measurement images** Set all measurements images as flagged or non-flagged *(see item 3 above, "Export Images", "Measures Only")*.
4	**DATES & REFERENCE EXAM** Each date is displayed in a column. One date can be set as a reference for comparison with other dates for all similar measurements performed by having a flag icon displayed on top of this date. To change the reference date, drag & drop the flag icon over the selected date or click the arrow icon below the any date and select **(Set as Reference)**. Comparison of all statistics for linked measurements will be computed as percentage change and/or as absolute change of the values to the reference date, but only for dates posterior to this reference date.

Item	Description
5	**MEASUREMENTS** Measurements of the same kind can be linked over time in a single finding. In this case, they will display the same statistics and will be aligned on the same row and highlighted. When 2 similar measurements of a finding are performed on different dates within a sphere of 10mm (based on their RAS coordinates), they will be automatically linked to the same finding, and thus displayed on same line and highlighted. If a measurement is not linked because of registration issue, simply drag and drop it over the corresponding measurement line in the expanded Summary Table to link it and display comparison statistics over time (absolute and/or relative). Drag and drop allow you to: • Link measurement to a similar measurement in another finding • Unlink a linked measurement in a new finding Compatible measurements and actions are highlighted during drag and drop action.
6	**FINDING NAME** The finding name can be modified manually directly in the expanded Summary Table (press **(Enter)** to validate modification).

Global Preferences

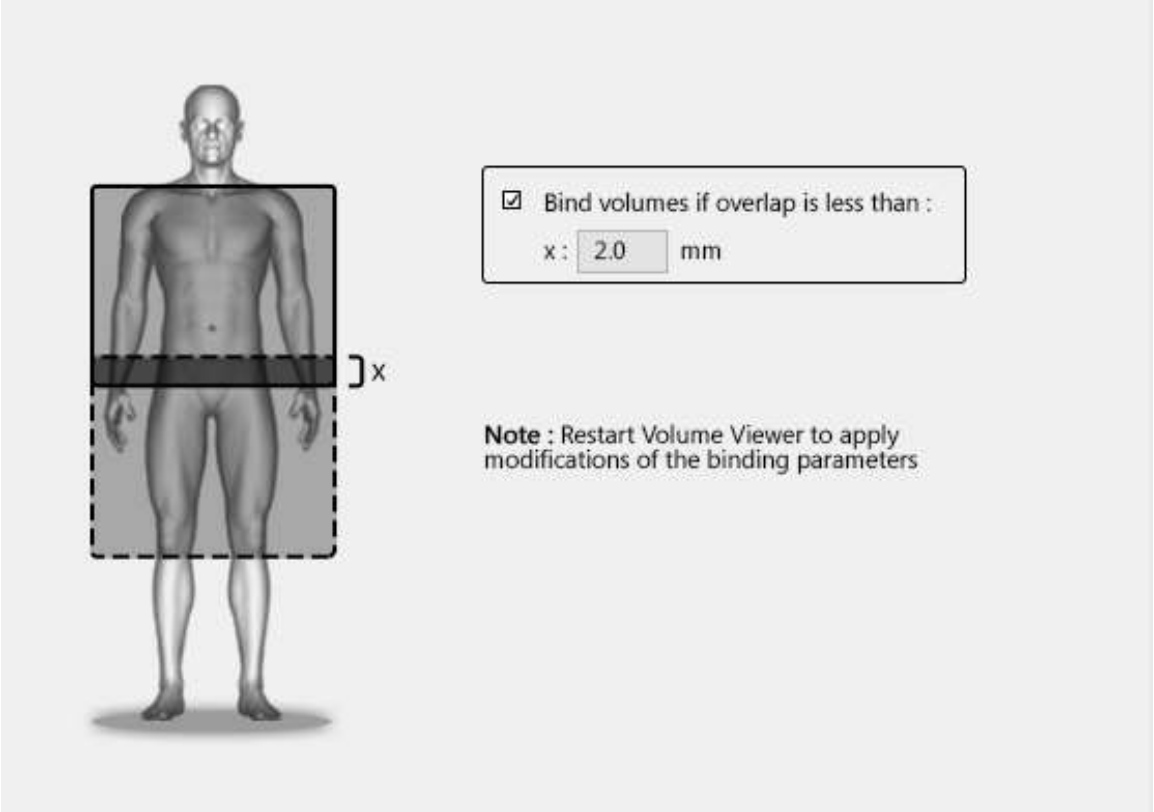
Global Preferences allows you to set preferences for Volume Viewer applications from a single location. Click  and select preferences category to be set.

Preference panel will be displayed at the corresponding preference category (Viewports, Annotations, Toolbar, Tools, Export, Integrated Registration and other VV applications).

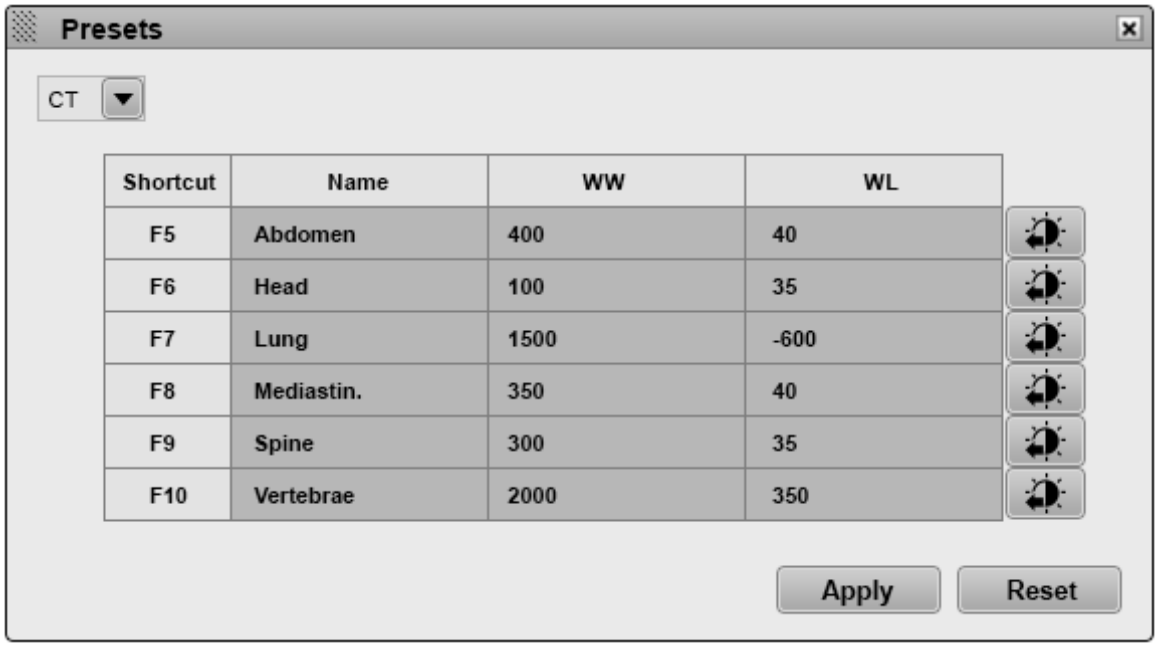
Loading *[CT only]*

When loading multiple CT series containing multiple acquisition volumes (multi-phase, multi-acquisition sequences…), it is possible to bind several volumes based on the overlap. Check the box and set up the maximum overlap allowed to automatically bind phases into a single volume at loading.

Note: If there is a gap between 2 volumes, an interpolation will be performed when loading these volumes.



Display



Set WW/WL presets linked to **<F5>** to **<F10>** keys in Volume Viewer.

Presets: select modality to display presets values (CT, MR, PET, NM, XACT).

Enter values or press  to capture current W/L from selected viewport.

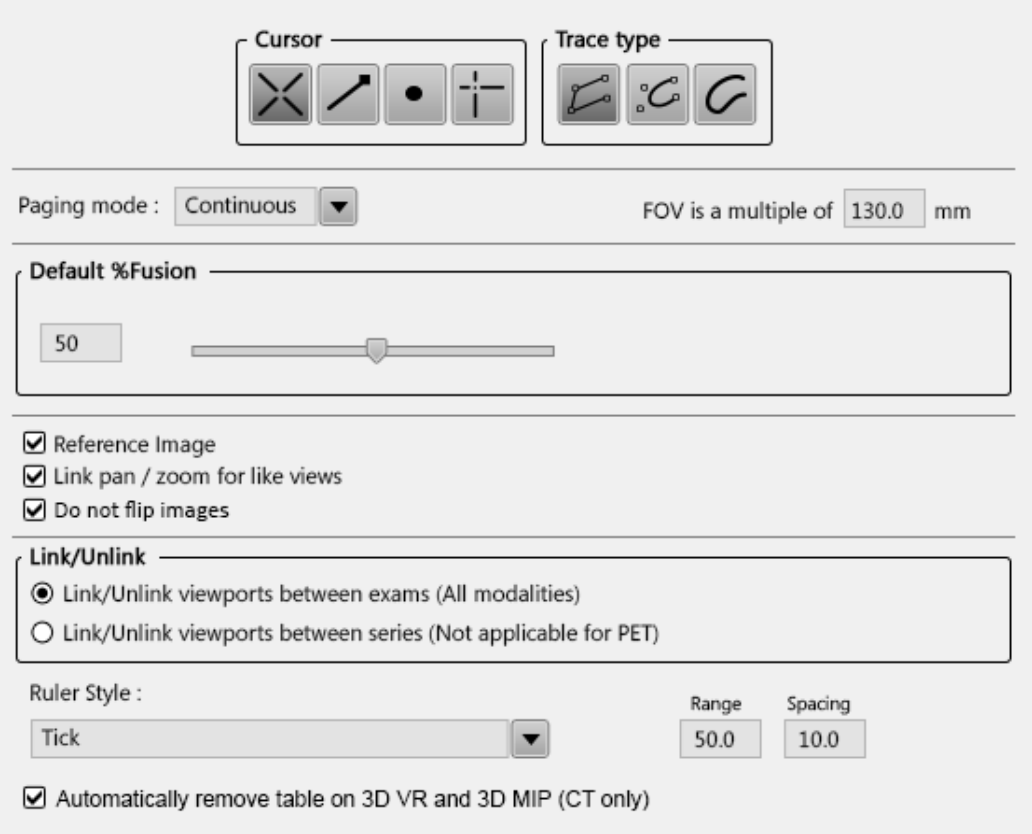
Click **[Apply]** to apply modification(s).

Click **[Reset]** to reset presets to factory values for selected modality.

Note: If a viewport containing one or more volumes is selected and the function keys <F5-F10> are used, then the WW/WL will be adjusted in every viewport where the first volume is displayed, including fused viewports.

Note: For PET presets, min and max will be applied with the current displayed SUV unit. To display the min and max with another SUV unit, change the unit first (refer to the SUV section in the PET in Volume Viewer chapter), then apply the min/max preset with <F5-F10> key.

Viewports



Cursor: set the cursor type used by default (Crosshair, arrow, dot, full cross, triangulation Cursor*).
* ***[Seamless integration]***

Trace type: set the trace type used by default (Polygon, Smooth trace or free hand).

Paging mode: Page through all individual slices, whatever the slice thickness (Continuous), or page through slabs (Contiguous, default mode).

FOV: Sets the "steps" when adjusting FOV with left/right mouse buttons. E.g. when setting 130mm, an original DFOV of 37.5 cm will decrease will left click to 26 cm, then 13 cm, then 6.5 cm…

Default % Fusion: sets the default fusion % when creating fused views via drag and drop.

Reference image: display/hide a reference image in the viewports corner.

Link pan/zoom for like views: if activated, pan and zoom all the viewports with same plane displayed (Axial, Coronal, Sagittal and Oblique views).

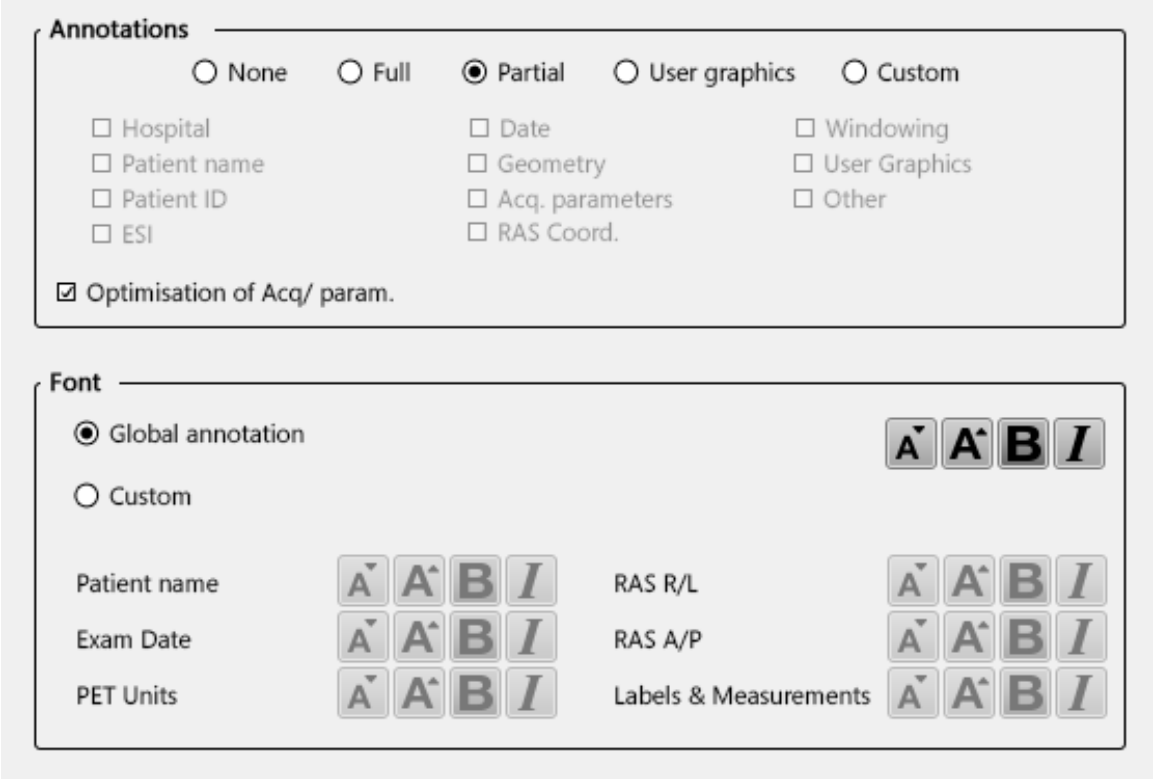
Do not flip images *[Volume Viewer only]*:
If checked (default mode), force oblique planes orientation to the closest standard point of view (inferior, anterior or right) and can lead to automatic image flip.
If unchecked, oblique planes orientation are free and can lead to image rotation (always check orientation annotations).

Link/Unlink: When multiple exams are loaded, unlink the views will apply to exams (i.e. series from the same exam will remain linked) or to series (i.e. each series will be unlinked from other series).

Ruler Style: Display/hide a ruler for distance references on viewports.

Table Removal: If activated, automatically removes table from CT images on 3D VR and 3D MIP viewports.

Annotations



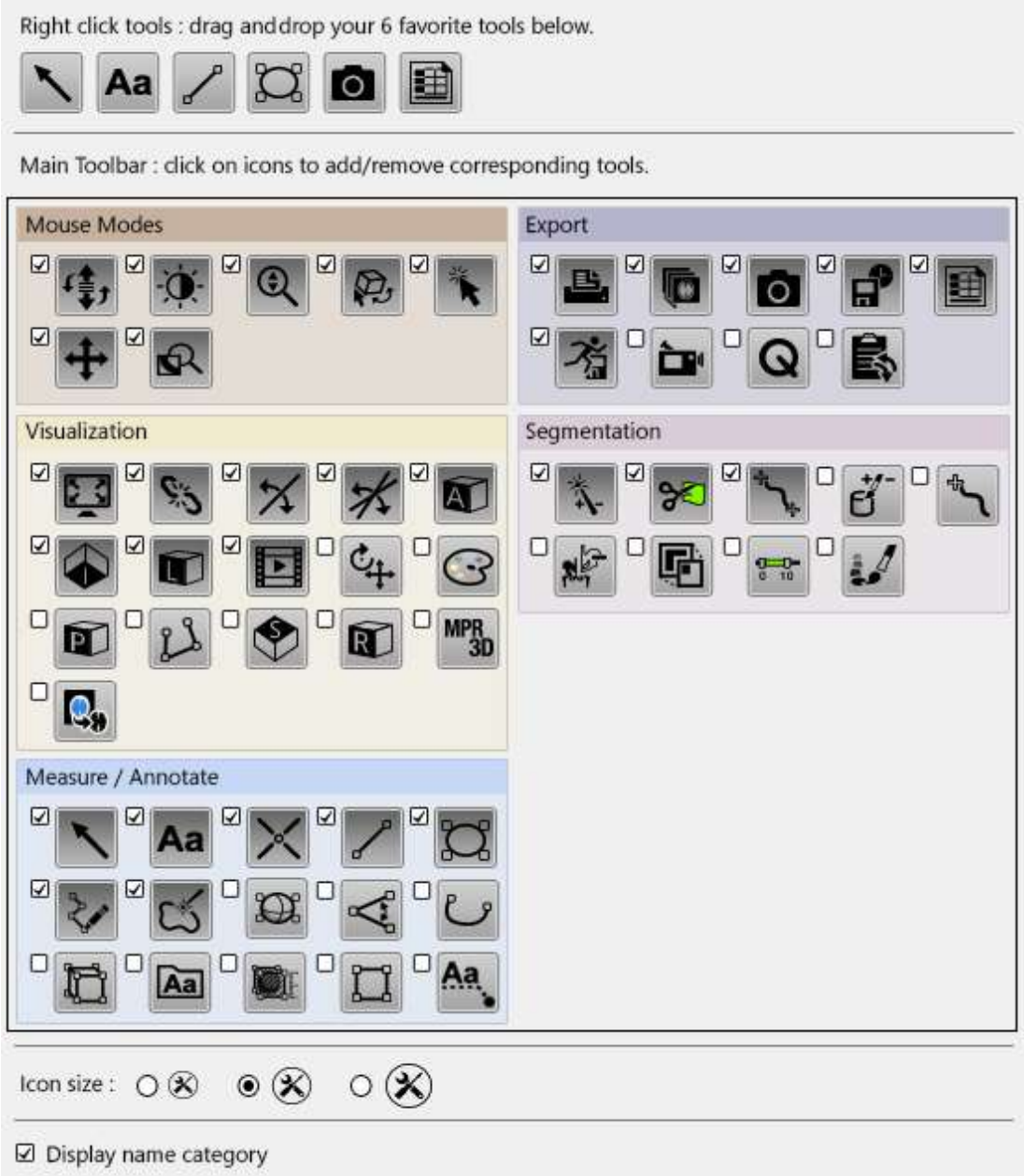
Annotations: Customize the annotations level in the default viewports with None, Full, Partial, User graphics (measurements and annotations only) or Custom.

Note: The “custom annotation” mode can be set as a preference only if at least the Patient name, Date, RAS coordinates, Windowing and Volumes annotations are selected. Otherwise, the next session will use “partial annotations” preference.

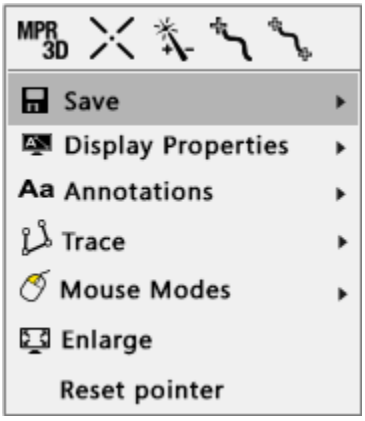
Optimization of Acq Parameter: (only if “Full” or “Custom”, with Acq Parameters checked, are set). If activated, displays the details of acquisition parameters only on 1 viewport per screen. If not activated, details of acquisition parameters will be displayed on all viewports.

Font: Set the font size displayed on viewports globally (Global Annotation) or by type of annotations (Custom). This preference is only for display in Volume Viewer. When sending images to the Filmer via F1 or F2 ***[AW and AW Server]*** the font will not be the same in the Filmer.

Toolbar


Right click tools : drag and drop your 6 favorite tools below.
Main Toolbar : click on icons to add/remove corresponding tools.
Mouse Modes
Export
Visualization
Segmentation
Measure / Annotate
MPR 3D
Icon size :
Display name category

Customize the right click menu:
6 tools can be accessed via the right click menu for each application (Volume Viewer, VesselIQ...).
Drag and drop the tools to be accessed from the right click menu.



Customize the main toolbar:

- Select the tools to be displayed for each category by checking them. Icon size in the toolbar can be adjusted and description text of tools categories can be displayed or not.

OR

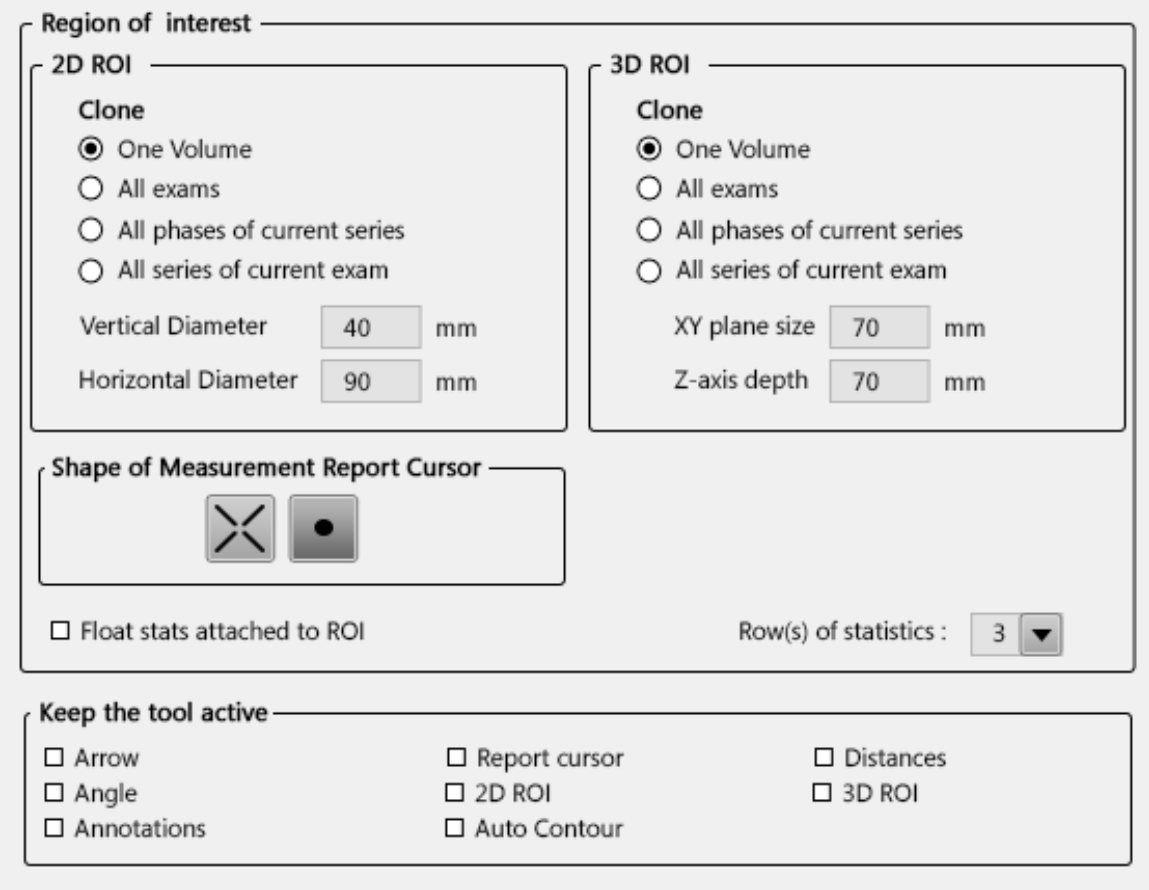
- Drag and drop the tools directly from the toolbar to remove them or insert them in the toolbar.

Display name category:
Displays/Hides the name of the toolbar category. By default, the toolbar category is displayed.

Display ON

Display OFF

Tools



Region of Interest:

- Auto-clone level when depositing a ROI (current volume, all series of all exams, all phases of current series of all series of current exams).
- Default ROI size when deposited in 1 click.

Shape of Measurement Report Cursor:
Set the measurement report cursor type used by default.

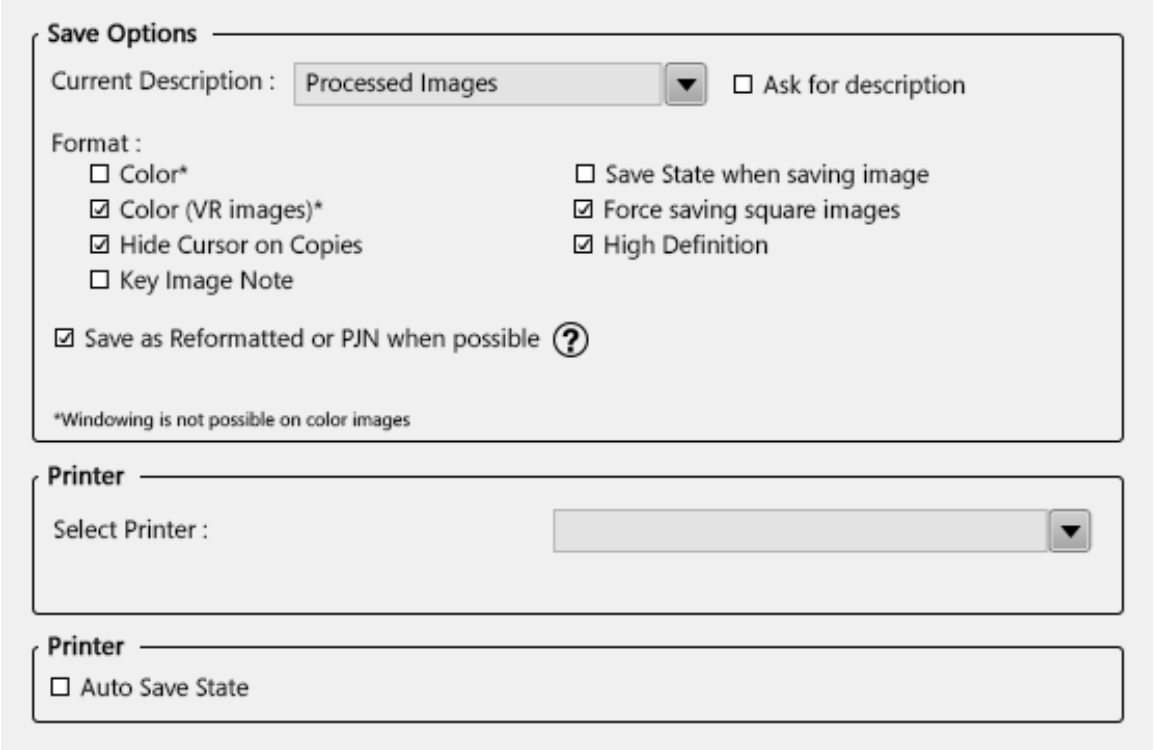
Float Stats attached to ROI:

- *Checked*: ROI statistics will be floating next to the measurement on the viewport.
- *Unchecked*: ROI statistics will be displayed in bottom right of the viewport. Number of ROI statistics lines displayed can be adjusted (1 to 3).

Keep the tool active:

- *Unchecked*: tool is not active after deposition. To deposit again the same type of measurement, user has to select again the tool.
- *Checked*: tool is still active after deposition (the mouse mode is still in deposition mode) until user selects another tool or another mouse mode or close the tool.

Export



Ask for description: if checked, displays a popup message to ask for description for saved image (i.e. "Save as…"). If unchecked, will use the default description set in **Current Description**.

Format:

- **Color**: saves non-VR images in Color SCPT. Due to DICOM format restrictions, Window Level and Width of color SCPT images cannot be modified. It is then recommended to unselect this option to be able to perform windowing adjustments when reading saved images in PACS or other DICOM viewers.
- **Color (VR images)**: saves VR images in Color SCPT.
- **Hide Cursor on Copies**: Saves images with cursor hidden.
- **Key Image Note**: when checked, all saved images are referenced into a single Key Image series (DICOM standard) when exiting Volume Viewer. This Key Image series can be opened in the Viewer or any compatible PACS or other workstation (all referenced images must be pushed on a remote host).
- **Save State**: saves the current status of Volume Viewer (3D Model, displays, ROIs…) at the same time as saving the image. This Saved State can be used later on to restore the Volume Viewer State.
- **Force Saving Square Images**: When sending rectangular viewport, adjusts the image in a square format (no resize but adding space around image). This option is mainly used for PACS or other DICOM systems not supporting rectangle images.
- **High Definition**: Saves the image in high resolution.

Save as Reformatted or PJN: Images saved under these formats contain geometrical information so that they can be reloaded in 3D software and freely windowed.

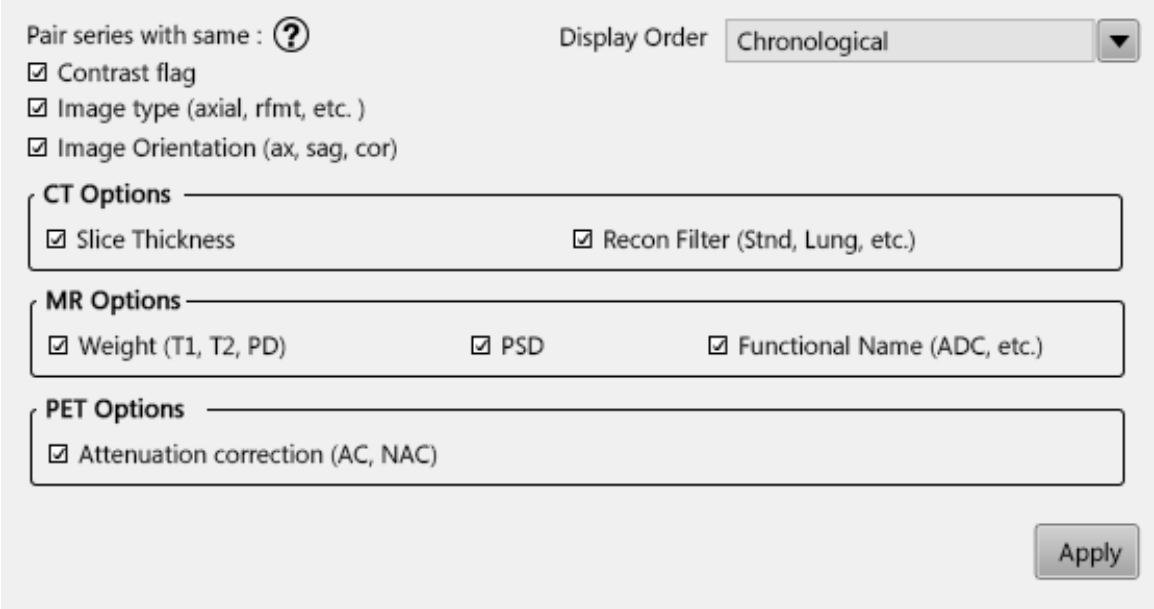
Check **Save as Reformatted or PJN** to save images in this format every time it is possible. Images saved under these formats contain geometrical information so that they can be reloaded in 3D software and freely windowed. Click the link [when possible] to display the list of image types that can be saved as Reformatted and PJN according to DICOM requirements.

Uncheck the option **Save as Reformatted or PJN** to benefit from **Color** and **Save State** capabilities every time you save an image.

Color and **Save State** options are not compatible with Reformatted DICOM format. These settings cannot apply to images which were saved as Reformatted.

The following viewports will be automatically saved in color (i.e. no W/L possible) whatever the export preferences:
- viewports with color map applied
- viewports with color ROI deposited
- viewports containing XA, NM, Fused or color SCPT images

General Review



This preference tab is available only from the protocol "**VV General Review**" (or "**Oncology Review**" which requires the OncoQuant license).

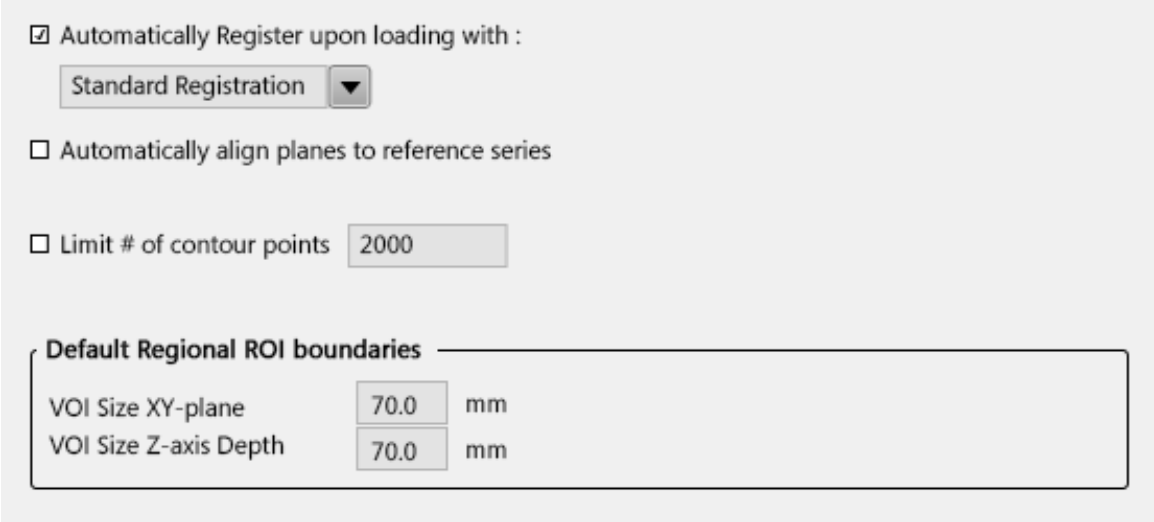
Pairing series:
Pairing of the loaded series between exams which display on the viewports is done automatically for the VV General Review protocol.
General pairing is based on series that have the same flags for contrast, image types and image orientations.
Specific pairing rules options can be found for CT, MR and PET modalities.
Uncheck an option if you don't want that criteria to be used for finding the matching pairs of series from other exams.

Example: if you want to review (side by side) 3 CT series from different exams that match in slice thickness, image orientation but maybe 1 of them does not have contrast, then uncheck contrast option to make them all pair up for the review. Click Apply button to update the viewports display.

Display order:
Select from the drop down the date order for review of your current and prior studies in VV General Review (from oldest to current or from current to oldest).

Refer to "Compare & Correlate" section below for more information about how to use "VV General Review" protocol.

Integrated Registration



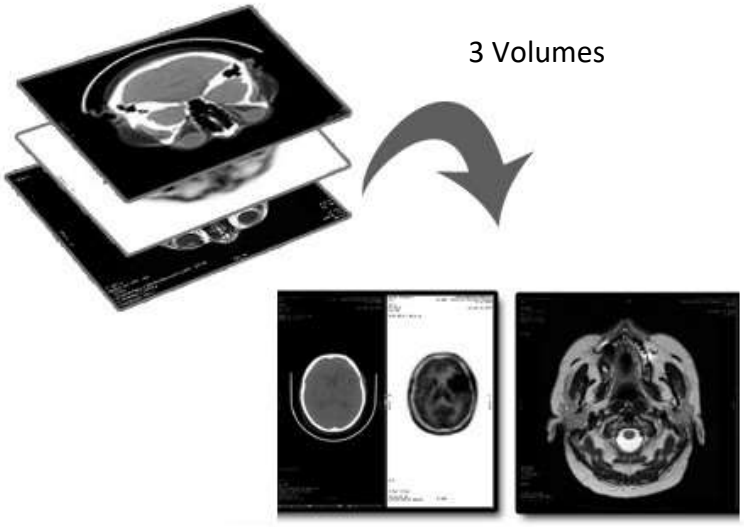
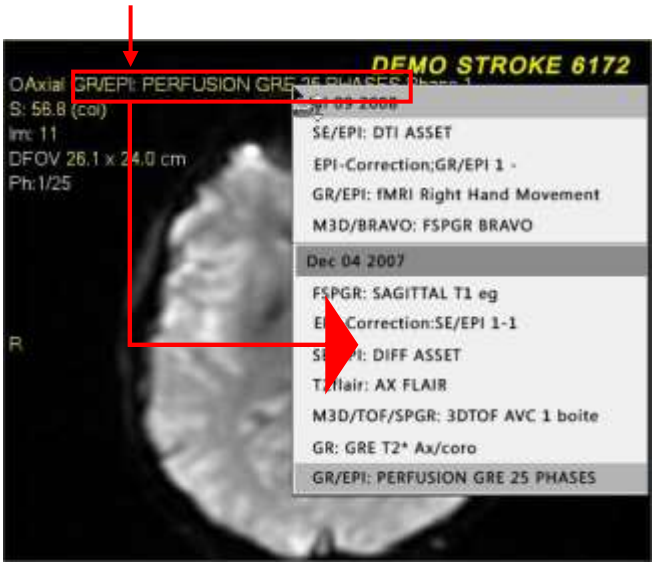
*(requires the **Integration Registration** license)*

Refer to Integrated Registration User Guide for more information on Integrated Registration preference parameters.

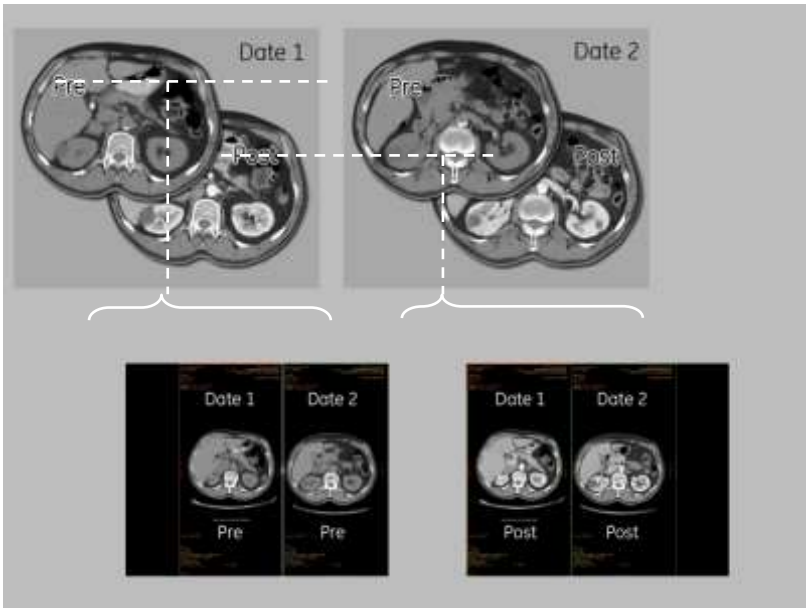
Compare and Correlate

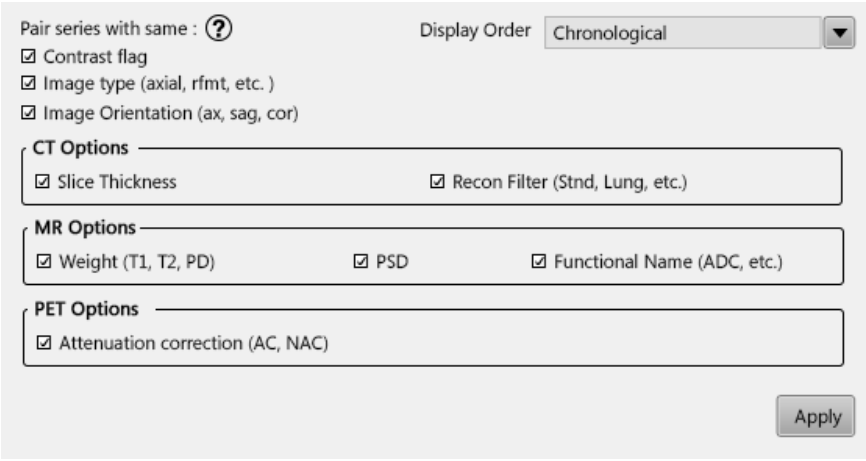
Using VV General Review

VV General Review is a standard protocol designed to create a simple PACS-like layout and with a built-in smart design finding “like” series between different exams to layout side by side for comparison/correlation. This protocol is for use with all modalities.

what	Description
	The number of volumes loaded will determine the default layout. If you load 3 volumes, then the layout will contain a total of 3 viewports. Loading: …4 volumes, 4 viewports, …5 volumes, 5 viewports, etc., up to 8 total viewports on AW workstation.
Drop-down series list 	If more than 8 volumes are loaded, the additional volumes are also loaded and available to view from the red drop-down menu on the viewports. If multiphase data is loaded, then an additional drop-down list will exist for phase selection. **1-monitor configuration:** When screen size is 1280x1024 or less, the max number of viewports will be 4 but the same general philosophy applies.

a





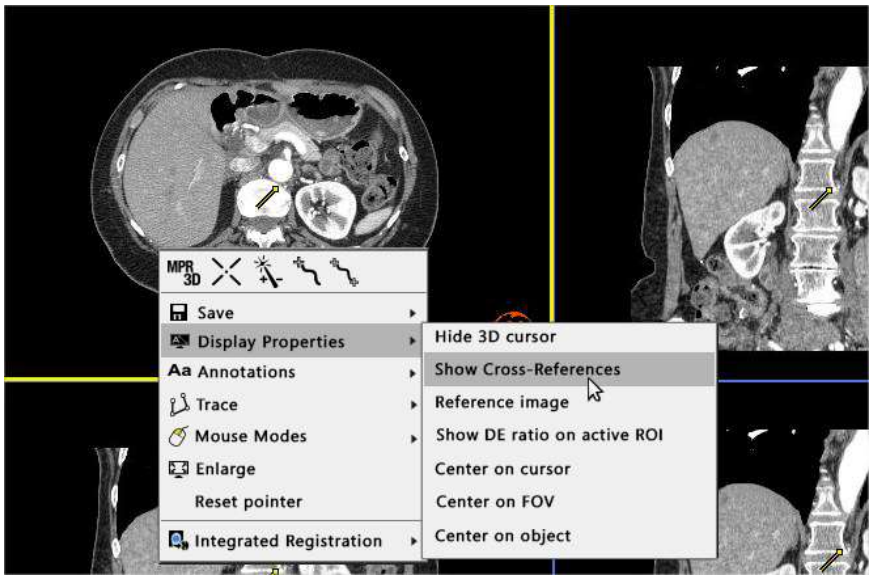
Intelligent Layout

This protocol has a built-in intelligence whereby it searches volumes to be loaded and tries to lay them out on the viewports according to “like” series.

Depending on the modality, different rules will apply:
For example:
(a) CT series in the same acquisition plane, reconstruction filter, slice thickness, etc. will display side by side on the views.
MR in the same acquisition plane, reconstruction filter, IV contrast information, etc. will display side by side on the views.
All volumes will load in the Axial plane for quick review but all other 3D MIP, VR, and multi-planar reformats will always be available from the red annotations on the viewports.

Pairing of the loaded series is done automatically for the VV General Review protocol. Adjust the Preferences to customize your pairing needs.
General pairing is based on series that have the same flags for contrast, image type, and image orientation.
Specific paring rules can be set for each modality.
Uncheck options in

General Review Paring Rules and modality pairing rules if you do not want to use the criteria. Set the display order for comparison exams in the Display Order drop down menu.



Cross Reference

Cross reference is available to display the location of the selected primary view on other viewports for correlation. Right mouse click on a primary view and Select Show Cross-References. A single cross reference line will display on corresponding views of the same exam.

A single cross reference line will display by default. After displaying a single line, the right mouse menu will display Hide Cross-References or Show all planes.

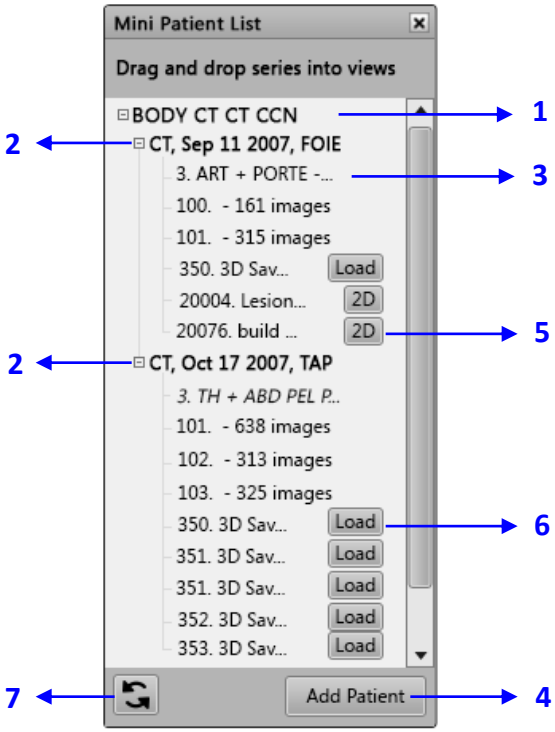
After posting all planes, the right mouse menu will allow users to return to a single plane (Show only current plane) or Hide Cross-Reference to turn off all cross-reference planes.

Using Dynamic Load

Dynamic Load is a feature allowing loading of extra series on-the-fly in Volume Viewer.

[AW and AW Server]
This feature is available in most Volume Viewer Review Protocols whereas advanced applications such as VesselIQ, LungVCAR, ColonVCAR, will only benefit from the 2D mini viewer feature described below.

Access to the panel is via the icon next to the Review Steps toolbar**.** 

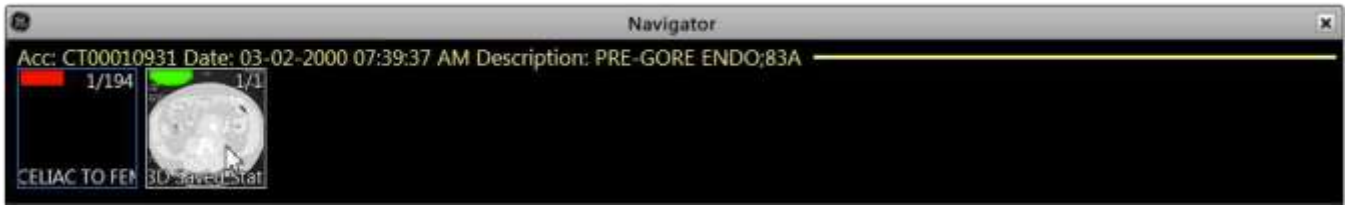


Item	Description
1	**Patient Name**
2	**Exam information**: modality, exam date, exam description All available exams on the local database from the currently loaded patient are listed.
3	**Drag & Drop** any 3D series (Axial, Reformatted, etc.) from the MiniPatientList to a desired viewport in order to display it. ***[AW Server only]*** **Drag & Drop** 2D series from the MiniPatientList to a desired viewport in order to display it. Only screen captures generated by Volume Viewer and single image series can be loaded in Volume Viewer.

Item	Description
	Note: Automatic registration can be performed when loading new volumes on-the-fly with the Integrated Registration option via Global Preferences. Refer to the Integrated Registration User Guide for more information. **Note**: Ensure that all images have been transferred on the local workstation prior to loading them from mini-patient list. Only images stored on the workstation will be loaded with drag and drop. If images are missing, please restart your Volume Viewer session.
4	***[AW only]*** When some exams from the active patient are stored on the local workstation but are not displayed in miniPatientList (misspelling, different patient ID, …): • Click **(Add Patient)** • Select desired exam from Patient List • Click again on **(Add Patient)** to validate
5	***[AW only]*** 2D series such as screen captures, DSA or single image series cannot be loaded in Volume Viewer. Click the **(2D)** button to load these series in the miniViewer which displays on top of bottom left viewport.
6	Click the **(Load)** button next to the "Save State" series in the miniPatientList to load it in a **new** Volume Viewer session (new tab on AW Server and right screen on dual screen AW). If the OncoQuant license is available, it is possible to load volumes referenced in the Save State series with corresponding measurements in **current** Volume Viewer session by using the **(Merge)** button. Refer to the OncoQuant User Guide for more information about this feature.
7	If all exams are not yet transferred when launching Volume Viewer, click the Refresh button to refresh the list of exams/series available on the local workstation.

[Seamless Integration]

To load images on the fly, open the **Series Navigator** from the PACS then drag and drop the desired series into the Volume Viewer viewport.
When dropping a Save State series, a popup asks whether the Save State series should be “Loaded” (i.e. replacing all series in current Volume Viewer session) or “Merged” (i.e. import referenced series and measurements from Save State in current Volume Viewer session).



MR in Volume Viewer

Volume Viewer MR is a Volume Viewer option which allows the recognition of MR image types (acquisition sequence, weighting, etc.) acquired on GE HDxt MR and later systems.
This option includes:

- Access to standard MR Review Protocols for dedicated anatomies (Brain, Knee, Breast, Liver, …)
- The possibility to customize MR Review Protocols (User Protocols)
- Fusion of MR sequences (as well as registration between MR sequences). Available from Integrated Registration MR option

Standard MR Review Protocols

Anatomy	MR Review Protocols

HEAD	• **MR Brain Review**
	  ○ MR Brain Review
	  ○ MR 3D Reformat
	  ○ MR 3D MIP
	
	• **MR Brain Stroke**
	  ○ MR Brain Stroke
	  ○ MR Brain FLAIR vs DIFFUSION
	  ○ MR Brain ADC vs MTT
	  ○ MR 3D Reformat
	  ○ MR 3D Multiple Oblique
	  ○ MR 3D MIP

CHEST	• **MR Breast Review**
	  ○ MR Breast Review
	  ○ MR Breast Diffusion
	  ○ MR Breast Dynamic
	  ○ Water/Fat/IP/OP

Anatomy	MR Review Protocols

CARDIAC	• **MR Cardiac AutoCine**
	  ○ MR Cardiac AutoCine
	  ○ CARDIAC Time Course vs MDE
	  ○ CARDIAC FIESTA vs MDE
	  ○ CARDIAC Time Course Stress-Rest

ABDOMEN	• **MR Prostate Review**
	  ○ MR Prostate Review
	  ○ MR Prostate Diffusion
	  ○ MR Prostate Contrast Uptake
	• **MRCP Review**
	  ○ MRCP Review
	  ○ MR MRCP 3D
	  ○ MR MRCP MS-MA
	• **MR Hips Review**
	  ○ MR Hips Review
	  ○ MR Hips Coronal
	  ○ MR Hips Sagittal
	  ○ MR Hips Axial
	• **MR Liver Review**
	  ○ MR Liver Review
	  ○ MR LAVA Dynamic
	  ○ MR LAVA Coronal
	  ○ MR LAVA 3D MIP
	  ○ Water/Fat/IP/OP

SPINE	• **MR Spine Review**
	  ○ MR Spine Review
	  ○ MR Spine Multi-View
	  ○ MR 3D Multiple Oblique

Anatomy	MR Review Protocols

UPPER LIMBS	• **MR Shoulders**
	  ○ MR Shoulders
	  ○ MR Shoulders Coronal
	  ○ MR Shoulders Sagittal
	  ○ MR Shoulders Axial

LOWER LIMBS	• **MR Knee Review**
	  ○ MR Knee Review
	  ○ MR Knee Coronal
	  ○ MR Knee Sagittal
	  ○ MR Knee Axial
	  ○ MR 3D Reformat
	  ○ MR 3D Multiple-Oblique

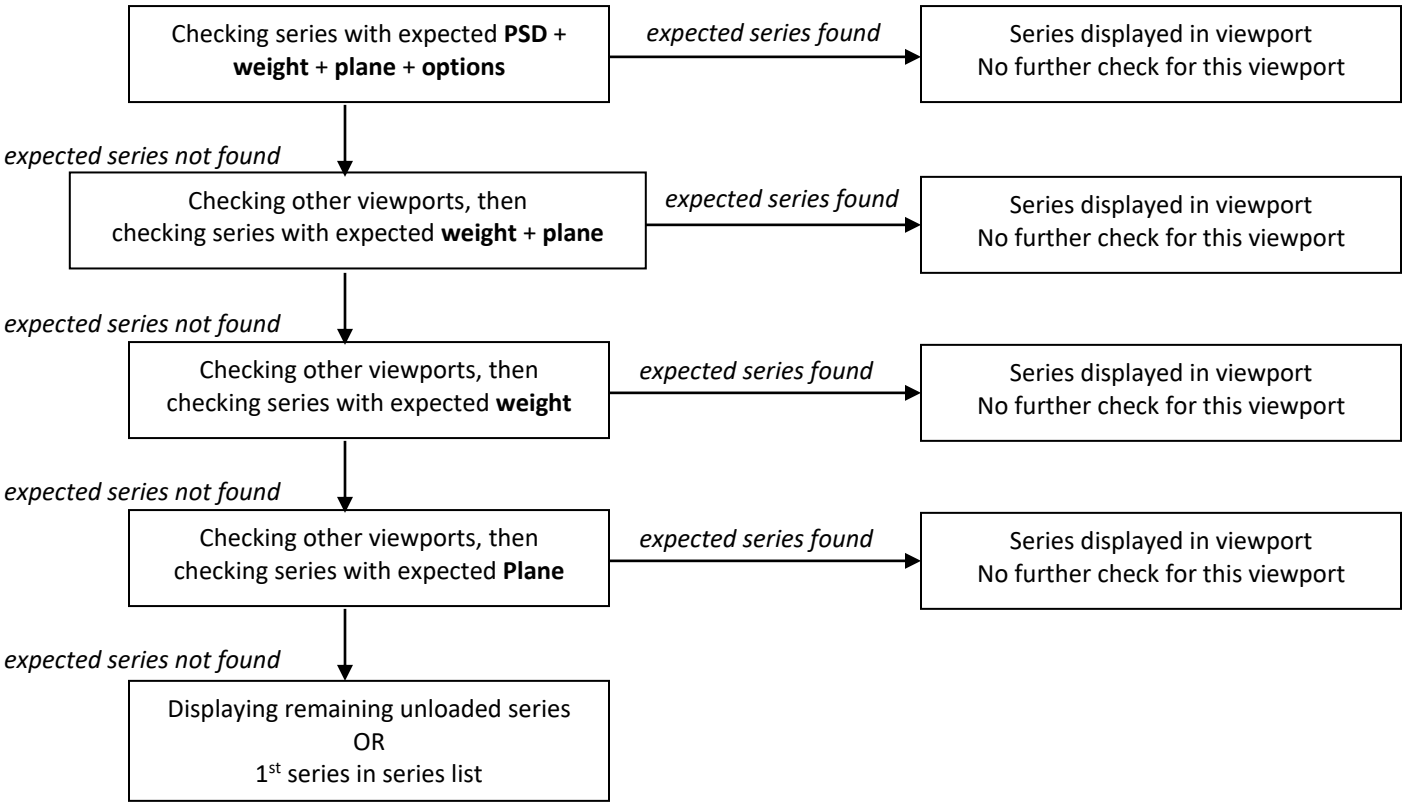
GENERAL	• **MR Review General**
	  ○ MR Review General
	  ○ MR 3D Reformat
	  ○ MR 3D Multiple Oblique
	  ○ MR 3D MIP
	  ○ MR Functool Outputs
	  ○ Water/Fat/IP/OP

Create a customized MR review protocol

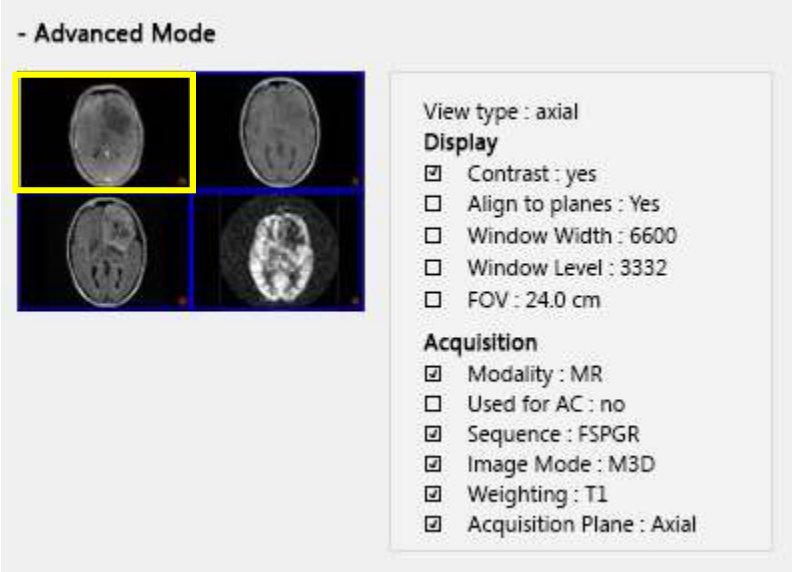
The save layout panel contains specific information for MR series (images acquired on GE HDxt MR and later). The following MR information can be set when creating new layouts, from **Advanced Mode** section in **Save Layout** panel:

- **Sequence name**: Pulse Sequence name of the acquired series.
- **Options**: acquisition options (EPI, Propeller, 3D, …). Displayed if applicable.
- **Weighting**: T1, T2, T2/T1, T2*
- **Bvalue**: b value for diffusion images. Appears when diffusion image is displayed.
- **Flex**: Water, Fat, In Phase, Out of Phase. Appears when Flex image is displayed.
- **Contrast**: Appears with "Yes" when contrast flag is set up on displayed series.
- **Funct**: functool type of image (ADC, MTT, etc.). Appears when a Functool image is displayed.
- **Slice Type**: if checked, forces the display of a series acquired in a specific plane (axial, sagittal, coronal).
- **Align to Plane**: if checked, the displayed series will be aligned to the actual acquisition plane.
- **Acquisition plane**: (for 3D acquisitions only) if checked, will display the 3D acquisition performed in a given plane.

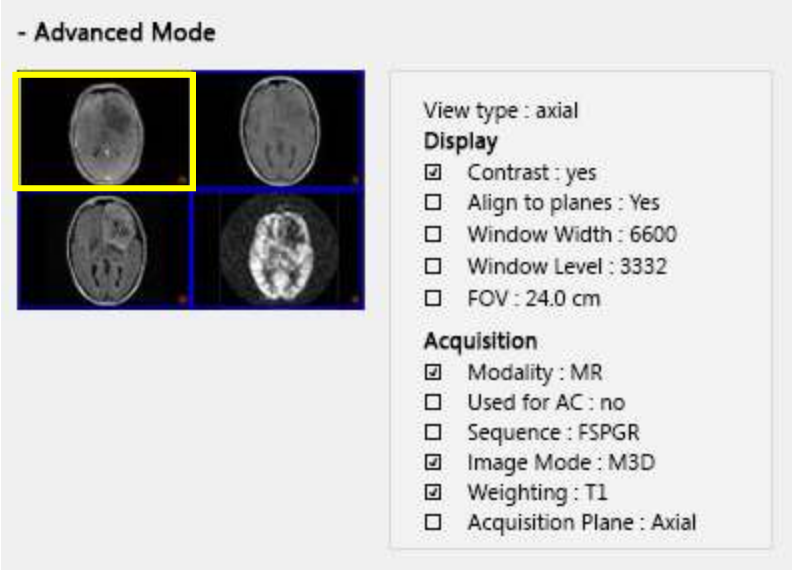
In order to maximize number of series displayed in MR Review protocols, 4 checks are performed for each viewport based on layout criterions:



***Example**: What will be displayed on top left viewport?*



Scenario 1:
Volume Viewer will try to find a 3D FSPGR sequence, with T1 weight acquired in an Axial plane.
If not found, it tries to find any T1 sequence acquired in an Axial plane.
If not found, it tries to find any T1 sequence or/and series acquired in an Axial plane.
The series found will be displayed in the acquisition plane.



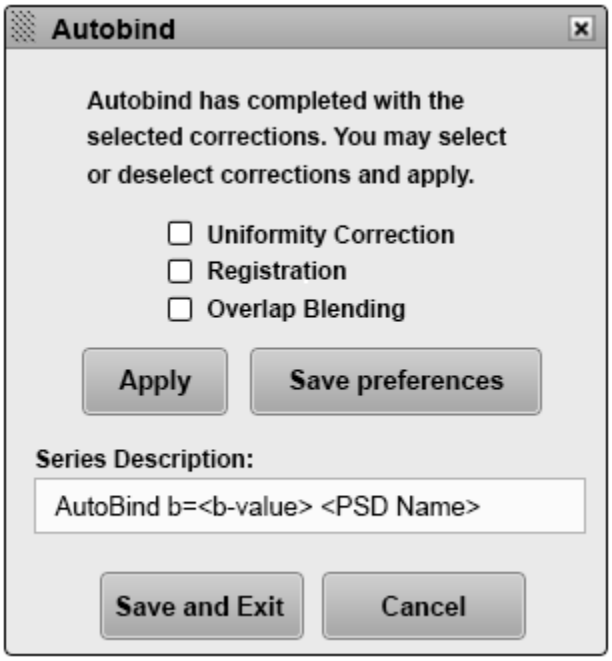
Scenario 2:
Volume Viewer will try to find any T1 series acquired in 3D mode, regardless of the PSD and acquisition plane (unchecked).
If not found, it selects the first unloaded series.

MR AutoBind

MR AutoBind protocol (available from the anatomy General) is designed to merge any single-phase MR axial series, Diffusion Weighted Images (DWI) or ADC maps. If multiple axial series were scanned and a whole-body view is needed, AutoBind may be used.

1. Protocol launch:
    a. ***[AW and AW Server*]*** Select the compatible MR series to be processed then select MR AutoBind protocol from the General anatomy.
    b. ***[Seamless Integration]*** Load MR exam in PACS viewer then select series viewports to be bound (using **<Ctrl>** key) and launch "AutoBind" from Oncology sub-menu in 3D Application menu.
    c. ***[MR console and PET/MR console]*** Select the compatible MR series to be processed then select AutoBind from Session Apps list.

2. After loading, the multiple selected series will be automatically bound in a single series and the resulting volume is displayed in reformat layout (Coronal and Sagittal) for preview. The AutoBind panel is displayed allowing you to:



- Recalculate the bind by applying several quality improving algorithms (uniformity correction, registration and overlap blending) which can be saved as preferences for further sessions.
- Edit the series description.
- Save the volume set and exit.
- Exit the application without saving.

3. Repeat the operation for each MR sequence (ADC, DWI …).

**For AW Server in Full integration, load the MR exam in PACS and launch MR AutoBind protocol. The series selection panel will be displayed to select which series should be used for binding.*

Optional corrections

Description

Use Uniformity Correction algorithm to improve visualization of bound data to provide similar window width and window length from head to feet.
Uniformity correction algorithm requires a minimum of 4 slices overlap between stations.

Use Registration algorithm to optimize continuity and alignment of anatomy from head to feet for DWI acquisitions acquired with same pixel size.
Registration algorithm requires both:

- A minimum of 4 slices overlap between stations on DWI acquisitions
- Reference images for DWI stations coverage (WATER: LAVA Flex series for MR system and WATER: MRAC series for PET/MR system). Reference images shall have same pixel size. Reference images might be automatically loaded by the software, if not, user would have to manually select corresponding reference images and DWI acquisitions at launch.

Use Overlap blending algorithm to get the images with improved intensity transitions at the overlap region and hence across the whole body.
Overlap blending algorithm requires both:

- A minimum of 4 slices overlap between stations
- Perfect match between overlap slices will improve algorithm results

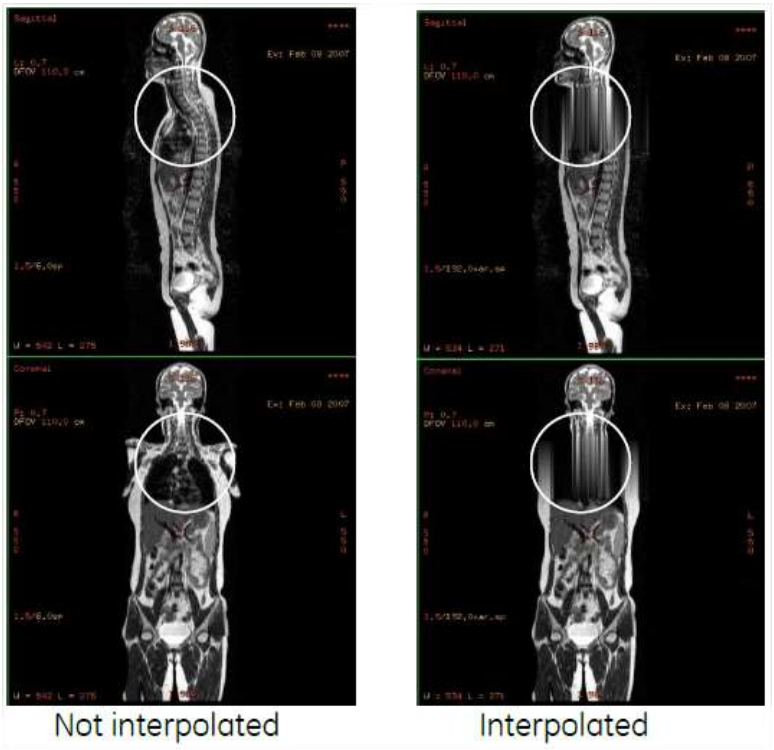
Corrections applicability

Uniformity correction and registration are available for axial DWI series only.
Uniformity correction and overlap blending are available by default for a limited set of PSDs including FSE-XL, FSE-IR, FRFSE, PROPELLER, LAVA, LAVA Flex, MRAC, SSFSE, Fast SPGR, efgre3d_aspir. Some PSDs will not propose those corrections by default and the user will have to select the corrections manually to apply them.

In case no corrections can be applied, input axial images will be simply stacked.

Troubleshooting

Always check the resulting volumes on the reformat views before saving them because the application does not limit you to series which share acquisition parameters or with the proper inclusion criteria. For example, if you accidentally miss loading one station, the application will use interpolation for that series that was not loaded (see image below).



Non-matching: If the patient moved during image acquisition, it may result in consecutive, non-matching series, which, if merged with AutoBind looks like image below on the left.

Non-matching

If the loaded series have both =0 and >0 b-values, the application generates as many new series as b values in the same exam from which the series were loaded. For 5 b-values, 5 bound series would be created.

After saving the automatically bound volume(s), always double-check the accuracy of the resulting series with the protocol you intended to use the bound images, and delete them if you find it necessary. Delete all erroneously or unintentionally saved series from the repository, and make sure that, if there were two series generated and saved, both of them are deleted.

For better identification, in the case of auto-bound series, the volumes are saved with the following series description by default:

<**AutoBind**> <other parameters> <date, format: YYYY-MM-DD hh:mm:ss> <b-value (**b=b-value**)>

If the loaded series have the same b value, then the *<b-value>* part is omitted.

<Other parameters> may include the combination of the following parameters:

1. *PSD name* and *weight* (if *PSD name* is available);

2. *weight* and *functional map name* (when *PSD name* is not available)
Note that the “Apparent Diffusion Coefficient” string is replaced with “ADC”.

The default series description can be edited by modifying the series description in the AutoBind interface.

When the input series have different resolutions, the saved series description will contain the text “Resized”.

PET in Volume Viewer

Overview

PET protocols allow the review of PET/CT exams in Single and Compare modes with specific PET features:

- Fused Views,
- SUV Quantification,
- Multi–Object Volume Rendering,
- Brain Study Reorientation,
- PET–MR Review.

Note: For PET datasets with matrix sizes over 256x256 some display performance issues may occur.

Display and Controls

Many of the basic viewing controls, such as those that you use to zoom in and out on the images, or adjust window width and level (contrast and brightness), are available directly on the views.

In the main toolbar, a dedicated category is available to allow a quick access of PET tools.

In the right click menu, the user is also able to customize a quick access of up to 6 different tools.

CT/PET Protocols

A set of protocols is available for PET category:

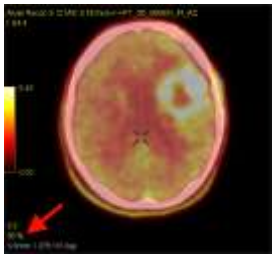
- **PET/CT Single Review**
- **PET/CT Follow up**
- **PET/CT QC Fused**

Additional PET protocols are available in Volume viewer PET:

- **Cardiac PET/CT QC**
- **PET 4D**
- **Reorient Guide**

Fused views

The percentage of fusion is automatically displayed on the left-hand side of fused views (see Figure below). Middle click and drag left/right the on–view annotation to adjust continuously the percentage of PET information displayed (from 0 to 100%) in the fused view. Or, with the mouse over the active annotation, type the new percentage of fusion desired.



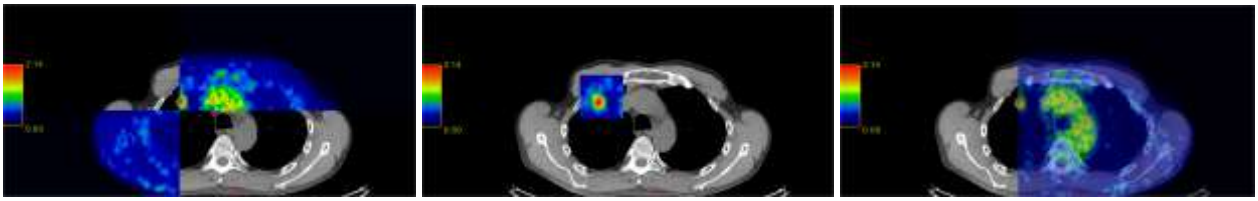
Adjusting PET image % on fused views

The color ramp of the PET image is automatically displayed in all fused views.
Note: On Linked views, the color ramp is only displayed in the first image view.

To modify the Window Level of the PET part of the fused image, click and hold the middle mouse button when over the max (resp. min) value active annotation above (resp. below) the color ramp and drag the mouse left and right to modify the max (resp. min) value. Or, to modify the min or max value, type in a new value with the mouse over the min or max value active annotation.
To modify the Window Level of the CT image, click and hold the middle mouse button anywhere else on the view then drag the mouse. If a viewport contains the CT used in the fused viewport, adjust the Window Level of the CT in this viewport (via the mouse or via keyboard shortcut) so it is synchronized in the fused viewport.

Right click in the fused view and select fusion rendering from **Blend Modes** menu:

Fused **Threshold Fused** **Inverse Fused**

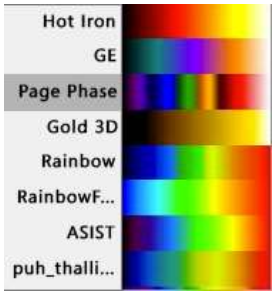


Tiled **Windowed** **Swipe**

Color map

To display/change a color map:

- Select the viewport(s) in which you would like to change the color map.
- Click directly on the color map (fused views) or click on the Set Color button available from the Visualization tools  . Select a predefined color map from the list.



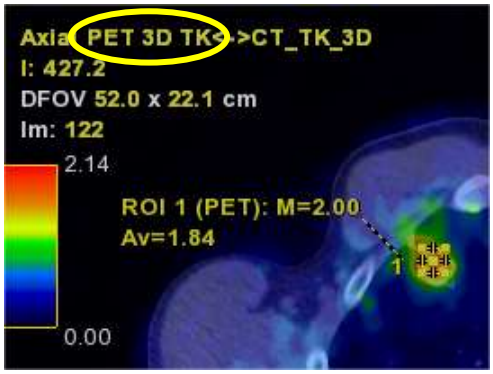
A color ramp is displayed on the left side of the viewport. The min/max values are displayed next to the color ramp. Once applied, a color map can be set as favorite for all fused views in the predefined protocols.

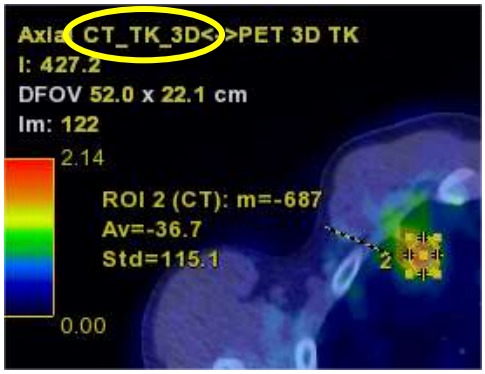
Note: Color map only applies to PET or fused views.
Note: There is no way to create a user defined color map.
Note: This is not applicable with user layouts in which the colormap is saved.

ROI statistics on fused views

Fused viewports contain 2 volumes: 1 main volume and 1 secondary volume, both displayed on top left of the viewport as "**main volume <-> secondary volume**".
Main volume and secondary volumes can be swapped by clicking the **<->** annotation.

When depositing a ROI on a fused view, the ROI will be attached to the main volume and the ROI will be displayed in all viewports containing the main volume. Modality will be displayed next to the ROI statistics in the fused viewport.





SUV

SUV calculation

Any ROI deposited on a PET view will provide statistics expressed in SUV values. Click the SUV unit in the bottom left of the PET viewport to change it, or to view/edit information for SUV calculation (patient weight, height, sex, tracer activity and measurement times, glucose level). Wrong value for one or more of these parameters can have a significant impact on SUV calculated value. Note that modifying information in the SUV calculation panel impacts only the current session, and will not be saved when exiting Volume Viewer.

Note: In Compare mode, the values in the SUV panel correspond to the selected view. These values are automatically updated when selecting another volume.

Information on unit of measure

Several SUV scales are available by right clicking the unit on–view annotation. The multiplicative factors used for each scale are defined as follows (WT=weight, HT=height):

- bw (g/ml) = WT
- lbm (g/ml*) = 1.10 WT – 120x(WT/HT)2 for males (Legacy *)
- lbm (g/ml*) = 1.10 WT – 128x(WT/HT)2 for males (Consensus **)
- lbm (g/ml*) = 1.07 WT – 148x(WT/HT)2 for females
- bsa (cm^2/ml) = WT0.425 x HT0.725 x0.007184

** Legacy: Based on reprint by Morgan et al. [1994] as 1.10 x WT – 120 x (WT/H)2, and consequently adopted (legacy) by the PET community [Sugawara et al. 1999]. Earlier versions of VV use this formula for Males. This is applied in the PET Preferences panel.*
*** Consensus: The original (consensus) formula for computing LBM for males was 1.10 x WT – 128 x (WT/H)2 [James 1976]. Newer versions of VV support this calculation for males when the preference is applied. This is applied in the PET Preferences panel.*

Default SUV display settings:

- The initial factory default unit setting for PET W/L is kBq/ml.
- If not enough information to compute SUVbw, the default secondary preference is KBq/ml.
- Though no longer the default for unit selection, an option to maintain last selected units when Volume Viewer PET is exited and reloaded is still available as a setting.
- Units are not saved in layouts.
- If SUV info is present but selected W/L units are kBq/ml, then m=0.0 M=(equivalent of 10.0 g/ml in KBq/ml).

SUV in comparison mode

SUV analysis is a frequently used tool to quantify and support a clinician's interpretation of variances in regional FDG uptake. They are relative (not absolute) values that aid in tumor management when tracked serially, and as such must be calculated identically to be comparable.

In order to compare SUVs between successive exams, they must be calculated identically to be accurately compared:

- Since the acquisition method (2D/3D) can influence the calculation of the SUVs, a message will pop up when the acquisition method is different between two exams.
- Differences in uptake time (injection time – start of acquisition time) may be invisible sources of errors for SUV calculation. A message will pop up when the differences between uptake times of two exams are too large.

When comparing maximum SUVs of an object with its appearance on a prior exam, ensure that the "hottest" pixel is actually being analyzed. It is important to ensure that it is contained within the VOI by changing the size of the VOI in all three planes.

Note: The values displayed on the SUV panel correspond to the selected view. When changing the selection, the values are automatically updated.

Volume Viewer supports both volumetric SUV analysis (3D) and 2D. In both 2D and 3D mode the SUV statistics are computed from the original transaxial data regardless of the orientation of the displayed image.

The following suggestions may help reduce discrepancies when reading follow up exams:

- If the prior exam has had SUV's reported on another workstation then we suggest utilizing the PET–CT compare mode layout for direct comparison between the current and prior exams.
- When comparing maximum SUVs of an object with its appearance on a prior exam, ensure that the "hottest" voxel is actually being analyzed. While Volume Viewer's 3D VOI performs this search automatically, it's important to ensure that it is contained within the VOI.

Note: It is important to note that Scanner calibration and other clinical factors also impact SUV variability.

Note: When comparing PET–CT exams, it is strongly recommended to load both native studies in the dedicated protocol PET–CT Compare.

Note: The position of the maximum pixel in the VOI can be in another slice that the one being displayed. A small blue dot is displayed on the correct location.

Note: When hitting the **<H>** key, the VOI box is hidden and only the contours are displayed.

Note: The contours are not displayed on slab thick views but only on views with the minimal slice thickness.

Statistics
Right click on the bookmark → Statistics
List of available statistics for PET ROI (deposited via **<Insert>** key or via AutoContour tool): Volume, Minimum, Maximum, Average, Standard Deviation, Relative Deviation, TLG (SUV only), Peak, Threshold

Note: A maximum of three statistics can be selected and displayed.

Note: The units of display of the VOI will always match the WL units displayed in the lower left of the viewport (VOI statistics in a fused viewport will be displayed in SUV, not HU).

Note: The TLG is the product between the volume of the tumor and its SUV average. TLG is only available for VOIs that are automatically thresholded.

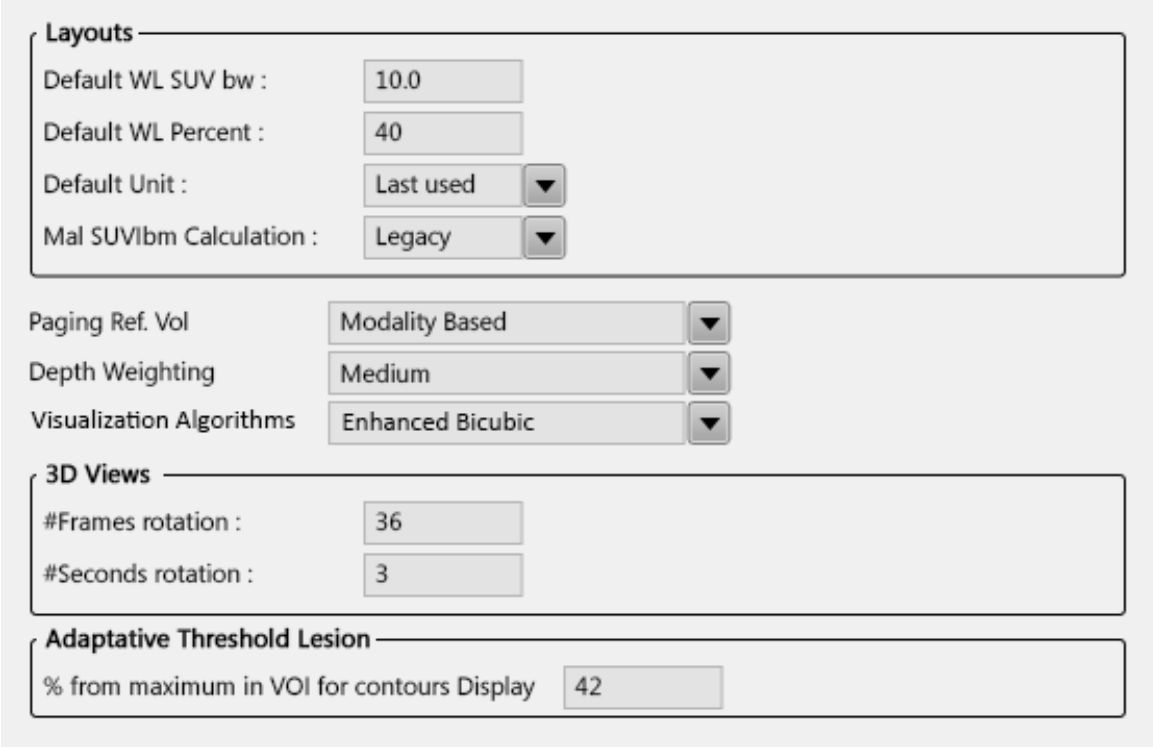
Note: The negative pixel values from PET images are not taken into account in the calculation of VOI statistics.

Contextual options
Right clicking a ROI/VOI when it is active will enable you to:

- Show/Hide statistics in the ROI/VOI (will show/hide statistics for all ROI's/VOI's in all viewports),
- Lock/Unlock ROI/VOI position, size and comments,
- Delete ROI/VOI,
- Clone ROI/VOI.
- Show/Hide max value in the VOI,
- Send cursor to max value.

PET Preferences

All the preferences for PET features are available from the Global Preferences panel, tab PET.



Note: All preferences are automatically saved when closing this panel.

Other PET protocols

Cardiac PET/CT QC

The Cardiac PET/CT QC protocol allows the review of alignment for cardiac PET/CT studies, by fusing PET images with the CT images that were used for attenuation correction in the PET reconstruction.

The fusion is composed of a CT series and a PET series.

- Need PET images and corresponding CT image series which was used for CTAC
- For each PET slice loaded its corresponding CT slice that was used for Attenuation Correction will be loaded and displayed fused to that PET slice

After images are loaded, the internal Cardiac registration can be analyzed in the axial, coronal, and sagittal views. The PET and CT images will remain linked as you scroll through all slices in all directions.

Note: Desired Alignment Correction measurements can be taken using the standard measurement tools but these values will not be transferred back to the PET system for reconstruction.

PET/MR Fused

The PET/MR Fused protocol allows the display and fusion of pre–registered PET & MR datasets. CT and MR series can be aligned by using the Fusion package.
After registration, you may want to reorient the dataset using Reorient Guides (see next section) to correctly align the 3D volumes for optimal review. This protocol may be used with PET and MR data, as well as PET–CT data.

Reorient Guide

Reorient Guide is a protocol used for re–orienting and saving a registered series (i.e. PET–MR, PET–CT). This is particularly useful in correcting for differences in the scan orientation and what is desired for review.

When the protocol is launched, follow the protocol panel instructions to re–orient CT series. Once the orientation is defined in CT series, it will be applied in PET series. You can then save both series with the same spacing and thickness as PET and these may be reviewed in the standard Volume Viewer layouts.

Objectives:
- used to correct for differences in the scan orientation against the desired review orientation
- used to create oblique reformats:
    - neuro cases (to align the head to standard review planes)
    - melanoma cases

Limitations:
- steps MUST be performed sequentially—work only in the currently active view

Reoriented CT series will save as:
- type: Reformat
- description: Average

Reoriented PET series will save as:
- type: Static Image
- description: Reformatted

New series can be loaded into Volume Viewer as if they were the original axial series.

Note: Weighted MIP image quality may be slightly degraded using reformatted series. If this occurs, change the view type to HD MIP.
Note: When a dataset is reoriented, the Standard Uptake Values (SUV) measurements may change as data are interpolated. Thus, the Max SUV may change, especially when the Max value is isolated.

PET 4D

PET 4D is a specialized protocol providing the ability to review a gated or dynamic (4D) PET exam.

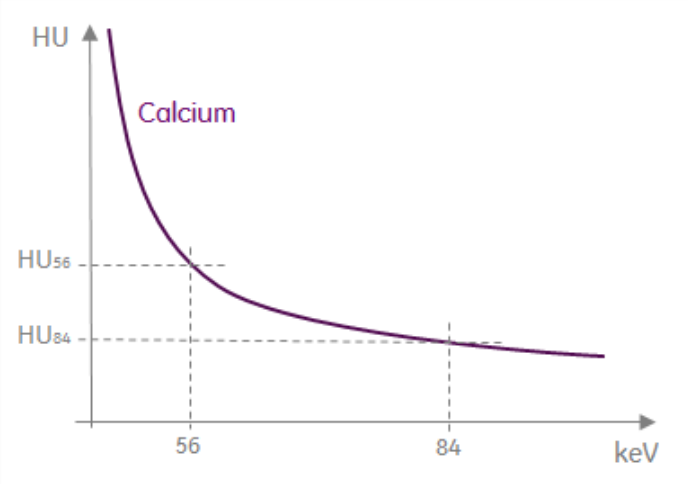
Objectives:
- Accurately localize active tumor
- Exclude non–active tissue
- Accurately quantify tumor volume in each of the respiratory phases
- See and quantify the tumor movement over time (4D)

For more information about the PET 4D tools available in this protocol, refer to the “PET/CT Tools” section in the “Volume Viewer – part 2: Deep Dive” User Guide.

Note: Only PET Gated series acquired on GE PET scanners are currently supported.

Dual energy CT

Material characterization can be performed based on dual energy acquisition. Indeed, HU values depend on the energy used during acquisition, closely linked to the voltage used. Below is the example of the HU values for calcium.



Considering that an acquisition made with 80 kVp corresponds roughly to 56 keV and an acquisition made with 140 kVp corresponds roughly to 84 keV, it is easy to imagine that materials can be characterized based on the HU ratio values between high kVp and low kVp.

$$\frac{HU(80kVp)}{HU(140kVp)} \approx \frac{HU(56keV)}{HU(84keV)}$$

Volume Viewer proposes 3 dual energy protocols based on similar workflow:

1. Check registration between low kVp and high kVp series which must have same slice thickness, same slice spacing, same reconstruction FOV and same reconstruction algorithm.
2. For Calcium and Uric Acid protocols, a material map is generated based on the values from literature*.
3. For Custom protocol, a map can be created adjusting the threshold on native image and the threshold based on ratio value.

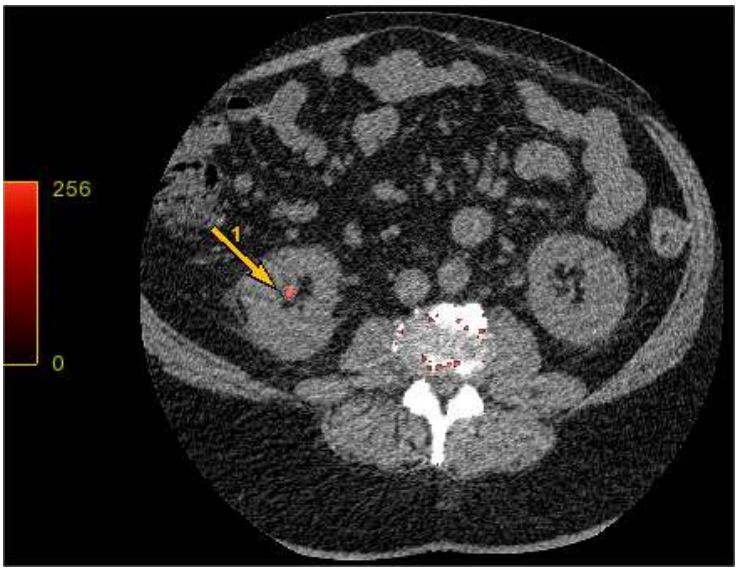
Refer to “Volume Viewer – part 3: Clinical scenarios” for more information about how to use these protocols.

** Refer to the literature for more information about the values used for Calcium and Uric Acid (“Dual-Energy CT as a Potential New Diagnostic Tool in the Management of Gout in the Acute Setting” - Savvakis Nicolaou, Charlotte Jane Yong-Hing, Sandro Galea-Soler, Daniel J. Hou, Luck Louis and Peter Munk – American Journal of Roentgenology, 2010; 194:1072-1078.)*

Once the 2 series, high kVp and low kVp are loaded and registered, 2 types of thresholds are applied automatically to generate the material map:

- Lower threshold and upper threshold, to specify the range of voxels to take into account for the material map creation (soft tissues, …). Default values for Dual Energy protocols are 150 and 500.
- Ratio threshold, lower OR upper:
    - For uric acid, upper threshold is set to 1.25 and cannot be modified
    - For calcium, lower threshold is set to 1.25 and cannot be modified
    - In custom protocol, upper threshold is set to 1.25 and **can** be modified (values + upper/lower).

Example: *Uric acid map with upper threshold 1.25 for HU in range [150-500]*



Refer to “Volume Viewer – Part 3: Clinical scenarios” for more information on how to use the Volume Viewer Dual Energy protocols.