

# **XD 3.6.11**

## **Help Guide**

# Table of Contents

• Notices	(page 5)
◦ Regulatory statement	(page 7)
◦ Warnings	(page 10)
◦ Data supported	(page 15)
• Overview	(page 18)
◦ Launching XD review modes	(page 19)
◦ Configuring your data	(page 21)
◦ The user interface	(page 23)
◦ Support	(page 26)
◦ Data quality control	(page 27)
• Viewing images	(page 28)
◦ Manipulating images	(page 29)
◦ Viewing a maximum intensity projection (MIP)	(page 33)
◦ Capturing an image	(page 35)
◦ Choosing a layout	(page 37)
◦ Interacting with active text	(page 38)
◦ Viewing cines	(page 40)
• Performing and managing registration of images	(page 41)
◦ Managing data bindings	(page 42)
◦ Performing automatic registration	(page 44)
◦ Performing manual registration	(page 47)
• Findings	(page 50)
◦ Segmenting an image	(page 51)
◦ Drawing a region	(page 53)
◦ Editing a region	(page 56)
◦ Creating and editing rulers	(page 58)
◦ Creating a ruler from a region	(page 60)
◦ Annotating an image	(page 61)

◦ Linking findings together	(page 62)
◦ Projecting findings	(page 64)
◦ Creating multiple threshold regions	(page 68)
◦ Creating quantification volumes	(page 70)
• Quantification	(page 71)
◦ Using the findings table	(page 72)
◦ Performing PERCIST	(page 74)
◦ Performing RECIST	(page 77)
• Customizing XD	(page 80)
◦ Setting user preferences	(page 81)
◦ Creating custom layouts	(page 85)
◦ Assigning hotkeys	(page 87)
• Saving, loading, and exporting data	(page 88)
◦ Saving a session	(page 89)
◦ Loading a session	(page 90)
◦ Exporting data	(page 91)
◦ Exporting a maximum intensity projection (MIP)	(page 94)
◦ Creating a DICOM viewer	(page 96)
◦ Exporting an RTSS	(page 97)
◦ Exporting secondary captures	(page 99)
• Equations and algorithms	(page 101)
◦ Statistics	(page 102)
◦ Calculation of statistics for gated data	(page 104)
◦ Derived statistics	(page 106)
◦ SUV Peak	(page 108)
◦ Volume doubling time	(page 111)
◦ PET SUV calculation by body weight	(page 112)
◦ PET SUV calculation by body surface area	(page 113)
◦ PET SUV calculation by lean body mass	(page 114)
◦ PET SUV from acquisition	(page 115)

# XD 3.6.11

Mirada Medical's XD 3.6.11 is a software application designed for the rigid registration of medical image datasets including PET, CT, MR, and SPECT as well as nuclear medicine planar, planar WB and planar dynamic. Additionally, XD 3.6.11 provides powerful image viewing capabilities including series image review, and region quantification and tracking.

## Topics in this help guide:

- [Notices](#)  
Find here important notices about the use of XD 3.6.10.
- [Overview](#)  
Topics describing installation, management, and the first steps of launching the XD application.
- [Viewing images](#)  
In this section you can find information about viewing images without making significant changes to your session data.
- [Performing and managing registration of images](#)  
Topics describing the registration of two images and the management of relationships between images.
- [Findings](#)  
Topics describing the creation and editing of regions and rulers.
- [Quantification](#)  
Topics describing the use of XD features to perform quantification.
- [Customizing XD](#)  
Topics describing the customization of XD.
- [Saving, loading, and exporting data](#)  
Topics describing the saving, importing, and exporting of data from XD.
- [Equations and algorithms](#)  
In this section you can find information about the equations and algorithms used to calculate various statistics in the XD application.

# Notices

**Summary:** Find here important notices about the use of XD 3.6.10.

In this section you can find information about the product that is of importance for safety or regulatory reasons.

You should also be aware of the following statement:

## 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.



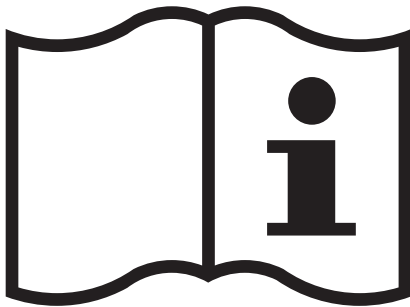
In compliance with Council Directive 93/42/EEC.



Manufactured by:  
Mirada Medical Ltd.  
New Barclay House  
234 Botley Road  
Oxford  
OX2 0HP  
United Kingdom



Date of manufacture: May 2019



<https://mirada-medical.com/eifu-xd-3-6-11-philips/>

## Alternative formats

An online version of the XD 3.6.11 instructions for use (including this help guide) is available at <https://mirada-medical.com/eifu-xd-3-6-11-philips/> and may contain updates that were made in the time since you were delivered your copy of XD 3.6.11.

A physical copy of the XD 3.6.11 instructions for use (including this help guide) is also available upon request from [support@mirada-medical.com](mailto:support@mirada-medical.com).

## Topics in this section:

- [Regulatory statement](#)

- [Warnings](#)

The warnings listed here relate to specific functions and modes of use for the software. These are also listed in applicable topics elsewhere in the user guide.

- [Data supported](#)

XD supports a range of data types.

# Regulatory statement

## Device Classification

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

**EU:** Class IIa

## Intended Use

XD 3.6.11 is intended to be used by trained medical professionals including, but not limited to, radiologists, nuclear medicine physicians, and physicists.

XD 3.6.11 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.

XD 3.6.11 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.

XD 3.6.11 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.

XD 3.6.11 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.

## Indications for Use

XD 3.6.11 is intended to be used by trained medical professionals including, but not limited to, radiologists, nuclear medicine physicians, and physicists.

XD 3.6.11 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.

XD 3.6.11 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.

XD 3.6.11 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.

XD 3.6.11 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.

## Contraindications for Use

None known.

## 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 XD 3.6.11, is a complement to these standard methods. XD 3.6.11 should not therefore be solely used to directly drive a clinical decision making process.

## Data Compression

XD 3.6.11 does not apply any data compression techniques. Lossy compressed data can be loaded into XD 3.6.11 at the discretion of users. It is important to understand that the use of lossy compressed data may result in lower quality images that can affect the accuracy of image display and quantification. Where lossy compressed data has been loaded into XD 3.6.11, the data will be labelled as such in the application.

## 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.



## Cyber Security

XD 3.6.11 is designed to use data sent to it in DICOM format only from sources within a hospital network as configured by users. XD 3.6.11 does not include any firewall or anti-virus protection and is not specifically designed to protect against malicious attack. Users are strongly advised to ensure that appropriate measures are in place in the infrastructure around XD 3.6.11 to protect against malicious attack as well as to comply with data protection regulations. Such measures may include, but are not limited to, secure local area networks (LANs), appropriate firewall provision, network directory permissions and anti-virus protection.

## User Credentials

XD 3.6.11 used Windows credentials for some functions. System administrators should ensure that XD 3.6.11 is secured for use by clinicians only, and users should not share their account details.

## Coexistence with other software

While there are currently no known safety issues or performance limitations with regard to XD 3.6.11 coexisting on the same workstation as other software applications, it is recommended that XD 3.6.11 is not used on a workstation with other software applications installed.

## 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.

# Warnings

**Summary:** The warnings listed here relate to specific functions and modes of use for the software. These are also listed in applicable topics elsewhere in the user guide.



**Warning:** 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.



**Warning:** 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.



**Warning:** 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.



**Warning:** 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.



**Warning:** Care should be taken to ensure that the slice numbering scheme chosen in XD 3.6.11 matches that of any system used to launch XD 3.6.11.



**Warning:** 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.



**Warning:** 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.




**Warning:** 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.





**Warning:** 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.


 **Warning:** 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.


 **Warning:** 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.

 **Warning:** 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.

 **Warning:** 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.

 **Warning:** 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.

 **Warning:** 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.

 **Warning:** 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.



**Warning:** 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.



**Warning:** 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 the 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.



**Warning:** 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.



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



**Warning:** 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.



**Warning:** XD 3.6.11 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 XD 3.6.11. 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.



**Warning:** Different interpolation methods may be used by XD 3.6.11 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 XD 3.6.11.



**Warning:** 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.



**Warning:** 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.



**Warning:** Many data roles can load multiple volumes so long as they share a common frame of reference. Once loaded, XD 3.6.11 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.



**Warning:** 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.



**Warning:** 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.



**Warning:** Depending on the regions used, it is possible that a region intensity distribution will not sum to 100%.

# Data supported

**Summary:** XD supports a range of data types.

## 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

## 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 XD 3.6 DICOM Conformance Statement contains a detailed description of supported modalities and data types.



**Warning:** 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.



**Warning:** 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.



**Warning:** Different interpolation methods may be used by XD 3.6.11 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 XD 3.6.11.



**Warning:** Many data roles can load multiple volumes so long as they share a common frame of reference. Once loaded, XD 3.6.11 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.



## Related topics:

- [Configuring your data](#)

Assign your data to particular roles to control how they are used and displayed.

- [Viewing images](#)

In this section you can find information about viewing images without making significant changes to your session data.

# Overview

**Summary:** Topics describing installation, management, and the first steps of launching the XD application.

## About

You install XD 3.6.11 using an installation package and must use a valid license.

Launch XD from ISP and assign your data to the correct roles for your aims.

## Topics in this section:

- [Launching XD review modes](#)  
Launch the XD application.
- [Configuring your data](#)  
Assign your data to particular roles to control how they are used and displayed.
- [The user interface](#)  
An overview of the user interface.
- [Support](#)  
If you require technical support, a support package provides additional information about your system.
- [Data quality control](#)  
You can review the attributes of your loaded data.

# Launching XD review modes

**Summary:** Launch the XD application.

## About

When launching XD, you select the data that you want to work with and the review mode that you want to use.

## Procedure

To launch XD, complete the following steps:

1. In ISP, select the data that you want to use. If you want to load a saved session, select the images included in the session and the session data.

**Note:** If loading data with multiple patient IDs, you will be presented with a warning. You should take particular care to ensure that the data loaded is appropriate in this case.

2. Click a review mode. If you want to guarantee that the Data Configuration window is displayed, press and hold the **Ctrl** key when you click the review mode.

Use the following review modes in the following circumstances:

- Use **XD General Fusion** when you want to use a generic set of layouts for viewing data from different modalities, phases, or sequences.
  - Use **XD General Oncology Review** when you want to use a generic set of layouts for viewing data from two or more time points.
  - Use **XD MR/PET/CT Review** when you want to perform a general review on MR, PET, or CT data.
  - Use **XD Basic NM Review** when you want to view NM data without any additional customization
  - Use **XD Single Volume Review** when you have a single volume that you want to view.
3. Depending on the data you loaded and the review mode you chose, you might be presented with the Data Configuration window. For more information about using the Data Configuration window see [Configuring your data](#).



**Warning:** Care should be taken to ensure that the slice numbering scheme chosen in XD 3.6.11 matches that of any system used to launch XD 3.6.11.



**Warning:** 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.

## Related topics:

- [Configuring your data](#)  
Assign your data to particular roles to control how they are used and displayed.
- [Saving a session](#)  
You can save your current session and return to it later.
- [Data quality control](#)  
You can review the attributes of your loaded data.

# Configuring your data

**Summary:** Assign your data to particular roles to control how they are used and displayed.

## About

When you launch XD, the application assigns data to a set of roles defined by the review mode that you are using. The data role into which an image or series is placed determines what can be done with the data and how it will be displayed.

If you are unsatisfied by the data assignments generated by XD, you can assign data to roles manually.

## Procedure



To manually assign data to roles, complete the following steps:

1. When you launch XD, press and hold the **Ctrl** key.

The data configuration window opens. In this window, you can drag and drop data from a list into roles. It is likely that XD has already assigned some data to roles.

**Note:** You can only assign valid data to a role. For example, some data roles must share a frame of reference.

You can sort the list at the top of the window by any of the columns.

2. (Optional) If you have not already launched the application by using a specific review mode, use the **Select a review mode** drop down menu to select the review mode that you want to use.
3. (Optional) To add a time point, click **Add Timepoint** at the bottom of the window. The added time point is always **Current**, with **Baseline** and **Prior** time points preceding it.
4. (Optional) To remove a time point, click the cross at the top right corner of the time point's panel in the window. Other time points have their labels adjusted to account for the removal of a time point.
5. To assign an image or volume to a data role, click the image or volume from the list and drag it to the data role.
6. To move an image or volume from one data role to another, click the image or volume from the first data role and drag it to the second.
7. (Optional) To remove an image or volume from a data role, select the image or volume in its data role and then, for that data role, click the **Clear role** icon . If you want to clear all images or volumes from the role, click the **Clear role** icon  without selecting any of the images or volumes in the role.

8. (Optional) To clear all assignments and delete all but one time point, click **Clear All**.
9. (Optional) To revert all assignments and removed or added time points to the state that was originally assigned by the application, click **Reset**.
10. Click **OK** to complete the application launch.

## Related topics:

- [Viewing images](#)  
In this section you can find information about viewing images without making significant changes to your session data.
- [Performing and managing registration of images](#)  
Topics describing the registration of two images and the management of relationships between images.


# The user interface

**Summary:** An overview of the user interface.

## The toolbar and the toolbox

The toolbar, at the top of the window, and the toolbox, on the left of the window, provide access to various functions regardless of the screen that you are viewing.

The toolbar provides commonly used tools for manipulating images and views, such as pan, zoom, segmentation, and showing and hiding various aspects of the user interface. The same tools in the toolbar are displayed for all screens.

The toolbox provides tools that are more specific to the screen you are currently viewing, such as access to secondary captures or a list of regions. The tools in the toolbox vary depending upon the screen you are viewing. You can show or hide the toolbox by clicking the **Select whether the toolbox is visible** icon  in the toolbar.

**Note:** By clicking the **Messages** menu at the top of the application window and selecting **Show messages**, you can view information from the application related to errors or unexpected data.

## Context menus

In XD right clicking in a view or menu presents a context menu. This menu contains different tools depending on where it is opened, and the tools provided can be customized through the Options window. For more information, see [Setting user preferences](#). All tools available in the context menu are also available through other menus, the toolbar, or the toolbox.

## Screens

XD provides several different screens, each of which serves a particular purpose. At the right end of the toolbar, you can use the **Screen** menu to switch between screens. You can also use the **Window** menu, or use buttons that are shown in the toolbox for certain screens.

- **Layout Screens** The layout screens provide a means to view your images. Different layouts suit different purposes, displaying a different selection of datasets, time points, and orientations. You can also create custom layouts.
- **Data QC** The Data QC screen provides a means to review the DICOM attributes associated with your data.
- **Registration Manager** The Registration Manager screen provides a means to assess and adjust the registration between images that you have loaded into the application.
- **Findings Table** The Findings Table screen displays the various statistics that can be calculated from the rulers and regions that you have created on your images.

- **Secondary Capture** The Secondary Capture screen displays your secondary captures that you have either loaded into the application or captured yourself.




## Layout screens



Layouts are the primary way of viewing images in XD. Each layout presents one or more views, where each view displays an orientation of an image.



Additionally, a view may display one image overlain on another image, using a customizable color map and transparency level.

In the corners of a view, information about the data is displayed either as static text or active text.

Each review mode makes available a different set of layouts and, if these are not sufficient, you can also create custom layouts. For more information, see [Creating custom layouts](#).

Data is displayed in views, including patient details and information about the image itself. To hide or show patient details, click the **Select whether patient information is displayed in the views** icon , to hide or show details for navigating the volume, click the **Select whether navigation controls are displayed in the selected view** icon  or, to hide or show all details in views, click the **Select whether the information overlays are visible** icon .

Crosshairs can be displayed in views, and by default are linked between orientations and registered images. The crosshairs allow statistics to be generated for a specific point and are used to position certain fixed-volume regions. To show or hide volume statistics at the crosshair location, click the **Select whether to calculate and display volume statistics at the crosshair location** icon , or, to hide or show the crosshairs and all associated information, click the **Select whether the crosshairs are visible** icon .

Annotations and findings are also displayed in views. To hide or show regions, click the **Select whether ROIs are displayed in the selected view** icon . To hide or show annotations, click the **Select whether annotations and rulers are displayed in the views** icon .

The toolbox provides tools for viewing layers, adjusting window and level settings, working with findings, accessing secondary captures, and controlling the display of dynamic data.

For more information, see the [Viewing images](#), [Performing and managing registration of images](#), and [Findings](#) topics.

**Tip:** When you have minimized the application window, the patient name is displayed when you hover your cursor over the application icon in the Windows taskbar.

## Data QC

The Data QC screen displays a table listing the different DICOM attributes.

The toolbox provides tools for setting your preferences for data quality control, and for accessing secondary captures.

For more information, see [Data quality control](#).



## Registration Manager

The Registration Manager screen is used to specify relationships between images and to perform or alter registration.

The toolbox provides tools for registration quality control, automatic registration, manual registration, and loading registrations.

For more information, see [Performing and managing registration of images](#).

## Findings Table

The Findings Table screen presents statistics and graphs that are generated from findings that you created on your volumes. Different tabs are available and show different sets of statistics, for example, the PERCIST tab provides statistics pertinent to PERCIST assessment.

Additionally, you can configure the statistics that appear in the findings table screen, for more information, see [Setting user preferences](#).

The toolbox provides tools for changing which datasets and time points are used to generate the findings table, for working with different findings, and for accessing secondary captures.

For more information, see [Using the findings table](#).

## Secondary Capture

The Secondary Capture screen displays a selected secondary capture in the main view.

The toolbox provides tools for choosing which secondary capture to view and for controlling how cines are played.

For more information, see [Capturing an image](#) and [Exporting secondary captures](#).

## Related topics:

- [Manipulating images](#)  
Adjust your view of an image.
- [Performing and managing registration of images](#)  
Topics describing the registration of two images and the management of relationships between images.
- [Findings](#)  
Topics describing the creation and editing of regions and rulers.
- [Creating custom layouts](#)  
You can create custom layouts for viewing a study.

# Support

**Summary:** If you require technical support, a support package provides additional information about your system.

## About

A support package includes the following information:

- Machine settings, such as Name and IP Address
- A configuration comparison list of files found in the XD 3.6.11 bin folder (comparing factory settings to current settings)
- Public and current user settings
- XD 3.6.11 logs that are present on the system, this includes the XD 3.6.11 log, the XD 3.6.11 debug log, and, if present, the XD 3.6.11 trace log

## Procedure

To generate a support package, complete the following steps:

1. Click the **Help** menu and select **Generate Support Package**.
2. Choose where to save your support package and click **Save**. It is not recommended to change the folder name.

You have generated your support package, attach this to your email to technical support.

# Data quality control

**Summary:** You can review the attributes of your loaded data.

## About

While you cannot edit DICOM attributes of your data, XD provides the means to review data attributes.

## Procedure

To review your data's attributes, complete the following steps:

1. Click the **Window** menu and select **Data QC**.
2. Click the tab of the data role that you want to review the attributes of.  
  
The table in each tab displays, for the data role, a selection of DICOM attributes at different time points.
3. (Optional) To copy the table to the system clipboard, click **Copy Table**.
4. (Optional) To save the table as a secondary capture, click **Snapshot Table**. For information about exporting secondary captures, see [Exporting secondary captures](#).
5. To configure the attributes that are displayed, click **Options** in the toolbox. For more information, see [Setting user preferences](#).

## Related topics:

- [Setting user preferences](#)  
Use the Options window to manage user preferences.
- [Exporting secondary captures](#)  
Export secondary captures as different image types or a DICOM object.

# Viewing images

**Summary:** In this section you can find information about viewing images without making significant changes to your session data.

In XD, you can view two-dimensional images and three-dimensional image volumes. The topics in this section of the user guide detail the methods by which you can view the image, such as the perspective of a viewport, by obtaining secondary captures, and as cines.

## Topics in this section:

- [Manipulating images](#)  
Adjust your view of an image.
- [Viewing a maximum intensity projection \(MIP\)](#)  
You can view a maximum intensity projection of your dataset.
- [Capturing an image](#)  
You can capture views for later reference or for use outside of XD.
- [Choosing a layout](#)  
Select the layout of images with which you want to view your data.
- [Interacting with active text](#)  
Blue text on an image is active text and can be used to manipulate the image.
- [Viewing cines](#)  
A cine displays a series of image frames or slices in order.

# Manipulating images

**Summary:** Adjust your view of an image.


## About

XD provides a range of tools for viewing your images. This topic covers the use of the following tools:

- Zoom
- Pan
- Scroll through slices
- Window and level settings
- Overlay transparency
- Rotation

## Procedure

To manipulate the manner in which your images are displayed, complete the following steps:


1. At any time, you can toggle between a viewport being maximized or part of a layout by double clicking the viewport. You can also toggle between the two settings by clicking the **Toggle whether the view is maximized** icon .

**Tip:** All the tools referred to in this topic can also be accessed by right-clicking the image.



2. (Optional) Specify the way in which your different viewports zoom together by clicking the **Image** menu, selecting **Zoom bindings** and choosing one of the following options:
  - Select **Axial/Coronal+Sagittal** to lock the coronal and sagittal planes together and zoom the coronal plane independently.
  - Select **Per-Plane** to lock all viewports of the same view together.
  - Select **All** to lock all views and viewports to the same zoom settings.
  - Select **None** to only zoom in the viewport that you are using.
3. (Optional) Specify the interpolation method used to visualize data by clicking the **Image** menu, selecting **Interpolation Method**, and choosing one of the following:
  - Select **Nearest Neighbor** to use the closest available value for each voxel.
  - Select **Linear** to use linear interpolation between the nearest available values for each voxel.

- Select **Cubic Spline** to use a cubic spline to interpolate between the nearest available values for each voxel.

4. To zoom the image to your desired scale, use one of the following methods:

- Hold the **Ctrl** key and use your scroll wheel to zoom in and out. Scroll up to zoom in and scroll down to zoom out.
- Click the **Zoom into the image** icon  and then click the image and drag in the vertical direction to zoom. Drag upwards to zoom out and drag downwards to zoom in.

5. To locate the views in other viewports to a position in your current viewport, drag the crosshairs to where you want the views to intersect.

If the crosshairs are not correctly linked between views and orientations, click the **Unlink the crosshairs to perform a manual alignment** icon , drag the crosshairs in different views to align correctly, and then click the **Link the crosshairs based on their current positions** icon .




**Warning:** 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 the 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.





**Warning:** 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.


6. To pan an image, use one of the following methods:

- Hold the **Shift** key and then drag the image with your cursor.
- Click the **Pan image** icon  and then drag the image with your cursor.

**Tip:** If you have multiple datasets within a timepoint and data role, such as multiple MR sequences or gates of CT data, you can switch between these by pressing the **Left** and **Right** arrow keys.

7. To scroll through slices of a plane, use one of the following methods:






- Use your scroll wheel to scroll through slices. The direction in which you scroll depends upon the orientation of the image.
- Click the **Navigate through the volume slices** icon  and then click and drag the image in the vertical direction.
- Display the navigation controls by clicking the **Select whether navigation controls are displayed in the selected view** icon  and then use the navigation slider bar in the viewport to navigate through the slices of the volume.


 **Warning:** 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.


8. To adjust the window and level settings, use one of the following methods:


- Use the sliders in the toolbox to adjust the level, by dragging the horizontal bar, and the window, by dragging the end markers.





- Click the **Adjust window and level** icon  or, if it is not displayed, select it from the dropdown menu beside the **Adjust the window maximum** icon . Then click the image and drag in the vertical direction to adjust the window and in the horizontal direction to adjust the level.
- Click the **Adjust window maximum** icon  or, if it is not displayed, select it from the dropdown menu beside the **Adjust the window and level** icon . Then click the image and drag in the vertical direction to adjust the maximum value of the window.
- To reset the window and level settings, click the **Reset Window/Level** icon .

9. To adjust the transparency of an overlay image, click the **Adjust the overlay transparency** icon  and then click on the image and drag in the vertical direction.

 **Warning:** 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.

10. To rotate your view in the current and linked viewports, click the **Rotate MPR views** icon  and then click and drag in the viewport.

When you have rotated a view, an MPR overlay cube is displayed, to show standard orientations in comparison to the current one. To toggle the display of this cube, click the **Select whether the MPR cube overlay is visible** icon .

11. (Optional) To reset the zoom, pan, and orientation of an image in all viewports, click the **Reset zoom, pan and orientation of all views** icon .

## Related topics:

- [Performing and managing registration of images](#)  
Topics describing the registration of two images and the management of relationships between images.
- [Findings](#)  
Topics describing the creation and editing of regions and rulers.
- [The user interface](#)  
An overview of the user interface.



# Viewing a maximum intensity projection (MIP)

**Summary:** You can view a maximum intensity projection of your dataset.

## About









Using the XD application, you can produce and view a maximum intensity projection (MIP) to view an apparently three-dimensional representation of the data.



**Warning:** 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.

## Procedure

To create and view a maximum intensity projection, complete the following steps:

1. Click the **Display the series in the selected view as a MIP in a floating window** icon . A new window opens, displaying the MIP.
2. Use the slider on the left of the window to rotate the direction from which the projection is taken.
3. To snap the view to the sagittal orientation, click the **Snap to sagittal orientation** icon .
4. To snap the view to the coronal orientation, click the **Snap to coronal orientation** icon .
5. To display a cine of the MIP rotating, click the **Start cine** icon .
6. To pause a playing cine of the MIP, click the **Pause cine** icon .
7. To reverse the direction in which the MIP rotates, click the **Change direction of cine** icon .
8. To toggle between rotating the MIP through 360° (rotating) and rotating through 180° then reversing (flicking), click the **Toggle between rotation and flick** icon,  when the image is currently rotating, or  when the image is currently flicking.
9. You can also use the **Image** menu to manipulate the MIP as you would a normal viewport.

## Related topics:

- [Exporting a maximum intensity projection \(MIP\)](#)  
You can export a maximum intensity projection.
- [Viewing cines](#)  
A cine displays a series of image frames or slices in order.

# Capturing an image

**Summary:** You can capture views for later reference or for use outside of XD.

## About

You can capture secondary images within the XD application that you can refer to later, after making other changes to the dataset, or that you can use outside of the application.

## Procedure

To capture an image and view this secondary capture within the application, complete the following steps:

1. You can capture a single viewport or a row or column of viewports.

- To capture a single viewport, complete the following steps:

i. On a layout screen, click the **Take snapshot of views** icon .

**Tip:** The **Take snapshot of views** icon is also available in the right-click menu.


ii. Click a viewport. The viewport is captured, including all active text.

**Tip:** To capture the entire application window instead of a single viewport, press **Ctrl+Shift+E**


- To capture a row or column, complete the following steps:

i. Select a viewport.

ii. Click the **Edit** menu and select either **Capture row view** or **Capture column view**. All viewports in the row or column, respectively, of your selected viewport are captured and stored as a single secondary capture.

2. To view a secondary capture, select the capture in the **Image Gallery** in the toolbox, and then click the **Switch to the secondary capture screen** icon . The Secondary capture screen opens.

3. To return to your layout, click **Back to Layouts** or, in the upper-right corner of the window, click **Secondary Capture** and then select the layout you want to return to.

4. (Optional) To delete one or more captures, select the capture or captures in the **Image Gallery** section of the toolbox and then click the **Remove selected images from the gallery** icon . You can select multiple captures by holding the **Shift** or **Ctrl** keys.

## Related topics:

- [Exporting data](#)  
Export data for use outside of your session.

# Choosing a layout

**Summary:** Select the layout of images with which you want to view your data.

## About

In XD, you can select from a number of different layouts, each of which will arrange images from a dataset in a different manner. Each review mode features several layouts and you can also create your own custom layouts.

## Procedure

To choose or change between layouts, use one of the following methods:

- In the upper-right corner of the application window, click the **View** button. The appearance of this button depends on your current view, but will be one of the following:
  - **Data QC**
  - **Registration Manager**
  - **Findings Table }**
  - **Secondary Capture**
  - The name of your current layout, for example, **1 Dataset - All Orientation**

Then click the layout that you want to change to.

- Click the **Window** menu in the menu bar at the top of the application window and then select the layout that you want to change to.
- Hold the **Ctrl** key and then cycle through available views, including layouts, by pressing the **Tab** key.

## Related topics:

- [Creating custom layouts](#)  
You can create custom layouts for viewing a study.
- [Launching XD review modes](#)  
Launch the XD application.

# Interacting with active text

**Summary:** Blue text on an image is active text and can be used to manipulate the image.

## About


In XD, two kinds of text are displayed on images. Blue text represents active text, and can be altered to change how the image is displayed, while black or white text, whose color depends upon the colormap in use, is static and for information only.

## Procedure

To manipulate an image by using its active text, complete the following series of steps:

- To edit the scale, complete the following steps:
  1. In the upper-right corner of the image viewport, click the blue text **Scale a:b**, where *a* and *b* represent the current scale of the image.
  2. Use the slider to choose a new scale.
  3. (Optional) Click **Zoom to Fit** to change the scale so that the entire image is displayed in the viewport.
  4. Click **Close**.

**Note:** The change in scale will apply to linked views as specified in the **Zoom Bindings** section of the **Image** menu. For more information, see [Manipulating images](#).

- To change the window and level settings, complete the following steps:
  1. In the upper-right corner of the image viewport, click the blue text **\*W = \*X L=Y \***, where *X* and *Y* represent the current window and level respectively.
  2. In the **Window and Level** section of the Visualization window, specify the window and level that you want to use.
    - If you want to specify values for your window and level, select **Custom** and specify a value for window, **W**, and level, **L**.
    - If you are using Hounsfield Units and want to use a common window and level, select it from the list.
    - You can save a window and level combination for later use by providing a name in the field below **W** and **L** and clicking the **Save Range** icon .
  3. Click **OK**.

**Note:** You can also use the sliders at the bottom of the Visualization window to set a custom window and level. For more information about using the sliders, see [Manipulating images](#).

- To edit the quantification options being used, complete the following steps:

1. In the lower-left corner of the image, click the blue text ***X Units*** where *X* is the intensity of the image at the crosshairs and *Units* is the units of that intensity.
  2. Select the units that you want to use.
  3. (Optional) If it is available, click **Quantification Options**, provide additional information, and click **OK** in the Quantification Parameters window.
  4. Click **OK**.
- To change which slice index you are viewing, complete the following steps:
    1. In the lower-right corner of the image, click the blue text **Slice *x/y* (*z*)** where *x* is the current slice index, *y* is the total number of slices, and *z* is the index of the current slice if the counting order is reversed.
    2. Enter a new slice index within the available range.

## Related topics:

- [Customizing XD](#)  
Topics describing the customization of XD.
- [Findings](#)  
Topics describing the creation and editing of regions and rulers.
- [Manipulating images](#)  
Adjust your view of an image.

# Viewing cines

**Summary:** A cine displays a series of image frames or slices in order.

## Prerequisites


To complete this task, you must have loaded into the application a dataset containing a time series or a three-dimensional volume.

## About

In XD, you can view images as a cine if they are either a time series or a three-dimensional volume. As a cine, the image frames or slices are displayed sequentially so that you can see how features change with time or space. You can also control the speed and direction of the cine.



## Procedure

To view a cine, complete the following steps:

1. Select the viewport containing the orientation that you want to use for the cine.
2. In the **Cine** section of the toolbox, select **Slices** or **Datasets** depending on whether you want your cine to display different spatial slices or datasets captured at different times.
3. Click the **Start cine** icon  to start the cine. The cine plays in all viewports, but when viewing slices only the selected orientation's image will change, while other orientations' crosshairs will move appropriately.



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

4. (Optional) Click the **Change direction of cine** icon  to reverse the order in which the cine plays.
5. (Optional) Click the **Pause cine** icon  to pause the cine.
6. (Optional) Use the slider in the **Cine** section of the toolbox to adjust the rate at which the cine plays or changes slice.

## Related topics:

- [Manipulating images](#)  
Adjust your view of an image.



# Performing and managing registration of images

**Summary:** Topics describing the registration of two images and the management of relationships between images.

## About

Images can be registered to one another within and between time points and datasets. You can perform registration automatically or manually.

## Topics in this section:

- [Managing data bindings](#)  
You can create, remove, and edit bindings between datasets and between time points.
- [Performing automatic registration](#)  
Have XD perform registration of two images.
- [Performing manual registration](#)  
If you want to control registration beyond using an automatic algorithm, you can perform manual registration.

# Managing data bindings

**Summary:** You can create, remove, and edit bindings between datasets and between time points.

## About

While XD creates data bindings automatically, these may not be correct and may require action.

A timepoint or dataset can be bound to one or more other timepoints or datasets. One-to-one bindings might be appropriate between two gated sets of data; all-to-one bindings might be appropriate between gated data and a static volume; and two-to-one bindings might be appropriate when two sets of gated data were sampled with different frequencies.

Data bindings have several effects:

- Changes made to ROIs in one dataset will be applied in other datasets that are bound to it, according to transformations.
- When viewing images, navigating through slices or timepoints in one dataset will navigate through slices or timepoints in the dataset to which it is bound.




## Procedure

To view and modify data bindings, complete the following steps:

1. Click the **Tools** menu and select **Data Management**. The Data Management screen is displayed.

Datasets are displayed as individual rows, while timepoints within a dataset are displayed as segments of a row.

Bindings between data are represented by lines joining timepoints or datasets. A dotted line indicates a binding between datasets where it is not possible to draw the line without crossing a third dataset.

2. To remove a binding, right click the link and select **Remove Binding**.
3. To create a binding, click one of the two datasets or timepoints and drag to the other dataset or timepoint.
4. (Optional) To cycle the display through timepoints within a dataset, click the **Cycle** icons  . Doing so does not affect the order of the data, but can be useful for viewing bindings that do not line up simply.
5. Each dataset with multiple timepoints has an anchor volume. This is the timepoint that is used for registration between datasets. The anchor volume is denoted by the **Anchor** icon .

To change the anchor volume, right click the timepoint that you want to become the anchor volume and select **Set as Anchor**.

6. (Optional) To revert all bindings to the automatically assigned bindings, click **Reset Links**.

## Related topics:

- [The user interface](#)  
An overview of the user interface.
- [Manipulating images](#)  
Adjust your view of an image.
- [Findings](#)  
Topics describing the creation and editing of regions and rulers.

# Performing automatic registration

**Summary:** Have XD perform registration of two images.


## About

XD is able to perform automatic registration by using various algorithms. The registration can be between time points, modalities, or both. In this manner, you can quickly register images in a study.

## Procedure

To perform automatic registration, complete the following steps:

1. Click the **Registration** menu and select **Registration Manager**.
2. In the pane at the top of the window, relationships between different images are displayed as lines between the roles of the images.

Black lines between roles indicate that the images share a frame of reference and are hardware locked in their registration. Images that are hardware locked to a reference image are also denoted by the **Locked** icon  and red lines between roles indicate that the images are subject to a rigid registration. Columns of images represent different time points.

To expand a time point and display additional volumes contained within the time point, click the column header of a time point, for example **Current** or **Baseline**. In the expanded view, click **Back** to return to the main view.

If the relationship that you want to register is locked, click the role and select **Unlock Image**, where *Image* is the name of the non-reference image.







If you want to change the relationships, use the Data Management page. For more information, see [Managing data bindings](#).

3. Click one of the roles that you want to register and select **Role 1 -> Role 2**, where the *Roles* are the data roles that you want to register. Views for each orientation are displayed with one image overlain on the other.
4. Perform one of the following registration types:
  - To perform automatic rigid registration, in the **Automatic Registration** section of the toolbox, click **Automatic Rigid**. To change the granularity with which the algorithm is run, click ... beside **Automatic Rigid** and select the granularity that you want to use.

**Note:** The granularity affects the quality of the registration and the time taken to perform it, with the **Fine** registration taking longest. The registration runs automatically when you select a granularity.

5. (Optional) To smooth a deformation so that displacements do not vary significantly between two near points, in the **Automatic Registration** section of the toolbox, click **Smooth Deformation**.

6. Use the following tools from the **Visualization Tools** section of the toolbox to review the registration. You can also use the standard image tools described in [Manipulating images](#).

- The left tool provides an overlay that represents the displacement arising from the registration. You can use one of the following overlays:
  - **Show Displacement Map**  Displays a heat map representing displacement.
  - **Show Displacement Grid**  Displays a grid that is deformed and displaced in the same manner as the image.
  - **Show Displacement Arrows**  Displays arrows showing the direction and scale of displacement at a given point.
- The middle tool allows you to display one image through a window instead as a transparent overlay. You can use the following window types:
  - **Checkerboard**  Displays the overlay and the base image in alternating squares.
  - **Inset**  Displays the overlay as a single square in the center of the view. The middle tool also enables the **Overlay size** slider, which you can use to adjust the size of the window.
- The right tool is the **Show Displacement Value** tool , which toggles the display of the displacement at the crosshairs on your image.



**Warning:** 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.

## Next actions

If you want to alter your registration, you can do so manually. For more information, see [Performing manual registration](#).

## Related topics:

- [Manipulating images](#)

Adjust your view of an image.

- [Managing data bindings](#)

You can create, remove, and edit bindings between datasets and between time points.

# Performing manual registration


**Summary:** If you want to control registration beyond using an automatic algorithm, you can perform manual registration.

## About

You can perform manual rigid registration either by translating an overlay image yourself or by placing landmarks that are then used to find a rigid transformation.

## Procedure

To perform manual registration, complete the following steps:

1. Click the **Registration** menu and select **Registration Manager**.
2. In the pane at the top of the window, relationships between different images are displayed as lines between the roles of the images.  
  
Black lines between roles indicate that the images share a frame of reference and are hardware locked in their registration. Images that are hardware locked to a reference image are also denoted by the **Locked** icon  and red lines between roles indicate that the images are subject to a rigid registration. Columns of images represent different time points.  
  
To expand a time point and display additional volumes contained within the time point, click the column header of a time point, for example **Current** or **Baseline**. In the expanded view, click **Back** to return to the main view.  
  
If the relationship that you want to register is locked, click the role and select **Unlock Image**, where *Image* is the name of the non-reference image.  
  
If you want to change the relationships, use the Data Management page. For more information, see [Managing data bindings](#).
3. Click one of the roles that you want to register and select **Role 1 -> Role 2**, where the *Roles* are the data roles that you want to register. Views for each orientation are displayed with one image overlain on the other.
4. In the **Manual Registration** section of the toolbox, choose how to display your images by performing one of the following actions:
  - To view your images in a single view per orientation, click **Fused**.
  - To view your images in two views per orientation, where one view displays both images and the second view only the overlay, click **Landmarks**.
5. Perform manual registration by completing one of the following sets of steps:
  - To perform manual rigid registration, complete the following steps:
    - i. Click **Manual Rigid**.

ii. In the view of your overlain images, drag the overlay into the correct position.

• To perform registration based on landmarks, complete the following steps:

i. If it is not active, click **Place Landmarks**.

ii. In a view in the top row of views, click where you want to place a landmark on the base image.

iii. In a view in the bottom row of views, click where you want to place a landmark on the overlay image. Place several landmarks and be careful to place a landmark on each image before placing the next landmark.

iv. (Optional) To delete a landmark, select the landmark in the **Marker** pane in the **Manual Registration** section of the toolbox, and then click **Delete**.

v. (Optional) To move the crosshairs to a landmark, select the landmark in the **Marker** pane in the **Manual Registration** section of the toolbox, and then click **Go To Source** to move your crosshairs in the source image, or **Go To Target** to move your crosshairs in the target image.

vi. When you have placed your landmarks, click **Landmark Rigid** to run the rigid registration.

6. Use the following tools from the **Visualization Tools** section of the toolbox to review the registration. You can also use the standard image tools described in [Manipulating images](#).

• The left tool provides an overlay that represents the displacement arising from the registration. You can use one of the following overlays:

▪ **Show Displacement Map** 

Displays a heatmap representing displacement.

▪ **Show Displacement Grid** 

Displays a grid that is deformed and displaced in the same manner as the image.

▪ **Show Displacement Arrows** 

Displays arrows showing the direction and scale of displacement at a given point.

• The middle tool allows you to display one image through a window instead as a transparent overlay. You can use the following window types:


▪ **Checkerboard** 

Displays the overlay and the base image in alternating squares.



- **Inset** 

Displays the overlay as a single square in the center of the view. The middle tool also enables the **Overlay size** slider, which you can use to adjust the size of the window.

- The right tool is the **Show Displacement Value** tool , which toggles the display of the displacement at the crosshairs on your image.

## Related topics:

- [Manipulating images](#)  
Adjust your view of an image.
- [Managing data bindings](#)  
You can create, remove, and edit bindings between datasets and between time points.

# Findings

**Summary:** Topics describing the creation and editing of regions and rulers.

## About

Findings can be either regions or rulers and can be created manually or by segmenting your volume. Additionally, you can project and link findings across datasets and time points.

## Topics in this section:

- [Segmenting an image](#)  
XD can perform automatic segmentation within an area that you define.
- [Drawing a region](#)  
You can draw a region on an image using the freehand region tool, or as an ellipse or rectangle.
- [Editing a region](#)  
You can edit the properties, location, and size of a region.
- [Creating and editing rulers](#)  
You can create permanent and temporary rulers and measure angles.
- [Creating a ruler from a region](#)  
You can create a bi-ruler from a region.
- [Annotating an image](#)  
Add annotations to an image that are included in the DICOM dataset.
- [Linking findings together](#)  
You can link findings to indicate a relation between the two.
- [Projecting findings](#)  
You can project and propagate findings between different images instead of creating each one separately.
- [Creating multiple threshold regions](#)  
You can create multiple regions within another region, where each new region is contoured based on a specific threshold level.
- [Creating quantification volumes](#)  
Create a cylindrical or spherical region with a specific volume.

# Segmenting an image






**Summary:** XD can perform automatic segmentation within an area that you define.


## About

XD provides several different tools for performing automatic segmentation. You can segment based on an absolute threshold, a percentage of maximum threshold, using Hounsfield units in a CT scan, or from a seedpoint.

## Procedure

To perform automatic segmentation of a volume, complete the following steps:

1. Click one of the following icons in the tool bar at the top of the window, depending on which tool you want to use. The tool you want to use might not be displayed, in which case use the drop down menu beside whichever of these icons is displayed. Alternatively, all the tools can be accessed through the **Quantify** menu.
  - Use the **Region with absolute threshold** tool  to generate a region based on an absolute threshold that is set in your contouring preferences. You can adjust the threshold within the bounding region later. For more information about setting the initial threshold, see [Setting user preferences](#).
  - Use the **Region with % max** tool  to generate a region based on a threshold derived from a percentage of the maximum intensity in the image. You can adjust the threshold within the bounding region later. For more information about setting the initial threshold, see [Setting user preferences](#).
  - Use the **Seedpoint Region** tool  to generate a region from a seedpoint and grow that region.
  - (CT image only) Use the **CT Region Segmentation** tool  to create a region that is segmented based on mutual information. Click and drag to create two concentric spheres, where the inner sphere approximates the region you want to segment. When you release the mouse button, the segmentation runs.
  - (CT image only) Use the **Adaptive CT Region Segmentation** tool  to create a region that is segmented based on mutual information, taking into account your current Window/Level settings. Click and drag to create two concentric spheres, where the inner sphere approximates the region you want to segment. When you release the mouse button, the segmentation runs.

 **Warning:** 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.

2. If you are using the Seedpoint Region tool, click the location from which you want to grow your region.

**Tip:** If you want to transfer a region from one image volume to another, either within or across timepoints, you can use the projection tools. For more information, see [Projecting findings](#).

3. If you are using another tool, click and drag to create the 3D volume within which segmentation will be performed. In the orientation that you are drawing the region on, the volume is drawn from corner to corner, while in other orientations the slice you are drawing on will be treated as the center.
4. Complete the following fields:
  - In the **Name** field, enter the name of the region, or select a standard region name from the drop down menu.
  - In the **Description** field, enter a description of the region.
  - Click the **Color** panel to select the color in which the region should be displayed.
  - Use the check boxes to specify whether the region is a lymph node and whether it should be quantified.
  - From the **Interpreted Type** drop down menu, select a type of region.
  - In the **Interpreter** field, provide the name of the interpreter.
5. Click **OK**.
6. In the **Threshold Settings** section of the Toolbox, adjust your threshold settings by completing the following steps:
  - a. Use the **Threshold by** drop down menu to select the units that a threshold uses.
  - b. Use the numeric fields to specify percentages or absolute values for your upper and lower thresholds (according to what you selected in the **Threshold by** field) or use the sliders to specify the range. The region updates dynamically as you adjust your range.

## Next actions

If you want to edit your region with other tools, see the [Editing a region](#) topic.

For information about using your new region for quantification, see [Quantification](#).

# Drawing a region



**Summary:** You can draw a region on an image using the freehand region tool, or as an ellipse or rectangle.

## About


As well as using automatic segmentation and generating volumes, you can draw a 2D or 3D region on an image manually.



## Procedure

To draw a 2D region on a single slice or a 3D region with its center on the current slice, complete the following steps:

1. Draw your region by using one of the following methods:
  - To draw your region as either an ellipse or a rectangle, complete the following steps:
    - i. Click the **Ellipse Region**  or the **Rectangle Region**  icon depending on which type of region you want to create.

If another region tool has been used more recently, use the drop down menu to select the appropriate tool instead.

Alternatively, you can select either the **Ellipse Region** tool or the **Rectangle Region** tool from the **Quantify** menu.
    - ii. In the position that you want to start, click the orientation and slice on which you want to draw a 2D region and drag the cursor across to create the region. The ellipse region's extremes in the vertical and horizontal directions are defined by where you drag your cursor.
  - To use the freehand tool to draw your region, complete the following steps:
    - i. Click the **Freehand Region** icon  in the toolbar at the top of the window.

If the **Paint**  or **Erase**  tool was used more recently, use the corresponding menu to select the **Freehand Region** tool.

Alternatively, you can select the **Freehand Region** tool from the **Quantify** menu.
    - ii. Click on the orientation and slice where you want to start drawing your 2D region and drag the cursor across the image in the shape of your region. The region will always be completed by a straight line joining the start and your cursor. If you are not satisfied with your first attempt, you can draw the region again or you can edit the region later.

- iii. Press **Esc** to exit the drawing tool.
  - iv. In the **Findings** section of the toolbox, double-click your newly created region.
- To create a 3D region, complete the following steps:

- i. Click the **Region** icon  in the toolbar at the top of the window.

If another region tool has been used more recently, use the drop down menu to select the appropriate tool instead.

Alternatively, you can select the **Region** tool from the **Quantify** menu.

- ii. Select the slice that you want to use as the center of the sphere or cuboid.
- iii. Click and drag to create the region.

**Note:** You can alter whether the Region tool creates a sphere or cuboid through the Options window. For more information, see [Setting user preferences](#).

**Tip:** If you want to transfer a region from one image volume to another, either within or across timepoints, you can use the projection tools. For more information, see [Projecting findings](#).

## 2. Complete the following fields:

- (Required) In the **Name** field, enter the name of the region, or select a standard region name from the drop down menu.
- In the **Description** field, enter a description of the region.
- Click the **Color** panel to select the color in which the region should be displayed.
- Use the check boxes to specify whether the region is a lymph node and whether it should be quantified.
- From the **Interpreted Type** drop down menu, select a type of region.
- In the **Interpreter** field, provide the name of the interpreter. Click **OK**.

## Next actions

If you want to edit your region with other tools, see [Editing a region](#).

For information about using your new region for quantification, see [Quantification](#).

# Editing a region

**Summary:** You can edit the properties, location, and size of a region.

## Prerequisites



To complete this topic, you must first have created a region. For more information, see [Segmenting an image](#) or [Drawing a region](#).

## About


Segmentation can be imperfect, or it can be easier to edit a region projected from a previous timepoint than to draw or segment a new region. XD provides tools for editing regions.

## Procedure

To edit a region, complete the following steps:

1. In the **Findings** section of the toolbox, or in a view, select the region that you want to edit.
2. To remove an area from a region, complete the following steps:
  - a. Click the **Erase** tool  in the toolbar at the top of the window. Alternatively, you can access it through the **Quantify** menu or through the keyboard shortcut by pressing **W**.
  - b. Adjust the size of your eraser by using the **Brush** and **Depth (%)** sliders in the **Region Editing Tools** section of the toolbox. You can also adjust the diameter by holding the **Shift** key and using your scroll wheel.
  - c. Erase a part of a region by clicking and dragging in that region. The eraser will have no effect outside of the selected region and erases as a three-dimensional cylinder.
3. To add an area to a region, complete the following steps:
  - a. Click the **Paint** tool  in the toolbar at the top of the window. Alternatively, you can access it through the **Quantify** menu or through the keyboard shortcut by pressing **Q**.
  - b. Adjust the size of your paint brush by using the **Brush** and **Depth (%)** sliders in the **Region Editing Tools** section of the toolbox. You can also adjust the diameter by holding the **Shift** key and using your scroll wheel.
  - c. Add a part of the image to the region by clicking and dragging on the image. The paintbrush will have no effect inside the selected region and paints as a three-dimensional cylinder.

**Tip:** If you want to transfer a region from one image volume to another, either within or across timepoints, you can use the projection tools. For more information, see [Projecting findings](#).

4. (Optional) To delete a region, ensure the region is selected and then click the **Delete the selected findings** icon  in the **Findings** section of the toolbox.



## Related topics:

- [Drawing a region](#)  
You can draw a region on an image using the freehand region tool, or as an ellipse or rectangle.
- [Segmenting an image](#)  
XD can perform automatic segmentation within an area that you define.

# Creating and editing rulers

**Summary:** You can create permanent and temporary rulers and measure angles.





## About


XD provides the facility to create rulers on your images. Standard one-dimensional rulers can be permanent or temporary, while two-dimensional rulers and angle measures are always permanent, though can be deleted.

These rulers are considered findings and can be used for quantification purposes.

## Procedure

To create and edit rulers, complete the following steps:

1. In the top toolbar, click one of the following tools according to what you want to do. If a different tool was used more recently, the tool you want to use might not be visible immediately; if this is the case, select the tool from the drop down menu beside one of the other tools. All of these tools are also available through the **Quantify** menu.
  - Use the **Temporary Ruler** tool  to draw a ruler that is only displayed while you hold the mouse button.
  - Use the **Ruler** tool  to draw a persistent ruler.
  - Use the **2D Ruler** tool  to draw a persistent two-dimensional ruler.
  - Use the **Angle** tool  to create a persistent angle measurement.
2. Click the image and drag to create the ruler. The angle or length is displayed. Release to complete the ruler or, if you are using the temporary ruler tool, to remove the ruler.
3. (Persistent rulers only) Complete the following fields:
  - (Required) In the **Name** field, enter the name of the ruler, or select a standard finding name from the drop down menu.
  - In the **Description** field, enter a description of the ruler.
  - Click the **Color** panel to select the color in which the ruler should be displayed.
  - Use the check boxes to specify whether the ruler is a lymph node and whether it should be quantified.
  - From the **Interpreted Type** drop down menu, select a type of ruler.
  - In the **Interpreter** field, provide the name of the interpreter.

4. (Persistent rulers only) Click **OK**.
5. (Persistent rulers only) To edit a ruler, click and drag the anchor points on the ruler to rotate and click the ruler itself to translate. When editing the angle tool, the anchor that does not have the angle displayed next to it can be used to change the angle, while other anchors move the ruler.
6. (Optional) To delete a ruler, ensure the ruler is selected and then click the **Delete the selected findings** icon  in the **Findings** section of the toolbox.



**Warning:** 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.

## Related topics:

- [Quantification](#)  
Topics describing the use of XD features to perform quantification.

# Creating a ruler from a region

**Summary:** You can create a bi-ruler from a region.

## About

Bi-rulers can be created from a region, identifying the long and short axes in the orientation in which they were created.

## Procedure

To create a ruler from a region, complete the following steps:

1. In the **Findings** section of the toolbox, select the region from which you want to derive a ruler.
2. Right click the region and select **Create Ruler from Region**. A ruler is created.



**Warning:** 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.



**Warning:** 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.

## Related topics:

- [Creating and editing rulers](#)  
You can create permanent and temporary rulers and measure angles.
- [Performing RECIST](#)  
Perform RECIST evaluation of solid tumors.

# Annotating an image


**Summary:** Add annotations to an image that are included in the DICOM dataset.

## About

In XD, you can add annotations to images to draw attention to features or provide information.

## Procedure

To annotate an image, complete the following steps:

1. Right click the view and select the **Create an annotation** tool . You can also access the tool by clicking the **Quantify** menu and selecting **Annotation**, or through the drop down menu containing other ruler tools.
2. Click the image and drag to create a line, which indicates to what the annotation pertains. The text is positioned at the end where you release the mouse button.

**Note:** The annotation only exists in the slice and orientation in which it is drawn, it is not visible elsewhere.

3. In the **Text** field, enter or select the text of the annotation.
4. (Optional) Use the **Color** panel to select the color in which you want the annotation to be displayed.
5. Click **OK** to save the annotation, or click **Cancel** to redraw the annotation.

## Related topics:

- [Manipulating images](#)  
Adjust your view of an image.
- [Creating and editing rulers](#)  
You can create permanent and temporary rulers and measure angles.

# Linking findings together

**Summary:** You can link findings to indicate a relation between the two.

## Prerequisites

To complete this task, you must have first created at least two findings. You must have two regions on the same data role but in different datasets or time points, two rulers, or a ruler and a region.

For more information about creating findings, see the following topics:

- [Segmenting an image](#)
- [Drawing a region](#)
- [Creating and editing rulers](#)

## About

To calculate certain statistics, you need to link one or more findings together. When linked, two findings are treated as a single finding that can be separated later.


You can link findings in the following circumstances:

- You can always link two rulers
- You can always link a region and a ruler
- You can link a region to another region that is drawn on the same role but on a different dataset
- You can link a region to another region that is drawn on the same role but on a different time point

You cannot link a region to a region when they have a different role, or when they share both a time point and a dataset.

## Procedure

To link two findings together, complete the following steps:

1. In the **Findings** section of the toolbox, select the findings you want to link. Select multiple findings by holding the **Shift** or **Ctrl** keys. You can link two or more findings.
2. Click the **Link the selected findings** icon . The findings are linked and use the name of the last selected finding in the list.
3. (Optional) To remove the link between findings, and to separate the findings again, right-click the combined finding and select **Unlink**. The separated findings all use the name of the combined finding.

## Related topics:

- [Segmenting an image](#)  
XD can perform automatic segmentation within an area that you define.
- [Drawing a region](#)  
You can draw a region on an image using the freehand region tool, or as an ellipse or rectangle.
- [Creating and editing rulers](#)  
You can create permanent and temporary rulers and measure angles.

# Projecting findings

**Summary:** You can project and propagate findings between different images instead of creating each one separately.

## Prerequisites

To complete this task, you must have already created a finding and you must have multiple datasets or time points.

## About

Instead of segmenting each image individually, you can project a finding from one image to one or more others.

## Procedure

To project a finding, complete the following steps:

1. Findings can be projected across either time points or data roles, but not both simultaneously. For example, you can project from a functional data role to another time point's functional data role, but not to another time point's anatomical data role.

To choose the data role from which you want to project, click a view that shows that data role. Fused views use the base layer.

2. In the **Findings** section of the toolbox, select the finding or findings that you want to project.
3. Depending on the manner in which you would like to project your finding, use one of the following approaches, a list of available projection methods can be found later in this topic.
  - Two tools are available directly from the **Findings** section of the toolbox.
  - The remaining tools are available through the context menu. Access the context menu by right-clicking the finding that you want to project.

The region is reproduced in the other volumes that you specified and is linked to the original region.



**Warning:** 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.



## Projection methods

The methods execute one of the three following actions upon a variety of targets:

- **Project by type**  
Use the same method of creation, such as a seedpoint or threshold region, to generate the finding in the new volume.
- **Transform**  
Use the same registration between volumes to transform the entire finding.
- **Project by volume**  
Use a point to point registration between volumes to transform the location of the finding, but make no changes to size or shape except to account for different voxel sizes.

The following volumes can be targeted:

- **All**  
Target all roles and time points.
- **Within time point**  
Target all volumes within the same time point (bins of a gated dataset)
- **Current**  
Target the most recent time point.
- **Remaining**  
Target all roles and times points that do not yet contain the finding.
- **Remaining within time point**  
Target all volumes within the same time point that do not yet contain the finding.

The following table lists all available methods of projection:

The first three tools are available through the context menu.

Projection method	Action
<b>Project to All by Type</b>	Generate the finding in all time points in the same manner as it was originally created
<b>Transform to Current</b>	Transform the finding by applying the same transformation as is used for registration to the whole finding
<b>Project to All within Timepoint by Type</b>	Generate the finding, in the same manner as the original, in all volumes within the same time point

The following tools are available in the context menu only and not all are available by default. For information about making them available, see [Setting user preferences](#). To open the context menu, right click the finding.

<b>Project to All by Volume</b>	Generate the finding in all time points by using a transformation that preserves the finding's shape and volume while adjusting for changes in voxel size
<b>Transform to All</b>	Transform the finding to all images occupying the same role by using the same transformation as used for registration
<b>Project to Remaining by Type</b>	Generate the finding in the same manner as the original in all images that share the same role but do not yet have the finding
<b>Project to Remaining by Volume</b>	Generate the finding in all time points that do not yet contain the finding by using a transformation that preserves the finding's shape and volume while adjusting for changes in voxel size
<b>Transform to Remaining</b>	Transform the finding to all time points that do not yet contain the finding by applying the same transformation as is used for registration to the whole finding
<b>Project to Current by Type</b>	Generate the finding in the same manner as the original in the most recent volume
<b>Project to Current by Volume</b>	Generate the finding in the latest time point by using a transformation that preserves the finding's shape and volume while adjusting for changes in voxel size
<b>Project to All within Timepoint by Type</b>	Generate the finding, in the same manner as the original, in all volumes in the same time point (bins of a gated dataset)
<b>Transform to All within Timepoint</b>	Transform the finding to all volumes within the same time point (bins of a gated dataset) by using the same transformations as used for registration
<b>Project to Remaining within Timepoint by Type</b>	Generate the finding, in the same manner as the original, in all volumes (bins of a gated dataset) in the same time point that do not already contain the finding
<b>Transform to Remaining within Timepoint</b>	Transform the finding to all volumes within the same time point (bins of a gated dataset) that do not yet contain the finding, using the same transformations as used for registration



**Warning:** 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.

## Related topics:

- [Segmenting an image](#)  
XD can perform automatic segmentation within an area that you define.
- [Drawing a region](#)  
You can draw a region on an image using the freehand region tool, or as an ellipse or rectangle.
- [Creating and editing rulers](#)  
You can create permanent and temporary rulers and measure angles.
- [Creating a ruler from a region](#)  
You can create a bi-ruler from a region.

# Creating multiple threshold regions



**Summary:** You can create multiple regions within another region, where each new region is contoured based on a specific threshold level.

## About


Multiple threshold regions are generated inside the same bounds within which another region was generated. Several findings are created, each of which segments the volume using at several threshold levels, which can be configured in the Options window.

## Procedure

To create a set of multiple threshold regions, complete the following steps:

1. Create a new region. Click the **Ellipse Region** icon  in the toolbar, or use the keyboard shortcut **Ctrl+L** and then click and drag over the area of an orientation in which you want to create multiple threshold regions. The **Rectangle Region**  tool can also be used.

**Note:** You can also use an existing region, in which case skip to step 4.

2. Complete the following fields:
  - (Required) In the **Name** field, enter the name of the region, or select a standard region name from the drop down menu.
  - In the **Description** field, enter a description of the region.
  - Click the **Color** panel to select the color in which the region should be displayed.
  - Use the check boxes to specify whether the region is a lymph node and whether it should be quantified.
  - From the **Interpreted Type** drop down menu, select a type of region.
  - In the **Interpreter** field, provide the name of the interpreter.
3. Click **OK**.
4. In the **Findings** section of the toolbox, ensure that your region is selected.
5. Click the **Create regions at preset thresholds within the selected area** icon .

You have created multiple threshold regions within your initially created region. You can alter the thresholds of each new region individually by selecting the region and using the **Threshold Settings** section of the Toolbox.

You can change the thresholds, delete thresholds, or add new thresholds in the Options window. For more information, see [Setting user preferences](#).

## Related topics:

- [Segmenting an image](#)  
XD can perform automatic segmentation within an area that you define.
- [Quantification](#)  
Topics describing the use of XD features to perform quantification.

# Creating quantification volumes

**Summary:** Create a cylindrical or spherical region with a specific volume.

## About

PERCIST requires the creation of regions with a specific volume, for use comparing different parts of the image volume. XD provides the means to create these.

## Procedure

To create a region with a fixed shape and volume, complete the following steps:

1. Place the crosshairs at the location in the image volume where you want to create the region. The crosshair location is used as the center of the sphere or cylinder.
2. To place a region centered on the crosshairs, click the **Quantify** menu and then select one of the following tools:
  - To place a cylindrical region with a diameter of 1cm, bevelled ends, and a total volume of 2cm<sup>3</sup>, select **Drop 1cm Diameter Cylinder**.
  - To place a spherical region with a diameter of 3cm, select **Drop 3cm Diameter Sphere**.
  - To place a spherical region with a diameter of 1cm, select **Drop 1cm Diameter Sphere**.
  - To place a spherical region whose diameter can be adjusted by holding the **Shift** key and using the scroll wheel, select **Drop Volume Crosshair Sphere**.

**Note:** You can adjust the diameter of the sphere only before placing it.

## Related topics:

- [Performing PERCIST](#)  
Use XD to perform PERCIST evaluation on lesions.
- [Performing RECIST](#)  
Perform RECIST evaluation of solid tumors.

# Quantification

**Summary:** Topics describing the use of XD features to perform quantification.

## About

You can view and export statistics from the findings table. Additionally, in this section you will find topics describing how to perform PERCIST and RECIST evaluation.

Statistics supported by XD include metabolic tumor volume (MTV), total lesion glycolysis (TLG), RECIST, WHO and PERCIST. For a description of the available statistics, see [Statistics](#), [Calculation of statistics for gated data](#) and [Derived statistics](#).

## Topics in this section:

- [Using the findings table](#)  
Use the findings table to view statistics calculated for various regions and rulers.
- [Performing PERCIST](#)  
Use XD to perform PERCIST evaluation on lesions.
- [Performing RECIST](#)  
Perform RECIST evaluation of solid tumors.

# Using the findings table

**Summary:** Use the findings table to view statistics calculated for various regions and rulers.

## Prerequisites

To take full advantage of this task, you must have created at least one finding. For more information, see the [Findings](#) section.

## About

The findings table displays the statistics available for your findings. It consists of several tabs, each of which groups a particular type of statistics.

## Procedure

To use the findings table, complete the following steps:

1. Access the Findings table by clicking the **View** button at the top-right of the screen and selecting **Findings Table** or by clicking the **Window** menu and selecting **Findings Table**.

The different tabs collate different types of statistics.

- The **Intensity Distribution** tab displays the intensity distribution values for all the categories of the current intensity distribution definition.
- The **PERCIST** tab displays statistics relevant to PERCIST.
- The **RECIST** tab displays statistics relevant to RECIST.
- The **Regions Tracking** tab displays information pertaining only to regions and not to rulers.
- The **WHO** tab displays statistics specific to WHO and bi-rulers.
- The **Advanced** tab is customizable and displays the statistics that you choose through the Options window.

The different columns of the findings table provide the following information:

- The **Finding Name** column lists the name of the finding on which a statistic is based.
- The **Lymph** column details whether a finding is marked as a lymph node.
- The **Dataset** column lists the dataset from which a statistic is calculated.
- The **Quantification** column provides the value of the statistic
- The **Unit** column details the unit of the quantification column



- The remaining columns represent the value of a statistic in a given time point or, for a tracking column, the percentage difference of that time point to the value indicated by the top entry of the column.

**Note:** If you have drawn regions on multiple datasets, you can confirm which dataset a region was drawn on by hovering your cursor over the region in the **Findings** section of the toolbox. The dataset on which it was drawn is displayed at the top of the tooltip.

**Note:** If you calculate the same statistic for the same region on multiple datasets, it is possible that differing image resolutions will result in the calculation of different values.

1. Click the tab that you want to view.
2. In the **Settings** section of the toolbox, use the **Tracking Mode** drop down menu to select the type of tracking used, where **Baseline** compares the statistic to the baseline time point's value, **Waterfall** compares it to the previous time point's value, and **Min. to Date** compares the statistic to the previous minimum.
3. In the **Settings** section of the toolbox, use the **Dataset** drop down menu to select the dataset that you want to use to calculate statistics.
4. In the **Findings** section of the toolbox, use the check boxes for each finding to control which are displayed in the findings table.
5. (Optional) To take a visual snapshot of the findings table and save it as a secondary capture, click **Snapshot Table**.
6. (Optional) To copy the table to your system clipboard for later use in another application, click **Copy Table**.
7. (Optional) To copy or save a graph, right-click the graph and select **Copy**, to copy the graph to your system clipboard, select **Save as** to save the graph as an image in your file system, or select **Save to Image Gallery** to save the graph as a secondary capture.

## Related topics:

- [Setting user preferences](#)  
Use the Options window to manage user preferences.
- [Findings](#)  
Topics describing the creation and editing of regions and rulers.

# Performing PERCIST

**Summary:** Use XD to perform PERCIST evaluation on lesions.

## About


The XD application provides tools that can be used to perform PERCIST evaluation. While these tools are described elsewhere in the user guide, this topic describes the particular steps needed for PERCIST.

This topic uses the PERCIST protocol as described in *Practical PERCIST: A Simplified Guide to PET Response Criteria in Solid Tumors 1.0* by Joo Hyun O, Martin A. Lodge and Richard L. Wahl.

## Procedure

To calculate the PERCIST threshold using XD, complete the following steps:

1. To confirm and, if necessary, edit the properties used to calculate patient's SUV Lean Body Mass, complete the following steps:
  - a. In the lower left corner of a PET view, click the active text showing the units of the view. Alternatively, click the **Image** menu and select **Quantification Options**.
  - b. In the Quantification Options window, click **Quantification Options**.
  - c. Check the **Height** and **Sex** fields are correct and, if necessary, correct them.
  - d. Click **OK** to save changes or **Cancel** to discard changes.
  - e. Select **PET SUV from Lean Body Mass**.
  - f. Click **OK**.
2. Place a reference region in your PET volume by performing one of the following sets of steps:
  - If the patient's liver is healthy, complete the following steps:
    - i. Use the pan and zoom tools to focus on the liver. For more information on the use of these tools, see [Manipulating images](#).
    - ii. Place the crosshairs where you want to center your reference region. Ensure that the crosshairs are correctly positioned in all orientations.
    - iii. Click the **Quantify** menu and select **Drop 3cm Diameter Sphere**.
    - iv. If necessary, click the region and drag it to adjust its position.
  - If the patient's liver is not healthy, and there is a clear area in the descending thoracic aorta where a cylinder can be placed, complete the following steps:
    - i. Use the pan and zoom tools to focus on the descending thoracic aorta. For more information on the use of these tools, see [Manipulating images](#).



- ii. Place the crosshairs where you want to center your reference region. Ensure that the crosshairs are correctly positioned in all orientations.
  - iii. Select the coronal view.
  - iv. Click the **Quantify** menu and select **Drop 1cm Diameter Cylinder**.
  - v. If necessary, click the region and drag it to adjust its position.
- If the patient's liver is not healthy, and there is no clear area in the descending thoracic aorta where a cylinder can be placed, complete the following steps:
    - i. Use the pan and zoom tools to focus on the descending thoracic aorta. For more information on the use of these tools, see [Manipulating images](#).
    - ii. Click the **Paint** tool  in the toolbar at the top of the window.
 

If the Freehand or Erase tools were used more recently than the paint tool, use the drop down menu to select the Paint tool. Alternatively, click the **Quantify** menu and select **Paint**.
    - iii. In the **Region Editing Tools** section of the Toolbox, use the **Depth** slider to specify the minimum possible depth.
    - iv. In the coronal view, click in the descending thoracic aorta to place the first disc of the region. The region is drawn only on the current slice.


**Tip:** You can hold the **Ctrl** key and use the scroll wheel to adjust the diameter of the brush.

- v. Move to the next slice and click again to place another disc. The discs are joined to form a contiguous region. Repeat this step to build up a cylinder or near-cylinder.
 

To check that a region is the correct size, use the ruler tools. For more information, see [Creating and editing rulers](#).
- vi. In the **Findings** section of the toolbox, double click your newly created region.
- vii. In the **Finding Name** window, from the **Name** drop down list, select **Reference**.

3. Identify the hottest lesion on the PET volume and then segment it, using the threshold calculated in Step 2 and the **Region with Absolute Threshold** tool . For more information about the tool, see [Segmenting an image](#).
4. In the **Findings** section of the toolbox, select your reference region and your areas of concern.
5. To track the identified lesion across time points, in the **Findings** section of the toolbox, right-click any of the regions and select **Project to All by Type**, and then, in the toolbox, click the **Projects the selected findings to all time points** icon .

**Note:** If Project to All by Type is not available in the context menu, you can enable it through the Findings tab of the Options window. For more information, see [Setting user preferences](#)

6. Click the **Show findings table** icon  to open the findings table. Alternatively, click the **Window** menu and select **Findings Table**.
7. Click the **PERCIST** tab. The table displays the percentage of change in tumor metabolism between the baseline and subsequent image volumes.
8. (Optional) To customize your findings table, click **Options** in the toolbox. You can specify which statistics are included and for which statistics graphs are created. For more information, see [Using the findings table](#).
9. Export your findings table in one of the following manners:
  - To export your findings table as an image, click **Snapshot Table**. The table is saved to your image gallery and can be exported in the same manner as a normal image. For more information, see [Exporting secondary captures](#).
  - To copy your findings table in another application, click **Copy Table**. Your table is available on your system's clipboard.

## Related topics:

- [Manipulating images](#)  
Adjust your view of an image.
- [Findings](#)  
Topics describing the creation and editing of regions and rulers.
- [Using the findings table](#)  
Use the findings table to view statistics calculated for various regions and rulers.

# Performing RECIST







**Summary:** Perform RECIST evaluation of solid tumors.

## About


XD provides functions that are useful for performing RECIST evaluation, and the findings table in particular will quantify tumour growth or shrinkage when findings are labelled appropriately.

## Procedure

To use the XD application to perform RECIST evaluation, complete the following steps:

1. On your Anatomical volume in your Baseline time point, create contours around the tumours either by automatic segmentation or by drawing the regions.
  - To create a contour by automatic segmentation, complete the following steps for each tumour or refer to the [Segmenting an image](#) topic:
    - i. In the toolbar, click the **Region with absolute threshold** , **Region with % of max**  or **CT Region Segmentation**  tool. These tools may be hidden under other segmentation tools, in which case select them from the drop down menu. Alternatively, you can access them through the **Quantify** menu.
    - ii. Navigate to the tumour in the orientation in which it is most easily visible. For more information, see [Manipulating images](#).
    - iii. Click the image and drag to define the volume in which the segmentation will be carried out. If the threshold levels are not correct, you can change them as described in the [Setting user preferences](#) topic.
    - iv. In the **Name** field, provide a name for your region.
    - v. If the region is a lymph node, click **Lymph Node**.
    - vi. (Optional) Fill out any additional fields that are part of your process.
    - vii. Click **OK**.
  - To create a contour by using the Draw or Paint tools, complete the following steps for each tumour or see [Drawing a region](#).
    - i. In the toolbar, click the **Freehand Region**  or **Paint**  tool. These tools may be hidden under one another or the Erase tool , in which case select them from the drop down menu. Alternatively, you can access them through the **Quantify** menu.

- ii. Navigate to the tumour in the orientation in which it is most easily visible. For more information, see [Manipulating images](#).
- iii. If using the **Paint** tool, click and drag on the image where you want to create region in a sphere around your cursor. Click a different viewport or select a different tool to complete the region.
- iv. If using the **Freehand Region** tool, click and drag on the image and draw the outline of the region in a single slice. Release the mouse button to complete the region.
- v. In the **Findings** section of the toolbox, double click your region to open the Finding Name window.
- vi. In the **Name** field, provide a name for your region.
- vii. If the region is a lymph node, click **Lymph Node**.
- viii. (Optional) Fill out any additional fields that are part of your process.
- ix. Click **OK**.

2. In the **Findings** section of the toolbox, select your regions. Hold **Ctrl** to select multiple findings at once.
3. Click the **Projects the selected findings to all time points** icon  or right click the findings and select **Project to all by type**. The findings are generated in all time points by using the same methods as you originally used.
4. Click **Baseline** in the upper-right corner of the window and select **Current** or **Prior X** depending on which time point you want to correct the findings of.
5. For each region, select the region and use the **Paint** and **Erase** tools to correct them. For more information, see [Editing a region](#).
6. For each region, right click the region in the **Findings** section of the toolbox and select **Create ruler from region** to create a bi-ruler in the currently selected orientation in all time opints.
7. Use the **Layout** button in the upper right corner of the window and select **Findings Table** or click the **Window** menu and select **Findings Table**.
8. Click the **RECIST** tab. The details of your regions, including the the Long Axis and Short Axis measurements of the region, are displayed. The BiRuler Auto statistic presents the Short Axis for a region marked as a lymph node and the Long Axis for a region not marked as a lymph node.

To save time when you have additional time points to consider, use the projection tools. For more information, see [Projecting findings](#).

## Related topics:

- [Findings](#)  
Topics describing the creation and editing of regions and rulers.
- [Using the findings table](#)  
Use the findings table to view statistics calculated for various regions and rulers.

# Customizing XD

**Summary:** Topics describing the customization of XD.

## About

XD is highly customizable. You can create custom layouts, assign hotkeys to specific functions, and alter a range of user preferences.

## Topics in this section:

- [Setting user preferences](#)  
Use the Options window to manage user preferences.
- [Creating custom layouts](#)  
You can create custom layouts for viewing a study.
- [Assigning hotkeys](#)  
You can customize key bindings for XD functions.



# Setting user preferences

**Summary:** Use the Options window to manage user preferences.

## About

XD provides a wide range of customization, much of it accessed through the Options window. These settings are managed on a per-user basis, unless otherwise stated.

To open the Options window, click the **Tools** menu and select **Options**.

Click **Apply** to apply changes and keep the Options window open, **OK** to apply changes and close the Options window, or **Cancel** to discard changes and close the Options window.

## User Preferences

The following user preferences are available through the Options window:

Preference	Tab	Description
Other Settings	Data QC	Specify whether the Data QC screen is hidden, prompted for, or displayed when launching the application.
SCP Configuration	DICOM	Add, edit and remove DICOM SCP details.
SCU Configuration	DICOM	Set the SCU AE title used for exporting data. (Requires administrative permissions)
Region Display	Findings	Specify how regions are displayed, including shading, outlines, transparency, and whether a findings table is displayed when hovering the cursor over the finding.
Region type	Findings	Specify whether 3D regions are ellipsoid or cuboid.
Default PET absolute threshold and Default percentage threshold	Findings	The default thresholds for when threshold regions are created.
Center views on new region and Draw bounding boxes from center	Findings	Specify whether views center on new regions and whether bounding boxes are drawn from a vertex or from the center.

Preference	Tab	Description
Prompt for name of new finding	Findings	Specify whether when creating new findings, the Finding Name window is displayed. Click <b>Suggestions</b> to configure the names that are available from a drop-down menu.
Multi-threshold region boundary values	Findings	Specify the threshold values of the boundaries between different regions that are generated with the <b>Create Multiple Threshold Regions</b> tool.
User Interface Settings	Findings	Specify which options are available in the context menu when right-clicking a finding and in the Findings section of the toolbox.
Viewer Options	Quantification	For the selected modality, specify which quantified values are displayed in the annotation of a finding.
Units	Quantification	Specify the units used for length and volume measurements.
Findings Table	Quantification	Specify the tabs and default tab of the Findings Table. Additionally, specify how timepoints are displayed in the table.
Review Mode Settings	Review Modes	Manage the availability of layouts in each review mode, which layouts are favorites and displayed at the top of the Toolbox, and default registration schemes that are run when the application is launched. You can also set window and colormap defaults.
Save and Export	Session	Specify whether prompts to save are provided when exiting the application or if the session is saved automatically.

Preference	Tab	Description
Restore Session	Session	Specify the behavior of the application when saved sessions are selected when launching the application.
Compatibility Options	Session	Specify whether saved sessions are exported as a single secondary capture DICOM object or as multiple objects.
User Interface Settings	User Interface	Specify whether or not, when multiple application windows are open, closing one window will close all windows. Additionally, select which tools and options are available in the toolbar at the top of the application window or in the context menu, accessed by right-clicking. For more information about configuring hotkeys, see <a href="#">Assigning hotkeys</a> .
Startup Options	User Interface	Set a range of default settings for when the application starts.
View Settings	Views	Specify a range of settings for how views appear. High contrast borders affect the currently selected view. Colored planes indicate image planes by color. Progress information indicates how complete a registration is while running.
Information Overlays	Views	Set font sizes and specify which optional information is displayed in a view. The font size of interactive text is applied to all text in the corners of views, though the color applies to only active text.
Slice numbering	Views	Specify the direction of slice numbering.

Preference	Tab	Description
Information Overlays	Views	Specify what information is displayed in a view or in a screen capture of that view type. The Default, Default Snapshot and Patient Only settings provide information on Patient Name, Sex, Age, Date of Birth, Institution Name, and Accession Number. The Default and Default Snapshot settings provide information on Scale Label, Window/Level Controls, Dataset Name, Quantification, View Code, View Type, Series Date, and Series Description. The Default, Default Snapshot and Slice Number only settings provide the Slice Number.
Window Level	Window Level	For the selected image modality, configure the default settings used when the application launches, including whether window/level settings defined in the data are used or not. Additionally, set hotkeys for defined window/level settings.
General Options	Window Level	Specify between which images window/level settings are linked when the application launches.

# Creating custom layouts

**Summary:** You can create custom layouts for viewing a study.


## About


In addition to the supplied layouts in XD, you can create layouts specifically tailored to your needs.

## Procedure

To create a custom layout, complete the following steps:

1. Click the **Tools** menu and select **Layout Editor**.
2. In the New Layout window, provide initial details about your layout:

**Note:** If you have begun editing a new layout and have not yet saved it, the New Layout window does not open and instead the layout editor is opened on the in-progress layout. You can create a new layout by clicking the **Create a new layout** icon .

- a. In the **Layout name** field, provide a name for your new layout.
  - b. From the **Applicable for** drop-down menu, select the review mode with which the layout can be used.
  - c. In the **Number of timepoints** field, specify the minimum number of timepoints that are required before the layout can be used.
  - d. Click **OK**.
3. To choose the number of viewports in your layout, click the **Select the grid dimensions for the layout** icon  and adjust the size of the grid that you want to arrange your viewports on.
  4. (Optional) To merge one or more viewports, click the viewports and then right click either viewport and select **Merge cells**. Deselect viewports by clicking them again.

**Note:** You can merge groups of cells only when they form a square or rectangle.

5. (Optional) To split previously merged viewports, right click the merged viewport and select **Split cells**.
6. Assign view types to your viewports by completing the following steps:
  - a. In the **View Types** section of the toolbox, from the **Select Type** drop down menu, select the type of view you want to assign.
  - b. Click the view type in the toolbox and drag it across to the viewport in which you want to display it.
  - c. (Optional) To overlay different datasets, drag additional view types across to an occupied viewport.

**Note:** You cannot overlay different types, orientations, or any 2D Slice and Planar Views.




**Warning:** 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.



**Warning:** 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.



**Warning:** 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.

- a. (Optional) To remove all assigned view types from a viewport, right click the viewport and select **Remove assignment**.
7. To customize default display options for a viewport, complete the following steps:
  - a. (Optional) To set a time point that should be used for the viewport, right click the viewport, select **Set timepoint**, and then select the time point that you want to use.
  - b. (Optional) To assign an offset to which dataset should be displayed, right click the viewport, select **Dataset Offset**, and then select the offset that you want to use. If you want to set an offset greater than 10, use the **Custom** option.
  - c. (Optional) To set a slice offset to the viewport, select **Slice Offset**, and then select the offset that you want to use. If you want to set an offset greater than 10, use the **Custom** option.
  - d. (Optional) To specify the default window and level settings, right click the viewport, select **Window/Level**, and then select one of the predefined settings.
8. Click the **Save the layout** icon . You must have filled all your viewports before you can save.
9. Click **This user** to save the layout for only the current system user, or click **All users** to save the layout for all users of the system. Depending on your user permissions, you might not be able to save for all users.

## Related topics:

- [Choosing a layout](#)  
Select the layout of images with which you want to view your data.
- [Manipulating images](#)  
Adjust your view of an image.

# Assigning hotkeys

**Summary:** You can customize key bindings for XD functions.

## About

Hotkeys in XD are highly configurable, many of the available functions can be assigned to new hotkeys, and existing hotkeys can be changed to suit your preferences.

## Procedure

To assign a function to a hotkey, or to edit an existing hotkey, complete the following steps:

1. Click the **Tools** menu and then select **Options**.
2. In the Options window, click the **User Interface** tab and then click **Hotkey configuration...**
3. Double-click the entry in the **Hotkey** column for the function that you want to assign a hotkey to or edit the hotkey of.
4. Press the hotkey, or the key combination, that you want to assign to the function.
5. (Optional) To remove a hotkey, select the entry and click **Clear**.
6. (Optional) To revert a hotkey to its default setting, select the entry and click **Default**.
7. (Optional) To revert a hotkey to its previous setting when you opened the window, click **Revert**.
8. Click **OK**.

# Saving, loading, and exporting data

**Summary:** Topics describing the saving, importing, and exporting of data from XD.

## About

You can export DICOM, image, or table data for use in other applications. Additionally, you can save and load sessions.

## Topics in this section:

- [Saving a session](#)  
You can save your current session and return to it later.
- [Loading a session](#)  
You can resume a previous XD session.
- [Exporting data](#)  
Export data for use outside of your session.
- [Exporting a maximum intensity projection \(MIP\)](#)  
You can export a maximum intensity projection.
- [Creating a DICOM viewer](#)  
You can create a folder containing everything needed to view your currently loaded images.
- [Exporting an RTSS](#)  
You can export a radiotherapy structure set (RTSS).
- [Exporting secondary captures](#)  
Export secondary captures as different image types or a DICOM object.



# Saving a session

**Summary:** You can save your current session and return to it later.

## About

When you save a session, the results of your actions are retained so that, when you resume your session, you can continue where you left off. This includes changes such as review mode, segmentation, registration, and quantification.

## Procedure

To save your current working session, complete the following steps:

1. Click the **File** menu and select **Save session...** The Save session window opens.
2. In the **Series information** section, from the drop-down menu select the image set that you want to associate the saved session with. When you launch XD using that image set as part of your selection, the saved session will be available.
3. In the **Series description** field, provide a description for your saved session.
4. From the **Destination** drop-down menu, select the destination of the saved session.
  - Selecting **File** will save the session as a file in your filesystem.
    - i. In the **Directory** field, provide the directory in which to save the file. You can also click ... to browse for your directory.
    - ii. In the **Filename** field, provide a file name for your session.
    - iii. From the **File format** drop-down menu, select the type of file you would like to save your session as.

## Related topics:

- [Loading a session](#)  
You can resume a previous XD session.

# Loading a session

**Summary:** You can resume a previous XD session.

## About

As part of the process of launching XD, you can load a saved session.

## Procedure

To load a saved session, complete the following steps:

1. In ISP, locate and select your saved session and the datasets with which it is associated. You can also load additional data, such as follow-up scans.
2. Launch XD. The Select session window opens.
3. Select your saved session and then click **OK**.
4. Perform data configuration as you would when launching XD normally. For more information, see [Launching XD review modes](#).

**Note:** Registrations loaded as part of a saved session will override any default registrations. You should ensure that these loaded registrations are correct.

## Related topics:

- [Saving a session](#)  
You can save your current session and return to it later.

# Exporting data

**Summary:** Export data for use outside of your session.

## About

You can export parts of your session to various destinations for later use or for record.

## Procedure

To export data from XD, complete the following steps:

1. (Optional) If you are intending to export a range of slices, click a view of the orientation that you want to export the slices of.
2. Click the **File** menu and select **Export**.
3. Depending on what you would like to export, complete one of the following sets of steps:
  - If you want to export a whole data series, complete the following steps:
    - i. Select **Original Data** and then click **OK**.
    - ii. From the **Data to export** drop down menu, select the specific data series that you want to export.
  - If you want to export volumes that have been resampled so that they are registered, and their slice thicknesses, resolutions, and geometries are equivalent, complete the following steps:
    - i. Select **Resampled Volumes** and then click **OK**.
    - ii. From the **Associate with** drop down menu, select the dataset to export.
    - iii. From the **Volume to export** drop down menu, select the volume that you want to resample and export.
    - iv. From the **Resample to match** drop down menu, select the volume that you would like to use the resolution, slice thickness and geometry of.
    - v. (Optional) In the **Series description** field, provide a description of your resampled volume.
    - vi. (Optional) In the **Performing physician** field, provide a name for the performing physician.
    - vii. (Optional) In the **Operator name** field, provide a name for the operator.
  - If you want to export the transformation of a registration as a DICOM registration object, complete the following steps:

- i. Select **Registration** and then click **OK**.
  - ii. From the **Associate with** drop down menu, select the data series that you want to associate the registration with.
  - iii. From the **Registration** drop down menu, select the particular registration that you want to export.
  - iv. (Optional) In the **Description** field, provide a description of the registration.
  - v. (Optional) In the **Creator Name** field, provide a name for the creator of the registration.
- If you want to export a subset of a volume's slices as a new volume, complete the following steps:
    - i. Select **Slice Range** and then click **OK**.
    - ii. Use the sliders on the image or the **Start** and **End** fields to specify a range of slices to use.
    - iii. Use the **Interval** field to specify the interval between slices in the original image for slices in the exported data. An interval of 0 will skip no slices and export every slice, while an interval of 1 will skip one slice between exported slices, and so on.
    - iv. Use the **Include patient information** check box to specify whether the exported slices should contain patient information.
    - v. Use the **Width** and **Height** fields to specify the size of the image to be exported.
    - vi. Click **Continue**.
    - vii. From the **Associate with** drop down menu, select the data series that you want to associate the registration with.
    - viii. (Optional) In the **Series description** field, provide a description of your resampled volume.
    - ix. (Optional) In the **Performing physician** field, provide a name for the performing physician.
    - x. (Optional) In the **Operator name** field, provide a name for the operator.
    - xi. (Optional) In the **Modality** field, enter the modality of the slices.
4. From the **Destination** drop down menu, select to where you want to export. Depending on the location you select you might have other fields to complete.

**Note:** You can export to File, to the launching application, or to any SCP configured through the Options window.

5. Click **OK**.

### **Related topics:**

- [Exporting a maximum intensity projection \(MIP\)](#)  
You can export a maximum intensity projection.
- [Exporting an RTSS](#)  
You can export a radiotherapy structure set (RTSS).

# Exporting a maximum intensity projection (MIP)

**Summary:** You can export a maximum intensity projection.

## About


Maximum intensity projections are exported as a set of two-dimensional images from different angles and can be exported in a number of file formats.



**Warning:** 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.

## Procedure

To export a maximum intensity projection, complete the following steps:

1. Select a viewport that you want to take an MIP from and then click the **Display the series in the selected view as a MIP in a floating window** icon . For more information on viewing and manipulating your MIP, see [Viewing a maximum intensity projection \(MIP\)](#).
2. Click the **File** menu and then select **Export...**
3. In the Export window, select **MIP Images** and then click **OK**.
4. Use the **Start** and **End** fields to specify a range of angle markers to create images for.
5. (Optional) Deselect **Include patient information** if you do not want the export to include patient information.
6. Use the **Width** and **Height** fields to specify the size of the image you produce, in pixels.
7. Click **Continue...**
8. (Optional) In the **Series information** section of the Export window, provide information about the image series. This information is only relevant when exporting in DICOM format.
  - From the **Associate with** drop-down menu, select an image with which to associate the exported MIP.
  - (Optional) Provide a description of the series in the **Series description** field.
  - (Optional) Provide the name of the performing physician in the **Performing physician** field.

- (Optional) Provide the name of the operator in the **Operator name** field.
  - If necessary, correct the modality listed in the **Modality** field.
9. In the **Send To** section of the Export window, specify details of the file and its location.
- a. From the **Destination** drop-down menu, select the manner in which you want to export the MIP. If you selected **File**, complete the following steps:
    - i. In the **Directory** field, specify the location in which the exported MIP should be saved. You can also browse for the location by clicking ...
    - ii. In the **Filename** field, provide a name for your file, this will have **\_X** appended to it, where *X* is the number of the angle marker.
    - iii. From the **File format** drop-down menu, select the format in which you would like to save your exported MIP.
10. Click **OK**.

## Related topics:

- [Viewing a maximum intensity projection \(MIP\)](#)  
You can view a maximum intensity projection of your dataset.

# Creating a DICOM viewer

**Summary:** You can create a folder containing everything needed to view your currently loaded images.

## Prerequisites

If you want to burn a viewer to CD, your system must be capable of writing to CDs.

## About

If you want to enable someone to view images and findings without installing the entire XD application, you can create and provide them with a DICOM viewer.

A DICOM viewer contains the data you are using in your current session, as well as a reduced form of the XD application with which to view the data.

## Procedure

To create and use a DICOM viewer, complete the following steps:

1. Click the **File** menu and select **Create Viewer**.
2. From the **Destination** drop down menu, select **Filesystem** to save the viewer as a folder in your file system, or select **Burn to CD** to burn the viewer to a CD.
3. (Filesystem only) In the **Folder name** field, enter the name of a new folder in which to save the viewer and use the **Location** field to specify where that folder should be saved. You can click the ... button to browse for a location.
4. Use the **Include regions, measurements and bookmarks** check box to specify whether you want to include findings and bookmarks in the viewer, as well as the DICOM data you loaded into the application originally.
5. Click **OK**.
6. To launch the viewer application, open the folder or disc drive and launch the **XDViewer** application. The viewer behaves in the same manner as the main XD application, but with limited functionality.

## Related topics:

- [Manipulating images](#)  
Adjust your view of an image.
- [Findings](#)  
Topics describing the creation and editing of regions and rulers.



# Exporting an RTSS

**Summary:** You can export a radiotherapy structure set (RTSS).

## Prerequisites

To complete this task, you must have created at least one region.

## About

Having created regions on an image, you can export a radiotherapy structure set for use outside of XD in a treatment planning system (TPS).



**Warning:** XD 3.6.11 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 XD 3.6.11. 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.



**Warning:** Different interpolation methods may be used by XD 3.6.11 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 XD 3.6.11.

## Procedure

To export an RTSS, complete the following steps:

1. Click **File** and select **Export**
2. Select **RTSS** and then click **OK**.
3. From the **Associate with** drop down menu, select the data series with which you would like to associate your exported RTSS.
4. From the **Export structures for** drop down menu, select the datasets from which you want to export regions.
5. From the **Regions to export** list, select the regions that you would like to export.
6. (Optional) In the **Label** field, enter the label of the RTSS.

7. (Optional) In the **Name** field, provide a name for the RTSS.
8. (Optional) In the **Description** field, enter a description of the RTSS.
9. (Optional) In the **Operator name** field, provide a name for the operator.
10. Use the **Export original dataset** check box to specify whether the original or modified dataset should be exported.
11. From the **Destination** drop down menu, select the location to which you would like to export. Depending on the destination you select, there might be additional fields to complete.
12. Click **OK**.

### **Related topics:**

- [Findings](#)  
Topics describing the creation and editing of regions and rulers.
- [Quantification](#)  
Topics describing the use of XD features to perform quantification.
- [Exporting data](#)  
Export data for use outside of your session.

# Exporting secondary captures

**Summary:** Export secondary captures as different image types or a DICOM object.

## Prerequisites

To complete this task, you must first have created at least one secondary capture. For more information, see [Capturing an image](#).

## Procedure

To export one or more secondary captures, complete the following steps:

1. In the **Image Gallery** section of toolbox, select the secondary captures that you want to export.

**Note:** You should ensure that the slice number is displayed in your secondary captures as there will be no other way of identifying the location of the image upon export.

1. Click **Export**.
2. From the **Associate with** drop down menu, select the dataset with which you want to associate the exported images.
3. (Optional) In the **Series description** field, provide a description of your image series.
4. (Optional) In the **Performing physician** field, provide the name of the performing physician.
5. (Optional) In the **Operator name** field, provide the name of the operator.
6. (Optional) In the **Modality** field, enter the image modality.
7. (If exporting multiple images) Use the **Export as single series** check box to specify whether the images are exported as one series or as multiple series.
8. From the **Destination** drop down menu, select the manner in which you would like to export your secondary captures. Depending on your choice, you might need to perform further configuration.
9. Click **OK**.

## Related topics:

- [Capturing an image](#)  
You can capture views for later reference or for use outside of XD.
- [Using the findings table](#)  
Use the findings table to view statistics calculated for various regions and rulers.

# Equations and algorithms

**Summary:** In this section you can find information about the equations and algorithms used to calculate various statistics in the XD application.

It is important to understand the means by which a statistic was calculated. The topics in this section provide details of the functioning of the algorithms and equations used by XD.

## Topics in this section:

- [Statistics](#)  
Standard statistics that can be included in the findings table.
- [Calculation of statistics for gated data](#)  
The method by which multiple statistics are calculated when multiple gates are available.
- [Derived statistics](#)  
The manners in which derived statistics are calculated.
- [SUV Peak](#)  
The SUV Peak calculation is a method to provide a robust measure of tracer activity in PET imaging.
- [Volume doubling time](#)  
The equation used to calculate the volume doubling time.
- [PET SUV calculation by body weight](#)  
The equation used to calculate PET SUV by body weight.
- [PET SUV calculation by body surface area](#)  
The equations used to calculate PET SUV by body surface area.
- [PET SUV calculation by lean body mass](#)  
The equations used to calculate PET SUV by lean body mass, for male and female patients.
- [PET SUV from acquisition](#)  
Scanner manufactures can calculate and store a PET SUV value.

# Statistics

**Summary:** Standard statistics that can be included in the findings table.

The statistics in this table are available across the **Intensity Distribution**, **PERCIST**, **RECIST**, **Regions Tracking**, **WHO**, and **Advanced** tabs. Their display for a given tab can be turned on or off by clicking **Options** in the **Settings** section of the toolbox, when viewing the Findings Table.

**Note:** All statistics can be displayed by the **Advanced** tab. Only relevant statistics are available in the other tabs

Further aggregated and derived statistics are also available in [Calculation of statistics for gated data](#) and [Derived statistics](#).

Statistic	Definition
Max	The maximum voxel intensity of all the voxels included in the region.
Min	The minimum voxel intensity of all the voxels included in the region.
Mean	The mean voxel intensity of all the voxels included in the region.
Median	The median voxel intensity of all the voxels included in the region.
StdDev	The standard deviation of the voxel intensity of all the voxels included in the region.
Threshold	The lower threshold value of an isocontour region. It is not generated for other finding types.
Upper Threshold	The upper threshold value of an isocontour region. It is not generated for other finding types.
Volume	The volume, in cm <sup>3</sup> , of the region.
MTV (Displayed as Volume)	Metabolic Tumor Volume. The product of the number of voxels in the region and the volume of each voxel.
Volume Doubling Time	The time, in days, that it would take the region to double in volume. For more information, see <a href="#">Volume doubling time</a> .
Peak	The PERCIST peak of the finding. For details of its calculation, see <a href="#">SUV Peak</a> .
BiRuler Long Axis	The long axis measurement of a 2D bi-ruler.
BiRuler Short Axis	The short axis measurement of a 2D bi-ruler.

Statistic	Definition
BiRulerAuto	If the finding has been marked as a lymph node, this is the short axis measurement of a 2D bi-ruler. Otherwise, this is the long axis measurement of a 2D bi-ruler.
UniRuler Length	The length of a 1D ruler.
Angle	The angle, in degrees, measured by an angle ruler.
BiRuler Product	The product of the long and short axes of a BiRuler.
Max Ratio to Reference Mean	The ratio of the maximum voxel intensity in a region to the mean voxel intensity of that region in the reference volume.
Mean Ratio to Reference Mean	The ratio of the mean voxel intensity in a region to the mean voxel intensity of that region in the reference volume.
Mean Range	The product of the maximum and minimum mean voxel intensity of the region when there are multiple volumes within a single time point.
Mean Ratio	The ratio of the maximum and minimum mean voxel intensity of the region when there are multiple volumes within a single time point.
TLG (Total Lesion Glycolysis)	For a PET region, this is calculated as the product of the MTV and the Mean activity across the region, using the SUV that is calculated as specified through the Quantification Options window.

**Note:** When datasets have been transformed for display, quantification calculations are performed on the original image space, not the resampled and transformed space.



**Warning:** 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.

# Calculation of statistics for gated data

**Summary:** The method by which multiple statistics are calculated when multiple gates are available.

## About

When a time point contains gated data, more than one value for a statistic might be created, depending on the statistic. When this is the case, an aggregate statistic is calculated, for each time point, from the statistics calculated from each gate.

## Aggregation methods

The following table details the methods used to aggregate statistics:

Statistic	Aggregation method
Max	The maximum value of any considered gate is used
Min	The minimum value of any considered gate is used
Mean	The mean value of the means calculated for each gate is used. This is equivalent to the overall mean of all the gates
Median	The mean value of the medians calculated for each gate is used.
StdDev	The mean value of the standard deviations calculated for each gate is used.
Threshold	The threshold is only presented when the threshold is equivalent across all considered gates.
Upper Threshold	The upper threshold is only presented when the upper threshold is equivalent across all considered gate.y
Volume	The mean of the volumes calculated for the region in each considered gate is used.
Volume Doubling Time	No value generated as aggregation takes place within a time point.
Peak	The maximum of the peaks of all the considered gates is used
BiRuler Long Axis	The maximum of the long axes of the bi-ruler in all of the considered gates is used.
BiRuler Short Axis	The maximum of the short axes of the bi-ruler in all of the considered gates is used.



Statistic	Aggregation method
BiRuler Auto	The maximum of the axis of the automatic bi-ruler in all of the considered gates is used.
UniRuler Length	The maximum of the length of the uni-ruler in all of the considered gates is used.
Angle	The mean of the angle measured in all of the considered gates is used.

# Derived statistics

**Summary:** The manners in which derived statistics are calculated.

## About

When a time point contains gated data, more than one value for a statistic might be created, depending on the statistic. Additionally, a derived statistic is calculated using one or more existing statistics. When a derived statistic is calculated for a gated time point, different methods are used to calculate the derived statistic.

## Aggregation methods

In the table later in this topic that describes the derivation of statistics from aggregated statistics, the following notation is used to describe aggregation methods:

Statistic representation	Aggregation method
$\text{mean}(\textit{Statistic})$	The mean of the statistic from each gate that is considered.
$\text{max}(\textit{Statistic})$	The maximum value of all the values of the statistic from each gate that is considered.
$\text{min}(\textit{Statistic})$	The minimum value of all the values of the statistic from each gate that is considered.
$\text{isSame}(\textit{Statistic})$	A value is only returned for the statistic when its value is equivalent in all gates. This extends to the whole of a derived statistic.

where, in all representations of an aggregation method, *Statistic* refers to a particular statistic of the same name.

More information on aggregation methods for different statistics can be found in [Calculation of statistics for gated data](#).

## Derivation methods

The following table details the methods used to derive statistics from aggregated statistics:

Statistic	Derivation method
BiRuler Product	$\text{max}(\textit{BiRuler Long Axis}) \times \text{max}(\textit{BiRuler Short Axis})$
Max Ratio to Reference Mean	$\frac{\text{max}(\textit{Max})}{\text{mean}(\textit{Reference Mean})}$

Statistic	Derivation method
Mean Ratio to Reference Mean	$\frac{\text{mean}(\text{Mean})}{\text{mean}(\text{Reference Mean})}$
Mean Range	$\text{max}(\text{Mean}) \times \text{min}(\text{Mean})$
Mean Ratio	$\frac{\text{max}(\text{Mean})}{\text{min}(\text{Mean})}$
PERCIST Threshold Blood Pool	<p>The threshold to use for PERCIST regions, relative to a defined reference bloodpool volume, using the SUV calculation specified through the Quantification Options window.</p> $2\text{mean}(\text{Reference Mean}) + 2\text{mean}(\text{Reference StdDev})$
PERCIST Threshold Liver	<p>The threshold to use for PERCIST regions, relative to a defined reference liver volume, using the SUV calculation specified through the Quantification Options window.</p> $1.5\text{mean}(\text{Reference Mean}) + 2\text{mean}(\text{Reference StdDev})$
Theshold % of Max	$100 \left( \frac{\text{isSame}(\text{Threshold})}{\text{max}(\text{Max})} \right)$

## Related topics:

- [Statistics](#)  
 Standard statistics that can be included in the findings table.
- [Calculation of statistics for gated data](#)  
 The method by which multiple statistics are calculated when multiple gates are available.

# SUV Peak

**Summary:** The SUV Peak calculation is a method to provide a robust measure of tracer activity in PET imaging.

## Occurrences

The algorithm described in this topic is used by the following functions of XD:

- [Performing automatic registration](#)
- [Using the findings table](#)

## Introduction

The algorithm calculates the maximum average SUV within a small ROI of a fixed size. The implementation used by XD 3.6.11 follows the definition provided in the PERCIST protocol.

## The algorithm

XD 3.6.11 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, thereby 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.

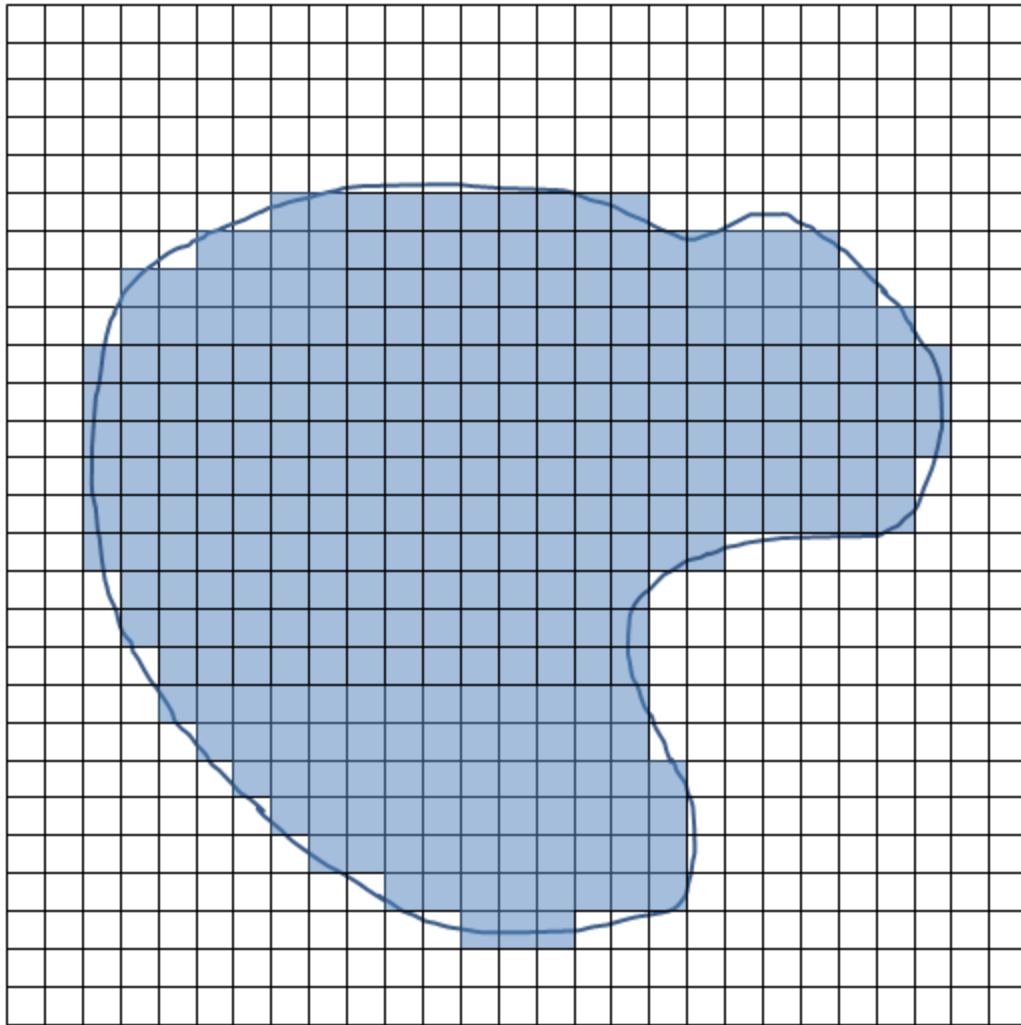


Figure 1: Quantified voxels are shaded

A sphere whose diameter is approximately 1.2cm (to produce a 1cm<sup>3</sup> 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.

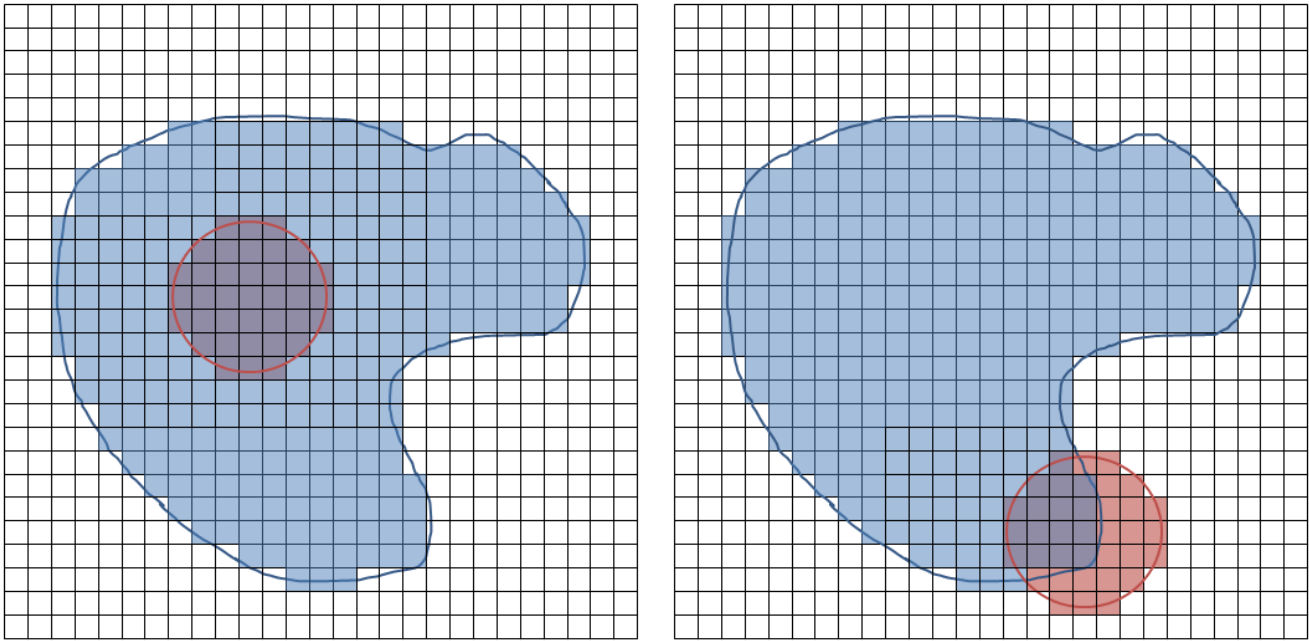


Figure 2: SUV Peak Kernel Counts Voxels Outside ROI

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.

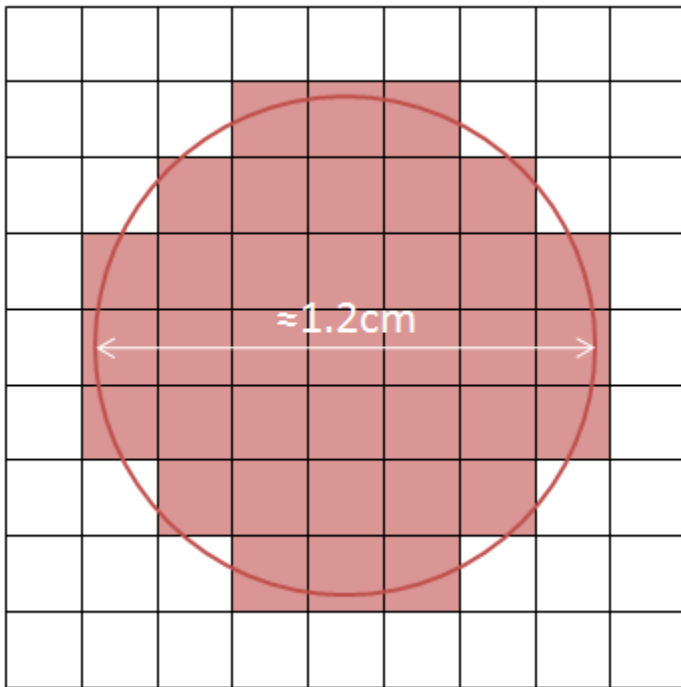


Figure 3: SUV Peak Kernel Voxels are Shaded

**Warning:** 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

**Summary:** The equation used to calculate the volume doubling time.

## Occurrences

The equation described in this topic is used by the following function of XD:

- [Using the findings table](#)

## Introduction

The volume doubling time is the estimated time that the volume will take to double, calculated from two time points.

## The equation

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 given by the following equation:

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

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.



**Warning:** 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.

# PET SUV calculation by body weight

**Summary:** The equation used to calculate PET SUV by body weight.

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

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

where SUV has units g/ml.

This calculation requires that the following information is available:

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

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.

**Note:** To change the method used to calculate PET SUV, click the active text for the units of the image layer in the bottom-left corner of a view and select the method that you want to use.

**Note:** All calculations are performed using metric units. However, it is possible to specify height and weight using Imperial units. In this case XD uses the Avoirdupois Pound and considers a stone equivalent to fourteen pounds.



# PET SUV calculation by body surface area

**Summary:** The equations used to calculate PET SUV 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 SUV has units  $cm^2/ml$  and the BSA is approximated using the following formula (by Du Bois and Du Bois):

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

This calculation requires that the following information is available:

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

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.

**Note:** To change the method used to calculate PET SUV, click the active text for the units of the image layer in the bottom-left corner of a view and select the method that you want to use.

**Note:** All calculations are performed using metric units. However, it is possible to specify height and weight using Imperial units. In this case XD uses the Avoirdupois Pound and considers a stone equivalent to fourteen pounds.

# PET SUV calculation by lean body mass

**Summary:** The equations used to calculate PET SUV by lean body mass, for male and female patients.

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 SUV has units g/ml and the lean body mass (LBM) is approximated by using the following formulae:

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

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

Note that the LBM must be converted into grams in order to be used in the SUV equation.

This calculation requires that 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.

**Note:** To change the method used to calculate PET SUV, click the active text for the units of the image layer in the bottom-left corner of a view and select the method that you want to use.

**Note:** All calculations are performed using metric units. However, it is possible to specify height and weight using Imperial units. In this case XD uses the Avoirdupois Pound and considers a stone equivalent to fourteen pounds.

# PET SUV from acquisition

**Summary:** Scanner manufactures can calculate and store a PET SUV value.

The PET SUV from acquisition is not calculated by XD and is instead retrieved from the DICOM data of the dataset.



**Warning:** 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.

**Note:** To change the method used to calculate PET SUV, click the active text for the units of the image layer in the bottom-left corner of a view and select the method that you want to use.