

Ambra ProViewer Guide

Ambra ProViewer is a zero-footprint diagnostic HTML 5 medical image viewer that can be accessed through the web or integrated into any PACS. Easy to use tools are available for visualizing and annotating; window, MPR, PET CT fusion, volume measurements, and more.

Indications for Use

510(k) Number: K202335

Device Name: Ambra PACS including ProViewer

Ambra PACS software is intended for use as a primary diagnostic and analysis tool for diagnostic images for hospitals, imaging centers, radiologists, reading practices and any user who requires and is granted access to patient image, demographic and report information.

Ambra ProViewer, a component of Ambra PACS, displays, modifies and manages diagnostic quality DICOM images including 3D visualization and reordering functionality.

Lossy compressed mammographic images and digitized film screen images must not be reviewed for primary image diagnosis or image interpretations. Mammographic images may only be viewed using cleared monitors intended for mammography display.

Not intended for diagnostic use on mobile devices.

Name and Place of Business

DICOM Grid (dba Ambra Health)
199 Water Street, 34th Floor
New York, NY 10038

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

Browser Requirements

Ambra supports the following browsers.

Windows OS

Minimum versions for basic features

Firefox (version 68.0 +)

Google Chrome (version 57.0 +)

Microsoft Edge (version 12.0 +)

Internet Explorer 11 (Requires Java 7+ to upload imaging)

Minimum versions for advanced features*

Firefox (version 68.0 +)

Google Chrome (version 57.0 +)

Microsoft Edge (version 79.0 +)

Internet Explorer (not supported)

Mac OS

Minimum versions for basic features

Firefox (version 68.0 +)

Google Chrome (version 57.0 +)

Microsoft Edge (version 79.0 +)

Safari (version 11.0 +)

Minimum versions for advanced features*

Firefox (version 68.0 +)

Google Chrome (version 57.0 +)

Microsoft Edge (version 79.0 +)

Safari (not supported)

*Advanced Features

- Surface Renderer
- Volume Renderer (which includes MIP)
- Multi-planar Reconstruction (MPR)
- PET/CT Fusion

Advanced features are not supported in Internet Explorer or Safari.

Measuring Systems and Standards

For diagnostic use, users must use base monitor standards or better per modality below.

Not intended for diagnostic use on mobile devices.

Recommended Monitor Standards

Modality Capture	Modality Matrix	Screen Size	Pixel Matrix	Color Required	Comments
Ultrasound IVUS	512, 768 & 1024 126 lines	18 to 19 in 15 to 18 in	$\geq 1280 \times 1024$ $\leq 1280 \times 1024$	Doppler	IVUS, avoid screen sizes above 18" diagonal
NUC/PET PET/CT	Variable	18 to 19 in 19 to 20.1 in	$\geq 1280 \times 1024$ $\geq 1600 \times 1200$	Encoding	Not recommended on 5 MP Pixel size: $\geq 0.206\text{mm}$
MRI/CT ~ 1mm/Slice Typical	256 & 512	19 to 20.8 in	$\leq 1536 \times 2048$	Enhanced 3d Re-construction	Not recommended on 5MP Large studies on 4 MP 30" di- agonal color. Pixel $\geq 0.206\text{mm}$
fMRI	256 & 512	19 to 20.8 in	$\leq 1536 \times 2048$	Contrast Enhancement	≤ 3 MP color or mono- chrome or 6MP @ $\geq 0.206\text{mm}$
Fluoro/R&F CT-Fluoro	1024 x 1024	18 to 20.1 in	$\leq 1600 \times 1200$	N/A	1280 x 1024 minimum for 1:1 aspect image w/in 5:4 screen. Gray-to-Gray cycle response time $\leq 13\text{ms}$
CR/DR (100-150) microns	4 MP	20.8 to 21.3 in	$\geq 1536 \times 2048$	N/A	Ideal t to 3 MP, color or monochrome $\geq 400 \text{ cd./m}^2$
Digitized Film (50-150)	8 MP ~ 8-10 lp/mm	20.8 to 21.3 in	$\geq 1536 \times 2048$	N/A	3 MP color or monochrome 5 MP monochrome
Mammography (50-100)	20MP+ ~ 18-20 lp/mm	21.3 in	2048 x 2560	N/A	Lossy compressed mammo- graphic images and digitized lm screen images must not be reviewed for primary image interpretations. Mam- mographic images may only be interpreted using cleared monitors intended for mam- mography display.

SMPTTE is the Society of Motion Picture & Television Engineers. This organization has developed several test patterns to ensure image quality viewing standards. This 1024 x 1024 test image is used to calibrate the monitor on any viewing station running DICOM software. Once the SMPTTE pattern is loaded and displayed, the user should ensure the 5% and 95% grey scales are clearly visible. If not, adjust the monitor's contrast and brightness.

The American Association of Physicists in Medicine (AAPM) Task Group 18 (TG-18) is a national task force consisting of medical imaging experts and organizational affiliates dealing with performance evaluation of electronic display devices. Used correctly, the AAPM QC test patterns will indicate immediately if there are any potential issues with the calibration and/or monitor.

The pixel spacing test images for DICOM developed by David Clunie allow the user to appropriately calibrate and confirm display resolution. Test image data with physical pixel spacing bars are rendered allowing the user to quantifiably check spacing.

User Interface

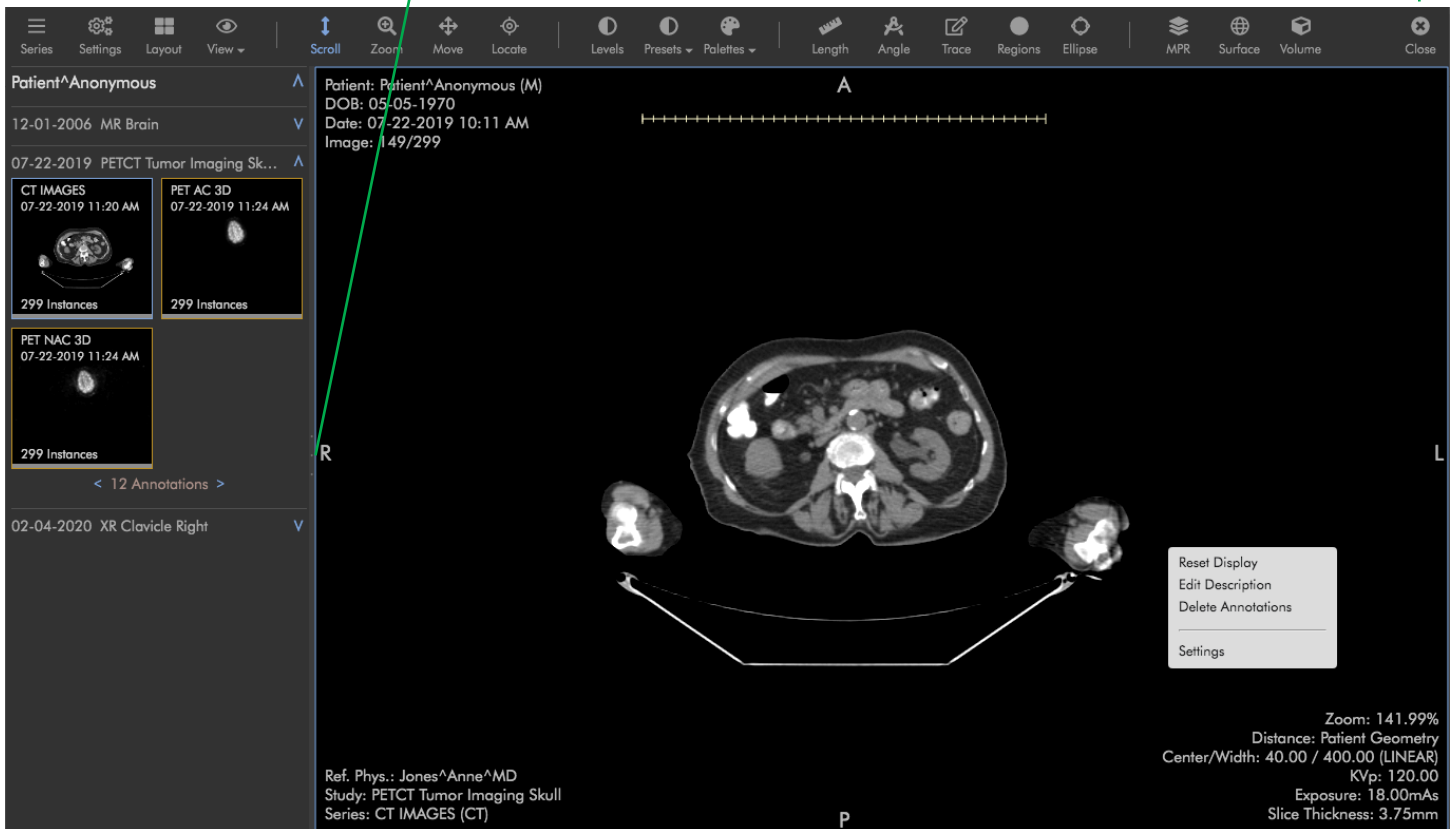
Overview

Main Toolbar

Thumbnails Pane Width

Slide divider to adjust width of thumbnails pane.

Closes ProViewer



Study Series Thumbnails

Studies are grouped by Series.
 Series contain one or more images.
 Click or drag a series thumbnail to load its images in the main image frame.

All series thumbnails display:
 Study description
 Date and time of study
 Number of instances

Thumbnails

When a study is opened the series for that study displays.
 Other studies for the patient that share the same MRN are available, with the series views closed.
 Click downward facing arrows to open study series.
 Studies display in chronological order from oldest to newest.

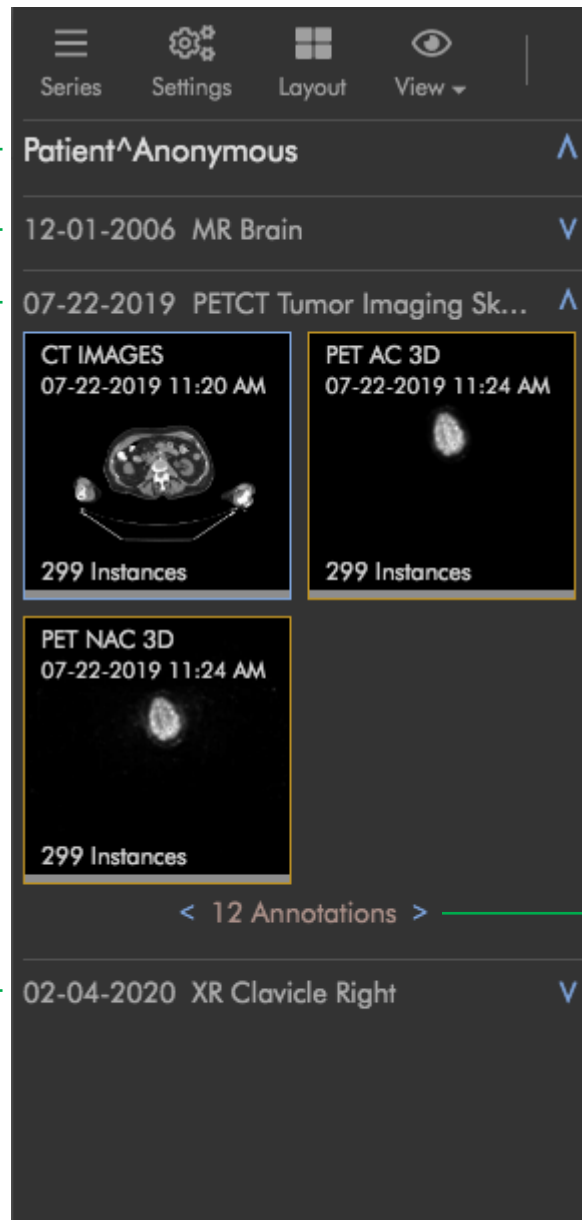
Labels

Patient name

Study #1: Date, Description

Study #2: Date, Description

Study #3: Date, Description



Show/Hide Functions

Hide all patient studies.

Show study thumbnails.

Hide study thumbnails.

Annotations Scrolling
 If annotations on a study have been made, click to scroll through images with annotations.

Show study thumbnails.

Images

Protected Health Information (PHI)

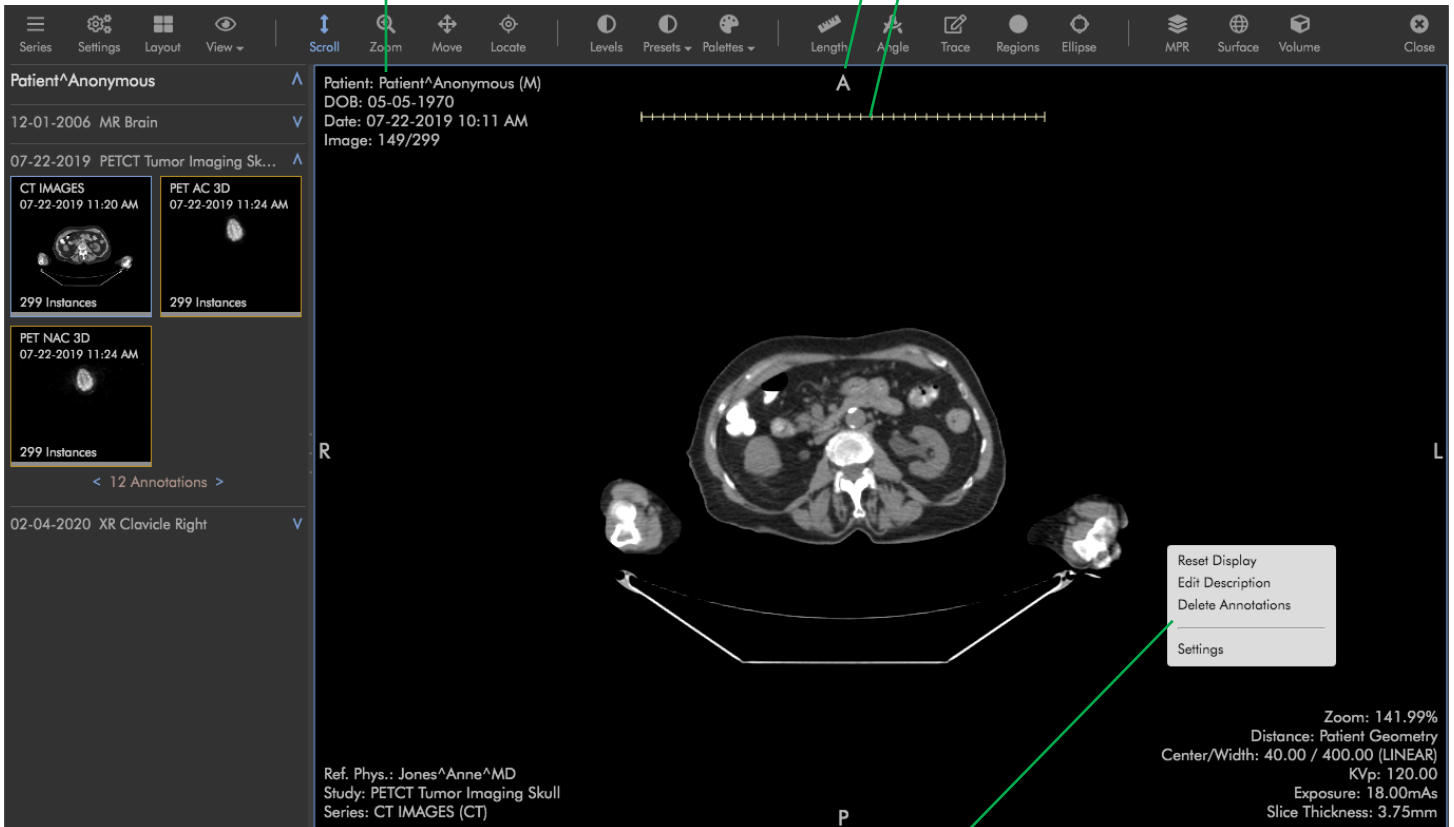
Patient: Name, and gender: (F) female, (M) male, (O) other
 DOB: Date of birth, MM/DD/YYYY
 Date: Study date, MM/DD/YYYY; time of day, HH24MMSS
 Image: 1/x: Image number in series

Patient orientation

Indicators appear at top, sides, and bottom:
 A: Anterior, S: Superior. P: Posterior, I: Inferior
 L: Left, R: Right

Ruler

Adjusts to scale on zoom in or out.



Protected Health Information (PHI)

Ref. Phys.: Referring physician
 Study: Description
 Series: Series description concatenated with modality in parentheses.

Context Menu

Displays with right-click, Windows;
 Control-click, Mac.

Zoom: Magnification level

Distance: Pixel spacing meaning

Center/Width: Window level

Indicates window level.

These items display only if the DICOM tags contain data:

kVp: Peak kilo voltage output of the device used

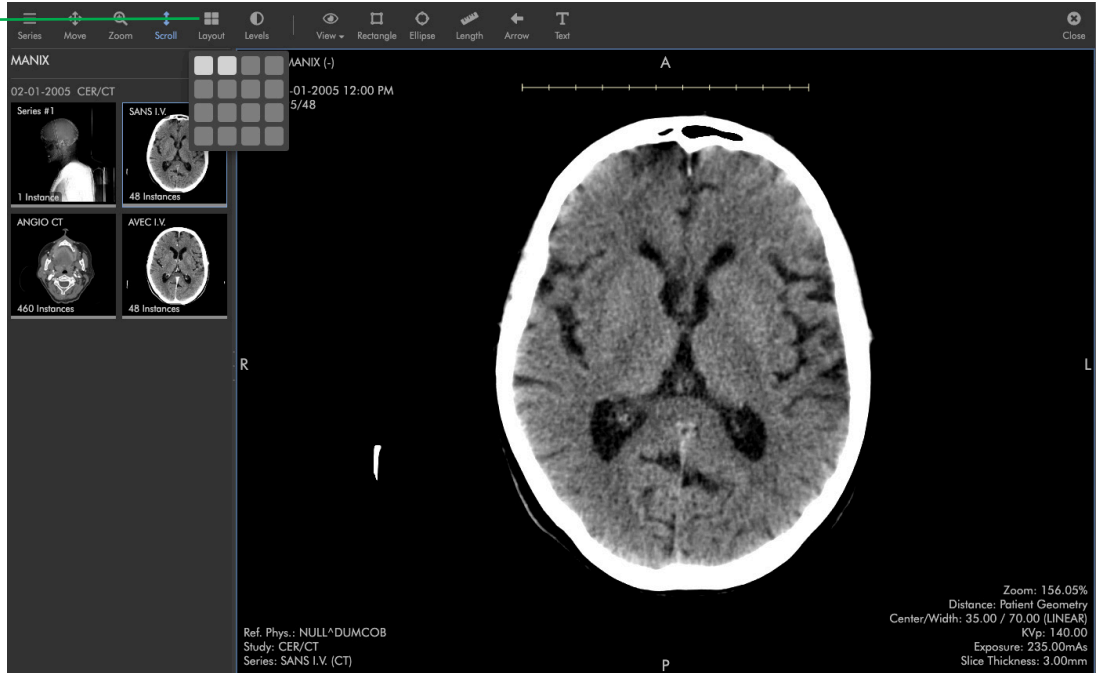
Exposure: The total exposure expressed in mAs

Slice Thickness: The slice thickness, in mm

Multiple Frames

Layout

Click 'Layout' to choose from one-up to sixteen-up layouts. One-up is shown here.

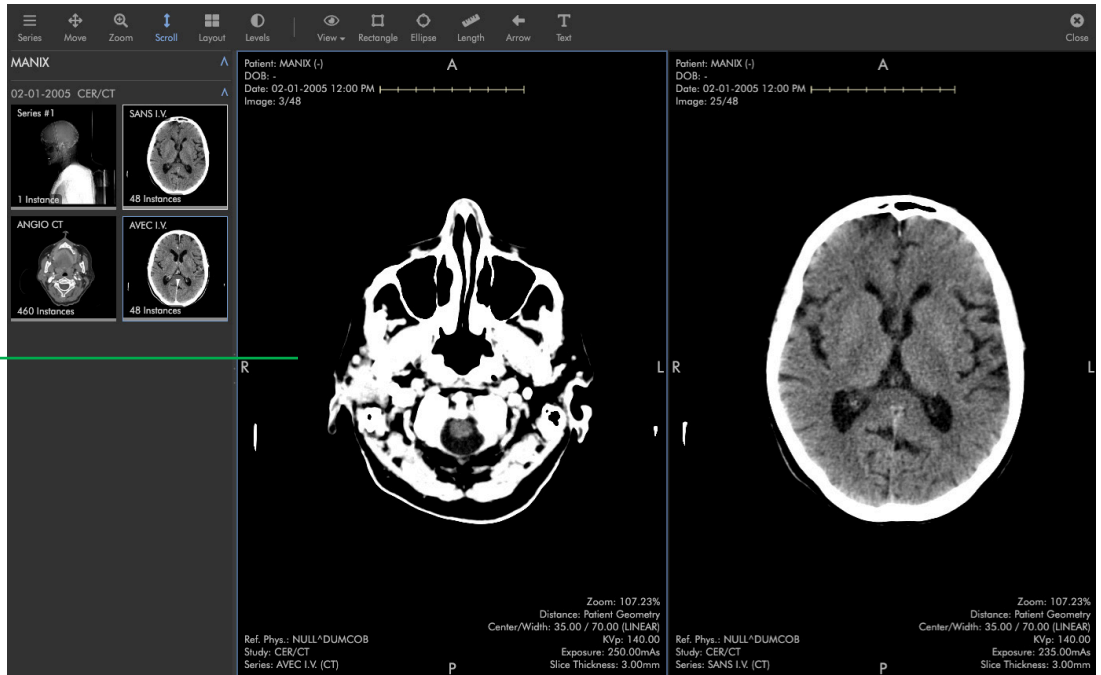


Layout

Two-up is shown here.

Active series

The active series is highlighted with a blue bounding box. Clicking another frame will make that frame active.



Tools

This is an inventory of Ambra ProViewer tools. ProViewer is typically customized for user requirements.

General



Help

Click to access help information in a new tab. The help URL is defined in General > Other settings.



Meet

Start a live collaborative meeting with other Ambra users. See a subsequent page for meeting instructions.



Settings

Opens the settings editor which allows you to set a customized toolbar, keyboard shortcuts, and other custom settings.

Visualization Tools



Cine

View images as a movie. Multi-frame studies are displayed with HTML5 video in actual frames per second. The cine sub-toolbar controls video playback.

Click 'Play' or 'Pause'. Click 'Increase Frame Rate' to increase playback speed. Click 'Decrease Frame Rate' to decrease playback speed. Click 'Set Frame Rate' to manually enter the frames per second.



Export

Select to show a menu of export options: As Image, As Image Download, As Image Download (De-identified), As Secondary Capture. "As Image" exports a PNG of the selected image in a new browser tab. "As Image Download" downloads a PNG of the selected image. "As Image Download (De-Identified)" downloads a PNG of the selected image without the PHI text overlay. "As Secondary Capture" generates a secondary capture DICOM file. All export options include any annotations on the image.



Flip H

Flips image horizontally.



Flip V

Flips image vertically.



Fullscreen

Click to enable full-screen mode. Use Escape key to exit.



Images

Select to display a menu of Key Image viewing options: Show Key Images, Show Collapsed Key Images, Show Flattened Key images, Clear All Key Images. "Show Key Images" displays one thumbnail per series that contains just the images that have been marked as key. "Show Collapsed Key Images" displays one thumbnail with all key images for that study. "Show Flattened Key Images" displays one thumbnail for each image that has been marked as key. Clicking "Show All" displays all study images again. "Clear All Key Images" removes all key image markers for the selected study.



Key

Select three points on the displayed image using the left mouse button to draw an angle measurement. A resizable circle will display automatically. The circle displays as a dotted line to indicate that it is for reference only. Click the dotted line and drag your mouse to re-position the circle. Click and drag the endpoint of each line segment to adjust the angle measurement. Click and drag the vertex to resize the circle and angle measurement.



Layout

Choose the number of series to display from the grid.



Levels

Sets the window width and window center for the selected series. You can change how window width and window level works with your mouse. Go to: Settings > General Settings > Mouse Controls, to make adjustments.



Link

When selected and either the mouse wheel or the scroll wheel is used to scroll through a series, non-orthogonal series will automatically scroll to the nearest parallel image.



Locate

A red cursor will display the corresponding location on all parallel and orthogonal series, and these series will automatically scroll to the nearest image.



Magnify

Click and drag to magnify the displayed area. Release your mouse and scroll to change the zoom level.



Move

Pans image.



Palettes

Click to apply a preset or custom color palette to the displayed study. Default options include Default (grayscale), Invert, Hot Iron, Hot Blue, and Fire.



Play

Click to view images as a movie.



Presets

CT supports window level presets for Bone, Head, Soft Tissue, and Lung.



Quadrant

Click to zoom the displayed MG image to the selected quadrant.



Reset

Returns series to original state while remaining on current image. Resets window level, rotation, and zoom.



Rotate

Rotates image in 90 degree increments.



Scroll

Scrolls through images in the selected series. Use mouse wheel or arrow keys.



Series

Click to collapse/expand the Series thumbnail pane.



View

Select to display a menu of show/hide options: Show/Hide Annotations, Patient Info, Overlays, Reference Lines, Ruler, and All.



Zoom

Zooms in and out on the selected image.

Annotation Tools

Annotation mark-up is not saved in the original DICOM file. However, you can use the GSPS export button to save a copy of the annotations, or use the secondary capture button on the Export menu to save a copy of the image with burned-in annotations. Annotation drawing functions can be set to automatically create measurements, or not. You can label any annotation by right clicking and selecting 'edit label'.



Angle

Select three points using the left mouse button. The angle at the middle point will be measured and displayed.



Arrow

Hold left click and move the mouse from point to point to drag an arrow from the source to the target. Then enter a label and click OK.



Drop Circle

Click to create a circle. The dimensions will be calculated automatically. Once the circle has been created, you can make it bigger or smaller by clicking inside the circle. Four dots will appear in a square outside the circle. Click and drag on any of the dots to make the circle bigger or smaller. To move a circle, click within the circle and drag.



Cobb

Locate the most tilted vertebra at the top of the curve and draw a parallel line to the superior vertebral end plate. Locate the most tilted vertebra at the bottom of the curve and draw a parallel line to the inferior vertebral end plate. The angle formed between the two lines is the Cobb angle.



Color

Before making an annotation, select a color. If you have multiple annotations with different colors, only measurements for annotations with the same color will show at the same time. You can toggle between different colors as needed.



Ellipse

Click to create an ellipse. The dimensions will be calculated automatically. Ellipses are also used with PET CT studies to generate SUV measurements.



Label

Left click to draw an ellipse around an area and then label it with a name. Please note that dimensions are not included by design. It is also useful to note that labels can be applied to any annotation by clicking 'edit label' in the right click/context menu.



Length

Hold left click and move the mouse from point to point to measure. Measurements display in millimeters to 100, then in centimeters. If you want the length to only show in mm, go to settings > general settings > annotations and tick the box 'Always Display in Millimeters'.



Ortho Axes

Hold left click and move mouse from point to point to create an orthogonal axes annotation. You can change the length of any end point or the location of the intersection by clicking on any of the circles and dragging. The measurement is displayed in millimeters to 100, then in centimeters. If you want the length to only show in mm, go to Settings > General Settings > annotations and tick the box 'Always Display in Millimeters'.



Polygon

Left click on each desired vertex point. The dimensions will be calculated automatically as long as the polygon is not self-intersecting.



Radius

Draw a circle and the radius measurement will be calculated automatically. Click and drag the mouse up or down to increase the size of the circle.



Rectangle

Click and drag the mouse to create a rectangle. The dimensions will be calculated automatically. Rectangles are also used with PET CT studies to generate SUV measurements.



Text

Click to create text annotations. After your text annotation has been created, you can make it bigger or smaller by clicking inside the text. The text editor will pop up. Click OK. Four dots will appear on the corners of the text box. Click and drag on any of the dots to make the font and text box bigger or smaller. To move an annotation, click within the text box and drag.

Annotation Trace Tools



Femoral

Select three points on the displayed image using the left mouse button to draw an angle measurement. A resizable circle will display automatically. The circle displays as a dotted line to indicate that it is for reference only. Click the dotted line and drag your mouse to re-position the circle. Click and drag the endpoint of each line segment to adjust the angle measurement. Click and drag the vertex to resize the circle and angle measurement.



Trace

Hold left click and move the mouse to create a freehand annotation. The dimensions will be calculated automatically as long as the annotation line is not self-intersecting. Also, to create a volume measurement, create traces on sequential slices. As long as the traces overlap the same anatomy, a volume measurement will be created. The feature supports adding n traces to the volume. Finally, trace areas are used with PET CT studies to generate SUV measurements.



Regions

The Regions tool is an advanced trace tool. It lets you make arbitrary shapes that can have non-contiguous parts, and it calculates the dimensions of the non-contiguous shape(s). The Regions tool also allows you to edit regions post creation. The Regions tool does not measure volumes across slices. There are two primary ways to use the Regions tool.

Use case #1:

Select the Grow Region tool from the Regions dropdown.

Pick an appropriate range.

In the viewport, click the center of the lesion in question. The dimensions will display in the top right of the viewport.

If you want to edit the region, select the Edit Region tool from the Regions dropdown and nudge adjust your trace. The dimensions in the top right will adjust to the new region.

If you want to grow the region, select the Grow Region tool from the Regions dropdown and click on the center of another lesion in question. The dimensions in the top right will add the new region.

Since the pixels in the lesion typically 'stand out' from the surrounding tissue, it is possible to pick a range that finds all lesion pixels and then stops at the border with the non-lesion tissue. In one click, you have drawn a region around the lesion that is more accurate and a lot faster than a manual trace.

Use case #2

Select the Shrink to Region tool from the Regions dropdown. The pixel intensity threshold will pre-fill with the Window Center pixel intensity.

All areas in the image with pixel intensity values above the pre-filled Window Center value will be traced, and the dimensions of these non-contiguous shapes will appear in the top right. The Shrink to Region tools removes any holes within a contiguous area for a cleaner view.

If you want to edit the region, select the Edit Region tool and nudge adjust your trace. The dimensions in the top right will adjust to the new region.

The Threshold to Region tool is similar to the Shrink to Region tool, but in the Threshold to Region tool, the holes within a contiguous shape are not removed. The resulting view is busier and more accurate. All areas in the image with pixel intensity values above the pre-filled Window Center value will be traced, and the dimensions of these non-contiguous shapes will appear in the top right.

The Range to Region tool is similar to the Threshold to Region tool in that holes within a contiguous shape are not removed. In the Range to Region tool, the user is prompted to enter minimum and maximum pixel intensity values to trace. The Window Center value pre-fills both prompts. All areas in the image with pixel intensity values within the min and max pixel intensity values will be traced, and the dimensions of these non-contiguous shapes will appear in the top right.

Advanced Visualization Tools



MPR

The Multiplanar Reconstruction (MPR) feature is used to display orthogonal orientations of a selected series. MPR supports series that meet the following criteria:

- Contain volumetric data.

- Contain at least 2 or more slices.

- All slices must have matching values for pixel spacing, rows, columns, and bit depth.

- All slices must have matching orientation.

If slices in the selected series do not have consistent slice spacing, a warning is displayed, as any gaps are ignored.

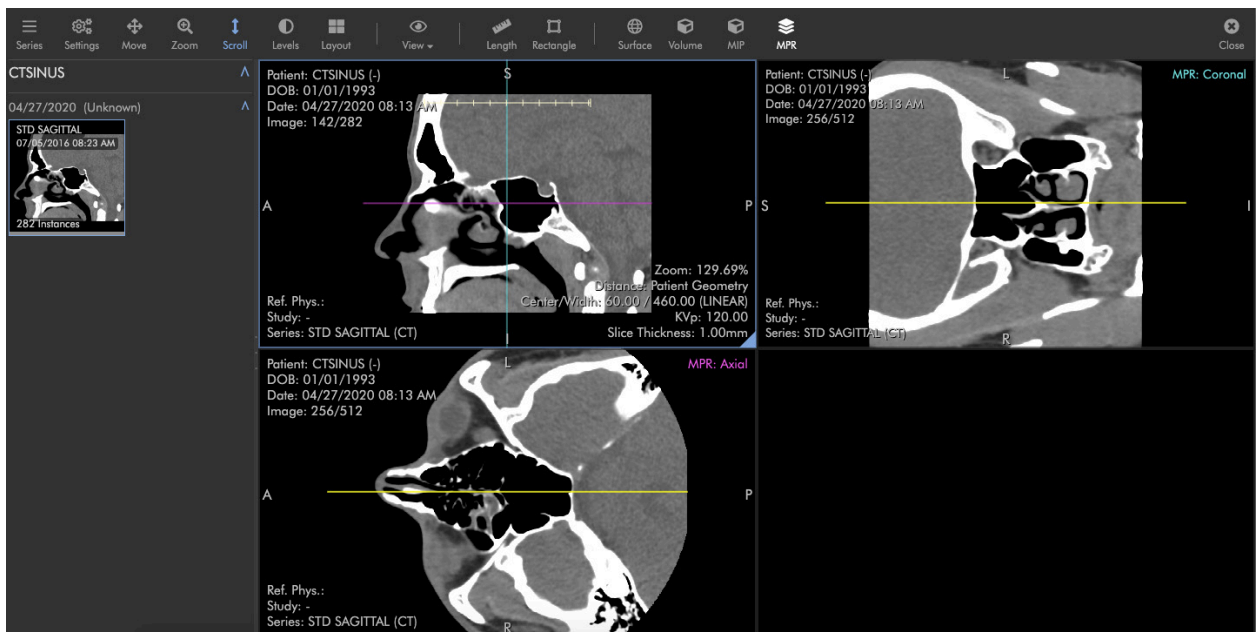
When MPR is enabled, two new viewports display, one for each of the two orthogonal orientations of the original series. The original series displays two reference lines indicating the current slice position of the two orthogonal series. Hovering your mouse over the intersection of these reference lines highlights a grabbable translation tool. You can click and drag this translation tool to adjust the current slice in both orthogonal series.

The series must meet further requirements to support oblique rotation:

- Slices must have square aspect ratio.

- Volume must not already be oriented at an oblique angle (according to image position metadata).

If the series meets these requirements, the two reference lines in the original series can be clicked and dragged, rotating around the intersection point. The orthogonal viewports are updated to display the data at this oblique angle.



PET CT Fusion

PET/CT Fusion is used to overlay PET and CT series data. The PET/CT Fusion feature is supported for series that meet the following criteria:

Both series must be from the same study.

One series must be modality CT and the other series must be modality PT.

Both series must contain volumetric data.

Both series must contain at least 2 or more slices.

Within each series, all slices must have matching values for pixel spacing, rows, columns, and have bit depth greater than 8.

All slices in both series must have matching orientation and must be axial.

Within each series, all slices must have consistent slice spacing.

Either volume must not be oriented at an oblique angle (according to image position metadata).

Two series can be overlaid if they meet these requirements. The PET series is highlighted in orange to indicate that it can be overlaid on the CT. The following metadata is used in calculating the alignment of the two series:

Image Position Patient.

Pixel Spacing.

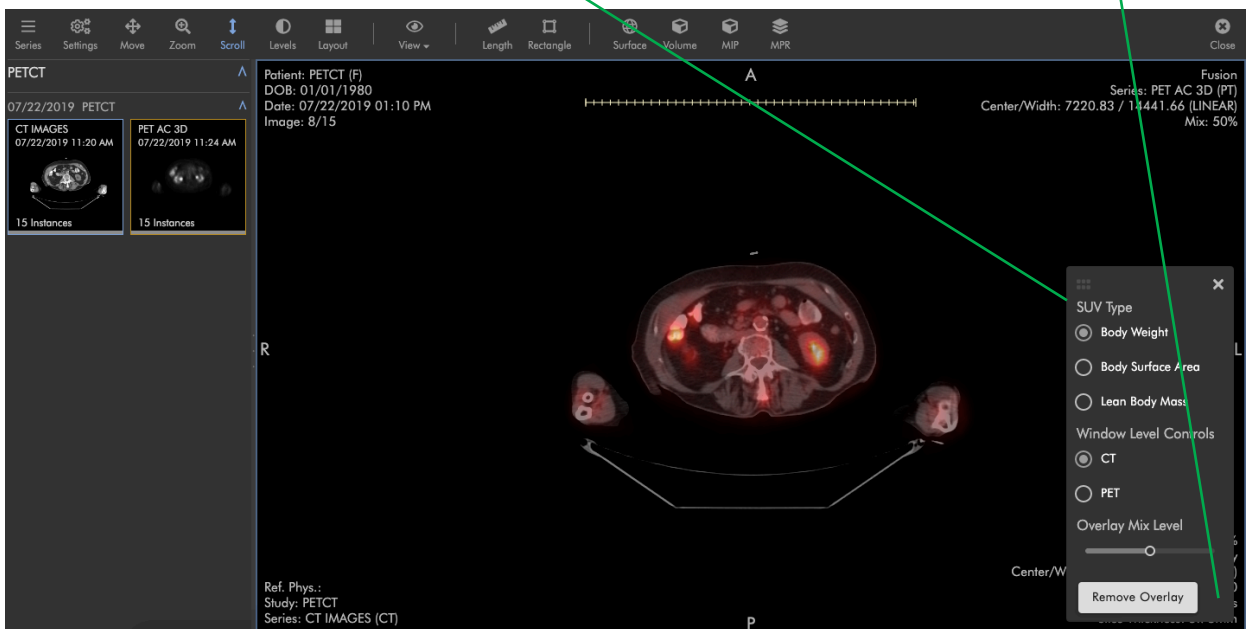
Rows.

Columns.

As the number and thickness of slices between the two series can differ, the closest PET slice is found for each CT slice, such that the distance between the two slices must be less than or equal to the slice distance between CT slices (i.e., the closest intersecting PET slice is found for each CT slice). The two series need not cover the same range of slices. If an intersecting PET slice is not found, none is displayed for that CT slice.

You can adjust the mix level of the two series.

SUV Type
Access 'SUV Type' by clicking the blue triangle (hidden here behind the SUV window. See next pages for illustration).



SUV Measurements

ProViewer will only display SUV measurements when the required metadata is found.

Concentration (Bq/ml)

 P: Pixel Value Measurement
 S: Rescale Slope (0028,1053)
 I: Rescale Intercept (0028,1052)
 $C = (P * S) + I$

Dose

 D = Injected Dose (0054,0016)

Decay Factor

 SeriesTime: Series Time (0008,0031)
 DoseStartTime: The injected dose start time comes from (0018,1072), if found, or (0018,1078) if not.
 DecayCorrection: The decay correction (0054,1102) must be either 'ADMIN' or 'START'.
 HalfLife: Half-life of radionuclide (0018,1075)

When DecayCorrection is 'START':
 $\Delta = (\text{SeriesTime} - \text{DoseStartTime}) / 1000$

When DecayCorrection is 'ADMIN':
 $\Delta = 0$

$d = 2^{(-1 * \Delta / \text{HalfLife})}$

SUVbw

 Weight: Patient Weight (0010,1030) in kilograms
 WeightGrams = Weight * 1000

$\text{SUVbw} = C / (D * d) * \text{WeightGrams}$

SUVbsa

 Weight: Patient Weight (0010,1030) in kilograms
 Height: Patient Size (0010,1020) in meters
 HeightCm: Height * 100

$\text{SUVbsa} = C / (D * d) * 71.84 * \text{HeightCm}^{0.725} * \text{Weight}^{0.425}$

SUVlbm

 Weight: Patient Weight (0010,1030) in kilograms
 Height: Patient Size (0010,1020) in meters
 HeightCm: Height * 100
 PatientSex: Patient Sex (0010,0040)

When PatientSex is 'M':
 $\text{SUVlbm} = C / (D * d) * ((1.10 * \text{Weight}) - (128 * (\text{Weight} / \text{HeightCm})^2)) * 1000$

When PatientSex is 'F':
 $\text{SUVlbm} = C / (D * d) * ((1.07 * \text{Weight}) - (148 * (\text{Weight} / \text{HeightCm})^2)) * 1000$



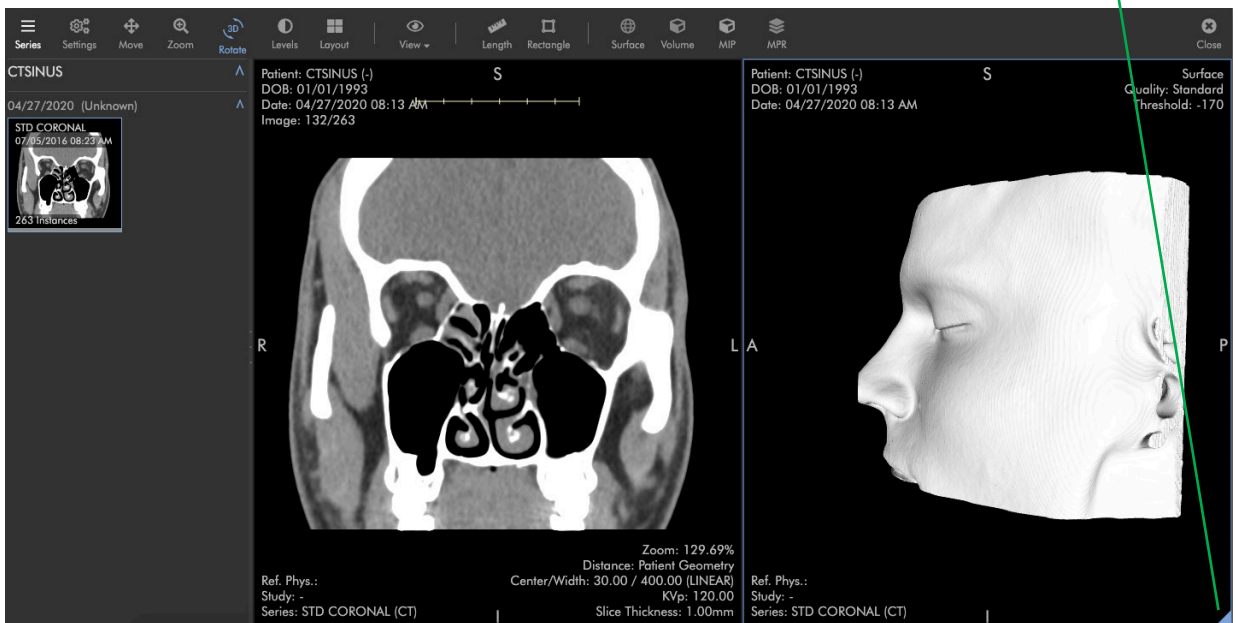
Surface

The Surface feature is used to generate a 3D rendering of volumetric data from a selected series. The Surface renderer supports series that meet the following criteria:

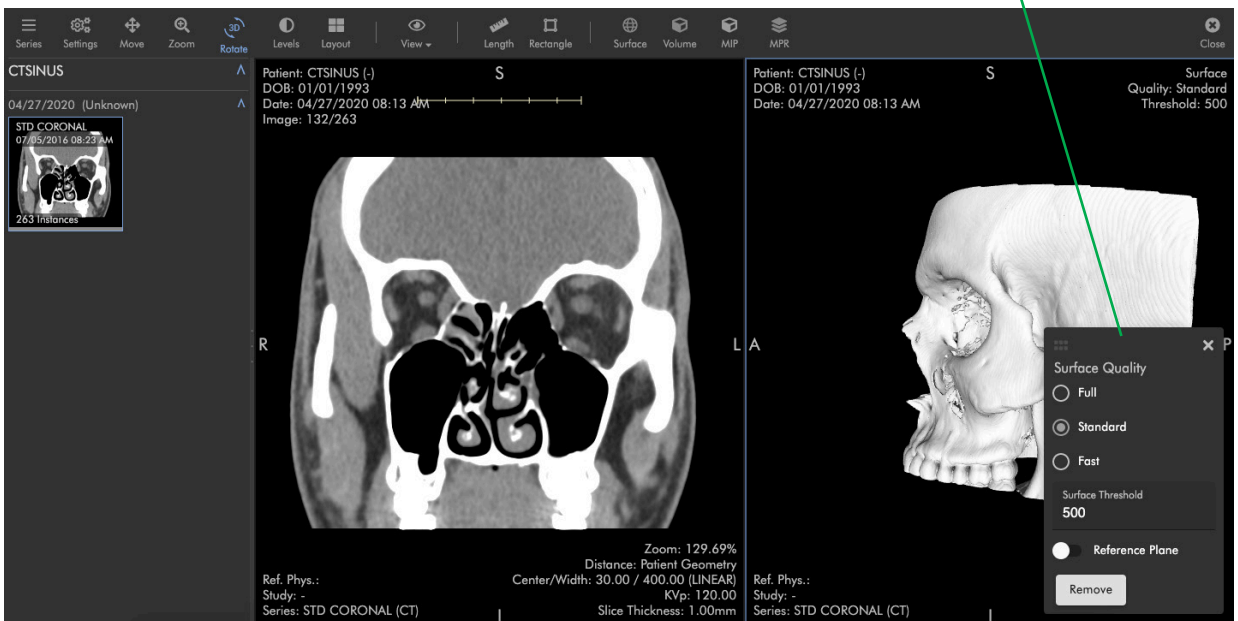
- Contain volumetric data.
- Contain at least 2 or more slices.
- All slices must have matching values for pixel spacing, rows, columns, and bit depth.
- All slices must have matching orientation.
- All slices must have consistent slice spacing.

When the Surface renderer is enabled, the image data is converted to surface data at the specified threshold using the “Marching Cube” algorithm. At this time, decimation and smoothing options are not supported. However, you may choose between three quality options: Full, Standard, and Fast. Standard quality reduces the within-slice resolution to 50%. Fast reduces the within-slice resolution to 25%. Across-slice resolution is always maintained at 100%. Full quality makes no reduction in resolution, but generates the most surface data.

Surface Quality
Access ‘Surface Quality’ by clicking the blue triangle.



The surface threshold can be dynamically adjusted and the surface render updates automatically.





Volume/MIP

The Volume feature is used to generate a 3D rendering of volumetric data. The Volume renderer supports series that meet the following criteria:



Contain volumetric data.

Contain at least 2 or more slices.

All slices must have matching values for pixel spacing, rows, columns, and bit depth.

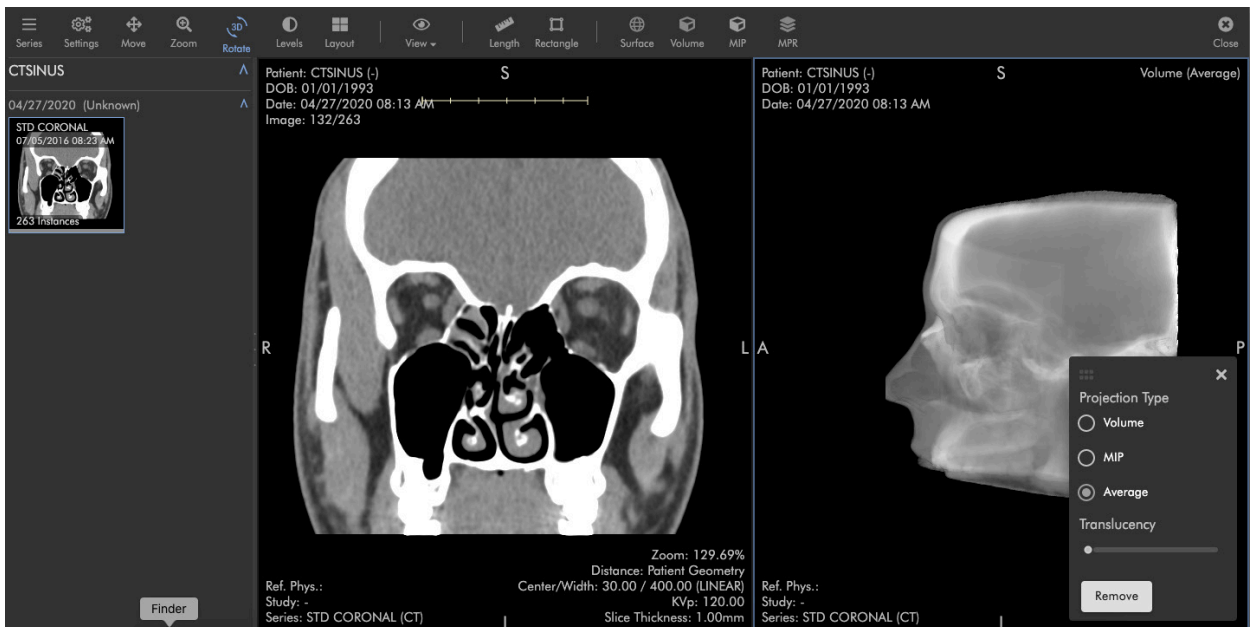
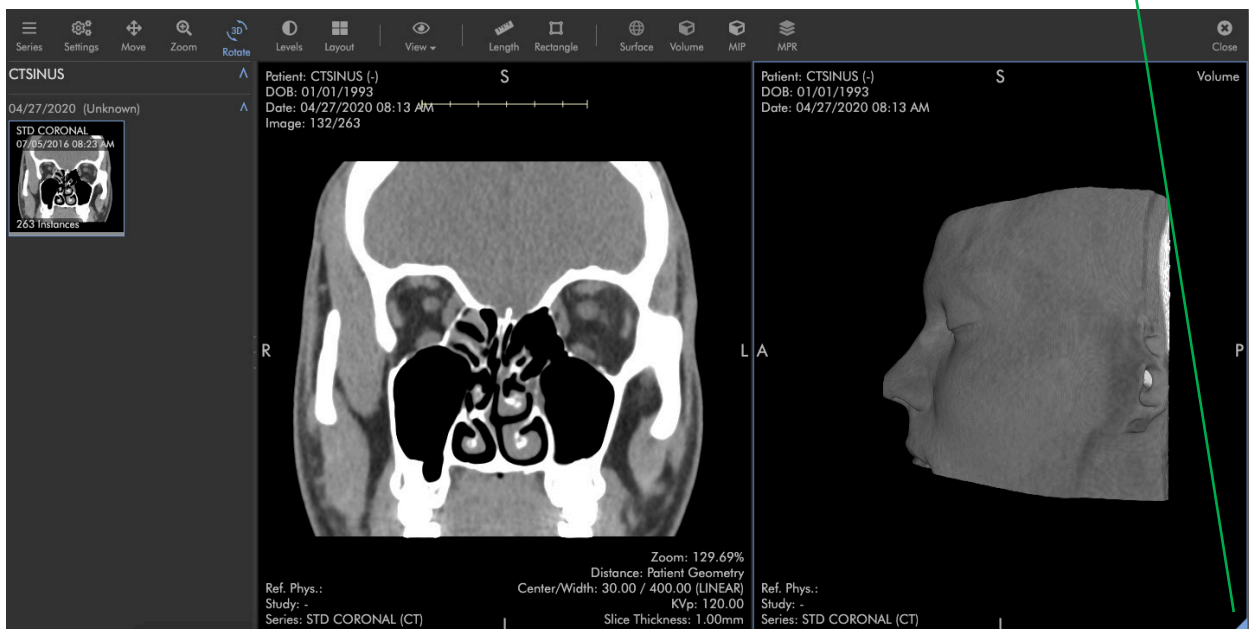
All slices must have matching orientation.

All slices must have consistent slice spacing.

When the Volume renderer is enabled, the image data is converted to a projection using a Ray Marching technique, implemented in a GPU shader using WebGL 2. The process takes the volumetric data, display transform, color palette, window levels, and translucency value as inputs.

The Volume renderer supports three modes: Volume, Maximum (MIP), and Average.

Projection Type
Access 'Projection Type' by clicking the blue triangle.



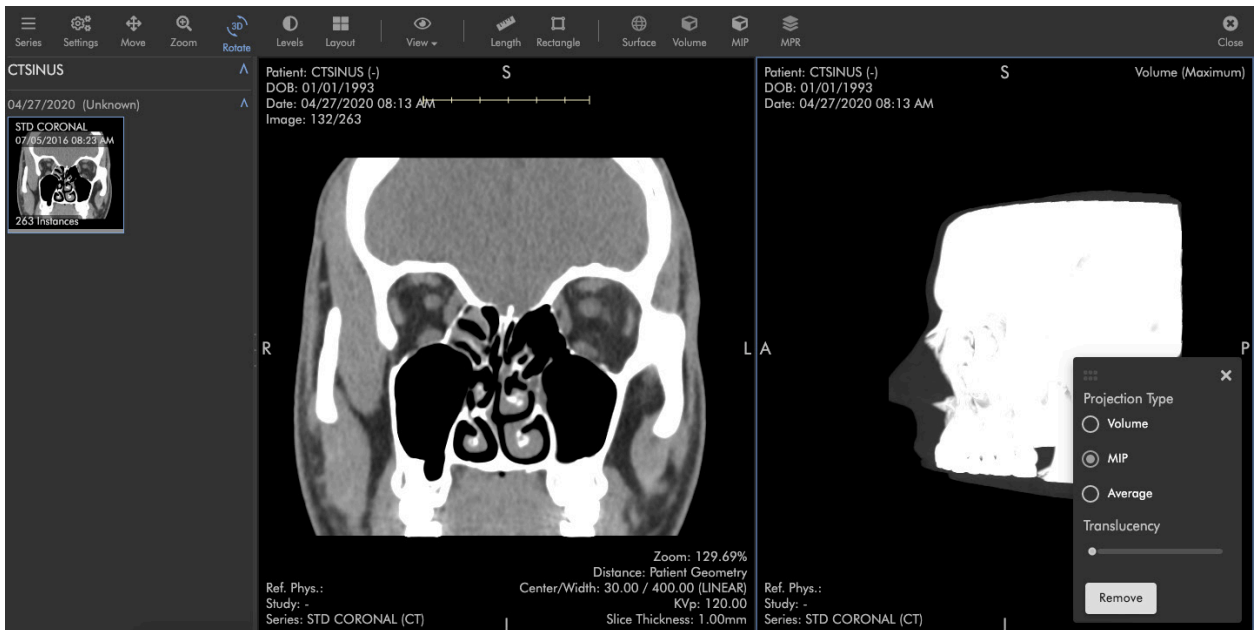
Volume Mode

The Volume mode, with zero translucency, produces a result similar to a surface rendering, as the ray marching stops its color computation early as it intersects image data. Increasing the translucency produces varying semi-transparent projections of the image data, allowing internal tissue structures to be visualized.

In Average mode, each ray marching step is fully computed, translucency ignored, and the result of each pixel intersection is averaged.

In Maximum mode (also called Maximum Intensity Projection or MIP), each ray marching step is fully computed, translucency ignored, and only the maximum value from all intersections is used in the projection.

MIP can be enabled using either the settings panel within the Volume renderer, or from the toolbar.



Quality Control Tools



Actions

The 'Actions' button displays for users with the 'Routing Rules: Create and run manual rules' role permission checked. Any routing rule with the 'Apply rule when a study is manually routed' setting enabled will be available from the 'Actions' button.



Analyze

The Analyze tool with horizontal lines icon creates a dialog that displays configured image level tag values. When you add a rule, the corresponding tag will always show the tag and value in white in the dialog. If the rule has a validation component and the tag value does not validate against the rule, the tag value is considered an exception and will show in orange. The user can hover over an orange value in the dialog, and the system will display the rule that the tag value is failing against. Also, when there is a tag value that fails against a rule, the system displays the number of images in the series where rule failures occur. The user can click on this orange value to scroll to the offending images. There is also a toggle in the dialog to show warnings only. Finally, the dialog also includes a filter. Enter the tag description or tag id to filter your list of surfaced tags.



Crop

Crop the selected series by drawing a rectangle annotation over the displayed image, then clicking this button. By default, a new study will be created with the cropped series. 'Settings > General Settings > Editing > Edit Current Study (No Copy)' can be enabled to crop the current study.



Delete

Click to display a menu with these options: delete annotations, delete the current image, delete the current series. Note that in order to delete annotations, you must have the role permission 'Annotations: edit and delete image annotations'. When you delete annotations, you are deleting all annotations created by you across the series, and you can only delete annotations created by you. You cannot delete annotations created by another user. You can also delete all annotations in a series by right-clicking and selecting 'Delete Annotations'. To delete images or series, you must have the role permission 'Studies: Delete images and series within a study.'



Metadata

Click to display the DICOM metadata for the selected image. The entire DICOM file header displays.



Redact

Click to display a menu of redact options: Draw Image Region, Draw Series Region, Draw Study Region, Clear All Regions, and Redact All Regions. To redact an area, select the Draw Image Region, Draw Series Region and/or Draw Study Region tool and draw your rectangular area(s). When executed, the Draw Image Region tool will put a mask over the defined rectangular area on the image where it was drawn. The Draw Series Region tool will do the same across all images in a series. The Draw Study Region tool will do the same across all images in all series in the study. When you are ready to create masks in your defined rectangular areas, select the Redact All Regions tool from the dropdown. Note that once you select the Redact All Regions tool, the masks will be drawn, and you cannot undo your masks. It is also important to note that if you have the Settings > General Settings > Editing 'edit current study (no copy)' setting enabled, the masks will be drawn on the current copy of the study, and you will need to close ProViewer and re-open to see your masks. If the 'edit current study (no copy)' setting is not enabled, when you click the Redact All Regions tool, the system will create a copy of your study and draw the mask(s) on the copy. You will need to close ProViewer and open the copy of your study to see your masks. Finally, if you have drawn image, series or study regions and you do not want to redact the defined areas, click the Clear All Regions tool to remove the rectangles from your viewport.



Reorder

Click to display a menu of reordering options: By Image Position, By Slice Location, Reverse Series, De-Interleave Series, Rearrange Series, Split Series, Merge Series, Edit Description, Reset to Previous, and Reset All.

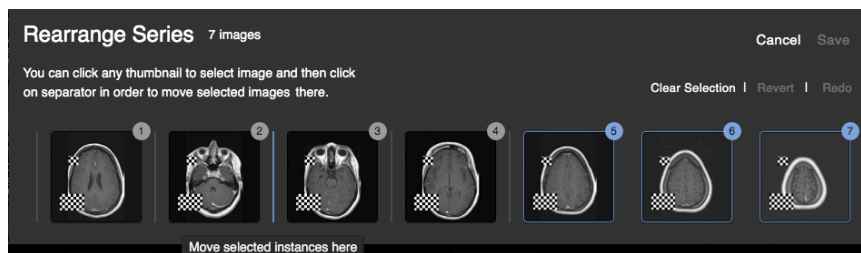
By Image Position: Rearranges how the images in a series present by image position patient. Image position patient is DICOM tag (0020,0032). By default, images are presented by instance number (0020,0013).

By Slice Location: Rearranges how the images in a series present by slice location. Slice location is DICOM tag (0020,1041). By default, images are presented by instance number (0020,0013).

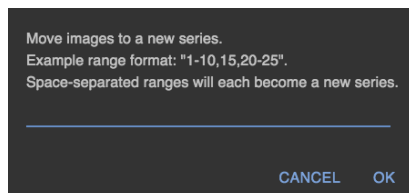
Reverse Series: Reverses the order of images in a series. For example, if there are 20 images in a series, image 1 becomes 20; image 2 becomes 19; image 3 become 18; and so on.

De-Interleave Series: Splits the selected series into two series. The first series contains the odd numbered images, and the second series contains the even numbered images.

Re-arrange Series: Opens a dialog that enables drag and drop of images within the selected series to the order preferred.



Split Series: Opens a dialog that enables the user to split defined images into a new series.



Merge Series: Enables the user to merge two or more series together. After clicking the 'Merge Series' button, select the series you want to merge from the series thumbnails (left side). When you select a series, its perimeter will change to yellow. Just above the top series thumbnails and below the toolbar, you will see a blue merge button. When you are ready to merge, click the blue merge button.

Reset to Previous: Enables the user to undo the prior action taken by a re-ordering tool.

Reset All: Enables the user to undo all prior actions taken by all re-ordering tools by all users over the life of a study in a namespace in Ambra.

Settings

All settings are per-user. Account-level settings can be edited by contacting support. Open the settings editor by clicking the 'Settings' button in the main toolbar.

General

Annotations

'Always Display in Millimeters'. This settings makes length and area-based measurements always display in millimeters instead of centimeters.

'Clear Anonymous User Annotations'. This setting clears all notations made by anonymous users.

'Drop Shape Width'. This setting sets the default diameter of a circle annotation.

'Show Creator'. This setting shows the name of the user who created an annotation. When you are looking at an image, annotations created by you do not show your name. Only other user's names are displayed.

'Enable Ultrasound Measurements'. This setting enables support for US measurements. The setting adds some overhead. If you do not make US measurements, it is best to leave this setting off for better performance.

Editing

'Edit Current Study (No Copy)'. This setting is off by default. In some workflows where the underlying DICOMs are being changed (e.g. when pixel masks are being applied to conceal PHI or when a user needs to crop an image), keeping the source data can be important.

Layout

'Default Layout (Columns)'. This setting defaults the number of image columns that are shown in the viewer tiles.

'Default Layout (Rows)'. This setting defaults the number of image rows that are shown in ProViewer.

'Display All Series In Minimal Layout'. This setting automatically displays the "best fit" layout for all series in the study, up to a 4x4 layout. For example, a study containing 9 series will display in a 3x3 layout. A study containing 4 series will display in a 2x2 layout.

'Automatically Prompt For Fullscreen'. This setting will automatically prompt the user to enter fullscreen.

'Automatically Tile Selected Series'. This setting displays the current series in a 4x4 layout, slice by slice. The PHI for the study displays in a banner across the top of the viewer when this setting is enabled.

Overlays

'Enable Colors'. This setting enables colored overlays. The overlay color defaults to red.

'Custom Overlay Colors'. This setting allows the user to choose a color for an overlay to display in.

Loading

'Find Related Studies'. This setting finds any related studies for a patient if they exist in the Ambra system.

'Automatically Load Related Studies'. This setting loads any related study's thumbnails alongside the existing study in the thumbnails panel.

'Display Series Only After All Images Loaded'. This setting only allows a series after all images in the series have been loaded.

'Enable Lan Accelerator'. Enable this setting when using an Ambra network accelerator.

'Enable Local Accelerator'. Enable this setting when using an Ambra personal accelerator.

Mobile

'Disable Mobile App Reminder'. If this setting is enabled, a user who logs in via browser on a mobile device (e.g., tablet) will not be reminded about Ambra's mobile app.

'Disable Mobile App Small-Screen Reminder'. If this setting is enabled, a user who logs in via browser on a small-screen mobile device (e.g., phone) will not be prompted to download Ambra's mobile app.

Toolbar

'Hide Toolbar Icons'. This setting hides the icons in the tools in the horizontal toolbar. When this setting is enabled, just the tool descriptions show in the toolbar. This gives the viewports more screen real estate.

Thumbnails

'Always Show Full Series Description'. This setting allows the user to always see the full series description regardless of length. If not enabled, long series descriptions will be cut-off with an ellipses in the thumbnail view.

'Thumbnail Columns'. This setting allows the user to set the number of columns in the thumbnail view.

Window Levels

'Reverse Window Levels (Horizontal)'. This setting reverses the window level behavior when the user drags their mouse horizontally. By default, the window width is decreased when the user drags their mouse to the left and increased when the user drags it to the right. When this setting is enabled, the window width is increased when the user drags their mouse to the left and decreased when the user drags their mouse to the right.

'Reverse Window Levels (Vertical)'. This setting reverses the window level behavior when the user drags their mouse vertically. By default, the window center is increased when the user drags their mouse up and decreased when the user drags their mouse down. When this setting is enabled, the window center is decreased when the user drags their mouse up and increased when the user drags their mouse down.

'Reverse Window Level Controls'. This setting allows a user to adjust the window center value by dragging their mouse left and right and adjust the window width value by dragging their mouse up and down.

'First Image Window Level Applies to Series'. This setting applies the default window level value from the first displayed image to all images in the series.

Other

'Help Link'. Define a URL to display when selecting the 'Help' toolbar button.

Toolbar

The toolbar is the horizontal bar at the top of the screen that has all the tools (Scroll, Zoom, Window Level, etc). When you click 'Toolbar' on the left, the dialog opens in 'General configuration' mode. This is your default toolbar for all modalities. If you want to create modality specific toolbars, you can do this by clicking the dropdown that is labeled 'General Toolbar', and clicking the modality you want to create a customized toolbar for.

To customize your toolbar, drag tools from the 'Available Tools' area on the left side and drop them in the 'Toolbar' area on the right side. Drop the tool in the place you want the tool to appear. The top tool in the 'Toolbar' area appears at the far left; the bottom tool appears at the far right.

If you enable more tools than your screen has space for, a dynamic 'More' icon will appear on the far right with the tools that have fallen off the screen.

If you want to create separation between sets of tools in your toolbar, drag the line just under the 'Actions' button to the 'Toolbar'. You can use as many line separators as you choose.

To clear the 'Toolbar', click 'Remove All'.

To reset the 'Toolbar' to the default configuration, click 'Reset to Default'.

Context Menu

Select and order context menu buttons.

Keyboard Shortcuts

Keyboard shortcuts or hot keys are a great way to engage tools quickly. Pick your operating system (Mac OS or Windows), and then click the 'Add shortcut' button. A list of tools that can become hot keys pops up. Click the tool you want to create a shortcut for. Click 'Key', select the key you would like to set as the shortcut, if desired select any key modifiers you would like to add to the shortcut (these will turn blue to indicate selection), and, finally, click 'Save'. At any point you may remove a shortcut by clicking the 'Remove' button on the far right of the line with that shortcut or remove all shortcuts by clicking the 'Remove All' button at the top of the shortcut list.

Mouse Tools

'Default left click hold mouse tool'. Select the left-click default behavior from a dropdown of available actions.

'Default right click hold mouse tool.' Select the right click mouse hold default behavior from a dropdown of available actions.

'Default middle/scroll click hold mouse tool'. Select the middle/scroll click default behavior from a dropdown of available actions.

'Default mouse scroll tool'. Select the scroll default behavior from a dropdown of available actions.

'Default mouse double-click tool'. Select the scroll default behavior from a dropdown of available actions.

Color Palettes

Add your own color palettes by modality to the palettes tool. The default palette options are grayscale, invert, hot iron, hot blue, and fire. To add your own custom color palette, select the modality. Click 'Add preset' in the top right. Give the preset a name. Add knots if necessary by clicking the 'Add knot' button. Enter a color code per knot or click the dot in the right side of each knot. A dialog will pop-up that enables you to set each knot's color. When you are ready, click 'Save'. Your color palettes will show at the bottom of the palettes tool dropdown.

Window Level

Configure Window Level presets per modality. Each preset consists of a center and width value.

Metadata Analysis

Select the modality from the dropdown in the top left, enter the image-level DICOM tag id, then select the rule type. For Must Match, Within Range, and Changes Consistently rules, enter a value in the Option field. Then click 'Add'.

Rule type options are:

'Show Only' which shows the tag in the dialog.

'Must Match' which requires the user to enter a value in the options column to match on.

'No Difference Across Series' which validates that the specified DICOM tag is the same across all images in a series.

'Within Range' which requires the user to enter a range in the options column.

'Changes Consistently' which requires the user to enter a delta value in the options column.

After you have added rules, click 'Save' in the top right corner.

Text Annotations

Select a modality. Configure patient and study text annotations for each of the four corners of the viewport.

Hanging Protocols

This setting specifies how studies of a particular type should be displayed on the screen. Users can configure hanging protocols per modality and study description.

The display on each monitor can be customized in the screen section. Change the columns and rows in the layout option to change the number of tiles in the viewport. Select the monitor that you would like the screen to be applied to in Display.

Filters on each screen can be added in the series section. Filter options include description, image type, view position, image laterality, and study type.

Save All

Save all settings, not just the current page.

Mobile Viewer Requirements

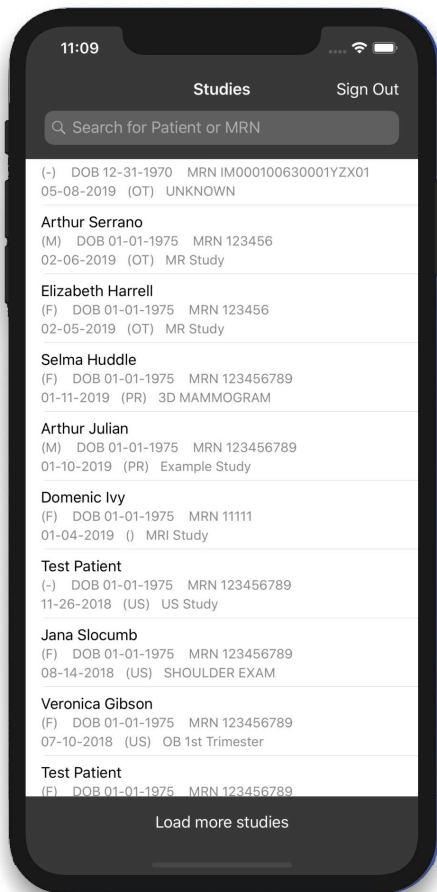
Ambra supports mobile devices (phones and tablets) that use Android and iOS operating systems. To use Ambra on your mobile device, you must download the Ambra app from Google Play (Android) or from the App Store (iOS).

The Android app requires Android 7.0 and later.

The iOS app requires iOS 10.0 and later.

Features Comparison

Description	Desktop	Mobile Phone	Mobile Tablet
Cybersecurity controls - login	√	√	√
Search	√	√	√
Import a study - web upload	√		
Import a Study - Email Request	√		√
Import a Study - Query/Retrieve	√		√
View images (zoom, move, rotate)	√	√	√
PHI overlay	√	√	√
Series thumbnails	√	√	√
Study metadata	√		√
Window/Level	√	√	√
Annotations (text, distance, area, angle, density)	√		√
3D (linked series, planar localization, and reference lines)	√		√
Layout	√		√
Cine	√		√
Delete	√		√
Related studies	√		√
Meetings	√		
Local viewing	√		
Settings	√		√
Printing	√		√



Mobile Phone Viewer

View images on your Android phone or iPhone. If you intend to use Ambra on your Android phone or iPhone, download the Ambra app from Google Play or from the App Store.

Not intended for diagnostic use on mobile devices.

Toolbar

- Toggle image info overlay
- Toggle window levels mode
- Reset window levels and zoom

Image Selection

- Drag slider to fast scroll through images
- Swipe left/right to increment

Series Selection

- Tap series list row to select series
- Swipe up/down to change current series

Zooming

- Pinch in and out to zoom
- Double tap image to toggle fullscreen
- Drag when zoomed to adjust pan



Mobile Tablet Viewer

View images on your Android tablet or iPad. If you intend to use Ambra on your Android tablet or iPad, download the Ambra app from Google Play or from the App Store.

Not intended for diagnostic use on mobile devices.

Toolbar

- Toggle image info overlay
- Link series
- Select multi-series layout
- Toggle window levels mode
- Reset window levels and zoom

Image Selection

- Drag slider to fast scroll through images
- Swipe left/right to increment

Series Selection

- Tap series list row to select series
- Swipe up/down to change current series

Zooming

- Pinch in and out to zoom
- Double tap image to toggle fullscreen
- Drag when zoomed to adjust pan