

eUnity 7.2

Enterprise Viewing, Integration, and Collaboration Platform

User Guide

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# Revision history

Revision number	Date	Author	Description of change
1.0	June 5, 2019	A. Newell	Initial release of new online help.
1.1	July 10, 2019	A. Newell	<ul> <li>Fixed white flash between page loads.</li> <li>Updated docs to indicate that the ability for a user to configure toolbar or context menu must be turned on by an administrator.</li> <li>Removed layouts topic for mobile (same layouts are available for desktop or mobile).</li> <li>Updated light test information for mobile.</li> <li>Moved SUV from Fusion menu to regular tools menu as SUV measurement tool is available without Fusion license.</li> </ul>
1.2	August 25, 2019	A. Newell	<ul> <li>Added new Screen Layout options for four monitor support.</li> <li>Studies in Series Tray are now shown as folders instead of study pills.</li> <li>Added minimum requirements for rad-reading sites.</li> </ul>
1.3	September 29, 2019	A. Newell	<ul> <li>Fixed the minimum iOS requirement.</li> </ul>

Revision number	Date	Author	Description of change
			<ul> <li>Fixed a screenshot in Screen Layout.</li> </ul>
1.4	October 9, 2019	A. Newell	<ul> <li>Fixed wording in Navigate         Relevant Priors and Navigate         Study List to reflect new         study ordering behavior.</li> </ul>
1.5	December 5, 2019	A. Newell	<ul> <li>Added ability to add custom text to help home page.</li> <li>Added note that Collaboration is not currently supported for Fusion</li> </ul>
1.6	February 4,2020	A. Newell	<ul> <li>Updated for 6.9</li> <li>Updated:</li> <li>spine labels are now shown in all planes</li> <li>MPR and Fusion now support discrete navigation and measurements in all planes</li> <li>removed information about immediate Key Image creation mode as the feature is now deprecated</li> <li>Curved MPR is now accessed directly from the Advanced Visualization menu</li> <li>platform differences and mobile hardware specifications</li> </ul>

Revision number	Date	Author	Description of change
			<ul> <li>Added:</li> <li>new topic for multiphase series splitting</li> <li>new topic for series and page navigation</li> <li>new information for automatic Key Image creation</li> </ul>
1.7	March 3, 2020	A. Newell	<ul> <li>Resolved printing issues and small navigation issues in User Guide</li> <li>Added note about saving Presentation States using new keyboard shortcut</li> </ul>
1.8	March 18, 2020	A. Newell	<ul> <li>Updated for 6.9.3</li> <li>Updated the hanging protocol section with new labels for viewer properties</li> </ul>
1.9	April 30, 2020	A. Newell	<ul> <li>Pemoved all distinctions between Flash and HTML5 clients.</li> <li>Added new navigation property to Hanging Protocol editor</li> </ul>
1.10	September 25, 2020	A. Newell	Updated for 6.10  Added  • Circle Markup

Revision number	Date	Author	Description of change
			<ul> <li>Ellipse Markup</li> <li>Ratio Tool</li> <li>Perpendicular Tool</li> <li>Video</li> <li>Manual Calibration</li> <li>Clone Series</li> <li>Switch Study</li> </ul>
1.11	November 13, 2020	A. Newell	<ul> <li>Updated for 6.10.2</li> <li>Clarified Series Tray behavior in Multi-monitor mode.</li> </ul>
2.0	February 24, 2021	A. Newell	Updated for 7.0  Updated:  • Clone Series and Close Cloned Series tools are now available for the toolbar.  • Added mouse shortcut for Clone Series tool.  • Changes to the hanging protocol editor  Added:  • Customize keyboard and mouse shortcuts  • Customize Window Level presets  • Customize screen layouts  • DICOM Header tool
2.1	June 22, 2021	A. Newell	Updated for 7.0.1 Updated:

Revision number	Date	Author	Description of change
			Point tool no longer requires left-click to activate
2.2	September 14, 2021	A. Newell	Updated for 7.1  Added documentation for:  • Close Study tool • Customizing the default presentation of the Series Tray • Download DICOM Study tool • Link Active Study tool • Mark Location tool • Multiple Reference Lines tool • Red Free Filter tool
2.3	November 3, 2021	A. Newell	<ul> <li>Updated for 7.1.1</li> <li>Added: <ul> <li>New hanging protocol property for ignoring zoom factor when viewing Presentation States</li> <li>Presentation States now show the name of the creator, if available</li> </ul> </li> <li>Updated: <ul> <li>The "Toggle Reference Lines" tool is now called "Reference Lines"</li> </ul> </li> </ul>
2.4	July 11, 2022	A. Newell	Updated for 7.2 Added:

Revision number	Date	Author	Description of change
			<ul> <li>Dock or undock the side panels</li> <li>Set the default side panel behavior</li> <li>Markup Color Picker</li> <li>Viewport Capture</li> <li>Multi-Segment Measurement</li> <li>Offset linking in the same study</li> <li>Smooth zoom feature</li> <li>View mammography CAD objects on a tomosynthesis slice</li> <li>Zoom / scale the viewer</li> </ul> Updated: <ul> <li>Tool icon images</li> </ul>
2.5	September 29, 2022	A. Newell	<ul> <li>Updated for 7.2.1</li> <li>Added Same Size tool to mammography</li> <li>Added Auto Cycle Colors to Markup Color Picker</li> <li>Updated platform differences for key images (now supported on mobile)</li> </ul>

## Regulatory information

### Contact us / regulatory

Viewer powered by eUnity™. For the specific release version number click = > About in the upper-right corner of the image viewer.

- Product name: eUnity™
- Product version: 7.2



#### CAUTION

Federal law restricts this device to sale by or on the order of a physician.



#### Manufacturer

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#### Solution overview

eUnity™ enables health care professionals to access, manipulate, and collaborate in real-time over full quality medical images using any web browser without installing client software. eUnity is a server-based solution that integrates with your existing hospital infrastructure. Once the eUnity server is installed, it connects to multiple PACS, VNA, Report, and other systems and displays DICOM images and other clinical content within and across the hospitals, securely from remote locations, or as an integrated part of an EHR or portal system.

#### Features

#### One viewer for the enterprise

eUnity is an enterprise-scale solution that gives everyone equal access to images with contextual performance for enterprise viewing, diagnostic radiology reading and breast imaging through one common zero-footprint platform. Image viewing can be accommodated from any location, on any device.

#### Powerful integration

eUnity integrates with your existing hospital infrastructure and performs federated queries to disparate systems, multiple PACS, or VNAs, to provide immediate access to the most recent studies available.

#### User concurrency

Thousands of users can be supported by a single eUnity server, eliminating complex hardware configurations and maintenance.

#### Security

eUnity does not store any image data or patient information on any device. All communication containing patient information is secure and encrypted.

### Business continuity / disaster recovery

eUnity can be used as:

- your primary enterprise and diagnostic viewing platform
- your PACS backup
- your method of redundancy during down times or for disaster recovery

#### Multi-Platform

Using your favorite web-browser and OS, eUnity™ runs on Microsoft Windows®, Mac OS® and Linux® in Microsoft Internet Explorer, Microsoft Edge, Mozilla Firefox, Google Chrome, Apple Safari and more

### Customer requirements

This documentation for use is intended to assist users in the safe and effective use of eUnity™. This documentation is primarily intended to describe the software supporting eUnity and does not describe the use of the IT equipment on which the eUnity software product solution is installed.

Before using eUnity, users must read this documentation thoroughly, paying particular attention to the warnings, cautions, and notes it contains.

#### Customer content requirements

#### DICOM waveform ECG review

eUnity has partial support of DICOM Waveform SOP class 1.2.840.10008.5.1.4.1.1.9.1.2 (General ECG Waveform Storage). For this reason, a site review must be made of this object type prior to clinical use within eUnity. The Mach7 Technologies Canada Inc. support & maintenance team can work with your site administrator to validate this SOP class for your site.

#### DICOM video object review

eUnity has support for the following DICOM video classes:

- 1.2.840.10008.5.1.4.1.1.77.1.1.1 (Video Endoscopic Image Storage)
- 1.2.840.10008.5.1.4.1.1.77.1.2.1 (Video Microscopic Image Storage)
- 1.2.840.10008.5.1.4.1.1.77.1.4.1 (Video Photographic Image Storage)

and the following transfer syntaxes:

- 1.2.840.10008.1.2.4.102 (MPEG-4 AVC/H.264 High Profile / Level 4.1)
- 1.2.840.10008.1.2.4.103 (MPEG-4 AVC/H.264 BD-compatible High Profile / Level 4.1)

Not all browsers support these transfer syntaxes. For this reason, a site review must be made of these object types prior to clinical use within eUnity. The Mach7 Technologies Canada Inc. support & maintenance team can work with your site administrator to validate these SOP classes and transfer syntaxes for your site.

#### DICOM Basic Text Structured Report and encapsulated PDF review

Due to the broad scope of the underlying formats and wide applicability in clinical workflow of DICOM Structured Reports and DICOM-encapsulated PDFs, a site review must be made of these object types prior to clinical use within eUnity. The requirement to do this is included in the documentation to highlight the risk associated with not maintaining these reviews.

#### Encapsulated PDF constraints

#### Lossy presentation

All encapsulated PDF objects are presented as lossy regardless of the underlying format type. eUnity communicates this to the clinician via the "lossy indicator."

#### Support for subset of PDF object types

PDF objects can contain a wide variety of formats, including image formats such as PNG, JPEG, JPEG2K, as well as vector text and other vector objects. Certain formats, such as JPEG2K, are not supported if embedded in a PDF document.

#### Structured reports constraints

In case of multiple associated reports with a given study, only the newest report will be displayed. This determination is based on comparing the Content Date (0008,0023), Content Time (0008,0033), Verification DateTime (0040,A030), and Observation DateTime (0040,A032) tags to derive the latest report.

#### Measurement, markup, and annotation

#### Accuracy of measurements

The user must be aware and account for the effects to the accuracy of measurements due to image quality, including, but not limited to:

- the accuracy of patient positioning and fixation
- patient motion
- the modality type and acquisition protocol
- image acquisition and reconstruction distortions
- image resolution: both spatial and contrast resolution

#### DICOM image calibration review

The methods used by existing modalities and new modalities (including any modality software updates) to determine medical image calibration values for subsequent measurements must be reviewed prior to clinical use within eUnity. While this is a standard operating procedure for most hospitals, the requirement to do this is included in the documentation to highlight the risk of incorrect measurement values which is associated with not maintaining these reviews. See the table within the <u>Calibration</u> section for how calibration is determined based on the source data from the DICOM header of an image.

#### Measurement use

The ability of the user to place measurement control points on an image displayed within a viewport is also one of the factors determining the accuracy of measurements. The user must take care when placing measurements. Settings such as zoom factor may affect how accurately users can place measurements. The user is responsible for determining the accuracy of the measurements.

#### Viewing

#### Collaboration

While the collaboration server attempts to synchronize all clients there may be issues related to networking that prevent the same image from being displayed to all users, or the cursor location being represented equally to all clients. If using collaboration for a diagnostic consultation, always verify which image and feature is being discussed.

#### Hanging protocols

Hanging protocols allow a rotation to be applied to the images within a series. Therefore, the images displayed may have a rotation applied. Check with your system administrator to see which hanging protocols with image rotations, if any, are configured.

Quality of reformatted (MPR/MIP) and volume rendered stacks

All reformatted and volume rendered views (MPR and 3D) are treated as 'Lossy' and will display a 'Lossy' indicator in the upper-right corner of the view

#### CINF module

When a DICOM Cine Module is present, eUnity attempts to play back the DICOM Series at the Frames Per Second (FPS) specified in the DICOM Cine module. In the absence of a DICOM Cine module, eUnity defaults to 30 FPS. eUnity presents a label during playback that describes, "currently presented fps / selected FPS (selected FPS as a percentage of the DICOM specified or default FPS)" e.g. 28 / 30 fps (100%). If the FPSs cannot be achieved, the FPS label will update to show how many FPS are being presented (e.g. 28 / 30 FPS (100%)). If frames are dropped, a yellow CINE icon will be displayed to communicate this to the user.

#### Images viewed

The user is responsible for ensuing they have viewed all relevant images for each study they view. When viewing a study, eUnity does not auto populate the study when new images as they arrive.

### Demographics

If the system is configured to display demographics from its local cache (not the source of truth), the system administrator is responsible for manually managing stale cache entries.

#### Third-party software

#### Antivirus software

Antivirus software or equivalent mitigation must be used to protect eUnity from downtime as a result of a virus or other malicious software.

#### Unauthorized third-party software

Do not install unsupported software on the eUnity servers. This could interfere with, or cause loss of or damage to patient-related data, introduce instability, or introduce computer viruses.

#### Network requirements

#### Network redundancy

eUnity is not a primary storage system and may be sold as software only. Network redundancy, manual workflows, back-up systems and other risk mitigation are recommended and are the responsibility of the customer to implement and manage.

#### For example:

- for longer or planned delays, users may use the PACS, modality or film to review medical images.
- daily backup procedures and or automated off site back-ups are the responsibility of the customer.

#### Privacy and security

#### Server SSL certificate

For privacy and security reasons eUnity must be run in HTTPS mode with a signed SSL certificate. The customer is responsible for obtaining a signed certificate from an authorized signing authority. The customer is responsible for ensuring all eUnity client communications with the eUnity server are over HTTPS connections.

#### Browser policies

For convenience some browsers store user names and passwords. eUnity does not limit this option as it may interfere with password managers, but when using any computer best practices and judgment should be followed before storing or remembering any authentication information.

#### Sale requirements

US federal law restricts this device to sale by or on the order of a physician (or properly licensed practitioner). For all other regions, customers must identify and adhere to their applicable laws.

#### Compatibility

#### Hardware requirements

The equipment is used according to the intended use and instructions provided in the Installation Guide and help documentation.

#### Software requirements

No software other than that which is distributed with this package or is sanctioned by Mach7 Technologies Canada Inc. will reside on the eUnity server.

eUnity has many configurations, settings, and other files (settings) that can be edited by users with access to the server(s) The settings are critical to proper functioning of the solution, editing the setting must only be edited by trained experienced users. Never make any changes without consulting the manufacturer. If you have any questions about making changes contact the manufacturer.

#### Environment requirements

eUnity must be operated in an environment where the minimum specified requirements for software, hardware and network performance are met.

#### Software updates

As updates for eUnity become available, customers should work with their appropriate support contacts to update their installation of eUnity. These software updates are essential to keep eUnity operating safely, effectively, and reliably.

#### Workstation settings

The following are the required workstation settings for radiology reading and diagnosis.

For information on changing any of the following settings, see the manufacturer's instructions for the relevant component (i.e. OS, graphics card, browser).

#### Desktop resolution (OS)

Desktop resolution refers to the number of pixels contained on a display monitor.

• Desktop resolution must be set to a value where images appear with a zoom factor that is appropriate for diagnostic use according to the requirements of the user's

radiological professional body.

• Monitors should be running at their native resolution. For example, a 5MP monitor should be running at 5MP.

#### Desktop scaling (OS)

Scaling refers to how much everything should be enlarged when measured in pixels. For example, with a halved resolution, the number of pixels is the same, but each pixel is twice as large.

• Desktop scaling must not be applied on imaging monitors.

#### Display bit depth (OS)

Bit depth refers to the number of color values that can be assigned to a single pixel in an image.

• The display bit depth must be set to a minimum of 32-bit color or 8-bit grayscale.

#### Graphics card (OS)

Graphics card refers to the graphics card that your browser is configured to use.

• Ensure the browser is configured to use the intended graphics card. For example, if your workstation has a dedicated graphics card, ensure the high performance option is selected in the browser graphics settings.

#### Browser zoom (browser)

Browser zoom refers to the zoom settings in your browser.

• Browser zoom must be set to 100%.

#### Hardware acceleration (browser)

• Hardware acceleration must be turned on in the browser (note that it is turned on by default). Hardware acceleration improves performance in the eUnity viewer.

#### Intended use

#### Overview

Supported modalities are listed in the DICOM Conformance Statement.

#### Legal information

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#### **United States**

eUnity™ is a software application that displays medical image data and associated clinical reports to aid in diagnosis for healthcare professionals. eUnity™ performs operations relating to the transfer, storage, display, and measurement of image data.

eUnity™ allows users to perform image manipulations, including Window / Level, rotation, zoom, measurement, and markup. eUnity™ provides 2D display, multi-planar reformatting, and 3D visualization of medical image data, and mobile access to images.

eUnity™ displays both lossless and lossy compressed images. For lossy images, the medical professional user must determine if the level of loss is acceptable for their purposes. Display monitors used for reading medical images for diagnostic purposes must comply with applicable regulatory approvals and with quality control requirements for their use and maintenance. For mobile diagnostic usage when a full workstation is not available.

Mobile usage for mammography is for reference and referral only.

#### Canada

eUnity™ is a software application that displays medical image data and associated clinical reports. eUnity™ performs operations relating to the transfer, storage, display, and measurement of image data.

eUnity™ allows users to perform image manipulations, including Window / Level, rotation, measurement, and markup. eUnity™ provides 2D display, MPR and 3D visualization of medical image data, and mobile access to images.

The communication and storage components of the eUnity™ system are primarily DICOM communication over TCP/IP networks, digital image storage on computer hard disk drives.

It is the user's responsibility to ensure that  $eUnity^{\mathbf{M}}$  is used with appropriate display hardware and that image type and quality are suitable for their intended clinical application based on the regulations and / or their professional association's guidelines pertaining to the anatomy and pathology being studied. When using on a mobile device, it is not intended to replace a full workstation images and mammography, or digital breast tomography images must not be used for diagnostic interpretations.

eUnity™ supports the following modalities: CR, CT, DX, ECG, MR, MG, NM, OP, PR, PT, RF, SC, SR, US, XA, VL.

#### Europe and Australia

eUnity™ is a software application that displays medical image data and associated clinical reports. eUnity™ performs operations relating to the transfer, storage, display, and measurement of image data.

eUnity™ allows users to perform image manipulations, including Window / Level, rotation, zoom, measurement, MIP/MPR/3D, and markup.

eUnity™ displays both lossless and lossy compressed images. For lossy images, the medical professional user must determine if the level of loss is acceptable for their purposes.

Display monitors used for reading medical images for diagnostic purposes must comply with applicable regulatory approvals and with quality control requirements for their use and maintenance.

#### Other

Certification for other regions is pending. Please contact Mach7 Technologies Canada Inc. for more information.

#### Document conventions

#### Quick reference

Many of the topics in the Tools section of the user guide have a "quick reference" at the top of the topic. This shows the tool icon, tool name, and a brief description of the tool's behavior so that you can quickly find the tool you're looking for.

#### Example:



#### Eraser

Erase a measurement or annotation.

#### Notes

Where applicable, key notes are provided in the documentation as follows:



#### NOTE

A key note of interest for the reader.

#### Caution

Where applicable, cautions are provided in the documentation as follows:



### CAUTION

This is a caution statement.

#### Warning

Where applicable, warnings are provided in the documentation as follows:



#### WARNING

This is a warning statement.

### Documentation warranty statement

Characteristics of the products described in this publication can be changed at any time without notice.

The information contained in this document is subject to change without notice. Mach7 Technologies Canada Inc. and its affiliates make no warranties or representations, express, implied or statutory, with regard to this material, including, but not limited to, the implied warranties of merchantability and fitness for a particular purpose.

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The information in this documentation is subject to change without notice.

### Hardware platform requirements

### Minimum requirements for web client for enterprise and cloud

When eUnity™ is used as an enterprise or cloud viewer, the following are **minimum** PC requirements:

	Minimum requirements
Operating system	Windows 8/8.1, Windows 10, MacOS®X 10.14+ (Intel)
Supported browsers  While eUnity™ stores no patient information on the client machine, we do recommend closing the browser when finished viewing images.	Safari® 10+, Internet Explorer 11+, Firefox 42+, Chrome™ 53+, Microsoft Edge 44+
Hardware	<ul> <li>Modern x64 Consumer CPU</li> <li>Intel® i3* or equivalent</li> <li>2+ Cores @ 1.5Ghz+</li> <li>4096 MB of RAM</li> <li>512MB+ of graphics memory</li> <li>10Mbit or higher network speed</li> <li>4G/LTE+ (cell network speed)</li> </ul>

<sup>\*</sup>Mobile, or low voltage class CPUs require on-site validation to be performed by customer prior to use

Note: Some default browser configurations are known to improperly handle the HTTP/1.1 no-store cache directive and cache information to the local disk. During site validation the enterprise browsers and configurations should be validated to ensure patient data is not unexpectedly cached.

### Recommended requirements for web client for enterprise and cloud

When used as an enterprise or cloud viewer, the following are **recommended** PC requirements:

	Recommended requirements
Operating system	Windows 10 MacOS® X 10.14+
Recommended browsers  While eUnity™ stores no patient information on the client machine, we do recommend closing the browser when finished viewing images.	Safari® 12+, Chrome™ 70+ Latest iOS Safari®, Android™ Chrome™
Hardware	<ul> <li>Modern x64 Consumer CPU</li> <li>Intel® i5* or equivalent</li> <li>4+ Cores @ 1.5Ghz+</li> <li>8192 MB of RAM</li> <li>Dedicated Graphics Card (NVIDIA® or AMD)</li> <li>DirectX 12 Compatible</li> <li>2GB+ of dedicated graphics memory</li> <li>30Mbit or higher network speed</li> <li>4G/LTE+, 5G (cell network speed)</li> </ul>

 $<sup>{}^*\!</sup>Mobile, or low voltage class CPUs require on-site validation to be performed by customer prior to use$ 

### Minimum requirements for web client for radiology reading

When eUnity is used as a radiology reporting station, the following are **minimum** workstation requirements:

	Minimum requirements
Operating system	Windows 10 MacOS® X 10.14+ (Intel)
Supported browsers  While eUnity™ stores no patient information on the client machine, we do recommend closing the browser when finished viewing images.	Chrome™ 70+ (64-bit)
Hardware	<ul> <li>Modern x64 Consumer or Business CPU</li> <li>Intel® i7 / i9 or equivalent*</li> <li>4+ Cores @ 3.6Ghz+</li> <li>16GB+ of RAM</li> <li>Dedicated Graphics Card (NVIDIA® or AMD)</li> <li>DirectX 12 Compatible</li> <li>3GB+ of dedicated graphics memory</li> <li>200Mbit+ or higher network speed</li> </ul>

 $<sup>{}^*\!</sup>Mobile, or low voltage class CPUs require on-site validation to be performed by customer prior to use.$ 

### Recommended requirements for web client for radiology reading

When eUnity is used as a radiology reporting station, the following are **recommended** workstation requirements:

	Recommended requirements
Operating system	Windows 10  MacOS® X 10.14+ (Intel)
Recommended browser  While eUnity™ stores no patient information on the client machine, we do recommend closing the browser when finished viewing images.	Chrome™ 70+ (64-bit)
Hardware	<ul> <li>Modern x64 Consumer or Business CPU</li> <li>Intel® i7 / i9 or equivalent*         <ul> <li>4+ Cores</li> <li>Minimum 7th generation high-end desktop CPU (i.e. non-mobile CPU)</li> <li>Non-power-optimized (i.e. not ending in H, HK, HQ, T, U, Y)</li> </ul> </li> <li>16GB+ of RAM</li> <li>Dedicated Graphics Card (NVIDIA® or AMD)         <ul> <li>DirectX 12 Compatible</li> <li>4GB+ of dedicated graphics memory</li> </ul> </li> <li>200Mbit+ or higher network speed</li> </ul>

## Mobile requirements

#### Mobile HTML

	iOS	Android™
Operating system	iOS 10+	Android™ 6+
Hardware	iPhone® 6+, iPad Air®+	Mobile devices that run Android™ OS 6.0 and up.

### Mobile app

	iOS	Android™
Operating system	iOS 10+	Android™ 6+
Hardware	iPhone® 6+, iPad Air®+	Mobile devices that run Android™ OS 6.0 and up.
App store	Apple App Store	Google Play Store

### Platform differences

There are a number of differences in supported features between eUnity clients on different platforms.

	Desktop web browsers	Mobile App / Mobile HTML (Phone and Tablet)
Angle Measurement	✓	<b>√</b>
Arrow Annotation	✓	✓
Cine	✓	✓
Circle Annotation	✓	✓
Circle ROI	✓	✓
Clone Series	✓	✓
Close Study	✓	✓
Cobb Angle Measurement	✓	✓
Collaboration	✓	✓
Context menu configuration	✓	N/ A
Download DICOM Study	✓	
Ellipse Annotation	✓	✓
Ellipse ROI	✓	✓
Eraser	✓	✓

	Desktop web browsers	Mobile App / Mobile HTML (Phone and Tablet)
Export	✓	
Flip and Rotate	✓	✓
Freeform ROI	✓	✓
Freehand Annotation	✓	✓
Hanging Protocols	✓	✓
Horizontal Series Tray	✓	✓
Image Sharpening	✓	✓
Invert	✓	✓
Key images	✓	✓
Keyboard shortcuts	✓	
Keyboard and Mouse Shortcut Preferences	✓	✓
Line Annotation	✓	✓
Linear Measurements	✓	✓
Linking	✓	✓
Linking offset / pause linking	✓	
Magnifying Glass	✓	✓

	Desktop web browsers	Mobile App / Mobile HTML (Phone and Tablet)
Mammography Tools	✓	<b>√</b>
Manual Calibration	✓	✓
Markup Color Picker	✓	✓
MPR/3D	✓	✓
Multi-Monitor Split Screen	✓	N/A
Multi-Segment Measurement	✓	✓
Multi-Study Display	✓	✓
Multiphase Tool	✓	✓
Multiple Reference Lines	✓	✓
Navigate	✓	✓
Paper Printing	✓	
Perpendicular Tool	✓	✓
PET / CT Fusion	✓	✓
Ratio Tool	✓	✓
Report / Comments	✓	✓
Revert to Original	✓	✓

	Desktop web browsers	Mobile App / Mobile HTML (Phone and Tablet)
Save (key image or presentation state)	✓	
Red Free Filter	✓	✓
Reference Lines	✓	✓
Screen Layout	✓	✓
Screen Layout Preferences	✓	✓
Series Paging	✓	✓
Series Reposition	✓	✓
Spine Labeling	✓	✓
Study List	✓	✓
Switch Studies	✓	✓
Text Annotation	✓	✓
Toggle Demographics	✓	✓
Toolbar configuration	✓	✓
Triangulation Mode	✓	✓
Vertical Series Tray	✓	
Video	✓	✓

	Desktop web browsers	Mobile App / Mobile HTML (Phone and Tablet)
Viewport Capture	<b>√</b>	<b>√</b>
Window/Level	✓	✓
Window / Level Preset Preferences	✓	✓
Zoom or Pan Images	✓	✓
Zoom/Scale the Viewer	✓	

# Calibration and compression information

### Calibration

The following table details how calibrations are determined based on the source data from the DICOM header of an image.



#### CAUTION

Users must consider the measurement types, units, and values and the source of a measurement's calibration. For example, with X-Ray-based modalities, the user must consider if the calibration takes magnification into account.

Calibration type	Used (Yes / No)	Description
(3D)	Yes	Calibration for a 3D modality (like CT and MR), using the Pixel Spacing field. This should be a correct calibration for all patient anatomy.
(fiducial)	Yes	For an X-Ray projection modality (like CR or XA), the Pixel Spacing field has been used, along with a Pixel Spacing Calibration Type field which describes this calibration as "FIDUCIAL" This means that a calibration has been done on the modality to some fiducial marker within the X-Ray image.
(geometry)	Yes	For an X-Ray projection modality (like CR), the Pixel Spacing field has been used, along with a Pixel Spacing Calibration Type field which describes this calibration as "GEOMETRY". The beam geometry has been used by the modality to get an approximate calibration for anatomy in the view. Alternately, for Enhanced XA SOP Classes, the Object Pixel Spacing In

Calibration type	Used (Yes / No)	Description
		Center Of Beam may have been used, which is also an automatic geometry-based calibration.
(imager)	Yes	For an X-Ray projection modality (like CR or XA), Imager Pixel Spacing (the detector plate pixel spacing) has been used. No Estimated Radiographic Magnification Factor has been found to correct it. It is possible that a Pixel Spacing field also exists, but if it does, it was found to be the same as Imager Pixel Spacing. Pixel Spacing is then ignored as just being a duplicate of Image Pixel Spacing
(imager/ERMF)	Yes	For an X-Ray projection modality (like CR or XA), both the Imager Pixel Spacing and the Estimated Radiographic Magnification Factor fields have been used. The calibration divides out the Estimated Radiographic Magnification Factor, providing a measurement that is closer to correct for the anatomy in the image, compared to the Imager Pixel Spacing (the plate dimensions) alone. It is possible that a Pixel Spacing field also exists, but if it does, it was found to be the same as Imager Pixel Spacing. Pixel Spacing is then ignored as just being a duplicate of Image Pixel Spacing.
(nominal scanned)	No	Nominal Scanned Pixel Spacing (pixel dimensions on a piece of scanned film) is not based on any anatomy or detector calibration and is therefore not used by the viewer. The text (unknown) will be displayed with measurements in pixels.
(unknown)	Yes	The calibration type is unknown, and the

Calibration type	Used (Yes / No)	Description
		modality is not a known 3D modality (like CT and MR), nor a projection modality with Imager Pixel Spacing information (like CR). If measurements are in mm, a Pixel Spacing field was found, but without any Pixel Spacing Calibration Type field to explain it. This often happens for Secondary Capture images. If the measurements are in pixels, then no calibration information exists.
(unknown recalibration)	Yes	For an X-Ray projection modality (like CR), the Pixel Spacing field has been used, but it doesn't match the Imager Pixel Spacing field. This indicates a recalibration in the modality, but there is no Pixel Spacing Calibration Type field to explain why this recalibration occurred.
(US region)	Yes	The Calibration comes from an Ultrasound Calibration Region in the DICOM object. These are usually set by the modality and should be correct.
(CW Doppler)	Yes	A subtype of US Region calibration representing Continuous Wave Doppler.
(PW Doppler)	Yes	A subtype of US Region calibration representing Pulsed Wave Doppler.
(presentation state)	Yes	The currently-used Presentation State for the image has a calibration value in the Presentation Pixel Spacing field, for a non-3D modality.  Note: Whether this is calibrated to a fiducial maker, the dimensions on the plate, or includes a geometric Estimated Radiographic Magnification Factor is

Calibration type	Used (Yes / No)	Description
		unknown. This will be displayed in cases where the calibration in the Presentation State does not match the calibration in the image header.
(presentation state 3D)	Yes	The currently-used presentation state for the image has a calibration value for a 3D imaging modality (like CT, MR, and NM) value in the Presentation Pixel Spacing field.
		This should be a correct calibration for all patient anatomy. This will be displayed in all cases where the calibration is (3D) and a presentation state is applied.
(user)	Yes	Manual calibration (that is, user-defined calibration) has been used. This means that a calibration has been manually done by the user to some fiducial marker within the image, series, or study.

# Lossy image display

Lossy images are displayed with an indicator in the demographics that identifies the image data as lossy compressed.

#### Lossy compression indicator

Shown in the viewport to identify the image data as lossy and summarize the compression ratio. Hover the cursor over the 1 to display the following information:

Lossy 9.9:1 **1** 

- the type of image compression
- the compression ratio
- derivation description, if one exists

If the image has multiple compression types and ratios, the tooltip displays all known type / ratio combinations.

# Lossy compression indicator (reformatted and rendered views)



#### WARNING

All reformatted and volume rendered views (MPR and 3D) are treated as Lossy and will always display a Lossy indicator.

In MPR, 3D , and Fusion modes, hover the cursor over the  $^{\scriptsize \textcircled{1}}$  to display the final JPEG render quality.

Lossy **(i)** 

# Getting started

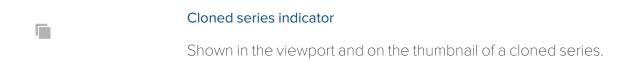
# Indicators overview

Indicators are displayed in the viewports to provide feedback on the state of the image.

# Flip and Rotate

Rotate 90°	Rotated 90° indicator	
	Shown in the viewport to indicate that the image has been rotated 90°.	
Rotate 180°	Rotated 180° indicator	
	Shown in the viewport to indicate that the image has been rotated 180°.	
Flip	Flipped indicator	
	Shown in the viewport to indicate that the image has been flipped.	

# Cloned series



# Curved MPR

CMPR Control Point Limit	CMPR Control Point Limit indicator  The curved MPR has reached the 20 control point maximum.
	Invalid Zoom indicator
Invalid Zoom 🛈	This indicator is displayed when the curve is too small to be rendered within the boundaries of the current viewport.

# Fusion

#### Limited Measurements indicator

Limited Measurements

Shown in the viewport to indicate that not all measurement types



# Partial Volume indicator

Partial Volume

Shown in the viewport to indicate that the complete 3D volume cannot be rendered. A partial volume occurs when the original 2D data does not provide contiguous 2D slices.

#### SUV not available indicator

SUV not available

Shown in the viewport to indicate that there is not sufficient data to perform SUV measurements. Click the for more information.

# Image error

#### Image error indicator



Shown in the viewport to indicate that there was an issue loading the image from the data source. Click More information to see additional information about the loading error.

# Image loading

# Image loading indicator

Shown in the viewport to indicate that data is being loaded.





# CAUTION

When you load an image or zoom further into an image, eUnity will typically need to load more data. Once loaded, the indicator will disappear. If the indicator is visible, you must wait for the full data to be loaded.

# Image sharpening



#### Image Sharpening indicator

Shown in the viewport to indicate that image sharpening is applied.

# Key Images



#### Key image indicator

Shown in the viewport to indicate that it is a key image.

# Source image indicator



Shown in the viewport on the source image from which a key image was created. The number represents the number of derived key images.

# Fk 🔑

### Unsaved key image indicator

Shown in the viewport on a manually created, unsaved key image.

# S R P

# Unsaved auto-generated key image indicator

Shown in the viewport on an automatically generated, unsaved key image.

# Linking





Shown in the viewport, a broken link indicator means that no matching slice could be found between the series. By default, the slices in linked series need to be within 5mm of each other to be considered for linking. If slices exceed the maximum threshold, the series will not be linked, and the broken link indicator will be displayed.



#### Series linked

Shown in the viewport, a link indicator means the series is successfully linked.

#### Link offset

Shown in the viewport, the link offset indicator means that the series' navigation has been manually offset from other linked series in the same study. That is, series linking was manually disengaged then the user navigated to a new point in the image stack and then relinked the series.

#### Offset not linked

Shown in the viewport, the offset broken link indicator displays when the series are no longer linked after a link offset is applied.

# Lossy compression

0

# Lossy compression indicator

Shown in the viewport to identify the image data as lossy and summarize the compression ratio. Hover the cursor over the 1 to display the following information:

Lossy 9.9:1 1

- the type of image compression
- the compression ratio
- derivation description, if one exists

If the image has multiple compression types and ratios, the tooltip displays all known type / ratio combinations.

# Lossy compression indicator (reformatted and rendered views)



# WARNING

All reformatted and volume rendered views (MPR and 3D) are treated as Lossy and will always display a Lossy indicator.

In MPR, 3D , and Fusion modes, hover the cursor over the  ${f 0}$  to



display the final JPEG render quality.

# Mammography

#### CAD markers displayed

CAD: Calc: 2 Mass: 1

Shown in the viewport to indicate that CAD markers are displayed. The numbers represent the count for every type of displayed marker.

#### No CAD findings

CAD: No Findings Shown in the viewport to indicate that CAD markers are NOT

displayed. That is, CAD exists, but there are no findings to display

for the image.

#### Error with CAD information

CAD: FAIL Shown in the viewport to indicate that CAD markers are NOT

displayed. That is, a fatal error with CAD information.

#### Image not related to CAD

No CAD for Image Shown in the viewport to indicate that CAD markers are NOT

displayed. That is, the image is not related to CAD.

# No CAD in study

No CAD for Study Shown in the viewport to indicate that CAD markers are NOT

displayed. That is, there is no CAD in the study.

# Percentage of certainty of malignancy

Case Score The case score displays the algorithm's level of confidence, per

study, that the study has malignant findings.

# Name and version of CAD algorithm

If enabled, the name and version of the Al algorithm that is used for

CAD objects is shown as part of the CAD overlay.



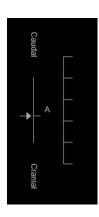
#### Quadrant View indicator

When in Quadrant View mode, this indicator is shown in the viewport on the non-breast wall side to indicate which quadrant of the breast is currently visible.

#### Related series indicator

In mammography studies, if the hanging protocol is set to Navigate Related Series, images of the same view type are stacked in the same viewport. This indicator is shown in the viewport to indicate how many images are stacked in the viewport and where you are in the stack.

System administrators can configure eUnity to include tomosynthesis images with the same view type in related series stacks.



# Tomosynthesis indicator

Shown in the viewport for breast tomosynthesis studies to show the location of the current slice in relation to the other images in the series. The indicator shows directional markers to indicate whether you are scrolling in a caudal / cranial, or a medial / lateral direction. If CAD objects are available, the indicator will show additional lines to show which slices contains the CAD objects.

#### Multiphase Series



#### Multiphase indicator

Shown in the viewport for a multiphase series that has not yet been split into virtual series. The dividers represent the start and end of a phase. The arrow represents the slice position in the stack.

# Partial Study

# Partial Study

Shown in the viewport to indicate that the study is only partially downloaded and may not display all of its images. When you initially open a study that is in a partial state, you will also receive a Partial Study warning dialog that shows the Accession Number of the study that is in a partial state.

# Presentation States



# Presentation state applied indicator

Shown in the viewport to indicate that a presentation state is applied.

# Red Free Filter



#### Red Free Filter indicator

Shown in the viewport to indicate that the red free filter is applied to the series.

# Viewport capture



# Unsaved viewport capture indicator

Shown in the viewport on an unsaved viewport capture.



# Saved viewport capture indicator

Shown in the viewport on a saved viewport capture.

# Log in and log out (desktop client)

For information on logging in and logging out on the mobile application, see <u>Log in or log out (mobile)</u>



# NOTE

If you have launched eUnity from a third-party application (such as an EMR or a worklist), do not also directly log in to eUnity in the same browser on the same workstation. Having multiple eUnity sessions running in the same browser may affect the session timeout and an unexpected log out may occur.

# Log in to eUnity™

To access the eUnity login screen, type the eUnity address in a web browser. For example: http://localhost

At the eUnity login screen, do the following:

- 1. Type your username and password. Note that both fields are case-sensitive.
- 2. Click Log In. If the login is successful, the Search screen is displayed.

eUnity supports secure LDAP, RADIUS, and local authentication so that users can log in with their enterprise username and password. As well, some sites that use LDAP integration allow users to change their enterprise password from the eUnity Search screen. For more information on configuring external authentication such as LDAP, see the eUnity™ Administration Guide.

# Log out of eUnity

To log out of eUnity, click in the upper-right corner of the Search screen.

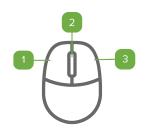
# Mouse actions

This section describes the default mouse button behaviors. Note that these behaviors may have been modified by your system administrator.

#### Left-click



- Drag up and down to scroll images
- Drag+ Ctrl + Shift to reposition series
- Double-click to enlarge viewport



#### Scroll wheel

- Roll up and down to scroll images
- Drag to zoom
- Drag + Ctrl to triangulate

# Right-click



- Drag left and right to change Window Width or drag up and down to adjust Window Level
- Drag + Ctrl to pan
- Click to show context menu

# Series tray

The series tray can be positioned horizontally or vertically. There are slight differences in functionality depending on how the series tray is positioned. There are also slight differences in behavior when you use the series tray in multi-monitor mode. For information on setting the default series tray presentation, see Customize the default presentation of the series tray.

#### Horizontal series tray

When the series tray is positioned horizontally, it shows series in thumbnail view.



#### Thumbnail mode

Each series is represented with a thumbnail image. To open a series, drag it into a viewport or click it to open it in the active (selected) viewport.



- The number of images in the series is shown in the upper-left corner of the thumbnail.
- The folded corner on the thumbnail indicates that at least one image in the series has been viewed.
- The series that is in the active viewport has an orange border around the thumbnail and an orange glow around the description text.
- The series that are currently open in the viewer have a blue border around the thumbnail and a blue glow around the description text.

# Study folder



Each rectangular folder represents a study that is available for the patient. Click a study folder to see its series. When the series tray is positioned horizontally, only one study folder can be expanded at a time

- The number in brackets on the right indicates how many series the study has. The number will change from bold text to regular text once at least one image in each series has been viewed.
- The study folder with the lighter gray background and the highlighted outside border is the study that is currently active in the series tray.
- The study folders with the darker gray background are the studies that are not currently active in the series tray.



#### Presentation states indicator

Indicates that there are presentation states available for the study. Click to select a presentation state.



# Study position indicator

Indicates the study position on the screen. If no screen position indicator is shown on the study folder, then the study is currently not shown in the viewer.



#### Pin the series tray

Pin the series tray so that it is always shown or unpin it so that it is hidden when it is not active.



# Reposition the series tray horizontally or vertically

Reposition the series tray at the top, bottom, left, or right of the screen.

# Vertical series tray

When the series tray is positioned vertically, it can show series in thumbnail view or text view and it can also show multiple expanded study folders at the same time. The image below shows the series tray in text view.



#### Text mode

In the series tray, show the available series as a text list instead of thumbnail images. This option is available only for the vertical series tray. For information on thumbnail mode in the series tray, see <a href="https://example.com/Thumbnail/Thumbnail/">Thumbnail/</a> modeabove.

Collapse

Click the arrow to collapse or show the series tray.

# Study folder

Each rectangular folder represents a study that is available for the patient.

Click a study folder to expand it and see the available series. See <sup>6</sup> for more information on expanding multiple study folders.

• The number in brackets on the right indicates how many series the study has. The number will change from bold text to regular text once at least one image in each series has been viewed.

- The study folder with the lighter gray background and the highlighted outside border is the study that is currently active in the series tray.
- The study folders with the darker gray background are the studies that are not currently active in the series tray.

#### Series list

In text view, the series are shown as text instead of thumbnails. To open a series, drag it into a viewport or click it to open it in the active (selected) viewport.

- The number of images per series is shown to the right in blue text.
- The series that is in the active viewport has an orange glow around the description text.
- The series that are currently open in the viewer have a blue glow around the description text.

# Study position indicator

Indicates the study position on the screen. If no screen position indicator is shown on the study folder, then the study is currently not shown in the viewer.

#### Expand multiple study folders

When the series tray is positioned vertically, more than one study folder can be expanded at a time. The number of study folders that can be open at one time is determined by the available screen space.

- Click a study folder to expand or collapse it.
- To expand or collapse multiple study folders, do either of the following:
  - To collapse all but one study folder, hold the Alt key and click the study folder that should remain open.
  - To re-expand the study folders that you collapsed, hold the Alt key and click again. Note that re-expanding works only if you have not made changes since you collapsed the study folders (for example, repositioning the series tray or expanding different study folders).

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# Reposition the series tray horizontally or vertically

Reposition the series tray at the top, bottom, left, or right of the screen.

8

# Viewed image indicator

The folded corner indicator means you have viewed at least one image in the series.

9

# Number of images

The number in brackets shows the number of images in the series.

10

#### Presentation states indicator

Indicates that there are presentation states available for the study. Click to select a presentation state.

# Series tray in multi-monitor mode

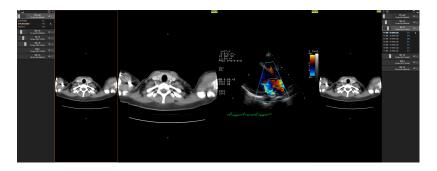
When the series tray is positioned horizontally in multi-monitor mode, the number of series trays that are shown depends on the monitor layout that you select in the Screen Layout options<sup>1</sup>. For example, selecting a 4 monitor layout results in 4 series trays.





In some cases, sites are configured so that the number of series trays is dictated by the monitor layout and the number of configured physical monitors. Under this configuration, the number of series trays will never exceed the number of physical monitors.

When the series tray is positioned vertically in multi-monitor mode, the series trays are shown only on the outside monitors. For example, in a 4 monitor layout the series tray will appear on the outer edges of the monitors.



When the series tray is opened, it shows the selected study's series thumbnails. In a new eUnity session, a study will be automatically selected and expanded in any of the following cases:

- If a new monitor is added to a layout (for example, the user has not yet changed the monitor layout and then changes from 1 monitor to 2 monitors), a new series tray is added. eUnity selects the first study in the monitor of that series tray (that is not already selected in another series tray).
- If a new study is loaded (for example, it is added from the study list), eUnity selects the newly loaded study in the first monitor in which that study appears.
- If a selected study is unloaded, eUnity selects the first study in the monitor of that series tray (that is not already selected in another series tray).

### Related

• Customize the default presentation of the series tray

# Tools overview

#### 3D

See 3D tools for more information.

#### Clip Box

Cut away some of the volume so that you can better see underlying anatomy.

Drag down to move the plane into the volume (cut more). Drag up to move the plane out of the volume (cut less). Selecting one of the edges of the clip box the orientation of the clip box can be changed without changing its size or the orientation of the volume.

#### **Cut Plane**

Use the Cut Plane tool to cut away some of the volume at a custom rotation.

Rotate the 3D volume to a desired view and click the Cut Plane icon. A cut plane normal to the current 3D view will be created. While in the cut plane mode, the cut plane can be moved into the volume by dragging the mouse down or out of the volume by dragging the mouse up.

# Scalpel Tool

Remove or isolate a section of an image by dragging the mouse along the border of the area to segment then clicking on the region you would like to keep.

#### Advanced MPR

See Advanced MPR tools for more information.

#### Create oblique

Every viewport is annotated with a color that directly corresponds to the reference line on other intersecting images in other viewports. To generate new planes, drag the controls corresponding to the color of the viewport you wish to change until desired orientation is achieved.

#### Advanced visualization

See MPR/3D or PET/CT Fusion for more information.

#### Advanced Visualization modes

Select Advanced Visualization modes such as 3D, MPR, Advanced MPR, Curved MPR, and Fusion. Note that the options in this menu are enabled / disabled depending on the active study or series type.

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

#### **Advanced Visualization Parameters**

View or change render types, render parameters, or SUV parameters. The tabs / options that are available in the panel depend on the visualization mode (i.e. Fusion vs 3D) and the series type (i.e. PET vs CT) or series orientation (i.e. same plane as the original series or not) that is selected in the viewer.

#### Annotations

See <u>Annotation tools</u> or <u>Annotations and measurements in MPR / 3D view modes</u> for more information.

#### Arrow

To add an arrow annotation, left-click to start the arrow and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

#### Circle

To add a circle annotation, left-click to start the circle and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

#### Ellipse

O To add an ellipse annotation, left-click to start the ellipse and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

#### Freehand

To add a freehand annotation, left-click and drag the mouse. Let go of the mouse button to end the annotation. The freehand annotation cannot be edited.

#### Line

To add a line annotation, left-click to start the line and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's handles to reposition.

#### Polygon

To add a polygon annotation, left-click to start to start the polygon. Each additional left-click adds another point to the polygon. To end the polygon, double-click or left-click on the polygon start point. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

# Rectangle

To add a rectangle annotation, left-click to start the rectangle and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

#### **Text Annotation**

Click the location that the text should start. A text box is displayed to enter up to 32 characters. To edit the text, double-click the annotation to select it and change the text. To move the annotation, drag it to a different location. Note that the Text Annotation tool cannot be used in Full Screen mode.

# Spine labeling

Spine Labeling

Add spine-related labels to images. In Spine Labeling mode, the **Spine Labeling** tab is activated to provide access to other spine labeling tools.

### Toggle Spine Labeling Markup

Hide or show spine labels. Note that Toggle Markup also hides / shows spine labels.

# Delete All Spine Labels

Delete all spine labels in the study.

#### Cine

See Cine for more information.

#### Toggle Cine mode / Play video



Play a series of images in succession (like a movie) or play a video. When Cine / Video mode is activated, the Cine toolbar is displayed in the active viewport. The default location of the Cine / Video toolbar can be configured by the system administrator.

#### Clone Series

# Clone Series



Clone a series so that you can see a copy of the series and the original series in the viewer at the same time. As a shortcut, right-click and drag a series from the series tray into the viewing area to clone it.

#### Close Clones Series



Close the cloned series and remove it from the series tray.

# Close Study

# Close Study



Close the study and remove it from the series tray and the Relevant priors and Switch studies lists, if they are enabled.

#### Collaborate

See Collaboration for more information.

#### Share this Session



Share your screen with other participants across all supported eUnity™ platforms (desktop web browser and mobile devices).

#### Curved MPR

#### Create Curved MPR



Click along curved anatomy in any of the 2D viewports and the perpendicular reconstruction is created in the CMPR viewport. Each point in the curve is along the center axis of the curved MPR view.

# Demographics

See Demographics for more information.

# 

# **Toggle Demographics**

Hide or show demographics in the viewport.

# **DICOM Header**



# **DICOM Header**

Show the DICOM header data for the selected series or image.

# Download DICOM Study

# Download DICOM Study



Download the selected study to your local machine as a DICOM file contained in a zip file.

# Eraser

#### Eraser

Erase a measurement or annotation.

# Export

See Export for more information.



# Export image to JPEG / PNG

Export an image to your local device in JPEG or PNG format.

# Flip and rotate

See Flip and Rotate for more information.

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# Flip (Horizontally)

Click to flip the image horizontally in the viewport.

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# Flip (Vertically)

Click to flip the image vertically in the viewport.

9

#### **Rotate Left**

Click to rotate the image counter-clockwise in the viewport.

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# Rotate Right

Click to rotate the image clockwise in the viewport.

# Free Rotate by Drawn Angle

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Rotate the image by a custom amount in the viewport. Draw a line to rotate the image.

#### Fusion

For more information, see <u>Advanced Visualization Parameters for Fusion</u>, <u>Fusion Blending</u>, Fusion Presets, SUV measurement tools

#### **Advanced Visualization Parameters**

View or change render types, render parameters, or SUV parameters. The tabs / options that are available in the panel depend on the visualization mode (i.e. Fusion vs 3D) and the series type (i.e. PET vs CT) or series orientation (i.e. same plane as the original series or not) that is selected in the viewer.

#### **Fusion Blending**

Left-click and drag the mouse up or down to increase or decrease the PET opacity. Increasing the opacity shows more of the functional (metabolic) data from the PET. Decreasing the PET opacity shows more of the anatomical data from the CT.

#### **Fusion Presets**

Apply presets such as Hot Iron to fused PET / CT studies so that the metabolic data of the PET information is assigned a preset pseudo color value from the Color Look Up Table (CLUT).

# **Point Tool**

#### Circle ROI

Draw a circular region of interest.

# Hanging protocols

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For more information, see Hanging protocols overview

#### Settings - Hanging Protocols

Open the hanging protocol panel (the Hanging Protocol tab in the Settings panel) to add, edit, copy, or delete hanging protocols.

# Add Hanging Protocol

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Captures the information on screen (display sets and layout) and creates a new hanging protocol.

# **Edit Hanging Protocol**

Edit the active hanging protocol.

This icon is available only when there is an active hanging protocol. Access non-active hanging protocols in the hanging protocol panel (the Hanging Protocol tab in the Settings panel).

# Select Hanging Protocol

This dropdown provides a list of "close match" hanging protocols. Choose a hanging protocol to apply to the current study in the viewer.

# **Presentation Steps**

Click the dropdown arrow to show the available presentation steps for the active hanging protocol. Click a Presentation Step to jump to it.

Hover the cursor over the icon to show which hanging protocol is currently applied.

#### Backward

Move to the previous presentation step in the hanging protocol.

# Forward

Move to the next presentation step in the hanging protocol.

#### Image sharpening

See Image sharpening for more information.

# **Image Sharpening Presets**

Click to apply a preset sharpening algorithm on an image in a viewport. Presets are configurable by the system administrator.

#### Invert

See <u>Invert</u> for more information.

#### **Invert Brightness**

Olick to apply a monochrome inversion to the selected series. Note that for mammography images, the viewport background retains its color when the image is inverted.

# Linking

See <u>Indicators</u> for more information.

#### **Link Studies**

Link series across all studies to apply zoom, pan, scroll, and optionally window level actions across all series from the same plane. Window level linking must be enabled by the system administrator.

# Link Active Study

Link series only within the active study to apply zoom, pan, scroll and optionally window level actions across series from the same plane. Window level linking must be enabled by the system administrator.

# Magnifying glass

See Magnifying glass for more information.

# Magnifying Glass

Click to enable the Magnifying Glass tool and magnify an area of an image. You can have up to four magnifying glasses open at a time.

# Mammography

See <u>Mammography CAD objects</u>, <u>Navigate Relevant Priors and Navigate Study List</u>, <u>Quadrant View and Fit to Window</u>, or <u>Toggle 2D and 3D views</u> for more information.

#### Fit to Window

Zoom the identified breast bounding box to fit the viewport and maintain "same size" on each viewport.

#### Mark Location

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Outline a region of interest with an ellipse and automatically add a line segment that measures from the edge of the ellipse to a landmark such as a nipple.

#### **Quadrant View**

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Divide the mammography image into four equally sized quadrants of "same size" to evaluate the entire breast in four separate sections.

#### Quadrant View Backward



Step through the four quadrants of the image moving backward (counterclockwise).



#### **Quadrant View Forward**

Step through the four quadrants of the image moving forward (clockwise).

# Toggle between 2D and 3D series



Switch between a tomosynthesis slice and the 2D reconstructed view for the selected series in a mammography study.



# Toggle CAD

Show or hide CAD data in mammography images.

# Markup Color Picker

#### Markup Color Picker



Use the Markup Color Picker on the toolbar to select a color for a measurement or annotation. Use the Markup Color Picker on the context

menu to edit the color of existing markup.

#### Manual Calibration

#### **Manual Calibration**



If the modality-provided calibration is not sufficient, manually set a calibration value for measurements.

#### Measurement tools

See Measurement tools for more information.

# **Angle Measurement**

Measure the angle between anatomical structures.

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- 1. Left-click to create the vertex.
- 2. Left-click twice more to set the end points of the angles arms.
- 3. To edit, click the measurement to select it and then drag the measurement handles.

# Cobb Angle Measurement

A Cobb angle is the angle formed at the intersection of the two lines, which typically intersect off-screen.



- 1. Left-click twice to draw the initial line segment.
- 2. Left-click twice more to draw the secondary line segment.
- 3. To edit the measurement, click the measurement to select it and then drag the measurement handles.

A dashed line connects the two segments and the Cobb angle, presented in degrees, is anchored to the connecting line.

#### Linear Measurement



Measure length in mm or measure time and velocity for echo ultrasound. Time doppler ultrasound regions will create peak velocity with a single click. Values are shown in mm and the source of the calibration is shown in brackets. For

more information on linear measurements in ultrasounds, see Ultrasound measurements.

- 1. Left-click to start the measurement and left-click again to end the measurement.
- 2. To edit, click the measurement to select it and drag the measurement handles.

#### Multi-Segment Measurement

Measure the distance of curved anatomical structures using multiple straight lines. Values are shown in mm and the source of the calibration is shown in brackets. Multi-segment measurements are not supported in advanced visualization modes.

- 1. Left-click to start the segment, and left-click again to set its endpoint. Repeat this process until the measurement is complete.
- 2. Double-click to end the measurement.
- 3. To edit, do either of the following:
  - To move a segment of the measurement, click and drag the segment handle.
  - To move the entire measurement, click between the segment handles and drag the measurement to the desired location.

#### Perpendicular tool

Use the perpendicular tool to draw two lines that intersect at a 90° angle and provide a measurement of each line. For example, use the Perpendicular tool to measure a nodule from top to bottom and from left to right.

- 1. Left-click to start the y-axis and left-click again to set its endpoint. Once the y-axis is drawn, a handle for the x-axis is automatically added.
- 2. Left-click to set each endpoint of the x-axis.
- 3. To adjust the measurement:
  - Drag the endpoint handles to lengthen or shorten the lines or to rotate the whole measurement.
  - Drag the center handle to change the intersection point for either axis.

Note that while the measurement can be rotated using the endpoint handles,





the intersection angle cannot be changed.

#### Ratio tool

Use the ratio tool to draw two separate lines and provide a measurement of each line as well as the ratio of the length of the first line (x) to the second line (y). That is, x/y. The ratio is calculated using the internal floating-point measurement value. The values that are displayed in the viewer are rounded to the nearest 2 or 3 decimal places (depending on if the value is less than or greater than 1).

X:Y

- 1. Left-click to start the first line (x) and left-click again to set its endpoint.
- 2. Left-click to start the second line (y) and left-click again to set its endpoint. The lines are connected with a dotted line to indicate that they are related.
- 3. To adjust the measurement:
  - Drag the endpoint handles to lengthen, shorten, or rotate the line.
  - Drag the center handle to move the line.

# Toggle Markup

Hide or show markup on images including markup on presentation states.

#### **ROI** tools

#### Circle ROI

Draw a circular region of interest. The source of the calibration is shown in brackets at the bottom of the overlay.

1. Left-click to start the measurement and left-click again to end the measurement.

2. To edit, click the measurement to select it and then drag the measurement handles.

# Ellipse ROI

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Draw an ellipse region of interest. The source of the calibration is shown in brackets at the bottom of the overlay.

- 1. Left-click to start the measurement and left-click again to end the measurement.
- 2. To edit a measurement, click the measurement to select it and then drag the measurement handles.

# Freeform ROI / Doppler Envelope

Draw a freeform region of interest. For cardiology, peak and mean velocity and peak and mean gradient are shown. The source of the calibration is shown in brackets at the bottom of the overlay. For information on using the Freeform ROI tool with ultrasound studies, see Ultrasound measurements.

- 1. Left-click to start the measurement.
- 2. Left-click on the first point selected or double-click to end the measurement.
- 3. To edit a measurement, click the measurement to select it and then drag the measurement handles.

#### **Point Tool**

--- Measure the value of a specific point. The unit of measure depends on the modality type. For example, in PET images it provides the SUV value, and in CT images it provides the Hounsfield units.

#### Rectangle ROI

Draw a rectangular region of interest. The source of the calibration is shown in brackets at the bottom of the overlay.

- 1. Left-click to start the measurement and left-click again to end the measurement.
- 2. To edit a measurement, click the measurement to select it and then drag the measurement handles.

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#### MPR/3D

For more information, see MPR / 3D.

#### Clip Box



Cut away some of the volume so that you can better see underlying anatomy. Drag down to move the plane into the volume (cut more). Drag up to move the plane out of the volume (cut less). Selecting one of the edges of the clip box the orientation of the clip box can be changed without changing its size or the orientation of the volume.

#### **Cut Plane**



Use the Cut Plane tool to cut away some of the volume at a custom rotation. Rotate the 3D volume to a desired view and click the Cut Plane icon. A cut plane normal to the current 3D view will be created. While in the cut plane mode, the cut plane can be moved into the volume by dragging the mouse down or out of the volume by dragging the mouse up.

# Scalpel Tool



Remove or isolate a section of an image by dragging the mouse along the border of the area to segment then clicking on the region you would like to keep.

# Multiphase



# Multiphase Tool

Split a multiphase series into multiple phase-based series or sort a multiphase series by phase.

# Navigation





Navigate study images using the mouse wheel, a left-click drag, touch drag, touch pad drag, or the up and down cursor keys.

# Triangulation

Navigate to a selected point in orthogonal series.

# Navigate Relevant Priors (Previous)

Open the previous relevant prior for the patient.

# Navigate Relevant Priors (Next)

Open the next relevant prior for the patient.

# Navigate Study List (Previous)

Open the previous study for the patient.

# Navigate Study List (Next)

Open the next study for the patient.

#### **Switch Studies**

Select a study to switch to. If you switch away from a study and then switch back to it, it is reopened to the state in which you left it.

# Paper Print

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See Paper Print for more information.

#### Paper Print

Print reports, images, or a set of images.

#### Red Free Filter



Turn on the red free filter to block red and blue wavelengths in color images.

#### Reference lines

See Reference Lines or Multiple Reference Lines for more information.

#### **Reference Lines**



Show where the selected image intersects other images from different planes.

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#### Multiple Reference Lines

Project reference lines from multiple series onto the selected series.

# Revert to original

# Revert to Original



Revert a series to its original presentation.

# Screen layout

See Screen Layout for more information.



#### Screen Layout

Access study compare mode or change the layout of each monitor.

# Series Reposition



# **Series Reposition**

Swap series between viewports.

# Series Page Backward / Forward



# Series Page Backward

Move to the previous series page.



# Series Page Forward

Move to the next series page.

## Spine Labeling

See Spine Labeling for more information.

#### Spine Labeling

Add spine-related labels to images. In Spine Labeling mode, the **Spine**Labeling tab is activated to provide access to other spine labeling tools.

## Toggle Spine Labeling Markup

Hide or show spine labels. Note that Toggle Markup also hides / shows spine labels.

# Delete All Spine Labels

Delete all spine labels in the study.

## Study Information

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See Study information panel for more information.

## Study List (if available)

Open a panel containing information grouped into the following tabs: Study List, Study Details, Report, and Notifications.

## Report / Comments

Open the study report in the Study Information panel, if available.

#### Ultrasound Measurements

See <u>Ultrasound measurements</u> for more information.

## Linear measurements in ultrasounds

Calibrated ultrasound images can use standard linear measurements. A single left mouse click starts the measurement and a second left click ends the measurement. To edit a measurement, drag the measurement handles.

When a linear measurement is placed within a region that has two different axes (i.e. units like time and velocity), it will show both units unless the measurement is parallel to one of the axes.

A special case exists for velocity-time Doppler Ultrasound regions. In this case, a single click will create the measurement by automatically snapping the other end-point to the zero-velocity axis.

- Moving the automatic end-point off the zero-velocity axis will transition the measurement into a standard Ultrasound linear measurement.
- Moving the user selected point will keep the automatic end-point locked, sliding it along the zero-velocity axis.

#### Freeform ROI in ultrasounds

The Freefrom ROI tool can be used to calculate the Doppler Envelope for velocity-time regions. ROIs will be locked to the zero-velocity axis and points can be added along the envelope. A double-click will end the ROI creation.

## Viewport Capture

#### Viewport Capture

Take a snapshot of the image in the selected viewport when you are in an advanced visualization mode. Viewport captures will be available in their own series and will include any modifications that were made to the original image such as markup, zoom, window level, etc.

#### **Delete Viewport Capture**

Delete the selected viewport capture as long as it has not already been saved. This button must be added to the context menu and will be available only after a viewport capture has been created.

#### Window Level

See Window Level for more information.



#### Window Level

Change the Window Level for the selected image. Note that for

mammography images, the viewport background retains its color when the Window Level is changed.

#### **Reset Window Level**

Reset the images to their original Window Level settings.

#### Window Level Presets

Select a predefined Window Level. Window Level presets are configurable by the system administrator.

## Window Level Scope

This feature must be enabled by the system administrator.

Change Window Level to apply to the study, the series stack, or only the image. By default, Window Level operations apply to the series stack.

## Zoom / Pan

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See Zoom / Pan Images for more information.

## Zoom / Pan

Zoom in on or pan an image in the selected viewport. When series are linked, zoom / pan is applied across all linked series.

## Viewer overview

The following section provides an overview of the viewer in eUnity™. Note that all features may not be available. Some features are enabled or disabled by your system administrator.

## Series tray



The Series Tray shows the available series for a study. From here, the series can be opened in the viewing area.

Series tray

#### Settings / user guide / viewer zoom

Note that the administrator can enable or disable any of the options / tabs in the Settings panel.

- Help: Open the online User Guide
- List Keyboard / Mouse Shortcuts: List your current keyboard and mouse shortcuts
- Zoom: Increase or decrease the size of the viewer components such as the toolbar, side panels, and series tray. Note that this feature does not affect the zoom factor for images in the viewer. Use the Zoom / Pan tool on the toolbar to zoom in on images.
- General Settings: Select options for saving Presentation States (Annotations / Markup, Window / Level, Spine Labels) and Key Images.
- Hanging Protocol: Edit hanging protocols
- Toolbar: Edit your toolbar
- Context Menu: Edit your context menu
- Keyboard Shortcuts: Edit your keyboard shortcuts
- Mouse Shortcuts: Edit your mouse shortcuts
- Screen Layouts: Edit your screen layout options
- Window Level Presets: Edit your Window Level presets

<u>Presentation</u> states

Customize the toolbar

Customize the context menu

Customize keyboard shortcuts

<u>Customize</u> mouse shortcuts

<u>Customize</u> screen layouts

Customize Window Level presets

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	version number and manufacturer information.	
3	Full screen mode  Expand the viewer to fill all available monitor space.	Screen Layout
4	Notifications  When a study is updated, the bell displays a red indicator to alert you that the study has changed.	Content change notifications
5	Screen Layout  Change to Study Compare mode, or change the number or monitors and viewports.	Screen Layout
6	Advanced visualization workflows  Access Advanced Visualization workflows such as 3D, MPR, MPR Advanced, and Fusion.  This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.	Screen Layout
7	Tools are categorized into different tabs. Tabs such a Spine Labeling, Mammography, and Advanced Visualization become available when these modes are activated.	Tools overview
8	Search screen  Access the eUnity Search screen.	Search in eUnity™
9	Study information panel  This panel contains information grouped into the following tabs: Study List, Study Details, Report, and Notifications. These panels can be enabled or disabled by the system administrator.	Study information panel

• About: See information about eUnity such as

## Viewport



Viewports are the individual partitions in the viewer. If a viewport is selected, it is outlined in orange. Double-click a viewport to enlarge the image and show it in one-up layout. Double-click again to return the viewport to its previous layout.

Screen Layout

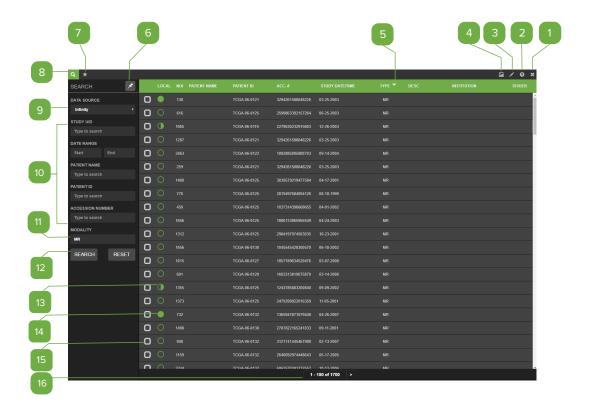
# Search

## Search screen overview

The following section provides an overview of the Search screen in eUnity™. Note that all features may not be available. Some features are enabled or disabled by your system administrator or, if you are using an older browser (Internet Explorer 8 and earlier) or if you have Compatibility Mode turned on in IE, you can access only the legacy Search screen.

The legacy search has all the functionality of the current search, with the exception of search templates, sort columns, collapse columns, hide / pin Search panel, or change theme.

Note: If the legacy Search screen is displayed and you are on a modern browser, it is most likely due to a site configuration setting. Contact your site administrator to enable the non-legacy search.



## Log out



Log out of eUnity.

See Log in and log out (desktop client) for more information.

#### Documentation

Click to open the eUnity User Guide.

See Document conventions for more information on the User Guide.

Change password

Change your system password. This feature must be enabled by the system administrator.

## Change Search screen theme

Note: Search screen themes are not supported in legacy search.

Change the Search screen from dark to light.

## Sort by column

Click a column to sort the Search list by that column. Click once to sort in ascending order. Click a second time to sort in descending order.

The column order is represented by the arrow in the column header.

- ascending
- descending

#### Pin the Search panel

Note: Hiding / pinning the search panel is not supported in legacy search

The search panel shows all of the search fields, and saved search templates.

- To pin the Search panel so that it is always visible, click
- To unpin the Search panel, so that it isn't visible when you
  navigate away from it, click
- ullet To access the Search panel when it is hidden, click  ${f Q}$



#### Saved searches



Your administrator may have pre-defined some common searches that can be accessed by clicking  $\bigstar$ . Note that saved searches are not available in legacy search.



#### Hide or show the Search panel

Click to hide or show the Search panel.

#### Select a data source



System administrators can configure eUnity™ to search remote data sources like a PACS. When remote data sources are available, they are shown in the Data Source dropdown list.

See Search in eUnity $^{\text{\tiny{M}}}$  for more information.

## Search fields



Enter search criteria in any combination of the search fields. Use the asterisk (\*) wildcard character in search fields to broaden search results. For example, entering 123\*5 in the Patient ID field returns all patients whose ID begins with 123 and ends in 5. The wildcard character can be at the start or middle of the string.

The search automatically puts an asterisk at the end of Patient Name and Patient ID searches.

See Possible search fields for more information.



#### Modality filter

Filter the search results by modality type.

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#### Search and Reset

After you have filled in the search fields, click Search to perform the search. Click Reset to clear all of the search fields.



#### Partially loaded in cache indicator

A half-filled circle indicates that the study is partially loaded in the

cache.

14

## Fully loaded in cache indicator

A filled-in circle indicates that the study is fully available in the cache.

15

## Multi-study selection

Click the checkboxes to select multiple studies for a patient. Then, click any of the selected studies to open them.

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## Search list pages

If there are multiple pages of results in the Search list, move backwards or forwards through the pages using the arrows.

# Search in eUnity™

To search from the eUnity Search screen, do the following:

- 1. Enter applicable criteria in the Search panel using any combination of the available search fields. If needed, you may use the asterisk (\*) wildcard character in search fields to broaden search results. For example, entering 123\*5 in the Patient ID field returns all patients whose ID begins with 123 and end in 5. The wildcard character can be at the start or in middle of the string. For more information, see the <a href="Possible search fields">Possible search fields</a> table
- 2. To filter results by modality type, click a modality in the Modality dropdown.
- 3. Click Search.

The results of the query are shown in the Search list. If there are multiple pages of information, page through the results using the **Previous** and **Next** buttons at the bottom of the screen.

#### Possible search fields

Note that site administrators can set constraints on search fields. If a search does not meet the constraints, a validation dialog will be displayed to indicate what properties are required for a valid search.

Search field	Notes
Date range	Search by study date or by using a date range in the following format: DD/MM/YYYY. Invalid formats will turn the box red. Alternatively, click the date field to select a pre-configured default or choose a range using the date picker.
Patient Name	Search by Patient Name.  The search automatically places an asterisk (*) at the end of the string.
Patient ID	Search by Patient ID.  The search automatically places an asterisk (*) at the end of the string.

Search field	Notes
Accession Number	Search by Accession Number.
Modality	Search by modality.  The list of searchable modalities is configured by the system administrator.
Referring Physician*	Search by Referring Physician Name.
Patient Birth Date*	Search by Patient Birth Date in the following format: DD/MM/YYYY. Invalid formats will turn the box red. Alternatively, click the date field to choose a date using the date picker.
Study Status*	Search by the status of the study.
Study UID*	Search by Study UID.
Study Description*	Search by Study Description.

<sup>\*</sup>Not available by default. Must be configured by the system administrator.

By default, the search list shows the following information for each study.

- Patient
  - Name
  - Patient ID
  - Patient Location
- Study
  - Accession Number
  - Date
  - Modalities in Study
  - Study Description
  - Referring Physician
  - Requesting Physician

# Open a study

From the results in the search list, launch a single study or compare two studies from the same patient .

- To quick launch a study, click on any row in the search list. This will immediately load the selected study into eUnity.
- To compare multiple studies, click on the empty checkbox that appears on the left side of each search result row. Selecting a row in this manner will add the study to the launch list. To launch the selected studies, click on any selected row. By default, the maximum number of studies that can be selected is 4.

By default, loading studies from different patients is not supported. If you select a study from a different patient, the launch list is reset.

# Open a remote study

#### Search for remote studies

In some cases, eUnity™ is configured to search beyond the local system to a remote data source like a PACS. When multiple data sources are configured, the **Data Source** field in the Search panel has a dropdown to select the desired source for searching. If only one data source is available, the dropdown will not be visible.

## Open remote studies

Depending on the eUnity integration with your DICOM archive, a full DICOM retrieve may be required before viewing a remote study. When this is the case, eUnity will display a "Downloading images" dialog. This dialog provides feedback on the state of the retrieve job. As images for the study arrive, the progress bar will approach 100%. When the retrieve job is complete, the dialog is closed and the full study is displayed. The dialog provides the following options:

- Click Cancel to return to the worklist
- Click View Partial Study to display the study data that has already been transferred. The
   Partial study dialog will be displayed to warn that not all images will be displayed. Click
   Yes to continue or No to finish downloading the images.

# User preferences

## Customize the context menu

Use the Context Menu tab in the settings panel to add, remove, or reorder context menu items or to make menu items available only for specific modalities. The context menu can be configured at a site, group, or user-level by the system administrator. Or, if the system administrator has enabled this feature for users, an individual user can configure their own context menu.

#### Add, edit, or delete menu items



#### NOTE

Clicking Reset will reset all context menu changes back to the defaults that were set by your system administrator. That is, all of your custom context menu settings will be reset.

- 1. In the upper-right corner of the viewer, click  $\equiv$  > Context Menu.
  - To add a menu item, click beside Context menu items. Select the item that you want to add and click **OK**.
  - To make a menu item available only for certain modalities, click . Choose the modality types and click OK.
  - To reorder a menu item, click the + handle and drag it to the desired position. The order of the menu items in the dialog is the order in which they appear in the context menu from top to bottom.
  - To remove an item from the context menu, click . If a menu item is removed, it can always be re-added.
- 2. If you are satisfied with your changes, click **Save**. To revert any changes you made since your last save, click **Cancel**.

# Customize keyboard shortcuts

Use the Keyboard Shortcuts tab in the Settings panel to add or remove keyboard shortcuts. Keyboard shortcuts can be configured at a site, group, or user-level by the system administrator. Or, if the system administrator has enabled this feature for users, an individual user can configure their own keyboard shortcuts.

## View keyboard shortcuts

To see the keyboard shortcut for a specific tool, hover your cursor over the tool on the toolbar. The keyboard shortcut is shown in brackets beside the tool name. To view a complete list of your keyboard shortcuts, do the following:

1. In the upper-right corner of the viewer, click  $\equiv$  > List Keyboard / Mouse Shortcuts.

## Add, edit, or delete keyboard shortcuts



#### NOTE

Clicking Reset will reset all keyboard shortcuts back to the default shortcuts that were set by your system administrator. That is, all of your custom keyboard shortcuts will be reset.

- 1. In the upper-right corner of the viewer, click  $\equiv$  > Keyboard Shortcuts.
- 2. To find a tool:
  - Type a tool name into the **Filter** field to find a specific tool.
  - Click  $\downarrow^{\mathbb{R}}_{\mathbb{Z}}$  to sort alphabetically by tool name.
  - Click 🏥 to sort by keyboard shortcut.
- 3. To add or edit a keyboard shortcut, click beside the tool name. Type the key combination you want to use. If the shortcut is already taken, a warning will display in the dialog. Click **OK**.

**NOTE**: The numbers along the upper part of the keyboard and the numbers on the number pad are treated as the same input. For example, if 9 is mapped to the LUNG W / L preset, pressing 9 in either location will apply the LUNG W / L preset.

- 4. To remove a keyboard shortcut, click  $\bar{\mathbb{m}}$  beside the keyboard shortcut.
- 5. If you are satisfied with your changes, click **Save**. To revert any changes you made since your last save, click **Cancel**.

## Restricted shortcuts

There are certain keyboard shortcuts (such as F12 or CTRL+L) that should not be set in eUnity because they are reserved for use by the browser. For more information about keyboard shortcuts used by your browser, see the browser's help documentation.

## Related

• Customize mouse shortcuts

# Customize mouse shortcuts

#### View mouse shortcuts

To view a list of the current mouse shortcuts, do the following:

1. In the upper-right corner of the viewer, click  $\equiv$  > List Keyboard / Mouse Shortcuts.

#### Add, edit, or delete mouse shortcuts



#### NOTE

Clicking Reset will reset all mouse shortcuts back to the default shortcuts that were set by your system administrator. That is, all of your custom mouse shortcuts will be reset.

- 1. In the upper-right corner of the viewer, click  $\equiv$  > Mouse Shortcuts.
- 2. To find a tool:
  - Type a tool name into the **Filter** field to find a specific tool.
  - Click  $\downarrow_z^{\mathbb{R}}$  to sort alphabetically by tool name.
  - Click to sort by mouse shortcut.
- 3. To add or edit a mouse shortcut, click beside the tool name. Select a mouse gesture and a modifier (Ctrl, Alt, or Shift) if desired. If the shortcut is already taken, a warning will display in the dialog. Click **OK**.
- 4. To remove a mouse shortcut, click beside the shortcut.
- 5. If you are satisfied with your changes, click **Save**. To revert any changes you made since your last save, click **Cancel**.

#### Restricted shortcuts

Left-drag is reserved for navigating images. To use left-drag for a mouse shortcut, it must be paired with Alt, Ctrl, or Shift.

#### Related

• Customize keyboard shortcuts

# Customize screen layouts

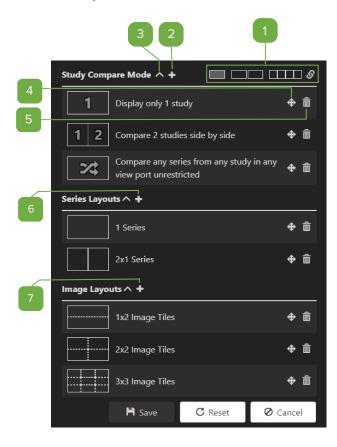
Use the Screen Layouts tab in the Settings panel to add, reorder, or remove screen layouts from the Screen Layout tool on the toolbar. Screen layouts can be configured at a site, group, or user-level by the system administrator. Or, if the system administrator has enabled this feature for users, an individual user can configure their own screen layouts.



#### NOTE

Clicking Reset will reset all screen layouts back to the default screen layouts that were set by your system administrator. That is, all of your custom screen layouts will be reset.

- 1. In the upper-right corner of the viewer, click  $\equiv$  > Screen Layouts.
- 2. Add study compare modes, series layouts, or image layouts. (See more details below.)
- 3. If you are satisfied with your changes, click **Save**. To revert any changes you made since your last save, click **Cancel**.



## Monitor layout

NOTE: Monitor layout applies only to study compare modes.

You can define a study compare mode per monitor layout (1, 2, or 4 monitor) or you can configure the same study compare modes across all monitor layouts. Select the monitor layout that you want to configure compare modes for.

1

For example, select single monitor and then click beside Study compare mode to add the study compare modes for single monitor.

Then, select 2 monitor and click to add the study compare modes for a two monitor layout, and so on.

If you customize study compare modes for any of the monitor layouts, and then click  ${\mathscr O}$ , all monitor layouts will be synchronized to the currently selected monitor layout. For example, if the 2 monitor layout is selected and then you click  ${\mathscr O}$ , the 1 and 4 monitor layouts will be synchronized to have the same study compare modes that are defined for 2 monitor. The viewer will provide a warning before it makes this change.

## Add study compare modes

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Study compare modes control the layouts when prior studies are in view in single or multi-monitor modes. eUnity comes with a predefined list of study compare modes. Click beside Study compare mode to see a list of available study compare modes. Select the compare modes you want to add and click OK.

3

## Collapse section

Click to collapse or to expand any of the sections in the panel.

#### Reorder

4

Click  $\ \Phi$  and drag the layout to the desired position. The order of the layouts in this panel corresponds to the order in which the layouts are displayed in the Screen Layouts tool on the toolbar.

#### Delete



Click beside the layout that you want to delete. If you delete a study compare mode, it will be available to re-add at any time. If you delete a series layout or image layout, you will have to manually recreate it to readd it.

## Add a series layout



Series layouts define the number of series to display from each study. There can be a maximum of 15 series layouts shown in the Screen Layout tool on the toolbar. Click beside Series layouts. Move your mouse across the grid to select the desired number of viewports and click to set it. Click **OK**. If the series layout already exists, a message will display in the dialog.

## Add an image layout



Image layouts define the number of images to display from a single series. These are also called image tile layouts. There can be a maximum of 6 image layouts shown in the Screen Layout tool on the toolbar. Click beside Image layouts. Move your mouse across the grid to select the desired number of viewports and click to set it. Click OK. If the image layout already exists, a message will display in the dialog.

# Customize the default presentation of the series tray

Customize how the series tray is presented when the viewer is first launched. The series tray can be configured at a site, group, or user-level by the system administrator. Alternately, if the system administrator has enabled this feature for users, users can configure their own series tray preferences.

- 1. In the upper-right corner of the viewer, click  $\equiv$  > General Settings.
- 2. Click in the Series tray section to expand it.
- 3. Select any of the following options:

Total Marila	
Text Mode	Select the default presentation for the vertical series tray.
	<ul> <li>Text mode: Represent series as text instead of thumbnails. If Text Mode is not selected, thumbnail view will be used instead.</li> </ul>
	When the series tray is horizontal (Top or Bottom), only thumbnail view is available. To see the difference between the thumbnail mode and text mode, see the <u>Series tray</u> overview.
Location	Select the default location for the series tray.
	• Top: Display the series tray horizontally across the top of the viewer.
	<ul> <li>Bottom: Display the series tray horizontally across the bottom of the viewer.</li> </ul>
	<ul> <li>Left: Display the series tray vertically on the left side of the viewer.</li> </ul>
	<ul> <li>Right: Display the series tray vertically on the right side of the viewer.</li> </ul>
	Note that the vertical series tray (Left or Right) displays on both the outer-left and outer-right monitors when you are in multimonitor mode.
State	Select the default state of the horizontal (Top and Bottom) series tray. The vertical series tray (Left or Right) is always

open until you manually collapse it by clicking

- Pinned open: The series tray is open and will remain pinned open.
- Open: The series tray is open and will close when you click outside of it.
- Closed: The series tray is closed and will open only when you click a study folder.

## Related

• Series tray

## Customize the toolbar

Use the Toolbar tab in the Settings panel to add, remove, or move tools. Toolbars can be configured at a site, group, or user-level by the system administrator. Or, if the system administrator has enabled this feature for users, an individual user can configure their own context menu.

## Add, edit, or delete tools



#### NOTE

Clicking Reset will reset all toolbars back to the default settings that were set by your system administrator. That is, all of your custom toolbar settings will be reset.

- 1. In the upper-right corner of the viewer, click  $\equiv$  > Toolbar.
- 2. Select the tab that you want to configure from the **Toolbar Tab** dropdown.
  - To add a tool, click beside Tools. Select the tools you want to add and click OK.
  - To move a tool to a new spot, click the  $\oplus$  handle and drag the tool to the desired position. The order of the tools in the dialog is the order in which they appear on the toolbar from left to right.
  - To remove a tool from the toolbar, click  $\overline{\mathbb{Q}}$  . If a tool is removed it can always be re-added.
- 3. If you are satisfied with your changes, click **Save**. To revert any changes you made since your last save, click **Cancel**.

# Customize Window Level presets

Use the Window Level Presets tab in the settings panel to add, edit, or delete window level presets. Window level presets can be configured at a site, group, or user-level by the system administrator. Or, if the system administrator has enabled this feature for users, an individual user can configure their own window level presets.

## View window level presets

To view a list of your current W / L presets, do the following:

- 1. In the upper-right corner of the viewer, click  $\equiv$  > Window Level Presets.
- 2. To filter the list, do either of the following:
  - In the **Modality** dropdown, select a modality so the list shows only W / L presets for that modality.
  - Type a value into the filter field to filter by a W / L preset name or value.

## Add a window level preset



#### NOTE

Clicking Reset will reset all window level presets back to the presets that were defined by your system administrator. That is, all of your custom window level presets will be reset.

- 1. In the upper-right corner of the viewer, click  $\equiv$  > Window Level Presets.
- 2. Click + beside Window Level Presets.
- 3. In the Add window level preset dialog select either of the following:
  - Choose Create custom to create a new W / L preset > Next. Add a Name, Window Width and Window Center value and click OK.
  - Choose Select from library to choose from the library of W / L presets > Next.
     Select the desired W / L presets from the list and click OK.
- 4. If you are satisfied with your changes, click **Save**. To revert any changes you made since your last save, click **Cancel**.

Edit, delete, or reorder a window level preset



## CAUTION

If you change or delete a window level preset it will be changed or deleted in any hanging protocol that uses it.

- 1. In the upper-right corner of the viewer, click  $\equiv$  > Window Level Presets.
- 2. Do any of the following:
  - To edit a W / L preset, click 🗹 beside the preset. Edit the values and click **OK**.
  - To remove a W/L preset, click beside the preset.
  - To change the position of a W/L preset in the list, click and drag the W/L preset to the desired location in the list. The location of the preset in the list corresponds to the order that the presets are shown in the W/L preset dropdown. It also corresponds to the order of the default W/L preset keyboard shortcuts (that is, number 1 in the list uses 1 as a keyboard shortcut, and so on).
- 3. If you are satisfied with your changes, click **Save**. To revert any changes you made since your last save, click **Cancel**.

# Dock or undock the side panels by default

- 1. In the upper-right corner of the viewer, click  $\equiv$  > General Settings.
- 2. Click in the Side panels section to expand it.
- 3. Select or clear the **Dock the side panels by default** checkbox.
- 4. Click Save.

## Related

• Study information panel

# Tools

## Annotation tools

Annotation tools allow users to apply markup to an image but do not supply any measurement information. These markups are added, removed, and edited in the same manner as the measurement tools. To cancel the annotation once you have started it, right-click or press the Esc key.

For information on using annotation tools in MPR / 3D, see <u>Annotations and measurements in MPR / 3D view modes.</u>

#### Arrow

To add an arrow annotation, left-click to start the arrow and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

#### Circle

To add a circle annotation, left-click to start the circle and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

## Ellipse

To add an ellipse annotation, left-click to start the ellipse and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

#### Freehand

To add a freehand annotation, left-click and drag the mouse. Let go of the mouse button to end the annotation. The freehand annotation cannot be edited.

#### Line

To add a line annotation, left-click to start the line and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's

handles to reposition.

## Polygon

To add a polygon annotation, left-click to start to start the polygon. Each additional left-click adds another point to the polygon. To end the polygon, double-click or left-click on the polygon start point. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

## Rectangle

To add a rectangle annotation, left-click to start the rectangle and left-click again to end it. To edit, click the annotation to select it and then drag the annotation's handles to reposition it.

#### **Text Annotation**

T Click the location that the text should start. A text box is displayed to enter up to 32 characters. To edit the text, double-click the annotation to select it and change the text. To move the annotation, drag it to a different location. Note that the Text Annotation tool cannot be used in Full Screen mode.

# Spine labeling

11/1

#### Spine Labeling

Add spine-related labels to images. In Spine Labeling mode, the **Spine Labeling** tab is activated to provide access to other spine labeling tools.

#### Toggle Spine Labeling Markup

Hide or show spine labels. Note that Toggle Markup also hides / shows spine labels.

## Delete All Spine Labels

Delete all spine labels in the study.



## Eraser

Erase a measurement or annotation.

## Related

• Markup Color Picker

## Cine

Use the Cine tool to play a series of images like a movie. When Cine is activated, you can select the target frame rate to control how quickly the Cine tool plays through the images. If the Cine module is present, eUnity™ attempts to play the series at the frame rate specified in the DICOM header.

A series must contain more than one image to activate the tool. By default, only one series at a time can display a Cine movie. When another series is selected, Cine plays the new series.

## Toggle Cine mode / Play video



Play a series of images in succession (like a movie) or play a video. When Cine / Video mode is activated, the Cine toolbar is displayed in the active viewport. The default location of the Cine / Video toolbar can be configured by the system administrator.

Note that while the button on the toolbar enables either Cine or Video mode (depending on the media type), the Cine toolbar differs between Cine and Video mode. For information on the video toolbar, see Video.

#### Cine toolbar

# $ight ightharpoons\Pi$

#### Play / Pause button

Located on the Cine toolbar, click to play or pause the Cine loop.

## Rock loop button



Toggle between looping through the images or rocking back and forth (that is, play from start to finish and finish to start).

#### Actual frame rate



The actual frame rate is displayed in the upper-right corner of the viewport. The actual frame rate is affected by a number of factors including the power of the client machine, memory, and data transfer rates.

# Target frame rate



Select the target frame rate for playing through images.



#### Trim slider

Trim the start or end frames of the series.

## **Current position**



Visual position of the current frame on the display slider.



#### Current frame

Textual identification of current frame position within the displayed series.



## Previous / Next Series

Open the previous or next series.

## Dropped frames indicator

The drop frames option can be optionally enabled by the site administrator. When enabled, it allows the Cine player to drop frames to achieve the desired frame rate.





## CAUTION

If the frame rate cannot be achieved, the frame rate label will show the actually achieved frame rate. If frames are dropped, a yellow Cine indicator is shown beside the frame rate label.

## Clone Series

#### Clone Series



Clone a series so that you can see a copy of the series and the original series in the viewer at the same time. As a shortcut, right-click and drag a series from the series tray into the viewing area to clone it.

#### Close Clones Series



Close the cloned series and remove it from the series tray.

Clone a series so that you can see a copy of the series and the original series in the viewer at the same time. Any annotations or measurements that are applied to the original series are also applied to the cloned series and vice versa, but any window / level adjustments are made only to the selected series. Your administrator determines the maximum number of cloned series that you can create.

Note that clones are only virtual, so the clones themselves cannot be saved as part of a presentation state, but any markup that is made to the clone will be made on the original series (when you refresh the viewer) and can be saved there. Since clones are virtual, this also means that if you click the Apply changes button (C) when you receive a content change notification, clones will be discarded.

## Note for toggling between tomosynthesis and mammography series

If you are viewing a clone of a tomosynthesis series and you switch to the corresponding mammography series using the  $^{20}$  tool, when you toggle back, the view toggles to the original tomosynthesis series, not the clone.

## Note for cloning in advanced visualization modes

You cannot clone a series once you are in an advanced visualization mode. Similarly, when a cloned series is displayed in an advanced visualization mode, you cannot close the cloned series.

#### Clone a series

The Clone Series tool may need to be added to the context menu or toolbar. For information on adding tools, see <u>Customize the context menu</u> or <u>Customize the toolbar</u> or contact your system administrator.

Note: Videos and key images cannot be cloned.

#### Do any of the following:

- Right-click and drag a series from the series tray into the viewing area. The series is cloned and shown in the viewing area.
- Right-click a series in the viewer and click **Clone Series** or select a series in the series tray and click on the Toolbar. Drag the clone from the series tray into the viewing area.

NOTE: If you are in structured layout mode, you must drag the cloned series into the viewing area (study slot) that contains the study that the series belongs to. See <a href="Study compare">Study compare</a>, structured layouts, and shuffle layout for more information.

#### Close a cloned series

To close a clone and remove it from the series tray, do either of the following:

- Right-click the cloned series in the viewer and click Close Cloned Series.
- Select the cloned series in the viewer or series tray and click  $\square$  on the toolbar.

#### Identifying cloned series in the viewer

Cloned series are marked by the Cloned Series indicator in the viewport and in the series tray thumbnail.



#### Cloned series indicator

Shown in the viewport and on the thumbnail of a cloned series.

The series number also changes to reflect the clone number. For example, if the DICOM number of the series is 3, and it was cloned 3 times, the clone series numbers will be 3 (1) and 3 (2) and 3 (3). This is shown in the annotation overlay (SE #: 3 (1)) and in the series label in the series tray.



# Close Study

#### Close Study

X

Close the study and remove it from the series tray and the Relevant priors and Switch studies lists, if they are enabled.

You can close studies when they are not relevant or when you want to view some different studies for the patient but you have reached the maximum number of loaded studies (i.e. studies in the series tray). You will not be prompted to save changes when you close a study, however, your changes (for example, annotations, window level adjustments, key images etc.) will be available if you reopen the study from the Study List.

The Close Study tool may need to be added to your toolbar or context menu. For more information, see <u>Customize the toolbar</u> or <u>Customize the context menu</u> or contact your system administrator.

- 1. To close a study:
  - Select the study in the viewer and click X on the toolbar.
  - Right-click the study in the viewing area or the study folder in the series tray and click **Close Study**. See the <u>Series tray</u> overview for an example of a study folder.

## Notes on Close Study behaviors

- Closed studies will not be available for the Navigate Study List, Navigate Relevant Priors, or Switch Studies tools (if those tools are enabled). To make a study available for those tools again, reload it.
- When you close a study, you will no longer receive change notifications for it.
- The Close Study tool cannot be used while you are in collaboration mode (if enabled).
- If you close a study in view while in a study compare mode, the viewport that contained the closed study will be left empty. (Note that this is not the case when you are in an advanced visualization mode.)
- If you close all studies that are in view, eUnity will display the left-most studies from the series tray in the viewing area.
- There must be more than one study loaded in the viewer for "Close Study" to be enabled. That is, you cannot close the only loaded study.

Notes on Close Study behaviors when studies are passed into the viewer from a worklist and have a status

- You cannot close the study that has a "NEW" or "CURRENT" status.
- If you close all studies that are in view, eUnity will automatically put the NEW or CURRENT study into the viewing area.

## Related

- View keyboard and mouse shortcuts
- Customize keyboard shortcuts
- Study List
- Series tray

### Collaboration

Share your screen with other participants across all supported eUnity™ platforms (desktop web browser and mobile devices). As no patient data (including images) pass through collaboration services, each participant must independently log in to eUnity in order to start or join a collaborative session. Note that collaboration is not available when eUnity is in multimonitor mode.

#### Share this Session



Share your screen with other participants across all supported eUnity™ platforms (desktop web browser and mobile devices).



#### CAUTION

While the collaboration server attempts to synchronize all clients, there may be issues related to networking that prevent the same image from being displayed to all users or the cursor location being represented equally to all clients. If using collaboration for a diagnostic consultation, always verify which image and feature is being discussed.

When collaborating, changes made to your view will be sent across to other participants. Similarly, changes made by other participants will be applied to your view. This includes cursors, markup, layout, thumbnail bar up / down and image manipulation such as Window Level and Invert. See below for the full list of shared actions.

The following actions are shared to (and from) other participants:

# 2D

- Cine
- Clone series
- Current on-screen studies / series / images
- Cursors
- Flip / Rotate
- Invert
- Layout
- Link Series
- Manual Calibration
- Mammography Fit to Window

- Mammography Quadrant View
- Markup\*
- Navigate
- Reference Lines
- Report panel
- Revert
- Series tray up / down / pinned
- Split Multiphase
- Study Information panel
- Triangulate
- Video\*\*
- Window/level
- Zoom/Pan

#### 3D

- 3D Clip box
- 3D Scalpel tool (segmentation)
- 3D Slice tool
- Curved MPR
- MPR/3D Actions
- MPR Navigation
- MPR Oblique tool
- Presets

#### Session indicators



#### Not connected

Collaboration is not yet connected or has failed to connect.



### Attempting to connect

Collaboration is attempting to connect to the collaboration server.

<sup>\*</sup>On mobile devices, markup creation is disabled, but mobile-based participants can still see markup created by desktop-based participants.

<sup>\*\*</sup>Video playback is not synchronized between devices in collaboration mode.



#### Connected

Collaboration is connected and working

#### Start a new session

To collaborate, both collaborators must have the same viewing environment. For example, if you have studies X and Y open in the viewer, and you start collaboration from study X, the collaborator must also be viewing X and Y. They cannot have only study X open in the viewer.

- 1. Log in to eUnity.
- 2. Open desired study or studies.
- 4. To quickly share the session with other users, copy the session URL and send it to other users.

# Join an existing session

Guest access is currently not supported.

- 1. Log in to eUnity. Do either of the following:
  - $^{ullet}$  Open the study or studies that are being viewed by other participants. Click
  - Click Paste the URL that another user has shared with you in to the browser address bar.

When the collaboration indicator has turned green , you have joined the session and your view should synchronize to match the other participants.

#### Leave a session

1. Click When the collaboration indicator turns red , you have left the session Anything you do from that point forward is not shared with other participants.

# Content change notifications

This feature must be enabled by the system administrator.

Content change notifications alert you when a study has changed outside the viewer and presents you with the option of loading the changed study into the viewer.

**NOTE**: If you receive a content change notification and you click to apply the change, you will delete any clones, split series, key images, or viewport captures that you have created in your current viewing session.

### Content change notifications enabled



When enabled, a bell icon is displayed in the upper-right corner of the toolbar in the viewer.

# Study update available

Depending on your site's configuration, content change notifications are shown in one of two ways:

- in a text notification on the toolbar and in the Study Information panel
- only in the Study Information panel



When a study update has occurred, the bell icon displays a red mark (

to indicate a change was detected. Click the bell icon to open the Notifications tab in the Study Information panel. This panel displays additional information about the updated study. As well, the following options are presented on the toolbar:

- C Apply the change to the view
- X Dismiss the notification

# Demographics

The content and location of demographics in the viewer are controlled by the system administrator.



# Toggle Demographics

Hide or show demographics in the viewport.

# Download DICOM Study

# **Download DICOM Study**

Download the selected study to your local machine as a DICOM file contained in a zip file.

If this feature is enabled, you can download the selected study to your local machine. The downloaded study (that is, all of the viewable images, associated reports, Key Images, and any Presentation States) will be downloaded to your local machine as raw DICOM files contained in a zip file with the naming format <patient id>\_<study date>\_<study description>.zip. Note that DICOM images will not be viewable on your local machine without a DICOM viewer.

The zip file also contains a readme.txt file that includes the number of images in the study, a list of downloaded image files, and the number of images downloaded. The file also shows the overall status of the download (that is, success, fail, or completed with errors). If there were any errors encountered while downloading images, the names of the missing images and their associated errors will be recorded in the readme file. For increased visibility when there is an error, the zip file will also contain a download-error.txt file that lists the errors and the images that failed to download.

#### To download a study:

- 1. In the viewer, select an image from the study you want to download.
- 2. On the **Export** tab, click ••
- 3. If prompted, enter a password for the zip file. Do not use your login credentials for the password. This password will be required to decrypt the downloaded zip file. If you are not prompted for a password, it is because the administrator has not enabled encryption for downloaded studies.
- 4. Click **Download**. The zip file will be downloaded and stored according to your browser's settings. Typically, files are saved to the Downloads folder on your local machine.



#### NOTE

If the system administrator has enabled AES-256 encryption, you will require third-party software such as 7zip, WinZip, or WinRAR to decrypt the zip file and extract the contents. Otherwise, native extraction tools can be used to decrypt and extract the contents the zip file.

# Export

Export an image in PNG or JPEG format. Only demographics that are burned in to the image are exported. That is, demographic overlays and user-added annotations are not exported.



#### Export image to JPEG / PNG

Export an image to your local device in JPEG or PNG format.

#### Export an image



#### CAUTION

Exported files are not diagnostic quality images.

- 1. Click the image to export.
- 2. On the **Export** tab, click  $\stackrel{1}{\checkmark}$
- 3. In the Export Image dialog, click either JPEG or PNG. If you choose JPEG, adjust the quality slider to increase or decrease the image quality.
- 4. Click Export. The file is exported to your default Download folder.

When exporting images, any presentation state-related markup will not appear on the image.

# External viewers

Administrators can configure eUnity™ to launch an external viewer from the right-click menu. The external viewer will be launch using the study that is currently loaded in eUnity.

#### Launch an external viewer

- 1. To launch an external viewer, right-click in the viewing area.
- 2. Select the desired viewer from the right-click menu. The external viewer launches the currently loaded study.

#### Related

• Customize the context menu

# Flip and Rotate

The flip and rotate tools can be accessed on the Flip + Rotate tab. Toggling a presentation state on or off will revert an applied rotate.

Flip (Horizontally)

Click to flip the image horizontally in the viewport.

Flip (Vertically)

**Rotate Left** 

Click to flip the image vertically in the viewport.

Click to rotate the image counter-clockwise in the viewport.

Rotate Right

Click to rotate the image clockwise in the viewport.

Free Rotate by Drawn Angle

Rotate the image by a custom amount in the viewport. Draw a line to rotate the image.

#### Note about rotating mammography images

- If a 2D mammography series is rotated and the user clicks the 2D / 3D toggle button, the 3D image will also be rotated, and vice versa.
- If the studies in view are hung using a hanging protocol that has the Navigation mode set to "Navigate through Related Series," and there are multiple related series stacked, then rotating one of the stacked series will rotate all related / stacked series.

#### Free rotate an image

- 1. On the **Flip + Rotate** tab, click
- 2. Left drag the mouse across the image.
- 3. Move the mouse left or right to create an angle to the perpendicular of the image. This angle corresponds to how the image will be rotated.
- 4. Once the desired angle is achieved, let go of the mouse button. The image is rotated to the desired orientation.

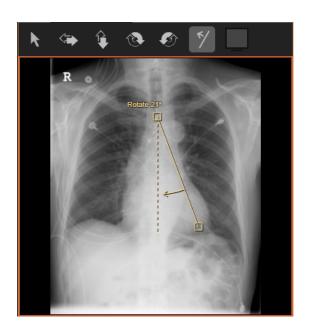


Figure 1: Left drag to set the free rotate angle



Figure 2: Release the mouse button to rotate the image to the set angle  $\,$ 

# Image sharpening

The image sharpening tool contains a number of preset sharpening algorithms that are defined by the site administrator. In the case where a study contains multiple modalities, the image sharpening dropdown shows only the presets for the modality of the currently selected series. If the selected series has no presets, image sharpening is disabled.

# **Image Sharpening Presets**

 $\triangle$ 

Click to apply a preset sharpening algorithm on an image in a viewport. Presets are configurable by the system administrator.

# $\blacktriangle$

# Image Sharpening indicator

Shown in the viewport to indicate that image sharpening is applied.

# Apply or remove image sharpening

- 1. Click a series to select it.
- 2. Click and select a preset from the dropdown. The image sharpening indicator appears in the viewport.
- 3. To remove image sharpening, click  $\triangle$  and click none in the dropdown.

# Invert

Use the Invert tool to invert image channels. When applied to a waveform, the invert tool will toggle the color scheme between light and dark themes. In mammography studies, the viewport background retains its color when an image is inverted.

# Invert Brightness

Click to apply a monochrome inversion to the selected series.

# Invert an image

- 1. Click the series to invert.
- 2. Click . The images in the series are inverted.
- 3. To revert inversion, click again. The Reset Window and Level tool will not reset the invert state of an image.

# View keyboard and mouse shortcuts

To view a list of your current keyboard and mouse shortcuts do the following:

1. In the upper-right corner of the viewer, click  $\equiv$  > List Keyboard / Mouse Shortcuts.

# Key Images

#### Key images overview

In  $eUnity^m$ , you can manually create key images using the "Create key image" option in the context menu or you can configure eUnity to automatically create key images each time you add markup to an image. Key images are shown in a dedicated series in the series tray. The key images series thumbnail in the series tray shows the unsaved key image indicator (the save icon with the vertical arrow). The upper-left corner of the icon shows the total number of key images.

Whether created manually or automatically, key images are added to the key images series as unsaved, temporary images. Key images must be saved before you do any of the following actions, otherwise, they will be lost:

- end your viewing session
- start a collaboration session
- load a different presentation state
- click the Apply changes button ( ) when you receive a content change notification



#### Key images series in series tray

When you create key images, they are added to their own series in the series tray. The number in the upper-left corner indicates the total number of key images. The number in brackets with the asterisk indicates how many of the key images are unsaved.

#### Key image indicators



#### Key image indicator

Shown in the viewport to indicate that it is a key image.



# Source image indicator

Shown in the viewport on the source image from which a key image was created. The number represents the number of derived key images.



#### Unsaved key image indicator

Shown in the viewport on a manually created, unsaved key image.



#### Unsaved auto-generated key image indicator

Shown in the viewport on an automatically generated, unsaved kev image.

#### Automatically create key images when you add markup or measurements

Set eUnity to automatically create key images from images that you add markup to. When key images are automatically created, they are added to the key images series as unsaved, temporary images. Key images must be saved before the session ends, otherwise, the changes are lost.

Turn on automatic key image creation and configure which types of markup will trigger it by doing the following:

- 1. In the upper-right corner of the viewer, click  $\equiv$  > General Settings.
- 2. Select the **Automatically create key images** option. By default, all available tools are selected.
- 3. Select or clear the checkbox for individual ROI tools, Markup tools, or Measurement tools. When any of the selected markup types are added to an image, eUnity will automatically mark those images as key images.
- 4. Click Save. To revert any changes you made since your last save, click Cancel.

Note: Clicking Reset will reset all key image settings back to the defaults that were set by your system administrator. That is, all of your key image settings will be reset.

#### Manually create or delete key images

When you mark an image as a key image, it is added to the Key images series as an unsaved, temporary image. Key images must be saved before the session ends, otherwise, the changes are lost.

- 1. Do either of the following:
  - Right-click the image > P Create Key Image.
  - Use a keyboard shortcut. You can see a list of keyboard shortcuts by clicking > List Keyboard / Mouse Shortcuts. Note that the same keyboard shortcut is used for both deleting and creating key images (the delete action is initiated when the Key images series is selected in the series tray).

The image is marked with the Source image indicator in the viewport  $^{1}$   $\nearrow$ 



# Delete key images

If you have not yet saved a key image, you can delete it from the Key image series in the series tray. The P Delete key image tool may need to be added to your context menu. For more information, see Customize the context menu or contact your system administrator.

- 1. In the series tray, click the Key image series to open it in the viewer and scroll to the key image that you want to delete. Do either of the following:
  - Use the same keyboard shortcut that you use to create key images.
  - Right-click the key image and click PDelete key image.

If you delete all key images, the Key image series will be removed from the series tray.

### Save key images

The Save dialog is used to save both key images and presentation states. Key images are saved in a key images series which can be accessed in the series tray. See View key images.

**Note**: Any options that are not selected in the Save dialog will be reverted. For example, if you do not select Spine labels, all unsaved spine labels will be removed from the study. Or if you do not select Save new key images, unsaved key images are discarded. Unsaved items are listed at the bottom of the Save dialog.

- 1. To save key images, click  $\blacksquare$  in the series tray.
- 2. In the Save dialog, select any options (described in the table below) and click Save.

After you save, eUnity checks the destination system to ensure the presentation state or key object was successfully saved. In rare cases (for example, a timing issue) eUnity may not be able to find the saved object when it rechecks. Consequently, the presentation state or key object is removed from the view. If this happens, and your annotations are removed from view after a save, it is likely that the save was successful, but you should contact your system administrator to make sure.

#### Set default Save dialog options

Set which options are selected by default in the Save dialog. For more information on each of these settings, see the <u>Save dialog options</u> table below.

- 1. In the upper-right corner of the viewer, click  $\equiv$  > General Settings.
- 2. Select any of the following:
  - Annotations / Measurements / Text
  - Window / Level (this option must be enabled by an administrator)
  - Spine labels
- 3. At the bottom of the Save dialog options section, click Save.

# Save dialog options

(applies to presentation states)	
Annotations / Measurements / Text	Select to save annotations, measurements, and text.
Window / Level	Select to save window / level adjustments.  Note that this option must be enabled by an administrator.
Spine labels	Select to save spine labels.
(applies to Presentation States)	
All images	Select to save the selected types of changes on all images.
Images used to create key images	Select to save the selected types of changes only on key image sources (that is, the images that key images are derived from).  Changes on images that are not marked as key images will be discarded.
(applies to key images)	
Save new key images	Select to save any newly created key images. If this option is not selected, the changes are saved as a presentation state only and any unsaved key images are discarded.

# View key images

Key images in eUnity are stored in a dedicated series that can be viewed from the series tray. In thumbnail view, the key images series is at the end of the series list and is marked with a key icon. As well, the number of images in the series is shown in the upper-left corner. The demographic overlay on a key image shows the original image number, frame number (if applicable), and series number.



# Key images series in series tray

When you create key images, they are added to their own series in the series tray. The number in the upper-left corner indicates the total number of key images. The number in brackets with the asterisk indicates how many of the key images are unsaved.

Figure 3: Key images series in the series tray

- 1. To view key images, open the series tray.
- 2. Click the key images series.

# Linking

eUnity provides linking tools so that you can perform common operations (navigate, zoom / pan, and optionally Window Level) across linked series. When you turn on Link mode, series are automatically linked by image plane (that is, all axial series are linked, all coronal series are linked, and all sagittal series are linked). When you scroll to navigate in one series, you will also scroll in all series that are part of the same link group. See more information on other Linking behaviors below.

The tool that you use to link series depends on if you want to link series across all studies (Link Studies) or if you want to link series only in the active study (Link Active Study). The Link Active Study tool may need to be added to the toolbar or context menu. For information on adding tools, see <u>Customize the context menu</u> or <u>Customize the toolbar</u> or contact your system administrator.

P+	Link Studies
	To link series across all studies, click 🕰
Alt	Pause linking across all studies
	To temporarily unlink series across all studies, press the Alt key on the keyboard while you navigate, zoom, pan or adjust window level. Linking will be resumed when you release the Alt key.
P	Link Active Study
	To link series only in the active (selected) study, click ${\mathscr S}$
Alt	Offset linking in the same study
	Press and hold the Alt key on the keyboard to temporarily pause linking while you navigate series that are linked within the same study. When you release the Alt key, the series are linked at the new offset location, and linked navigation is resumed. The link offset indicator $(^{\circ\circ})$ will display in the viewport on the image where the offset started.

through the image stack until you reach the slice where the offset started, then, release the Alt key. Alternately, close the viewing session.

### Indicators

#### Not linked

Shown in the viewport, a broken link indicator means that no matching slice could be found between the series. By default, the slices in linked series need to be within 5mm of each other to be considered for linking. If slices exceed the maximum threshold, the series will not be linked, and the broken link indicator will be displayed.

#### Series linked

Shown in the viewport, a link indicator means the series is successfully linked.

#### Link offset

Shown in the viewport, the link offset indicator means that the series' navigation has been manually offset from other linked series in the same study. That is, series linking was manually disengaged then the user navigated to a new point in the image stack and then relinked the series.

#### Offset not linked

Shown in the viewport, the offset broken link indicator displays when the series are no longer linked after a link offset is applied.

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# Linking behaviors

# Navigation

For series that share frames of reference (that is, when the series contain information about the current anatomical position), the linked series will jump to the same slice position as the selected series. If a linked series does not have a slice within 5mm of the selected series location, the link is broken and the  $\mathcal{O}$  indicator is displayed in the viewport.

Series that do not share frames of reference will simply navigate from whatever starting position they are at. If the series are out of sync, you can temporarily disengage linking by pressing the Alt key and scrolling the mouse wheel to manually re-sync them.

If a series contains multiple planes, eUnity tries to find the closest slice that is the same orientation to the navigating series. If none is found, the link is broken and one of the broken link indicators is displayed in the viewport.

Images without a plane will be linked under a separate linking group.

# Zoom and pan

In Link mode, the current zoom factor and panning position is used from each on-screen image. Zooming and panning of the images is then relative to the selected image. That is, if you have already zoomed in or panned one image, that zoom / pan will not reset to its original state once linked. It will keep zooming and panning from its current state.

#### Window level

For window level operations, series are linked by image plane and modality. That is, window level adjustments are only applied to series if they are both the same image plane and the same modality type. Note that window level linking is not turned on by default. It must be enabled by an administrator.

# Magnifying glass

The magnifying glass magnifies an area of an image without markups and overlays. When activated, the magnifying glass is initially applied to the image in the currently selected viewport, but can be dragged into any other viewport. You can have up to 4 magnifying glasses open at a time.

Note: If you change layouts, magnifying glasses are removed from any viewports that are removed by the layout change.

## Magnifying Glass

(Click to onable

Click to enable the Magnifying Glass tool and magnify an area of an image. You can have up to four magnifying glasses open at a time.

# Turn on the magnifying glass

- 1. Select the viewport that contains the image to magnify.
- 2. Click to turn on the magnifying glass tool and drag the magnifier to the desired location.
- 3. Place your cursor over the magnifier and roll the scroll wheel to zoom in on the area.

#### Add additional magnifying glasses

1. To add another magnifying glass (up to 4), click on the magnifier. Drag additional magnifiers to their desired locations.

#### Remove magnifying glasses

1. To remove all magnifying glasses, click again. To remove only one, click on the magnifier.

# Mammography

# Mammography overview

eUnity™ supports the display of mammography images / exams with modality type as MG or CR and one of the following SOP class UIDs:

- Digital Mammography X-Ray Image Storage for Presentation (1.2.840.10008.5.1.4.1.1.1.2)
- Breast Tomosynthesis Image Storage (1.2.840.10008.5.1.4.1.1.13.1.3)
- Computed Radiography Image Storage and other DICOM elements, Organ Exposed=Breast, Body Part Examined=Breast (1.2.840.10008.5.1.4.1.1.1)

Mammography images with the following SOP class UID are not displayed by default. If desired, contact your system administrator to have this SOP class configured to be viewable.

• Digital Mammography X-Ray Image Storage - for Processing (1.2.840.10008.5.1.4.1.1.1.2.1)

#### Mammography tools

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

This section provides an overview of the mammography tools. See <u>Mammography CAD</u> <u>objects</u>, <u>Navigate Relevant Priors and Navigate Study List</u>, <u>Quadrant View and Fit to Window</u>, or <u>Toggle 2D and 3D views</u> for more information.

# Fit to Window Zoom the identified breast bounding box to fit the viewport and maintain "same size" on each viewport. Toggle between 2D and 3D series Switch between a tomosynthesis slice and the 2D reconstructed view for the selected series in a mammography study. Toggle CAD Show or hide CAD data in mammography images. Quadrant View

Divide the mammography image into four equally sized quadrants of "same size" to evaluate the entire breast in four separate sections.

#### Quadrant View Backward



Step through the four quadrants of the image moving backward (counterclockwise).

# **a**

#### **Quadrant View Forward**

Step through the four quadrants of the image moving forward (clockwise).

# Mammography indicators

The following indicators may be displayed in the viewport when viewing mammography studies:

CAD: Calc: 2 Mass: 1	CAD markers displayed
	Shown in the viewport to indicate that CAD markers are displayed. The numbers represent the count for every type of displayed marker.
CAD: No Findings	No CAD findings
	Shown in the viewport to indicate that CAD markers are NOT displayed. That is, CAD exists, but there are no findings to display for the image.
CAD: FAIL	Error with CAD information
	Shown in the viewport to indicate that CAD markers are NOT displayed. That is, a fatal error with CAD information.
No CAD for Image	Image not related to CAD
	Shown in the viewport to indicate that CAD markers are NOT displayed. That is, the image is not related to CAD.
No CAD for Study	No CAD in study
	Shown in the viewport to indicate that CAD markers are NOT displayed. That is, there is no CAD in the study.

#### Case Score

#### Percentage of certainty of malignancy

The case score displays the algorithm's level of confidence, per study, that the study has malignant findings.

#### Name and version of CAD algorithm

If enabled, the name and version of the Al algorithm that is used for CAD objects is shown as part of the CAD overlay.

#### Quadrant View indicator

When in Quadrant View mode, this indicator is shown in the viewport on the non-breast wall side to indicate which quadrant of the breast is currently visible.

#### Related series indicator

In mammography studies, if the hanging protocol is set to Navigate Related Series, images of the same view type are stacked in the same viewport. This indicator is shown in the viewport to indicate how many images are stacked in the viewport and where you are in the stack.

System administrators can configure eUnity to include tomosynthesis images with the same view type in related series stacks.

#### Tomosynthesis indicator

Shown in the viewport for breast tomosynthesis studies to show the location of the current slice in relation to the other images in the series. The indicator shows directional markers to indicate whether you are scrolling in a caudal / cranial, or a medial / lateral direction. If CAD objects are available, the indicator will show additional lines to show which slices contains the CAD objects.

# Mammography base view









#### WARNING

When the breast zoom to fit feature is applied on a series basis, the resulting zoom to fit action on the images with different orientation may zoom the anatomy of any of the images out of the field of view.

To avoid this, create a hanging protocol to split out the images of the series into single series so each series consists of a single orientation.

When a mammography study is first opened, eUnity automatically presents a consistent layout for evaluation and interpretation. This default layout is referred to as base view. eUnity will not apply the base view to mammography studies if the following required DICOM attributes are missing, and the Orientation Marker is set as an Unknown View.

- Patient Orientation (0020,0020)
- Image Laterality (0020,0062)
- View Code Sequence (0054,0220)
- View Code Modifier Sequence (0054,0222), when present

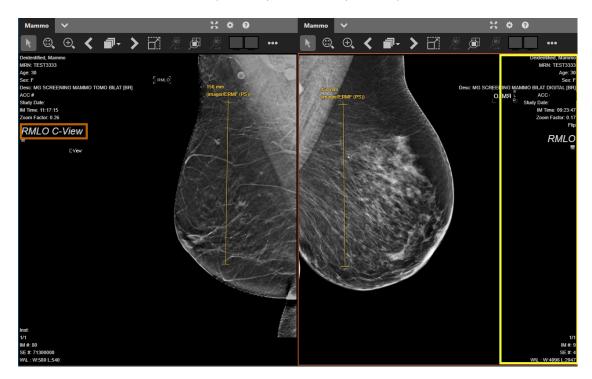


Figure 4: eUnity mammography base view

Ventral view

The viewer displays the left breast with the nipple pointing to the right of the viewport and a right breast displays the nipple pointing to the left of the viewport.

#### Chest wall alignment

The chest walls are aligned to the viewport edge.

#### Same size

Images are scaled in the viewport so that images from the same patient, performed at different times on different detectors can be displayed at the same size. This allows for evaluation of developing densities and allows the radiologist to evaluate for a change in size of known lesions during temporal comparison with prior digital images or even film mammograms. See the yellow measurement lines in the above image.

#### Demographic overlay

The viewer shows the demographic overlay opposite the chest wall by default so it does not cover the relevant anatomy. The demographic overlay is outlined in yellow in the above image.

#### Orientation marker

The orientation marker is always shown opposite the chest wall and it cannot be turned off. If C-View (Hologic: Synthesized 2D Mammographic Imaging) is present, it is added to the orientation marker so that the user is always aware that they are viewing a synthesized image (for example, RCC C-View). The orientation marker is outlined in orange in the above image.

#### Flip images

eUnity always flips images that would otherwise present upside down. When an image is flipped, the viewer shows the rotate indicator in the viewport.

#### Breast tomosynthesis viewing

eUnity shows a breast tomosynthesis indicator in the viewport to show the type of breast tomosynthesis and location of the current slice in relation to the other images in the series.

# Air gap suppression

eUnity uses air gap suppression so that the air gap area (the viewport background) retains its color when the Window Level is changed or an image is inverted in a mammography study. For air gap suppression to work, the image cannot be a secondary capture, color, or lossy and the Pixel Padding Value (0028,0120) and Pixel Padding Range Limit (0028,0121) tags must be populated in the DICOM header. If these values are missing or incorrect, air gap suppression may not work as expected. Note that air gap supression can be disabled by a system administrator.

# Mammography CAD objects

eUnity™ supports the display of Mammographic Computer-Aided Detection objects. Mammo CAD markers are not displayed on key images, on printed images, or under the Magnifying Glass. See the Mammo CAD markers and outlines table below for information on what each marker means.

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.



#### Toggle CAD

Show or hide CAD data in mammography images.

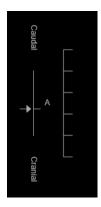
### Turn on CAD objects

1. To turn on CAD objects, on the **Mammo** tab, click \*>. CAD markers are displayed on the image.

#### View CAD objects on a tomosynthesis slice

Depending on the CAD manufacturer, CAD objects may be displayed on both the synthetic 2D image and on the individual tomosynthesis slices. The tomosynthesis indicator contains a line for each CAD finding to indicate where in the stack the CAD objects are located. To see the CAD marker on a specific slice in a breast tomosynthesis stack, do the following:

- 1. On the **Mammo** tab, click \* to turn on CAD objects.
- 2. Scroll to the slice that contains the CAD object.
- 3. Click to view the synthetic 2D image.



# Tomosynthesis indicator with CAD finding

Shown in the viewport for breast tomosynthesis studies to show the location of the current slice in relation to the other images in the series. The indicator shows directional markers to indicate whether you are scrolling in a caudal / cranial, or a medial / lateral direction. If CAD objects are enabled, the indicator will show additional lines to show which slices contains the CAD objects.

#### Mammo CAD markers and outlines

Note that CAD outlines can be enabled or disabled by administrators. Certain vendors may not display markers, outlines, or the certainty of finding percentage for CAD objects. See Vendor-specific display below for more information.

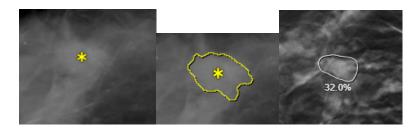


Figure 5: CAD marker (left) CAD outline (center) and CAD outline with certainty of finding percentage (right)

<b>A</b>	Calcification cluster
Δ	Individual calcification
*	Mass (density)
<b>*</b>	Mass with calcifications
32.0%	Outline with certainty of finding percentage  Outlines can either trace the boundary of the CAD finding or show the general region of the finding. The certainty of finding represents the algorithm's confidence, expressed as a percentage, that the detected lesion is malignant. For information how the certainty of finding percentage is calculated, see the CAD vendor documentation.

# Vendor-specific display

R2

No outlines are displayed by default (that is, only markers are shown).

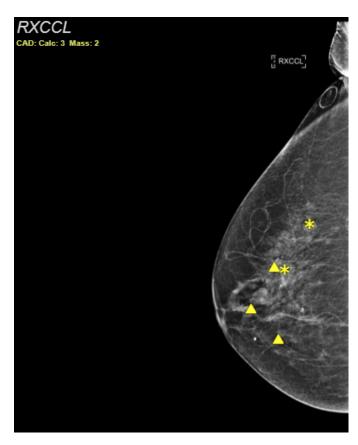


Figure 6: CAD markers shown with no outlines

### Hologic and iCAD

Outlines are displayed. If the CAD object doesn't contain an outline, the viewer will fall back to showing the CAD marker.

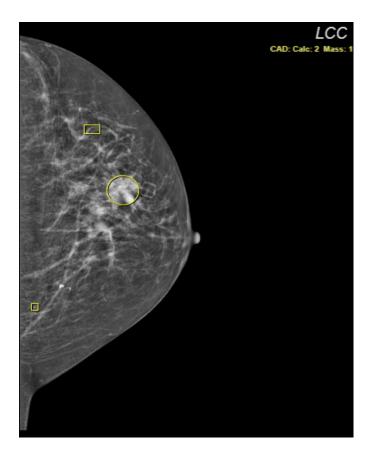


Figure 7: Outlines displayed with no markers

#### Mammo CAD indicators

Mammo CAD indicators are shown in the viewport to give additional information about the CAD objects.



Figure 8: Example of Mammo CAD indicator in the viewport

# CAD markers displayed

CAD: Calc: 2 Mass: 1

Shown in the viewport to indicate that CAD markers are displayed. The numbers represent the count for every type of displayed marker.

CAD: No Findings

# No CAD findings

Shown in the viewport to indicate that CAD markers are NOT

displayed. That is, CAD exists, but there are no findings to display for the image.

#### Error with CAD information

CAD: FAIL

Shown in the viewport to indicate that CAD markers are NOT displayed. That is, a fatal error with CAD information.

#### Image not related to CAD

No CAD for Image

Shown in the viewport to indicate that CAD markers are NOT displayed. That is, the image is not related to CAD.

#### No CAD in study

No CAD for Study

Shown in the viewport to indicate that CAD markers are NOT displayed. That is, there is no CAD in the study.

## Percentage of certainty of malignancy

Case Score

The case score displays the algorithm's level of confidence, per study, that the study has malignant findings.

#### Name and version of CAD algorithm

If enabled, the name and version of the Al algorithm that is used for CAD objects is shown as part of the CAD overlay.

#### Quadrant View and Fit to Window

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

#### Fit to Window



Zoom the identified breast bounding box to fit the viewport and maintain "same size" on each viewport.

#### **Quadrant View**



Divide the mammography image into four equally sized quadrants of "same size" to evaluate the entire breast in four separate sections.

#### Quadrant View Backward



Step through the four quadrants of the image moving backward (counter-clockwise).



#### **Quadrant View Forward**

Step through the four quadrants of the image moving forward (clockwise).

#### About Quadrant View and Fit to Window



#### WARNING

While the Fit to Window and Quadrant View tools can be used to view images, it is not intended to be the default and only method to view images. Never view an entire study in these modes as it risks not seeing the entire original image.

The Quadrant View and Fit to Window tools are available in Mammography mode to zoom in on a breast image for diagnostic reading. These tools can be turned on after initial load or invoked as an action of a hanging protocol. Quadrant View and Fit to Window maintain the "same size" property, so images in different viewports may be updated with a new zoom factor whenever the screen layout is changed, the series is navigated, or a new series is dragged in.

The Fit to Window and Quadrant View tools calculate the area that contains anatomical content for each image in a mammography study. The output of these tools' calculation creates a Breast Bounding Box for each image that is zoomed to fit whole breast area or breast quadrant area to each viewport when the tool is activated.

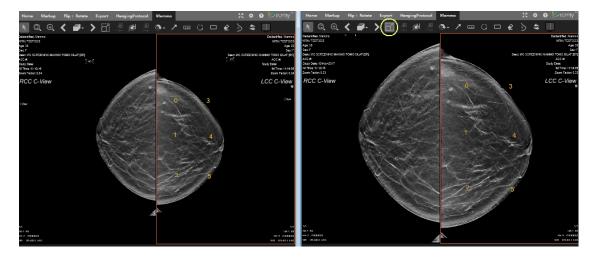
**NOTE**: Fit to Window and Quadrant View cannot be applied if any of the following conditions are met. In any of these cases, these images are reverted to "image fit to viewport" and the tools are disabled.

- The DICOM object does not contain pixel spacing.
- The image contains an invalid MammoView marker.
- A presentation state (GSPS) with a zoom factor or rotation is applied to images. Note that if the presentation state is unselected (or set to None), these tools should be enabled.
- The breast bounding box cannot be identified (ex. image contains spot compression device or biopsy needle).

#### Fit to Window

In Fit to Window mode, eUnity zooms in on the breast bounding box to fit the viewport and maintains "same size" on each viewport.

- 1. Select an image in the viewing area.
- 2. On the Mammo tab, click



#### Quadrant View

In Quadrant View mode, eUnity divides the mammography image into four equally sized quadrants of "same size" so you can evaluate the entire breast in four separate sections. The first quadrant is displayed in the active viewport.

#### Quadrant View indicator



When in Quadrant View mode, this indicator is shown in the viewport on the non-breast wall side to indicate which quadrant of the breast is currently visible.

- 1. Select an image in the viewing area.
- 2. On the **Mammo** tab, click
  - Click  $\stackrel{\textstyle \bigcirc}{}$  to step forward (clockwise) to the next quadrant.
  - Click  $\stackrel{ ext{loc}}{ ext{loc}}$  to step backward (counter-clockwise) to the previous quadrant.

#### Same Size



#### Same Size

Scale a patient's mammography images in the viewer so that they are

displayed at the same relative physical size.

When same size is turned on, a patient's mammography image views are scaled up or down in the viewer so that they are displayed at the same relative physical size. This feature can be used in conjunction with mammography views such as quadrant view and fit to window.

The same size feature allows radiologists to evaluate developing densities and size changes of known lesions during comparison with prior digital images or film mammograms even when imaging was performed at different times on different detectors. The following behaviors are expected when same size is turned on:

- In cases where images are too small to scale up, larger images will be reduced in size to maintain an acceptable resolution.
- Magnified mammography views will not be scaled relative to other mammography images, and other images will not be scaled relative to magnified views.

By default, same size is turned on. To have same size turned off by default, please contact your system administrator. The Same Size tool may need to be added to your toolbar or context menu. See <u>Customize the toolbar</u> or <u>Customize the context menu</u> or talk to you system administrator for more information.

To turn on same size in the viewer:

1. On the Mammo tab, click (5)

The same size display property can also be set in mammography hanging protocols. For more information, see Create a hanging protocol.

# Toggle 2D and 3D views

#### Toggle between 2D and 3D series

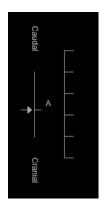


Switch between a tomosynthesis slice and the 2D reconstructed view for the selected series in a mammography study.

# Toggle between 2D and 3D view

When viewing a breast tomosynthesis slice, quickly switch between the current slice and the 2D reconstruction in the selected series.

- 1. In a tomosynthesis stack, click . The 2D reconstruction is shown.
- 2. Click again to switch back to the tomosynthesis slice you were previously viewing.



# Tomosynthesis indicator

Shown in the viewport for breast tomosynthesis studies to show the location of the current slice in relation to the other images in the series. The indicator shows directional markers to indicate whether you are scrolling in a caudal / cranial, or a medial / lateral direction. If CAD objects are available, the indicator will show additional lines to show which slices contains the CAD objects.

#### Mark Location

#### Mark Location

Outline a region of interest with an ellipse and automatically add a line segment that measures from the edge of the ellipse to a landmark such as a nipple.

Use the Mark Location tool in mammography studies to outline a region of interest with an ellipse and automatically add a line segment that measures from the edge of the ellipse to a landmark such as a nipple. The tool provides a number of labels (such as Microcalcification, Asymmetry etc.) that you can select from that will be used to label the measurement. The measurement can then be saved as a key image or presentation state.

NOTE: The Mark Location tool cannot be used in Advanced Visualization modes.

The Mark Location tool may need to be added to your toolbar or context menu. For more information, see <u>Customize the toolbar</u> or <u>Customize the context menu</u> or contact your system administrator.

- 1. On the toolbar, click  $\mathfrak L$  and select a label for the measurement.
- 2. Place your cursor near the region of interest, left-click to start the ellipse and left-click again to end it.
- 3. The line segment will be drawn automatically as soon as you move the cursor. Left-click to set its end point.

To discard the measurement before it is completed, press the Esc key.

### Edit a measurement

- 1. Click the measurement to select it and do any of the following:
  - To resize the ellipse, drag the handles on the edge of the ellipse.
  - To reposition the entire ellipse, drag from the center of the ellipse.
  - To resize the linear measurement, drag the handle at the end of the line segment.
  - To reposition the entire measurement, drag the handle in the center of the line segment.
  - To reposition the measurement label, drag it to the desired location.

### Related

- Customize keyboard shortcuts
- Presentation states

# Manual Calibration

#### Manual Calibration



If the modality-provided calibration is not sufficient, manually set a calibration value for measurements.

For cases where a modality does not provide calibration information or where modality-provided calibration is not sufficient, use the Manual Calibration tool to set a measurement calibration value for an image, series, or study.

The Manual Calibration tool works by having users provide the measurement of an object in the image that has a known dimension (such a calibration marker, ruler, or templating sphere). The object should have approximately the same geometric magnification as the anatomy. Any existing or new measurements (that are made in eUnity) are calibrated to that value. That is, any measurement from other vendors will not be updated with new calibration information.



### WARNING

Manual calibration takes precedence over any other calibration that can apply to the image, including calibration from the modality. Users are responsible for ensuring that manual calibration values are accurate and applied to the correct scope. Do not apply manual calibration using a broad scope (i.e. at the study or series level) unless all images within that scope are from the same modality, have the same pixel aspect ratio, and have the same zoom factor.

Manual calibration is not available in the following cases:

- the study, series, or image contains an ultrasound calibration region
- the study, series, or image contains 3D calibration data
- the modality of the study, series, or image is MG (mammography)
- the image is a Key Image

## Add manual calibration information

The Manual Calibration tool works only with modalities defined by your system administrator. The Manual Calibration tool may need to be added to the toolbar. For information on adding buttons to the toolbar, see Customize the toolbar or contact your system administrator.

Manual calibration is applied to new and existing measurements on all images that are within the scope of the calibration. The measurements will indicate that manual calibration is applied by showing (user) in the measurement annotation.

Note that manual calibration measurements cannot be edited once they are created. Even if the manual calibration measurement is deleted, the calibration information is persisted for the viewing session. To remove manual calibration, use the Revert to Original  $\checkmark$  tool. To change a manual calibration measurement, erase and redo the measurement.

- 1. Open an image that contains an object with a known measurement (such as a calibration marker, ruler, or templating sphere).
- 2. Click A to activate the Manual Calibration tool.
- 3. In the image, left-click to set the start point of the measurement and left-click again to set the endpoint of the measurement.
- 4. In the Manual Calibration dialog, type the length of the measurement in millimeters (mm) and select the scope (Image, Series, or Study) of the measurement. Note that the maximum number of digits (including the decimal point) is 8.
- 5. Click Apply.

When measurements are saved as a Presentation State, manual calibration values and their associated markup are saved along with them.

# Markup Color Picker

The Markup Color Picker may need to be added to the toolbar or context menu. For information on adding tools, see <u>Customize the context menu</u> or <u>Customize the toolbar</u> or contact your system administrator.

NOTE: You cannot change the color of spine labels.

### Change the markup color for new annotations or measurements

When you change the markup color, the color will be used for any markup that you add until you change the color again or you change the patient context.

- 1. On the toolbar or in the context menu, click a markup color from the Markup Color Picker
- 2. Add the desired markup.

# Automatically cycle through colors

1. To change to a new color each time you add markup, select **Auto Cycle Colors** from the Markup Color Picker dropdown.

# Change the markup color for existing markup

When you change the color of existing markup, the color does not remain selected for the next markup that you add.

- 1. Right-click the markup that you want to change.
- 2. In the context menu, click a new color from the Markup Color Picker.

# Measurement tools

Use measurement tools to apply measurements to an image. To cancel the measurement once you have started it, right-click or press the Esc key.

Some measurement tools may need to be added to the toolbar or context menu. For information on adding tools, see  $\underline{\text{Customize the context menu}}$  or  $\underline{\text{Customize the toolbar}}$  or contact your system administrator.

# Multi-modality measurement tools

### **Angle Measurement**

Measure the angle between anatomical structures.

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- 1. Left-click to create the vertex.
- 2. Left-click twice more to set the end points of the angles arms.
- 3. To edit, click the measurement to select it and then drag the measurement handles.

# Cobb Angle Measurement

A Cobb angle is the angle formed at the intersection of the two lines, which typically intersect off-screen.



- 1. Left-click twice to draw the initial line segment.
- 2. Left-click twice more to draw the secondary line segment.
- 3. To edit the measurement, click the measurement to select it and then drag the measurement handles.

A dashed line connects the two segments and the Cobb angle, presented in degrees, is anchored to the connecting line.

### Linear Measurement



Measure length in mm or measure time and velocity for echo ultrasound. Time doppler ultrasound regions will create peak velocity with a single click. Values are shown in mm and the source of the calibration is shown in brackets. For more information on linear measurements in ultrasounds, see Ultrasound measurements.

1. Left-click to start the measurement and left-click again to end the

- measurement.
- 2. To edit, click the measurement to select it and drag the measurement handles

### Multi-Segment Measurement

Measure the distance of curved anatomical structures using multiple straight lines. Values are shown in mm and the source of the calibration is shown in brackets. Multi-segment measurements are not supported in advanced visualization modes.

- 1. Left-click to start the segment, and left-click again to set its endpoint. Repeat this process until the measurement is complete.
- 2. Double-click to end the measurement.
- 3. To edit, do either of the following:
  - To move a segment of the measurement, click and drag the segment handle.
  - To move the entire measurement, click between the segment handles and drag the measurement to the desired location.

### Perpendicular tool

Use the perpendicular tool to draw two lines that intersect at a 90° angle and provide a measurement of each line. For example, use the Perpendicular tool to measure a nodule from top to bottom and from left to right.

- 1. Left-click to start the y-axis and left-click again to set its endpoint. Once the y-axis is drawn, a handle for the x-axis is automatically added.
- 2. Left-click to set each endpoint of the x-axis.
- 3. To adjust the measurement:
  - Drag the endpoint handles to lengthen or shorten the lines or to rotate the whole measurement.
  - Drag the center handle to change the intersection point for either axis.

Note that while the measurement can be rotated using the endpoint handles, the intersection angle cannot be changed.

#### Ratio tool

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Use the ratio tool to draw two separate lines and provide a measurement of each line as well as the ratio of the length of the first line (x) to the second line (y). That is, x/y. The ratio is calculated using the internal floating-point measurement value. The values that are displayed in the viewer are rounded to the nearest 2 or 3 decimal places (depending on if the value is less than or greater than 1).

- 1. Left-click to start the first line (x) and left-click again to set its endpoint.
- 2. Left-click to start the second line (y) and left-click again to set its endpoint. The lines are connected with a dotted line to indicate that they are related.
- 3. To adjust the measurement:
  - Drag the endpoint handles to lengthen, shorten, or rotate the line.
  - Drag the center handle to move the line.

# Toggle Markup

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Hide or show markup on images including markup on presentation states.

## **ROI** tools

### Circle ROI

Draw a circular region of interest. The source of the calibration is shown in brackets at the bottom of the overlay.

- 1. Left-click to start the measurement and left-click again to end the measurement.
- 2. To edit, click the measurement to select it and then drag the measurement handles.

# Ellipse ROI

Draw an ellipse region of interest. The source of the calibration is shown in brackets at the bottom of the overlay.

- 1. Left-click to start the measurement and left-click again to end the measurement.
- 2. To edit a measurement, click the measurement to select it and then drag the measurement handles.

# Freeform ROI / Doppler Envelope

Draw a freeform region of interest. For cardiology, peak and mean velocity and peak and mean gradient are shown. The source of the calibration is shown in brackets at the bottom of the overlay. For information on using the Freeform ROI tool with ultrasound studies, see Ultrasound measurements.

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- 1. Left-click to start the measurement.
- 2. Left-click on the first point selected or double-click to end the measurement.
- 3. To edit a measurement, click the measurement to select it and then drag the measurement handles.

#### Point Tool

### Rectangle ROI

Draw a rectangular region of interest. The source of the calibration is shown in brackets at the bottom of the overlay.

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- 1. Left-click to start the measurement and left-click again to end the measurement.
- 2. To edit a measurement, click the measurement to select it and then drag the measurement handles.

#### Ultrasound measurements

The following tools can be used to make ultrasound measurements on images with the appropriate calibration information.

#### Linear measurements in ultrasounds

Calibrated ultrasound images can use standard linear measurements. A single left mouse click starts the measurement and a second left click ends the measurement. To edit a measurement, drag the measurement handles.

When a linear measurement is placed within a region that has two different axes (i.e. units like time and velocity), it will show both units unless the measurement is parallel to one of the axes. See image below.

A special case exists for velocity-time Doppler Ultrasound regions. In this case, a single click will create the measurement by automatically snapping the other end-point to the zero-velocity axis. See image below.

- Moving the automatic end-point off the zero-velocity axis will transition the measurement into a standard Ultrasound linear measurement.
- Moving the user selected point will keep the automatic end-point locked, sliding it along the zero-velocity axis.

#### Freeform ROI in ultrasounds

The Freefrom ROI tool can be used to calculate the Doppler Envelope for velocity-time regions. ROIs will be locked to the zero-velocity axis and points can be added along the envelope. A double-click will end the ROI creation. See image below.



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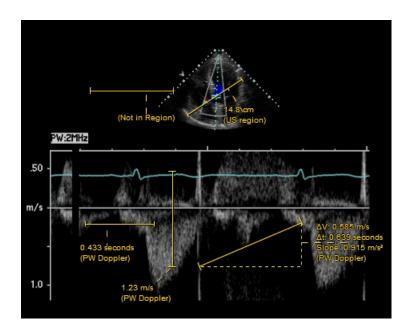


Figure 9: Linear measurements in ultrasound

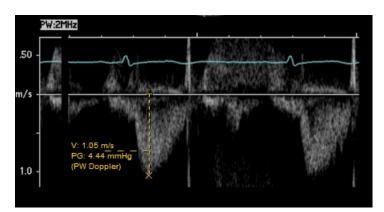


Figure 10: Linear measurements in velocity-time doppler ultrasound regions

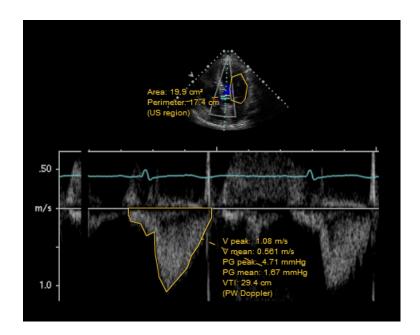


Figure 11: Freeform ROI to calculate doppler envelope for velocity time regions

# Related

• Markup Color Picker

# MPR/3D

#### MPR, Advanced MPR, and 3D overview

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

If enabled in eUnity™, the Advanced Visualization menu is available to create MPR, obliques, curved MPR, and 3D volume rendered views.



#### WARNING

All reformatted and volume rendered views (MPR and 3D) are treated as Lossy and will display a Lossy indicator in the upper-right corner of the viewport. For more information, see Lossy image display

- 1. Click and select the desired view mode. The differences between the modes is explained below.
  - MPR
  - Advanced MPR
  - Curved MPR
  - 3D

### **MPR**

These layouts will generate axial, sagittal, and coronal planes from the selected series and display them in 3 horizontal or 3 vertical views. Slice navigation in this mode is similar to 2D stack navigation (e.g. mouse wheel and drag advances by the slice thickness). Basic MPR uses slice-based navigation, where possible. When it is not possible, for example, the gantry is tilted relative to the patient, or the patient is rotated relative to the table, it uses volume-based navigation. When slice-based navigation is used, the annotation overlay shows the slice numbers. When volume-based navigation is used, the annotation overlay displays NA in place of slice numbers.

In slice-based navigation, measurements that you make on a slice are retained for the duration of your session. Note however that annotations and measurements on reconstructed series cannot be saved as a Presentation State.

# Advanced MPR

These layouts will generate axial, sagittal, and coronal planes from the selected series. Advanced MPR uses volume-based navigation and provides advanced features such as

changing the slice thickness, changing the rendering type, and creating oblique / non-orthogonal stacks.

In volume-based navigation, measurements that you make will not be retained when you navigate away from the image containing the measurements.

#### **Curved MPR**

Use the Curved MPR tool to drop control points on curved anatomy to build a perpendicular sectional reconstruction.

#### 3D

These layouts will generate volume-based axial, sagittal, and coronal planes from the selected series, and will also show a 3D volume rendered stack in one of the viewports.

#### Interactive mode in MPR / 3D view modes

Interactive mode is a special low-latency mode that prioritizes frame-rate and is enabled in fast operations such as adjusting Window Level on the fly, navigating the stack, or adjusting the 3D image render function or volume orientation on volume rendered stacks.

Note: Viewports in Interactive mode will display <sup>5</sup> in the upper-right corner of the viewport to indicate that higher quality images are in progress.

For information on adjusting the quality of interactive or final images, see <u>Advanced Visualization Parameters for 3D and MPR</u>.

#### Annotations and measurements in MPR / 3D view modes

Certain annotations and measurements can be made in MPR, Advanced MPR, and 3D modes, however, they cannot be made on 3D MIP, 3D, and curved MPR series. Annotations and measurements that you make in MPR, Advanced MPR, 3D modes are available only for your session. That is, annotations and measurements on reconstructed series cannot be saved as a Presentation State.

To avoid incorrect measurements in rendered volumes, images that contain nonsquare pixels will not be rendered in Advanced Visualization modes. In this case, eUnity will display the following error message: "MPR not supported on this series. The image pixels are nonsquare."

### Navigating in reconstructed stacks

When you hold down the left mouse button and drag to navigate through a reconstructed stack (for example, an MPR stack), navigation will jump dynamically based on the length of the drag action. That is, images will be skipped so that you can quickly find the general location

you are looking for. To move through images one at a time, use the mouse wheel or arrow keys.

#### Advanced Visualization Parameters for 3D and MPR

#### **Advanced Visualization Parameters**

View or change render types, render parameters, or SUV parameters. The tabs / options that are available in the panel depend on the visualization mode (i.e. Fusion vs 3D) and the series type (i.e. PET vs CT) or series orientation (i.e. same plane as the original series or not) that is selected in the viewer.

#### Render Parameters tab

### Change the quality of interactive or final images

The Interactive Quality and Final Quality options scale up or scale down the quality of interactive images (images generated during on-the-fly rendering) and final images (images generated at rest, when no user commands are applied to the volume stack).

- 1. Click  $\square$  and click the Render Parameters tab.
- 2. Click and drag the handle on the Interactive Quality or Final Quality scales.

### Change the slice thickness

This feature is available for Advanced MPR, Curved MPR, and MPR / 3D. It is also available for basic MPR and Fusion if slice-based navigation is not applicable to the reconstructed volume (for example, when a volume is tilted).

- 1. Click a volume rendered image.
- 2. Click  $\square$  and click the Render Parameters tab.
- 3. Click and drag the handle on the Slice Thickness slider.

# Render Types tab

The Render Types tab is available when you select an axial, sagittal, or coronal reconstruction in Advanced MPR, Curved MPR, and MPR / 3D modes. It is also available for basic MPR and Fusion if slice-based navigation is not applicable to the reconstructed volume (for example, when a volume is tilted).

## Change the render type

- 1. Click  $\square$  and click the Render Types tab.
- 2. Select one of the following render types:
  - Maximum Intensity Projection (MIP)
  - Minimum Intensity Projection (MinIP)
  - Faded Maximum Intensity Projection (Faded MIP)
  - Average Intensity Projection (Average)

### Advanced MPR tools

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

### Create oblique



Every viewport is annotated with a color that directly corresponds to the reference line on other intersecting images in other viewports. To generate new planes, drag the controls corresponding to the color of the viewport you wish to change until desired orientation is achieved.

### Turn on Advanced MPR mode

- 1. Click and click Advanced MPR.
- 2. On the MPR / 3D tab, click an Advanced MPR layout:
  - Advanced MPR with oblique 2 x 2 layout
  - Advanced MPR with oblique custom layout

# Create non-orthogonal / oblique reformatted stacks

When reference lines are turned on, every viewport is annotated with a color that directly corresponds to the reference line on other intersecting images in other viewports. To generate new planes, drag the controls corresponding to the color of the viewport you wish to change until desired orientation is achieved.

# Create Oblique

- 1. On the MPR/3D tab, click
- 2. Draw an additional reference line to draw a second oblique in the lower-right viewport.

# Curved MPR

#### Create Curved MPR

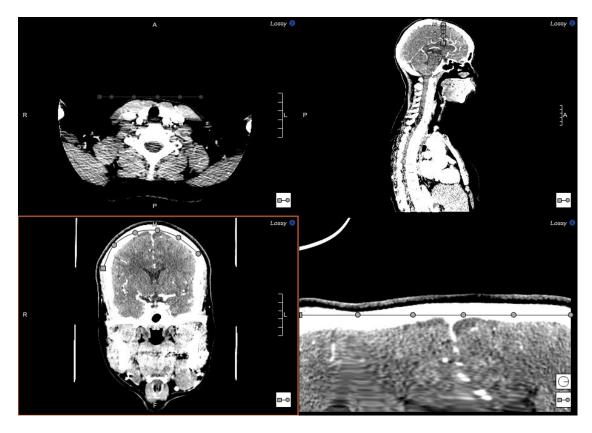


Click along curved anatomy in any of the 2D viewports and the perpendicular reconstruction is created in the CMPR viewport. Each point in the curve is along the center axis of the curved MPR view.

### Create a curved MPR view

You can drop your control points in any of the 2D viewports. That is, you can drop all of the control points in one 2D viewport or drop some in one 2D viewport and the rest in another. The curve is defined in 3D space and can be manipulated from anywhere within any of the 2D viewports (that is, the axial, sagittal, and coronal views).

- 1. Click and click Curved MPR.
- 2. Click
- 3. Click in any of the 2D views along the desired anatomy to add up to 20 control points. Once you have added at least two points, the curved MPR view will be rendered in the curved MPR viewport. Each point will be along the center axis of the curved MPR view.



Curved MPR viewing features

- In any of the views, double-click to maximize the viewport. Double-click again to go back to the original layout.
- In any of the three orthogonal views, drag the control points to reposition them.
- In the curved MPR view, click a control point to synchronize the three orthogonal views to the selected point.
- In the curved MPR view, drag the mouse side to side to traverse a curved reconstruction. Alternately, drag the mouse up and down to rotate all the views around their axes. If the curved MPR view is rotated so that the curve is vertical, the opposite actions apply (side to side to rotate, and up and down to traverse).
- The current orientation angle is shown by the icon in the curved MPR view. Click this icon to reset the orientation angle back to the original.
- Click to toggle the line and control points on and off.
- On the Curved MPR toolbar, change the curved MPR layout (if desired).
  - Curved MPR with 2 x 2 layout (curved MPR view in the lower-right viewport)
  - Curved MPR with custom layout (curved MPR view to the right of the other series)

#### Curved MPR indicators



### **CMPR Control Point Limit indicator**

The curved MPR has reached the 20 control point maximum.

#### Invalid Zoom indicator



This indicator is displayed when the curve is too small to be rendered within the boundaries of the current viewport.

#### 3D tools

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

#### Clip Box



Cut away some of the volume so that you can better see underlying anatomy. Drag down to move the plane into the volume (cut more). Drag up to move the plane out of the volume (cut less). Selecting one of the edges of the clip box the orientation of the clip box can be changed without changing its size or the

orientation of the volume.

#### Cut Plane

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Use the Cut Plane tool to cut away some of the volume at a custom rotation. Rotate the 3D volume to a desired view and click the Cut Plane icon. A cut plane normal to the current 3D view will be created. While in the cut plane mode, the cut plane can be moved into the volume by dragging the mouse down or out of the volume by dragging the mouse up.

# Scalpel Tool



Remove or isolate a section of an image by dragging the mouse along the border of the area to segment then clicking on the region you would like to keep.

#### Turn on 3D mode



- 2. On the MPR / 3D tab, click a 3D layout:
  - III 3D with 3 MPR views
  - 🔊 3D with custom layout

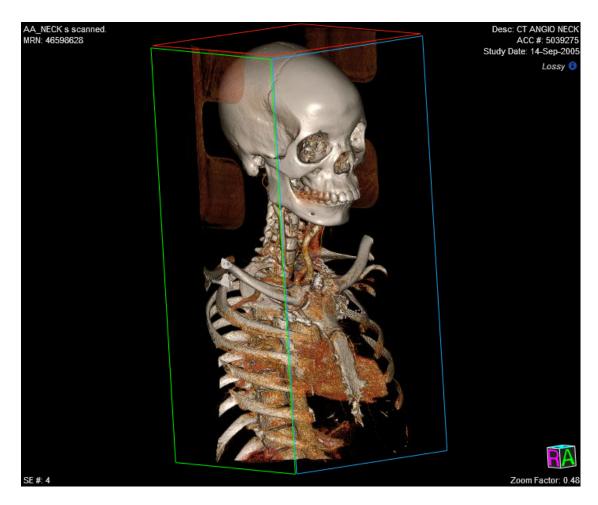
### Clip Box

Use the Clip Box tool to cut away some of the volume so that you can better see underlying anatomy. Each plane is represented with a colored border. Click outside the edges of the clip box and drag to change the orientation of the clip box without changing its size or the orientation of the volume.





- 2. Click within one of the sides and do either of the following:
  - Drag into the volume (cut more).
  - Drag out of the volume (cut less).



### Cut Plane

Use the Cut Plane tool to cut away some of the volume at a custom rotation.

- 1. Rotate the 3D volume to a desired angle.
- 2. On the MPR /3D tab, click . A cut plane normalized to the current 3D view is created.
  - Drag the mouse down to move the cut plane into the volume.
  - Drag the mouse up to move the cut plane out of the volume.

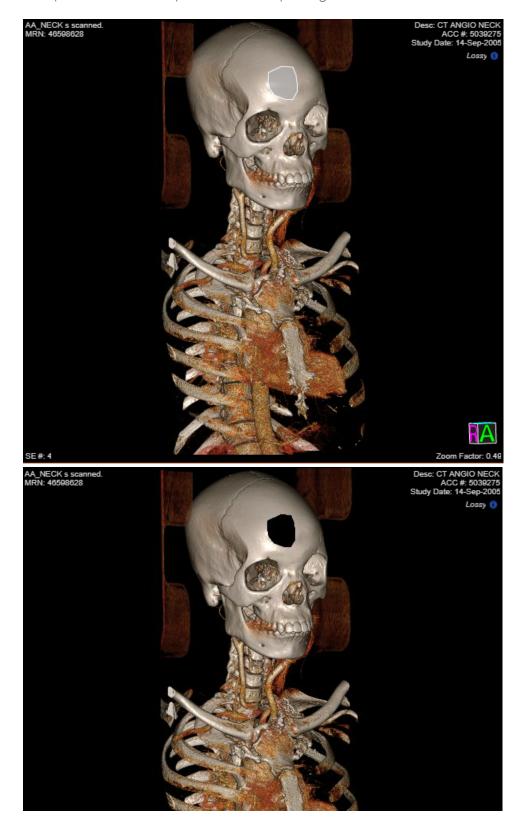
# Scalpel

Use the Scalpel tool to remove or isolate a segment of the image.

- 1. On the MPR / 3D tab, click
- 2. Drag the mouse along the border of the area you wish to segment. Once the desired region has been selected you should see the selection similar to the first image below.

3. Click on the region you would like to keep. For example, clicking outside of the segment will remove the selected region and the result will be similar to the second image below.

This process can be repeated for multiple regions. The reset tool will revert all segments.



# Adjust the rendering presets

The rendering preset can be adjusted on-site and may differ from the default. Changing the presets will re-render the volume, highlighting different features, or even completely changing the method or type of rendering.

- 1. Select the 3D view.
- 2. Click and click the **Presets** tab.
- 3. Click a rendering preset.

# Multiphase Tool

Multiphase series are typically created by CT / MR, or enhanced CT / MR modalities to acquire the same anatomic region over time to visualize functions such as perfusion, cardiac cycle, and so on. When all multiphase images are stored in a single series and the series is loaded and selected in the viewer, the Multiphase Tool will be enabled on the toolbar.

### Multiphase Tool



Split a multiphase series into multiple phase-based series or sort a multiphase series by phase.

The following indicator is shown in the viewport for a multiphase series to provide a visual representation of the phases.



### Multiphase indicator

Shown in the viewport for a multiphase series that has not yet been split into virtual series. The dividers represent the start and end of a phase. The arrow represents the slice position in the stack.

Use the Multiphase Tool to rearrange multiphase series for easier comparison. The Multiphase Tool can split a selected multiphase series into multiple phase-based virtual series, or it can reorder a multiphase series so that it is sorted by phase. For example, some series may be ordered by anatomic position where the phases are interleaved:

- ▼ slice 1/ phase 1
- ▼ slice 1/ phase 2
- ▼ slice 2 / phase 1
- ▼ slice 2 / phase 2

In this case, the "Sort by Phase" option will be available in the Multiphase Tool dropdown so that the series can be reordered:

- ▼ slice 1/ phase 1
- ▼ slice 2 / phase 1

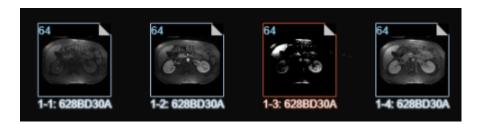
- ▼ slice 3 / phase 1
- ▼ slice 4 / phase 1
- ▼ slice 1/ phase 2
- ▼ slice 2 / phase 2
- ▼ slice 3 / phase 2
- ▼ slice 4 / phase 2

### Split, reorder, or reset a multiphase series

The Multiphase Tool may need to be added to the toolbar. For information on adding buttons to the toolbar, see <u>Customize the toolbar</u> or contact your system administrator.

- 1. Select a multiphase series from the series tray.
- 2. Hover your cursor over the  $\stackrel{\diamondsuit}{=}$  tool on the toolbar to see how many phases the series contains.
- 3. Click  $\otimes$  on the toolbar and do any of the following:
  - To split the series into phase-based virtual series, click Split.
  - To keep the series as one, but sort it by phase, click Sort by Phase.
  - To undo splitting or sorting, click **Reset**.

Once the series is split, the series number changes to reflect the virtual series number. For example, if the DICOM number of the series is 1, and it was split into 4 virtual series, the virtual series numbers will be 1-1, 1-2, 1-3, 1-4. This is shown in the annotation overlay (SE:1-1) and in the series label in the series tray.



Note that the split is a virtual split only, so the split cannot saved as part of a presentation state, but any markup that is made to the split series will be made on the original series (when you refresh the viewer) and can be saved there. Since the split series are virtual, this also means that if you click the Apply changes button ( $^{\bigcirc}$ ) when you receive a content change notification, split series will be discarded.

# Multiple Reference Lines

To help visualize how images from different planes are oriented to each other, the Multiple Reference Lines tool projects reference lines onto the selected series, where each line represents an image that intersects the series you are projecting to. Reference lines can be projected from specific series of your choosing, all series in currently in view, or all series, including off screen series once they are dragged into view. Note, however, that reference lines will be projected from a series only if it is in view and it is from a different plane than the series it is being projected on.

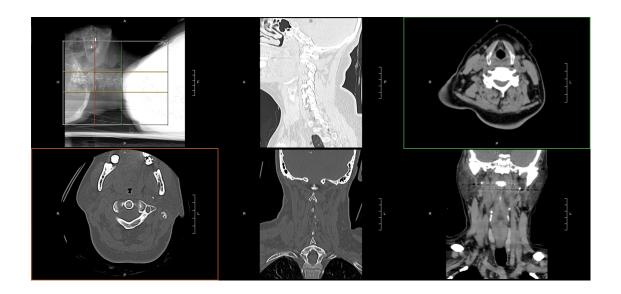
Unlike the basic Reference Lines tool which projects from the active series, Multiple Reference Lines are always displayed on the originally selected series regardless of what series is currently active. Since Multiple Reference Lines do not depend on the active series, they will remain visible while you perform measurements and you can also display Multiple Reference Lines on multiple series simultaneously. For example, if you select series A and project all series in view to it, and then you select series B and project all series in view to it, both series A and series B will show references lines for all intersecting series that are currently in view.

NOTE: The Multiple Reference Lines tool cannot be used in advanced visualization modes.

# Turn on multiple reference lines

- 1. Select the series to project the reference lines to.
- 2. Click and select any of the series that are listed in the dropdown. Alternately, select one of the following options:
  - Project Automatically: Project reference lines from all series that are currently in view and automatically project reference lines from off-screen series when they are dragged into view.
  - Select All In View: Project reference lines from all series that are currently in view, but do not automatically project reference lines from off-screen series that are dragged into view.

If the series are in view and they intersect the selected series, the currently displayed images from each of the series will be projected onto the selected series as a yellow reference line. For more information on the different reference line colors, see <u>Reference line colors</u>.



# Reference line colors

Reference Line Color	Description
Yellow	Series  Each yellow reference line represents a series.
	Eddit yellow reference line represents a series.
Orange	Active series  An orange reference line represents the currently selected series.
Green	Highlight series  Reference lines turn green when you hover over them (or when you tap them on a mobile device) so that you can easily find their corresponding series. See <a href="Map a reference line to a series">Map a reference line to a series</a> for more information.
White	Boundary lines  White reference lines are displayed only on scout images to represent the first and last images of the series.

# Map a reference line to a series

NOTE: This feature is not available when using Cine or Collaboration.

1. Hover over a reference line or if you are on a mobile device, tap a reference line.

The reference line and the viewport of its corresponding series will be highlighted in green. If references lines from multiple series overlap, the viewports of all applicable series will be highlighted in green.

### Clear individual reference lines

Individual reference lines cannot be cleared if you are automatically projecting reference lines.

- 1. Select the series that you want to clear the reference lines from.
- 2. Click and clear the check mark beside any of the individual series in the dropdown.

### Clear all reference lines

- 1. Do either of the following:
  - To clear all reference lines from a specific series, select the series and click
     Clear Selected Viewport.
  - To clear all references lines from all series, click > Clear All Viewports.

### Related

• Reference Lines

# Navigate

Navigate is the default mode in  $eUnity^{\mathbb{M}}$ , however, some browsers do not automatically give their content focus, and the mouse and keyboard interaction do not apply. In these cases, click anywhere on  $eUnity^{\mathbb{M}}$  and the mouse and keyboard will interact with your selections.

## Navigate



Navigate study images using the mouse wheel, a left-click drag, touch drag, touch pad drag, or the up and down cursor keys.

# Navigate images

The default behavior is navigating all of the images within a series within a single drag from the top to the bottom of the viewport.



### CAUTION

The default scroll behavior will skip images. If this is not desired, contact your site administrator. The default behavior can be changed to not skip images (for non-reconstructed stacks). Reconstructed stacks (for example, MPR) will always skip images when you drag to navigate. To move through reconstructed stacks one image at a time, use the mouse wheel or arrow keys.

- 1. To navigate through a stack of images, click  $\ ^{f k}$  and do any of the following:
  - Mouse Wheel Up: Scrolls images from a higher number image to a lower number image.
  - Mouse Wheel Down: Scrolls images from a lower number image to a higher number image.
  - Left-Click Drag Up: Scrolls images from a higher number image to a lower number image.
  - Left-Click Drag Down: Scrolls images from a lower number image to a higher number image.

# Navigate Relevant Priors and Navigate Study List

By default, the Navigate Relevant Priors and Navigate Study List tools are available on the Mammo tab, but they can be used for any modality type. See <u>Customize the toolbar</u> for information on customizing the toolbar.

## Navigate Relevant Priors (Previous)

Open the previous relevant prior for the patient.

### Navigate Relevant Priors (Next)

Open the next relevant prior for the patient.

### Navigate Study List (Previous)

Open the previous study for the patient.

# Navigate Study List (Next)

Open the next study for the patient.

### Navigate Relevant Priors

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Depending on your site's configuration, when you open a study from your worklist, the worklist may choose a number of relevant priors for eUnity™ to open along with it. Relevant priors are typically studies that provide meaningful context to the current study (for example, for a mammography study, relevant priors may be older or newer mammography, breast ultrasound, or breast MR studies). You can quickly navigate through these relevant priors by doing the following:

- On the Mammo tab, click to open the previous relevant prior (newer than the currently loaded relevant prior).
- On the **Mammo** tab, click to open the next relevant prior (older than the currently loaded relevant prior).

If, for example, the study compare mode is (meaning the current study is on the left and the relevant prior is on the right), the current study will remain in view on the left and the relevant priors will cycle through the viewing area on the right. When there are no more relevant priors to move through, the button is disabled. Depending on your site's

configuration, the "current" study can either be defined by your worklist, or it can be the study with the newest date and time. The study order method is configured by your system administrator.

# Navigate Study List

Depending on your site's configuration, all of a patient's historical studies may be shown in the eUnity Study List. To quickly move through the studies in the Study List, do the following:

- On the Mammo tab, click to open the previous study (newer than the currently loaded study).
- On the Mammo tab, click to open the next study (older than the currently loaded study).

If, for example, the study compare mode is \_\_\_\_\_\_ (meaning the current study is on the left and other studies are on the right), the current study will remain in view on the left and the other studies will cycle through the viewing area on the right. When there are no more studies to move through, the button is disabled. Depending on your site's configuration, the "current" study can either be defined by your worklist, or it can be the study with the newest date and time. The study order method is configured by your system administrator.

# Page through series or images

When you open a study that contains more content than can be shown at one time, you can replace all the content that is currently in view with the next "page" of unseen content by paging through series or images.

Series Page Backward

Move to the previous series page.

Series Page Forward

Move to the next series page.

# Shortcuts

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Page Down	Show the next series page (series page forward)
Page Up	Show the previous series page (series page backward)
Shift + Page Down	Show the last series page
Shift + Page Up	Show the first series page
Up arrow	Scroll backward through the image stack (image page backward)
Down arrow	Scroll forward through the image stack (image page forward)
Home	Jump to the first images in the stack
End	Jump to the last images in the stack

# Page through series

Move to the next set of unseen series. For example, if you are using a 2x1 series layout where series 1 and 2 are showing, use Series Page Forward to show series 3 and 4. Note that series paging is not available when the screen layout is in shuffle mode. The Series Page Forward

and Series Page Backward buttons may need to be added to the toolbar. For information on adding buttons to the toolbar, see <u>Customize the toolbar</u> or contact your system administrator.

- 1. Do any of the following:
  - On the Toolbar, click to move to the next series page. Click to move to the previous series page.
  - On the keyboard, press the Page Down key to move to the next series page and the Page Up key to move to the previous series page.
  - On the keyboard, press Shift + Page Down to move to the last series page or Shift + Page Up to move to the first series page.

### Note on series page order

The contents of a series page is determined by:

- the series order as it is stored in the study
- the series layout in the viewer

When series are loaded out of page order, the viewer will jump to the page of the currently selected series when you page forward or backward. For example, if the series layout is 4x1, the first series page should consist of series 1-4, but they may be loaded out of page order, as shown in the image below:



When you page forward or backward, the viewer loads the page that belongs to the currently selected series. In this case, the selected series belongs to the first page, so page 1 is loaded.



# Page through images

Move to the next image page. For example, if you are using a 2x2 image layout and images 1-4 are showing, press the down arrow on the keyboard to move to the next image page and show images 5-8.

- 1. On the Home tab, click Screen Layouts ( ) and click an image layout.
- 2. On the keyboard, do either of the following:
  - Press the down arrow key to move forward one image page and the up arrow key to move back one image page.
  - Press the End key or Home key to go to the last or first page of images, respectively.

# Paper Print

Use the Paper Print tool to print the study report (if available), the selected image, or up to 24 images.



### Paper Print

Print reports, images, or a set of images.

# Print images



# CAUTION

Printed images are not intended for diagnostic reading.

- 1. Select a viewport. Selected viewports are indicated by an orange border around the image.
- 2. On the Export tab, click
- 3. Select the desired settings. Use the information in the Print settings table below.
- 4. Click Print.

# Print settings

Study Report	Select this option to print the report for the selected study. The study that is currently selected is shown below the checkbox.
Image Print Options	<ul> <li>Print with demographics: When selected, the printed image includes the demographic information.</li> <li>Print with markup: When selected, the printed image includes all annotation and measurement markups.</li> </ul>
Image Print Layout	<ul> <li>Layouts are presented in a per-page format with the option to print 1, 2, 4, 6, 8 or 12 images per page.     When using the Current View option in the Images to Print options, the print layout will automatically be assigned to match the current screen layout.</li> <li>Select Portrait or Landscape orientation.</li> </ul>

After clicking Print, the browser's Print dialog will appear so that you can select a printer and other print options.

**NOTE**: Some older browsers will overwrite the Portrait or Landscape setting. You may have to reset the orientation setting in the the browser's Print dialog.

### **Images to Print**

Set which image(s) will be printed. A maximum of 24 images can be included in a single print job.

- Current View: The current view option prints images as they are currently laid out on screen. A short description will appear next to this option indicating the number of images and layout.
- Marked Images: When images have been marked within the viewer, users have the option to print the set of marked images. In the event that more than 24 images are marked, the first 24 images selected will be printed. To mark an image, right-click on an image and click Mark Image. Marked images have a star indicator.
- Selected Series: Print images from the currently selected series. The range selector can be used to choose the subset of images (up to 24 images) to be printed.

# Presentation states

eUnity™ supports display of DICOM Greyscale Softcopy Presentation State (GSPS) and Color Softcopy Presentation State (CSPS) objects. These objects can alter the display of an image by changing window level, zoom factor, shutters, or markup.

**	Presentation state applied indicator
	Shown in the viewport to indicate that a presentation state is applied.
	Presentation state available indicator
录	Shown in the study folder in the series tray to indicate that presentation states are available. Click the arrow to show the available presentation states. If available, the name of the person who created the presentation state will be shown in brackets beside the presentation state name.

# Apply a presentation state

By default, the newest presentation state will automatically be applied to a study. When a presentation state exists for a study, the study folder in the series tray will include a presentation state context menu . The label displayed in the menu comes from the presentation name and may include one or more related presentation state instances.

**NOTE**:Unsaved key images will be removed when you apply a presentation state. To keep your current markup and key images, save them before you apply a presentation state.

- 1. Open a study that has available presentation states in the viewer.
- 2. To activate or disable presentation states, click in the series tray.
- 3. Click the presentation state that you want to apply. To remove all presentation states, click **None** .

When an image has a presentation state applied, the  $\overline{\mathbb{R}}$  indicator appears in the viewport. As well, the indicator on the study folder in the series tray changes from  $\overline{\mathbb{R}}$  to  $\overline{\mathbb{R}}$ .

**NOTE**: When exporting images, any presentation state-related markup will not appear on the image.

### See the name of the presentation state creator

If available, the name of the person who created the presentation state will appear in brackets beside the presentation state name. If the creator's name is not available, nothing will be displayed.

- 1. Open a study that has available presentation states in the viewer.
- 2. Click in the series tray. If available, the name of the presentation state creator is shown in brackets beside the presentation state name.

### Save presentation states (markup-only)

If this feature is enabled by the system administrator, markup can be saved to the PACS. If

your administrator has enabled saving presentation states, a grayed out save icon shown in the study folder in the series tray. The icon will be enabled once you add markup.

**Note**: If using a keyboard shortcut to save, you are initiating a save only on the currently selected study.

- 1. To save a DICOM presentation state, click on the study folder in the series tray.
- 2. In the Save presentation state dialog, select the types of changes that you want to save and click **Yes**.
- 3. To hide the dialog in future, select **Do not prompt me again**. If this option is selected, the default save values (see below) are selected.

After you save, eUnity checks the destination system to ensure the presentation state or key object was successfully saved. In rare cases (for example, a timing issue) eUnity may not be able to find the saved object when it rechecks. Consequently, the presentation state or key object is removed from the view. If this happens, and your annotations are removed from view after a save, it is likely that the save was successful, but you should contact your system administrator to make sure.

### Configure default presentation state save options

If available, default presentation state save defaults can be set in the Settings menu. Note that the Settings menu must be enabled by the system administrator. The options that you choose will be selected in the confirmation dialog next time you save a presentation state. If the Save presentation state dialog option is disabled, the default save options will be used when saving.

- 1. Click = > General Settings.
- 2. In the Save Dialog Options section, select any of the following options (the system administrator may not make all of these options available):

### Save Dialog Options

Annotations / Measurements / Text	Have Annotations, measurement, and text selected by default in the <b>Save presentation state</b> confirmation dialog.		
Window / Level	Have Window / level selected by default in the Save presentation state confirmation dialog. This option must be enabled by an administrator.		
Spine Labels	Have Spine labels selected by default in the <b>Save</b> presentation state confirmation dialog.		
Disable Prompts	When selected, clicking will no longer cause a Save presentation state confirmation dialog to display and the save will proceed automatically.		
Save Changes On (available in the Save dialog only when Key Images are enabled)			
All Images	Have "All images" selected by default in the <b>Save</b> presentation state confirmation dialog. When selected, changes will be saved on all images.		
Images used to create Key Images	Have "Images used to create key images" selected by default in the <b>Save presentation state</b> confirmation dialog. When selected, changes will be saved only on Key Image sources (that is, the images that key images are derived from).		

### Red Free Filter

# B

#### Red Free Filter



Turn on the red free filter to block red and blue wavelengths in color images.

Use the red free filter to block red and blue wavelengths of light in color images. The red free filter transforms images by applying a green filter and then converting the images to grayscale. This tool can be used to improve contrast in color retinal fundus images. The Red Free Filter tool may need to be added to your toolbar or context menu. For more information, see <u>Customize the toolbar</u> or <u>Customize the context menu</u> or contact your system administrator.

**NOTE**: The red free filter image transformation will not be saved as part of a presentation state or as a key object. That is, if you save an image that has the red free filter applied, the image will be saved in its original color format.

- 1. Select the image or series to apply the filter to.
- 2. On the toolbar, click  $^{\odot}$

The filter is applied at the series level and the Red Free Filter indicator displays in the viewport. Note that if the series contains a mix of color and grayscale images, only the color images will have the Red Free Filter indicator as the filter is not applied to the grayscale images.

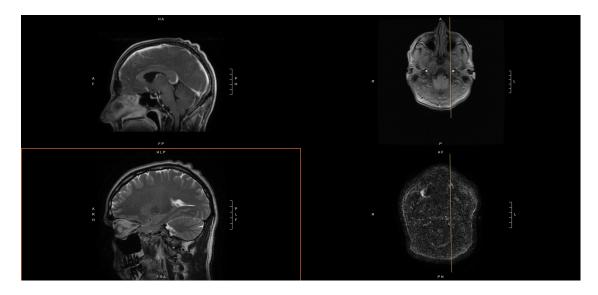
## Reference Lines

Use the Reference Lines tool to show where the selected image intersects other images from different planes. Unlike the Multiple Reference Lines tool where the reference lines remain static no matter which series is selected, when you use the Reference Lines tool, the reference lines will always project from the active series. For example, if you select series A and you turn Reference Lines on, reference lines representing series A will be projected onto all orthogonal series that have an intersection point. If you then select series B, the series A reference lines are removed and reference lines representing series B are projected.

# Turn on Reference Lines

- 1. Select the series that you want to project onto other images.
- 2. Click I

If the series intersects images from different planes, it will be projected onto those images as a yellow line.



# Project reference lines to a scout image

All scout images in a study are combined into a single series and placed at the start of the <u>Series tray</u>.

- 1. Drag the scout series into view.
- 2. Select the series that you want to project onto the scout.
- 3. Click

4. If there are multiple scout images, navigate them using the standard <u>Navigate</u> commands.

Three lines will appear on the scout image:

- two white lines indicate the intersection of the first and last images of the series
- a single yellow line represents the currently displayed image of the selected series

If no lines appear, then the selected series does not intersect the scout image.

### Related

• Multiple Reference Lines

### PET / CT Fusion

#### PET / CT Fusion overview

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

If the PET / CT Fusion module is enabled in eUnity™, Fusion is available in the Advanced Visualization menu so that you can generate fused PET and CT stacks. Fusion uses slice-based navigation, where possible. When it is not possible, for example, the gantry is tilted relative to the patient, or the patient is rotated relative to the table, it uses volume-based navigation. When slice-based navigation is used, the annotation overlay shows the slice numbers. When volume-based navigation is used, the annotation overlay displays NA in place of slice numbers.



#### WARNING

All reformatted and volume rendered views (PET / CT Fusion) are treated as Lossy and will display a Lossy Indicator in the upper-right corner of the viewport. See Lossy image display for more information.

#### Turn on PET / CT Fusion

- 1. Open a PET / CT study.
- 2. Click and click Fusion.
- 3. Drag the CT or PET into the viewer from the Series Tray.
- 4. On the Fusion toolbar, click the desired Fusion layout.

These layouts will generate slice-based axial, sagittal, and coronal fusion planes from the selected series and display it in the following layout formats. Note that the tiling (i.e. 3x3) is drawn on the icon.

- 🔳 3x3 basic fusion layout with CT(non-fused), PET(non-fused), and fused views
- 📠 3x1 fused axial, sagittal, coronal views
- 📠 3x1 fused axial, sagittal, coronal views + 3D MIP
- 3x1 axial only
- 3x1 sagittal only
- 3x1 coronal only

Custom layouts (can be added to the toolbar using the <u>Customize the toolbar</u> editor)

- 2x2 axial CT, PET, and fused view with 3D MIP PET
- 3x2 axial CT, PET, and fused view, coronal PET, coronal fused, and 3D MIP PET

### PET / CT Fusion Tools

NOTE: Collaboration is not currently supported for PET / CT Fusion.

#### **Advanced Visualization Parameters**

View or change render types, render parameters, or SUV parameters. The tabs / options that are available in the panel depend on the visualization mode (i.e. Fusion vs 3D) and the series type (i.e. PET vs CT) or series orientation (i.e. same plane as the original series or not) that is selected in the viewer.

### **Fusion Blending**

Left-click and drag the mouse up or down to increase or decrease the PET opacity. Increasing the opacity shows more of the functional (metabolic) data from the PET. Decreasing the PET opacity shows more of the anatomical data from the CT.

### **Fusion Presets**

Apply presets such as Hot Iron to fused PET / CT studies so that the metabolic data of the PET information is assigned a preset pseudo color value from the Color Look Up Table (CLUT).

#### **Point Tool**

#### Circle ROI

O Draw a circular region of interest.

### PET / CT Fusion indicators

### Image loading indicator

Shown in the viewport to indicate that data is being loaded.





#### CAUTION

When you load an image or zoom further into an image, eUnity will typically need to load more data. Once loaded, the indicator will disappear. If the indicator is visible, you must wait for the full data to be loaded.

### Lossy compression indicator (reformatted and rendered views)



### WARNING

Lossy 1

All reformatted and volume rendered views (MPR and 3D) are treated as Lossy and will always display a Lossy indicator.

In MPR, 3D , and Fusion modes, hover the cursor over the 1 to display the final JPEG render quality.

#### Limited Measurements indicator

Limited Measurements

Shown in the viewport to indicate that not all measurement types are available for the series. Click the for more information.

#### Partial Volume indicator

Partial Volume

Shown in the viewport to indicate that the complete 3D volume cannot be rendered. A partial volume occurs when the original 2D data does not provide contiguous 2D slices.

### SUV not available

#### SUV not available indicator

Shown in the viewport to indicate that there is not sufficient data to

perform SUV measurements. Click the U fo



#### Interactive view mode in PET / CT Fusion



#### CAUTION

The images presented in eUnity PET / CT Fusion Display Layouts are derived from a continuous-space volume which is constructed from the original 2D images. As a result, the user-presented 2D images may not have a direct spatial mapping to the original 2D images. More specifically, navigating in volume space is different from navigating the original 2D slices.

As the user-presented 2D images are derived from a different location and may be rendered with different thickness, the applied pseudo color palette may be different from the intensity values on the original 2D PET images as they are subject to interpolation algorithms used in the rendering process.

If there is ever any doubt concerning the fusion image(s), users should always reference the closest images from the original 2D PET images.

Interactive mode is a special low-latency mode that prioritizes frame-rate and is enabled in fast operations such as adjusting Window Level on the fly, navigating the stack, or adjusting the 3D image render function or volume orientation on volume rendered stacks.

Note: Viewports in Interactive mode will display  $^{\circ}$  in the upper-right corner of the viewport to indicate that higher quality images are in progress.

For information on adjusting the quality of interactive or final images, see <u>Advanced</u> <u>Visualization Parameters for Fusion</u>.

### Annotations and measurements in Fusion mode

Annotations and measurements that you make in Fusion are available only for your session. That is, they cannot be saved as a Presentation State.

However, if an ROI measurement is made on the original 2D PET stack, it can be saved as a Presentation State. Note that if any of the SUV parameters were changed, they will be saved along with the Presentation State. For information on using ROI tools in Fusion mode, see SUV measurement tools .

Advanced Visualization Parameters for Fusion

#### **Advanced Visualization Parameters**

View or change render types, render parameters, or SUV parameters. The tabs / options that are available in the panel depend on the visualization mode (i.e. Fusion vs 3D) and the series type (i.e. PET vs CT) or series orientation (i.e. same plane as the original series or not) that is selected in the viewer.

#### Render Parameters tab

#### Change the quality of interactive or final images

The Interactive Quality and Final Quality options scale up or scale down the quality of interactive images (images generated during on-the-fly rendering) and final images (images generated at rest, when no user commands are applied to the volume stack).

- 1. Click  $\square$  and click the Render Parameters tab.
- 2. Click and drag the handle on the Interactive Quality or Final Quality scales.

### Render Types tab

### Change the render type

The **Render Types** tab is available when you select a non-fused, reconstructed image in a fusion layout. For fused images, the render type is always MIP.

- 1. Click  $\square$  and click the Render Types tab.
- 2. Select one of the following render types:
  - Maximum Intensity Projection (MIP)
  - Minimum Intensity Projection (MinIP)
  - Faded Maximum Intensity Projection (Faded MIP)
  - Average Intensity Projection (Average)

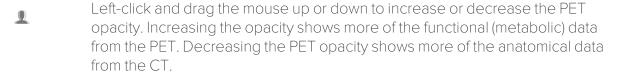
#### SUV Parameters tab

See SUV measurement tools.

### **Fusion Blending**

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

### **Fusion Blending**



- 1. Select a fused image. Do either of the following:
  - On the Fusion tab, click . Left-click and drag the mouse up or down to increase or decrease the PET opacity.
  - Click  $\square$  > Render Parameters. Drag the handle in the PET Blending slider.

### **Fusion Presets**

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

CT and PET modalities acquire and natively display the resulting images using grayscale. When fusing the two data sets together, eUnity™ applies a pseudo color from the Color Look Up Table (CLUT) to the PET data so that the metabolic data of the PET information has a pseudo color value.

#### **Fusion Presets**

Apply presets such as Hot Iron to fused PET / CT studies so that the metabolic data of the PET information is assigned a preset pseudo color value from the Color Look Up Table (CLUT).

### Change the color preset

- 1. On the Fusion tab, click <sup>(9)</sup>
- 2. In the dropdown, select a color preset.

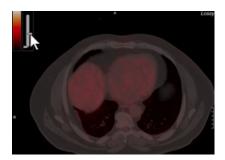
#### Alternately,

- 1. Hover the cursor over the vertical color palette in the upper-left corner of the fusion viewport.
- 2. Left-click the color palette to cycle through the available presets. Press and hold the Shift key during the mouse clicks to cycle through the fusion presets in opposite order.

### Filter grayscale range

Use the slider control in the upper-left corner of the fusion viewport to filter out (trim) the hottest (high-end) or coldest (low-end) grayscale values from the PET data displayed in the fused viewport. Once the filter range has been adjusted, the entire color palette in the viewer is reassigned to the filtered range set by the user.

**NOTE**: The entire color palette in the viewer will be reassigned across the filtered range that you set.



## Link color palette to PET Window Level

Link the color palette in fused PET /CT images with the Window Level in PET images. When this switch is toggled on, if you change the Window Level in a PET image, the color palette range in the fused PET / CT is also changed, and vice versa. For example, if you increase the Window Width, you also increase the color palette range.

- 1. Select a fused image.
  - Toggle the Link Palette with Pet W/L switch to the on position to link the color palette to the PET Window Level.
  - Toggle the Link Palette with Pet W/L switch to the off position so that changes to the Window Level do not affect the color palette, and vice versa.

# Revert to Original



# Revert to Original

Revert a series to its original presentation.

# Screen Layout

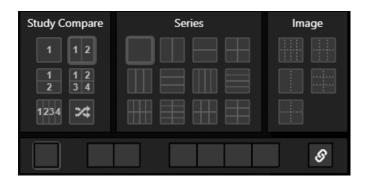
Screen layouts are accessed by pressing the Screen Layout button on the toolbar. From the Screen Layouts menu, you can choose the monitor layouts, study compare layouts, and the layouts for series within a monitor or the layout for images within a series.



### Screen Layout

Access study compare mode or change the layout of each monitor.

# Single monitor



### **Dual monitor**



### Four monitor



Screen layouts are grouped into the following categories:

Study Compare	These layouts control layout behavior when prior studies are inview in single or multi-monitor modes. If you change study compare modes to a layout that displays priors, the selected viewport will always remain in one of the study slots.
Series	Choose the number of series to display from each study. The gray lines represent the number of series within study.
Image	Choose the number of images to display from a single series. These are also called image tile layouts. The dotted lines represent images within the same series.

# Monitor layouts



If multi-monitor mode is enabled by the system administrator, the screen layout drop-down will provide the following display options: single monitor, dual monitor, four monitor, and synchronized multi-monitor. When dual monitor or four monitor are selected, eUnity will enter multi-monitor mode.

### NOTE

- Due to browser limitations, the maximize browser button is disabled when the software detects that there is more than one monitor.
- Collaboration mode is not available in Multi-Monitor mode.

Single Monitor	In Single Monitor mode there is one toolbar and one Series Tray.
Dual Monitor	The view is split between two monitors. This mode can be used even if there is only one physical monitor. In this case, eUnity splits the view into two virtual monitors. Each virtual partition that holds a study is referred to as a study slot. Each physical monitor or study slot has its own layout, toolbar, and series tray.

Four Monitor	Split the view among four monitors. This mode can be used even if there is only one or two physical monitors. In this case, eUnity splits the view into four virtual monitors. Each virtual partition that holds a study is referred to as a study slot. Each physical monitor or study slot has its own layout, toolbar, and series tray.
Synchronize Layouts	Synchronize each study slot so that they both use the same layout or view mode. For example, if you change the layout for one study slot, that layout will be applied to all study slots.

### Study compare, structured layouts, and shuffle layout

In all multi-monitor modes (Single Monitor, Dual Monitor and Four Monitor) the Study Compare Display options include Structured Layouts and a Shuffle Layout. The Shuffle Layout is only available if it is configured by the system administrator.

Typically, PACS workstations either present studies in a prescribed manner to help users keep an organized view of what series belongs to what study. Some users find this too restrictive and prefer PACS workstations that allow the user to drag any series to any viewport on any monitor. Through the use of both structured layouts and shuffle layout, eUnity supports both scenarios.

When shuffle layout is selected <sup>32</sup> the user can drag any series from any study to any available viewport. Structured layouts, on the other hand, define study slots to prevent series from different studies being mixed together. For example, the structured layout icon showing

two study slots with two studies will keep all the series from study 1 in study slot 1 and all the series from study 2 in study slot 2.

#### Multi-study ordering

System administrators can set either of the following modes of behavior when displaying more than one study in Structured Layouts (that is, the time ordering described below does not apply to the Shuffle Layout).

- Strict Time Ordering On: Studies displayed in a multi-study layout are always ordered from newest study date to oldest from left to right. This time-based ordering is always maintained when new studies are brought into view.
- Strict Time Ordering Off: Studies can be displayed in any order.



### Study slots

A study slot can only contain a single study. If a series is dropped into a slot containing a different study, the entire study slot, including all enclosed series cells, will be changed to the dropped study.

The same study cannot be displayed in two different study slots. This restriction causes different behavior depending on the time ordering configuration. If Strict Time Ordering is on, attempting to drag-and-drop a series for a study already on screen will only permit dropping into the existing study slot. When Strict Time Ordering is off, a series can be dropped into any study slot with the result that, if the study is elsewhere on screen, the studies will be swapped.

## Load studies from the Study List

Clicking on an item from the Study List will display that study in the first empty study slot. If there are no empty study slots, then the currently selected study will be replaced. If the selected item is not currently loaded into the viewer (that is, it is not available from the series tray) it will be loaded. When the maximum loaded studies limit is reached, the currently selected study will be unloaded.

When a study is displayed, the on-screen location is indicated using an icon on the Study List item with a corresponding icon in the series tray for the matching study. For example, the icon below from the Study List indicates that the study is displayed in the upper-left quadrant of the screen. For more information on how multi-monitor screen layouts affect hanging protocol layouts, see the  $eUnity^{\mathbb{N}}$  Administration Guide.



### Related settings

• Customize screen layouts

# Series Reposition



# **Series Reposition**

Swap series between viewports.

# Series Reposition on desktop

- 1. To reposition series in the viewports click to turn on series reposition mode.
- 2. Click a series to select it and drag it to another viewport.

# Series Reposition on mobile

1. Long-press the screen to pickup the series and drag it to another viewport.

# Spine Labeling

#### Spine Labeling

1/1/1

Add spine-related labels to images. In Spine Labeling mode, the **Spine Labeling** tab is activated to provide access to other spine labeling tools.

### Toggle Spine Labeling Markup

Hide or show spine labels. Note that Toggle Markup also hides / shows spine labels.

₽.

# Delete All Spine Labels

Delete all spine labels in the study.

### About spine labels



### CAUTION

The Spine Labeling tool does not perform any automatic detection of the individual vertebra in DICOM images. It uses the 3D spatial information within the DICOM images to apply spine label annotations to other spatially related series within the same DICOM study. This tool is intended only to assist a user to more easily add spine label annotations - it is the responsibility of the user to ensure that the labels are presented on the appropriate vertebrae within the study.

Annotations on vertebral bodies can help you to more easily understand the approximate position of an image within a patient's body. Typically, spine labeling should be used on studies with multiple views such as CT and MR so that eUnity™ can use the 3D information contained within the DICOM header of an image to automatically apply spine label annotations to other spatially related images. That is, if you apply labels to a sagittal series, eUnity automatically adds those labels to the corresponding vertebrae in the associated axial and coronal series.

Studies such as CR do not have DICOM information within the DICOM header that spatially relates multiple series. For these types of studies, the Spine Labeling tool can still be used to manually annotate a single image at a time. Images from such modalities are treated as sagittal views with the assumption that the top of the spine is at the top of the image. There is no automatic labeling of images in these non-spatially related modalities.

When you start labeling, eUnity will use the information in the DICOM header and the cursor position relative to the other spine labels to determine whether you are labeling ascending or descending order. The tool icon on the toolbar changes to display the vertebra that will be

added on the next click. For example, the Spine Labeling icon ( ) will change to and continue to increase or decrease as the mouse position changes. Sagittal and coronal views display the spine labels to the side of the image with a dashed indicator line and axial views display a text label centered at the top of the image. Text labels and indicator lines can be repositioned in any of the views.

For more information on spine labeling in different series and study types, see <u>Spine labeling</u> workflows below.

### Add spine labels



### CAUTION

The precision of the system placing spine labels depends on the user placing labels as close as possible to center of the vertebrae.



### NOTE

For DICOM studies with multiple views, such as CT and MR studies, spine labels can be applied on coronal, sagittal, and axial images. Spine labels are not projected on scout images or other 2D images in the study.

To add spine labels, do the following:

- 1. Click the series that you want to label. For CT and MR studies, this will typically be a sagittal view.
- 2. On the Markup tab, click to turn on Spine Labeling mode and display the **Vertebral Bodies** menu. Once Spine Labeling mode is turned on, the **Spine Labeling** tab is activated and it is available until the end of the session.
- 3. In the Vertebral Bodies menu, click the vertebra that you want to start with.
- 4. In the image, left-click on a vertebra center to add a spine label. If necessary, click and drag the text label to reposition it. Alternately, to add and reposition the label in one step, click and hold the vertebra center and then drag the cursor to position the text label (note that this behavior does not apply to axial series).
- 5. Move your cursor to the next vertebra. The **Spine Labeling** icon on the toolbar indicates which label will be added on next. In case the toolbar displays no vertebra label or a vertebra label different from what you want to add, click the **Spine Labeling** icon again

and select the desired vertebra from the **Vertebral Bodies** menu. See below for how to Add C8, T13, or L6 labels.

To turn off spine labeling, and return to Navigation mode, click

## Add C8, T13, or L6 labels

To apply C8, T13, and L6, simply skip those vertebrae and apply the labels immediately before and after them. When you return your cursor to the skipped vertebra, eUnity will automatically switch to the missing label so you can apply it. For example, to add the C8 vertebra, do the following:

- 1. Add the C7 label, skip C8, and apply T1.
- 2. Move your cursor between the C7 and T1 labels. The **Spine Labeling** tool icon on the toolbar changes to C8.
- 3. Left-click the image to apply the C8 label.
- 4. Move the mouse to the vertebra below T1. The **Spine Labeling** tool icon will change to T2.

### Edit or delete spine labels

To edit a spine label, do any of the following:

- On sagittal or coronal views, drag the text label or indicator line to a new location. Ensure that you keep the end point of the indicator line as close as possible to vertebra center.
- For non-spatially related studies, drag the text label or indicator line to a new location.
- On axial views, drag the label anywhere in the image.

To delete spine labels, do any of the following:

- Click to show the **Vertebral Bodies** menu. Clear the vertebra that you want to remove.
- Click the spine label that you want to remove and press the Delete key on your keyboard.
- To remove all spine labels in the study, on the **Spine Labeling** tab, click

### Navigate using spine labels

1. Double-click the spine label on a sagittal or coronal series to display that vertebra in all series.

### Spine labeling workflows

The typical scenarios where spine labeling is used are:

- Labeling a sagittal or coronal series (e.g. a CT or MR)
- Labeling an axial series (e.g. a CT or MR)
- Labeling an image (e.g. a CR or DX)



### NOTE

For DICOM studies with multiple views, such as CT and MR studies, spine labels can be applied on coronal, sagittal, and axial images. Spine labels are not projected on scout images or other 2D images in the study.

### Labeling workflow for sagittal series

The most common use of spine labeling is to label images within a sagittal series of a DICOM study. This workflow is similar for labeling coronal series. In this scenario, the common steps are:

- 1. Left-click a vertebra on a sagittal image to apply a spine label. For example, C2. The Spine Labeling tool will do the following:
  - Apply a spine label of C2 to every image in the selected image's series.
  - Copy a matching spine label of C2 to every image in any spatially related sagittal images within the same study.
  - Apply a spine label of C2 to any spatially related axial image within the same study that are near the point selected in the sagittal image.
  - Apply a spine label of C2 to any spatially related coronal image within the same study that are near the point selected in the sagittal image.
  - Apply a spine label of / C2 to any spatially related axial image within the same study that are anatomically above the image labeled C2.
  - Apply a spine label of C2 / to any spatially related axial image within the same study that are anatomically below the image labeled C2.

**NOTE**: If you move your mouse above and below the C2 spine label annotation, you can see that the spine label tool icon will update its spine label vertebra to C1 and C3, respectively.

Select a second vertebra on a sagittal image to apply another spine label of below the first spine label of C2. The Spine Labeling tool will do the following:

- Apply a spine label of C3 to every image in the selected image's series.
- Copy a matching spine label of C3 to every image in any spatially related sagittal images within the same study.
- Apply a spine label of C3 to any spatially related coronal image within the same study that are near the point selected in the sagittal image.
- Update the spine label(s) of C2 / to C3 to the images within the selected series and any spatially related axial image within the same study that are near the point selected in the sagittal image.
- Update the spine label(s) of C2 / to C2 / C3 to the images within the selected series and any spatially related axial image within the same study that are between the images identified as C2 and C3.
- Update the spine label(s) of C2 / to C3 / to the images within the selected series and any spatially related axial image within the same study that are below the images identified as C3.
- This process continues for each spine label the user selects to apply.

### Labeling workflow for axial series

This workflow is similar to labeling a sagittal series. It is used when the study does not contain spatially related sagittal or coronal images. Reference lines are useful for adding spine labels on studies that do not have sagittal images. In this scenario, the user selects the axial image they would like to apply a spine label on (for example, C2) and click to apply the spine label. The Spine Labeling tool does the following:

- Apply a spine label of C2 to the selected image and any spatially related axial image within the same study that are near the point selected in the axial image.
- Apply a spine label of / C2 to any spatially related axial image within the same study that are anatomically above the image labeled C2.
- $\bullet$  Apply a spine label of C2 / to any spatially related axial image within the same study that are anatomically below the image labeled C2.

The user navigates to the image that has the vertebra C3 and clicks to apply a spine label. The Spine Labeling tool does the following:

- Update the spine label(s) of C2 / to C3 to the selected image and any spatially related axial image within the same study that are near the point selected in the axial image.
- Update the spine label(s) of C2 / to C2 / C3 to the images within the selected series and any spatially related axial image within the same study that are between the images identified as C2 and C3.
- Update the spine label(s) of C2 / to C3 / to the images within the selected Series and any spatially related axial image within the same study that are below the images identified as C3.

### Labeling workflow for non-spatially related studies

Spine labels can be applied to modalities that have no image orientation and position information, (that is, studies other than CT and MR). Images from such modalities are treated as sagittal views with assumption that the top of the spine is at the top of the image. There is no automatic labeling of images in these non-spatially related modalities.

# Study information panel

The Study information panel is displayed on the left side of the viewer. It contains various tabs that provide information about the study. Each of the tabs are made available based on configuration settings and the availability of systems integrated to the eUnity™ server. If none of the tabs are available, the Study Information button is not displayed.

- Click in the upper-right corner of the panel to undock (float) the panel and drag it to the desired location in the viewer area.
- If the panel is undocked, click  $\square$  to dock it on the left side of the screen.

See Dock or undock the side panels by default to change the default behavior of the panel.

### Study List (if available)

 $\equiv$ 

Open a panel containing information grouped into the following tabs: Study List, Study Details, Report, and Notifications.

# Study List

The Study List tab displays a list of other studies for the current patient. Click any study in the Study List to load it. The study will replace the study in the currently active viewport. Note that the number of studies that can be loaded at a time is configured by your administrator. For more information, see <u>Load studies from the Study List</u>.

**NOTE**: The image number that is shown beside the Modality label represents the DICOM value for the number of instances in the study. This value may not correlate with the actual number of images available for viewing. The study could, for example, contain unsupported GSPS objects or images that are not for clinical processing.

### Study Details

The Study Details tab displays basic information and study comments for the currently selected study. Note that the availability of Study Comments depends on a source system being available for, and integrated to, the eUnity server.

#### Report

If eUnity has been configured to retrieve report information from a report system / archive, the report text for the currently selected study appears in this panel. Note that you can launch directly into the report panel by clicking

**NOTE**: If there are multiple DICOM SR reports associated with the study, eUnity will only display the most current by date.

Notifications

See Content change notifications

# SUV measurement tools

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

SUV can be measured in a PET study in 2D mode or in Fusion mode. In eUnity™, SUV can be measured only for BQML (becquerel / milliliter) units using any of the following measurement methods: body weight (bw), lean body mass (lbm), and body surface area (bsa). For more information on how these measurements are calculated, see SUV measurement methods.

Note that some essential data must be available in the DICOM header to perform SUV measurements (see Required DICOM attributes to calculate uptake values). If essential data is missing, the SUV measurement cannot be performed and the "SUV not available" indicator will display in the viewport with a tool tip that provides details about the missing information. If necessary, non-essential data such as sex, weight, height, dose, half life, radiopharmeceutical, and time of administration can be manually edited in the Advanced Visualization Parameters panel.



### IMPORTANT NOTE ON SUV CALCULATIONS

SUV calculations in eUnity are based on industry-accepted standards and equations. They may differ from the methods of the customer. The customer is responsible for evaluating and approving the use of SUV measurements in their facility before the tool is approved for widespread use.

This section contains the following information:

- Overview of SUV measurement tools
- Change SUV parameters
- Change the SUV measurement method
- Measure SUV using an ROI tool
- Measure SUV using the Point Tool
- Save SUV measurements
- SUV measurement methods

Overview of SUV measurement tools



Circle ROI

Draw a circular region of interest.

# Ellipse ROI

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W

Draw an ellipse region of interest.

### Rectangle ROI

Draw a rectangular region of interest.

# Freeform ROI / Doppler Envelope

Draw a freeform region of interest. For cardiology, peak and mean velocity and peak and mean gradient are shown.

### **Point Tool**

### Change SUV parameters

If non-essential parameters such as patient weight or administration time are entered incorrectly at the time of acquisition, you can manually update these parameters in the Advanced Visualization Parameters panel and optionally save them as a presentation state.

- 1. On the Fusion tab, click  $\square$  to open the Advanced Visualization Parameters panel.
- 2. In the panel, click the SUV Parameters tab.
- 3. Change any of the non-essential parameters such as sex, weight, height, dose, half life, radiopharmeceutical, and time of administration.
  - Click Apply to apply your changes to the current view.
  - Click Cancel to discard any un-applied changes.
  - Click on the Home tab to reset all parameters back to the values you started with (if it is the original study, the values are set back to the DICOM values, and if it is a presentation state, the values are set back to the original presentation state values).
  - Click Reset (to the right of the associated parameter) to reset the parameter's value back to the original DICOM value (even in a presentation state, this will revert to the original DICOM value).

4. To save the parameters that you have changed, click **Apply** to apply the changes and then save the study as a presentation state. Note that the study must also contain markup on the 2D PET (for instance an ROI measurement) to be able to save it as a presentation state. For more information, see <u>Save SUV measurements</u>.

In the Advanced Visualization Parameters panel, a missing parameter displays a yellow warning marker and a modified parameter displays a checkmark beside it. Updated parameters are also shown in the SUV measurement overlay as shown in the image below. The units of measure, shown on the first line of the SUV overlay, indicate that they are based on "updated" parameters and the changed parameters are listed in the last line of the SUV overlay.

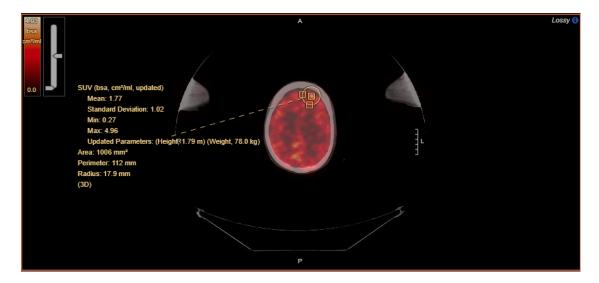


Figure 12: Updated height and weight parameters in SUV measurement overlay

### Change the SUV measurement method

The measurement method and the units are shown in the SUV measurement overlay. The available measurement methods and units are:

- gram per milliliter (g/ml) for body weight (bw) and lean body mass (lbm)
- centimeter-squared per milliliter (cm2/ml) for body surface area (bsa)
- 1. On the Fusion tab, click  $\square$  and click the SUV Parameters tab.
- 2. Select a measurement method.
- 3. Click Apply.

#### Measure SUV using an ROI tool

When you measure SUV using an ROI tool, the SUV overlay shows the average and standard deviation as well as the minimum and maximum pixel values within the boundaries of that ROI. System administrators can configure what is shown in the overlay.

- 1. On the Markup tab, click any of the ROI measurement tools or click the Circle ROI tool from the Fusion tab.
- 2. Click and drag to outline the region of interest. (In the case of the polygon ROI, double-click to end the measurement.)
- 3. The SUV values are displayed in the measurement overlay.

### Measure SUV using the Point Tool

The Point Tool measures the exact SUV value for a specific point.

- 1. On the Fusion tab, click -|-
- 2. Move the cursor to the location that you want to measure. The SUV value is displayed.

#### Save SUV measurements

SUV measurements that are made on the original 2D axial PET images can be saved as a presentation state. If any SUV parameters have been changed and those changes have been applied to the study, they will be saved as part of the presentation state.

- 1. On a 2D axial PET image, measure SUV using an ROI tool.
- 2. To save a presentation state, click  $\blacksquare$  on the study folder in the series tray.
- 3. In the confirmation dialog, select the markup that you want to save and click Yes.

#### SUV measurement methods

eUnity supports the following measurement methods: body weight (bw), lean body mass (lbm), and body surface area (bsa). This section explains the calculation details for each of these methods.



#### NOTE ON SUV MEASUREMENTS IN FUSION IMAGES

Since fusion images are constructed from a volume, SUV computation is subject to interpolation algorithms.

### Required DICOM attributes to calculate uptake values

The following DICOM attributes are required to calculate uptake values.

DICOM attribute	Alternative Name Used in This Documentation	Tag
Corrected Image		(0028,0051)
Decay Correction		(0054,1102)
Radiopharmaceutical Information Sequence  Radionuclide Total Dose (in Becquerel) Radionuclide Half-Life (in Second) Radiopharmaceutical Start Time Radiopharmaceutical Start Date Time	Radiopharmaceutical Injected Dose Radiopharmaceutical Administration Time	(0054,0016) (0018,1074) (0018,1075) (0018,1072) (0018,1078)
Series Date Series Time	Scan Time	(0008,0021)
Acquisition Date  Acquisition Time	Frame Acquisition Start Time	(0008,0022)
Frame Reference Time		(0054,1300)
Actual Frame Duration	Frame Duration	(0018,1242)
Patient's Weight (in Kilogram)		(0010,1030)
Patient's Size (in Meter)	Patient's Height	(0010,1020)
Patient's Sex		(0010,0040)
Philips SUV Scale Factor	Philips Body Weight SUV Scale Factor	(7053,1000)

DICOM attribute	Alternative Name Used in This Documentation	Tag
Philips Activity Concentration Scale Factor		(7053,1009)
GE Scan Date and Time		(0009,100d)

### PET exam background information

A PET exam starts by administering a certain dose of a radiopharmaceutical to a patient. A delay is necessary for patient's metabolic processes to deliver the radiopharmaceutical to the target of the study. After this delay, the PET scan is performed. The result of the scan is a series of PET images. A scan is divided into multiple frames (or bed positions) and the data acquired in each frame is used to generate several slices which belong to that frame.

### Decay correction calculation

The radiopharmaceutical decay is a continuous process throughout the exam. As a result, the pixel data obtained at different times during the exam may have different interpretation. A correction is necessary to unify this interpretation across the series; this correction is usually applied in two steps, one at the modality and one in the viewer application.

eUnity allows the calculation of SUV if the underlying series is corrected for decay with respect to the scan time at the modality. This condition is satisfied if (a) corrected image attribute contains the value DECY, and (b) decay correction attribute has the value START. Note that this correction does not account for the decay from the radiopharmaceutical administration time to the scan time. eUnity does correct for that decay as described below.

Denote by  $m{D}$  the radiopharmaceutical injected dose at the administration time, and by  $m{H}$  the half-life of the radionuclide used in the radiopharmaceutical. The values of  $m{D}$  and  $m{H}$  have the units Becquerel (Bq) and second, respectively. Also, denote by  $m{\Delta T}$  the time interval from the radiopharmaceutical administration time to the scan time. If the scan time is valid, the corrected dose at the scan time is given by:

$$C=D2^{-rac{\Delta ext{T}}{H}}$$

#### Scan time calculation

The scan time is valid if it has a value in compliance with the DICOM specification, and if it precedes the acquisition time of any frame in the exam. When the series is post-processed

after acquisition, the scan time is overwritten and hence no longer valid. The actual scan time can still be indirectly calculated if the following information is available:

- 1. Acquisition date and time The combination of acquisition date and time denote the frame acquisition start time
- 2. Frame reference time The time interval from the actual scan time to the average activity time. The average activity time for a frame is defined as the time instant within that frame where the instantaneous rate of radionuclide disintegration (or activity) is equal to the average activity over the frame.
- 3. Frame duration The time interval from the frame acquisition start time to the frame acquisition end time.

The procedure to indirectly calculate the scan time is as follows:

1. Calculate the time interval from the frame acquisition start time to the average activity time as follows. Let the frame acquisition start time coincide with the time origin t = 0. Denote by Nt the number of radionuclides at time t. We have

$$N_t=N_02^{-t/H}=N_0e^{-\lambda t}$$

where  $\lambda = \ln 2/H$  is known as the decay constant. The disintegration rate (or activity) at time t is given by  $-\frac{dN_t}{dt}$ . From the definition of the average activity time, the interval of interest is the solution for t of the following equation:

$$-rac{d}{dt}N_t \; = rac{1}{T}\int_0^T -rac{d}{d au}N_ au\;d au$$

where  $m{T}$  is the frame duration. The solution is given by:

$$t=rac{1}{\lambda}lnrac{\lambda T}{1-e^{-\lambda T}}$$

- 2. Subtract the value calculated in Step 1 from the frame reference time; the result is the length of the time interval from the actual scan time to the frame acquisition start time.
- 3. Subtract the value calculated in Step 2 from the frame acquisition start time; the result is the actual scan time.

#### SUV measurement calculations

The SUV is a normalized measure of radioactivity concentration and has the following generic form:

$$SUV = fP$$

In the above formula,  $\boldsymbol{f}$  is the normalization factor and  $\boldsymbol{P}$  is the activity concentration.  $\boldsymbol{P}$  is replaced with either the minimum or maximum pixel value within the boundaries of an ROI drawn over a PET or PET / CT fusion image, or the average value of all pixels within that ROI. The pixel values are directly read from the original full-resolution DICOM images before any transformation (such as Window Level) is applied.

We first consider a case where  ${\pmb P}$  has the unit BQML (Bq / Milliliter). In this case, the normalization factor can be defined in several ways.

### Body weight SUV calculation

For body weight SUV, the normalization factor is the ratio of the patient's weight  $m{W}$  in gram to the corrected dose  $m{C}$  in Bq, i.e.,

$$SUV_{bw} = rac{W}{C}P$$

The SUV unit for body weight is gram / milliliter.

#### Lean body mass SUV calculations

For lean body mass SUV, the normalization factor is the ratio of the patient's lean body mass in gram to the corrected dose  $m{C}$  in Bq, i.e.,

$$SUV_{lbm} = rac{LBM}{C}P$$

The lean body mass in kilogram is calculated from the patient's weight  $m{W}$  in kilogram, height  $m{H}$  in centimeter and sex using James formula for females and Morgan formula for males:

$$LBM_{male} = 1.10~W~-~120 \left(rac{W}{H}
ight)^2$$

$$LBM_{female} = 1.07 W - 148 \left(\frac{W}{H}\right)^2$$

The SUV unit for lean body mass is gram / milliliter.

#### Body surface area SUV calulations

For body surface area SUV, the normalization factor is the ratio of the body surface area in centimeter-squared to the corrected dose  $m{C}$  in Bq, i.e.,

$$SUV_{bsa} = rac{BSA}{C}P$$

The body surface area in centimeter-squared is calculated from the patient's weight  $m{W}$  in kilogram and height  $m{H}$  in centimeter using Du Bois formula:

# $BSA = 71.84 \; H^{0.725} \; W^{0.425}$

The SUV unit for body surface area is centimeter-squared / milliliter.

#### Remarks

- 1. Radiopharmaceutical administration date is implicitly inferred from radiopharmaceutical administration time, scan date and scan time. If the radiopharmaceutical administration time is before the scan time (e.g., radiopharmaceutical administration time = 14:27:00:000000 and scan time = 15:27:00:000000), it is assumed that the radiopharmaceutical administration date is the same as the scan date. If the radiopharmaceutical administration time is after scan time (e.g., radiopharmaceutical administration time = 23:29:00:000000 and scan time = 00:29:00:000000), it is assumed that the radiopharmaceutical administration date is one day before the scan date, i.e., the PET exam crosses midnight.
- 2. Radiopharmaceutical start date time attribute is ignored. This DICOM attribute, if present, provides the explicit date on which the radiopharmaceutical is administered.
- 3. We do not support GE private tag for scan date and time.

#### References

https://dicom.innolitics.com/ciods/pet-image/pet-image/00541300

 $\underline{\text{http://qibawiki.rsna.org/images/8/86/SUV\_vendorneutral\_pseudocode\_20180626\_DAC.pdf}$ 

### Switch Studies

#### **Switch Studies**

Select a study to switch to. If you switch away from a study and then switch back to it, it is reopened to the state in which you left it.

If this feature has been enabled by your administrator, the Switch Studies tool provides a list of the loaded relevant exams for a patient so that you can quickly select one to open. If you switch away from an exam and then switch back to it, it is reopened to the state in which you left it (that is, any markup and layout changes will be as you left them).

### Switch to another study

The Switch Studies tool may need to be added to the toolbar or context menu. For information on adding buttons to the toolbar or context menu, see <u>Customize the toolbar</u> or <u>Customize the context menu</u> or contact your system administrator.

- 1. Do either of the following:
  - On the toolbar, click 🏝 and select a study to open.
  - Right-click to open the context menu and click Switch Studies. Select a study to open.

# Toggle Markup

### Toggle Markup

Hide or show markup on images including markup on presentation states.

### Triangulation



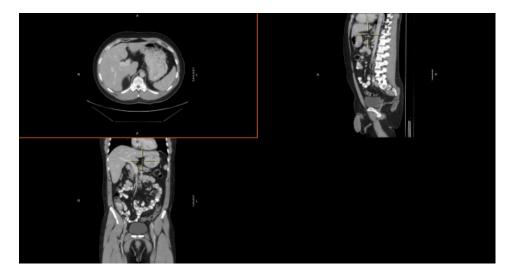
#### Triangulation

Navigate to a selected point in orthogonal series.

The Triangulation tool and <u>Reference Lines</u> tool work together to help you navigate orthogonal series.

- 1. Click  $\diamondsuit$  to turn on Triangulation.
- 2. Left-click and drag the mouse over a series to display the crosshair indicator on the other series in the view. The crosshair indicates the corresponding point on the different planes.

To navigate series, click on the scout and the corresponding series will navigate to the selected point.



#### Video

#### Toggle Cine mode / Play video



Play a series of images in succession (like a movie) or play a video. When Cine / Video mode is activated, the Cine toolbar is displayed in the active viewport. The default location of the Cine / Video toolbar can be configured by the system administrator.

Videos loop (replay) until you pause the video playback. Multiple videos can be played at the same time, but only one video can be unmuted at a time.

**NOTE**: Due to a limitation with Internet Explorer, videos in that are encoded with the AC3 audio codec will not be able to play in eUnity when you are using Internet Explorer. These videos will cause a "Study Content Not Supported" error to display in the viewer.

- 1. Play videos in eUnity™ by pressing on the toolbar.
- 2. Jump to the start or the end of the video using the Home and End keys. If the video has been trimmed using the trim slider, the Home and End shortcuts ignore the trim boundary and go to the start / end of the source video.

#### Video toolbar



#### Play / Pause button

Click to play or pause the video.

#### Target frame rate



Select the target frame rate to either speed up or slow down the video playback. Note that the video speed is not actually being changed, but rather the refresh rate of the screen. That is, a 2 minute video will still take 2 minutes to play.



#### Trim slider

Change the start or end point of the video.



#### **Current position**

Visual representation of the current video position on the slider.

### 00:00 / 00:31

### Current video position

Textual identification of current position in the video.



#### Mute

Turn on or turn off the video volume.



#### Previous / Next Series

Open the previous or next series (can be video or non-video).

### Viewport Capture

#### Viewport Capture

Take a snapshot of the image in the selected viewport when you are in an advanced visualization mode. Viewport captures will be available in their own series and will include any modifications that were made to the original image such as markup, zoom, window level, etc.

#### **Delete Viewport Capture**

Delete the selected viewport capture as long as it has not already been saved. This button must be added to the context menu and will be available only after a viewport capture has been created.

#### Create a viewport capture

Viewport captures are a snapshot of an image that include any markup or modifications, but exclude the demographic overlays. Once you create the viewport capture, it will be available to save, to print, or to export in JPG or PNG or DICOM format. The viewport captures cannot be edited after they are created. That is, if you create a viewport capture and make changes to it before you save it, those changes will not be saved. Either make the changes on the original image and redo the viewport capture, or save the viewport capture, make your changes, and save it again.

The Viewport Capture tool may need to be added to your toolbar or context menu. For more information, see <u>Customize the toolbar</u> or <u>Customize the context menu</u> or contact your system administrator.

- 1. Select the viewport that contains the image to capture. For the best image quality, make the viewport as large as possible (for example, double-click the image so that only a singular viewport is displayed).
- 2. Click ... The viewport capture is added to the viewport capture series in the series tray.

#### Viewport Capture series



The viewport capture series is created in the series tray after you create a viewport capture. If you delete all unsaved viewport captures, the viewport capture series is removed from the series tray. The number in the upper-left corner represents the total number of viewport captures. The number in brackets with an asterisk represents the number of unsaved viewport

captures.

#### View a viewport capture

You cannot open a viewport capture while in an advanced visualization mode.

- 1. Do either of the following:
  - Click  $\Longrightarrow$  > 2D to change back to 2D mode. In the series tray, click the viewport capture series to open it in the viewing area.
  - Drag the viewport capture from the series tray into a 2D viewing area.
- 2. In the viewing area, scroll to the viewport capture that you want to see.

#### Viewport capture indicators

The following indicators are shown in the viewport when you open a viewport capture.



#### Unsaved viewport capture indicator

Shown in the viewport on an unsaved viewport capture.



#### Saved viewport capture indicator

Shown in the viewport on a saved viewport capture.

#### Save a viewport capture

If your administrator has enabled saving viewport captures, a dark save icon is shown in the study folder in the series tray. The icon will be enabled () once you create the viewport capture. Viewport captures must be saved before your session ends, before you start a collaboration session, or before you hit the refresh button () when you receive a content change notification, otherwise, the viewport captures are lost. Your administrator will configure a maximum number of viewport captures that you can create before you are prompted to save.

**Note**: If using a keyboard shortcut to save, you are initiating a save only on the currently selected study.

- 1. To save a viewport capture, click  $\stackrel{\square}{=}$  on the study folder in the series tray.
- 2. In the Save dialog, select Save new viewport captures and click Save.

#### Delete an unsaved viewport capture

If you have not yet saved a viewport capture, you can delete it from the viewport capture series in the series tray. The Delete Viewport Capture tool may need to be added to your context menu. For more information, see <u>Customize the context menu</u> or contact your system administrator.

- 1. Do either of the following:
  - Click  $\Rightarrow$  2D to change back to 2D mode. In the series tray, click the viewport capture series to open it in the viewing area.
  - Drag the viewport capture from the series tray into a 2D viewing area.
- 2. In the viewing area, scroll to the viewport capture that you want to delete.
- 3. Right-click the viewport capture and click Delete Viewport Capture.

The viewport capture is deleted from the viewport capture series. If you delete all viewport captures, the viewport capture series will be removed from the series tray.

#### Window Level

In mammography studies, the viewport background retains its color when the Window Level is changed. For more information, see Air gap suppression .

### **\**-

#### Window Level

Change the Window Level for the selected image.



#### Reset Window Level

Reset the images to their original Window Level settings.





Select a predefined Window Level. Window Level presets are configurable by the system administrator.

#### Window Level Scope



This feature must be enabled by the system administrator.

Change Window Level to apply to the study, the series stack, or only the image. By default, Window Level operations apply to the series stack.

#### Manually change the Window Level

The Window Level operation can be mapped to middle-mouse button or right-mouse button by the system administrator.

- 1. Click \* to turn on the Window Level tool.
- 2. Click and hold the left mouse button in the viewport.
  - Drag the cursor up and down to adjust Window Level.
  - Drag the cursor left and right to adjust Window Width.

To get fine Window Level control, press and hold the CTRL key while you drag. The Window Level will be adjusted in smaller increments.

3. To reset the Window Level to its initial presentation, click

#### Apply a Window Level preset

The Window Level Presets dropdown provides access to site-level, modality-specific Window Level presets. The Window Level Presets button is shown only if there are presets available for the study being displayed. If a study contains multiple-modalities, the dropdown will be populated with the presets matching the modality of the selected series. If the selected series has no presets, the icon is disabled. Additional presets can be defined by the system administrator.

1. Click 4 and select a preset.

#### Change the Window Level Scope

NOTE: This feature must be enabled by the system administrator.

By default, Window Level operations apply to all of the images in a series. To instead apply Window Level changes at the study or image level, do the following:

- 1. Click and select any of the following options:
  - W/L Image Scope
  - W/L Series Scope
  - W/L Study Scope

When the Window Level scope is changed, the icon on the toolbar changes to reflect the current selection:

- Window Level Image Scope
- Window Level Series Scope
- Window Level Study Scope

## Zoom/Pan Images

#### Zoom / Pan

Zoom in on or pan an image in the selected viewport. When series are linked, zoom / pan is applied across all linked series.

- 1. Select an image.
- 2. Click
  - To zoom in incrementally, roll the mouse wheel forward.
  - To zoom in using a smooth motion, click and hold the mouse wheel and move the mouse forward.
  - To pan, left-click and drag the mouse left or right.

The zoom factor in the demographic overlay details the zoom factor.

#### Related

• Zoom/scale the viewer

#### 700m / scale the viewer

Use the viewer's Zoom feature to increase or decrease the size of the main viewer components (for example the toolbar, series tray, and side panels). The viewer components can be scaled up to 140% of their original size or scaled down to 70%. When you change the viewer zoom factor, it does not affect the zoom factor for images in the viewports, but demographic overlays may adjust based on the zoom factor and the amount of space that is available.

If your administrator has enabled preference saving, your zoom settings will automatically be applied the next time you log into the viewer as long as your monitors are the same height as the monitors that you used when you last set your viewer zoom settings.

- 1. Click  $\equiv$ . In the Zoom section, do either of the following:
  - Click or + to decrease or increase the size of the viewer components.
  - Click **Auto** to have the viewer automatically set the size of the viewer components based on the height of the monitor.

NOTE: This feature is not available on mobile devices or on Internet Explorer.

#### Related

• Zoom / Pan Images

# Hanging protocols

### Hanging protocols overview

This feature requires a separate license and may not be available. Contact your system administrator to have this feature licensed and enabled.

Hanging protocols (HPs) are a set of instructions that are used to position and manipulate images in the eUnity™ viewer. Users can create HPs that are available only for themselves, and administrators can create HPs for entire groups or for an entire site.

In eUnity, you create an HP by manually arranging series in the viewer and then "capturing" the viewer state as a new HP. In order to capture the viewer state, eUnity needs to be able to tell what it is looking at (i.e. what kind of study it is and what type of series is in what viewport). eUnity determines study type and series type using **Study Selectors** and **Series Selectors**. Selectors take the manual work out of creating an HP. Instead of the HP author telling eUnity what series to put where, eUnity intelligently determines what is on the screen by comparing the study and series DICOM attributes against the HP selector library. The more robust your selector library, the less you have to manually edit the HP.

#### Study selectors

Study Selectors define what content will trigger a specific hanging protocol to be applied. These answer the question, what kind of study is it? eUnity comes with a broad set of Study Selectors (for example, the "CT" Study Selector which will match any kind of CT). It is up to administrators to define more specific Study Selectors for the site (for example, CT chest).

#### Series selectors

Series Selectors evaluate the DICOM attributes in a series to define what is unique about each series. Is it an AXIAL? An AXIAL T2? When you identify the unique pieces of information about a series, that series type can be consistently mapped to the desired location on the screen. The more detailed the selector, the more precise you can make the hanging protocol. eUnity comes with a basic set of Series Selectors (for example, view position is PA or AP). It is up to administrators to expand the Series Selector library with data that is specific to your site. For example, with a basic set of Series Selectors, the hanging protocol can perhaps identify that you have a CORONAL series in the upper-left viewport. If you have more detailed Series Selectors, the hanging protocol could identify that you have a CORONAL PD FAT-SAT in the upper-left viewport. With the more detailed selector, the next time the hanging protocol is applied, the CORONAL PD FAT-SAT series will be in the upper-left viewport instead of just any CORONAL series.

#### Display set

Display sets are the series in the study. Display sets are listed so that you know what series are available to be arranged in the viewer. Display sets identify the series that are available in the study by matching series selectors to the attributes in the series. If no series selectors are defined, the viewer creates display sets based on series descriptions. If no series descriptions are defined, the viewer creates display sets based on series number.

#### Presentation steps

Presentation steps are the views that you step through in a hanging protocol. For example, step one of a mammography hanging protocol may be to read the CC views (LCC, RCC) and step two is to read the MLO views (LMLO, RMLO) and step three may be to view all images with CAD markers turned on. Each of these states is captured as a presentation step.

#### Note on strict hanging of display sets

When display sets are mapped to viewports in a hanging protocol, you have the option to enable strict hanging. When strict hanging is enabled, if a study does not contain the display set that is defined for the view, the viewport will be left blank. When strict hanging is not enabled, the next available series will be shown in the viewport.

For information on enabling strict hanging for display sets, see <u>Edit the presentation step</u> view.

### Putting it together

- Study selectors connect the study to the hanging protocol.
- ▼ Series selectors connect the series to the display set.
- ▼ Display sets are mapped to viewports as presentation steps.

#### Example

Dr. Smith wants to create a new HP that she will use to read MR studies of the brain. She opens a brain MR, sets the screen layout to  $2 \times 2$ , and then drags the series into the viewports. In the first step of the read, she wants to look at the SCOUT, AXIAL, SAGITTAL, CORONAL, in that order. Dr. Smith drags each series to the desired viewport and clicks  $\stackrel{\square}{=}$  on the Hanging Protocol tab. eUnity does the following:

- identifies the study type by comparing the study metadata to the **study selectors**: in this case, an MR study of the brain
- identifies the device type and number of screens: in this case, a web viewer with one monitor

- identifies the series types using **series selectors**: in this case, a SCOUT, AXIAL, SAGITTAL, CORONAL, AXIAL T1 FLAIR, and CORONAL T1 FLAIR
- maps the series to **display sets**: in this case a SCOUT, AXIAL, SAGITTAL, CORONAL, AXIAL T1 FLAIR, and CORONAL T1 FLAIR
- identifies the location of the series on the screen as a **presentation step**: In this case, the SCOUT: upper-left, AXIAL: upper right, SAGITTAL: lower-left, and CORONAL: lower-right, and AXIAL T1 FLAIR and CORONAL T1 FLAIR: not shown

In the next step of her read, Dr. Smith wants to look at the same kinds of images, but with reference lines turned on. Dr. Smith adds a new presentation step named "Reference Lines". In the **Presentation step properties**, she selects Reference lines and saves the presentation step.

eUnity makes a new presentation step where the layout is the same, but the reference lines are on

In the next step, Dr. Smith wants to look at all of the FLAIR images. Dr. Smith adds a new presentation step named "FLAIR". In the viewer, she drags all of the FLAIR series onto the screen and then in the presentation step editing panel of the hanging protocol editor, she clicks **Get Viewer State**.

• eUnity creates a new presentation step where only the FLAIR series are shown on the screen.

Once finished, Dr. Smith saves the hanging protocol. Since she is not an administrator, it will be available only for her. The next time she opens an MR study of the brain, her MR - BRAIN hanging protocol will be automatically applied.

- When the study opens. the viewer shows the SCOUT, AXIAL, SAGITTAL, and CORONAL series, in that order.
- Clicking on the Hanging Protocol tab moves to the next presentation step. The viewer shows the same series, but with reference lines on.
- Clicking on the Hanging Protocol tab moves to the next presentation step. The viewer shows the FLAIR series.

### Create a hanging protocol

Before reading this section, see <u>Hanging protocols overview</u>. It contains explanations of hanging protocol concepts and terms that are used in these instructions. If you are an administrator, see the hanging protocol section in the  $eUnity^{\text{\tiny M}}$  Administration Guide.

#### Quick guide

The following is a set of basic instructions so you can quickly get started with hanging protocols. To learn more about the more advanced fields in the Hanging Protocol editor, see the Advanced guide below.

- 1. Open a study and arrange the series in the viewports as you'd like them to be seen in the first step of the hanging protocol.
- 2. On the **Hanging Protocol** tab, click . eUnity opens the hanging protocol editor. The viewer state is captured as the first presentation step in the hanging protocol.
- 3. In the Name field, add a descriptive name for the hanging protocol.
- 4. Edit the Display Sets, if needed.
- 5. To add a new presentation step, click + in the Presentation Steps section.
- 6. To edit the presentation step, click in the new step. The Presentation Step dialog opens.
- 7. In the Presentation Step dialog, in the **Name** field, add a name for the new presentation step.
- 8. Rearrange the series in the viewer and click Get Viewer State. The viewer state is captured as a new presentation step.
- 9. In the Study Slots section of the Presentation Steps dialog, click the individual viewports to edit the display sets or set Display Set properties.
- 10. Click OK.
- 11. Repeat steps 5-10 for each presentation step that you want to add.
- 12. Click **Apply** at the bottom of the Hanging Protocol editor to apply the changes to the current view.
- 13. Click **Save** to save the changes.

#### Advanced guide

The number of steps that it takes to create a hanging protocol depends on the quality and quantity of your system's Study Selectors and Series Selectors. After you lay out the study in the viewer, if your selector library is detailed enough, eUnity should be able to precisely identify study types and series types. If your selectors need a little more detail, there may be a few extra steps needed to create a hanging protocol. The following table represents two

possible hanging protocol workflows. Detailed instructions for each step of the workflow are available below.

# Selectors identify study and series Selectors identify study and series precisely Arrange series and capture the Arrange series and capture the viewer state Set hanging protocol matching Set hanging protocol matching criteria criteria Add Presentation Steps, if necessary Refine the Study Selector Define the view for the Refine the selection criteria for the Presentation Step study Add viewer-level properties, if Add or edit Display Sets necessary Add Presentation Steps, if Apply and save changes necessary Define the view for the Presentation Step Add viewer-level properties, if necessary

Apply and save changes



### Hanging Protocol tab overview

The following buttons are available on the Hanging Protocol tab of the toolbar for managing, adding, and editing hanging protocols. For information on navigating through a hanging protocol after it is applied, see Select a hanging protocol and step through it.

#### Settings - Hanging Protocols



Open the hanging protocol panel (the Hanging Protocol tab in the Settings panel) to add, edit, copy, or delete hanging protocols.

#### Add Hanging Protocol



Captures the information on screen (display sets and layout) and creates a new hanging protocol.

#### **Edit Hanging Protocol**



Edit the active hanging protocol.

This icon is available only when there is an active hanging protocol. Access non-active hanging protocols in the hanging protocol panel (the Hanging Protocol tab in the Settings panel).

Lay out the study in the viewer and capture the viewer state

#### Arrange series and capture the viewer state

- 1. Open a study and arrange the series in the viewports as you'd like them to be seen in the first step of the hanging protocol.
- 2. On the Hanging Protocol tab, click . Alternately, if the hanging protocol panel is already open, click Add in the upper-left corner of the panel and then and click obeside Add Hanging Protocol. eUnity captures the selection criteria for the study and series, and captures the overall layout. This information is displayed in the hanging protocol editor as the Study Selector, Display Sets, and the first Presentation Step. Note that properties such as Window Level, rotation, etc. are not captured; they must be set manually.

**NOTE**: If Shuffle mode is turned on when you capture the viewer state, the screen layout will be captured, but not the study information. To capture the study compare mode, turn off Shuffle mode before you capture the viewer state.

#### Name the hanging protocol and set matching criteria

This part of the hanging protocol defines criteria that the study and viewer must meet for the hanging protocol to be chosen.

- 1. In the Name field, add a descriptive name for the hanging protocol.
- 2. In the **Priority** field, select a priority. When multiple hanging protocols match a study, the hanging protocol with the higher priority will be chosen. If multiple matching hanging protocols have the same priority, a user's own hanging protocol will be chosen over the group or site hanging protocols and a group hanging protocol will be chosen over a site hanging protocol. If there are no user-level or group-level matches, the hanging protocol with the more specific selection criteria is used. Note that the priority will be shown in the priority column in the hanging protocol panel as long as the browser window is large enough to display the column.
- 3. In the **Device** field, select the device type that the hanging protocol should be used for. For example, only choose this hanging protocol when the user is on a tablet.
- 4. In the **Screens** field, select the number of screens that the hanging protocol should be used for. For example, only choose this hanging protocol when the user has 2 monitors.
- 5. If necessary, add additional Study Selectors. In the Study Selector

field, start typing the name of a Study Selector and select it from the list. The Study Selectors will be separated by "OR". For example, MRI knee with contrast OR MRI knee without contrast OR MRI knee with / without contrast.

#### Refine the selectors

If the Selectors identify the study and series at a general level, but you would like something more specific, you can further refine the Study Selectors by removing some of their selection criteria or you can add your own selection criteria to the hanging protocol. You can also edit the Display Sets to further refine the Series Selectors.

For example, if the Study Selector used by the hanging protocol has selection criteria that says Modality is equal to MR AND Manufacturer is equal to ACME, but you want to remove the manufacturer criteria, you can clear that criteria in the Study Selector Refinements section. Conversely, if the Study Selector has selection criteria that says Modality is equal to MR, but you want this hanging protocol to apply only to MR studies from a ACME machines, you can add Manufacturer is equal to ACME in the Selection Criteria section.

Or, for example, a Series Selector identifies an AXIAL series, but you were actually interested in that series because it was an AXIAL T2, you can add additional selection criteria to the AXIAL Display Set in the Display Set section. For example, MR repetition time is greater than 2000 AND MR echo time is greater than 80 AND Flip angle is equal to 90.

#### Refine the Study Selector

Optionally remove selection criteria from the Study Selector. This does not edit the actual Study Selector; it is refined only for the specific hanging protocol. Once you make refinements to the Study Selector in the hanging protocol, the hanging protocol will no longer automatically inherit changes that are made to the Study Selector by an administrator. You will be notified that there are changes available and you can choose to accept them. See <a href="Accept Study Selector updates">Accept Study Selector updates</a> below.

- 3
- 1. Click beside Study Selector Refinements to expand the section.
- 2. Click a checkbox to clear any of the selection criteria. Click the checkbox beside the operator (AND / OR) to clear all the selection criteria in the expression.

When a Study Selector has been refined, three asterisks are

displayed beside the label in the hanging protocol editor.

### Study Selector Refinements\*\*\* (Optional) >

The asterisks are also displayed beside the Study Selector in the hanging protocol panel.

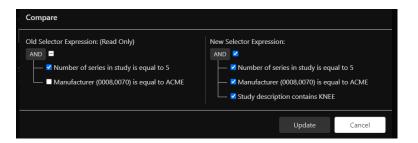


#### Accept Study Selector updates

If an administrator makes changes to a Study Selector, any hanging protocols that use that Study Selector and have Study Selector refinements will show a message in the hanging protocol editor indicating that "One or more expressions have changed".

#### Study Selector Refinements\*\*\* (Optional) ✓ One or more expressions have changed

- 1. To view the changes, click to expand the Study Selector Refinements section and click to view a comparison of the old Study Selector and the new Study Selector.
  - A Compare dialog opens. On the left, it shows which Study Selector selection criteria are currently used in the hanging protocol in a read-only view. On the right, it shows the new selection criteria that the hanging protocol will use if you choose to accept the Study Selector update.
- To update the hanging protocol to use the new Study Selector expression, click Update. To continue to use the old Study Selector expression, click Cancel. Note that if there are multiple new selection criteria and you only want some of them, you can clear any of the checkboxes in the New Selector Expression section before clicking Update.



#### Refine the selection criteria for the study

- 1. In the Selection Criteria section, select AND or OR. If the all selection criteria must be true to match a study, select AND. If any of the expressions can be true to match a study, select OR.
- 2. Click to add a selection criterion field.
- 3. For each selection criterion, select the DICOM attribute, the operator, and the value. For example, to use the hanging protocol for a study without priors, add "AND Number of studies is equal to 1". To use the hanging protocol for a study with priors, add "AND Number of studies is greater than or equal to 2".

For information on creating more advanced expressions, see the eUnity™ Administration Guide.

Note: Selection criteria is appended to the Study Selector (see step

2). So, if the study selector is MR and you add selection criteria of AND Manufacturer is equal to ACME, then the hanging protocol will apply to studies where Modality is equal to MR AND Manufacturer = ACME.

#### Add or edit display sets

- 1. To add a Display Set, click † in the Display Set section. To edit a Display Set, click on the display set.
- 2. In the Name field, add or edit the display set name.
- 3. Select AND or OR. If the all selection criteria must be true to match a series, select AND. If any of the expressions can be true to match a series, select OR.
- 4. Click to add a selection criterion field.
- 5. For each selection criterion, select the DICOM attribute, the

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- operator, and the value. For example, Series description contains PD.
- 6. Apply any desired properties to the display set. For more information, see Display Set properties.

For information on creating more advanced expressions, see the eUnity™ Administration Guide.

#### Add Presentation Steps and define the presentation step view

Presentation steps are the views that you step through in a hanging protocol. For example, step one of a mammography hanging protocol may be to view the left breasts (LCC, LMLO) and step two is to view the right breasts (RCC, RMLO) and step three may be to view all images with CAD markers turned on. Each of these states is captured as a Presentation Step. You can define a different study compare mode and monitor layout for each presentation step in the hanging protocol.

#### Add a Presentation Step

- 1. To add a new Presentation Step, click in the Presentation Steps section or click to copy an existing Presentation Step.
- 2. Click 🗹 in the newly added step.
- 3. In the **Name** field, add a name for the new Presentation Step.
- 4. Select the Monitor Mode, Study Compare Mode, and Monitor
  - layout or click Get viewer state to automatically capture these fields from the current layout in the viewer.
- 5. If there are any properties that should be applied to all of the Display Sets in the Presentation Step, set those properties. For more information, see <u>Presentation Step properties</u>.

#### Edit the presentation step view

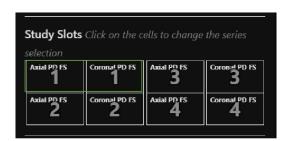
Set which display set is shown in which viewport and optionally override some of the properties that are set on the presentation step. To do this, you can either change the layout in the viewer and click

Get viewer state to automatically capture the layout and display sets (if available), or manually configure the view in the Presentation Step dialog. These instructions explain manual configuration.



NOTE: When you click Get viewer state, properties such as window level, rotation, etc. are not captured. Properties must be set manually.

The numbers on the screens in the Study Slots section represent studies. The current study is 1, the most recent prior is 2, the next most recent is 3, and so on. A "study slot" is the physical space that a study occupies. For example, if the current study is spread across 2 monitors then study slot one will appear on monitors 1 and 2. This is represented with the number 1s below.



- 1. In the Study Slots section of the Presentation Steps dialog, click a viewport.
- 2. In the Series Selection dialog, choose the display set that you want to display in the viewport.
- 3. To add alternate display sets, click beside Display Sets.
  Alternate display sets are useful for studies that are missing series. If, for example, your first choice for the view is a Sagittal PD FS, but if that wasn't available, you would prefer to see any Sagittal instead, you add a Sagittal PD FS display set first and then Sagittal display set after that.
- 4. If necessary, select property overrides for the view (for example, set strict hanging of display sets). For more information, see <u>View</u> properties.
- 5. Click OK.

#### Set viewer-level properties



 Select any properties that should apply at the viewer / study level.
 For more information on the available properties, see <u>Viewer</u> properties. **NOTE**: Most viewer-level properties can be overritten at the display-set level, presentation-step level, or the view level.

#### Apply and save changes

- 1. Click **Apply** to see your current hanging protocol settings in the current view. Note that Apply does not save changes.
- 2. Click **Save** to save the hanging protocol. The hanging protocol will be available only for you.



If you edit a hanging protocol and save it, but do not click Apply to apply the changes to the current view, you will continue to see the old hanging protocol in the viewer. To update the viewer to show the changes you made to the hanging protocol, reselect it from the Select

Hanging Protocol dropdown on the toolbar.

If you changed the name of the hanging protocol, you will see the old

hanging protocol name when you hover over \_\_\_. The name will be updated once you select the new hanging protocol in the dropdown.

#### Hanging protocol properties

Hanging protocols, use properties to control what tools or modes are enabled or disabled, what panels or tools are shown in the viewer, and what kind of effects (such as inversion, rotation, window level etc.) are applied to the series. Properties are inherited, so most can be set at the viewer-level and then overridden in the display set, presentation step, or the individual views in the presentation step.

- Viewer properties
- Display Set properties
- Presentation Step properties
- View properties

The labels beside the properties have the following meanings:

Action: true Enable the property.

Action: false Disable the property.

Action: none

Take no action on the property. That is, leave it in its current state. For example, if CAD Markers Action is true in presentation step 1, and Action is none is step 2, the CAD markers will remain turned on in step 2.

#### Viewer properties

With the exception of Breakout modality images and Combine series modalities, any of the properties that are set at the viewer-level can be overridden at another stage of the hanging protocol.

For example, if you want a mammography hanging protocol to have CAD markers turned on only for the first 2 steps of the hanging protocol, you can select CAD markers in the viewer properties and then deselect CAD markers in the third Presentation Step.

Toolbar mask	Hide unused tools from the toolbar. All tools are available to hide.
Navigate mode*	<ul> <li>Change the series navigate mode to one of the following options:</li> <li>Navigate through images— scroll only the selected series</li> <li>Navigate through series— scroll to the next series in the study when you reach the end of the series (i.e. scroll across series stacks). Once you reach the end of the study, eUnity will not loop back to the first series unless the configuration property EnableNavigateWrapAround is set to true.</li> <li>Navigate through studies (shuffle mode only)— Scroll to the next series in the study, and when the end of the last series is reached, continue to the first series of the next loaded study. Note that this option will skip over any series that are already on screen. This navigation option works only in Shuffle Mode.</li> <li>Navigate related series (mammo only) - In mammography studies, stack images that are the same view type together (for example, stack all CC views together). The view types that are stacked</li> </ul>
	together are configured by the administrator. When images are stacked, an indicator (such as 1/2)

	shows in the viewport to indicate that multiple images are stacked. Note that key images are not included in related series.
Mammography view	<ul> <li>Original view – Do not apply quadrant view or fit to window.</li> <li>Quadrant – Breaks the images in 4 quadrants and allows the user to step through each quadrant.</li> <li>Fit to window – Zooms in on the breast bounding box to fit the viewport.</li> <li>Note that the mammography view is also affected by the Mammo same size property. If Mammo same size is selected, the mammography view (i.e. original view, quadrant view, or fit to window) will be scaled up or down to match the relative physical size of other mammography images from the patient.</li> </ul>
Modalities to break out to separate series	Set which modalities should separate each image into a separate series. For example, if this property is set to DX, each image in a DX series will be broken out into its own series. Separate multiple values with a comma.
Modalities to combine to a single series	Set which modalities should combine all series into a single series. For example, if this property is set to CR, all series in CR studies will be combined into a single series. Separate multiple values with a comma.
Display demographics	Show or hide demographics.
Display reference lines*	Show reference lines on initial display.
Display CAD markers	Show the CAD markers for mammography studies by default. If you have CAD markers on in the first presentation step, they will be on as you scroll through the presentation steps unless CAD markers are explicitly turned off in the step or the CAD markers are off on the viewer properties.
Mammo same size	Scale mammography images so that they are displayed

	at the same relative physical size.
Auto shuffle mode	Automatically switch to shuffle mode if a series is dragged to a restricted location (for example, series from study 1 dragged to study 2 viewport).
Spine label	Toggle spine labels on or off.
Show report	Show the report panel on initial display.
Show study list	Show the study list on initial display.
Play cine	Start playing cine / video on initial display.
Series linking	<ul> <li>Series linking for studies: Link series from the same plane across all studies</li> <li>Series linking for active studies: Link series from the same plane only within the active study</li> <li>No Series Linking: Do not link any series</li> </ul>
Allowskipping	Skip over presentation steps when the study does not have the required display sets. Note that this applies only when the Strict property is selected.
Apply newest presentation state*	Applies the newest presentation state on initial display.
Presentation steps wrap around	Cycle back to the first presentation step in the hanging protocol once the final presentation step has been reached. This property will also cycle from the first to the last step when reversing through presentation steps.
Ignore saved zoom	Any zoom factor that was saved as part of a presentation state is ignored when you view the presentation state. If you are viewing a presentation state when this property is enabled, and you save a new presentation state or key image, the zoom factor from the original presentation state will not be saved in the new presentation state or key image. Note that the presentation state indicator is

still shown in the viewport even when zoom is being ignored.

#### Display Set properties

The Display Set properties apply to any matching series even if it is not hung in the Presentation Step view. The Display Set view properties are mainly used to set the desired default presentation of the series. For example, if a study contains a scanned document which is usually white and very bright, it is nice to invert the series with the associated Display Set even if it is not hung in one of the Presentation Steps. It will be inverted when it is dragged into view from the available series.

These properties can be overridden in the view properties.

Rotation

Apply a rotation to the images in the series:

- No rotation
- Rotate 90°
- Rotate 180°
- Rotate 270°
- Flip horizontal
- Flip horizontal + rotate 90°
- Flip vertical
- Flip horizontal + rotate 270°



#### WARNING

Since this option will change the orientation of the image it is critical that the images have pre-existing orientation markers either burned into the pixel data or the annotation indicator in the demographic overlay. In the absence of these indicators, the system administrator should configure the annotation overlay to include the image rotation indicator.

Window Level Preset

Select a window level preset to apply to the series.

<sup>\*</sup>These properties apply to prior studies as well. All other properties are for the current study only.

Sharpening	Apply a sharpening preset of High, Medium, or Low to the
	series.

#### Presentation Step properties

The presentation step view properties would be configured to step through different views of the series. For example: first show a series with a BONE Window Level then a SOFT TISSUE window level. If the window level of the series was just wrong, it would be best to correct it in the display set view properties.

Note that presentation step view properties are only applied if a specific display set matches the viewport. For example, if the view is not strict and the next available series is placed in the viewport, the presentation step view properties for the viewport will not be applied to the series. The presentation step view properties are usually specific to the series, so it normally would not make sense to apply them.

The presentation step properties are the same as the Viewer properties except for Breakout modality images and Combine series modalities.

#### View properties

Set properties that will apply at the view-level (that is, the individual display sets in the viewport). In the view properties, you can override the image rotation, window level presets, or sharpening properties. You can also set two additional properties:

Strict Selection	If a study does not contain the display set that is defined for the view, the viewport will be left blank, when this option is selected.
	If this option is not selected, the next available series will be shown in the viewport.
	For example, in a mammography study, if there is no LCC, you may want to select "Strict" to leave the viewport blank rather than show the next available series.
Invert image	Select to invert the image.

### Copy or edit a hanging protocol

#### Copy or edit a hanging protocol from the hanging protocol tab

If you select a site or group hanging protocol, eUnity creates a copy of the hanging protocol that will be available only for you. The Save button will be updated to say "Save for me" to indicate that you are not editing a site or group-wide hanging protocol.

- 1. On the **Hanging Protocol** tab, click to open the hanging protocol panel.
- 2. Optionally, use the Filter field at the top of the hanging protocol panel to filter the list and find the desired hanging protocol.
- 3. Select the checkbox beside the hanging protocol that you want to edit.
- 4. Do either of the following:
  - To edit the hanging protocol, click **Edit** at the top of the panel.
  - To make a copy of the hanging protocol so that the original hanging protocol is not changed, click **Copy**.
- 5. Make any changes and click the **Save** button at the bottom of the hanging protocol editor.

#### Edit the currently applied hanging protocol

If the currently applied hanging protocol is a site or group hanging protocol, eUnity creates a copy of the hanging protocol that will be available only for you.

- 1. On the **Hanging Protocol** tab, click  $\checkmark$  to open the hanging protocol editor.
- 2. Make any changes and click the **Save** button at the bottom of the hanging protocol editor.

### Select a hanging protocol and step through it



#### WARNING

If a presentation step changes the layout to a study compare mode that displays priors, the study in the selected viewport will always remain in one of the study slots.

### **Select Hanging Protocol**



This dropdown provides a list of "close match" hanging protocols. Choose a hanging protocol to apply to the current study in the viewer.

#### **Presentation Steps**



Click the dropdown arrow to show the available presentation steps for the active hanging protocol. Click a Presentation Step to jump to it.

Hover the cursor over the icon to show which hanging protocol is currently applied.

#### Backward



Move to the previous presentation step in the hanging protocol.

#### Forward

Move to the next presentation step in the hanging protocol.

# Mobile app

### Mobile regulatory information and safety guidelines

Adhere to the safety guidelines in this section for the use of this software on mobile devices.

- For diagnostic display mode, the light test must be performed.
- For mobile diagnostic usage when a full workstation is not available.
- This software is not intended for use with high native resolution diagnostic radiology images (if applicable).
- Mammography images and digitized film screen images must not be used for diagnostic interpretations.

#### Recommended viewing conditions

Contrast of the display can be significantly reduced under improper ambient lighting. Degraded contrast leads to reduced ability of perceiving subtle image features. It is the responsibility of the user to verify the viewing environment by performing the light test. The device should be used under the following recommended viewing conditions for diagnostic viewing:

#### Lighting conditions

Recommended viewing lighting conditions for diagnostic display are in a dimly lit office environment, away from overhead fluorescent lights and exterior windows. This is an environment similar to a radiology reading room.

#### Screen adjustments recommendations

- The screen should be clean (make sure the screen is free of dust, dirt, smudges and fingerprints) before using the viewer. The screen should be viewed straight on (perpendicularly).
- The screen should not be tilted, as tilting degrades image quality.
- To avoid specular reflections, the screen should be viewed in a location away from bright light sources (such as windows, bright walls, light boxes, and overhead lighting).

#### Screen brightness settings

Automatic brightness should be off and the brightness of the screen display should be set to maximum. The light test should be performed so that the environment is close to the ideal radiology reading area.

## Perform the light test

1. To start the light test, in the viewer click the bulb icon ( ) and click Launch Light Test.



#### Lighting environment user assessment

TG18-CT and TG18-MP standard test patterns will be displayed for subjective visual evaluation of screen luminance and lighting conditions. The user is responsible for validating the viewing environment by performing the light test. The user must verify that:

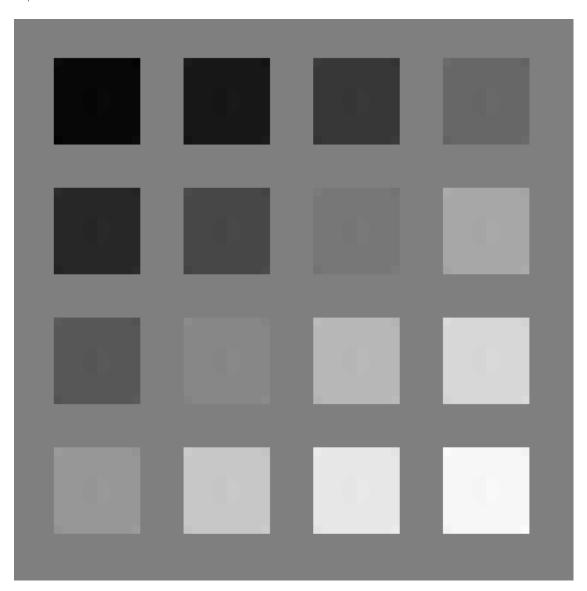
- 1. The device is set to a maximum brightness.
- 2. The recommended viewing conditions are present.

Please refer to the  $\underline{\text{Mobile regulatory information and safety guidelines}}$  in the User Guide for optimal settings recommendations.

**NOTE**: Once the test is performed, the user may accept that the lighting conditions in the viewing environment are ideal for making a diagnostic decision. If the user declines the current viewing environment, then it is recommended the user finds an environment with more appropriate lighting conditions and repeat the test, before making a diagnostic decision.

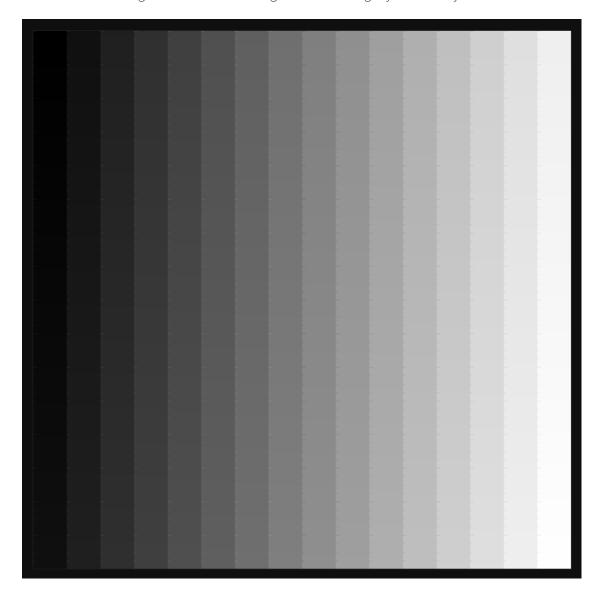
#### TG18-CT Test pattern

The luminance response of the display should be evaluated using the TG18-CT test pattern. This pattern contains 16 zones with differing luminance levels upon a uniform background. The pattern should be examined from a viewing distance of 30 cm. Please verify that all squares and inner half-moons are visible.



#### TG18-MP test pattern

The bit-depth resolution of the display should be evaluated using the TG18-MP test pattern. This pattern contains vertical grayscale ramps. The pattern should be examined from a viewing distance of 30 cm. Please verify the continuous luminance level variations of the vertical contouring bands and the diagonal inverse grayscale is symmetrical.



### Log in or log out (mobile)

If you have logged into eUnity on a mobile device before, the "Recent Connections" area on the login screen shows past URLs that you have logged into. Tap one to connect to it. If it is your first time logging in, the mobile login requires three pieces of information:

- server
- username
- password

The username / password are your standard eUnity™ login credentials.

Since the installed mobile application might connect to different eUnity instances, the server must be specified. The server can be entered a number of ways and resolves to the following:

- hostname → https://hostname:443
- hostname:8443 → https://hostname:8443

When left unspecified, the default access will always resolve to https on port 443.



#### CAUTION

Always use https for communications; never use http. http is not encrypted, which risks exposing patient and personal information.

#### Log out

Tap X in the upper-right corner of the Search screen. This will return you to the login screen.

### Search (mobile)

The mobile search provides many of the same options found in the desktop search. It is also subject to the same constraints that provide for a more targeted results set. When a search is performed, the 50 results will be displayed per page. Users can swipe up and down to scroll through the list. Tapping the **Next** or **Prev** will advance to the next page of results. When a tablet is held in landscape mode, the search fields are shown. When held in portrait mode, only the results are shown.

#### Search list columns

The width of the screen when you are on a mobile device determines which columns are hidden and which are shown. The order of the columns is controlled by the system administrator. To view the information in the collapsed columns, press the caret down character on the right side of the search results. To hide the columns, press the caret again.

NOTE: Column collapse is not supported in legacy search.

#### Display A Study

To display a study, tap on any row in the results.

### Mobile navigation

Once the study is launched in the viewing portion of the application, tools are presented across the top and the series tray is displayed on the bottom.

#### Navigation

In all modes there is a special **navigation zone** on the left and right borders of the viewport. These zones are not visible but remain active at all times when viewing a study. Inside these zones certain touch commands will perform navigation functions instead of their regular operations. This is to provide easy access to navigation no matter what mode is active.

- When viewing multiple images or series on the screen, each viewport has its own navigation zone.
- When viewing multiple images from the same series, navigation performed in one of the viewport navigation zones will be applied to all images.
- When viewing multiple series, navigation performed within one viewport will apply only to that series.



#### One finger tap

- on the top toolbar, selects a tool
- in the Series Tray, swap the series in display
- at the bottom of a navigation zone, move forward one image page
- at the top of a navigation zone, move backward one image page



#### Double-tap

In a viewport, the double-tap gesture will toggle between the currently selected viewport layout and a 1 up viewport layout.



#### Touch drag up / down

In a navigation zone, this motion navigates forward and backward through the image stack.



#### Pinch zoom

In the viewing area, these motions will incrementally zoom in on or out from the displayed image.



#### Touch drag multi-direction

When Window Level mode is active, pressing and dragging will modify window level values. When zoom mode is enabled, pressing and dragging will pan the image around the viewport.



#### Two finger drag

The two finger drag, in a left or right direction on a viewport, will move to the previous or next series.

# About the company

At Mach7 Technologies Canada Inc. we build innovative IT solutions that provide Health Professionals with secure access to the information they need at the point of care. eUnity provides clinicians access to medical images through their favorite web-browser, regardless of their location and with no client software to manage. eUnity does all this real-time and keeps medical images where they belong, with the PACS they reside on. This ensures clinicians are viewing the most up to date medical data.

### Privacy notice

Version date: February 28, 2020

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