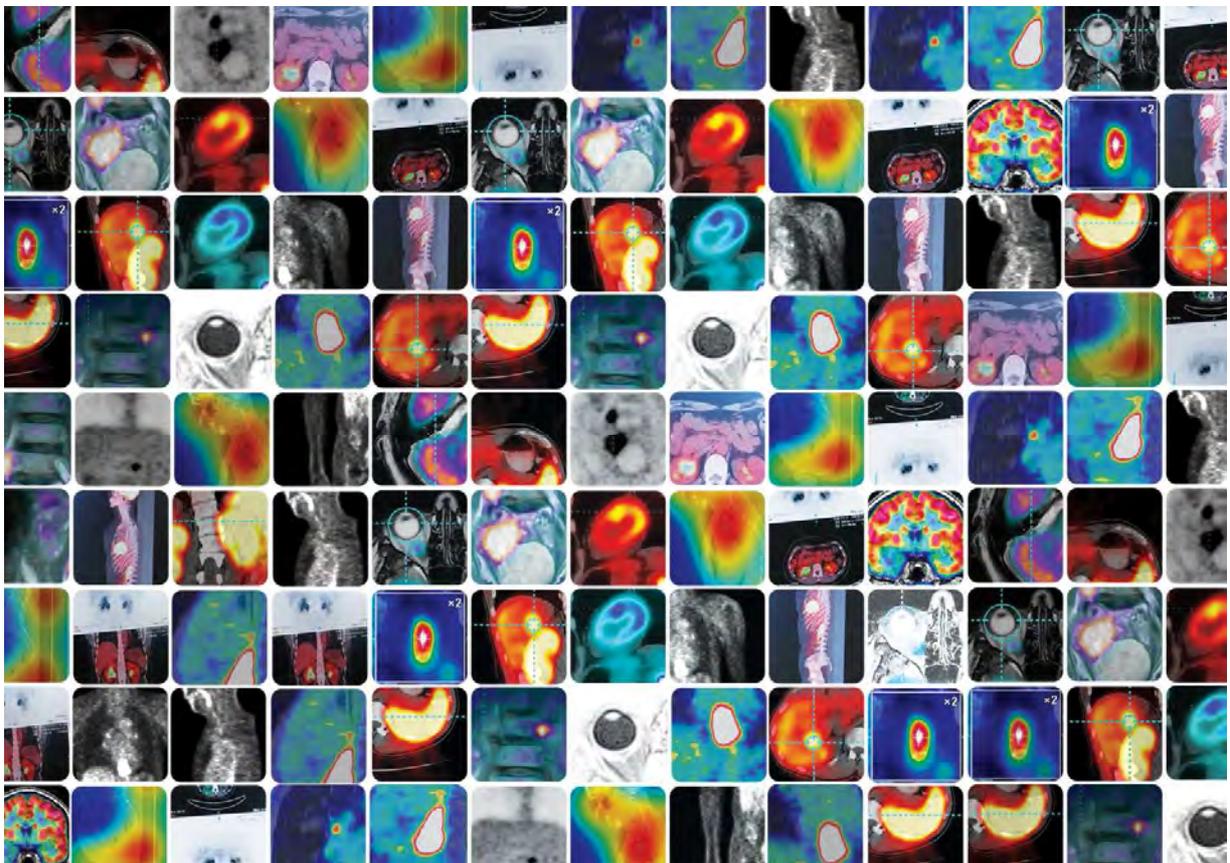


XD₃

Help Guide



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Introduction to XD3

Mirada Medical’s XD 3.6 is a software application designed for the rigid and deformable registration of medical image datasets including PET, CT, MR, and SPECT as well as nuclear medicine planar, planar WB and planar dynamic. Additionally, XD3 provides powerful image viewing capabilities including series image review, region quantification and tracking and a customizable reporting tool.

XD3 is available in both Standard and Advanced tiers. This user documentation provides instruction for the Advanced Tier. Some functionality described may not be available to you, depending on the license tier you have installed. The following table lists differences in the two tiers.

Feature	Standard	Advanced
Follow up scan comparison	Yes	Yes (unlimited)
Support for 4D (gated) data	No	Yes
Support for multi-sequence MR	No	Yes
Support for multi-phase, multi-time point CT	No	Yes
Support for multiple time points	No	Yes
Rigid Fusion of images	Yes	Yes
Deformable fusion of images	No	Yes
Three way fused views	No	Yes
Advanced modality optimized deformable image registration	No	Yes
Save regions as RTSS	Option	Yes
Load and display RTSS	Option	Option
Export rich fusion viewer to disk	Option	Yes
Save state, bookmarks, ROIs rulers to PACS	Yes	Yes
Derive ruler from ROI	Yes	Yes
CT-specific segmentation	Option	Option

Review Mode	Standard	Advanced
General Fusion	Yes	Yes
General Oncology Review	Yes	Yes
Nuclear Medicine Review	Yes	Yes
PET Review	Yes	Yes
PET/CT Whole Body Review	Yes	Yes
Single Volume Review	Yes	Yes
Head/Neck Review	No	Yes
Melanoma Review	No	Yes
MR/PET/CT	No	Option

New in XD 3.6

The following are some of the key features that have been added to the application in this release:

- CT-specific segmentation tools.

- RTSS Import
- Fast navigation mode using the right mouse button

Regulatory Statement

Device Classification

Class II (Picture Archiving and Communications System) device with reference to Section 892.2050, Product Code: LLZ Image Processing System.

Intended Use

XD3 is intended to be used by trained medical professionals including, but not limited to, radiologists, nuclear medicine physicians, and physicists.

XD3 is a software application intended to display and visualize 2D & 3D multi-modal medical image data. The user may process, render, review, store, print and distribute DICOM 3.0 compliant datasets within the system and/or across computer networks. Supported modalities include, static and gated CT and PET, and static MR, SPECT and planar NM. The user may also create, display, print, store and distribute reports resulting from interpretation of the datasets.

XD3 allows the user to register combinations of anatomical and functional images and display them with fused and non-fused displays to facilitate the comparison of image data by the user. The result of the registration operation can assist the user in assessing changes in image data, either within or between examinations and aims to help the user obtain a better understanding of the combined information that would otherwise have to be visually compared disjointedly.

XD3 provides a number of tools such as rulers and region of interests, which are intended to be used for the assessment of regions of an image to support a clinical workflow. Examples of such workflows include, but are not limited to, the evaluation of the presence or absence of lesions, determination of treatment response and follow-up.

XD3 allows the user to define, import, transform and store and export regions of interest structures and dose volumes in DICOM RT format for use in radiation therapy planning systems.

Cautions

The device presents medical image information, acquired from scanner systems, which can be used as part of a clinical diagnostic process, in particular for the diagnosis, staging, treatment assessments and follow up of disease. The clinical diagnostic process uses many other sources of information to form the assessment of the condition of the patient, including blood tests, clinical examination, case history and genetic profiles. The information that medical imaging provides, as presented by XD3, is a complement to these standard methods. XD3 should not therefore be solely used to directly drive a clinical decision making process.

Prescription Statement

Caution: Federal law restricts this device to sale by or on the order of a licensed healthcare practitioner.

Computational Performance

Unless explicitly agreed to by Mirada Medical, no responsibility is taken for the duration required to perform functions within the software environment. Specific performance requirements can only be agreed to if the product is delivered on Mirada Medical specified hardware.

Accuracy

The actions of the user may directly affect the accuracy of functions within the software environment. Therefore it is the responsibility of the user to determine if the results of image visualization are satisfactory.

Reporting

While the device is a quality product, manufactured under a rigorous quality control program, it is not a secure repository for clinical reports. Any comments, images or annotations compiled into any form of report and provisionally stored by the software environment are at the user's risk. No responsibility is taken by Mirada Medical for damaged reports, incomplete record manipulation, storage/retrieval problems or network-based security issues unless specifically agreed.

Security

The software tool may, by virtue of its usage, contain confidential patient information. The security and configuration of the computing hardware used to execute the software is the responsibility of the end-user. This includes secure imaging local area networks (LANs), appropriate fire-wall provision, network directory permissions, etc.

Printing

Mirada Medical takes no responsibility for the faithfulness or quality of a generated hard-copy result of a printing device not supplied by Mirada Medical and/or installed/configured by Mirada Medical.

User Installation/Operation

User-performed installation and configuration of the software is entirely at the user's risk unless otherwise agreed by Mirada Medical (on the basis of an extended EULA/service contract). This includes any disruption to existing installations, software (or software licenses) or data loss.

Diagnostic and Therapeutic Restrictions

Use of the software as a primary viewing or diagnostic device

The software is designed as an aid to diagnosis, enabling information to be used as an input into a diagnostic process. Other methods and procedures should be in place to enable a diagnosis to be reached without the aid of this software. The software should not be used as the sole basis for forming a diagnosis, to do so would constitute a misuse of the software.

Use of the software for Biopsy Planning

The software is designed as a visual aid and as such it is not recommended for use in applications where the image geometry or the fused image geometry (as displayed by the software application) cannot be confirmed by other means. The software should not be used as a direct control mechanism for biopsy guidance mechanisms (either hardware or software based).

Use of the software for Surgical Planning

The software is designed as a visual aid and as such it is not recommended for use in applications where the image geometry or the fused image geometry (as displayed by the software application) cannot be confirmed by other means. The software should not be used as the sole basis for surgical planning, the preparation, execution or post-operative assessment of surgical practices.

Use of the software for Radiotherapy and Treatment Response

The software is designed as a visual aid and as such it is not recommended for use in applications where the image geometry or the fused image geometry (as displayed by the software application) cannot be confirmed by other means. The software should not be used as a direct control mechanism for delivery of treatment, either via radiation or chemotherapeutic methods. The software should not be used as the sole basis for evaluating the success/response to treatment.

Warnings

The warnings listed here relate to specific functions and modes of use for the software. These are also listed in the applicable sections of this Help Guide.



Unsupported modalities, data or image types may cause the software to function incorrectly, to return invalid results or to reject the data if an attempt is made to load them into the software. Attempt to load invalid data along with valid data may cause both sets of data to be rejected by the software.



Lossy compressed data, by design will reduce image quality. This may impact the ability to view images with the same accuracy and detail as with non-lossy data. All loaded lossy data is labeled as such in the viewing window.



The Maximum Intensity Projection or MIP Renderer is a tool for data visualization in 3D and is useful for obtaining an overview of the areas within the image data of a high intensity and as a tool to navigate to those regions. The MIP should not be used as the sole view used to interpret the image data.



Fused images are displayed within system provided layouts and can be included in user defined layouts. The modality, quantification information, time point and dataset designation within the current review mode are displayed for each layer in the fused view to allow identification of each layer.



Care should be taken to ensure that the slice numbering scheme chosen in XD3 matches that of any system used to launch XD3.



The slice navigation slider is specifically designed to be able to navigate quickly to a desired area within an image view. As such the slice navigation slider does not display every slice in the view being navigated from the currently displayed slice to the slice represented by the slider position set.



The PET SUV from Acquisition calculation underlying the display of this quantification option is outside the control of Mirada Medical. When PET SUV from Acquisition displays values, the number displayed is based on the stored value in the image data. Please contact your vendor for further information on this topic.



If the **Go To Hottest Voxel** tool is used on a region with more than one voxel with the highest intensity value, then only one of these voxels will be identified.



When an automatic registration scheme is set to be run on application load, the results should be reviewed using the crosshair alignment and the quality control tools available via **Registration -> Registration Manager** to ensure that the registration is satisfactory. This is particularly important before propagation of ROIs between time points.



When an automatic registration scheme is run with data assignments containing multiple related series (e.g. Gated CT or PET, Multi-phase CT, Multi-sequence MR), the first series/volume assigned is the one used for registration for registrations involving that assignment. This may or may not be the optimal series/volume to use for registration depending on the acquisition protocol. This can be modified on the Data Management screen by changing the 'Anchor' for the assignment and reviewed on the **Registration -> Registration Manager** to ensure that the registrations are satisfactory.



When propagating ROIs between time points, it is important to check that the threshold used is appropriate for the data in the time points. For meaningful comparison statistics to be displayed, the threshold should be the same in each time point.

To see the threshold used, select the region in the time point and view the threshold slider or hover the mouse over the Region defined in the Regions of Interest panel in the Toolbox.

The threshold is also visible on the Regions Table.



When defining a 2D ruler, the measurement associated with a line is displayed in the same color as the line to which it pertains. When the measurements are similar, the colors should be checked to identify the pertaining line.



The Create Ruler from Region tool calculates the long and short axes from the ROI selected using mathematical approximations of the smooth ROI boundary. However, the resulting bi-ruler may not correspond to what the user considers to be the long and short axes that best characterize the lesion from a clinical point of view. It is important that the resulting Biruler is visually inspected and compared with the region used for creation to ensure the results are as desired.



The Create Ruler from Region tool uses mathematical approximations to the smooth ROI boundary when calculating the best bi-ruler placement. However, in some rare cases the approximations may result in a ruler that does not correspond exactly to the displayed boundaries or one that passes slightly outside the lesion boundary. The user should check the result of the tool to confirm that the ruler meets their expectations.



When viewing fused images, artifacts may be introduced by poor alignment of findings between the image layers in the fused view. It is recommended that the registration accuracy is checked prior to image interpretation and the transparency of the layers is adjusted appropriately to view the layers in the fused views.



When a layout image segment contains multiple planar NM Images from one or more series, the only way to distinguish to which planar series an image pertains is by the series description text label on the image segment.



Gallery images do not individually contain patient identification information due to the potentially limited size of the image segments. To identify to which images the gallery pertains, system provided gallery views contain a patient information view segment.

The layout editor allows patient information views to be added to all user defined layouts and should be used when creating Gallery views.



The Data QC validation is performed on a per user basis using the validation criteria specified by each user. The validation does not perform any image quality or registration checks.

This feature requires an advanced license to perform and report validation results. Care should be taken when utilizing the floating license deployment and using this feature, as launching with a Standard license after an Advanced license will not perform validation on the data as may be expected.

It should be noted that not all fields are validated, some are for display only. These fields cannot be set to validate the contents when specifying which fields to validate.



The Voxel Intensity Distribution feature relies on the accuracy of the registration when the ROI was created on one dataset and the intensity distribution statistics are viewed for the other datasets within the same time point. The registration should be checked for accuracy using the Registration Manager prior to using this feature.



Functions that rely on the inversion of the registration deformation map such as the cross-hair alignment and Region of Interest propagation may exhibit inconsistent and asymmetrical behavior in certain situations. For example in Adaptive Planning review mode, if the user were to navigate the cross-hair to a location A in the Baseline Planning the software will automatically place the cross-hair at a particular corresponding location, B, in the Current Planning. However, if the user were then to move the cross-hair around in the Current Planning and then place it back at location B, the position of the cross-hair in the Baseline Planning may not be at location A.

This applies to any deformable registration either within a timepoint or across timepoint. For example, in Fusion Analytics in which a deformable registration exists between the Planning and MR images, the Planning dataset should be used for cross-hair navigation.



When using the Volume Crosshair tool, due to the discrete nature of the image data, quantization effects may result in a small difference in the statistics displayed on the same data viewed in fused and non-fused views. This effect may be greater in the presence of a large deformable registration between the layers. Such differences are generally not clinically significant. However, we recommend that the user check the magnitude of any differences by comparing the statistics visible in the fused and non-fused views when using this tool. If the user considers the difference significant for their purposes then the non-fused statistics should be used. This effect does not occur with the other ROI tools available in the application.



The frames in a dynamic flow study are played at a uniform rate and not in real-time.



Due to its definition, the peak value may include voxel values from outside the ROI boundaries when the ROI is near an adjacent area of the image with high PET values. The user should treat the peak value with caution where high PET voxels are within 0.7 cm of the ROI boundaries.



XD3 creates the DICOM RT Structure Sets from the selected region as specified in the DICOM Standard. RTP systems may apply interpolation between the encoded contour control points that differs from their display in XD3. We recommend that the user takes screenshots of the regions used to create the contours, on an acquisition orientation view, and uses these to compare to the contour displayed within the RTP system to ensure that the imported contour is an accurate representation.



Different interpolation methods may be used by XD3 and TPS systems when displaying contours. This means that when viewing findings in the acquisition orientation, they may appear visually different between systems. It is recommended that screenshots of loaded findings be taken in the acquisition view and compared to the same findings as displayed on the TPS to ensure that the imported structures are accurately represented in XD3.



Regions resulting from performing the **Transform to All**, **Transform to Remaining**, **Transform to All within Timepoint** and **Transform to Remaining within Timepoint** actions are highly dependent on the quality of the registration that exists between the dataset on which the source region exists and all the datasets to which the region is to be transformed. It is recommended that quality checks be performed within the Registration Manager screen on the accuracy of the registrations prior to performing a region transformation action.



The volume doubling time statistic is derived from the volume statistic. It is an estimate of the true tumor volume doubling time and depends on the accuracy of the regions drawn. The region should be checked on every slice on which it exists to ensure it is as accurate as possible.



The volume doubling time calculation becomes more robust the larger the regions become. At small volumes where the region volume consists of only a few voxels, the potential error in the reported volume may be quite large. The user is advised to use the Data QC screen to check the voxel dimensions when making a judgement as to how to interpret the volume doubling time. In addition, the volume doubling time calculation may become very large and sensitive when the volumes in consecutive timepoints are similar.



Many data roles can load multiple volumes so long as they share a common frame of reference. Once loaded, XD3 will attempt to sort the volumes into a logical order. For gated data, this will be in a temporal order. Multiple reconstructions of the same raw data can also be loaded, however in such use cases it may not be possible to consistently order the volumes. While the application is not designed to support multiple reconstructions of the same data for PET and SPECT (such as FBP and TOF), it is possible to load these reconstructions simultaneously into the same data role. In this case it is not possible to guarantee that the same order is maintained over multiple timepoints. The user must check within the Data Management screen to ensure that the same reconstructions have been assigned to the anchor role.



Automatically shadowed regions will be quantified in the resolution of the dataset onto which the region was shadowed. Only voxels whose center lies within the region are considered when calculating statistics. If the dataset on which the original region was defined and the dataset onto which the region was shadowed are of a different resolution, the regions may have a different Volume statistic as the volume will always be a multiple of the voxel volume of the dataset on which the region is defined. For instance, a region defined on a CT dataset and automatically shadowed onto the PET may have a different Volume statistic when calculated on the CT compared the Volume statistic calculated on the PET if the CT dataset is of a different resolution to the PET.

It follows that any statistic derived from the Volume statistic (e.g. Volume Doubling Time) will be different for a finding shadowed between a pair of datasets if the Volume statistic is different for that finding.



The CT Region Segmentation tools estimate a lesion boundary based on image contents and the user initialization and does not attempt any automated detection of lesions. The quality of the results need to be checked for accuracy by the user prior to being used.

Notes

Note 1

When using SUV calculation during PET assessment certain assumptions are made with regard to the reference time for the acquisition of the data series. Variability in interpretation of requirements outlined in the DICOM Standard with regard to determination of the start reference time during acquisition and the time of tracer injection may result in variability in the SUV values calculated by different vendors.

It is important to note that due to inconsistency of approach throughout the industry, the acquisition time used in SUV calculation may be any of the acquisition times presented in the DICOM data. It is equally important to note that SUV is affected by a number of physiological factors which cause variability. Taking these two factors into account, SUV can be thought of as a simplified measure of radiopharmaceutical uptake which has a complementary rather than directive role in the assessment, treatment and staging of disease.



In compliance with Council Directive 93/42/EEC.

Manufactured by:

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Oxford

OX1 1BY

United Kingdom

Date of manufacture: March 2012

Getting Started

Launching the application

This launch instruction assumes that XD3 will be launched via the Mirada Application Launcher (data browser) software.

From the desktop of your workstation, double click on the gray Application Launcher icon.



Application Launcher

See **Application Launcher** online help for comprehensive user documentation. Application Launcher help is accessed by pressing **F1**, or selecting **Help** from the menu in the Application Launcher screen.

Once the application is launched, you will see a screen with available patient data listed. The data may be arranged:



Patient-study-series view



Study-series view



Series view

Expanded:



Expand the whole tree

Sorted:



Sort the selected column in descending order

And grouped by Study or Patient via the drop down menu.

Select the appropriate datasets by clicking left and dragging to include study/series data arranged in order, or use **Ctrl** and click the left mouse button to select individual datasets.

If XD3 is launched with data from more than one patient, the system will display a warning to the user and allow the option to confirm or cancel the launch.

File Menu

From the **File** Menu you may select from a series of options for importing patient data into the application or exporting files from the application. These options include **Manual Import**, **Folder Search/Import**, **DICOM Query/Retrieve**, and **DICOM Export**.

Data Menu

From the Data menu you may select:

- **Refresh** to update the Application Launcher database if series or studies have been imported or deleted. You can also use the keyboard shortcut **Ctrl + R**. Note that the Application Launcher refreshes automatically every 5 seconds.
- **Delete** datasets by selecting the patient, series or study you wish to delete by clicking left with the mouse to select the data. You can also use the keyboard shortcut **Ctrl + D**.

View Menu

You may select your preference for data arrangement on the Application Launcher screen. This is an alternative to the icons showing the views seen at the beginning of the Application Launcher section of this document.

Administration Menu

From the Administration menu you can:

- Change and manage database information
- Change and manage logging
- View logs
- Configure the system and set favorites
- Upgrade your license

NOTE: These settings are generally set by your systems administrator or by the installer when the software was installed. Most users do not need to change any of these settings. With the exception of setting your Favorites, it is strongly recommended not to change these settings unless advised to do so by customer support or your systems administrator.

Help Menu

This allows you to access the online Help. Help may also be accessed by pressing the **F1** key. The **About** selection gives pertinent information about the Application Launcher, including the version and copyright information.

Data Supported

Supported Image Modalities

The following data types are supported:

- CT
- MR
- PET
- SPECT/NM

Supported Image Types

The following image types are supported:

- Gated CT, NM, PET
- Multi-sequence MR
- Multi-phase CT

Supported Non-Image Data Types

The following non-image types are supported:

- RTSS

Supported Data Types

The following data types are supported:

Uncompressed:

- Explicit Big Endian
- Implicit Little Endian
- Explicit Little Endian

Compressed:

- Lossless JPEG First Order
- Lossless JPEG
- Deflated
- Lossy JPEG Baseline
- Lossy JPEG Extended
- Lossless JPEG 2000
- Lossless or Lossy JPEG 2000

NOTE: The XD3 DICOM Conformance Statement contains a detailed description of supported modalities and data types.



Unsupported modalities, data or image types may cause the software to function incorrectly, to return invalid results or to reject the data if an attempt is made to load them into the software. Attempt to load invalid data along with valid data may cause both sets of data to be rejected by the software.



Lossy compressed data, by design will reduce image quality. This may impact the ability to view images with the same accuracy and detail as with non-lossy data. All loaded lossy data is labeled as such in the viewing window.



Different interpolation methods may be used by XD3 and TPS systems when displaying contours. This means that when viewing findings in the acquisition orientation, they may appear visually different between systems. It is recommended that screenshots of loaded structures be taken in the acquisition view and compared to the same structures as displayed on the TPS to ensure that the imported structures are accurately represented in XD3.



Many data roles can load multiple volumes so long as they share a common frame of reference. Once loaded, XD3 will attempt to sort the volumes into a logical order. For gated data, this will be in a temporal order. Multiple reconstructions of the same raw data can also be loaded, however in such use cases it may not be possible to consistently order the volumes. While the application is not designed to support multiple reconstructions of the same data for PET and SPECT (such as FBP and TOF), it is possible to load these reconstructions simultaneously into the same data role. In this case it is not possible to guarantee that the same order is maintained over multiple timepoints. The user must check within the Data Management screen to ensure that the same reconstructions have been assigned to the anchor role.

Review Modes

Review modes are used to create a simplify the steps involved in matching the XD3 application to a particular task such as deformable fusion for multi-modal contouring or using an atlas for automatic contouring. Functionality, the number of supported data sets, layouts, defaults, etc. are customized to each particular Review Mode. For instance, pressing F5 'Auto Deformable' does something different depending on whether you are in General Oncology or MR/PET/CT review mode..

Review Modes are accessed from the icons on the right side of the **Application Launcher** screen or from the 'Select a review mode' drop-down menu on the **Data Configuration** screen.

When selecting data and launching a review mode, the XD3 application window may be displayed without any further user interaction. If certain conditions are present, the data configuration screen is displayed so the data assignments can be reviewed or modified manually. The following are those conditions:

- The system is not launched with a specified Review Mode
- The automatic data assignment leaves some data unassigned
- There is a different collection of data available for each time point (e.g. CT and Dose in one time point, and only a CT in another time point).

Holding down the **Ctrl** key and clicking any review mode icon will force display of the data configuration screen.

The following **Available Review Modes** section of this document lists all Review Modes and a description of each.

Available Review Modes

XD3

This is a generic way to launch XD3 which displays the data configuration screen allowing the review mode to be selected manually from the drop down menu and the data assignments to be confirmed or modified manually.

General Fusion

This review mode supports one time point and allows the registration of up to three datasets. One dataset is designated the source and the other dataset(s) targets. The targets are registered to the common source.

General Oncology Review

This review mode is designed to allow you to review one or more time points of PET/CT or SPECT/CT data. An MR may replace one or more of the CTs. This review mode supports multi sequence MR and multi-phase CT.

MR/PET/CT

This review mode is designed to allow you to load multiple sequences of MR data along with PET and CT for review. This review mode supports multiple time points.

Nuclear Medicine Review This review mode allows you to load planar NM images as well as SPECT or SPECT/CT volumes for multiple time points.

PET Review

This review mode is designed for follow-up PET reviews. It supports PET images only (with optional NAC reconstructions).

PET/CT Head and Neck Review

This review mode allows you to read data including WB plus additional regional scans in a meaningful way with respect to the layouts and registrations performed.

PET/CT Melanoma Review

This review mode allows you to load a WB PET/CT and a PET/CT of the legs. NACs may also be loaded as they are particularly important for these cases. Single or multi time-point review is supported

PET/CT Whole Body Review

This review mode is designed for review of one or more time points of PET/CT. Optical Flow (CT-CT registration) is performed and datasets are labeled as PET and CT.

Single Volume Review

This review mode is available for quick review of a single dataset. You may choose a single PET, CT, MR or SPECT dataset for viewing and quantification.

Review Mode Preferences

For each review mode there are several user preferences which may be selected via the **Tools -> Options** menu on the Review Modes tab.

- **Automatic registration scheme:** this may be selected from the dropdown menu at the top of the window. It is the registration that is performed upon data load into the application.
- **Default report template:** this may be selected from the dropdown menu, and may be a Mirada provided report template or a user-defined custom template.
- **Layouts:** You may place a tick in the box next to any layout that you would like to have available in a given review mode. Each user (per login) may also identify five favorite layouts which will appear as icons in the upper left on the screen at the top of the Toolbox. Any layout may also be set to a hotkey by double-clicking left in the Hotkey column until the cell turns yellow and then typing the keystroke of the desired hotkey. If a hotkey is already in use, a dialogue will appear alerting you that it is already in use by another function.
- **Window Defaults:** this allows you to choose the default layouts for your review mode, and others to use if the default selection does not support the data loaded. Window 1, Window 2 and Window 3 correlate to multiple monitors.
- **Colormap Defaults:** this allows you to set default colormaps for your base and overlay images in fused views.

NOTE: Changes made on this screen will be applied upon the next launch of the application

Data configuration screen

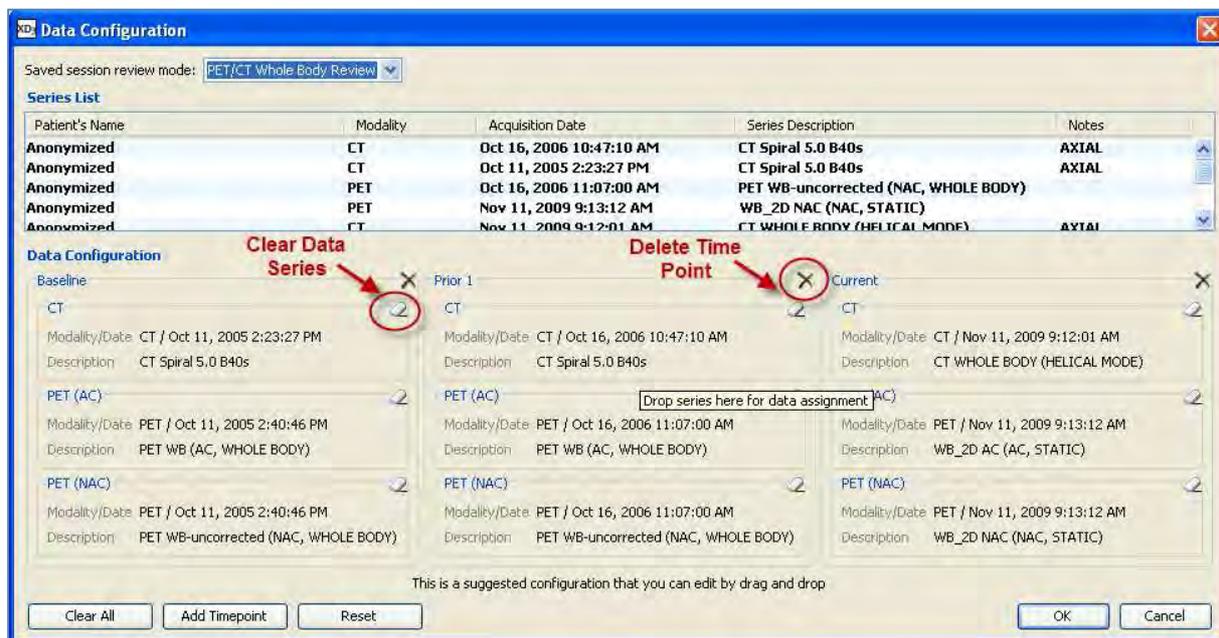
The data configuration screen allows you to review and/or manually select how the datasets for each time point are configured and loaded into the software for viewing and/or manipulation. This screen will appear automatically if:

- The system is not launched with a specified Review Mode
- The automatic data assignment leaves some data unassigned
- There is a different collection of data available for each time point (e.g. CT and PET in one time point, and only a PET in another time point).

The **Data Configuration** screen may also be displayed manually by pressing the **Ctrl** button and clicking left on the appropriate **Review Mode** in the Application Launcher screen.

You may change your selection of Review Mode by using the drop down menu at the top of the screen.

The files available for review are listed near the top of the window in the Series List. Each series is placed in the appropriate position as shown in the **PET/CT Whole Body Review** mode example below:



If multiple time points are loaded, the first or oldest dataset is loaded into Baseline, Prior studies are loaded in chronological order and the current study is loaded into Current position. Use the eraser tool to remove any dataset from its pre-assigned position. Drag and drop datasets from the Series List to the appropriate position in the Data Configuration grid. Using the buttons in the lower left of the window, you may **Clear All** assignments to start over, **Add Timepoint** to include another study, or select **Reset** to return to the original configuration. Continue until you are satisfied with the placement of data and click 'OK'.

Certain assignments are mandatory and this varies between review modes. Generally it is the Anatomical role that is required. If you select the 'OK' button without these assignments populated, a warning will be displayed which will detail the mandatory assignments.

This opens the image workspace with images displayed in the default layout.

Data QC

Data QC Feature

The **Data QC** tool is provided to allow you to view attributes from datasets loaded into the application for review. Generic attributes that apply to all modalities or those such as acquisition date will be available for display only. Several attributes that can be validated such as slice thickness, kVP, X-ray tube current and several others may be displayed for the CT data. Likewise, software version, injected dose, delay time, half-life, patient height, patient weight and additional attributes are available for validation on the PET data.

If you wish, you may perform validation of this data based on limits that you define. For example, you may want to be warned if the delay time variance from the time of injection to time of scan between time points is greater than a certain amount of time. Remember that attributes are for display only and cannot be validated. The Data QC screen will show you the attributes and flag any that are outside the tolerance levels you have set. Additionally, the Data QC screen may be included in a custom report. You may choose which attributes are visible and whether you would like to be prompted to display the Data QC screen on startup if there are validation warnings.

Configuring Data QC

The **Data QC** screen may be displayed via the Window menu, on the toolbar layout selector, from the on-screen layout selector (Ctrl + Tab) or via a hotkey set in **Tools -> Options** on the User Interface Tab. See User Preferences section for detail on setting hotkeys.

See **User Preferences** section for detailed instruction on setting up the Data QC items that you wish to have visible on your Data QC screen and which attributes you wish to validate when data are loaded.

When loading gated data, multi-phase CT or multi-sequence MR, variance checks are carried out between the different phases or sequences and the results reported.

There are some fields for PET data whose values come from the Quantification Options dialog rather than the underlying data. These fields are Delay Time, Half Life, Height, Injected Dose, Sex and Weight. These fields are editable by the user in the Quantification Options dialog and any changes made are reflected live in the Data QC screen.

NOTE: Validation requires an Advanced license. Attributes can be viewed with a Standard or Advanced license.

NOTE: The way that validation is performed varies slightly between the type of data being validated. Textual data is validated against the input validation values, and is not case sensitive. If this textual data is not present for data being validated within a time point, then the cross time point variance check will also fail and be reported as such.

Numeric data is validated against the minimum, maximum and variance (i.e. the range) values entered. The values entered are checked inclusively, so if a variance of 10 is entered and the variance is 10, it will pass the check. If this numeric data is not present for data being validated within a time point, then the cross time point variance check will pass and be reported as such. The within time point check will fail.

Item	Baseline	Current	Variance
Functional (AC)			
Manufacturer	CPS	CPS	
Manufacturer Model Name	1023	1023	
Software Version			
Protocol			
Series Description	PET WB	PET WB	
Slice Thickness	3.4 mm	3.4 mm	
Row Spacing	5.307 mm	5.307 mm	
Column Spacing	5.307 mm	5.307 mm	
Radio pharmaceutical Name			
Number of Slices	226	226	
Injected Dose	610.13 Mbq	471.38 Mbq	×
Delay Time	00:51:55	00:53:44	✓
Half life	1 hours 49 mins 46.2 s	1 hours 49 mins 46.2 s	✓
Weight	125 lb 1.797 oz	125 lb 1.797 oz	✓
Height			
Reconstruction Method	OSEM 218s	OSEM 218s	

Warnings were found based on your settings ☹️



The Data QC validation is performed on a per user basis using the validation criteria specified by each user. The validation does not perform any image quality or registration checks.

This feature requires an advanced license to perform and report validation results. Care should be taken when utilizing the floating license deployment and using this feature, as launching with a Standard license after an Advanced license will not perform validation on the data as may be expected.

It should be noted that not all fields are validated, some are for display only. These fields cannot be set to validate the contents when specifying which fields to validate.

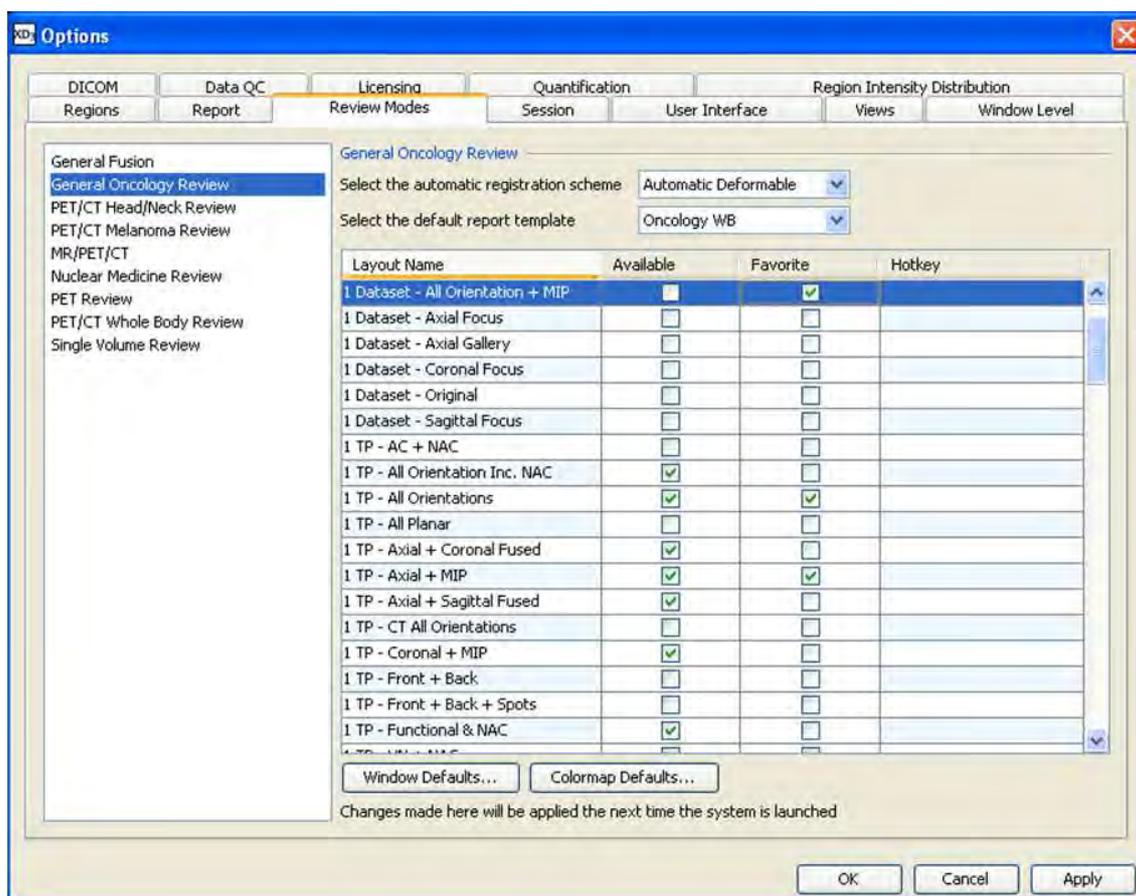
Layouts

Provided Layouts

Layouts are the hanging protocols used to display images. Each Review Mode contains a selection of available layouts. These layouts may be accessed either from the dropdown menu in the upper right corner of the image window, via the **Window** menu, or by using **Ctrl** and **Tab** keys simultaneously to bring up an on-screen layout selection menu (see below). When using **Ctrl** and **Tab**, hold down on the **Ctrl** key and toggle the **Tab** key to scroll through the on-screen menu of layouts. Layouts may also be selected by clicking on them in the on-screen layout selection window.

Any layout may be assigned to a hotkey of your choice via **Tools -> Options** menu and under the Review Modes tab. See User Preferences section for detailed instruction on creating hotkeys for your layouts. In addition, each user may choose five favorite layouts for display and access in the Favorite Layouts area in the Toolbox. Favorites may be defined on the Review Modes tab in Preferences via the **Tools -> Options** menu as shown below.

Please take caution when making layouts available in a review mode for which they were not created as the data will likely not be displayed as expected.

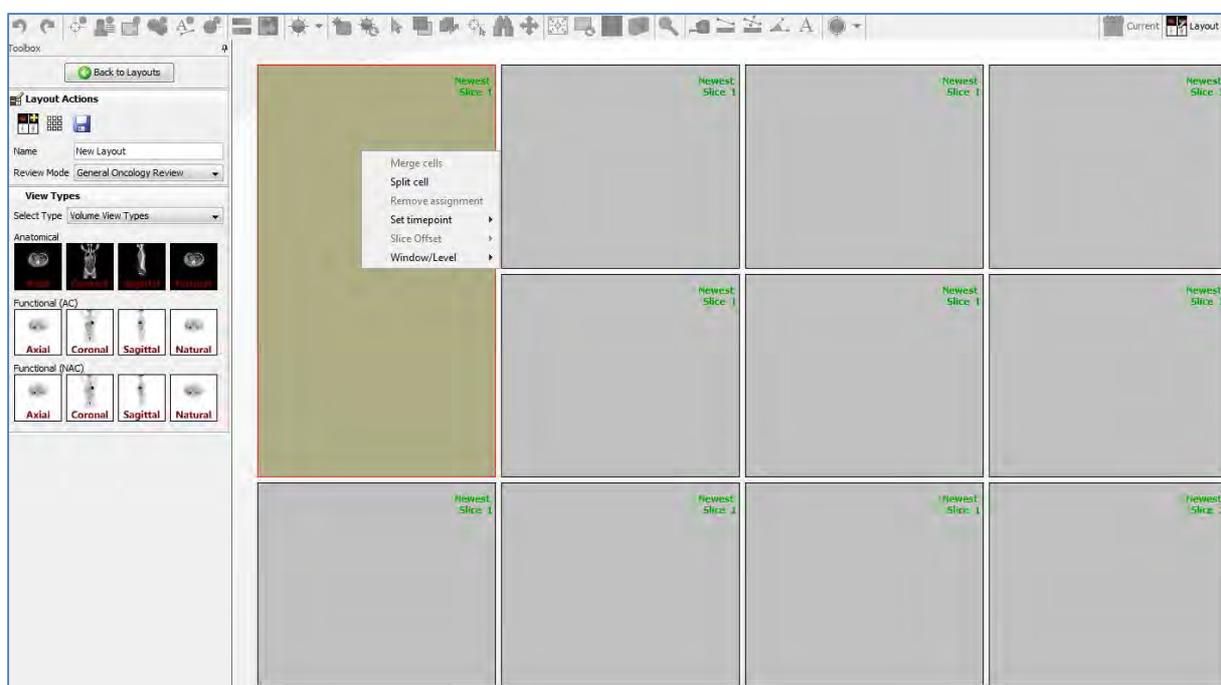


Data QC, Registration Manager, Findings Table, Reportt Screen, and Secondary Capture will always be available in the selection of layouts regardless of the Review Mode.

Custom Layouts

Custom layouts may be created from the **Tools** menu by selecting **Layout Editor**. The New Layout window will appear. Provide the name you wish to assign to the new layout, select the Review Mode for which you want the layout to be available, and select the number of time points you would like it to support. Select **Continue**.

Next select the grid size that you would like to use in creating the layout by selecting the  icon from the Layout Actions are of the Toolbox. Click and drag your mouse to highlight the number of rows and columns that you would like to include. Each square represents an image view and is highlighted in orange to identify the number and arrangement you would like to see in your layout. By clicking left in the lower right square of your highlighted grid, that array is saved as your layout grid. You may merge adjacent cells by clicking left on the cells you wish to merge and then click right to select **Merge Cells** from the dropdown menu. For example, you may wish to display a MIP using two or three merged cells.



If you merge cells and then decide you do not want them merged, click the right mouse button within that cell and select **Split Cell** from the dropdown menu.

View Types

Select the type of images you want to include in your layout by selecting from the drop down menu. The choices are:

- **Volume View Types** – for axial, coronal, sagittal and acquisition orientation images from PET/CT/MR/SPECT datasets
- **Gallery View Types**

- **Info Views** – these views contain textual overlays containing patient information only; they may be added to the beginning of a gallery view or any image view where images may be too small to show the full patient information overlay
- **MIP View Types**
- **2D Slice and Planar Views** - for displaying NM planar data

NOTE: Acquisition orientation views allow data to be viewed in the same orientation it was acquired. For example, an off-axis MR scan can be scrolled through without having to view partial slices created from post-acquisition reorientation to axial.

Each cell within the layout has a context menu that can be accessed by clicking the right mouse button. This menu allows the following to be set:

- **Time point offset** – Defines the time point to display for a multi-time point layout.
- **Window/Level** – Select a window/level preset to apply to the base layer of the dataset loaded into the cell.
- **Slice Offset** – This is only available for 2D Slice and Planar Views. This is used to display a particular image from a multi frame series. For instance, use Slice Offset to display the second image in a sequence of spot images.
- **Dataset Offset** – This is useful for gated CT or PET, multi-phase or multi-sequence MR or dynamic SPECT. This allows the initial dataset within the group to be set. For instance, the third volume in a multi-sequence MR series.

Continue defining your layout by dragging and dropping the image sets on the left into the desired positions on your new layout grid. If more than one image view is dragged and dropped into the same cell, a fused view will be created. The layers will be created in the order that they are dropped on the cell. Once all positions are filled, click **Save Layout**. The layout editor will not allow you to save a layout with empty cells.

You may change the name you have given the layout prior to saving it by retyping in the Layout name field. Also, use the drop down menu to preview the layout for all Review Modes for which the layout will be available.

Layouts may be made available for various Review Modes, selected as Favorites, or set as Hotkeys in Review Modes tab in **Preferences** found by selecting **Tools -> Options** from the menu.

It is also possible to create layouts that do not match the currently loaded data in the application. In this case, the layouts will not be available for selection until the data in the application matches that defined by the layout.

NOTE: Certain layouts such as three way fused views require an Advanced license. These layouts can be created with the Standard license, but will not be available for selection.



Fused images are displayed within system provided layouts and can be included in user defined layouts. The modality, quantification information, time point and dataset designation within the current review mode are displayed for each layer in the fused view to allow identification of each layer.



When a layout image segment contains multiple planar NM Images from one or more series, the only way to distinguish to which planar series an image pertains is by the series description text label on the image segment.



Gallery images do not individually contain patient identification information due to the potential limited size of the image segments. To identify to which images the gallery pertains, system provided gallery views contain a patient information view segment.

The layout editor allows patient information views to be added to all user defined layouts and should be used when creating Gallery views.

Layout Selection and Time Points

System provided layout selection

Each system created layout displays a fixed number of time points. The actual time points displayed in the layout can be modified. For example, with three time points loaded, when selected for the first time, a two time point layout may have the Prior 1 and Current time points displayed. This can be changed to Baseline and Current if so desired. When another system provided two time point layout is selected, this Baseline and Current time point selection is maintained in the newly selected layout.

In summary, the time points displayed are remembered when switching to system provided layouts with the same number of layouts. The time point selection is not remembered across application windows.

Custom layout selection

As with system provided layouts, each custom layout is defined with a fixed number of time points. The initial time points to be displayed in the layout are set when creating the layout (newest, oldest etc). When switching to a custom layout, the time point selection is reset unless the time points defined in the current layout and the one to switch are identical, in which case the time point selection will be maintained. A two time point layout created with **oldest** and **newest** time points is not considered identical to a two time point layout created with **newest** and **newest-1**, as these will resolve to different time points, depending on the number of time points loaded.

As with system provided layouts, the time point selection is not remembered across application windows for custom layouts.

Image Window

Active Text

In the image window there is information about the patient, study and images displayed. Some of the text is for information only and other is 'active text' that may be used to adjust the image. The default colors of the text are blue and black/white. The black/white colored text is inactive and represents information such as patient name, sex, age, birth date, identification number, hospital or facility name, the currently displayed field-of-view, series name and date obtained from the DICOM header.

The blue colored text is the active text. When the mouse pointer hovers over any setting that may be adjusted in this manner, the text becomes underlined. Click on the text to display the available control.

Available Active Text Controls

In the image window there are active text controls for:

- Scale
- Window and Level
- Quantification Options (SUV)
- Slice Index

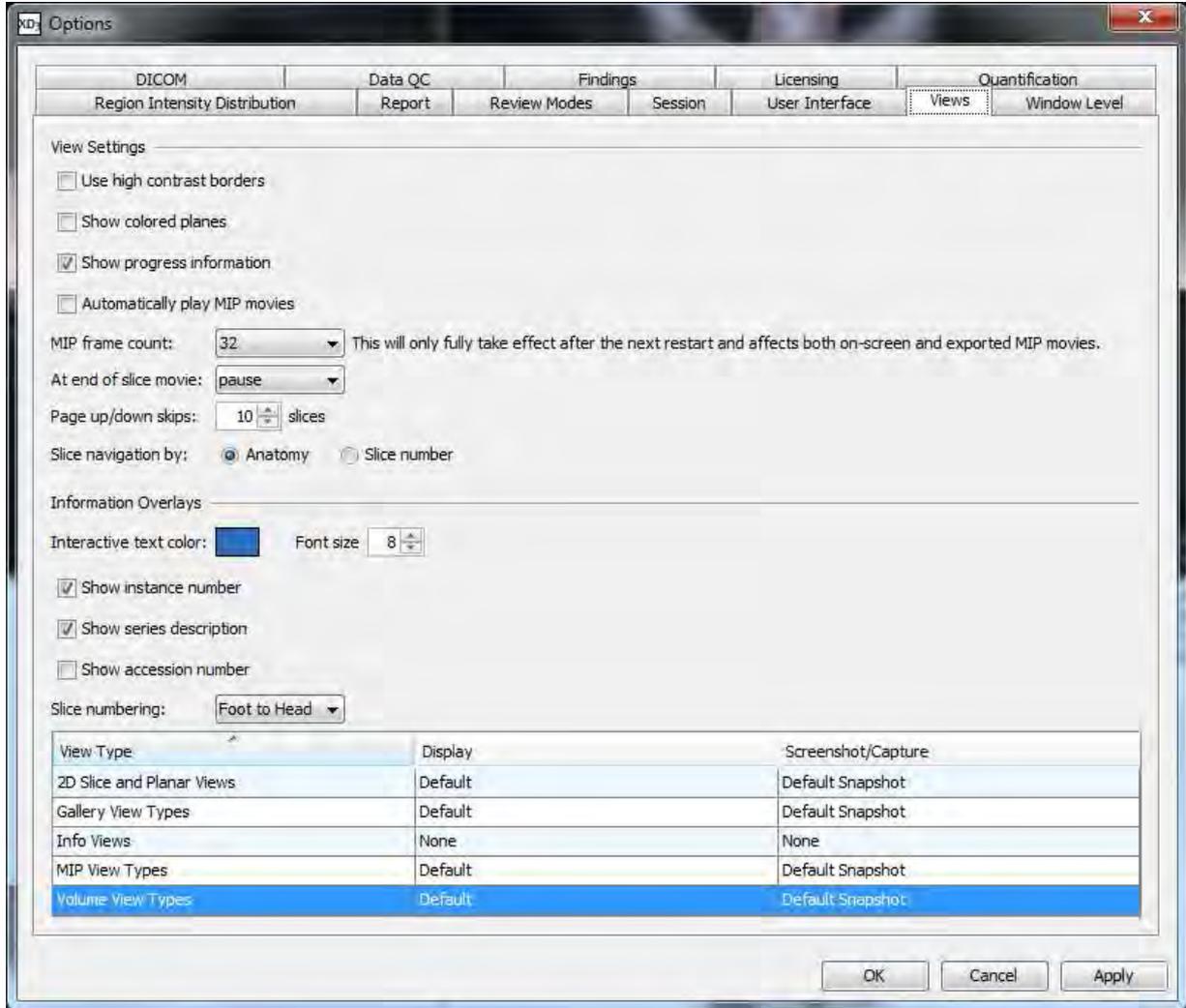
Custom color and font size for the on screen text may be set in user Preferences via the **Tools -> Options** menu on the **Views** tab. Click on the Interactive text color shown to display the color palette and select a new color. Font size may be changed by using the up and down arrows or double-clicking and entering the desired size.

Image View Labels

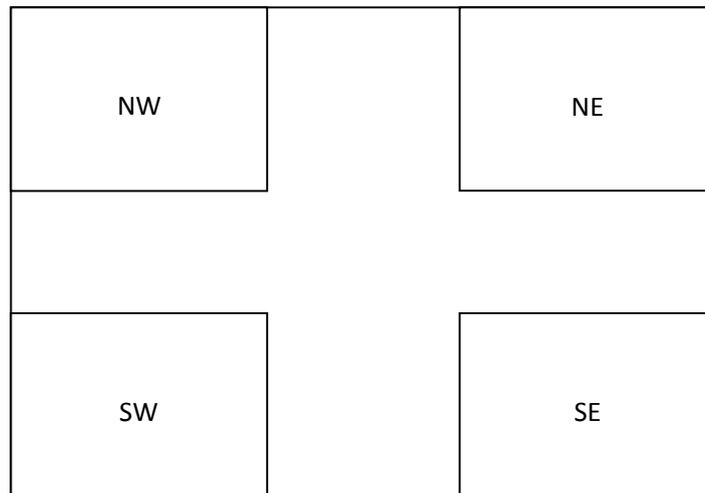
In XD3 an image view can be customized to display only the information the user wants. Each view has two configurations: the information to display on-screen and the information to imprint into the view when a screen capture is taken of that view.

There are five view configurations available in XD3: Default, Default Snapshot, Patient Only, None and Slice Number Only. Each of the different view types (see View Types) can have a different configuration selected for on-screen display and for when a screen capture is taken.

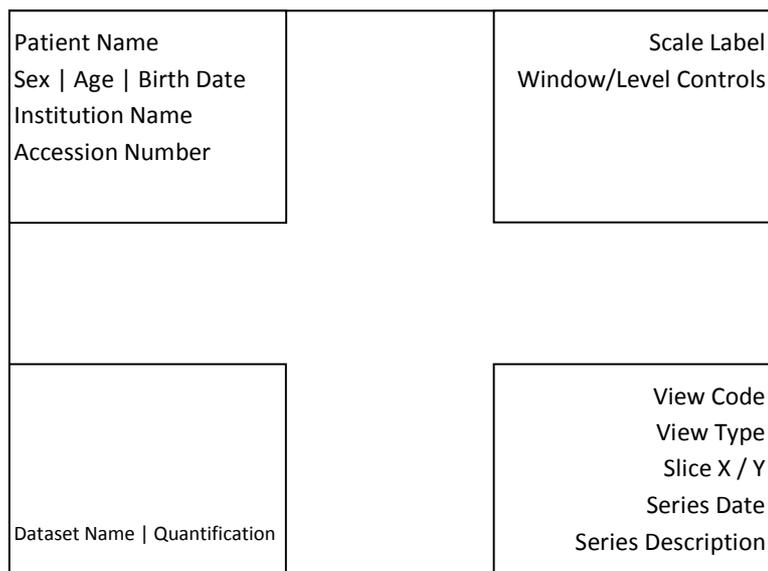
The selected configurations can be changed as a user preference via the Tools -> Options menu on the **Views** tab.



The different configurations control which information is visible in the four corners of the views.



Default



Patient Name, Patient Sex, Patient Age, Patient Birth Date, Institution Name, Accession Number, View Code, View Type, Series Date and Series Description come from the underlying DICOM data that is being displayed as the bottom layer in the view.

Scale label is the current zoom factor being applied. The window/level controls are the active text controls that allow the user to modify the displayed window/level.

Dataset Name is the review mode-specific name of the data role to which the data has been assigned. E.g. "Anatomical" or "Source". The Quantification label is the value at the crosshair location displayed in the appropriate units.

View Code is only applicable to NM data and comes from the NM Detector Information Sequence in the NM Detector Module. The View Type displays something appropriate for the type of view. For instance, this could be Axial, Coronal, Sagittal, MPR, Original, MIP, *et cetera*.

Default Snapshot

This is currently the same as the Default configuration.

Patient Only

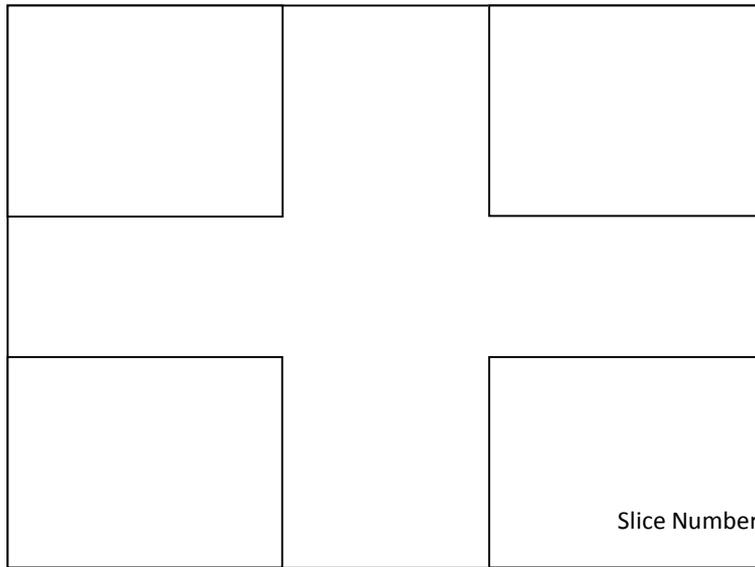
Patient Name Sex Age Birth Date Institution Name Accession Number		

Patient Name, Patient Sex, Patient Age, Patient Birth Date, Institution Name and Accession Number come from the underlying DICOM data that is being displayed as the bottom layer in the view.

None

No information is displayed in any part of the view

Slice Number Only



Slice number is a single number relating to slice number of the crosshair position in the orientation of the view.

Toolbox

Toolbox

This bar on the left side of the image window is used to display a number of control panels. Some of these are open by default and some are disabled. The open/collapsed contents can vary per monitor (i.e. application window) and per task.

Showing or Hiding the Toolbox



The toolbox may be hidden from display, thus allowing additional space for images by selecting the button on the toolbar or by selecting 'Show Toolbar' from the View menu. This function may be set to a hotkey. This setting applies to all windows as the toolbox may not be removed from just one window.

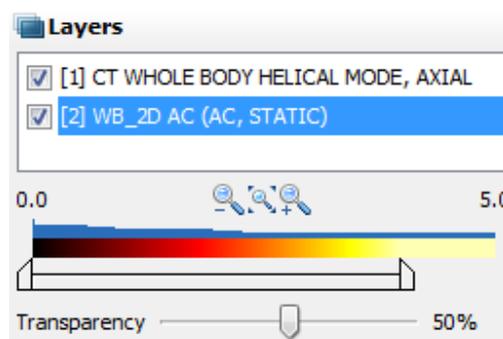
Favorite Layouts

Each user may select up to five favorite layouts to be included in the display at the top of the Toolbox for quick access. Those favorites can be set up in **Options** on the **Review Modes** tab, by selecting **Tools -> Options** from the menu. Click to place a check mark in the box next to any available layout to select as a favorite. These or other layouts may be given hotkeys to allow you to switch quickly between different layouts. If a hotkey has been assigned to any of the favorite layouts, when you hover your mouse over the layout the hotkey will be displayed.

The layouts that you have chosen as favorites will be available for selection once the application has been restarted.

Layers

The **Layers** Panel in the **Toolbox** displays a row for each dataset displayed in the selected view. Next to each layer is a box to check to include or remove that dataset from the current image view. By highlighting a particular layer (that row is highlighted in blue), you choose the layer for which controls are active. For example, when using the Transparency Tool, the system adjusts the transparency of the selected layer within the current image view.



In the example above, both CT and PET (AC) datasets are visible in the view, and the controls are active for the PET (AC) dataset .

The window/level slider control resides in this area of the toolbox as well, and adjusts the window and level of the selected layer. The units of the control will be appropriate for the modality of the layer. If you select the adjust transparency control, the system displays the Transparency slider in the **Layers** panel.

Pressing the 'O' key on the keyboard makes the overlay invisible if it is currently visible or it will make it visible if it is currently invisible. The removal of the overlay applies to all fused views within the application. All **Layers** within the view other than the base layer are removed.

Findings

The findings include regions, measurement, and annotations created on an image. You may modify the created findings' names, colors and viewed statistics by double-clicking the finding name. When the mouse hovers over any ROI or Ruler in this panel, the tooltip will display statistics or measurements. This feature is most useful with ROIs if a region has been projected.

Role	Dataset	Min	Max	Mean	Median	RMS	σ	Volume	Units
Baseline PET (AC) PET WB (AC, WHOLE BODY)	PET WB (AC, WHOLE BODY)	2.5	5.0	3.3	3.1	3.3	0.6	3.2	SUV BW
Baseline CT	CT Spiral 5.0 B40s AXIAL	-995.0	208.0	20.2	47.0	167.2	166.0	2.8	HU
Baseline PET (NAC)	PET WB-uncorrected (NAC, WHOLE BODY)	-	-	-	-	-	-	-	US
Prior 1 PET (AC) PET WB (AC, WHOLE BODY)	PET WB (AC, WHOLE BODY)	2.5	5.8	3.5	3.3	3.6	0.8	6.1	SUV BW
Prior 1 CT	CT Spiral 5.0 B40s AXIAL	-1016.0	182.0	-85.2	28.0	313.1	301.3	6.1	HU
Current PET (AC) PET WB (AC, WHOLE BODY)	PET WB (AC, WHOLE BODY)	2.5	10.5	4.4	3.8	4.8	1.9	12.7	SUV BW
Current CT	CT Spiral 5.0 B40s AXIAL	-1022.0	194.0	3.5	48.0	214.7	214.7	12.2	HU

The Findings panel toolbar contains the following options:

- Delete the selected finding
- Go To the selected finding
- Show or hide the selected findings
- Display the Findings Table
- Link the selected findings
- Show Dose-Volume Histogram

 Projects the selected finding to all time points

 Projects the selected finding within its time point

Click the right mouse button on any selected finding to:

- **Delete**
 This action is also available from the toolbar.
- **Copy Statistics to Clipboard**
- **Copy Statistics to the Image Gallery**
- **Display Findings Graph**
 This action is also available from the toolbar.
- **Go To** the selected finding.
 This action is also available from the toolbar.
- **Go to hottest voxel**



If the **Go To Hottest Voxel** tool is used on a region with more than one voxel with the highest intensity value, then only one of these voxels will be identified.

- **Create a ruler from the region**
- **Toggle to indicate lymph node**
- **Unlink**
- **Link Findings:** There are two types of findings: rulers and regions. Rulers include uni-rulers, bi-rulers and angles (annotations are not classed as findings). Regions include isocontour regions (with threshold), filled regions, 2D rectangles, 2D ellipses and regions painted with the freehand paint tools. Ruler findings can always be linked to other ruler types. They can also always be linked to region types. Region structures can be linked to ruler findings but are restricted as to which other regions they can be linked. A region can only be linked to another region that was defined on the same data role. E.g. a region defined on the Anatomical data role in General Oncology Review can only be linked to another region defined on the Anatomical role and not to one defined on the Functional role. This is further restricted to only being able to be linked to another region defined on the same role but not on the same dataset. E.g. a region defined on gate 1 of a gated CT assigned to the Anatomical role can be linked to a region defined on gate 2 of the same gated CT, but not to another region defined on the same gate 1. This restriction does not apply across time points. A region on gate 1 of a CT on the baseline time point can be linked to a region defined on gate 1 of a CT on the current time point.
 This action is also available from the toolbar.
- **Show/Hide regions**
 This action is also available from the toolbar.

- **Project to all by type** : with a region selected, this option will propagate a finding to the equivalent dataset designation in all time points by recreating the region in each time point using the means by which the region was originally created (i.e. absolute threshold, % max threshold). If the region exists in multiple time points, then the value will be taken from the selected time point.
 This action is also available from the toolbar.
- **Project to all by volume**: with a region selected, this option will project the region to the equivalent datasets designations in all time points by maintaining the volume of the original region. If the region exists in multiple time points, the volume value will be taken from the selected time point.
- **Project to all within volume by type**: with a region selected, this option will project the region to all datasets from the same frame of reference (i.e. bins of a gated dataset, phases of a multi-phase CT or sequences of multi-sequence MR) and create shadows on each of them. If the region exists in multiple datasets, then the absolute threshold value is taken from the selected dataset.
 This action is also available from the toolbar.
- **Transform to all**: with a region selected, the region will be transformed to the equivalent dataset designation in all time points using the existing registration to transform the ROI shape. If the region exists in multiple time points, then the selected time point will be propagated.
- **Options ...** (displays the Findings tab in Tools -> Options)

There are additional options for projecting and transforming findings which are turned off in the menu by default, but may be enabled via Tools-> Options on the Findings tab. These additional tools are:

- **Project to remaining by type**: with a region selected, this option will propagate the selected region to the equivalent dataset designation in time points where the region does not already exist by recreating the region in each of the time points using the means by which the region was originally created (i.e. absolute threshold, % maximum threshold)
- **Project to Remaining by volume**: with a region selected, this option will propagate the region to the equivalent dataset designation in time points where the region does not already exist by maintaining the volume of the propagated region. If the region exists in multiple time points, then the volume value will be taken from the selected time point
- **Transform to remaining**: with a region selected, this option will propagate the region to the equivalent dataset designation in all time points that do not contain the region. The existing registration will be used to transform the ROI shape. If the region exists in multiple time points, then the selected time point will be propagated.

- **Project to remaining within timepoint by type:** with a region selected, this option will project the region to all datasets from the same frame of reference (i.e. bins of a gated dataset, phases of a multi-phase CT or sequences of multi-sequence MR) where the region is not currently defined and create shadows on all datasets to which the role on which the region was defined are linked. If the regions exists in multiple datasets, the absolute/threshold value will be taken from the selected dataset.
- **Transform to all within timepoint:** with a region selected, this option propagates the region to all datasets within the same frame of reference (i.e. bins of a gated dataset, phases of a multi-phase CT or sequences of multi-sequence MR) using the existing registration to transform the ROI shape. If the region exists in multiple datasets within the same frame of reference, the selected region will be propagated.
- **Transform to remaining within timepoint:** with a region selected, this option projects the region to the other datasets within the data designation (same frame of reference) that do not contain the region, using the existing registration to transform the ROI shape. If the region exists in multiple datasets within the designation, the selected region will be propagated.



Regions resulting from performing the **Transform to All**, **Transform to Remaining**, **Transform to All within Timepoint** and **Transform to Remaining within Timepoint** actions are highly dependent on the quality of the registration that exists between the dataset on which the source region exists and all the datasets to which the region is to be transformed. It is recommended that quality checks be performed within the Registration Manager screen on the accuracy of the registrations prior to performing a region transformation action.

Threshold Settings

The threshold of the selected iso-contour or seed point region may be adjusted using the slider or by typing in an absolute value or percentage of maximum. Select the region in the image window to view the threshold setting in the Toolbox.

Note that if you have a linked region in different time points, each time point can have a different threshold. Therefore, selecting the image sets the threshold slider to the correct value for the selected time point.

The threshold used when projecting findings is taken from the time point or dataset (when viewing gated data) that is selected in the image views for the region. For example, let's say you create a region on a Baseline study with a threshold of 3 SUV, and a Prior study with a 4 SUV threshold and then link the findings before projecting to unused by type. If the Prior image view is selected, a threshold region will be created on the current time point using 4 SUV. Likewise, if the Baseline study is selected when projecting, then it will create a threshold region on the Current study using 3 SUV.

Image Gallery

The Image Gallery houses any bookmarks, key images, snapshots or secondary captures that have been created during a reading session. The objects in the image gallery may be included in a report, exported as .BMP, .PNG, .JPEG or DICOM Secondary Capture. Note that the image gallery may be filtered by time point by selecting the desired time point from the drop down menu.

Upon double clicking a bookmarked image within the image gallery, the following will be restored:

- Layout
- Window/Level
- Zoom
- Crosshair position
- Selected dataset/Phase (gated data, multi-phase CT data, multi-sequence MR data)

If a session is restored that includes a DICOM secondary capture it will be displayed in the Image Gallery. You may choose that image and then select the 'Switch to Secondary Capture screen' icon () to view it.

Cine

Any displayed MIPS or other data with multiple gates, sequences or phases may be controlled from this area. Tools are present for playing the MIP, reversing the direction of the MIP cine, and pausing the MIP cine. The slider bar is available to adjust the speed. There are also tools in the MIP window that may be accessed by hovering over the blue shaded area at the bottom of the MIP window.

If you wish to have the MIP spinning upon load, you may set the preference in **Tools -> Options** on the **View** tab. Check the box next to 'Automatically play MIP cine'.

When gated data, multiple sequences of MR or multiple phases of CT are loaded, there is an option from the dropdown menu to select **Items** or **Slices**. Items refer to gate, sequence or phase depending on the data. Select **Items** to cine through the gates, sequences or phases, and select **Slices** to cine through the slices (or frames in a dynamic NM series)

The cine may also be controlled by turning on the navigation controls on the toolbar. These controls are displayed by default on MIP views.



The frames in a dynamic flow study are played at a uniform rate and not in real-time.

Setting Window and Level

Window Level Control Mode



Window and Level may be manually adjusted using the icon from the toolbar or click the right mouse button to access the context menu. The following describe the functionality:

- Dragging right increases the brightness (decreases level)
- Dragging left decreases the brightness (increases level)
- Dragging up increases the contrast (increases window width)
- Dragging down decreases the contrast (decreases window width)



Window Max tool changes the upper end of the window/level spectrum while the lower end is locked (i.e. For PET data, the lower value never goes below zero).



Normalize window and level tool allows you to click the left mouse button and drag the mouse to define an area on an image for which images are 'normalized'.



Reset window and level tool returns to the original window/level settings that were displayed on initial launch.

Window Level Active Text Control

You may adjust window and level by clicking on the interactive text on the image window. As the mouse pointer hovers over these settings, the blue text becomes underlined. Click on that text to display the dialog box to define and select presets.

You may set a custom color for the interactive text in **Tools->Options** on the **Views** tab.

Visualization dialog box

The visualization dialog opens for the study chosen as the active window. If the active window is a fused view, select the study for which you wish to set the visualization parameters from the list of available studies on the left. The study highlighted in blue is the selected study for which the settings will apply.

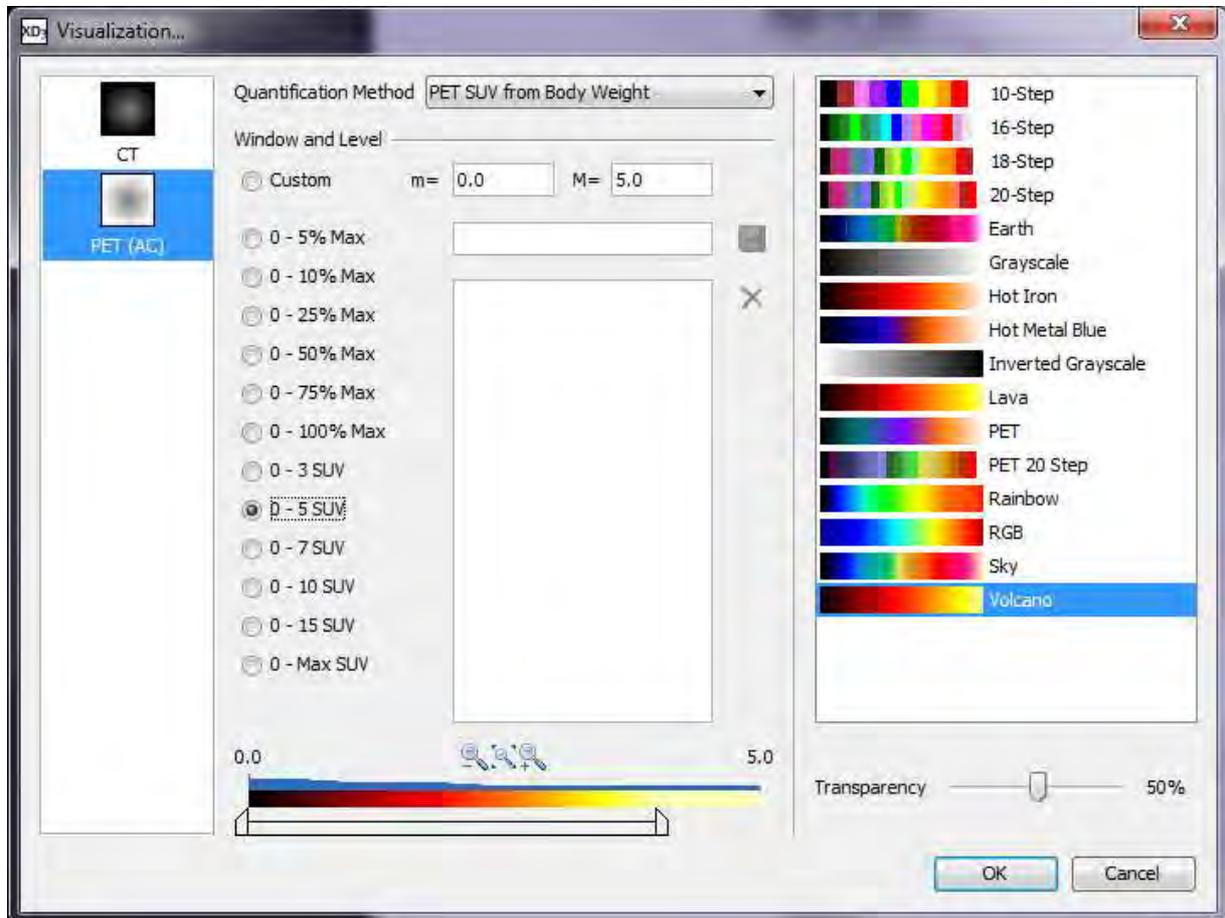
The system supplies a selection of preset values as radio buttons on the Visualization dialog.



Custom presets may be created by entering custom values, a new name and then selecting the **Save** icon.

Custom presets can be deleted by selecting them and then choosing the **X** button. For both PET and CT displays the default window and level settings applied upon launch may be overridden by ticking the box in the Window Level tab accessed from the **Tools -> Options** menu.

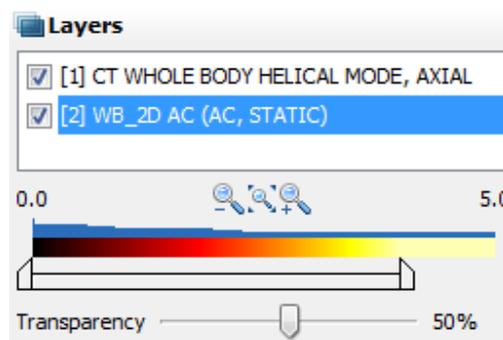
Window and level may also be set using the slider control at the bottom of the screen. The color map may be changed in this dialog box as well, along with transparency setting for fused views.



NOTE: Window/level settings may be assigned to shortcut keys via the Tools -> Options menu.

Window Level Slider Control

Window and level settings for all datasets may also be adjusted using the slider control in the Toolbox. This control is available for whatever layer is selected in the layers panel. The units and values that the slider displays match those currently selected via the Window and Level Settings.



Normalize Window Level



XD3 provides a tool to normalize the window and level settings by selecting an area of an image that becomes the baseline from which the window and level settings are determined. This action can be accessed from **Image -> Normalize Window and Level** from the menu. This tool may be assigned to a hotkey or added to the toolbar via **Tools -> Options** on the User Interface tab.

Use the left mouse button to click and then drag the mouse over the area to be used as baseline. Upon release of the left mouse button, the window and level changes instantly to reflect the baseline you have selected for normalization.

Reset Window Level



Use the Reset Window Level tool to return to the original settings. This tool may be selected from the toolbar or selected from the menu via **Image -> Reset Window/Level**.

This tool may be assigned to a hotkey via **Tools -> Options** on the User Interface tab.

The original setting is determined by the same criteria as used to set the window and level on application start as described below:

- If a window level preset applies to the layout it will be used.
- Otherwise, if a modality specific preset has been set to override the values in the data on loading that will be used.
- Otherwise, if window and level values are defined in the data, it uses the values in the data if they exist.
- Otherwise, the window and level will be set to 0 – 100%.

Regions of Interest

ROI Display

ROIs are displayed as smooth regions within a shaped bounding box such as an ellipsoid or cuboid that can itself be used to obtain simple quantification statistics (e.g. Maximum PET SUV) in some circumstances. Regions may be displayed as voxel masks by selecting Quantify -> Show Smooth Contours. This allows a user to see all voxels included in a region for region quantification purposes.

ROIs can be displayed differently within a time point depending on the review mode that is being used. One general rule is that they can only be displayed on registered datasets. Specifically, an ROI created on the CT can only be displayed on other data sets (e.g. the PET) if there is a meaningful registration between the two datasets. The datasets where shadowed regions are displayed can be modified via the Data Management Screen available from the Tools menu. This is particularly useful when viewing multiple gated datasets.

Note that it will only be possible to edit (i.e. adjust position and size) ROIs on the dataset that they were created, however, the ROI can still be selected and its threshold adjusted.

You may view and modify the PET quantification options by clicking on the SUV value in the image window (Quantification active text control). See **Active Text Control** section for more information.

Creating an ROI

ROIs may be created on any orthogonal image view using a variety of ROI tools from the **Quantify** menu or from the ROI drop-down menu on the toolbar. The tool you select to create a region will be remembered and that one will be displayed on the toolbar until another is selected. The other tools will still be available via the drop-down menu or may be added to the toolbar individually via the toolbar configuration on the user interface tab in **Tools -> Options**.

ROI Tools



Region With Absolute Threshold: Click the left mouse button and drag to create a region using absolute threshold value set in Contouring preferences.



Region with % of Max Threshold: Click the left mouse button and drag to create a region using % of maximum threshold value set in Contouring preferences. The threshold value is expressed as a percentage of the maximum value within the bounding box of the region.



Region: Click the left mouse button and drag to create an ROI with threshold set at minimum. Used to quickly find max SUV in an area of interest.



Ellipse Region: Click the left mouse button and drag ellipse to create a region on a single slice.

 **Rectangle Region:** Click the left mouse button and drag rectangle to create a region on a single slice.

 **Seedpoint Region:** Click the left mouse button anywhere in an area of interest to automatically generate an ROI based on a threshold value. The threshold may be adjusted using the Threshold Settings in the Toolbox on the left side of the screen. Use the slider for a manual adjustment or choose to use a percentage of maximum or a fixed value. A default threshold value may be set via **Tools -> Options** on the Regions tab.

 **CT Region Segmentation:** Click the left mouse button inside the lesion and drag the bounding sphere outside the lesion to automatically generate a 3D region.

 **Adaptive CT Segmentation:** Click the left mouse button inside a lesion on a CT volume and drag the bounding sphere outside the lesion to automatically create a 3D region.

 **Paint:** Use to define or edit an ROI by painting voxels in an orthogonal/MPR image view.

 **Freehand Region:** Click and drag to create a 2D region. Use paint and erase tools to edit.

NOTE: Any of the ROI tools may be assigned to a hotkey via Tools -> Options on the User Interface tab.

Editing an ROI

Once a region has been created it can be edited, using either the controls specific to that region or the paint brush tools. A region may only be edited on the dataset on which it was created (i.e. not on a dataset on which the region is mirrored). A region created on a fused view may be edited on either dataset.

Paint Brush Tools

 **Paint:** Use to define or edit an ROI by painting voxels in an orthogonal/MPR image view. The paint tool operates from within a region.

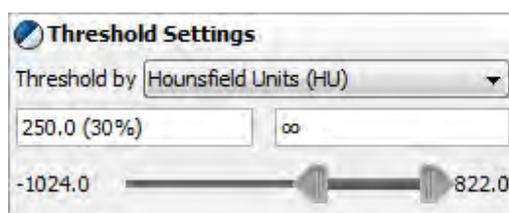
 **Erase:** Use to delete voxels from an ROI by moving the mouse over the region. The erase tool operates outside the region.

 **Freehand Region:** Click and drag to scribble a region on a single slice. Use paint and erase tools to edit.

To resize the ROI, select the ROI by clicking on it within the image views then dragging the handles from the desired corner. To move an ROI, drag the center of the region. Once edited via Paint or Edit, regions are no longer threshold regions and cannot be moved or resized.

Tool Settings

All of the ROI creating and editing tools have per-tool settings that are accessed from the toolbox. The **Region with Absolute Threshold**, **Region from % Max**, **Region**, **Ellipse** and **Rectangle Region** tools are all analogous and share the same settings. Each of these tools creates a region with different initial settings but each can be made to behave like any of the other types by adjusting the settings in the **Threshold Settings Panel**.



Threshold Settings Panel

The top drop-down allows the region type to be switched between thresholding by absolute values in the selected quantification method, and thresholding by percentage of the maximum value within the region bounding box. The two text fields allow entering the lower and upper threshold values. A value of ∞ signifies that the threshold is unbounded. The slider allows setting the threshold values directly. Pushing one of the thumbs to the limit of the slider will make that threshold value unbounded.



Region With Absolute Threshold: Creates a region with an unbounded upper threshold and a lower threshold defined in the preferences dialog. The threshold values are expressed in the currently selected quantification method of the dataset on which the region was defined. The threshold values are absolute values which may be modified in the **Threshold Settings** panel of the toolbox by entering values into the lower and upper threshold fields, or by modifying the lower and upper thumbs of the threshold slider.

Contouring Preferences are found by selecting **Tools -> Options** from the menu and choosing the **Findings** tab.



Region with % of Max Threshold: Creates a region with an unbounded upper threshold and a lower threshold defined in the preferences dialog. The threshold values are expressed as percentages of the maximum value within the 3D bounding box of the region. The threshold values are percentages which may be modified in the **Threshold Settings** panel of the toolbox by entering values into the lower and upper threshold fields, or by modifying the lower and upper thumbs of the threshold slider.

Contouring Preferences are found by selecting **Tools -> Options** from the menu and choosing the **Findings** tab.



Region: Creates a region with an unbounded upper and an unbounded lower threshold. This has the effect of creating an entirely filled region. The filled region may be turned into a thresholded region by modifying the lower and upper threshold values.

 **Ellipse Region:** Creates a region with an unbounded upper and an unbounded lower threshold. This has the effect of creating an entirely filled region. The filled region may be turned into a thresholded region by modifying the lower and upper threshold values.

 **Rectangle Region:** Creates a region with an unbounded upper and an unbounded lower threshold. This has the effect of creating an entirely filled region. The filled region may be turned into a thresholded region by modifying the lower and upper threshold values.

 **Seedpoint Region:** Creates a region with an unbounded upper threshold and a lower threshold defined in the preferences dialog. The threshold values are expressed in the currently selected quantification method of the dataset on which the region was defined. The threshold values are absolute values which may be modified in the **Threshold Settings** panel of the toolbox by entering values into the lower and upper threshold fields, or by modifying the lower and upper thumbs of the threshold slider. Unlike the other region types, the Seedpoint Region can only threshold by absolute value and cannot be changed to percentage of region max.

Contouring preferences are found by selecting **Tools -> Options** from the menu and choosing the **Findings** tab.

 **Paint:** Use to modify the selected region by painting additional areas.

 **Erase:** Use to modify the selected region by removing areas.

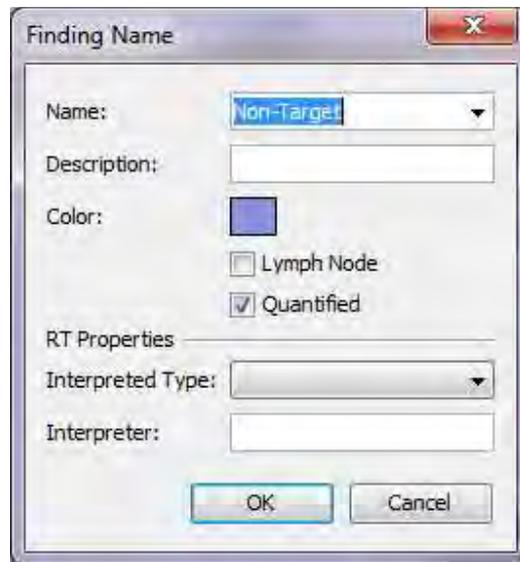
Naming a Finding

When a finding is created, whether a region, ruler or bi-ruler, it may be linked to other types of findings. For example you may wish to link a region with a ruler for a single finding.

Upon creation of a region of interest, a dialog box will display which allows you to name and describe your region. Type in a name or select from the dropdown list of optional names. You may add to, delete or edit the 'Name' list via **Tools -> Options** on the **Findings** tab.

You may also type a description and if you'd like, select the color of the region by clicking on the pink box and choosing from the color palette.

Indicate that the region is a lymph node by ticking the box. The box labeled 'Quantified' indicates whether statistics are calculated for the created region. This would be ticked by default. Enter a description you wish and click OK.



If you do not wish to be prompted to name each new finding you may disable this feature via **Tools -> Options** on the **Findings** tab. In addition, the list of preset structures names may be modified there as well by selecting the **Suggestions** button on the Findings tab.

Linking Selected ROIs

Linking selected ROIs allows you to manually link a selected ROI to an ROI in a different time point for region tracking. Linking an ROI means that comparison statistics can be displayed between the ROIs that have been linked. In the Regions of Interest panel, use Ctrl and click the left mouse button to choose the regions you wish to link, and then simply click on the link button.



Projecting an ROI

To project an ROI to multiple time points, select the tool from the Findings panel. This will project any ROI created in a single time point to all other time points that are loaded into the layout at that time. The region will be created by threshold or percent of maximum depending on the method used to create the original ROI. The statistics for each time point will be displayed on the screen. The ROI can also be projected by volume and to a subset of time points. To do this, click the right mouse button on the ROI in the Findings panel and select the required option from the displayed menu.



When propagating ROIs between time points, it is important to check that the threshold used is appropriate for the data in the time points. For meaningful comparison statistics to be displayed, the threshold should be the same in each time point.

To see the threshold used, select the region in the time point and view the threshold slider or move the mouse pointer over the Region defined in the Regions of Interest panel in the Toolbox to display the tooltip.

The threshold is also visible on the Regions Table.

Deriving a ruler from an ROI

You may create a ruler from any previously created region of interest. A bi-ruler will be created in the slice with the greatest long axis and corresponding short axis within the boundaries of the selected region in the orientation of the selected view. The auto-ruler first finds the longest axis, then for that plane will find the longest short axis. Select the image view with the orientation from which you wish to derive the ruler, then in the Findings section of the Toolbox highlight the region you wish to use, click right and select **Create Ruler from Region**.



The Create Ruler from Region tool calculates the long and short axes from the ROI selected using mathematical approximations of the smooth ROI boundary. However, the resulting bi-ruler may not correspond to what the user considers to be the long and short axes that best characterize the lesion from a clinical point of view. It is important that the resulting Biruler is visually inspected and compared with the region used for creation to ensure the results are as desired.



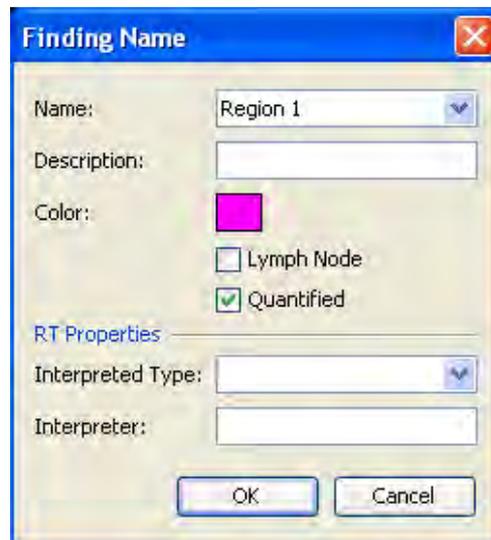
The Create Ruler from Region tool uses mathematical approximations to the smooth ROI boundary when calculating the best bi-ruler placement. However, in some rare cases the approximations may result in a ruler that does not correspond exactly to the displayed boundaries or one that passes slightly outside the lesion boundary. The user should check the result of the tool to confirm that the ruler meets their expectations.

Creating and Exporting RTSS

It is possible to save and export as Radiation Therapy Structure Sets (RTSS) any volumes of interest created in XD3 for use in radiation therapy treatment planning systems.

Upon creation of a region of interest, a dialog box will display which allows you to name and describe your region. Type in a name or select from the dropdown list of optional names. You may also type a description and, optionally, select the color of the region by clicking on the box showing the currently selected color, and choosing from the color palette. The chosen color will be the one used for the contours when creating the RTSS.

If you are creating a region to use as an RTSS, you may select the appropriate type of structure from the 'interpreted type' dropdown list. You may add to, delete or edit this list via **Tools -> Options** on the **Findings** tab. Enter your name if you wish and click OK.



Once you are satisfied with the region, after creating and editing it, select **File -> Export** from the menu. Select RTSS from the **Export** dialog box and click OK. A second Export dialog box displays, as shown below. Select the study with which the RTSS should be associated, and select the dataset containing the region from the dropdown.

Ensure the appropriate regions you wish to export are visible; and enter label, name, and description as desired. Click to place a tick in the box if you wish to have the original dataset exported along with the region(s); the original dataset is the one containing the region to be exported.

Select the export destination and click OK. You must enter a label in order for the RTSS to be exported.

Name	Interpreted Type
Primary	GTV



XD3 creates the DICOM RT Structure Sets from the selected region as specified in the DICOM Standard. RTP systems may apply interpolation between the encoded contour control points that differs from their display in XD3. We recommend that the user takes screenshots of the regions used to create the contours, on an acquisition orientation view, and uses these to compare to the contour displayed within the RTP system to ensure that the exported contour is an accurate representation.

It is also important to note that when exporting RTSS, XD3 creates contours in the geometry and slices of the original image data and not the geometry and orientation of the current MPR views. Therefore, it is important to review regions on acquisition orientation views before exporting to an RTP system. Similarly, if the system that imports structures generated within XD3 re-samples the image data for display, the contours may not appear to be in the same position as when displayed in XD3.

Importing and Displaying RTSS

XD3 can import DICOM RT Structure Sets (RTSS). RTSS do not appear in the Timepoint Selection dialog but are automatically loaded if the dataset that they reference is also loaded.

To be able to display the structures on reconstructed views, the loaded structures are converted into an internal volumetric representation. This allows all loaded structures to be displayed in any MPR view. The original contours in the RTSS are defined in the acquisition plane of the dataset. When comparing structures displayed in XD3 to the same structures displayed on a different system, the acquisition orientation must be used.

All imported structures are added to the Findings panel in the Toolbox. By default, quantification is turned off for loaded structures. If quantification statistics are required for loaded structures then quantification must be explicitly turned on for those structures. To do this, double-click the name of the structure in the Findings panel and check the **Quantified** option.

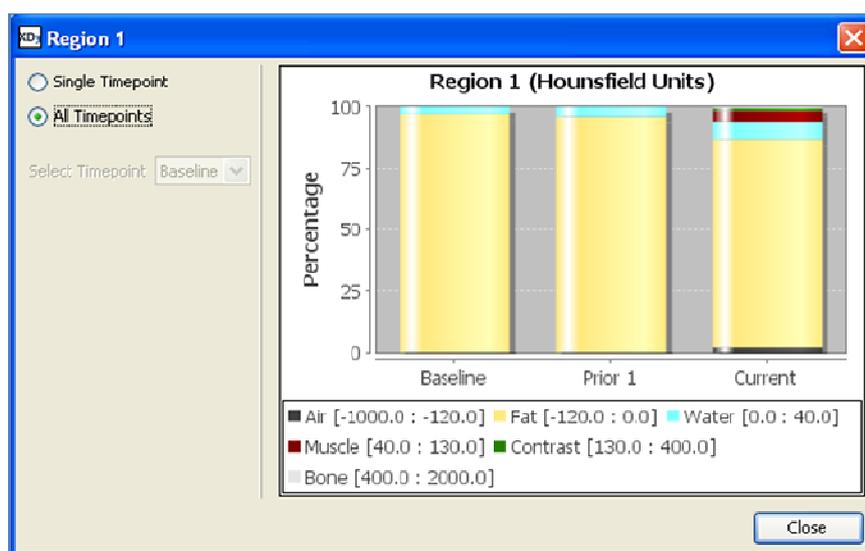


Contour interpolation is applied to RTSS for display, however methods may vary between different vendors. XD3 uses a particular contour interpolation method which may differ to that used by other systems (such as TPS). This means that structures may display differently in XD3 when compared to other systems. In most cases such differences will be trivial and affect only the visualization, however it is recommended that screenshots of loaded structures be taken in the XD3 acquisition view and compared to the same structures as displayed on other systems.

Display Findings Graph

Depending on the findings created (i.e. rulers or regions) the findings graph will display a line profile for a ruler and the region intensity distribution for a region.

The **Region Intensity Distribution** tool allows you to set categories for voxel intensities within a region of interest. These categories are reported in parts of the application that report the region statistics. These are reported via the image view statistics, the intensity distribution graphs from the Findings Table and from the regions tracking tab on the Findings Table. See the example below.



NOTE: The density values displayed in this example are for demonstration purposes only

You may click the right mouse button to copy the intensity distribution graph to a Windows clipboard or to image gallery to send to PACS as DICOM Secondary Capture.

NOTE: If an ROI is modified with an intensity distribution graph displayed, the updates will not be reflected until the intensity distribution graph is closed and re-displayed. This also applies if the intensity distribution categories are modified via the user preferences.

The categories may be set in **Options** via **Tools -> Options** on the **Region Intensity Distribution** tab.

Select the modality for which you wish to set intensity ranges from the list on the left. Select the quantification method from the dropdown menu. Click on **New** to create a new region intensity distribution definition. This will open the dialog box which allows you to set the number and range of intensity levels.

Use the green '+' to add a category and use the red 'X' to delete a category. For each category, add lower and upper bounds for the category range.

Enter the names for your categories by double clicking the default name (i.e. air, water, contrast, bone, etc.), and click on the colored square to the left of the category name to select the color to represent that category in the graphical display. Click **OK** to continue and save your selections. Intensity distributions are per-user. Any intensity distributions that are added or modified by the user will be available for that user only.

There is no restriction on the category ranges allowed within an intensity distribution. If two categories have overlapping ranges then it is possible for the sum of the percentages of the classification to be greater than 100%. Similarly, if there are gaps between the category ranges then it is possible for the sum of the percentages of the classification to be less than 100%. For instance, an intensity distribution for PET SUV by body weight can be created with the following ranges: Type1 [1 – 3], Type2 [2 – 4] and Type3 [3 – 10]. If a region is created that contains only voxels whose SUV is greater than 2.0, then every voxel will be included in the Type1 category (100%), every voxel will be included in the Type2 category (100%), possibly, a non-zero amount of voxels will be included in the Type3 category. In this case the sum of the percentages will be greater than 200%.

Region Intensity Distributions may be viewed, edited, cloned or created from the Region Intensity Distribution tab in the **Tools -> Options** menu.



The Voxel Intensity Distribution feature relies on the accuracy of the registration when the ROI was created on one dataset and the intensity distribution statistics are viewed for the other datasets within the same time point. The registration should be checked for accuracy using the Registration Manager prior to using this feature.

PET SUV Calculation

PET SUV calculations are based on variables defined in the loaded data. These include patient's weight, height and sex, *et cetera*. XD3 allows these variables to be modified in the Quantification Parameters dialog. In certain circumstances, the application will correct the values stored in the data based on the DICOM Conformance statement information of particular scanners. For example, data from particular scanners will store the Radionuclide Total Dose in MegaBecquerels rather than Becquerels as specified in the standard. In this case, XD3 will perform the conversion automatically and raise a warning in the messages panel.

Calculation by Body Weight

One of the methods of calculating PET SUV in this application is by body weight. The following formula is used in this calculation:

$$SUV = \frac{\text{average activity in ROI (Bql/ml)}}{\text{injected dose (Bql)}} * \text{patient weight (g)}$$

Unit is g/ml.

This method requires that all of the following information is available:

- Administration date/time
- Acquisition date/time
- Injected dose
- Radionuclide half-life
- Decay correction method
- Patient weight

Calculation by Body Surface Area

SUV by Body Surface Area (BSA) is calculated by using an approximation of the Body Surface Area. The following formula is used for this calculation:

$$SUV = \frac{\text{average activity in ROI (Bql/ml)}}{\text{injected dose (Bql)}} * BSA (cm)^2$$

Where the BSA is approximated using the following formula (by Du Bois and Du Bois):

$$BSA (cm^2) = [\text{patient weight (kg)}]^{0.425} * [\text{patient height (cm)}]^{0.725} * 71.84$$

Unit is cm²/ml.

This method requires that all of the following information is available:

- Administration date/time
- Acquisition date/time
- Injected dose
- Radionuclide half-life
- Decay correction method
- Patient weight
- Patient height

Calculation by Lean Body Mass

SUV by Lean Body Mass (depending on the sex of the patient) is calculated using the following formula:

$$SUV = \frac{\text{average activity in ROI (Bql/ml)}}{\text{injected dose (Bql)}} * LBM (g)$$

Where the LBM is approximated using the following formulae:

$$LBM_{MALE} (kg) = 1.10 * [patient weight (kg)] - 128 * \left[\frac{patient weight (kg)}{patient height (cm)} \right]^2$$

$$LBM_{FEMALE} (kg) = 1.07 * [patient weight (kg)] - 148 * \left[\frac{patient weight (kg)}{patient height (cm)} \right]^2$$

Unit is g/ml (remember to multiply LBM formulae above by 1000 to get them in g).

This method requires that all of the following information is available:

- Administration date/time
- Acquisition date/time
- Injected dose
- Radionuclide half-life
- Decay correction method
- Patient weight
- Patient height
- Patient sex

For more information please see:

Reevaluation of the Standardized Uptake Value for FDG: Variations with Body Weight and Methods for Correction, by Sugawara et al, **Radiology**, November 1999.

PET SUV from Acquisition

PET SUV from Acquisition displays the SUV that certain scanner manufacturers calculate and store in the image data.



The PET SUV from Acquisition calculation underlying the display of this quantification option is outside the control of Mirada Medical. When PET SUV from Acquisition displays values, the number displayed is based on the stored value in the image data. Please contact your vendor for further information on this topic.

Active Text Control

In the image window there is information about the patient, study and images displayed. Some of the text is for information only and other is 'active text' that may be used to adjust the image. The default colors of the text are blue and black/white. The black/white colored text is inactive and represents information such as patient name, sex, age, birth date, patient ID, hospital or facility name, the currently displayed field-of-view, series name and date obtained from the DICOM header.

The blue colored text is the active text. When the mouse pointer hovers over any setting that may be adjusted in this manner the text becomes underlined. Click on the text to display the available control.

Available Active Text Controls

In the image window there are active text controls for:

- Scale
- Window and Level
- Quantification Options (SUV)
- Slice Index

Custom color and font size for the on screen text may be set in user Preferences via the **Tools -> Options** menu on the **Views** tab. Click on the Interactive text color shown to display the color palette and select a new color. Font size may be changed by using the up and down arrows or double-clicking and entering the desired size.

Toolbar and Menus

Toolbar icons

 **Undo:** Click the left mouse button to undo the last operation in the Registration Manager.

 **Redo:** Click the left mouse button to redo the last operation in the Registration Manager.

 **Toolbox:** Toggle to show or hide the toolbox.

 **Patient Information:** Toggle to add or remove patient information from image window.

 **Information Overlays:** Toggle to add or remove information overlays from image window.

 **MPR Cube Overlay:** Select whether the MPR cube overlay is displayed.

 **Navigation Controls:** Select whether navigation controls are displayed in the selected view.

 **Crosshairs:** Toggle to add or remove crosshairs from image window

 **Crosshair ROI:** Toggle to show statistics at the crosshair location. Use shift + mouse wheel to adjust size of ROI.

 **ROIs:** Toggle to show ROIs in the image windows.

 **Annotations and Angles:** Toggle to show annotations and angles in the image windows.

 **Visualization:** Click to display the Visualization dialog box to change window, level, color palette and transparency.

 **Invert Color map:** Click to invert the color map in the base image.

 **Adjust Window and Level:** Use left mouse button to click and drag up, down, right and left to adjust contrast and brightness.

 **Window Max:** Click to adjust the upper end of the window/level spectrum while the lower end is locked (e.g. for PET data, the lower value never goes below zero). This tool is accessed via drop down under Adjust Window and Level icon.

 **Normalize window and level:** Click the left mouse button and drag the mouse over an area on an image; this draws a square which is the area for which images are 'normalized'. Note that this button is not present on the toolbar by default.

 **Reset window and level:** Click to return to the original window/level settings.

 **Selection Mode:** Puts cursor into a click-to-select mode for various on-screen objects like rulers, and simultaneously takes you out of any other mode such as zoom.

 **Transparency Tool:** Click the left mouse button and drag up and down to change Overlay Transparency.

 When viewing fused images, artifacts may be introduced by poor alignment of findings between the image layers in the fused view. It is recommended that the registration accuracy is checked prior to image interpretation and the transparency of the layers is adjusted appropriately to view the layers in the fused views.

 **Slice Navigation:** Click the left mouse button to move through the slices in an image set.

 **Place cross hair:** Click the left mouse button and then place cross hair in image window where cursor will determine location from which to triangulate.

 **Image Zoom:** Click the left mouse button and drag the cursor down across the image to enlarge, up to reduce in size.

 **Image Pan:** Click the left mouse button and drag to move an image within its window. Used when areas of the image cannot be seen within the boundaries of the image window.

 **Rotate MPR Views:** Click the left mouse button to rotate MPR views in the active image window.

 **Maximize view:** Toggle to maximize an image window to full screen.

 **Reset pan and zoom:** Click the left mouse button to restore original pan and zoom settings.

 **MIP:** Click to display series in the selected view as Maximum Intensity Projection (MIP) in a floating window.

 **Snapshot:** Click the left mouse button icon then click the left mouse button in image window to save a snapshot as a key image.

 **Magnifying glass:** Click and drag small square to move over images and magnify to various levels.

 **Link/Unlink Crosshairs:** Toggle to link and unlink crosshairs to perform a manual alignment.

NOTE: The Ruler Tools below may be grouped into a 'Favorites' drop down menu on the toolbar where the last one used is remembered and displayed on the toolbar. This may be set in Tools -> Options on the User Interface Tab under Toolbar Configuration.

 **Temporary Ruler:** Click the left mouse button and drag to measure a distance within an image view; ruler disappears after measurement is made.

 **Ruler:** Click the left mouse button and drag to measure a distance within an image view; ruler remains visible after measurement is made.

 **2D Ruler:** Click the left mouse button and drag to measure short and long axis of a lesion simultaneously within an image view. The axes are always maintained at 90 degrees; adjustments may be made to either short or long axis by clicking left and dragging ends of ruler.

 **Angle:** Click the left mouse button to place, expand and adjust to measure an angle.

 **Add Annotation:** Click the left mouse button to identify the finding you wish to annotate, and then drag to place the annotation. Use the Rulers and Annotation window on the left of the screen to edit the label, delete the annotation or to show or hide a selected region.

NOTE: The Region Tools below may be grouped into a 'Favorites' drop down menu on the toolbar where the last one used is remembered and displayed on the toolbar. This may be set in Tools -> Options on the User Interface Tab under Toolbar Configuration.

 **Region With Absolute Threshold:** Click the left mouse button and drag to create a region using absolute threshold value set in Contouring preferences.

 **Region with % of Max Threshold:** Click the left mouse button and drag to create a region using % of maximum threshold value set in Contouring preferences.

 **Filled Region:** Click the left mouse button and drag to create a ROI with threshold set at minimum. Used to quickly find max SUV in an area of interest.

 **Ellipse Region:** Click the left mouse button and drag ellipse to create a 2D region on a single slice.

 **Rectangle Region:** Click the left mouse button and drag rectangle to create a 2D region on a single slice.

 **Seed point Region:** Click the left mouse button anywhere in an area of interest to automatically generate a ROI based on a threshold value.

 **CT Region Segmentation:** Click the left mouse button inside the lesion and drag the bounding sphere outside the lesion to automatically generate a 3D region.

 **Adaptive CT Segmentation:** Click the left mouse button inside a lesion on a CT volume and drag the bounding sphere outside the lesion to automatically create a 3D region.

 **Paint:** Use to define or edit an ROI by painting voxels in an orthogonal/MPR image view. The paint tool operates from within a region.

 **Erase:** Use to delete voxels from an ROI by moving the mouse over the region. The erase tool operates outside the region.

 **Freehand region:** Click and drag to create a 2D region. Use paint and erase tools to edit.

Many of these region and ruler creation tools may be grouped into a single drop-down menu on the toolbar which will remember the last used tool within the group. It is possible to configure the system to place each of these tools directly onto the toolbar by going to **Tools -> Options...**, selecting the **User Interface** tab and then selecting the **Toolbar Configuration** option.



Time Point Selector: Click to display and select the time point you wish to display.



Layout Selector: Click to display Registration Manager, Data QC, Findings Table, Report, Secondary Capture viewer or the layout of your choice.

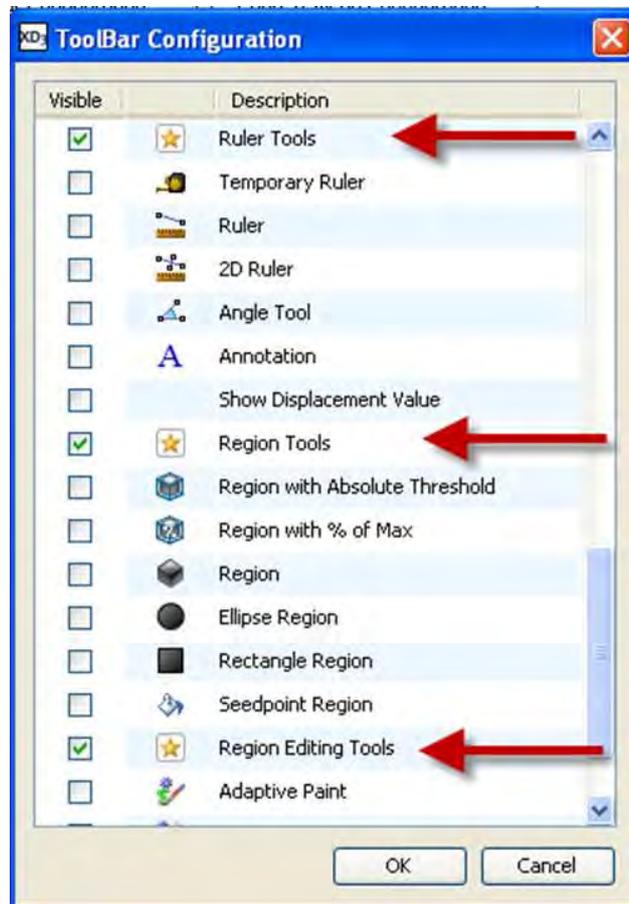
Show or Hide the Toolbar

If desired, the toolbar may be hidden by selecting **View -> Show Tool Bar** from the menu. Tools located on the toolbar are also available from the menus and from the context menu found in the right mouse button when in an image window. This function may also be set to a hotkey in **Tools -> Options**.

Configure the Toolbar

You may configure the toolbar to show as few or as many of the tools that you wish to be displayed. From the **Tools -> Options** menu, select the **User Interface** tab and choose **Tool Bar Configuration**. Place a check in the box next to the tools you wish to include in the toolbar. When you are satisfied with your selections, press OK. The toolbar will update with your new selections immediately.

There are options in the toolbar configuration window to enable Favorites: options are Ruler Tools, Region Tools and Region Editing Tools.



By placing a check in the box next to the Favorite tools, this group of tools is available as a dropdown on the toolbar, with the most recently used of the set displayed on the toolbar as the favorite. To avoid having the individual tools visible on the toolbar (in addition to the dropdown), you should uncheck the boxes next to the individual tools in the Tool Bar Configuration window.

Context Menu

There is a context menu (also known as the floating toolbar) accessed by clicking the right mouse button anywhere in the image window. This toolbar contains the same functions as the main toolbar.

You may configure the context menu to show as few or as many of the tools that you wish to be displayed. From the **Tools -> Options** menu, select the **User Interface** tab and choose **Context Menu Configuration**. Place a check in the box next to the tools you wish to include in the context menu. When you are satisfied with your selections, press OK. The context menu will update with your new selections immediately.

Displaying a MIP



The Maximum Intensity Projection or MIP Renderer is a tool for data visualization in 3D and is useful for obtaining an overview of the areas within the image data of a high intensity and as a tool to navigate to those regions. The MIP should not be used as the sole view used to interpret the image data.

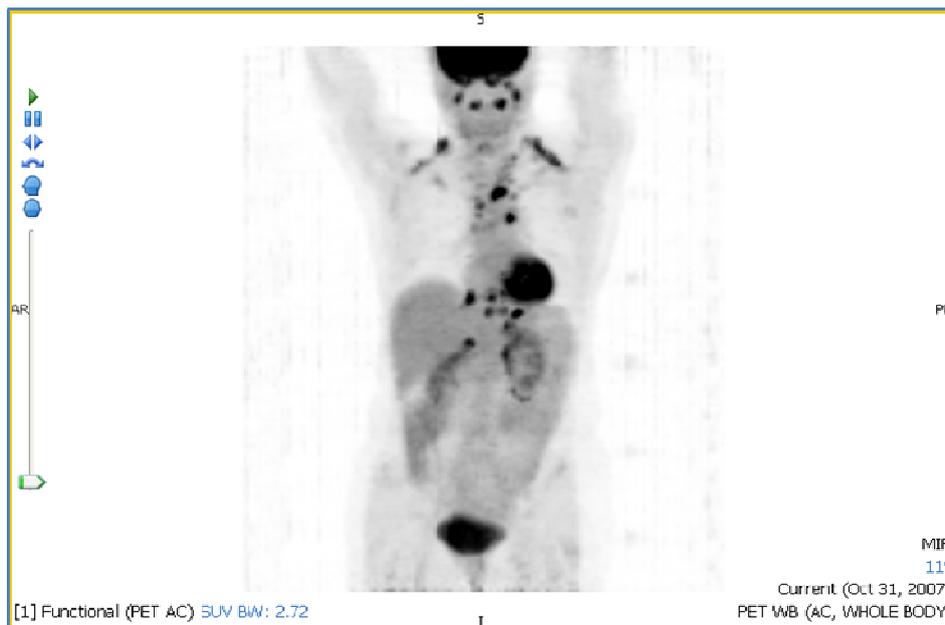


Selecting the MIP icon from the toolbar, context menu or selecting **Image -> Show as MIP** from the menu will display a floating MIP window.

Alternatively, you may use the MIP icon on the Toolbar, from the context menu or by using a hotkey.

If you wish to have the MIP automatically spinning upon launch, you may set that preference in **Tools -> Options** on the **Views** tab. Place a check in the box next to 'Automatically play MIP cine'.

Additionally, you may also set the number of frames to be displayed for MIPs. This applies to exporting them as well.



MIP tools are visible within the MIP window on the left side as shown in the example above. These buttons allow manual control of the MIP image, playing and pausing of the MIP cine, reversing direction of the cine, changing from 360° to 180° rotation, snapping to a sagittal view, and snapping to a coronal view. The speed of the cine is controlled with the slider in the Cine section of the Toolbox.

Exporting a MIP

To export a MIP file, you must be in a layout that includes a MIP display. Be certain that your MIP window is the active window. Select **File -> Export** to display the Export window. Select MIP Images from the list and click **OK**. Select the range of MIP frames to export and click on **Continue**. Input Series Information and choose destination, browse for destination directory, provide filename and choose file format from the dropdown menu. Click **OK** to export the file. The number of frames exported will be the same as set in **Tools -> Options** on the Views tab.

File Menu

Export

Options for exporting include:

- **Original Data** – the Export screen will display for you to select which series you wish to export. The dataset selected in the 'Associate with' field will be exported. Provide the information about the destination and select **OK**.
- **Resampled Volumes** – the system will display the Export Selection Screen to allow you to save a resampled volume to the destination of your choice. The resampled volume creates a new series that has registration applied so that the new series could look like it was from a hybrid scanner (i.e. slice thickness, geometry, resolution are the same). You will also be prompted to specify to which dataset the exported one should be re-sampled. Upon selecting **OK** from the Export Selection Screen, the system will save the re-sampled dataset to the specified destination
- **Registration** – the system will display the Export Selection Screen to allow you to save a registration to a destination of your choice. This exports a spatial registration DICOM object – this object along with the two original series when reloaded are in a saved state, and are displayed as a record of the prior registration. There are other fields present to select which registration relationship is being exported. Upon selecting **OK** from the Export Selection Screen, the system will save the selected registration to the specified destination. Multiple restores registrations can be reapplied via the registration manager in the Loaded Registrations panel.
- **Slice Range** - This option allows you to export a range of slices from an image of your choice. Upon selection, the system will display an **Export Slice Range** screen for the selected view. You will be able to preview the image of the view to be exported (the preview will not be available for off axis slice ranges. In this case, the slices should be reviewed prior to selecting the export slice range option). Use the start and end markers on the image preview to set the range of slices to be exported. The larger the width and height settings, the larger the output files will be. Place a check in the box if you wish to include patient information in the exported file. Likewise, place a check in the box if you wish to use default volume size on export. When the range is set, select **Continue**.

Use the Cancel button to dismiss the dialog.

Input information about the series using the drop down menu and by typing in desired **descriptions and information** about the data series. Use drop down menu to select the destination and file format. Browse to select the destination directory, and then type in a name for the file. Click **OK** to export the file. An Export window will appear to confirm successful export.

Slice ranges may be exported as DICOM SC, JPEG, PNG, BMP and AVI. The available formats will depend on the export destination selected. Note that the AVI file will be uncompressed data and may be quite large depending on the range selected.

- **MIP Images** - You must be in a layout that includes a MIP and have the MIP window as the active window in order to export MIP data. The **Export MIP slices** window allows you to select the number and range of MIP frames you wish to export. Type in the numbers or use the arrows to scroll to reach the desired value. Check the box to include the patient information in your export. You may check the box to use default volume size. Press Continue to input Series and Destination information.

Select the series with which you want the exported MIP slices associated from the dropdown menu. You may type in additional information in Series Description, Performing Physician and Operator Name fields. Use the Send To dialog box to select the destination, directory, file name, and file format for the export. Note that you may export the MIP as AVI file via the **Destination** drop down menu. Select OK to export the data. You will see a progress bar during the export and a dialog box confirming a successful export.

NOTE: The number of frames displayed in MIPs can be set in Tools ->Options. The displayed number of frames is what will be exported.

- **RTSS** – This option allows you to export RT Structure Sets generated from volumes of interest. Select the study with which the RTSS should be associated, and select the dataset containing the region from the dropdown. Ensure the appropriate regions you wish to export are visible; and enter label, name, and description as desired. Click to place a tick in the box if you wish to have the original dataset exported along with the region(s); the original dataset is the one containing the region to be exported. Select the export destination and click OK. You must enter a label in order for the RTSS to be exported.

NOTE: Series Description, Performing Physician and Operator Name are remembered on a per user basis.

Save Session

Under the **File** menu, you will find an option to **Save Session**. This option allows you to exit the current session, but save all of your work. The following items are saved as DICOM objects so you can reload them along with the images and begin where you left off at the end of the previous session:

- Registrations
- Findings
- Key Images
- Bookmarks
- Rulers
- Bi-rulers
- Annotations
- Angles

- Modified PET Quantification Parameters (e.g. weight, height)
- Data Management screen order/anchor settings (e.g. for gated data)

These items are stored using standard DICOM objects and may be sent to and retrieved from PACS. There is an option to save these objects as a single series for compatibility with PACS. Compatibility mode is enabled by default and is useful if your PACS does not support the other DICOM objects. If you choose to disable this feature, you may do so via **Tools -> Options** on the Session tab.

If there is a study loaded for review when you choose a new dataset for review, you will be prompted to choose whether or not you would like to save your current session. You may wish to automatically save each session upon exit. This preference may be set via the **Tools -> Options** on the Session Tab.

Create a Viewer

From the File menu, you may select **Create a Viewer** to generate a volumetric DICOM viewer of the dataset(s) you are currently viewing. The viewer may be burned to a CD or saved to the file system for transfer to other output device (USB drive) and shared with a referring physician or patient, for example.

When the Create Viewer dialog box appears, select from the dropdown menu whether you wish to save the viewer to a destination on the file system or burn directly to CD. If you choose file system as your destination, enter a name for the folder where the viewer will be stored and browse to select the location for the folder. Select OK to continue. A progress bar will be displayed as the viewer is created. Along with the images, any bookmarks, registrations, ROIs, rulers, annotations, and angles that were created during the reading session will be written to the viewer.

If you are using a thin client system, you will save to the file system on the local machine and then burn to CD using Windows Explorer.

To run the viewer, double click on the **Start Viewer** file.

Send to Casebook

When the Casebook plug-in is installed you may export a dataset(s) to a location on the file system from which they may be imported in Casebook.

Send to Caseaccess

When Caseaccess plug-in installed you may send a dataset(s) and report to the Caseaccess server where it can be accessed remotely. See Caseaccess User Guide for detailed information on the Caseaccess product.

Send to Casemeeting

When the Casemeeting plug-in is installed you may export a dataset(s) to the Casemeeting server where it may be accessed remotely for a tumor board meeting or other multidisciplinary conference. See Casemeeting User Guide for detailed information on the Casemeeting product.

Exit

This action will exit the application. Using this method to exit the application preserves the number of displayed XD3 windows for re-display on the next launch.

Edit Menu

Undo

Undo the previous step. Also **Ctrl + Z**.

Redo

Redo the previous step. Also **Ctrl + Y**.

Capture View

Adds currently selected view to the Image Gallery. Also **Ctrl + E**.

Copy View to Clipboard

Copies the currently selected view to the clipboard. Also **Ctrl + K**.

Capture Screenshot

Adds a screenshot of this window to the Image Gallery. Also **Ctrl + Shift + E**.

Copy Screenshot to Clipboard

Copies a screenshot of this window to the clipboard. Also **Ctrl + Shift + K**.

Cut

Cut a currently selected report item. Also **Ctrl + X**.

Copy

Copy a currently selected report item. Also **Ctrl + C**.

Paste

Paste a currently selected report item. Also **Ctrl + V**.

View Menu

Show Toolbar

Select to add or remove the Toolbar from the top of the image window.

Show Toolbox

Select to add or remove the Toolbox from the left side of the image window.

Show Patient Information

Select to add or remove patient information in the image window.

Show Timepoint Information

When launched with more than one timepoint, select to show timepoint label and date in the image window.

Show Information Overlays

Select to add or remove information overlays in the image window.

Show Fused Overlays

Select whether the fusion overlays are visible.

Show Volume Bounds

Select to add or remove volume bounds in the image window.

Show MPR Cube

Select whether the MPR cube overlay is visible.

Show Navigation Controls

Select whether navigation controls are displayed in the selected view.

Show Crosshairs

Select to add or remove crosshair in the image window.

Show Volume Crosshair

Select to calculate volume statistics at the location of the crosshair. Use shift + mouse wheel or ‘-’ and ‘=’ to adjust size.

Show ROIs

Toggle whether regions of interest are displayed in the image windows.

Show Annotations

Toggle whether annotations and rulers are displayed in the views.

Show Region Statistics

Select whether region statistics are visible in the views.

Image Menu

Invert Color Map

Click to invert the color map in the base image.

Window/Level

Use left mouse button to click and drag up, down, right and left to adjust contrast and brightness.

Window Max

Use the left mouse button to adjust only the upper level of the window/level spectrum.

Normalize Window/Level

Click the left mouse button and drag the mouse over an area on an image. This draws a rectangle to define the area for which images are 'normalized'.

Reset Window/Level

Click to restore initial window and level settings.

Select

Puts cursor into a click-to-select mode for various on-screen objects like rulers, and simultaneously takes you out of any other mode such as zoom.

Overlay Transparency

Click the left mouse button and drag up and down to change Overlay Transparency.

Navigate Slices

Click the left mouse button to move through the slices in an image set.

Place Crosshairs

Click the left mouse button and then place cross hair in image window where cursor will determine location from which to triangulate.

Zoom

Click the left mouse button and drag the cursor down across the image to enlarge, or up to reduce in size.

Image Pan

Click the left mouse button and drag to move an image within its window. Used when areas of the image cannot be seen within the boundaries of the image window.

Rotate

Click the left mouse button and rotate the orthogonal orientation in the active image window.

Maximize View

Toggle to maximize an image window to full screen.

Zoom Reset

Resets zoom and pan for all views.

Show MIP Window

Click to display a floating MIP window. MIP controls are present on the left hand side of the view. Controls are present for playing and pausing of the MIP cine, speed adjustment, snapping to a sagittal view, snapping to a coronal view and reversing direction.

Snapshot

Click the left mouse button icon then click the left mouse button in image window to save a snapshot as a key image.

Switch Timepoint

Select to change the displayed time point when multiple time points are loaded.

Quantification Settings

Select which quantification method to use for the datasets in the current view. For datasets that have configurable quantification parameters, a **Quantification Options** button is also available. Selecting the Quantification Options button will bring the relevant modality-specific dialog box for setting the parameters.

PET

The PET Quantification Parameters dialog allows the following parameters to either added, updated or removed: patient sex, height, weight, acquisition date and time, administration start date and time, dose and radiopharmaceutical half-life.

Window/Level Presets

Select to choose from a list of preset window and level settings. Preset window and level settings may be set to hotkeys via **Tools -> Options** on the Window/Level tab.

Visualization

Select to display a dialog box to choose Quantification Method, Window/Level setting and Color Map

Crosshair Bindings

Select to configure crosshair bindings. Choose from:

- All
- None
- Single Series
- Single- Timepoint

Zoom Bindings

Select to configure zoom bindings. Choose from:

- Axial + Coronal/Sagittal
- Per Plane
- All
- None

Pan Bindings

Select to configure pan bindings. Choose from:

- Per Plane
- None

Window/Level Bindings

Select to configure window/level bindings. Choose from:

- All
- By Timepoint
- Base and Overlay
- Base and Overlay by Timepoint

MPR Orientation Bindings

Select to configure MPR orientation bindings. Choose from:

- Per Plane
- Single Series
- None

Interpolation Method

Select the interpolation method to use for all views. Choose from:

- Nearest neighbor
- Linear
- Cubic Spline

Crosshair Style

Select the crosshair style to be used for all views. Choose from:

- Target
- Plain
- Open
- Fade
- Frame Marker

Volume Crosshair Size

Increase or decrease the size of the crosshair volume when using the crosshair as an ROI. The size of the crosshair volume may also be increased or decreased using shift + mouse wheel or using '-' and '=' hotkeys.

Registration Menu

Run Automatic Rigid

Select to automatically run the rigid registration algorithm. You may also use the **F2** key for this.

Run Automatic Deformable

Select to run the automatic deformable algorithm. You can also use the **F5** key for this.

Smooth Deformation

Takes an existing deformable registration and filters it to reduce large deformations. Successive iterations of the Smooth Deformation command further reduce the deformation field until it reaches a maximum smoothness. This tool may be useful when applying CT deformable registrations to PET overlays.

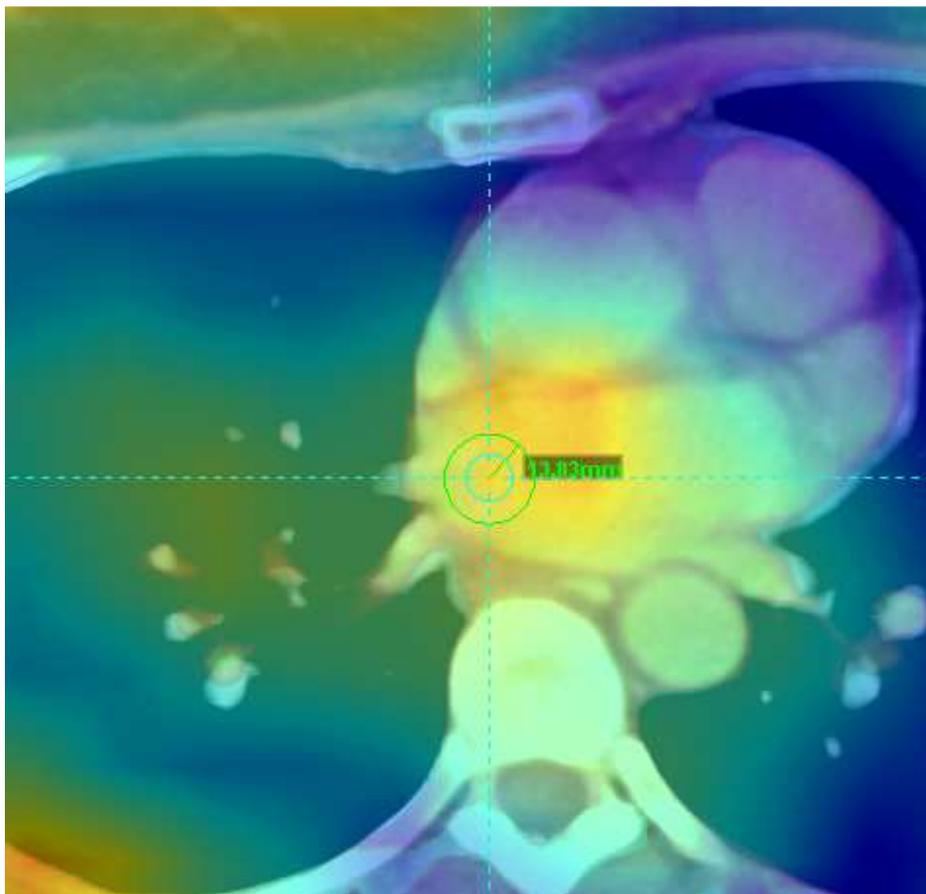
Show Displacement Value

The system displays a circle, an equal distance around the crosshair, with the distance being equivalent to the amount of deformation. The system will indicate the distance in millimeters. If there is zero deformation, the Displacement Value will be the same size as the crosshair.

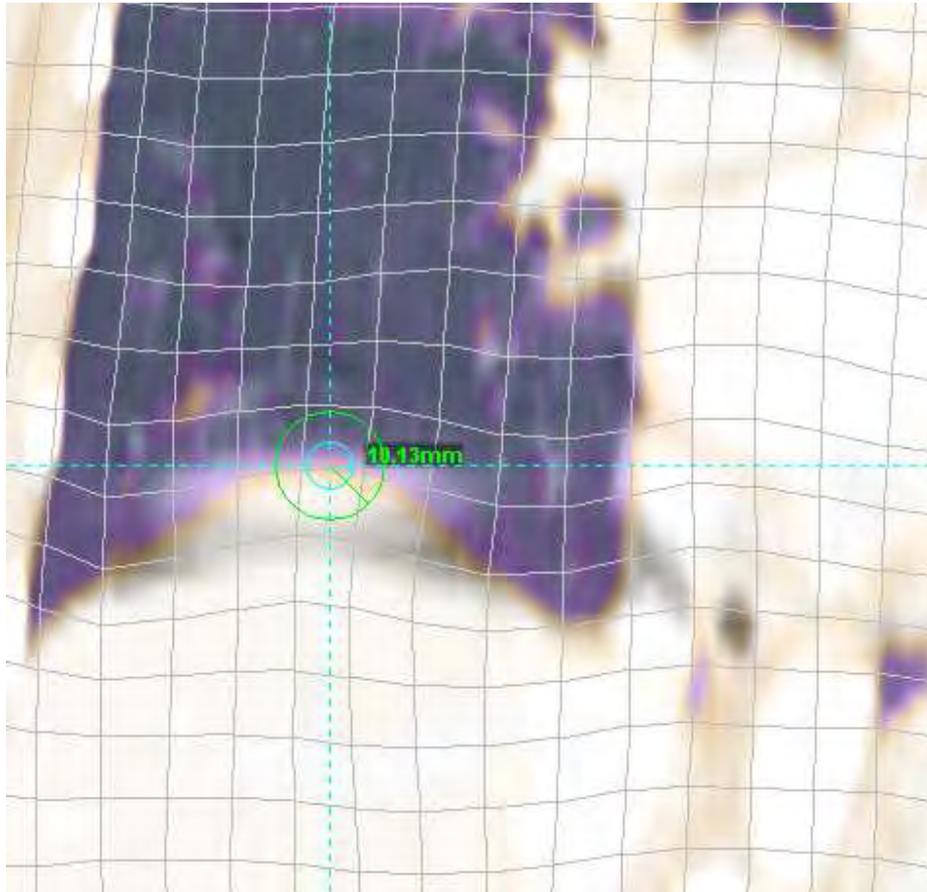
Displacement View

These are Quality Assurance tools which allow you to visualize the extent of the deformable registration applied. The deformation of the data may be shown as a Displacement Map, a Displacement Grid, or Displacement Arrows. These controls are only available when the registration applied has been either automatic CT to CT deformable or multi-modal deformable.

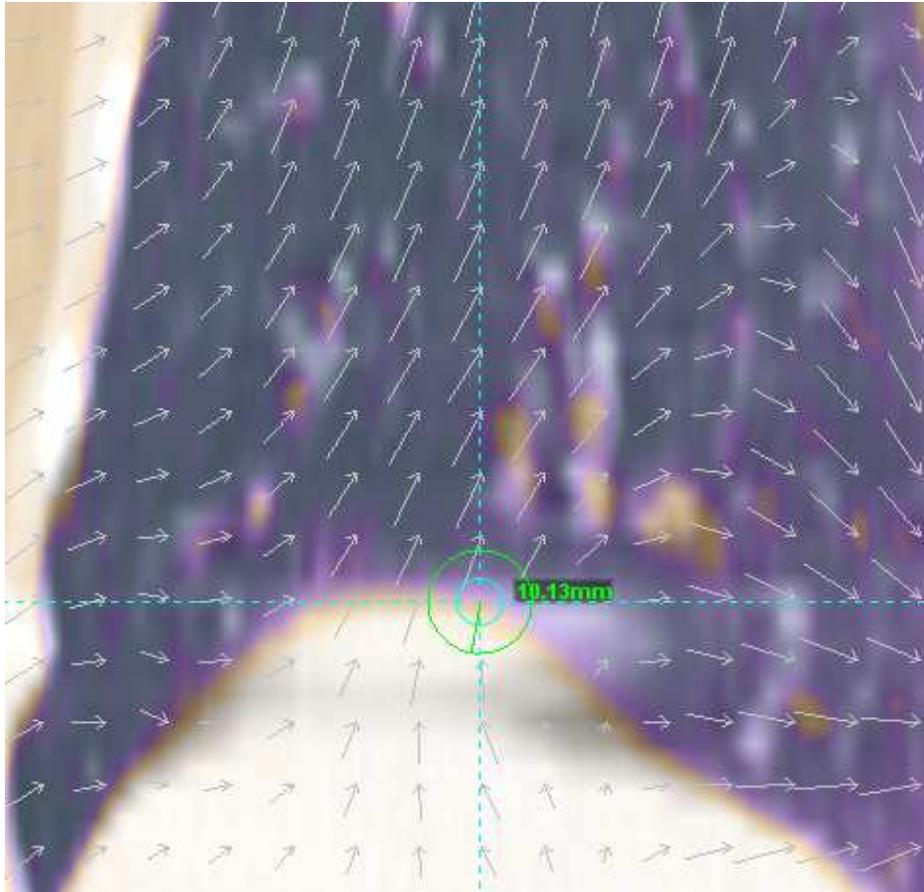
When viewing the **Displacement Map**, the areas of deformation are indicated by a color map. Warm colors such as red and yellow indicate high areas of deformation; cool colors such as blue and green indicate areas of low displacement.



When viewing the **Displacement Grid**, the grid is shown over the target-overlaid-on-source view which indicates areas of low and high displacement. Areas of high grid displacement indicate high areas of deformation.



When viewing the **Displacement Arrows**, the amount and direction of deformation or displacement are indicated by arrows, where the length is proportional to the amount of deformation.



Overlay Type

Select registration overlay type. Choose from checkerboard or inset.

Unlink Crosshairs

Click to unlink the crosshairs between time points to allow scrolling of each study separately. Unlinking the crosshairs changes the crosshair bindings to 'Single Timepoint'.

When linking crosshairs, the inter-time point registrations will be replaced with a translation based on the current crosshair positions in each time point.

This functionality is the same as the Link/Unlink tool () on the toolbar.

Registration Manager

Registrations other than the automatic schemes defined in the review modes are performed from the registration manager. This is the only place these tasks can be performed. The Registration Manager screen may also be displayed from any of the layout selectors.

See **Registration Manager** section of this document for details.

Quantify Menu

Drop 1cm Sphere

Place your cursor where you would like to define a reference region. Select **Quantify -> Drop 1 cm³ sphere** to drop a 1.0cm diameter region. Name the region as '**Reference**' in the Regions of Interest section of the Toolbox or select Reference from the dropdown menu of the Findings dialog box. This reference region will enable ratio statistics in the PERCIST and Advanced tabs in the Findings Table.

Drop 3cm³ Sphere

Place your cursor where you would like to define a reference region. Select **Quantify -> Drop 3cm³ sphere** to drop a 3.0cm diameter region. Name the region as '**Reference**' in the Regions of Interest section of the Toolbox or select Reference from dropdown menu in the Findings dialog box. This reference region will enable ratio statistics in the PERCIST and Advanced tabs in the Findings Table.

Drop Volume Crosshair Sphere

Place your cursor where you would like to show statistics at the crosshair location. Use shift + mouse wheel or the '-' and '=' keys to change the size of the region.

Temporary Ruler

Click the left mouse button and drag to measure a distance within an image view; ruler disappears after measurement is made.

Region with Absolute Threshold

Click the left mouse button and drag to create a ROI based on absolute threshold values set in Contouring Preferences. Region statistics will be displayed next to the region on the image window.

Contouring Preferences are found by selecting **Tools -> Options** from the menu and choosing the Findings tab.

Region with % of Max

Click the left mouse button and drag to create a ROI based on a percentage of maximum value set in Contouring Preferences. Region statistics will be displayed next to the region on the image window.

Contouring Preferences are found by selecting **Tools -> Options** from the menu and choosing the Regions tab.

Region

Click the left mouse button and drag to create a ROI. The threshold is set at minimum and the region statistics will be displayed next to the region on the image window. This is a quick way to measure a max SUV.

Ellipse Region

Click the left mouse button and drag to create an elliptical 2D region on a single slice.

Rectangle Region

Click the left mouse button and drag to create a rectangular 2D region on a single slice.

Seedpoint Region

Click the left mouse button anywhere in an area of interest to automatically generate an ROI based on a threshold value that is then used to grow the region from the selected point for all connected voxels that exceed the threshold.

CT Region Segmentation

Click the left mouse button within the lesion and drag to expand the sphere to identify the lesion to segment. The outer solid circle is a firm boundary for the segmentation, therefore the region will not extend beyond this line. The inner dotted line indicates the area used to indicate the interior of the lesion and guides the segmentation algorithm. It may be necessary to initiate the segmentation from a non-central area in the lesion to exclude nearby structures to be avoided, such as ribs or mediastinal structures. The tool will remain active in the event that multiple attempts are needed for desired segmentation. Use 'Esc' or the 'Select' function to deactivate the segmentation tool or to begin segmentation of a new lesion. Once the lesion is segmented, a biruler may be automatically derived.

Adaptive CT Region Segmentation

Click the left mouse button within the lesion and drag to expand the sphere to identify the lesion to segment. The outer solid circle is a firm boundary for the segmentation, therefore the region will not extend beyond this line. The inner dotted line indicates the interior of the lesion and guides the segmentation algorithm. It may be necessary to initiate the segmentation from a non-central area in the lesion to exclude nearby structures to be avoided, such as ribs or mediastinal structures. The tool will remain active in the event that multiple attempts are needed for desired segmentation. Use 'Esc' or the 'Select' function to deactivate the segmentation tool or to begin segmentation of a new lesion. This tool differs from the CT Region Segmentation tool in that it will use the current window and level to aid in the identification of boundaries.

Note that Findings created using the CT Region Segmentation Tools will Project by Volume, meaning that the algorithm is not re-applied on project. Instead the shape is preserved and the position in the target volume is calculated from the transformation between the source and target volumes.



The CT Region Segmentation tools estimate a lesion boundary based on image contents and the user initialization and does not attempt any automated detection of lesions. The quality of the results need to be checked for accuracy by the user prior to being used.

Ruler

Click the left mouse button and drag to measure a distance within an image view; ruler remains visible after measurement is made.

2D Ruler

Click the left mouse button and drag to measure short and long axis of a lesion simultaneously within an image view. The axes are always maintained at 90 degrees; adjustments may be made to either short or long axis by clicking left and dragging ends of ruler.



When defining a 2D ruler, the measurement associated with a line is displayed in the same color as the line to which it pertains. When the measurements are similar, the colors should be checked to identify the pertaining line.

Angle Tool

Click the left mouse button to place, expand and adjust to measure an angle.

Annotation

Click the left mouse button to identify the finding you wish to annotate, and then drag to place the annotation. Use the Rulers and Annotation window on the left of the screen to edit the label, delete the annotation or to show or hide a selected region.

Region Painting Brush Size

Use menu to increase or decrease the size of the region painting brush or to select from a list of predefined brush sizes Paint

Select to define an ROI by painting voxels in an orthogonal/MPR image view.

Erase

Select to erase from an ROI by moving the mouse cursor over the voxels in a region.

Delete All

Select to delete all the regions and rulers created during the current session.

Show Smooth Contours

Select to show ROIs with smooth contours

Finding Tools

Although the following tools are available from the menu, it would be most efficient to assign them to hotkeys via **Tools -> Options** and selecting the **Configure Hotkeys** button on the **User Interface** tab.

- **Delete**
- **Copy Statistics to Clipboard**

- **Copy Statistics to the Image Gallery**
- **Create Ruler from Region**
- **Go to the Finding**
- **Display Finding Graph**
- **Go to hottest voxel**



If the **Go To Hottest Voxel** tool is used on a region with more than one voxel with the highest intensity value, then only one of these voxels will be identified.

- **Toggle to indicate lymph node**
- **Unlink**
- **Link:** There are two types of findings: rulers and regions. Rulers include uni-rulers, bi-rulers and angles (annotations are not classed as findings). Regions include isocontour regions (with threshold), filled regions, 2D rectangles, 2D ellipses and regions painted with the freehand paint tools. Ruler findings can always be linked to other ruler types. They can also always be linked to region types. Region findings can be linked to ruler findings but are restricted as to which other regions they can be linked. A region can only be linked to another region that was defined on the same data role. E.g. a region defined on the Anatomical data role in General Oncology Review can only be linked to another region defined on the Anatomical role and not to one defined on the Functional role. This is further restricted to only being able to be linked to another region defined on the same role but not on the same dataset. E.g. a region defined on gate 1 of a gated CT assigned to the Anatomical role can be linked to a region defined on gate 2 of the same gated CT, but not to another region defined on the same gate 1. This restriction does not apply across time points. A region on gate 1 of a CT on the baseline time point can be linked to a region defined on gate 1 of a CT on the current time point.
- **Show/Hide regions**
- **Project to all by type :** with a region selected, this option will propagate a finding to the equivalent dataset designation in all time points by recreating the region in each time point using the means by which the region was originally created (i.e. absolute threshold, % max threshold). If the region exists in multiple time points, then the value will be taken from the selected time point.
- **Project to all by volume:** with a region selected, this option will project the region to the equivalent datasets designations in all time points by maintaining the volume of the original region. If the region exists in multiple time points, the volume value will be taken from the selected time point.
- **Project to all within volume by type:** with a region selected, this option will project the region to all datasets from the same frame of reference (i.e. bins of a gated dataset, phases of a multi-phase CT or sequences of multi-sequence MR) and create shadows on each of them. If the region exists in multiple datasets, then the absolute threshold value is taken from the selected dataset.

- **Transform to all:** with a region selected, the region will be transformed to the equivalent dataset designation in all time points using the existing registration to transform the ROI shape. If the region exists in multiple time points, then the selected time point will be propagated.;
- **Project to remaining by type:** with a region selected, this option will propagate the selected region to the equivalent dataset designation in time points where the region does not already exist by recreating the region in each of the time points using the means by which the region was originally created (i.e. absolute threshold, % maximum threshold)
- **Project to Remaining by volume:** with a region selected, this option will propagate the region to the equivalent dataset designation in time points where the region does not already exist by maintaining the volume of the propagated region. If the region exists in multiple time points, then the volume value will be taken from the selected time point
- **Transform to remaining:** with a region selected, this option will propagate the region to the equivalent dataset designation in all time points that do not contain the region. The existing registration will be used to transform the ROI shape. If the region exists in multiple time points, then the selected time point will be propagated.
- **Project to remaining within timepoint by type:** with a region selected, this option will project the region to all datasets from the same frame of reference (i.e. bins of a gated dataset, phases of a multi-phase CT or sequences of multi-sequence MR) where the region is not currently defined and create shadows on all datasets to which the role on which the region was defined are linked. If the regions exists in multiple datasets, the absolute/threshold value will be taken from the selected dataset.
- **Transform to all within timepoint:** with a region selected, this option propagates the region to all datasets within the same frame of reference (i.e. bins of a gated dataset, phases of a multi-phase CT or sequences of multi-sequence MR) using the existing registration to transform the ROI shape. If the region exists in multiple datasets within the same frame of reference, the selected region will be propagated.
- **Transform to remaining within timepoint:** with a region selected, this option projects the region to the other datasets within the data designation (same frame of reference) that do not contain the region, using the existing registration to transform the ROI shape. If the region exists in multiple datasets within the designation, the selected region will be propagated.
- **Options...** (displays the Findings tab in Tools -> Options)



Regions resulting from performing the **Transform to All**, **Transform to Remaining**, **Transform to All within Timepoint** and **Transform to Remaining within Timepoint** actions are highly dependent on the quality of the registration that exists between the dataset on which the source region exists and all the datasets to which the region is to be transformed. It is recommended that quality checks be performed within the Registration Manager screen on the accuracy of the registrations prior to performing a region transformation action.

Tools Menu

Options

Select to display **Preferences** Window. XD3 allows certain preferences to be applied on a per user basis. These settings are remembered between runs of the application. See the **User Preferences** section for further detail.

Magnifying Glass

Click and drag a small rectangle to move over images and magnify to various levels. Right click to change magnification factor. The magnifying glass may also be resized by dragging its corner.

Layout Editor

Select to create and save a custom layout. See **Custom Layout** section of this document for details.

New Color map

Select to create and save a simple custom color map. Provide a name for the color map, then right click to add and define a point on the color spectrum. To remove a point, click and drag it away from the color bar. Select OK to save the color map and indicate whether you would like it saved for the current user or all users. If you need to create a more complex color map, please contact Mirada Customer Support or the vendor through which you purchased Mirada software.

Data Management

The Data Management screen is available in review modes which support either gated data, multiple-sequence MR or multi-phase CT. This screen allows the user to specify the shadowing behavior for regions for the data loaded into the review mode. It also contains the default shadowing logic for each review model. Modifications made to this screen are reflected in any saved session.

The contents of this screen are included in saved and restored sessions.

See the **Data Management** section for more information.

Window Menu

New Window

Allows you to open an additional window for multi- monitor display. Window size and placement is saved between launches of the application.

Full Screen

Allows you to maximize the amount of screen space that is available for displaying images. The Toolbox and Toolbar are removed from the view. This function is assigned to a hotkey (F11).

Back to Layouts

Select Back to Layouts from the Data QC, Registration Manager, Findings Table, RT Planning or Report screens to return to the previous image window.

Data QC

The **Data QC** tool is provided to allow you to view attributes from datasets loaded into the application for review. Attributes such as scanner manufacturer, software version, slice thickness, kVP, X-ray tube current and several others may be displayed for the CT data. Likewise, software version, injected dose, delay time, half-life, patient height, patient weight and additional attributes are available for PET data.

If you wish, you may perform validation of this data based on limits that you define via **Preferences** found on the **Data QC** tab from **Tools -> Options** menu. For example, you may want to be warned if the delay time variance from the time of injection to time of scan between time points is greater than a certain amount of time. This Data QC screen will show you the attributes and flag any that are outside the tolerance levels you have set. Additionally, the Data QC screen may be included in a custom report. You may choose which attributes are visible and whether you would like to be prompted to display the Data QC screen on startup if there are validation warnings.

The Data QC screen may be displayed via the Window menu, on the toolbar layout selector, from the on-screen layout selector (Ctrl + Tab) or via a hotkey set in **Tools -> Options** on the User Interface Tab. See User Preferences section for detail on setting hotkeys.

See User Preferences section for detailed instruction on setting up the Data QC items that you wish to have visible on your Data QC screen and which attributes you wish to validate when data are loaded.

Registration Manager

Registrations other than the automatic schemes defined in the review modes are performed from the registration manager. This is the only place these tasks can be performed. The Registration Manager screen may also be displayed from any of the layout selectors. See the **Registration Manager** section of this document for details.

Findings Table

Displays the Findings Table which displays the statistics for any regions of interest that have been defined on the currently displayed images. Findings Table may also be accessed from any list of available layouts including drop down lists and transparent list accessed with **Ctrl + Tab**. Also, Findings Table may be found in the Toolbox from either the **Regions of Interest** panel or **Rulers and Annotation** panel.

Report

Displays the reporting feature which allows you to create custom reports based on report templates. Default templates are provided for each review mode, but you can make modifications and save them back to the same or a new template. Report Screen may also be chosen from any list of available layouts including the drop down lists and the on-screen list accessed with **Ctrl + Tab**. See the Reporting Section of this document for details on creating and editing custom reports.

Secondary Capture

This screen allows the interactive viewing of secondary capture images created within the application. It also allows images loaded (prior bookmarks, image stacks) to be interactively viewed and a cine played where appropriate.

Available Layouts

The hanging protocols available for display of images within each review mode are displayed via the **Window** menu. Each Review Mode contains a selection of Layouts suitable for the selected data sets. These layouts may also be accessed either from the dropdown menu in the upper right corner of the image window or by using **Ctrl + Tab** keys simultaneously to bring up a transparent layout selection menu. When using **Ctrl + Tab**, hold down on the **Ctrl** key and toggle the **Tab** key to scroll through the on-screen menu of layouts. Layouts may also be selected by clicking on them in the transparent layout selection window.

Help Menu

Help

Displays this Help documentation. Help may also be accessed by using the **F1** key.

License

Displays license details. License details may not be visible if your Mirada software is integrated into a third party workstation.

Generate Support Package

Select to initiate the creation of a zip file to a location of your choice containing the following readable information that is often required during a Customer Support inquiry. The following information is included:

- Machine settings such as Name and IP Address
- A configuration comparison list of files found in the XD3 bin folder (Factory vs. Current)
- Public and current user settings
- XD3 logs present on the system: XD3 log, XD3 debug log, XD3 trace log (if present)

Enable Debugging

Select to allow a development environment to connect to the running XD3 instance. This is applied until the XD3 process is restarted. **This feature should only be enabled on advice of Mirada support personnel.**

Update XD3

This feature allows any online updates to be installed and should only be used with involvement of Mirada Customer Support.

About

Displays the version of the application and associated copyright and license information.

Messages

Show Messages

Displayed in this area are messages that may include reports of things that happened during a data load or initial registration. If an icon (yellow or red, indicating warning or error) appears next to the Messages menu item, this indicates that a new message is available and should be reviewed. This icon disappears after the message has been viewed.

Occasionally, there will be messages displayed that you do not need to explicitly acknowledge, as they may be part of a hazard mitigation or messages that help with the use of the application.

Information presented in the messages window is also stored with additional detail in the application log file.

Loading a Saved Session

When the application is launched with one or more saved sessions, the user is presented with the choice of which saved session to restore or, alternatively, the option to start a new session.

When a session has been selected to be restored, the system will attempt to assign the data from the previous session to the same data designations. Any new timepoints will be inserted where appropriate. The following information will be restored:

- Registrations
- Findings
- Key Images
- Bookmarks
- Rulers
- Bi-rulers
- Annotations
- Angles
- Modified PET Quantification Parameters (e.g. weight, height)
- Data Management screen order/anchor settings (e.g. for gated data)

Items can only be restored if the data on which they were defined has been reloaded. For instance, consider a saved session for a two timepoint PET/CT case where a region was defined on each PET. If the session were subsequently restored but with only one of the PET/CT timepoints supplied to the application, only one of the regions will be restored.

The application allows the hardware registration between hybrid datasets to be overridden by a custom registration. If a custom registration has been applied, it will be saved as part of a session. Upon restoring the session the custom registration will be reapplied overriding any hardware registration that may have been present. If this occurs the application will warn the user.

Data Management



This screen is used to specify two different types of binding behavior: **Bindings for Timepoint** and **Bindings for Dataset**. **Bindings for Timepoint** allows the viewing and editing of bindings between different data roles in the same time point. **Bindings for Dataset** allows the viewing and editing of bindings between the same data role across time points. In the case that only a single time point is loaded, **Bindings for Dataset** is not available and the **Bindings for Timepoint** is simply called **Bindings**.

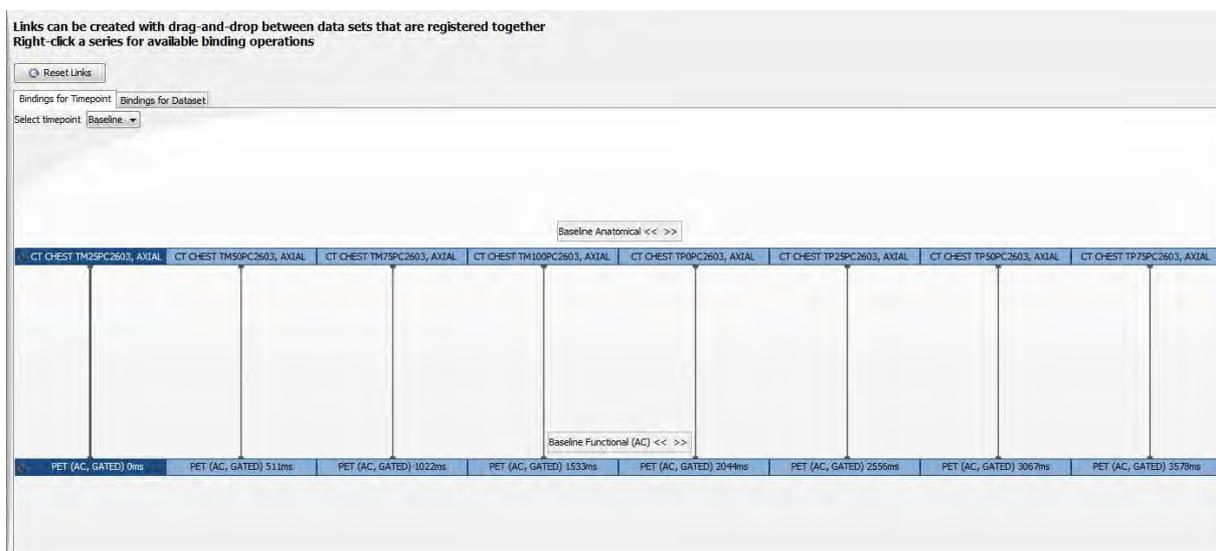
Bindings for Timepoint

This allows viewing and editing of links between different volumes of multi-volume data assigned to different data roles.

XD3 makes certain logical assumptions about how the bindings in one timepoint relate to those in another. These bindings may not be optimal if the acquisition protocols used in each study are not the same.

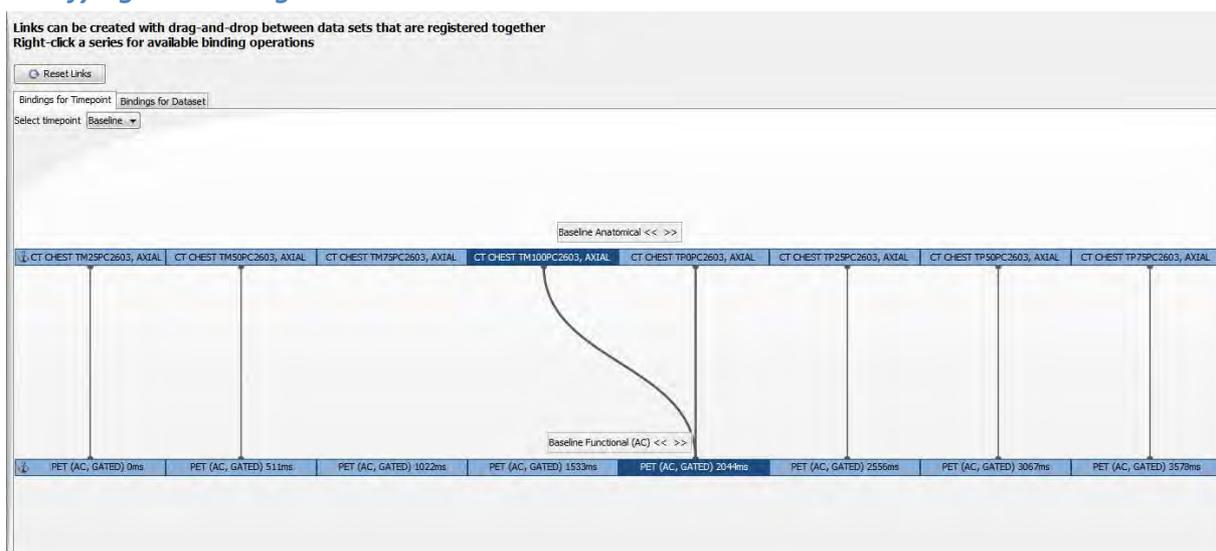
The screenshot below shows the dataset bindings between a gated PET assigned to the Functional role and a gated CT assigned to the Anatomical role. In this instance, there are equal numbers of PET and CT bins and the default bindings are one-to-one. What these bindings represent are links along which shadow regions are created. Drawing a region on the first bin of the PET dataset will automatically create a shadow region on the first bin of the CT. Similarly, creating a region on the second bin of the CT will automatically create a shadow region on the second bin of the PET dataset.

The binding links also affect the volume displayed in the layout views. In the example displayed below, changing the displayed PET volume in a Functional view affects the volume displayed in other Functional views in the layout and it also affects the volume displayed in Anatomical views. This means that switching the view from displaying the first PET bin to displaying the second PET bin makes all views in the layout displaying PET show the second bin. It will also update all Anatomical views in the layout to display the second CT bin as that bin is linked to the second PET bin. This also works on fused views. Cycling through the PET bins on the overlay will update the CT base layer in the view to display the appropriate bin based on the links in the data management screen.



The tab for Bindings for Timepoint displayed above also includes a time point selector. Use this drop-down to select the time point for which bindings are to be viewed/edited.

Modifying the Bindings

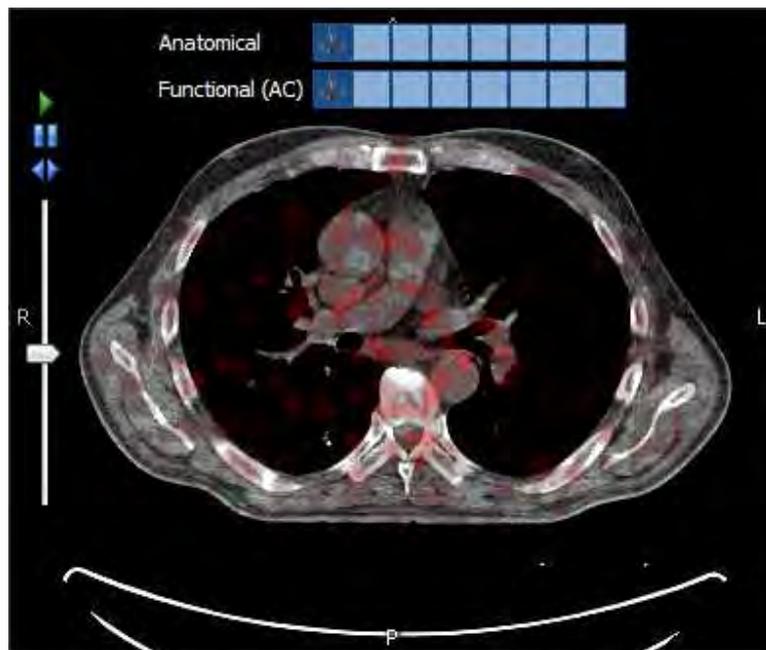


The screenshot above shows modifications made to the default bindings. A link can be removed by first clicking it and then selecting **Remove Binding** from the popup menu. A binding can be added by dragging a volume label to the target volume label. In this example a binding was added between the fourth bin of the CT to the fifth bin of the PET by dragging the fourth CT bin box to the fifth PET bin box.

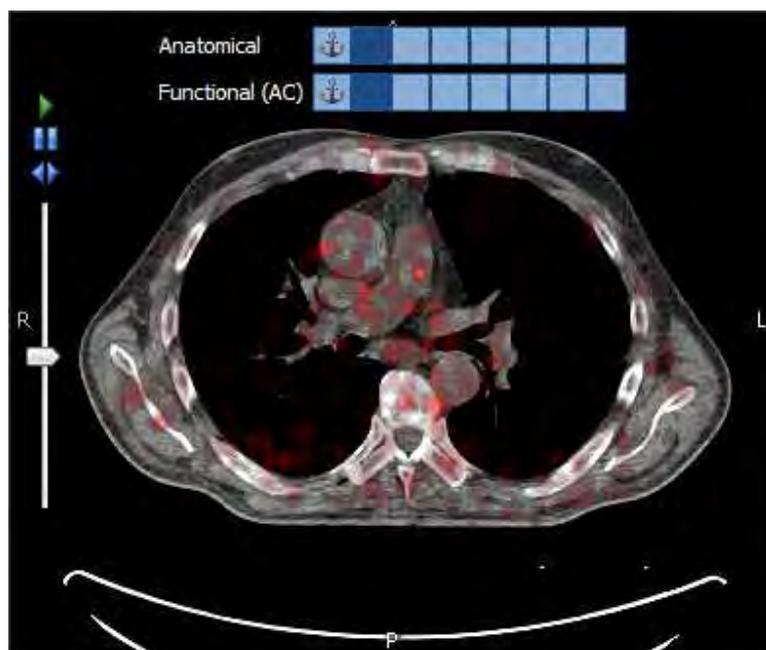
In the example above, drawing a region on the fifth PET bin will create a shadow region on both the fourth and fifth CT bins. Drawing a region on either the fourth or fifth CT bin will create a shadow region on the fifth PET bin. Drawing a region on either the third or fourth PET bins does not create a shadow region on any CT bin. Similarly, drawing a region on the third CT bin does not create a shadow on any PET bin.

To understand how the modified bindings displayed above affect the views displayed in layouts, consider the following procedure:

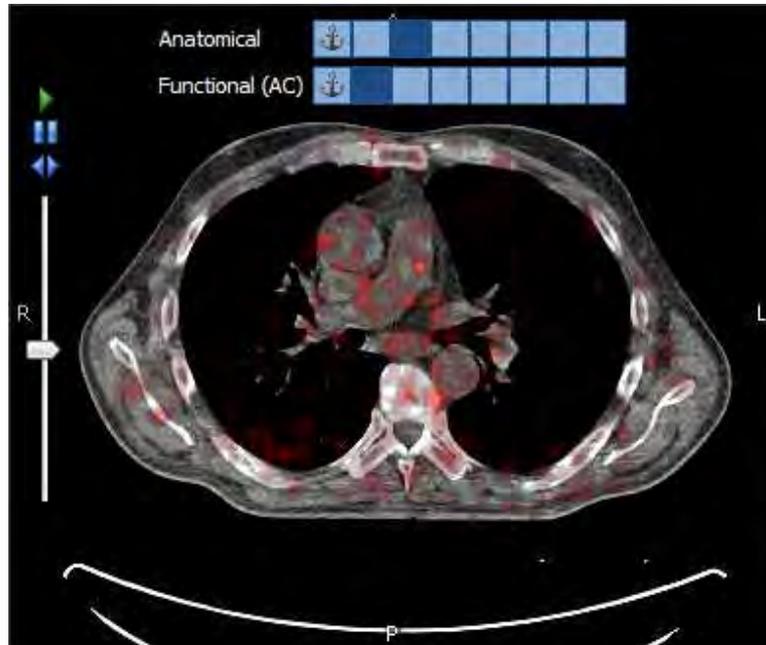
1. In a fused view, enable the navigation controls and select the first bin of the CT (this can be done by clicking the first box next to the Anatomical label). Note that the first bin of the PET is selected as those two bins are bound. See the image below.



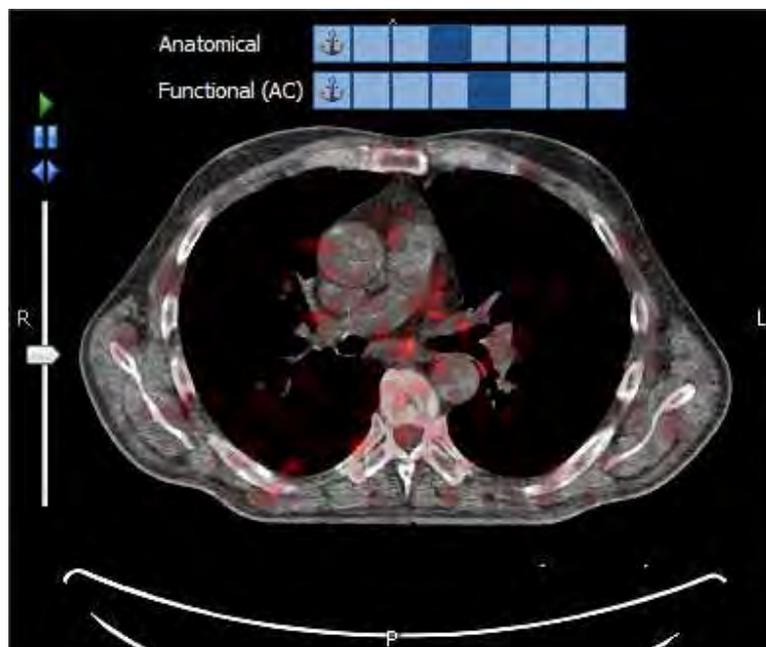
2. Select the second bin of the CT by clicking the second box next to the Anatomical label. Note that the second bin of the PET dataset becomes selected and displayed. See the image below.



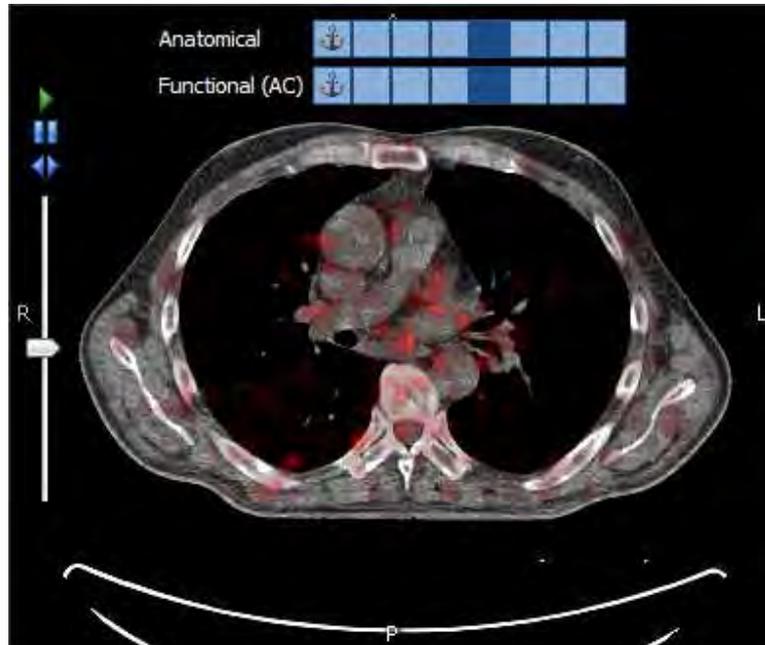
3. Select the third bin of the CT by clicking the third box next to the Anatomical label. Note that the selected PET overlay does not change. This is because the third bin of the CT is not bound to any PET volume. See the image below.



4. Select the fourth bin of the CT. Note that the fifth PET bin becomes selected and displayed as those volumes are bound in the data management screen. See the image below.



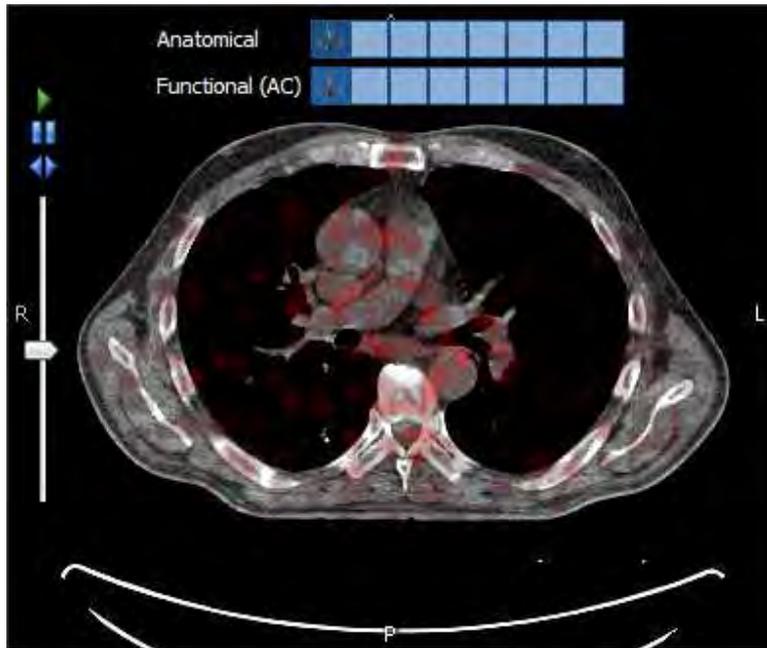
5. Select the fifth bin of the CT. The fifth bin of the PET is also selected as those datasets are bound. In this instance the fifth PET bin was already selected, but had it not been then selecting that CT bin would have changed the selected PET bin. See the image below.



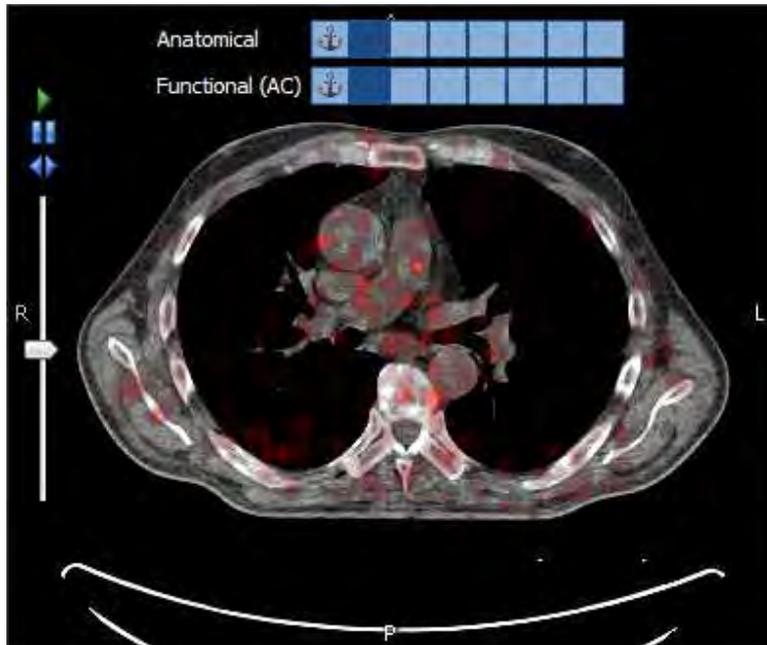
6. From here on there is a direct link between each of the CT and PET bins and they move lockstep as the CT bins are visited in turn.

The same procedure can be carried out by stepping through the PET bins. This is detailed below as there is a special case for dealing with a single bin being bound to many bins on a different data role.

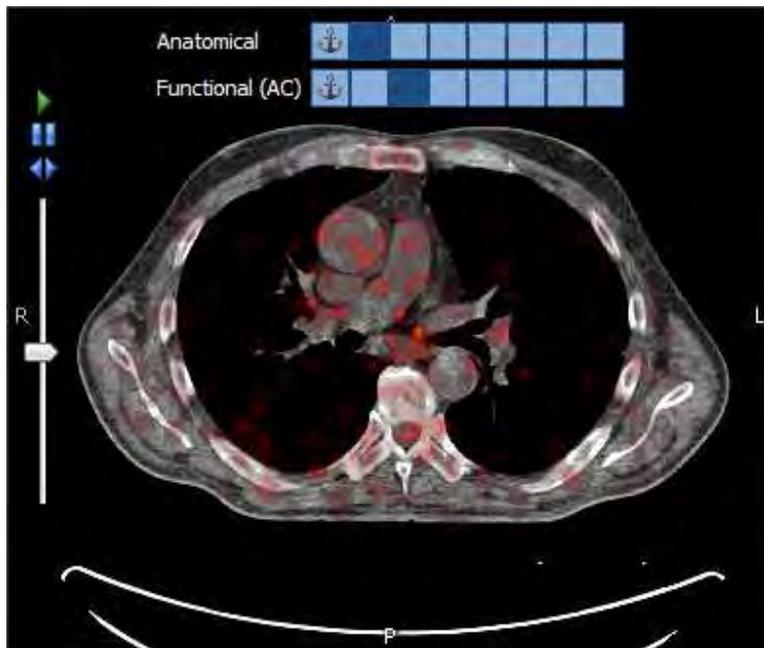
1. Select the first bin of the PET by clicking the first box next to the Functional (AC) label. Note that the first bin of the CT is selected and displayed. See the image below.



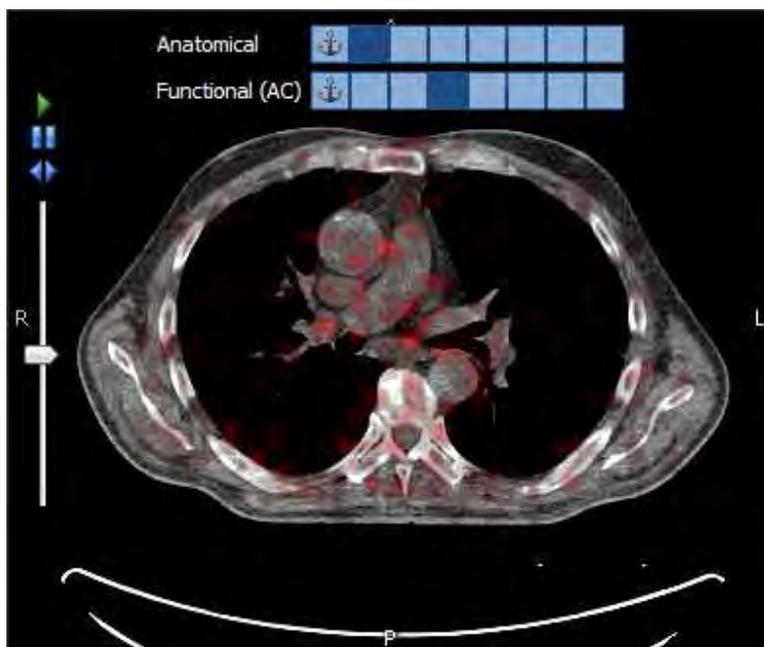
2. Select the second bin of the PET by clicking the second box next to the Functional (AC) label. Note that the second bin of the CT is selected and displayed. See the image below.



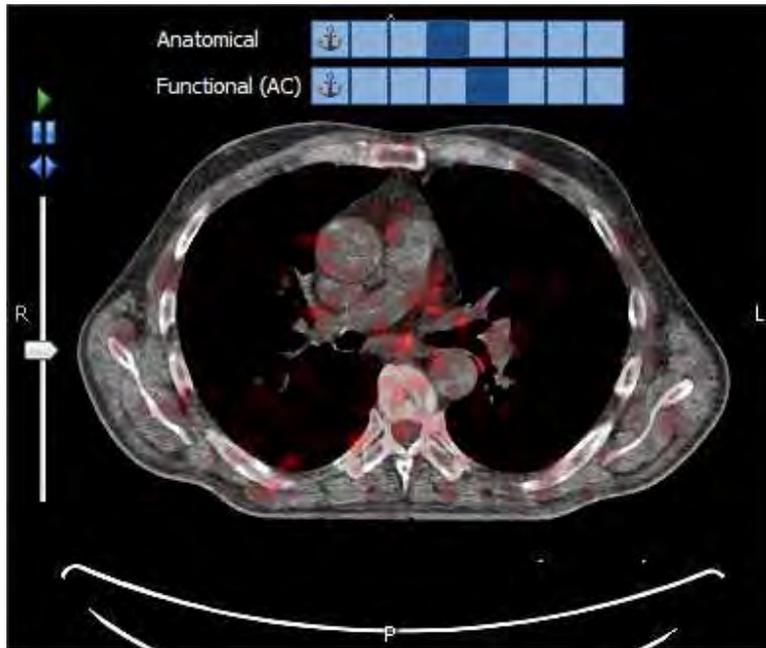
3. Select the third bin of the PET. Note that the selected CT bin does not change. This is because the third bin of the PET is not bound to any CT bin. See the image below.



4. Select the fourth bin of the PET. Note that the selected CT bin does not change because the fourth bin of the PET is also not bound to any CT bin. See the image below.



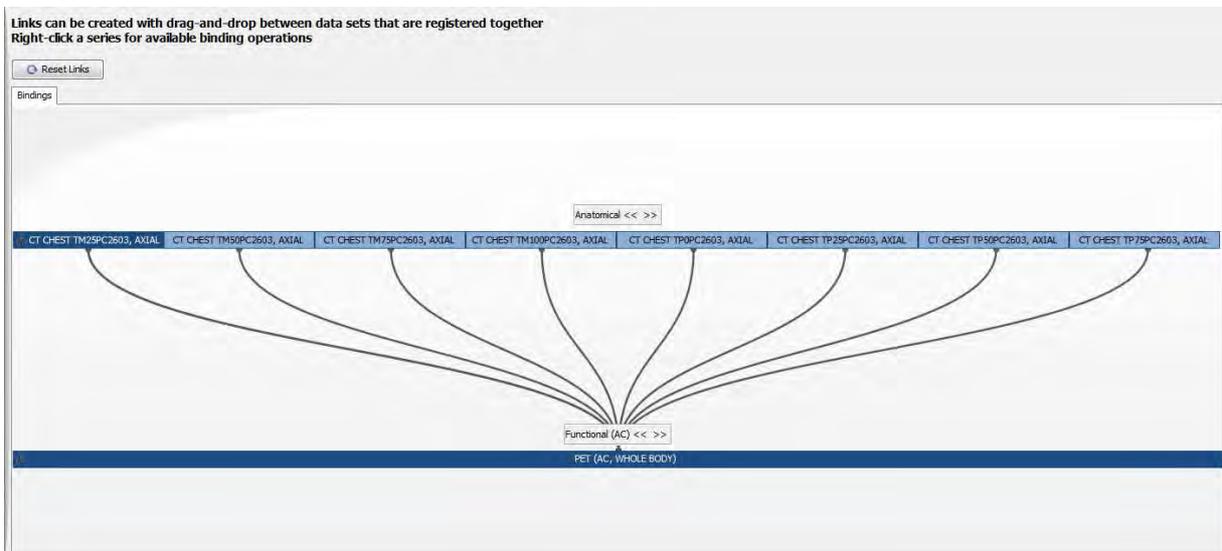
5. Select the fifth bin of the PET. In the data management screen, the fifth bin of the PET is bound to both the fourth and fifth bins of the CT. This ambiguity is always resolved by selecting the first bin to which the PET bin is bound. In this case, that is fourth bin of the CT. See the image below.



- From here on there is a direct link between each of the CT and PET bins and they move lockstep as the PET bins are visited in turn.

The examples considered so far have involved CT and PET data where the numbers of bins were equal in each dataset. The principles covered extend to more complex cases that will be briefly mentioned below.

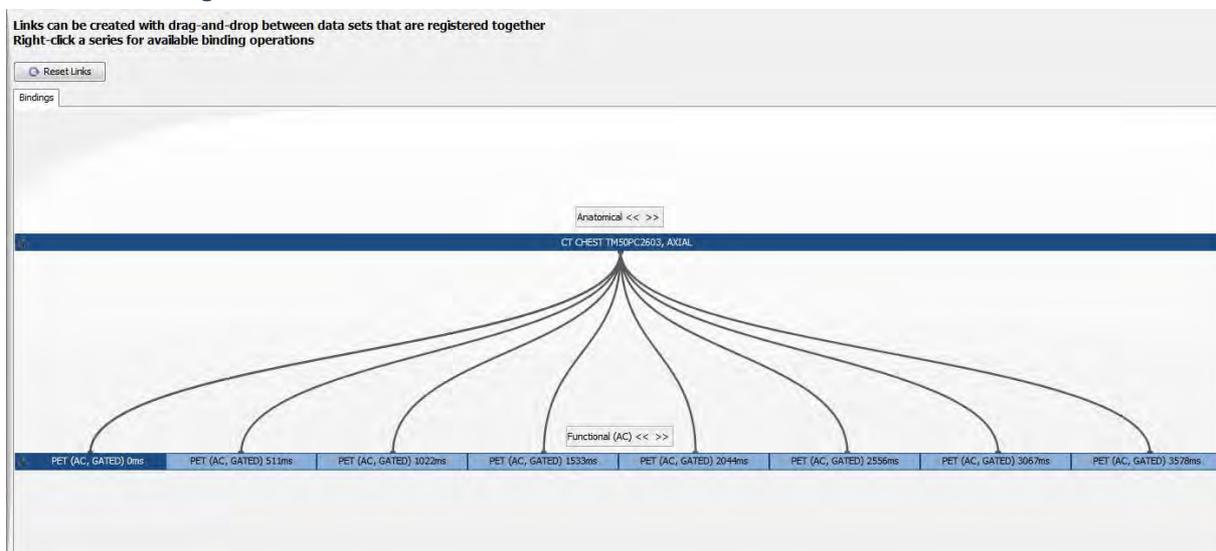
Static PET on Gated CT



By default, all bins of the CT are bound to the PET. Drawing a region on any CT bin automatically creates a shadow on the PET. Drawing a region on the PET automatically creates a shadow region on each of the CT bins.

In a layout, cycling through the displayed CT bins always displays the same PET.

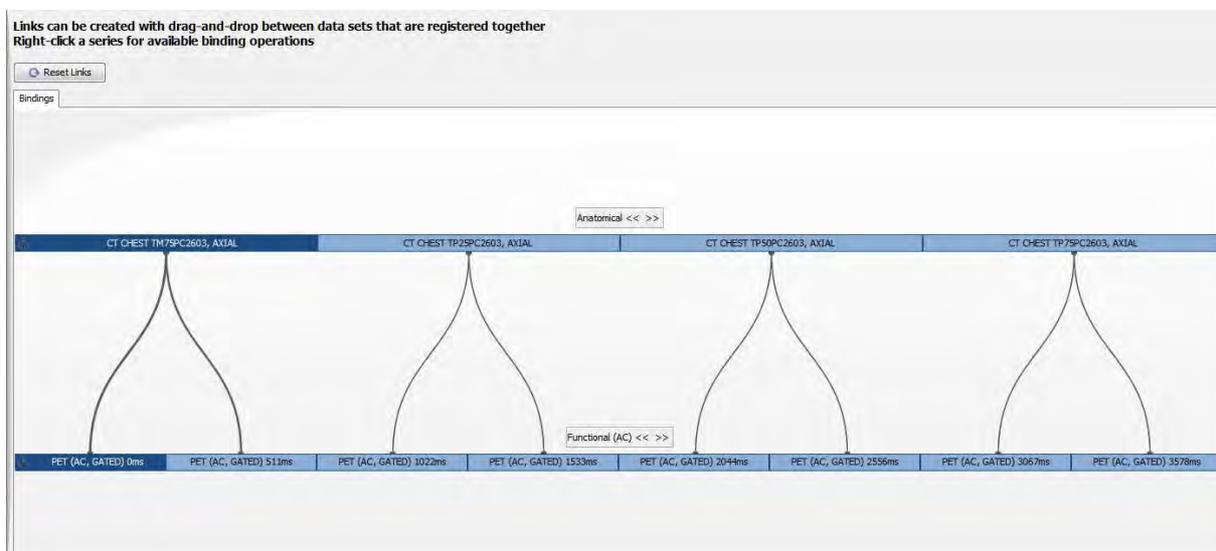
Gated PET on Single CT



By default, all bins of the PET are bound to the CT. Drawing a region on any PET bin automatically creates a shadow on the CT. Drawing a region on the CT automatically creates a shadow region on each of the PET bins.

In a layout, cycling through the displayed PET bins always displays the same CT.

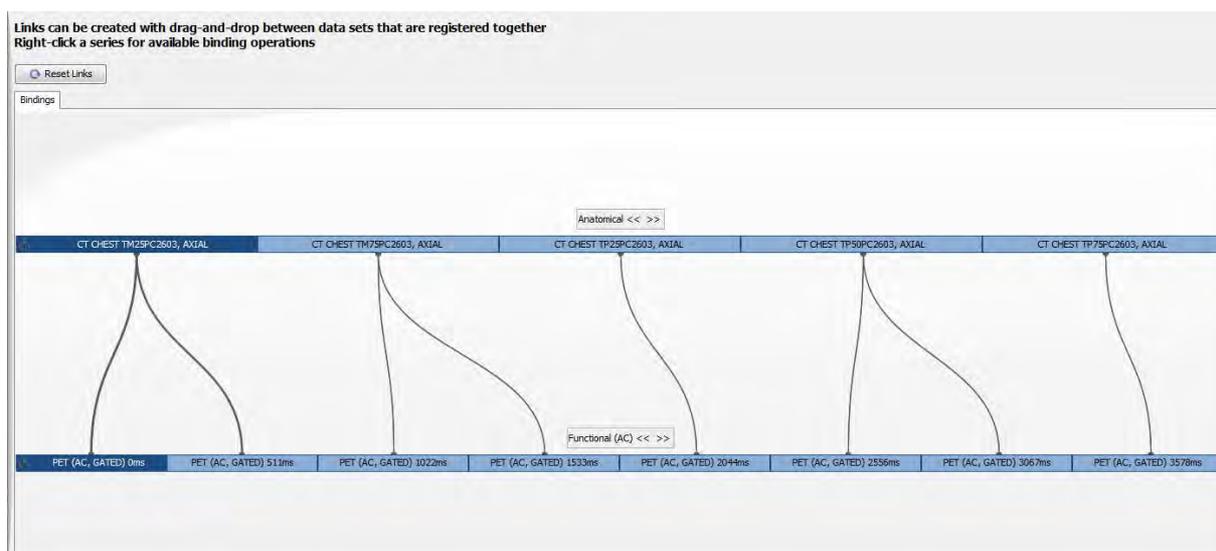
Gated PET on Gated CT – Different Number of Bins



In the above case, eight bins of PET have been loaded against four bins of CT. The default links created have bound two PET bins to every CT bin. Drawing a region on a PET bin automatically creates a shadow region on the associated CT bin. Drawing a region on a CT bin automatically creates a shadow region on the two PET bins to which it is linked.

In a layout, cycling through the displayed PET bins will update the displayed CT bin for every other PET bin visited. Cycling through the CT bins will update the displayed PET bin every time the CT bin changes. As each CT bin is bound to two PET bins, the ambiguity is resolved by picking the first PET bin to which the CT is bound. For instance, selecting the second bin of the CT will select and display third bin of the PET as that is the first bin to which it is bound.

Pictured below is an even more degenerate example of mismatching numbers of bins. In this instance there are five CT bins and eight PET bins.



By default the application will bind each volume to at least one other volume so that nothing is left unbound. It is up to the user to determine whether the default bindings are appropriate and change them accordingly.

Bindings for Dataset

This section allows the viewing and editing of links between the same dataset across different time points. For instance, in a multi-time point gated CT read, the links between the CT bins across different time points can be viewed and edited. See the image below.

This section is only available if multiple time points have been loaded. **Bindings for Dataset** only affect view bindings and, unlike **Bindings for Timepoint**, do not impact shadowing behavior. These bindings are further simplified by being constrained to allowing only single-to-single bindings.



The tab for **Bindings for Dataset** displayed above also includes a dataset selector. Use this drop-down to select the dataset for which bindings are to be viewed/edited.

The image above shows how each bin of the baseline CT relates to the bins of the current CT. In the case shown above, eight bins of CT were loaded into the Anatomical role for the baseline time point and eight bins of CT were loaded into the Anatomical role for the current time point. The default links created by the application have paired them in a simple fashion. Bin 1 of the baseline CT is bound to bin 1 of the current CT. Bin 2 of the baseline CT is bound to bin2 of the current CT *et cetera*.

These links affect the views displayed in the layouts. When the first bin of the baseline CT is selected in a view for display, all other views of the baseline CT are updated to display the same bin. Additionally, all views of the current CT are updated to show the first bin as those bins are linked.

These bindings can be removed by first clicking on a link and then selecting **Remove Binding** from the popup menu that appears. Bindings can be created by dragging and dropping the boxes to each other.

Anchor Volumes

Each data role that supports multiple volumes has the notion of an anchor volume. There is always exactly one anchor volume per multi-volume data role. The anchor volume is the volume that is used when performing registrations. For more information see the **Multi-volume data in the Registration Manager** subsection of the **Registration Manager** section.

The Data Management screen is the place where the volume designated as anchor can be set. To change the anchor volume of a role simply click the right mouse button in any volume box and select **Set as Anchor** from the popup menu.

Registration Manager



The Registration Manager screen contains the following areas, which are described below.

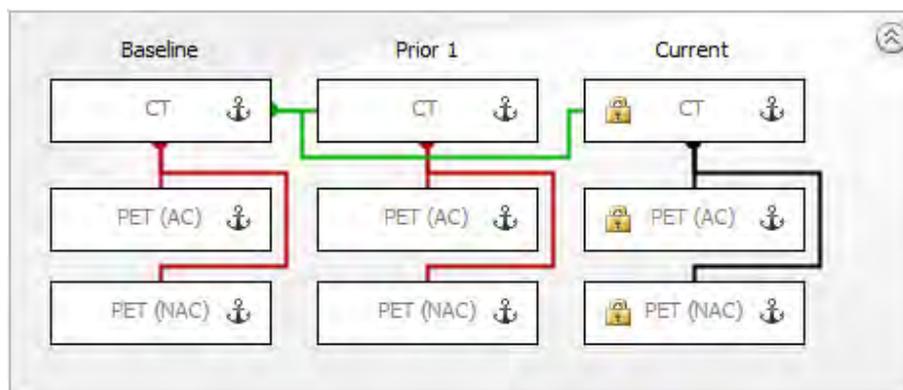
- Toolbar
- Registrations area
- Image area
- Layers Panel
- Visualization Tools Panel
- Automatic Registration Panel
- Manual Registrations Panel
- Image Area context menu

Toolbar

The toolbar contains the same tools that are available elsewhere in the application. The tools are also available via the context menu and may alternatively be assigned to hotkeys. See the **Toolbar and Menus** section of this document for detailed descriptions for each tool.

Registrations Area

This area displays a graphical representation of the relationships between the datasets loaded into the review mode. In the example below, there are three time points of PET/CT data loaded. The black, red and green lines illustrate datasets with registration relationships that may be viewed, evaluated or reregistered.



Each column represents a single time point. Each box represents a data role within the time point.

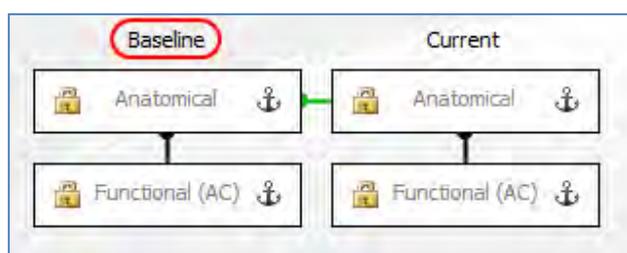
The black lines represent datasets that share the same frame of reference and are hardware locked. Those datasets that are hardware locked will be displayed with a lock icon, as above. A context menu with dataset-specific options is available by clicking the right mouse button within the dataset rectangle. Selecting the 'Unlock' action will unlock the frames of reference so that registrations can be performed with other datasets.

The red lines represent rigid registrations, including the implicit center alignment created when clicking 'Reset Registration'. Green lines represent deformable registrations.

Click on the lines to select a relationship. Once a relationship is selected, the datasets will be displayed in the image area and a number of tools will be available to review, evaluate or manipulate the registrations.

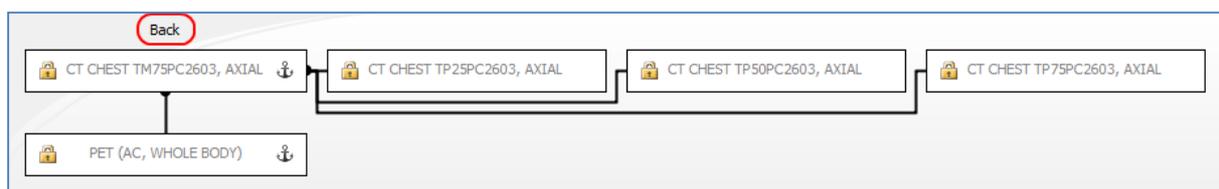
Many review modes allow the loading of multiple volumes into a data role. This may be gated CT, gated PET, multi-phase MR or multi-sequence MR. When multiple volumes are loaded into a role, one of them is designated the **anchor**. There is always exactly one anchor volume per role. In the case that a data role contains a single volume, that volume is always the anchor. The anchor is a special volume. All registrations that are performed by the application are between anchor volumes. In the case of a gated PET and a gated CT loaded into General Fusion review mode, the registration that exists between the Functional (AC) role and the Anatomical role is the registration performed between the anchor Functional (AC) volume and the anchor Anatomical volume.

By default, the registration manager displays an overview matrix where only one box is displayed per data role. See image below.



In this case, two time points of data were loaded. Both the current and baseline Anatomical roles were populated with four gates of CT. The Functional (AC) roles were populated with a static PET series. In total, 10 volumes have been loaded (8 gates of CT and two PET volumes). The registration matrix displays only one box for each role and the registration relationships between those roles. To see a detailed view of each time point, click its time point label above the grid (highlighted in red above).

Expanding a time point displays the relationships between all volumes loaded into that time point. An example is displayed below.



The expanded baseline time point shows the four gates of CT and how they relate to static PET. All the gates of the CT are linked to the anchor CT gate. The anchor CT gate is also the volume that is related to the anchor PET volume.

This expanded view behaves much like the overview view of the registration matrix. Click a link between any two volumes to view the registration between those two volumes. The registrations can be manually edited as expected and automatic registrations can be run. For datasets that share a frame of reference (denoted by lock icons), it is necessary to first unlock those datasets before the registration between them can be modified.

To return to the overview registration matrix, click the **Back** button highlighted in the image above.

To change the anchor volume for a data role see the **Anchor Volumes** subsection of the **Data Management** section.

Image Area

This is the area where the selected datasets are displayed.

Layers Panel

The **Layers** Panel in the Registration Manager **Toolbox** displays a row for each dataset selected and displayed in the image area. Next to each layer is a box to check to include or remove that dataset from the current image view. By highlighting a particular layer (that row is highlighted in blue), you choose the layer for which controls are active. For example, when using the Transparency Tool, the system adjusts the transparency of the selected layer within the current image view.

Visualization Tools Panel

These QA tools are available to visualize the displacement following image registration:

There is a drop down menu which includes the following QA tools to show the displacement after image registration:



Show Displacement Map displays the area of displacement with a color map; warm colors indicate high areas of deformation and cool colors indicate areas of low displacement.



Show Displacement Grid displays the area of displacement with a grid; areas of high grid displacement indicate high areas of deformation.



Show Displacement Arrows the amount and direction of deformation or displacement are indicated by arrows, where the length is proportional to the amount of deformation.

These overlay tools are available to assess the registrations in a drop down menu:



Show Checkerboard Overlay: both layers are represented with alternating squares to evaluate registration between the two.

 **Show Inset Overlay:** All layers except the base layer are drawn in the region outside the inset window with the transparency settings adjusted as though the base layer had been hidden.

The size of the overlay tools may be adjusted with the slider bar.

 **Show Displacement Value** allows the displacement value for any specific point in the registration to be assessed. Use the cursor to point to any area on the registered datasets in the Image Area and view displacement value.

Any of the visualization tools may be set to hotkeys via **Tools -> Options** by selecting the **Hotkey Configuration** button on the User Interface tab.



Functions that rely on the inversion of the registration deformation map such as the cross-hair alignment and Region of Interest propagation may exhibit inconsistent and asymmetrical behavior in certain situations. For example in Adaptive Planning review mode, if the user were to navigate the cross-hair to a location A in the Baseline Planning the software will automatically place the cross-hair at a particular corresponding location, B, in the Current Planning. However, if the user were then to move the cross-hair around in the Current Planning and then place it back at location B, the position of the cross-hair in the Baseline Planning may not be at location A."

This applies to any deformable registration either within a timepoint or across timepoint. For example, in Fusion Analytics in which a deformable registration exists between the Planning and MR images, the Planning dataset should be used for cross-hair navigation.

Automatic Registration Panel

Automatic Registration tools are:

- **Reset Registration** – Datasets are aligned using the field of view center of the displayed datasets for the current registration relationship.
- **Automatic Rigid** – Selected datasets are aligned using the automated rigid algorithm.

The following presets are available by selecting the  next to the Automatic Rigid button:

- **Medium** – The default setting.
- **Fast** – Runs faster as it works at a coarser resolution and for fewer iterations than the Medium setting.
- **Fine** – Runs slower as it works at a finer resolution and for more iterations than the Medium setting.

This choice is saved between launches of the application.

- **Multi-Modal Deformable** – Selected datasets are aligned using the automated multi-modal deformable algorithm.

The following presets are available by selecting the  next to the Multi-Modal Deformable button:

- Default – This is a generic preset that works well over a wide variety of multi-modal registration use-cases.
- CT-PET Emission – A preset optimised for CT-PET registration. It is largely the same algorithm as Default, but with stronger constraints on transformation smoothness to account for weaker structural information.
- CT-MR – A preset optimised for CT-MR use-cases. It is slower than the default, but generally gives more accurate registrations.
- CT-CT – A preset optimized for CT-CT registration where the images have been acquired from different scanners, or for registering contrast enhanced CT with a non-contrast enhanced CT.
- CT-CBCT – A preset optimized for registering a planning CT to a conebeam CT.
- MR-MR – A preset optimized for registering MR to MR.

This choice is saved between launches of the application.

- CT Deformable – Selected datasets are aligned using the CT to CT deformable algorithm.
- Smooth Deformation - Takes an existing deformable registration and filters it to reduce large deformations. Successive iterations of the Smooth Deformation command further reduce the deformation field until it reaches a maximum smoothness.



When an automatic registration scheme is run with data assignments containing multiple related series (e.g. Gated CT or PET, Multi-phase CT, Multi-sequence MR), the first series/volume assigned is the one used for registration for registrations involving that assignment. This may or may not be the optimal series/volume to use for registration depending on the acquisition protocol. This can be modified on the Data Management screen by changing the 'Anchor' for the assignment and reviewed on the **Registration -> Registration Manager** to ensure that the registrations are satisfactory.

Manual Registrations Panel

Manual Registration tools provide a means of defining your own transformation between two datasets by dragging the mouse to slide (translate and rotate – rigid transformations) the base image overlay with respect to the base image. This technique relies on a visual examination of the registration by the user.

With the layout set to **Fused**, the manual rigid registration control is active over the entire registration view. Dragging on the green circle controls rigid *rotations*; dragging elsewhere controls rigid *translations*.

With the layout set to **Landmarks**, you may define your own registration between two datasets by defining two equally numbered sets of landmark points at corresponding sites on the source and target views of the data. Use the left mouse button to place a landmark in any orthogonal view for the source or target data sets. An unpaired landmark will display as a cross on the image, place your mouse on the corresponding dataset. When landmarks are placed on both the source and target datasets, a label will be assigned and displayed on the image window. That label will also be added to the Marker table. You may visualize a particular marker by highlighting it in the Marker table and selecting the **Go To** button. Markers may be deleted by highlighting the marker in the table and selecting the **Delete** button.

The **Image Area** initially displays the axial, coronal and sagittal views for the two datasets that are selected in the registrations area. The image views behave as any other orthogonal image view in the main application. For example, double clicking enlarges the currently selected image to fill the image area.

Loaded Registrations

This area allows a loaded registration to be applied when the relationship for which it was created is displayed. Select a relationship to see the available registrations that can be applied.

Findings Table

About the Findings Table



The **Findings Table** is where detailed statistics and graphs for regions and ruler measurements are displayed. The screen has a number of tabs predefined in the software. Each tab on the **Findings Table** has a statistics table and a graph area. The statistics that are displayed by default as appearing in the statistics table or plotted on the graph are defined for each tab.

Saving the Tables and Graphs for Use Outside the Application

Use the **Snapshot Table** button to save a table as a snapshot in the Image Gallery. Objects saved in the Image Gallery can be exported as DICOM Secondary Capture, .BMP, .PNG, or .JPEG files.

Use the **Copy Table** button to copy the table to a Windows clipboard for use in any application that accepts data from a Windows clipboard. Examples include Microsoft Excel, Word, etc.

Click the right mouse button on any graph to:

- Copy to Windows clipboard
- Save to a file destination of your choice
- Save the graph to the image gallery to be exported as DICOM Secondary Capture, .BMP, .PNG, or .JPEG files.

Accessing the Findings Table



The **Findings Table** may be accessed from several points within XD3:

- By selecting the **Findings Table** icon from the Regions of Interest panel of the Toolbox
- By selecting the **Findings Table** icon from the Rulers and Annotation panel of the Toolbox
- A list of available layouts including drop down lists and transparent list accessed with **Ctrl + Tab**
- By selecting **Window -> Findings Table** from the menu

The tables found under each of the tabs include the following columns:

- Region Name
- Lymph Column (indicates if a region has been set as a lymph node)
- Dataset column
- Quantification measure column (Rows displayed for each measure set for display on the tab)
- Unit column (displays the unit of measure)
- One column per time point using the time point naming convention (e.g. baseline)
- Tracking column (displays the tracking mode) showing the percentage relative to the value being tracked

To get back to the image window, select the **Back to Layouts** button in the upper left of the screen.

Findings Table Toolbox

Settings

Tracking mode specifies the way in which the comparison statistics are calculated and displayed for rulers and regions in the statistics table.

- Baseline calculates the statistics relative to the baseline scan
- Waterfall calculates statistics relative to the previous study
- Min to Date calculates statistics relative to the time point containing the minimum value for the statistic being calculated; only time points prior to the one being calculated are considered when looking for the minimum value

The **Dataset Selector** indicates for which set of data the statistics table and graphs will be displayed.

The **Options** button allows you to choose whether or not you want to include graphs and tables in your display. Place a check mark in the column to indicate your preference. Use the buttons at the bottom of the Quantification Options dialog box to include All Tables, No Tables, All Graphs or No Graphs

Findings

The findings include regions, measurement, and annotations created on an image. You may modify the created findings' names, colors and viewed statistics by double-clicking the finding name. When the mouse pointer hovers over any ROI or Ruler in this panel, the tooltip will display statistics or measurements. This feature is most useful with ROIs if a region has been projected.

The screenshot shows the Findings Table Toolbox interface. It includes a list of regions (Region 1, Region 2) and a table of statistics. The table has columns for Role, Dataset, Min, Max, Mean, Median, RMS, σ , Volume, and Units. The data is as follows:

Role	Dataset	Min	Max	Mean	Median	RMS	σ	Volume	Units
Baseline PET (AC)	PET WB (AC, WHOLE BODY)	2.5	5.0	3.3	3.1	3.3	0.6	3.2	SUV BW
Baseline CT	CT Spiral 5.0 B40s AXIAL	-995.0	208.0	20.2	47.0	167.2	166.0	2.8	HU
Baseline PET (NAC)	PET WB-uncorrected (NAC, WHOLE BODY)	-	-	-	-	-	-	-	US
Prior 1 PET (AC)	PET WB (AC, WHOLE BODY)	2.5	5.8	3.5	3.3	3.6	0.8	6.1	SUV BW
Prior 1 CT	CT Spiral 5.0 B40s AXIAL	-1016.0	182.0	-85.2	28.0	313.1	301.3	6.1	HU
Current PET (AC)	PET WB (AC, WHOLE BODY)	2.5	10.5	4.4	3.8	4.8	1.9	12.7	SUV BW
Current CT	CT Spiral 5.0 B40s AXIAL	-1022.0	194.0	3.5	48.0	214.7	214.7	12.2	HU

The Findings panel toolbar contains the following options:

-  Delete the selected finding
-  Go To the selected finding
-  Show or hide the selected findings
-  Display the Findings Table
-  Link the selected findings
-  Show the Dose-Volume Histogram
-  Projects the selected finding to all time points
-  Projects the selected finding within its time point

Right click on any selected Finding to:

- **Delete**
 -  This action is also available from the toolbar.
- **Copy Statistics to Clipboard**
- **Copy Statistics to the Image Gallery**
- **Display Structure Graphs**
 -  This action is also available from the toolbar.
- **Go To Finding**
 -  This action is also available from the toolbar.
- **Go to Hottest Voxel**



If the **Go To Hottest Voxel** tool is used on a region with more than one voxel with the highest intensity value, then only one of these voxels will be identified.

- **Create a ruler from the region**
- **Toggle to indicate lymph node**
- **Unlink**

- **Link:** There are two types of findings: rulers and regions. Rulers include uni-rulers, bi-rulers and angles (annotations are not classed as findings). Regions include isocontour regions (with threshold), filled regions, 2D rectangles, 2D ellipses and regions painted with the freehand paint tools. Ruler findings can always be linked to other ruler types. They can also always be linked to region types. Region findings can be linked to ruler findings but are restricted as to which other regions they can be linked. A region can only be linked to another region that was defined on the same data role. E.g. a region defined on the Anatomical data role in General Oncology Review can only be linked to another region defined on the Anatomical role and not to one defined on the Functional role. This is further restricted to only being able to be linked to another region defined on the same role but not on the same dataset. E.g. a region defined on gate 1 of a gated CT assigned to the Anatomical role can be linked to a region defined on gate 2 of the same gated CT, but not to another region defined on the same gate 1. This restriction does not apply across time points. A region on gate 1 of a CT on the baseline time point can be linked to a region defined on gate 1 of a CT on the current time point.



This action is also available from the toolbar.

- **Show/Hide regions**



This action is also available from the toolbar.

- **Project to all by Type** : with a region selected, this option will propagate a finding to the equivalent dataset designation in all time points by recreating the region in each time point using the means by which the region was originally created (i.e. absolute threshold, % max threshold). If the region exists in multiple time points, then the value will be taken from the selected time point.



This action is also available from the toolbar.

- **Project to all by Volume:** with a region selected, this option will project the region to the equivalent datasets designations in all time points by maintaining the volume of the original region. If the region exists in multiple time points, the volume value will be taken from the selected time point.
- **Project to all within Volume by Type:** with a region selected, this option will project the region to all datasets from the same frame of reference (i.e. bins of a gated dataset, phases of a multi-phase CT or sequences of multi-sequence MR) and create shadows on each of them. If the region exists in multiple datasets, then the absolute threshold value is taken from the selected dataset.



This action is also available from the toolbar.

- **Transform to All:** with a region selected, the region will be transformed to the equivalent dataset designation in all time points using the existing registration to transform the ROI shape. If the region exists in multiple time points, then the selected time point will be propagated.
- **Options ...** (displays the Findings tab in **Tools -> Options**)

There are additional options for projecting and transforming findings which are turned off in the menu by default, but may be enabled via Tools-> Options on the Findings tab. These additional tools are:

- **Project to remaining by type:** with a region selected, this option will propagate the selected region to the equivalent dataset designation in time points where the region does not already exist by recreating the region in each of the time points using the means by which the region was originally created (i.e. absolute threshold, % maximum threshold)
- **Project to Remaining by volume:** with a region selected, this option will propagate the region to the equivalent dataset designation in time points where the region does not already exist by maintaining the volume of the propagated region. If the region exists in multiple time points, then the volume value will be taken from the selected time point
- **Transform to remaining:** with a region selected, this option will propagate the region to the equivalent dataset designation in all time points that do not contain the region. The existing registration will be used to transform the ROI shape. If the region exists in multiple time points, then the selected time point will be propagated.
- **Project to remaining within timepoint by type:** with a region selected, this option will project the region to all datasets from the same frame of reference (i.e. bins of a gated dataset, phases of a multi-phase CT or sequences of multi-sequence MR) where the region is not currently defined and create shadows on all datasets to which the role on which the region was defined are linked. If the regions exists in multiple datasets, the absolute/threshold value will be taken from the selected dataset.
- **Transform to all within timepoint:** with a region selected, this option propagates the region to all datasets within the same frame of reference (i.e. bins of a gated dataset, phases of a multi-phase CT or sequences of multi-sequence MR) using the existing registration to transform the ROI shape. If the region exists in multiple datasets within the same frame of reference, the selected region will be propagated.
- **Transform to remaining within timepoint:** with a region selected, this option projects the region to the other datasets within the data designation (same frame of reference) that do not contain the region, using the existing registration to transform the ROI shape. If the region exists in multiple datasets within the designation, the selected region will be propagated.



Regions resulting from performing the **Transform to All**, **Transform to Remaining**, **Transform to All within Timepoint** and **Transform to Remaining within Timepoint** actions are highly dependent on the quality of the registration that exists between the dataset on which the source region exists and all the datasets to which the region is to be transformed. It is recommended that quality checks be performed within the Registration Manager screen on the accuracy of the registrations prior to performing a region transformation action.

Findings Table Tabs

The Findings screen is populated with different tabs that contain subsets of the statistics available. Each tab is described in turn below. Each tab contains a table of results and a chart area where charts that have been enabled are displayed. The table contains statistics calculated for each finding at each time point in which it exists. The statistics calculated depend on the tab selected. There will be one row in the table per statistic per finding.

Statistics

Statistics for regions are calculated from the values of all voxels whose center is included within the region. The following, primary, statistics are available within the application.

- Max – The maximum intensity of all the included voxels.
- Min – The minimum intensity of all the included voxels.
- Mean – The mean intensity of all the included voxels.
- Median – The median intensity of all the included voxels.
- StdDev – The standard deviation of all the included voxels.
- Threshold – The lower threshold value of an isocontour region. This statistic only applies to isocontour regions.
- Upper Threshold – The upper threshold value of an isocontour region. This statistic only applies to isocontour regions.
- Volume – The volume in cubic centimeters of the region.
- Volume Doubling Time – The time in days that it would take the region to double in volume.
- Peak – The PERCIST peak.
- BiLongAxis – The long axis measurement for a 2D ruler.
- BiShortAxis – The short axis measurement for a 2D ruler.
- BiRulerAuto – If the finding has been marked as a lymph node, then this statistic has the value of the short axis measurement for a 2D ruler. If the finding has not been marked as a lymph node, then this statistic has the value of the long axis measurement for a 2D ruler.
- UniRuler – The length of a ruler.
- Angle – The angle in degrees for an angle measurement.

NOTE: As only voxels whose center lies within the region are considered when calculating statistics, the Volume statistic will always be a multiple of the voxel volume of the dataset on which the region is defined. Partial volume correction is not applied.



Automatically shadowed regions will be quantified in the resolution of the dataset onto which the region was shadowed. Only voxels whose center lies within the region are considered when calculating statistics. If the dataset on which the original region was defined and the dataset onto which the region was shadowed are of a different resolution, the regions may have a different Volume statistic as the volume will always be a multiple of the voxel volume of the dataset on which the region is defined. For instance, a region defined on a CT dataset and automatically shadowed onto the PET may have a different Volume statistic when calculated on the CT compared the Volume statistic calculated on the PET if the CT dataset is of a different resolution to the PET.

It follows that any statistic derived from the Volume statistic (e.g. Volume Doubling Time) will be different for a finding shadowed between a pair of datasets if the Volume statistic is different for that finding.

SUV Peak

The SUV Peak calculation is a method to provide a robust measure of tracer activity in PET imaging. It refers to the maximum average SUV within a small fixed-size ROI. The implementation used by XD3 follows the definition provided in the PERCIST protocol.

XD3 displays smooth images and contours, meaning that both the displayed images and contours are interpolated to produce a display without square edges around each voxel. However, quantification is always performed on the original voxels avoiding any form of interpolation or partial volume correction. For all ROIs, the quantified voxels are those whose centers fall inside the curve. This is illustrated in Figure 1, where the quantified voxels have been shaded for the region defined by the blue contour.

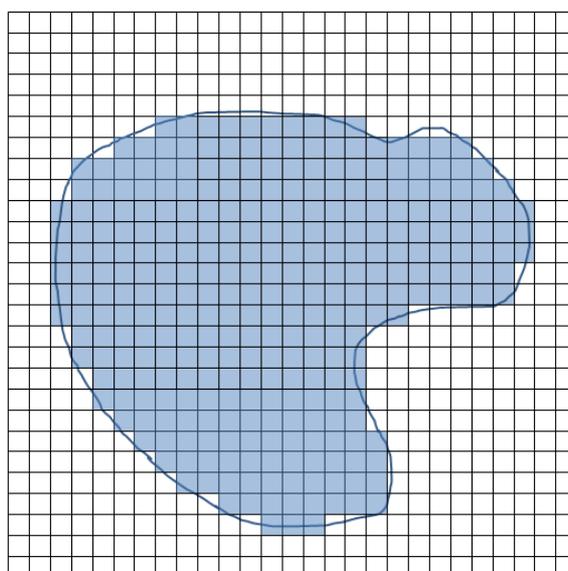


Figure 1: Quantified Voxels are Shaded

A sphere of diameter approximately 1.2cm (to produce a 1cm^3 volumetric sphere) is used to calculate the Peak value. This is referred to as the SUV Peak kernel. For all voxels in a region, the SUV Peak kernel is placed such that the center of the kernel is over the center of the voxel being assessed. The mean intensity of all voxels within the kernel is computed. The SUV Peak is the maximum of all the mean values computed from placing the kernel at each voxel in the ROI. For voxels near the edge of the ROI, some voxels within the SUV Peak kernel are used in the calculation of the mean SUV whether or not those voxels are inside the region as illustrated in Figure 2. The SUV Peak kernel is also quantized using the same approach as illustrated in Figure 3, specifically each voxel whose center is inside the kernel is used for the mean calculation.

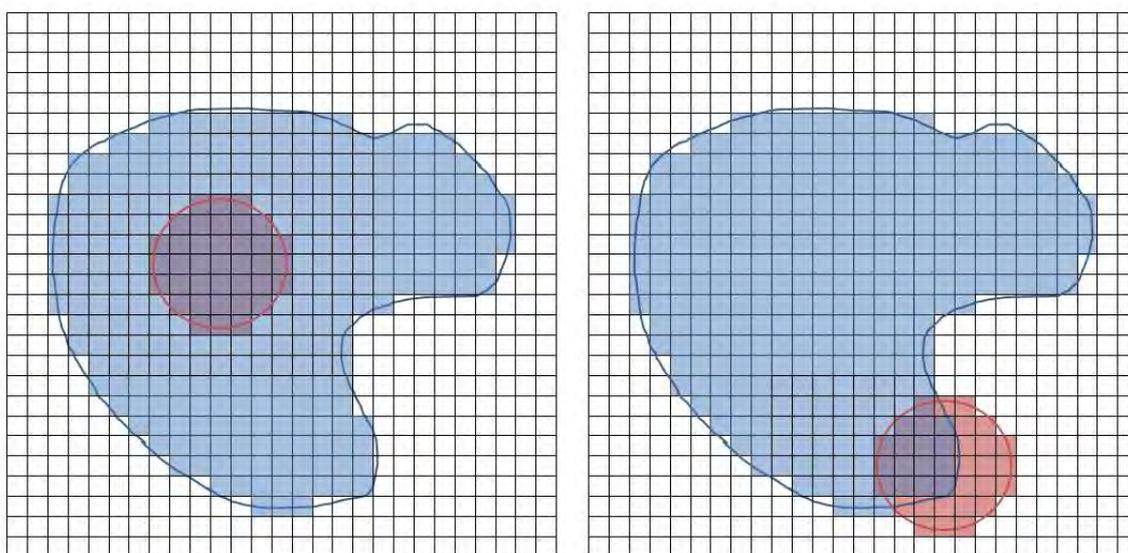


Figure 2: SUV Peak Kernel Counts Voxels Outside ROI

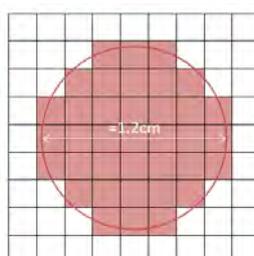


Figure 3: SUV Peak Kernel Voxels are Shaded



Due to its definition, the peak value may include voxel values from outside the ROI boundaries when the ROI is near an adjacent area of the image with high PET values. The user should treat the peak value with caution where high PET voxels are within 0.7 cm of the ROI boundaries.

Volume Doubling Time

The volume doubling time can only be calculated when more than one timepoint of data has been loaded. It is based on the rate of change of the volume statistic. The rate of change is calculated from the volume of a region at a particular timepoint and the volume of the same (linked) region in the immediately preceding timepoint. This means that the volume doubling time cannot be calculated for the baseline timepoint (as there is no preceding timepoint), nor can it be calculated for a region if a linked region does not also appear in the immediately preceding timepoint.

The formula for the volume doubling time, t_D , is:

$$t_D = \frac{t \cdot \log 2}{\log\left(\frac{V(t)}{V_0}\right)}$$

Where V_0 is the volume of the region and the preceding timepoint, $V(t)$ is the volume of the region at the current timepoint, and t is the time, in days, between the two volume measurements.

Volume Doubling Time is not computed for a data role when a finding contains more than one region on the data role. For instance, if two linked regions are defined on a gated CT, Volume Doubling Time is not computed for that gated CT as there is no definitive Volume statistic.



The volume doubling time calculation becomes more robust the larger the regions become. At small volumes where the region volume consists of only a few voxels, the potential error in the reported volume may be quite large. The user is advised to use the Data QC screen to check the voxel dimensions when making a judgement as to how to interpret the volume doubling time. In addition, the volume doubling time calculation may become very large and sensitive when the volumes in consecutive timepoints are similar.



The volume doubling time statistic is derived from the volume statistic. It is an estimate of the true tumor volume doubling time and depends on the accuracy of the regions drawn. The region should be checked on every slice on which it exists to ensure it is as accurate as possible.

Aggregation of Statistics

Typically, only a single value is calculated for a particular statistic for a finding in a time point. For instance, if a linked finding contains two linked regions: one on the baseline PET and one on the current PET, then there would be one Max value calculated for the finding at the baseline time point and one Max value calculated for the finding at the current time point. This would be displayed as a row in the table.

In the case where the baseline PET is a gated PET and the current PET is also a gated PET then potentially many more values are calculated. If each of those PET datasets contained four bins then it is possible to define a region on each of the PET bins on the baseline time point and on each of the PET bins on the current time point and then link all of those regions into a single finding. When displayed in the findings table, an aggregate statistic is calculated for each time point. In this example, the four regions on the baseline PET could have Max SUVs of 4.1, 4.3, 3.9 and 4.0. The aggregate Max is the maximum of those values which is 4.3 in this case. The following table shows the operation used to aggregate the primary statistics for display in the table.

Statistic	Aggregation Method
Max	maximum
Min	minimum
Mean	mean
Median	mean
StdDev	mean
Threshold	a value is only displayed if all values being aggregated are equal
Upper Threshold	a value is only displayed if all values being aggregated are equal
Volume	mean
Volume Doubling Time	N/A
Peak	maximum
BiLongAxis	maximum
BiShortAxis	maximum
BiRulerAuto	maximum
UniRuler	maximum
Angle	mean

These aggregate statistics are also displayed in the image views. For linked findings the value calculated for the region in the view is displayed and the aggregate value is displayed in parentheses next to the individual region value.

Aggregation of Derived Statistics

Typically only a single value is calculated for a particular derived statistic for a finding in a time point. For instance, for a linked finding contains two regions: one on the baseline CT and one on the current CT, then there would be one TLG value calculated for the finding at the baseline timepoint and one TLG value calculated for the finding at the current time point. This would be displayed as a row in the table.

In the case where the baseline CT is a gated CT and the current CT is a gated CT then, potentially, many more values are calculated. If each of those CT datasets contained four gates then it is possible to define a region on each CT gates on the baseline time point and on each of the CT gates on the current time point and then link all of those regions into a single finding. When calculating the TLG, aggregate values for the primary statistics are used. The TLG calculated for a particular timepoint is the aggregate mean multiplied by the aggregate volume. For instance, consider a linked Finding with a region on Gate 1 of the CT with a Mean of $mean_1$ and a Volume of $volume_1$ and another region on Gate 2 of the same ct with a Mean of $mean_2$ and a Volume of $volume_2$. The TLG calculated is the aggregate Mean multiplied by the aggregate Volume. From the table above, the aggregate Mean is $\left(\frac{mean_1+mean_2}{2}\right)$ and the aggregate Volume is $\left(\frac{volume_1+volume_2}{2}\right)$. This means the aggregate TLG is:

$$\left(\frac{mean_1 + mean_2}{2}\right) \times \left(\frac{volume_1 + volume_2}{2}\right)$$

NOTE: An aggregate statistic is only computed when more than one linked item exists on the same data role within the same timepoint.

If we define the following aggregation operations:

- $mean(Statistic)$ – This is the mean of the individual Statistic values.
- $max(Statistic)$ – This is the maximum of all the individual Statistic values.
- $min(Statistic)$ – This is the minimum of all the individual Statistic values.
- $isSame(Statistic)$ – This aggregation method only returns a value if all the individual Statistic values are identical.

Additionally, we define that Reference Mean is the Mean statistic for the Finding named “Reference” and that Reference StdDev is the Standard Deviation of the Finding named “Reference”. Then the derived statistics can be defined as follows:

Statistic	Aggregation Method
BiRuler Product	$max(BiLongAxis) \times max(BiShortAxis)$
Max Ratio to Reference Mean	$\frac{max(Max)}{mean(Reference\ Mean)}$
Mean Ratio to Reference Mean	$\frac{mean(Mean)}{mean(Reference\ Mean)}$
Mean Range	$max(Mean) \times min(Mean)$
Mean Ratio	$\frac{max(Mean)}{min(Mean)}$
PERCIST Threshold Blood Pool	$2mean(Reference\ Mean) + 2mean(Reference\ StdDev)$
PERCIST Threshold Liver	$1.5mean(Reference\ Mean) + 2mean(Reference\ StdDev)$

Threshold % of Max	$100(\max(Max) \times isSame(Threshold))$
TLG	$mean(Mean) \times mean(Volume)$

Intensity Distribution Tab

This tab displays the intensity distribution values for all the categories set for the currently active Intensity Distribution definition. The values are displayed as Hounsfield units (HU).

Intensity Distribution definitions may be set via **Tools -> Options** on the **Region Intensity Distribution** tab. See User Preferences section for details.

PERCIST Tab

Designed for users wishing to display the PERCIST specific statistics and/or tracking information for regions. By clicking on the **Options** button in the Toolbox, the following quantification options are available for plotting in the Findings Table and as graphs:

Derived Statistics are available for:

- Mean
- Maximum
- Standard Deviation
- Peak
- Volume
- TLG
- Max Ratio to Reference Mean
- Mean Ratio to Reference
- PERCIST Threshold Liver
- PERCIST Threshold Blood Pool

In addition, **summary quantification** data for plotting in the Findings Table and as graphs is included for:

- Sum of Peak
- Track Peak
- Sum of TLG
- Track Max Ratio
- Track Mean Ratio

NOTE: Reference statistics will not be available until a region has been created and named 'Reference'. You may use any ROI as your reference or use the Drop 1 cm Sphere or 3 cm Sphere tools to create regions of a specific size. See the Quantify menu section of this manual for details on the Sphere tool.

RECIST Tab

Designed for users wishing to display RECIST specific statistics and/or tracking information for rulers and bi-rulers only. No regions information is displayed on this screen. By clicking the **Options** button in the Toolbox, the following quantification options are available for plotting in the Findings Table and as graphs:

- BiRuler Long Axis
- BiRuler Short Axis
- Bi Ruler Auto (chooses the long axis if lymph node flag is off, short axis if it is on)
- UniRuler length

The software also includes **summary quantification** data for plotting in the Findings Table and as graphs on the RECIST tab. Summary quantification is included for:

- Sum of BiRuler Auto
- Sum of Uni Ruler length

Regions Tracking Tab

Designed for users wishing to display statistics and / or tracking information for regions only. There is no ruler information displayed on this screen. By clicking on the **Options** button in the Toolbox, the following derived quantification options are available for plotting in the Findings Table and as graphs:

- Max
- Mean
- Median
- Threshold
- Volume
- Volume Doubling Time

In addition, **summary quantification** data for plotting in the Findings Table and as graphs is included for:

- Track Max
- Mean of Mean

WHO Tab

Designed for users wishing to display WHO specific statistics and/or tracking information for bi-rulers only. No other ruler or region information is displayed on this screen. By clicking the **Options** button in the Toolbox, the following quantification options are available for plotting in the Findings Table and as graphs:

- BiRuler Long Axis
- BiRuler Short Axis

Derived statistics are available for BiRuler Product.

Summary statistics are available for Sum of BiRuler Product.

Advanced Tab

Designed for users wishing to display statistics and/or tracking information for regions, rulers and bi rulers together. By clicking the **Options** button in the Toolbox, the following quantification options are available for plotting in the Findings Table and as graphs:

Quantification

- Intensity Distribution

Derived statistics are available for:

- Angle
- BiRuler Long Axis
- BiRuler Product
- BiRuler Auto
- BiRuler Short Axis
- Max
- Max Ratio to Reference Mean
- Mean
- Mean Ration to Reference
- Mean Range
- Mean Ratio
- Median
- Min
- Peak
- PERCIST Threshold Blood Pool
- PERCIST Threshold Liver
- Standard Deviation
- Threshold
- Threshold % of Max
- TLG
- UniRuler Length
- Volume
- Volume Doubling Time

Summary Statistics are available for:

- Mean of Mean Range
- Mean of Mean Ratio

- Mean of Mean
- Mean of Peak
- Mean of Volume
- Sum of BiRuler Auto
- Sum of BiRuler Product
- Sum of Mean
- Sum of Peak
- Sum of TLG
- Sum of UniRuler Length
- Sum of Volume
- Track Max Ratio
- Track Max
- Track Mean Ratio
- Track Mean
- Track Peak

NOTE: Reference statistics will not be available until a region has been created and named 'Reference'. You may use any ROI as your reference or use the Drop 1cm3 Sphere or Drop 3cm3 Sphere tools to create regions of a specific size. See the Quantify menu section of this manual for details on the Sphere tool.

Creating a Custom Quantification Tab

You may wish to create a custom tab with quantification statistics that you choose to include. You can accomplish this from the **Advanced** tab in the Findings Table. In the toolbox, select the **Options** button from the **Settings** area to display the Quantification Options window. Place checks in the boxes next to the quantification statistics you wish to include in your new tab. You can specify whether you want the statistics displayed as graphs, tables or both. Use the buttons below the selections to choose all or none of the tables or graphs.

When you are satisfied with your selections select **OK**. You will be able to preview your new tab on screen to make certain you are satisfied with your selections. Once you are satisfied, click **Save View** in the Toolbox to enter a name for your custom tab and select **OK**. Then choose whether you want the tab available for current user only or all users (you must have appropriate permission to save for all users). You will see a confirmation window that the tab has been saved and it will be immediately available for selection.

Gated Data

XD3 supports the display of gated CT, PET, Planar NM and SPECT. Multiple time points of gated data are supported.

Findings

You may perform any ruler measurement or region definitions on any of the bins of the gated data. Regions can be projected and transformed to other bins or time points. Regions will be projected/transformed as set in the bindings in Tools -> Data Management. Defaults are provided but can be modified. See the **Data Management** section of this document for further details.

Layouts

When creating layouts for gated data, if you wish to display all of the bins individually in a layout, use the 'Data Offset' in the right mouse button menu within the cell. This will allow you to separate out the bins as 'Dataset 1', 'Dataset 2', 'Dataset 3', etc. If you prefer to view the gated data as a cine, create the layout using the axial, coronal or sagittal views you wish to include and the bins may be displayed one at a time using the 'left and right arrow keys or played as a cine.

The image below illustrates the navigation tools for viewing gated data. In this example, the 10 bins of gated data are represented by the blue boxes at the top of the image window. You may click on the boxes to view the various bins of gated data.



Multi-phase CT Data

In the General Oncology Review Mode, PET/CT/MR Review Mode and Single Volume Review Mode, XD3 allows the display of multiple CTs acquired in the same frame of reference, such as multi-phase CT. The CT phases may all be displayed on the screen at one time or one view at a time with the ability to manually switch between the loaded CT phases using the left and right arrow keys, or by using the navigation tools.

The image below illustrates the navigation tools within the image view. The blue boxes at the top of the image represent the three phases of this CT study. You may click on the boxes to display the various phases. The slider bar is present on the left side of the image window to allow scrolling through the slices.



Registration

If desired, you may choose to adjust the registration between the CT phases, as in the event of patient motion between acquisitions. The frame of reference may be unlocked in the registration manager to adjust the registrations.

Findings

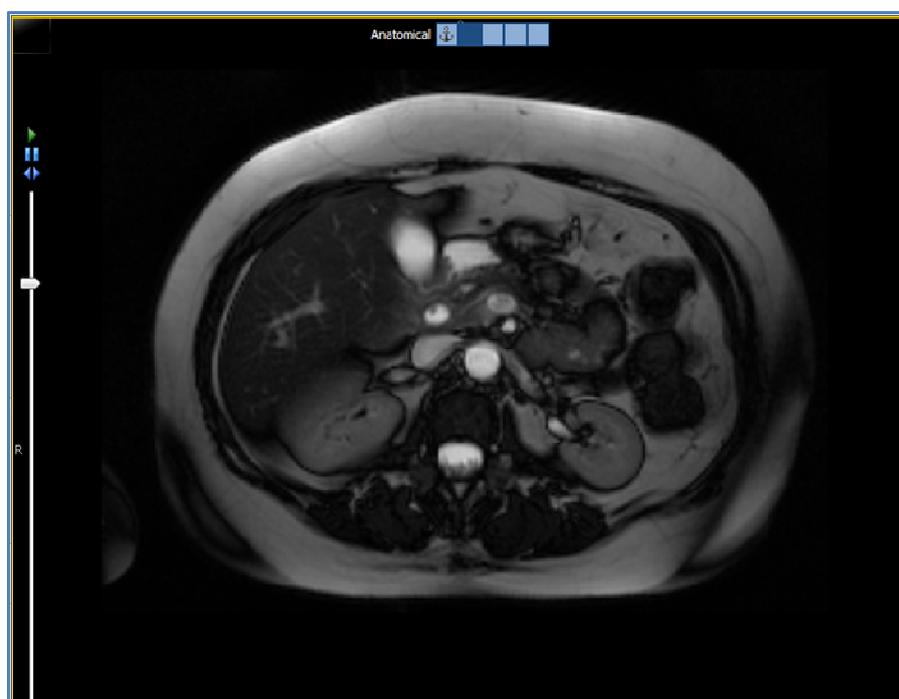
You may perform any ruler measurements or region definitions on any of the CTs. Rulers and regions defined on one CT are shadowed as defined on the Data Management screen.

Layouts

When creating layouts for multi-phase CT data, if you wish to display all of the phases at one time in a layout, use the 'Data Offset' in the right mouse button within the cell. This will allow you to separate out the phases as 'Dataset 1', 'Dataset 2', 'Dataset 3', etc. If you prefer to view the sequences one at a time, create the layout using the axial, coronal or sagittal views you wish to include and all sequences may be displayed one at a time using the left and right arrow keys.

Multiple Sequence MR Data

In the General Oncology Review Mode, PET/CT/MR Review Mode and Single Volume Review Mode, XD3 allows the display of multiple MRs acquired in the same frame of reference, such as multiple sequences. The MR sequences may all be displayed on the screen at one time or one view at a time that allows you to manually switch between the loaded MR sequences using the left and right arrow keys, or by using the navigation tools as shown below. The blue boxes at the top of the image window represent the five sequences of MR data loaded into the application. You may click on the individual boxes to navigate through the sequences. The slider bar on the left side of the image window allows you to scroll through the slices.



Registration

If desired, you may choose to adjust the registration between the MR sequences, as in the event of patient motion between acquisitions. The frame of reference may be unlocked in the registration manager to adjust the registrations.

Findings

You may perform any ruler measurements or region definitions on any of the MRs. Rulers and regions defined on one MR are displayed on the other MRs that the system configuration specifies.

Layouts

When creating layouts for multi-sequence MR data, if you wish to display all of the sequences at one time in a layout, use the 'Data Offset' in the right mouse button within the cell. This will allow you to separate out the sequences as 'Dataset 1', 'Dataset 2', 'Dataset 3', etc. If you prefer to view the sequences one at a time, create the layout using the axial, coronal or sagittal views you wish to include and all sequences may be displayed one at a time using the left and right arrow keys.

Reporting

Creating a Report



The reporting screen is available by selecting **Window ->Report Screen** from the menu or by selecting **Report Screen** from any of the layout menus. The reporting feature allows you to create reports based on report templates. Default templates are provided for each review mode, but you can make modifications and save them back to the same or a new template. The intent is to auto-populate the reports as much as possible, so you only have to insert captured images and free text from your findings.

Once you've entered the **Report Screen**, the **Image Gallery** and **Reporting Tools** are available from the Toolbox. The Image Gallery is accessible if you have saved key images or bookmarks during your reading session. If you have key images or bookmarks in the gallery, the gallery will display an enlarged view of the image when the mouse pointer hovers over the image thumbnail. You may double click on any image to transfer it to the report or you may drag and drop any key image into the report.

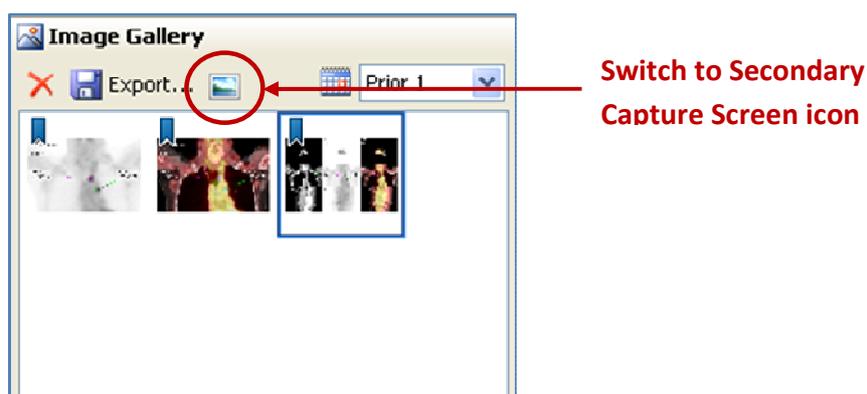
Image Gallery

The Image Gallery panel is where screenshots, image view captures, bookmarks, snapshots and DICOM secondary captures are stored in a thumbnail view. These images may be exported or added to a report once the report screen is displayed. Images can also be previewed in a larger form by hovering your mouse over them, or they may be removed from the image gallery entirely, by highlighting the image and clicking the **Remove** button.

Bookmarks are available in order for you to stop what you are doing and return at a later time without losing your previous work. You may double click on bookmarked images to restore a particular layout and crosshair position (when not previewing the report), as well as window/level and zoom settings. Bookmarks may also be exported to Casebook. Double clicking an image when viewing the report adds the image to the report page.

The Image Gallery may be filtered by time point by using the dropdown menu at the bottom of the Image Gallery window.

If a DICOM secondary capture image is present in the Image Gallery it may be displayed by selecting the 'Switch to Secondary Capture Screen' icon.



Reporting Tools

It is recommended that the application window be full screen when creating the report. When converting to PDF, conversion of the report contents is based proportional to the screen height and width.

The reporting tools panel is available in the Toolbox whenever the reporting screen is selected. This contains a number of controls which can be used to add information to the report or to manage the information contained in the report.



Items available to add include:

- Text – this adds a text box to the currently displayed report page if there is space to do so. If there is insufficient space on the current page then a new page should be inserted and the text box placed there.
- Statistics – this allows addition of the quantification statistics table displayed on the quantification screen to the report, allowing you to specify the tab from quantification screen statistics to include (Basic Tracking, RECIST, etc.) and for which datasets the statistics are to be included (i.e. CT, PET AC, etc.).
- Data QC – this allows information configured for display from the applicable modality attributed defined in the Data QC options.
- Patient Information – this adds the patient’s name, sex and date of birth to the report.

Also included in the Reporting Tools is a section called **Manage Report**. This allows manual addition or removal of a report page. The report may be refreshed to update any manipulation to the data that may have been done during the report creation. Additionally, the page may be flipped from portrait to landscape layout.

Saved Templates are listed in a drop down menu. The **Restore** button allows you to discard all changes and creates a new report based on the current template. **Save Template** allows you to name and save a custom template after selecting which Review Mode(s) the template is valid.

The Export button prompts you to select which data series you would like the report associated, provide a series description, add the physician's name, and add operator's name. You may then select the destination from a drop down menu to choose File, SCP or Application Launcher. You may browse to select a destination directory, type in a file name and select the file format from a drop down menu. File format choices are DICOM, BMP, PNG and JPEG.

The report may also be saved as a PDF. You will be prompted to specify a location on the local file system for the file to be saved.

The **Settings** button allows you to enter and save your institution name, paper size and a logo for the header of your reports. You may also specify whether you would like to be prompted to refresh report content when exporting or if you would like the report to be automatically refreshed when exporting.

You may right click on any of the page tabs at the top of the report to :

- Remove a page
- Add a page
- Flip the page from landscape to portrait
- Add a text box
- Add statistics
- Add Data QC
- Add patient information
- Select Options – to set preferences for your report.

Secondary Capture Screen



The Secondary Capture screen is a dedicated screen for viewing loaded secondary capture images and any bookmarks or screenshots created within XD3. Additionally, any RT Image objects loaded within XD3 will be added to the Image Gallery. To view an image, double-click the left mouse button on an image icon within the Image Gallery. The selected image will be displayed in the main viewing area at its natural size or, if it is larger than the display area, a scaled size that fits the view. The images can be manipulated with the standard Zoom, Pan and Window and Level controls.

If the selected image series has multiple frames such as a multi-frame secondary capture, it is possible to scroll through the different image slices using the mouse wheel or the slice navigation slider.

Setting User Preferences

XD3 allows certain preferences to be applied on a per user basis. These settings are remembered between runs of the application. The preferences can be set via the **Tools -> Options** menu.

Unless stated otherwise, all preferences described in this section apply on a per-user basis. Changes made will affect the currently logged-in user. In deployments where multiple users share the same user account, preference settings will also be shared. Changes made by one user will affect all users sharing that account so care must be taken to check important settings on startup. To avoid this it is strongly recommended that all unique users of the system have an individual user account.

The following sections describe each tab in the Preferences section.

DICOM

This allows you to define DICOM nodes to which you wish to send data. These are global settings and hence require sufficient access rights to save changes. The access privileges required are those required to write to public or shared document areas. It is recommended, for example, to use a local administrator account when making system-wide changes such as defining DICOM preferences.

NOTE: In general, this tab applies settings on a system-wide basis. All other preference tabs are applied on a per user basis. However, on some integrations, this may not be present at all or may apply on a per user basis rather than a global one.

Data QC

The **Data QC** tool is provided to allow you to view attributes from datasets loaded into the application for review. Attributes such as scanner manufacturer, software version, slice thickness, kVP, X-ray tube current and several others may be displayed for the CT data. Likewise, software version, injected dose, delay time, half-life, patient height, patient weight and additional attributes are available for PET data.

If you wish, you may perform validation of this data based on limits that you define. For example, you may want to be warned if the delay time variance from the time of injection to time of scan between time points is greater than a certain amount of time. This Data QC screen will show you the attributes and flag any that are outside the tolerance levels you have set.

Additionally, the Data QC screen may be included in a custom report. You may choose which attributes are visible and whether you would like to be prompted to display the Data QC screen on startup if there are validation warnings.

To set your preferences:

1. Select the modality from the list on the left to view the list of attributes available for inclusion and validation on the Data QC screen.

2. Double-click on an item in the list to indicate whether you want this row to be visible in the table and if you want to perform validation. Note that some items are for display only and the validation settings are disabled upon selection.
3. Enter validation settings – most of the attributes allow you to set a minimum value (you will be warned if the value falls below this number), a maximum value (you will be warned if the value falls above this number) and a variance. The variance can be used if you wish to be notified of variances between time points. For example, you may want to be alerted if the injected dose varies by more than 5 mCi between any number of scans.

At the bottom of the screen you can indicate whether you would like to be prompted to display the Data QC screen on startup if there are validation warnings, or if you want to automatically switch to the Data QC screen if there are validation warnings. Place a check in the box next to your preference and click **Apply** and **OK** to save your selections.

Findings

This tab allows you to choose whether to draw Regions as Outline, Shaded or Outline and shaded. Additionally, you may select to set the ROI Transparency percentage using a slider.

The context menu may be configured by selecting the Context Menu button and ticking the items you wish to have available on the findings context menu (accessed by clicking right on any highlighted finding).

Place a tick in the box if you wish to show tooltips in the Findings panel table.

You may also set preferences for contour creation including Type of Region: Cuboid or Ellipsoid from drop down menu.

A preference for default *absolute* threshold or default *percentage* threshold may be input as well from this screen. These settings will be applied when you use the corresponding region tools elsewhere in the application.

Place a check in the box if you would like to center image views when you create a new region.

Place a check in the box if you wish to be prompted for a name upon creation of a new finding. The **Suggestions** button allows you to add, edit and delete from the list of suggested finding labels.

Click **Apply** and **OK** to save your selections.

Licensing

This option should be provided by your system administrator or by Mirada Customer Support personnel during installation.

Quantification

Allows you to select the ROI statistics to display in the on-screen labels within the image views. The options are configurable on a per-modality basis. Any combination of the following statistics may be configured for display:

- Mean
- Max
- Min
- Threshold
- Upper Threshold
- Median
- Peak
- Volume
- Intensity Distribution
- Volume Doubling Time

You may select whether you want your rulers to display measurements in mm or cm.

Findings Table preferences allow you to select the enabled statistics tabs in the Findings Table view. Options are:

- Intensity Distribution
- PERCIST
- RECIST
- Regions Tracking
- WHO
- Advanced

If you have created any custom tabs, they will be available for selection in this space as well.

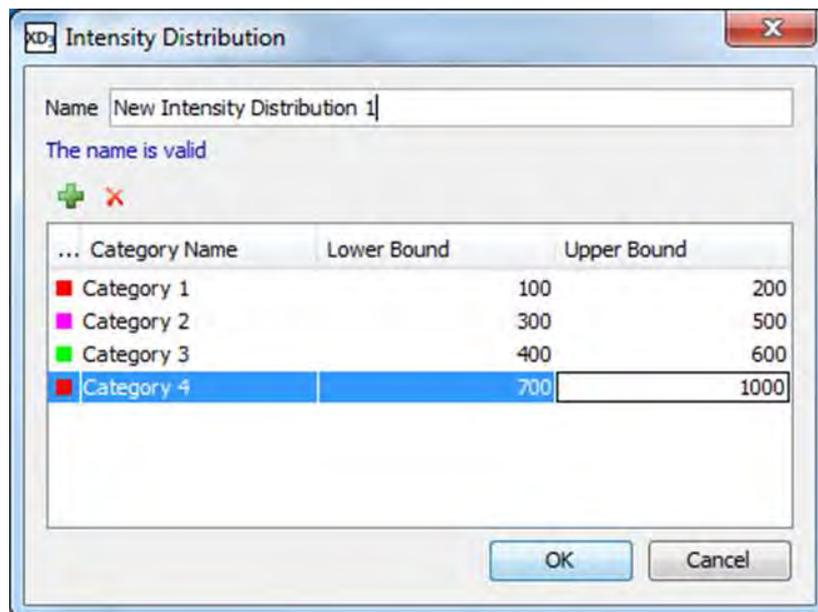
Select your default statistics tab for display in the Findings Table from the drop down menu.

Click **Apply** and **OK** to save your selections.

Region Intensity Distribution

The **Region Intensity Distribution** tool allows you to set categories for voxel intensities within a region of interest. For example, you may wish to assign categories for air, water, bone, contrast, fat, etc. in a CT region of interest. These categories are reported in parts of the application that report the region statistics. These are reported via the image view statistics, the intensity distribution graphs from the Regions Table and from the regions tracking tab on the Regions Table. The categories may be set in **User Preferences** via **Tools -> Options** on the **Region Intensity Distribution** tab.

Select the modality for which you wish to set intensity ranges from the list on the left. Select the quantification method from the dropdown menu. Click on **New** to create a new region intensity distribution definition. This will open the dialog box which allows you to set the number and range of intensity levels. Intensity Distribution definitions can also be cloned from existing ones and then modified. They cannot be edited once created.



Use the green '+' to add a category and use the red 'X' to delete a category.

You may enter the values for the ranges in the **lower bound** and **upper bound** boxes (double click in the box to enter numbers). Ranges may be defined with gaps between one category upper bound and the next category lower bound. In a similar way, they can be set to overlap so a voxel could be counted in multiple categories. It should be noted that gaps or overlapping voxels will likely result in the reported percentages not adding up to 100% for any given region.

Enter the names for your categories (e.g. air, water, contrast, bone, etc.) by double clicking the category name. The category color can be changed by selecting the colored squares to the left of the category name. This sets the color to represent that category in the graphical display (i.e. Intensity Distribution graphs). Click **OK** to continue and save your selections.

When a registration exists between a pair of datasets, it is possible to draw a region on one and the system will automatically create a shadowed region on the other. For example, when creating a region on the PET dataset, the system will automatically create the same region on the CT. The accuracy of the intensity distribution is limited by the quality of the registration. When relying on quantification statistics of a shadowed region created by the system, the quality of the registration should be checked in the Registration Manager first. In the example below the PET/CT has been deliberately misregistered to highlight the issue. A thresholded PET region has been automatically shadowed to the CT dataset and Hounsfield-based intensity distribution statistics are displayed for the CT region. The region has been classified as 62.5% air due to the misregistration placing the lesion in the lung.



Report

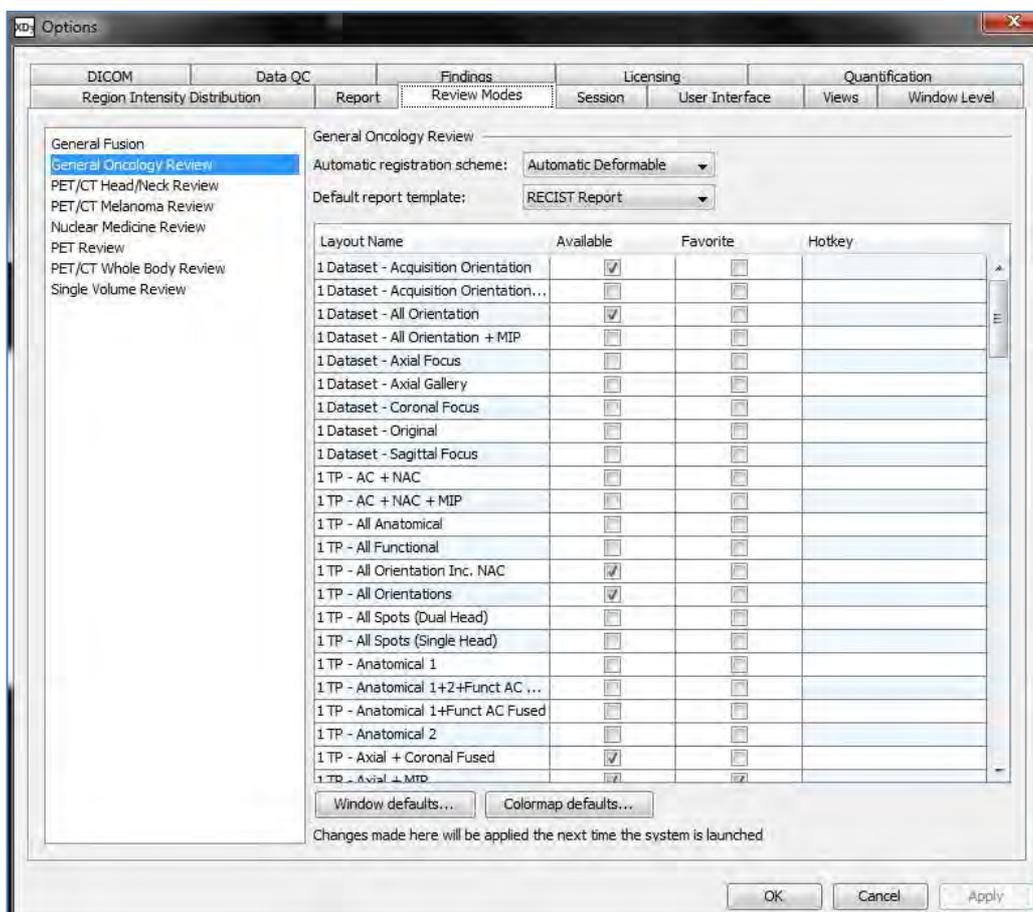
Allows you to customize your report. The following preferences are available:

- Insert your Institution Name
- Select whether you want to be prompted to refresh data included in the report or if you want the system to automatically refresh your report upon export
- Select Paper Size
- Insert a Logo to be displayed on your report

Click **Apply** and **OK** to save your selections.

Review Modes

This allows you to select a **Review Mode** and then select a default report template, an automatic registration scheme, and select from a list of **Layouts** which you would like to have available for that Review Mode.



Both Mirada provided layouts and custom layouts are listed. Check the box for layouts you wish to have available. To select layouts to be displayed as **Favorites** in the **Toolbox** in the upper left-hand corner of your screen, check the box under the **Favorite** heading.

If you wish to assign a layout to a hotkey, simply double-click in the hotkey field in the table and press the keystroke you would like to use as the shortcut. You may use single letters or complex hotkeys such as "ctrl+shift+1". After you have pressed your keystroke, the hotkey or combination will be displayed. When you have assigned the hotkeys click **Apply**. The hotkeys will be available for use upon restarting the XD3 application and the Application Launcher.

Under the list of Layouts is a **Window Defaults...** button. Use this screen to define layouts for single or for multiple Windows. This allows you to define default layouts for a single, dual or triple screen monitor setup. The Fallback layouts are available to use if the defaults are not available. For example, if you have a 2 Time Point Layout selected as default for Adaptive Planning Review mode and you load a single time point study, the Fallback layout would be used.

Use the **Colormap Defaults** button to choose color maps for base and overlay datasets in any of the Review Modes.



When an automatic registration scheme is set to be run on application load, the results should be reviewed using the crosshair alignment and the quality control tools available via **Registration -> Registration Manager** to ensure that the registration is satisfactory. This is particularly important before propagation of ROIs between time points.

Session

This page allows you to set a preference whether you would like to be prompted to save your session upon exit of the application, or if you want to automatically save each session.

Click **Apply** and **OK** to save your selections.

User Interface

Select the **Hotkey Configuration** button to set any of the tools in the toolbar or any of the menu items to hotkeys. Double-click in the Hotkey column and type the key or keystroke combination you wish to use.

Select the **ToolBar Configuration** button to select which tools you want to have visible on your Toolbar. Place a check in the box next to those items you want to include. Select **OK** to save your selections and update the toolbar.

Select the **Context Menu Configuration** button to select which tools you want to have visible in your context menu. The context menu is accessed via the right mouse button in any image window. Place a check in the box next to those items you want to include. Select **OK** to save your selections and update the context menu.

Startup Options allow you to make changes which do not take effect until the application is re-launched. Items you may change are:

- Crosshair Style: may be set to Plain, Open, Target, or Frame Marker
- Zoom Binding: may be set to Axial/Coronal + Sagittal, All, or None; where
 - None = Only the image view being manipulated is adjusted.
 - All = All image views are adjusted.

- Axial + Coronal/Sagittal – If an axial image is manipulated, all axial images are zoomed. If a coronal or sagittal image view is zoomed, all coronal and sagittal image views are adjusted.

NOTE: MIPS and Orthogonal views do not share zoom factors.

- Pan Binding: may be set to Per-Plane, or None, where:
 - Per-Plane = If a plane (e.g. axial) is manipulated, then all the image views of that plane are panned
 - None = Only the image view being manipulated is adjusted

NOTE: MIPS and Orthogonal views do not share pan adjustments.

Select **compact display mode** for optimized display when using the application on a laptop.

Enable Direct3D Acceleration is enabled by default. This setting allows optimized performance with certain monitors and should only be disabled in the event of performance issues that are thought to be monitor related.

Click **Apply** and **OK** to save your selections.

Views

View Settings allow you to:

- Enable the use of high contrast borders
- Show colored planes – displays colored frames around each plane displayed
- Show progress information
- Automatically play MIP cine
- Select the MIP frame count from the dropdown menu – this selection takes effect only after a new launch of the application and affects both on-screen and an exported MIP cine
- Select the behavior at the end of a slice cine – choose loop, pause, reverse from the dropdown menu
- Determine how many slices are skipped when using Page Up and Page Down keys
- Set whether you want to navigate slices by anatomy or slice number

The **Information Overlays** section allows you to:

- Change the interactive text color
- Adjust the font size in the image windows
- Set whether or not you want to show the instance number on slices
- Set whether or not you want to show series description
- Set whether or not you want to show accession number
- Set the option for slice numbering (i.e. head to foot or foot to head)



Care should be taken to ensure that the slice numbering scheme chosen in XD3 matches that of any system used to launch XD3.

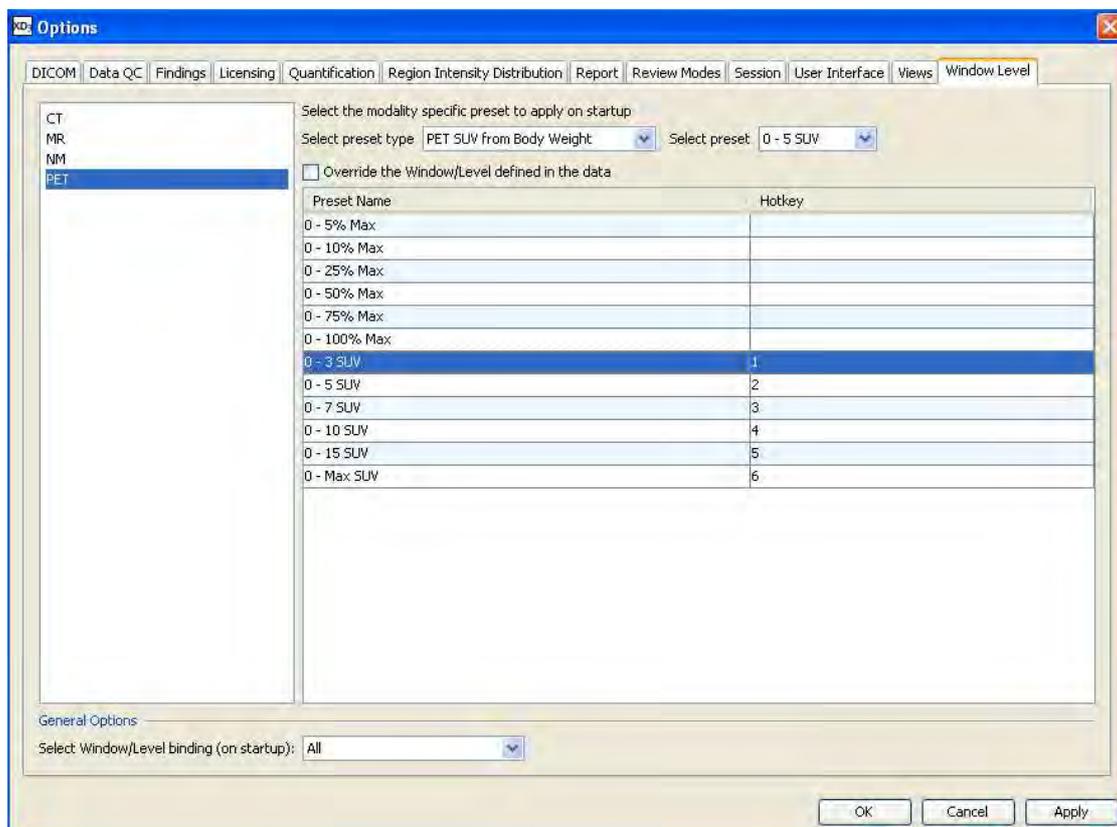
The slice number option determines which numbering scheme will be used for display in the axial view only. Head to Foot will number the most superior slice as 1 and then slice numbers increment towards the feet. Foot to Head will number the most inferior slice as 1 and then slice numbers increment towards the head. It is important to note that these numbers refer to the slice number of the reconstructed 3D volume. It is possible for a reconstructed 3D volume to have greater or fewer slices than the number of individual instances from which it was reconstructed. This happens when the slice thickness or slice spacing varies within the original series slices. The Views configuration page has an option to display the image instance number. This number is the slice instance number of the slice from which the voxel at the crosshair location was taken. When reporting a slice number, the original instance number should be used rather than the reconstructed slice number. This will guarantee interoperability with other systems. The slice numbers displayed in the views are of the form: a/b (c) where a is the reconstructed slice number, b is the number of reconstructed slices in the current plane and c is the image instance number.



The slice navigation slider is specifically designed to be able to navigate quickly to a desired area within an image view. As such the slice navigation slider does not display every slice in the view being navigated from the currently displayed slice to the slice represented by the slider position set.

Window Level

Allows you to select modality-specific Window and Level settings to apply on start-up for CT, PT, NM, and MR datasets. Use the drop down menus to select the **preset type** and the **preset values** you wish to apply on startup for the initial data load.



You may specify whether to override the window level values contained within the data with your selected preset by checking the box.

To assign a window level setting to a hotkey of your choice, double-click in the Hotkey field in the table and press your keystroke as normal. For example, press control key and F1 to assign a shortcut of “ctrl + F1”. Because the keys are set per modality, the same key may be used for different modalities. The hotkeys will be available for use upon restarting the XD3 application and the Application Launcher.

Use the drop down box at the bottom of the window to select **window/level binding** on startup. You may specify whether you want bindings applied to all displayed datasets or by time point.

Click **Apply** and **OK** to save selections.

Keyboard Shortcuts

Keyboard Shortcut Mappings

Action	Keyboard Shortcut	Description
Toggle between Time Points	Space Bar	Toggles between time points when multiple time points are loaded in a review mode and a single time point layout is used.
Zoom	Ctrl + mouse wheel	Magnifies images in the selected image window.
Pan	Ctrl + left mouse button	Pans images in the selected image window.
Undo	Ctrl + Z	Undo last step.
Redo	Ctrl + Y	Redo last step.
Copy	Ctrl + C	Only available from the Report Screen – copies items from a page on the report to allow them to be pasted on the same or a different page.
Cut	Ctrl + X	Only available from the Report Screen – cuts items from a page on the report to allow them to be pasted (moved) to an area on the same or a different page.
Paste	Ctrl + V	Only available from the Report Screen – Pastes a previously cut or copied item from a page on the report.
Delete Report Item	Delete	Only Available from the Report Screen – deletes the selected item on a report page.
Capture View	Ctrl + E	Sends the selected view to the Image Gallery.
Capture Screenshot	Ctrl + Shift + E	Sends a screenshot of the selected application window to the Image Gallery.
Copy View to Clipboard	Ctrl + K	Copies the image in the currently selected view to the clipboard.
Copy Screenshot to Clipboard	Ctrl + Shift + K	Copies a screenshot of the currently selected application window to the clipboard.
Help	F1	Opens the help file.
Full Screen	F11	Displays the application as full screen, removing toolbar and side bar
Return to Layouts	CTRL + Left	Returns the selected window from specific screens to the image layouts
Rigid Registration	F2	Applies the automatic rigid registrations defined in the review mode.
Deformable Registration	F5	Applies the automatic Deformable registrations defined in the review mode.
Show Displacement Field	SHIFT+CTRL+F	Shows the displacement field when a deformable registration exists between the datasets visible in a fused

		image view
Show Displacement Grid	SHIFT+CTRL+G	Shows the deformation grid when a deformable registration exists between the datasets visible in a fused image view
Show Displacement Map	SHIFT+CTRL+M	Shows the deformation map when a deformable registration exists between the datasets visible in a fused image view
Increase Slice Index	Up Arrow	Increases the slice index by one in the selected view. E.g. if the currently selected view is a Coronal view at slice index 314, pressing the up arrow increases the slice index in the Coronal view to 315.
Decrease Slice Index	Down Arrow	Decreases the slice index by one in the selected view. E.g. if the currently selected view is a Sagittal view at slice index 112, pressing the down arrow decreases the slice index in the Sagittal view to 111.
Increase by 10 slices	Page up	
Decrease by 10 slices	Page down	
Restore Object selection mode	Escape	Exits control modes such as window level control mode
Increase Slice Index	Up Arrow	Increases the slice index by one in the selected view; for example, if the currently selected view is Coronal view at slice index 314, pressing the up arrow increases the slice index in the Coronal view to 315.
Decrease Slice Index	Down Arrow	Decreases the slice index by one in the selected view; for example, if the currently selected view is a Sagittal view at slice index 112, pressing the down arrow decreases the slice index in the Sagittal view to 111.
Show/Hide Volume Bounds	B	Toggles display of Volume Bounds in the display window.
Toggle Annotations	A	Removes annotations from the image views
Toggle Navigation Controls	N	Show/Hide navigation controls
Remove Crosshairs	C	Removes crosshairs from the image views.
Remove Information Overlays from the image views	I	Removes the Information Overlays from the image views
Show Timepoint Information	T	When launched with more than one timepoint, displays the timepoint name and date in the image views.
Toggle Overlay	O	Toggles the overlay between the current transparency setting and fully transparent. This has the effect of showing and hiding the overlay. This is only available if the currently selected view has both a base and overlay dataset.

Remove Patient Information overlays from image views	P	Removes the Patient Information from Image Views.
Show/Hide Region Statistics	S	Toggles display of region statistics on and off in the display window.
Toggle ROIs	R	Removes ROIs and associated text from the image views
Toggle Region Crosshair Display	V	Displays the crosshair ROI
Increase Volume Crosshair Size	=	
Decrease Volume Crosshair Size	-	
Define Ellipsoid Region	CTRL+L	
Define Rectangular Region	CTRL+R	
Paint Tool	Q	
Eraser Tool	W	
Toggle PET AC/NAC	T	Replaces the selected PET or SPECT AC dataset with the PET or SPECT NAC dataset.
Delete Object	Delete	Deletes the currently selected annotations, rulers, angles or regions.
View Context Menu	Right Mouse button	Displays the floating toolbar (also known as context menu) in an image window.
Move to Start	Home	<p>This action depends on the currently selected view and preference setting:</p> <p>System preferences set to navigate by slice number:</p> <ul style="list-style-type: none"> • Axial: moves to the axial slice index at the bottom of the patient • Coronal: moves to the coronal slice index with the highest value • Sagittal: moves to the sagittals slice index with the highest value <p>System preferences set to navigate by anatomy:</p> <ul style="list-style-type: none"> • Axial: moves to the most inferior slice in the axial view • Coronal: moves to the most posterior slice in the coronal view • Sagittal: moves to the most leftward slice in the sagittals view

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