



# NilRead

## User Guide

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### **Contact Us**

U.S. (toll free): 1-877-201-0001

Direct: 913-227-7030

Customer Portal: <https://www.onbase.com/community>

### **Manufacturer**

Hyland Software Canada ULC

120 Carlton Street, Suite 217

Toronto Ontario, Canada

M5A 4K2

### **Authorized European Representative**

Emergo Europe

Prinsessegracht 20

2514 AP The Hague

The Netherlands

Web: [www.emergogroup.com](http://www.emergogroup.com)

### **Australian Sponsor**

Emergo Australia

Level 20, Tower II, Darling Park

201 Sussex Street

Sydney, NSW 2000

Australia

**Brazil Registration Holder**

Software

Anvisa Registration #: 80117580529

Responsible Technician: Júlia Zema Parente Pinto / CRF – DF 2508

IMPORTER:

Emergo Brazil Import Importação e Distribuição de Produtos Médicos Hospitalares Ltda.

Address: SIA Trecho 3, Lot 2010/2020, 1º floor, Ed. Myriam - District: Zona Industrial (Guará) Post code: 71.200-030 -

City: Brasília / State: DF

Tax number: 04.967.408/0001-98

e-mail: [brazilvigilance@emergogroup.com](mailto:brazilvigilance@emergogroup.com)

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# 1. Intended use

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## About NilRead

NilRead is a web-based, no installation, diagnostic viewer. NilRead provides physicians with secure, interactive processing, viewing, and sharing of 2D, MPR, 3D, Fusion and other imaging exams. The product is designed for use by qualified medical practitioners to review and interpret imaging studies and reports. NilRead provides interactive image visualization tools and rule-based hanging protocols for exam viewing according to physician preference and multi-monitor display configuration. NilRead can be easily integrated with any DICOM or HL7 network, connected with a VNA, and can be invoked from a RIS or workflow/reporting solution. NilRead can also query-retrieve remote DICOM nodes, XDS repositories and other medical archives.

Physicians can easily customize how a patient study is presented using a number of configurable layouts, then further arrange images by dragging and dropping series into viewports. This allows each physician to review images based on their personal preferences.

Access NilRead using your mobile device or desktop computer. NilRead runs on all major browsers and supports multi-touch gestures on mobile devices (for details, see “Device specifics” on page 6). For hardware requirements and supported browsers, see “Hardware requirements” on page 5. Please also review the “Warnings and precautions” on page 2.

NilRead uses industry standard security mechanisms (HTTPS, SSL) and does not transfer any patient data to the client device running the viewer. This allows radiology departments and other health care organizations to provide secure access to referring physicians and radiologists on the go without having to setup and maintain an IT infrastructure on devices outside the organization. NilRead supports many modalities (see “Supported modalities” on page 5).

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



0413



View additional regulatory information including warnings and precautions (see “Warnings and precautions” on page 2).



## Version number

The NilRead version number can be viewed by hovering over the NilRead logo.



## Warnings and precautions

Before attempting to use NilRead, you must read this manual thoroughly, paying particular attention to all Warnings and Cautions incorporated in it.

<b>WARNING</b>		Directions, which if not followed, could cause fatal or serious injury to an operator, patient or any other person, or could lead to a misdiagnosis or mistreatment.
<b>CAUTION</b>		Directions, which if not followed, could cause damage to the equipment described in this Instructions for Use and/or any other equipment or goods, and/or cause environmental pollution.

### General Usage



NilRead is intended for use by physicians trained in reviewing and interpreting medical images.



Users are to ensure that the appropriate study is loaded based on the identification on the timeline and in the viewport.



It is recommended that NilRead be installed on the minimum hardware requirements (see "Hardware requirements" on page 5). Users are to ensure guidelines and warnings (including maintenance provisions) provided by the hardware manufacturer are adhered to, and that hardware is used under safe operating conditions. Users shall not install any additional third party software on the NilRead server to prevent compromising the software performance.



A user's access to the NilRead software is dependent upon the connectivity of their computer or mobile device to the NilRead server. A NilRead site should maintain the network integrity since the network is a critical part of the distributed image viewing system.



NilRead uses compressed images during interactive manipulation, clearly marking them on the screen as "lossy" images. The diagnostic quality image is presented at the end of the manipulation, as part of a progressive refinement display.



NilRead has been qualified on a variety of operating system and browsers (see "Device specifics" on page 6). However, operating system and browser version updates may affect the NilRead software.

We recommend verifying the NilRead functionality after a modification to the operating system or browser.



NilRead could be used as a temporary data cache and local changes might be out of synch with the master database. If NilRead is configured as a temporary cache, it is recommended that either the data correction functions are disabled or that an appropriate data lifecycle policy is setup to propagate changes to the master database.



Patient data may be incorrectly removed by improperly configuring a data lifecycle policy. The system administrator shall make sure that when NilRead is used as primary data storage, data lifecycle is setup to include hierarchical storage endpoints, including a long term archive. This will prevent purging policies from automatically deleting studies when the local cache is full.



The system administrator shall ensure that when NilRead is used as primary data storage, that the site implements an appropriate backup and recovery procedure of the NilRead database.



The system administrator shall ensure that Data QC privileges are assigned to users familiar with the hospital's workflow.

## Use on Mobile Devices



Users are to ensure guidelines and warnings provided by the mobile device manufacturers are adhered to regarding care and operation of the mobile devices.



Before conducting a diagnostic assessment, clean the device screen so it is free from dust, dirt and fingerprints, and stop using NilRead if the screen becomes damaged. Use screen protectors or any covering material with caution as they may adversely impact the reading conditions.



LCD displays have angular dependence characteristics. During a diagnostic assessment on a mobile device, view any image from the front with a viewing angle of less than 15 degrees.



Some mobile devices are equipped with ambient light detection to self-adjust the output luminance level and luminance response according to ambient light changes. It is recommended that for a diagnostic read on a mobile device, the auto-brightness adjustment be disabled and any settings which automatically reduce the brightness (e.g. due to low battery) be disabled. The hardware and power settings should be set to ensure maximum brightness.



NilRead may be subject to factors not typical for reading room workstations (e.g. lighting conditions, screen size) when used on mobile devices. It is therefore required that the user follows the operating instructions properly, and use NilRead's Reading Environment Verification tool to verify the reading environment conditions (see "Reading environment verification" on page 6).

## Measurements



On MPR and 3D views, interpolation may be done depending on the spacing between the original slices (as the spacing increases, the amount of interpolated data increases). For any image, when displaying images on the monitor at a scale other than 100%, data is interpolated. Measurement results are affected when interpolation is done. Interpolation always implies a certain inaccuracy.



Do not perform pixel value measurement on compressed images. Compressed images are marked as "lossy" on the screen.



NilRead allows 3D measurements to be performed. 3D measurements can change significantly with small changes in a line's location or with changes in opacity.



The accuracy of any measurement also depends on the user's ability to select appropriate measurement points on the display device.



The accuracy of calibrated measurements should be visually verified with the size of an anatomical object.

## Intended use within Canada

The NilRead software application provides desktop and portable access to multi-modality softcopy medical images, reports and other patient-related information for conducting diagnostic review, planning, and reporting through the interactive display and manipulation of medical data. NilRead also allows users to collaborate by sharing application sessions. NilRead is for use with MRI, CT, Ultrasound, Digital Fluoroscopy, Digital Angiography, X-ray, Mammography, DBT, ECG and DICOM RT and Nuclear Medicine images.

On portable (mobile) platforms, this device is not intended to replace full workstations and should be used only when there is no access to a workstation. It is the user's responsibility to ensure the software is used on appropriate hardware and to verify image quality is suitable for the clinical application. Mobile use is not intended for diagnostic review of Mammography and DBT.

## Intended use outside Canada and the USA

The NilRead software application provides desktop and portable access to multi-modality softcopy medical images, reports and other patient-related information for conducting diagnostic review, planning, and reporting through the interactive display and manipulation of medical data, including mammography. NilRead also allows users to collaborate by sharing application sessions.

Mammographic images should only be viewed with a monitor approved by the FDA for viewing mammographic images, or monitors with similar specifications. On portable (mobile) platforms, this device is not intended to replace full workstations and should be used only when there is no access to a workstation. It is the user's responsibility to ensure the software is installed on appropriate hardware and to verify display image quality is suitable for the clinical application. Mobile use is not intended for diagnostic review of Mammography and DBT.

NilRead is intended for use by physicians trained in reviewing and interpreting medical images.

## Supported modalities

NilRead provides imaging data to physicians in many different specialties. Modalities such as MR, CT, Xray, fluoroscopy, ultrasound, mammography, and many more are supported by NilRead.

For a full list of supported modalities, see the NilRead DICOM Conformance Statement.

## Hardware requirements

The computer or device used for NilRead must meet the following hardware requirements.

### Desktop computers

The minimum hardware requirements for desktop computers running NilRead are:

- CPU: 1GHz Intel processor
- Available Memory: 500MB

The minimum network connection speed for a desktop computer is 1Mbps download, 256Kbps upload.

NilRead functions on any browser that supports JavaScript but has only been formally verified on the following browsers:

- Microsoft® Internet Explorer® (8.0 and higher)
- Mozilla® Firefox® (3.0 and higher)
- Google Chrome™ (3.0 and higher)
- Apple® Safari® (4.0 and higher)

## Mobile devices

NilRead is verified to work on the following mobile devices:

- Apple® iPhone® (iOS 3.0 and higher)
- Apple® iPad®
- Android™ devices (2.3 and higher)
- Microsoft® Surface™
- Windows® Phone (8.0 and higher)

NilRead requires mobile devices to have a minimum network connection of 3G or WiFi.

## Device specifics

NilRead is available for desktop computers with a diagnostic monitor and for mobile devices. For details, see “Hardware requirements” on page 5.

It is the user’s responsibility to ensure NilRead is used on appropriate hardware and that image quality, including display monitors, image resolution and environment lighting, are suitable for the clinical application. It is recommended that users comply with the applicable regulatory guidelines for the anatomy and pathology being studied. For reference:

- American College of Radiology Practice Guidelines (<https://www.acr.org/Clinical-Resources/Practice-Parameters-and-Technical-Standards>)
- Canadian Association of Radiologists Practice Guidelines (<https://car.ca/patient-care/practice-guidelines/>)

Using NilRead is slightly different on desktop computers and mobile devices.

### Desktop computer with a diagnostic monitor

All NilRead features are available.

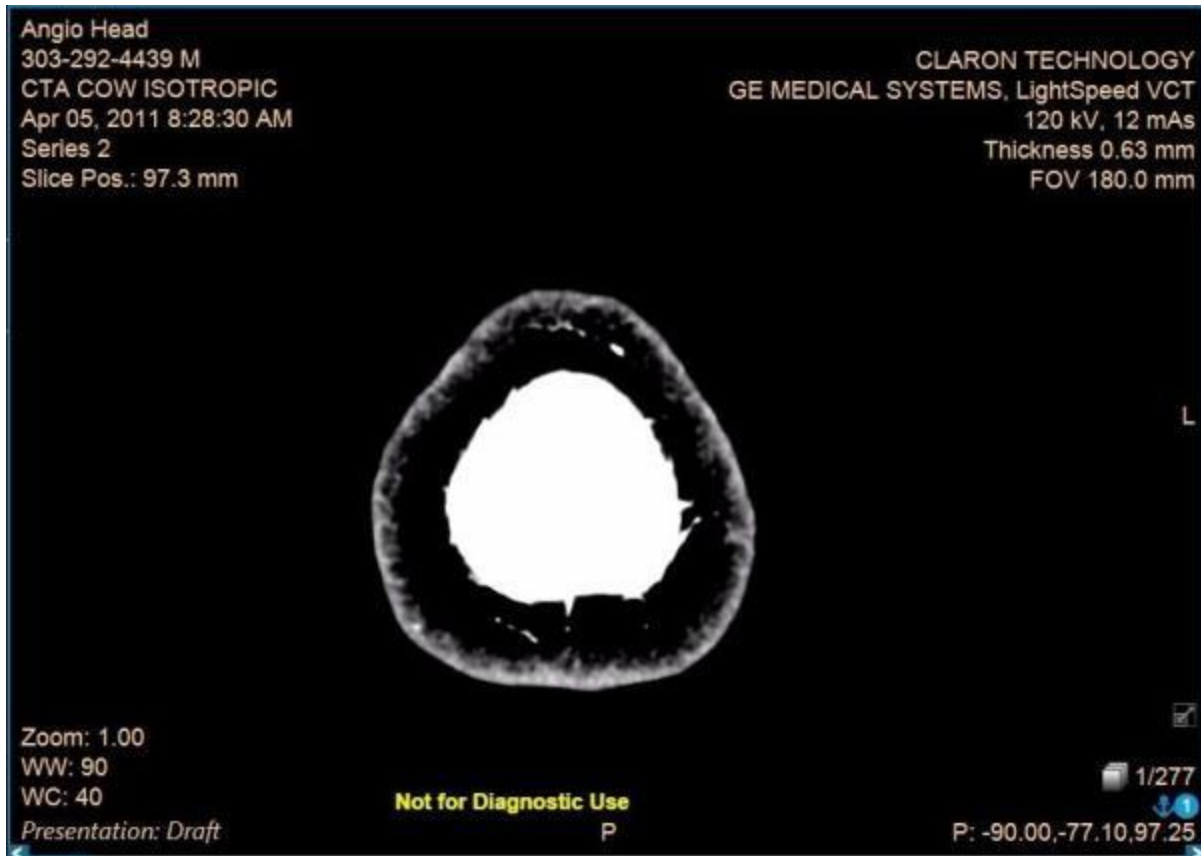
### Mobile devices

Multi-touch gestures are supported (tap, double-tap, drag, swipe, pinch, flingable toolbar). Collaboration is not supported on smartphones.

## Reading environment verification

NilRead requires the user to assess the reading environment to confirm the user can view images accurately on a mobile device. When viewing a study on a mobile device, the message “Not for diagnostic use” will be shown on the screen until a reading environment verification is accepted.

NilRead will automatically display the “Not for diagnostic use” message every 60 minutes when images are viewed on a mobile device.



When in a collaboration session, a user can verify the reading environment only if the “Not for diagnostic use” message is on the screen. Once the message is removed or if it is not visible because the environment has been verified recently, it is not possible for the user to verify the read environment without stopping the collaboration session. If starting a collaboration session on a tablet, the user is instructed to verify the read environment prior to starting the collaboration session using the following instructions.

Follow these steps to perform a reading environment verification.

1. Select **Settings**. Under **Preferences**, select **Reading environment verification**.  
or  
Select the “Not for diagnostic use” message on the screen.
2. A low contrast pattern is shown in the viewport. Note that in the following example, the contrast has been highlighted for demonstration purposes.



3. Touch the low contrast pattern to indicate its location.

If you do not select the correct location, the lighting conditions may be too bright or the device's screen may not be at maximum brightness. For a diagnostic read on a mobile device, it is recommended that the auto-brightness adjustment is disabled and the presence of thumbprints in critical parts of the screen is checked frequently. A bright and clean display is the best starting point for a diagnostic reading environment assessment. Also note that LCD displays have angular dependence characteristics. During the assessment, it is recommended that the images are viewed from the front within 10-20 degrees of the viewing angle.

You can adjust the reading environment and try again (select the **Try Again** button) or you can continue with a non-diagnostic read (select **Continue Non-diagnostically**). You can also access the Help instructions (select **Read Instructions**).

## Mobile device calibration

NilRead allows you to calibrate your mobile device using the DICOM grayscale standard display function (GSDF). The DICOM GSDF defines the luminance response of a display such that an observer's perception of image contrast is consistent throughout the pixel value range of a displayed image.

1. Select **Settings**.
2. Under **Preferences**, select **Mobile Device Calibration**.
3. Select **Instructions**. Follow the instructions to calibrate your mobile device.

4. Select Apply.



## 2. Review studies

---

### Open a study

NilRead provides several methods to open a study. The easiest method is the Patient Directory.

#### Note

The studies you can view depend on your privileges in NilRead. You may be given access to specific studies or you may be able to view the full directory.

#### Note

Other methods to open a study include a more detailed search, worklists, folders, and a list of recently opened studies. For details, see "Access studies" on page 73. You can also open multiple studies at once. This allows you to review multiple studies in a single session without having to return to the Patient Study Directory. For details, see "Open multiple studies" on page 76.

1. In the Patient Study Directory, select **Patient Directory**.

Status	Source	Patient's Name	Modalities in Study	# Images	Date Of Birth	Patient ID	Accession No.
ALL							
■	Local	Addison, Barry W	CT PR	647	Oct 18, 1928	055703	0001301
■	Local	Arienne, Franchesca [ * ]	CT SR	3	Aug 7, 1635	[Patient ID.1]	[Accession Nu.6
■	Local	boost, breast	CT RTDOSE RTPLAN R	102		123456	
■	Local	Brown, Barry	ECG DOC PR	3	Mar 22, 1934	12345	
■	Local	Bugs, Bunny	XC PR	2		32dfg345fdg45	
■	Local	Dean, Deangelo	ECG PR	2	Jun 6, 1975	296892	45167947
■	Local	Explicit Little Endian Image 16bits-1f	CT	1		634370223005578170	
■	Local	FHIR, CareEvolution	CR PR	4	Mar 2, 1996	6	6A23C1EC
■	Local	Fhir, EPIC	CR	2	Feb 20, 2014	203579	I28077718
■	Local	Fhir, IBP	CR	2	Feb 20, 2014	8099093	I28077718
■	Local	FHIR, IPB	CR PR	4	Mar 2, 1996	5	I28077718
■	Local	Gatti, Claudio	US KO PR	81	Feb 11, 1965	3911359	24746994
■	Local	GEMINI TF, Lung ca	PT CT PR	368		SLU_0022	
■	Local	GEMINI TF, Lung ca	PT CT	368		SLU_0022	
■	Local	GEMINI TF, Lung ca	PT CT	368		SLU_0022	
■	Local	Jaqueline, Kymberly V. [ * ]	US KO PR	81	Mar 7, 1604	[Patient ID.1]	[Accession Nu.6
■	Local	John, Doe	XA	1	Mar 2, 1996	303-292-4239	
■	Local	John, Doe	US KO PR	81	Feb 11, 1965	303-292-4239	24746994
■	Local	John, Doe	CT RF PR	285	Mar 2, 1996	303-292-4239	8036388
■	Local	John, Doe	CT KO PR	669	Mar 2, 1996	303-292-4239	6826921
■	Local	John, Doe	CR PR	4	Mar 2, 1996	303-292-4239	6819547
■	Local	John, Doe	ECG PR	2	Mar 2, 1996	303-292-4239	
■	Local	John, Doe	US	1	Mar 2, 1996	303-292-4239	5465432-2
■	Local	Johnson, Scott	ECG PR	2	Feb 11, 1965	303-292-5555	
■	Local	Miss, Madaline [ * ]	CT	192	Aug 6, 1805	[Patient ID.1]	[Accession Nu.6
■	Local	MMEDIA, Carl	OT	3	Sep 12, 1958	129-075-362	201405090005
■	Local	Test, Jane K	CT KO PR OT	438	May 10, 1983	907838558	903779E

All studies are shown. If multiple studies exist for a patient, they are listed on separate lines.


**Note**

Studies are loaded on demand as you scroll down the page. On mobile devices, you can also swipe to move through the pages.




2. To open a study, click (or tap) anywhere on the directory entry for the study.

To find a study in the directory:

1. Enter information about the study in the blank row below the column headings (patient name, patient ID and so on).
2. To find a study based on status, select one of the following options in the **Status** column:
  - **All** Show all studies.
  - **Available** Show studies containing at least one report.
  - **Not Available** Show studies with no reports.
  - **Approved** Show studies containing at least one approved report.
  - **Locked** Show locked studies.

3. To view all studies again, select **Clear** .

To customize the columns:

- Select **Customize**  in the top-right corner. To add a column, drag a column from the **Customize** list to the location where you want to place it. To remove a column, drag it to the **Customize** list.
- Click (or tap) a column heading to sort the studies. Click (or tap) the column heading again to sort the studies in the reverse order.
- To rearrange the columns, drag a column heading to a new location.
- Select **Reset**  to reset the columns to the default sort order, remove any custom columns and reload all studies.
- Select **Refresh**  to refresh the studies list and view the latest changes made by all users.

## Use presentations

The measurements and annotations you apply to an image are saved in a presentation.

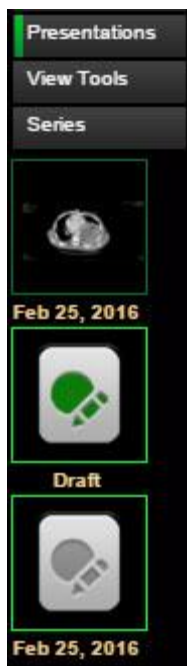
A draft presentation is automatically created when you open a study (if a draft does not already exist). Your changes will continue to be added to the draft until you approve the presentation. Once a presentation is approved, it cannot be modified.

When viewing an image, you can apply presentations in order to view different measurements and annotations you have saved.

### Note

A bookmark is a special kind of presentation. In addition to measurements and annotations, bookmarks also store image visualization settings such as layout, window, level, and zoom. For more information, see “Share bookmarked images” on page 152.

Presentations are shown in the side panel with the most recent presentation at the top of the list. Bookmarks are listed first, then draft presentations, then approved presentations. For approved presentations, the approval date is shown. The following example shows a bookmark, a draft presentation, and an approved presentation:



The list may also include presentations that originated from a third-party, such as PACS or VNA. These presentations are automatically marked as approved and use the following icon:



#### Note

If you do not have permission to use persistent presentations (for example, if you are a guest user), you will be able to create annotations and measurements but your changes will not be saved.

## Select presentations

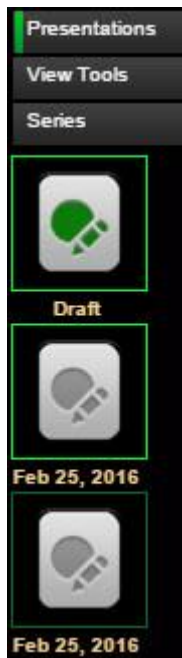
You can apply one or more presentations to the image you are currently viewing. When you open a study, the most recent draft presentation and the most recent approved presentation are automatically applied. Use the Presentations side panel to manually select the presentations you want to apply.

#### Note

Applying a bookmark may change the current draft presentation for the image. When you view a bookmark, the following settings that were captured during the bookmark creation will be applied: the layout, the series selected for each viewport, and the presentations applied to the displayed images.

1. Select **Presentations** (side panel) to view the presentations for a study.
2. Select one or more presentations to apply them.

The presentations you have selected are highlighted in the side panel. In the following example, the draft presentation and the first approved presentation have been applied to the image:



To remove a presentation from an image, select the highlighted presentation in the side panel. The presentation is no longer applied to the image and is no longer highlighted in the side panel.

### Approve a presentation

Right-click (or touch and hold) a presentation, then select **Approve**.

An approved presentation cannot be modified. Annotations in approved presentations are shown with dashed lines, indicating that they cannot be modified. The Presentations label in the bottom-left corner of the image will contain the word "Approved" and the approval date.

Note that a typical NilRead implementation will automatically push back to PACS or VNA presentations through a lifecycle rule.

### Create a draft presentation

If you approve or delete a draft presentation, a new draft presentation is not automatically created during the current viewing session. To create a new draft presentation, right-click (or touch and hold) any existing approved presentation, then select **Make Draft**. A blank draft presentation is created.

If you attempt to apply annotations or measurements to an image and a draft presentation does not exist, you will be given the choice to:

- Make a new draft presentation which will be used to save your changes.
- Allow transient in-session overlays. This allows you to apply annotations and measurements during your current session. These changes are temporary and will not be saved.

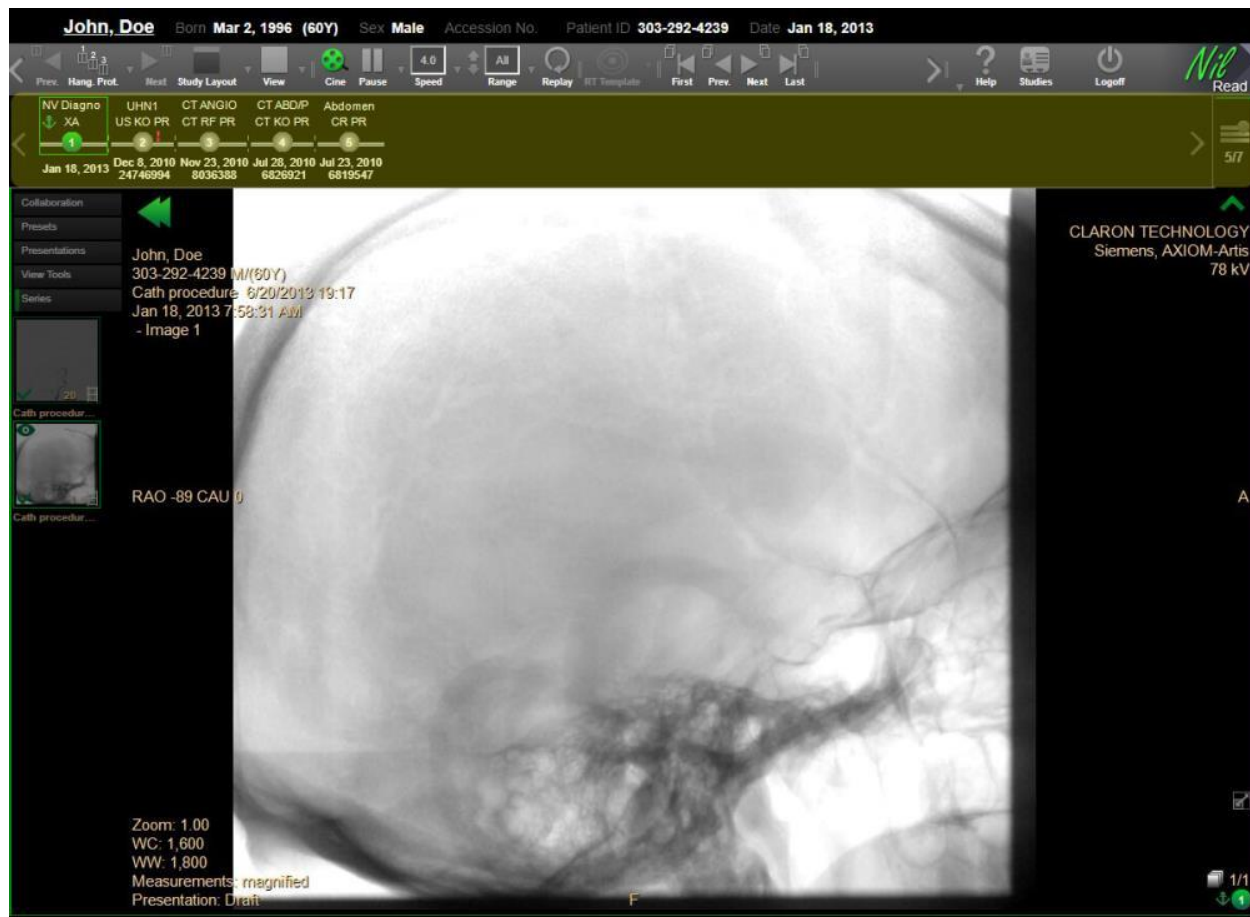
If you choose to allow transient in-session overlays, the Presentations label in the bottom-left corner of the image will contain the word “Transient”, indicating that your changes will not be saved.

### Delete a presentation

Right-click (or touch and hold) a presentation, then select **Delete**.

## Use the patient timeline

When you open a study, a timeline with additional studies and reports for the patient is shown at the top of the image viewing area. The current study is also included in the timeline and is marked with an anchor.



### Note

The timeline is only shown if prior studies exist for the patient in the database or are accessible through an XDS registry or a query to connected DICOM devices.

The following information is shown on the timeline:

- Prior studies and DICOM embedded PDF reports are shown in chronological order.
- The studies in the timeline are numbered.
- For studies, the modality and date are shown. For reports, the date is shown.
- An exclamation mark is shown if a warning exists for a study or report.
- The current study is marked with an anchor.

In each viewport, the number of the currently loaded study is shown in the bottom-right corner.



## View study or report details

Hover over a study or report in the timeline to view more detailed information, such as the number of series and images in a study or the title of a report.

## View a study

Select a study in the timeline to load it in all viewports. The study is opened using the default hanging protocol for the study.

or

Drag a study from the timeline to a viewport. This allows you to place different studies in different viewports. A warning appears near the top of the image viewing area stating that multiple studies are displayed.



## View a report

Select a report in the timeline. The report opens below the timeline. The following options are available when viewing reports:


- **Save** Save a PDF copy of the report.
- **Print Report** Print the report from your browser.
- **Vert/Horiz** Place the report area on the right side (Vert) or bottom (Horiz) of the screen.
- **Maximize/Restore** View the report area only and hide the image viewing area (Maximize) or view both the report area and the image viewing area (Restore).
- **Close** Close the report.

### Note


To resize the image viewing and report areas, drag the divider between the two areas.

## Select priors to include in the timeline

You can select the prior studies to include in the timeline.

1. Select  on the right side of the timeline.

### Note

The number under  indicates how many studies are displayed in the timeline (for example, All or 2/3).

2. The Extended Patient Timeline window appears. The available priors are shown at the top of the window.
3. To load a prior in the image viewer, select the prior, then select **Load** in the bottom-left corner.
4. To filter the available priors, select one of the following options beside **Select relevant priors**:
  - **All** Include all priors.
  - **Manual Selection** Select the checkboxes beside the priors to include.
  - **Filtered** Enter search information in the blank row below the column headings. You can select priors based on age, modality and description.
5. To view more information about a prior, select the prior, then select one of the following options at the bottom of the window:
  - **Study Info** View details about the study.
  - **Reports** View the reports in the study. Select a report to view a preview. When done, select **Close**.

- **Images** View thumbnails of the images in the study. Select a thumbnail to view a preview of the image. When done, select **Close**.
6. Select **Set as relevant**. The selected prior studies are shown in the timeline.

## Hide the timeline

Use the arrow below the timeline to hide or view the timeline.



### Note

The timeline content and visibility can also be controlled using hanging protocols (see "Set up hanging protocols" on page 206). Use the **Relevant patient history** section to automatically display only relevant priors in the timeline. Use the **Application preferences** section to keep the timeline closed when that specific hanging protocol is in use.

## Retrieve prior studies

Use the prior icon in the timeline to trigger a background retrieve of prior studies while reading the current (anchor) study. This icon is only available if all of the prior studies have not yet been loaded.

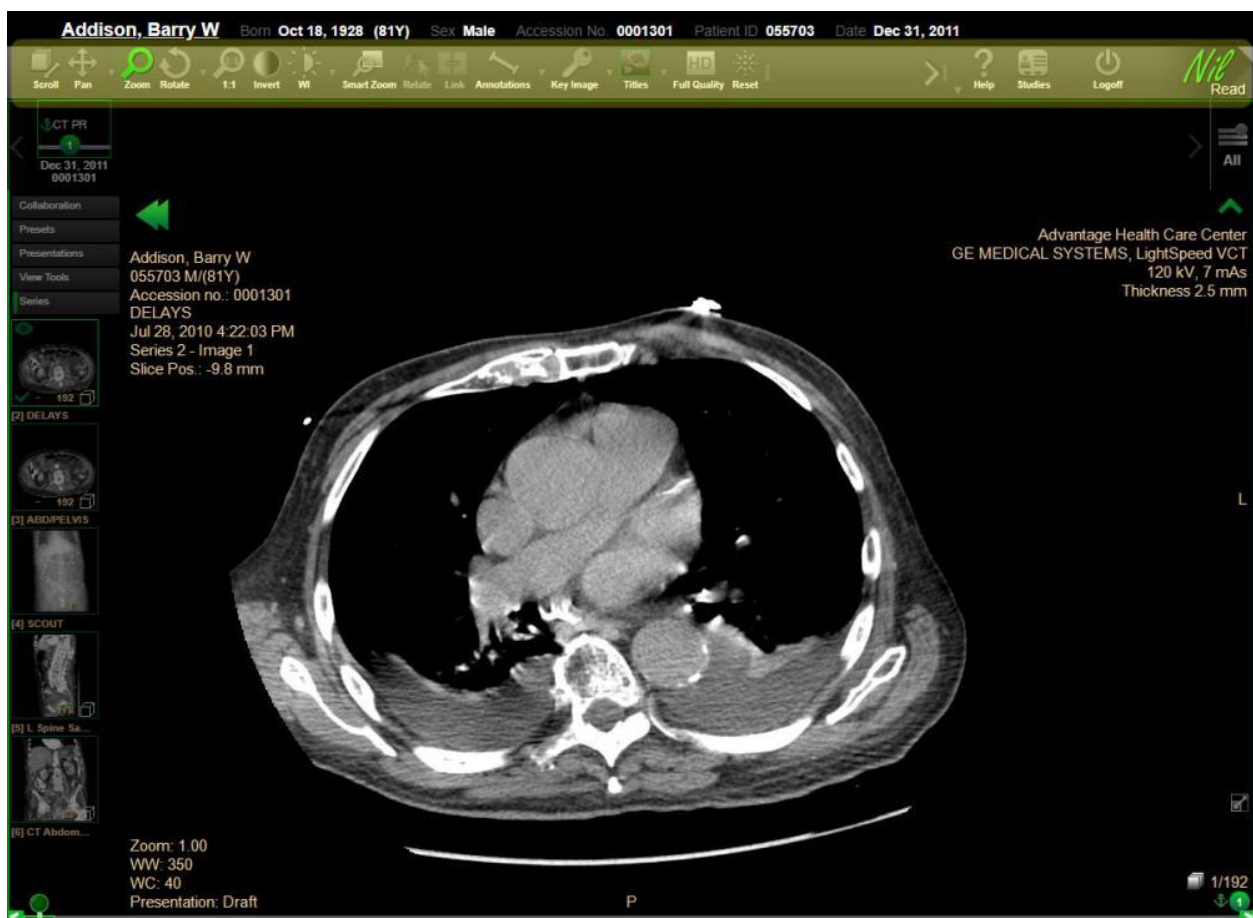
## Hide images on the screen

When viewing a study, you can hide the images on the screen without closing the study. This allows you to quickly hide sensitive information from others who may be able to see the screen.

To hide images, select Close (toolbar). To view the images, select Open (toolbar).

## Use image visualization tools

The NilRead toolbar provides quick access to the most important commands for working with images. To move through the tools, use the arrows at the ends of the toolbar. On touch devices, fling the toolbar.



You can use the tools in any viewport. Changes to one viewport affect all viewports displaying the same series. If the Link feature is active, then changes to one series will affect all series in all viewports.

#### Note

You can right-click (or touch and hold) a viewport to access the tools. You can also customize the toolbar (see “Change tool preferences” on page 171) and assign tools to mouse buttons, keyboard shortcuts and touch gestures (see “Change mouse and keyboard preferences” on page 169).

After using a tool, your changes are saved unless you select **Reset** (to remove changes from all images in the series) or **Annotations > Delete Last/Delete All** (to removes changes from current image) before closing the study.

The following sections describe the tools available in the toolbar. Note that some tools are only available for specific modalities and views.

## Scroll



Drag or use the mouse wheel to scroll through images.

- **2D** Drag to scroll forwards or backwards through the images in a series.
- **MPR** Drag to navigate forwards or backwards through the stack of images. The navigation step depends on the slice thickness that is currently selected.
- **3D** Drag to rotate an image with a full three degrees of freedom.
- **Sculpting** Drag to navigate forwards or backwards through the stack of images. The navigation step depends on the slice thickness that is currently selected.
- **ECG** Drag to navigate forwards or backwards in time.

You can also scroll through images using the arrow keys on your keyboard, the arrows at each end of the scroll bar below an image, or by dragging the scroll bar.

## Pan



Drag to move an image within a viewport. Panning is applied to all images in the series.

- **Oblique** Drag to move an image in any direction within a viewport.
- **Constrained** Drag to move an image vertically or horizontally within a viewport.

#### Note

To move an image at any time, hold ALT while dragging the image.

#### Note

To focus on a specific area, pan the image so the area is centered in the viewport, then zoom in. On mobile devices, use pinch-to-zoom to pan and zoom simultaneously.

## Zoom



Drag up to zoom in on an image; drag down to zoom out. Zooming is applied to all images in the series. When mammography images are linked, the zoom remains consistent between the viewports and is based on physical distance (not the magnification factor).

#### Note

To zoom an image at any time, hold CTRL while dragging on the image.

#### Note

To focus on a specific area, pan the image so the area is centered in the viewport, then zoom in. On mobile devices, use pinch-to-zoom to pan and zoom simultaneously.

## Rotate



- **MPR** Drag to rotate an image in any direction. Rotation is applied to all images in the series.
- **3D** Drag to rotate an image with a full three degrees of freedom.
- **Sculpting** Drag to rotate an image in any direction. Rotation is applied to all images in the series.
- **Fusion 3D** Drag to rotate an image with a full three degrees of freedom.

#### Note

The orientation figure and orientation information is updated when you rotate an image (see "View image orientation" on page 71).

## 1:1 display mode



You can choose to view images using a 1:1 display mode where 1 image pixel equals 1 monitor pixel. This allows you to view all pixels as they were acquired, without any interpolation. You may also want to use the 1:1 display mode for monitor quality control when using synthetic images such as AAPM test patterns.

Before using the 1:1 display mode, you must configure your monitor and browser. You must also enable the 1:1 toolbar icon in your tool preferences.

### Configure your environment to use the 1:1 display mode

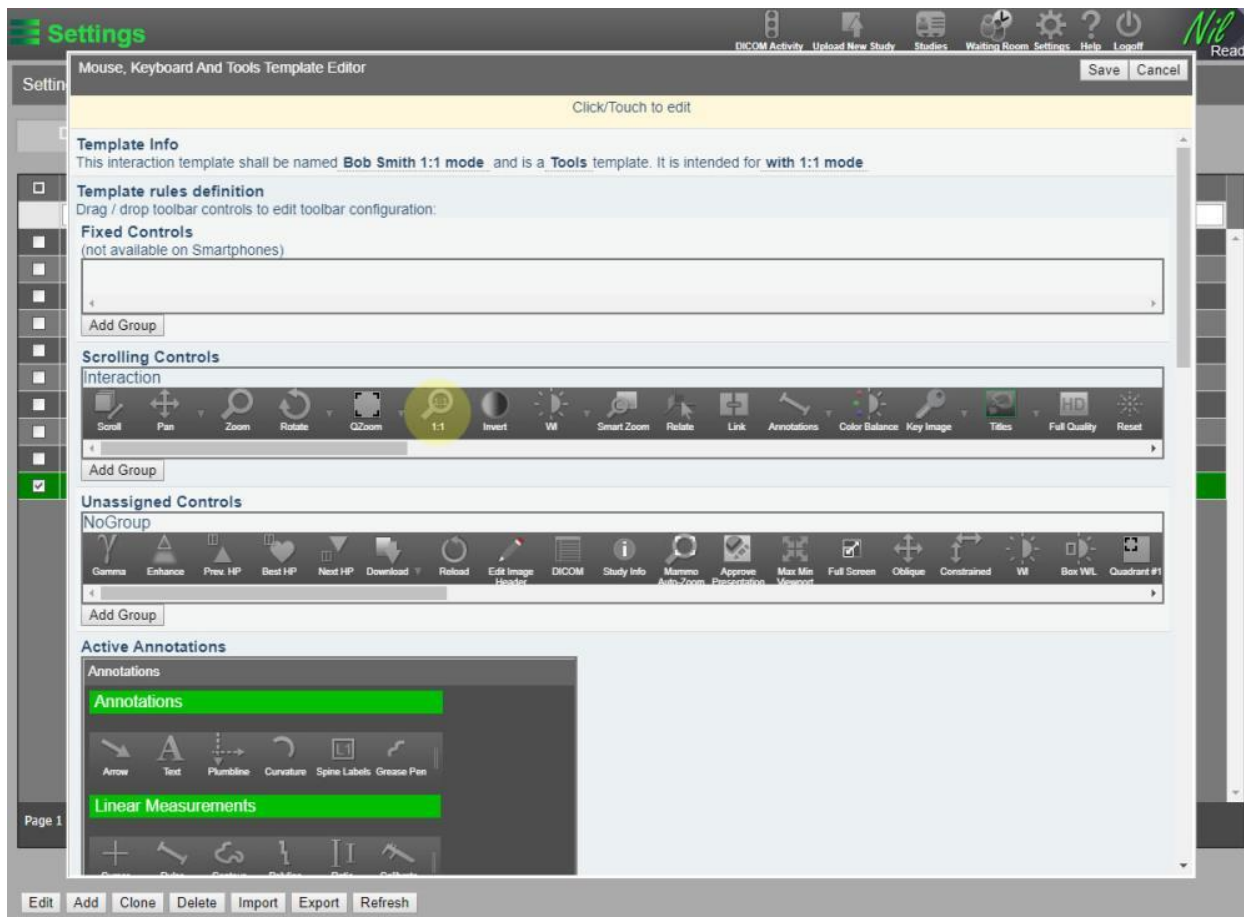
Check the following display settings for your monitor.

1. Use the recommended screen resolution.
2. Use a 100% display scale.
3. Use a 100% text DPI scale.

In your browser settings, set the zoom to 100%.

### Enable the 1:1 display mode

Create a Tools template that includes the 1:1 tool. For details, see “Change tool preferences” on page 171.





### Apply the 1:1 display mode

1. Select 1:1 (toolbar).
2. To remove the 1:1 display mode, select Reset (toolbar). The 1:1 display mode will also be removed if the image zoom factor is changed.

### Quadrant Zoom



For mammography images, Quadrant Zoom presents a magnified view of the four quadrants.

- To switch quadrants, select .
- To select a specific quadrant, select the arrow beside  and select a quadrant.

- To exit quadrant zoom, select the arrow beside  and select **Zoom to Fit**.

## Invert



Invert grey images. Will be applied to all images in the series.

## Window Level



You can adjust the window level based on the entire image or based on a region of interest.

- **Overall window level** Select the **WL** tool. Drag to adjust the window level. Window level changes are applied to all images in the series. (To change the window level for an image at any time, hold SHIFT while dragging on the image.)
- **Region of interest** Select the **Box WL** tool. Click (or tap) and drag to highlight a region of interest. The window level is adjusted to maximize the contrast of the area you selected.

### Note

Use presets (side panel) to apply common window levels (see “Apply presets” on page 47).

## Gamma



Drag up or down to adjust the gamma correction. You can adjust the gamma correction for both color and monochrome images.

The gamma value is shown in the lower-left corner of the image.

## Enhance



Drag up to sharpen the image. Drag down to blur the image.

The enhancement level is shown in the lower-left corner of the image. A negative value is shown if the image is blurred (maximum is -3); a positive value is shown if the image is sharpened (maximum is +3).



## Smart Zoom



To use the Smart Zoom box:

- Using the handles on the sides of the box, drag the box to an area on an image.
- To resize the box, drag the handles on the corners of the box.
- Select **Reset** to reset the Smart Zoom box to the default settings. You can change the Smart Zoom default settings in your user preferences (see “Change your user preferences” on page 168).
- To remove the Smart Zoom box, select the **Smart Zoom** icon in the toolbar.

### Zoom In on a Portion of an Image

You can use Smart Zoom to increase the magnification and window level for a selected area.

Place the Smart Zoom box on the area you want to magnify. Select the box, then use the Zoom tool to change the magnification within the box. You can also change the Window Level within the Smart Zoom box.

### Compare Images

You can use Smart Zoom to compare two series. To overlay a series on top of another series, drag a series from the Series panel or the patient timeline into the Smart Zoom box. You can also drag a preset into the Smart Zoom box.

You can use the following tools on an overlay series. Select the Smart Zoom box, then select the tool.

#### Zoom

Change the magnification factor for the overlay series. Note that if you change the magnification factor for the underlay series, the overlay series will also be affected.

#### Window Level

Change the window level for the overlay series. Note that if you change the window level for the underlay series, the overlay series will also be affected.

#### Scroll

Change the overlay image by scrolling through the images in the series.

#### Pan

Pan the overlay series.

### Rotate

Rotate the overlay series.

### Gamma

Adjust the gamma correction.

### Rendering

Change the rendering mode for the overlay series.

### Thickness

Change the plane thickness for the overlay series.

## Relate



Not available for 2D views. Modify the reference lines. Reference lines are shown on all series on the current screen that are in the same frame of reference. The intersection of the reference lines represents the corresponding position in all viewports.

Click (or tap) an image where you want to place the intersection of the reference lines. You can also drag the horizontal and vertical lines individually, or drag the intersection to move both lines simultaneously.

### Note

Use Reference to show or hide the reference lines.

## Link



Link or unlink all currently open series. This allows you to scroll through the linked series in a synchronized manner. Changes (such as Rotation and Zoom) applied to one series are also applied to the other series.

When mammography images are linked, the zoom remains consistent between the viewports and is based on physical distance (not the magnification factor).

## Annotations and measurements



Use these tools during image analysis to mark and measure features on an image. Use the arrow beside **Annotations** to select a tool.

### Note

A draft presentation is automatically saved when you add annotations and measurements to an image (see “Use presentations” on page 12).

### Note

Measurement units are set in your user preferences (see “Change your user preferences” on page 168).

## Propagate annotations and measurements

For cross-sectional images, you can propagate an annotation or measurement across all images in the series.

1. Add an annotation or measurement to a cross-sectional image.
2. Right-click (or touch and hold) the annotation or measurement, then select **Propagate**.

Note that when an annotation or measurement is applied to a multiframe image while a cine is playing, the annotation or measurement is automatically propagated across all images in the series. If a propagated measurement cannot be calculated for all images in the series, the measurement value will be \*\*\*.



## Annotations

### Arrow

Add a arrow pointing to a feature of the image.

1. Click (or tap) and drag to add an arrow.
2. Add a note, then select **OK**. Select **Cancel** if you do not want to add a note.

To adjust an arrow:


- To move the arrow, drag the arrow to a new position.
- To adjust the arrow length, drag  at either end of the arrow.
- To move the note, hover over the note until  appears, then drag the note to a new position.
- To edit the note, click (or tap) the note. Edit the text, then select **OK**.

## Text

Add a note to an image.

1. Click (or tap) where you want to add the note.
2. Add text and select **OK**.

To adjust the note:

- To move the note, hover over the note until  appears, then drag the note to a new position.
- To edit the note, click (or tap) the note. Edit the text, then select **OK**.

## Plumbline

Add plumbines to an image. The angle where the lines intersect is shown.

1. To create vertical lines, click (or tap) and drag up or down.
2. To create horizontal lines, click (or tap) and drag left or right.

To adjust a line:


- Drag a line to move it to a new position.

## Curvature

Measure the radius between two points.

1. Click (or tap) and drag to draw a line between two points.
2. Move the mouse to define the curve radius, then click (or tap) to set the radius.

To adjust the curve:

- To adjust the curve radius, drag  in the center or on an end of the curve.
- Drag the curve to move it to a new position.

## Spine Labels

Label spinal vertebrae in an image.

1. Click (or tap) on the first spinal vertebra, then select a label.
2. Click (or tap) on the remaining vertebrae to apply consecutive labels. When done, right-click + beside a label, then select **Complete Labeling**.
3. To display the labels across all views of this body location in the current study, select **Study**. Select **Not Shared** to display the labels on the current viewport only.
4. If sharing labels across views, set the **Display Threshold** to indicate how many neighboring slices the label should be displayed on. Labels are displayed on consecutive slices up to the **Display Threshold** (in mm).

To adjust the labels:

- To change a label, right-click + beside the label, then select **Edit**.

- To delete a label, right-click + beside the label, then select **Delete**. To delete the last label added to the image, select **Delete Last**. To delete all labels, select **Delete Annotation**.

### Grease Pen

Highlight a region of interest using a freeform shape. No measurements are shown.

1. Click (or tap) and drag to create a shape.
2. Drag the shape to move it to a new position.

## Linear Measurements

### Cursor

Click (or tap) to display a point intensity measurement. The value is shown in measurement units appropriate for the study type. You can also choose to show the cursor position. For details, see “Change your user preferences” on page 168.

### Ruler

Click (or tap) and drag to create a linear measurement. After the line is drawn, the line length is calculated and displayed. Measurements are not shown on uncalibrated images.


If two lines intersect, the angle between the lines is shown. You can turn off the angle measurement (see “Change your user preferences” on page 168).

### Contour

Click (or tap) and drag to create a free hand curve and measure its length. Measurements are not shown on uncalibrated images.

### Polyline

Use to create a multi-segment line.


- Click (or tap) to create each point in the line. Right-click (or touch and hold) after creating the final point.
- Drag  on a point to move the point to a new position.


### Ratio

Use to measure the ratio between two lines. Two ratios are shown: from the shorter line to the longer line, and from the longer line to the shorter line.

1. Click (or tap) and drag to draw the first line.
2. Drag to draw the second line. The ratio is shown between the lines.

To adjust the lines:

- Drag  at the end of a line to adjust a line's length.

- Drag  in the center of a line to adjust the line's position.
- Drag the dashed connecting line to move the entire measurement to a new position.

### Calibrate

Enabled for images that need to be calibrated due to missing size attributes in the image (for example, an analog image that has been scanned). The **Calibrate** tool should only be used when a scale or an object of known size is present on the image.

Drag to draw a line between scale marks on the image or to cover a known object, then enter the distance. After this calibration, the measurement tools are available for the image.

### Area Measurements




You can define patterns for area measurement tools in your user preferences (see "Change your user preferences" on page 168).

#### ROI-Free

Create a border around a region of interest using a freehand shape. Statistics for the area are shown as appropriate for the study type (for example: average intensity, standard deviation, area and main diameters).

- Click (or tap) and drag to create a border around the region of interest.

To adjust the measurement:

- Drag a  to move the measurement to a new position.
- To increase the measurement area, click (or tap) anywhere on the border (do not select ). Draw a line outside the border that connects to another point on the border. This area is added to the measurement.
- To decrease the measurement area, click (or tap) anywhere on the border (do not select ). Draw a line inside the border that connects to another point on the border. This area is removed from the measurement.

#### Note



To increase or decrease the measurement area, the ROI-Free tool must be selected.

#### ROI-Ellipse

Create a border around a region of interest using an elliptical shape. Statistics for the area are shown as appropriate for the study type (for example: average intensity, standard deviation, area and main diameters).

- Click (or tap) and drag to draw an ellipse.

To adjust the measurement:




- Drag the center  to move the measurement to a new position.
- Drag an outer  to adjust the length of the corresponding axis of the ellipse.

### Circle

Create a circular border around a region of interest. Statistics for the area are shown as appropriate for the study type (for example: average intensity, standard deviation, area and main diameters).

- Click (or tap) and drag to draw a circle.

To adjust the measurement:


- Drag an outer  to adjust the measurement size.
- Drag the center  to move the measurement to a new position. You can also drag anywhere on the circumference of the circle (except on an outer ).

### Polygon

Create a border around a region of interest using a polygon shape. Statistics for the area are shown as appropriate for the study type (for example: average intensity, standard deviation, area and main diameters).

1. Click (or tap) to create each point in the line.
2. Right-click (or touch and hold) after creating the final point.

To adjust the measurement:


- Drag a  to adjust the measurement size.
- Drag the measurement to move it to a new position.

### Square and Rectangle

Create a square or rectangle around a region of interest. Statistics for the area are shown as appropriate for the study type (for example: average intensity, standard deviation, area and main diameters).

1. Click (or tap) to create the first corner of the square or rectangle.
2. Click (or tap) to create the opposite corner.

To adjust the measurement:

- Drag a  to adjust the measurement size.
- Drag the measurement border to move it to a new position.
- Drag a circle to rotate the measurement.

### ROI - Threshold

Available for PET images. Highlight areas above a certain threshold within a region of interest.

To apply a threshold:




1. Click (or tap) and drag to create a border around a region of interest.
2. Enter a threshold, then select **OK**. Any areas within the region of interest that are above the threshold are circled.

**Note**

The default threshold is 2.5 SUV. To change the default threshold, see “Change your user preferences” on page 168.

3. To apply the ROI threshold measurement to all images in the series, right-click (or touch and hold) the measurement, then select **Propagate**.

To adjust the measurement:




- Drag a  to move the measurement to a new position.
- To increase the measurement area, click (or tap) anywhere on the border (do not select ). Draw a line outside the border that connects to another point on the border. This area is added to the measurement.
- To decrease the measurement area, click (or tap) anywhere on the border (do not select ). Draw a line inside the border that connects to another point on the border. This area is removed from the measurement.

**Area Ratio**

Available for OP images. Measure the area ratio between two regions.

1. Click (or tap) and drag to create a border around the first region.
2. Click (or tap) and drag to create a border around the second region. The area of the two regions are shown. The ratio of the smallest area to the largest area is also shown.

To adjust the measurement:

- Drag  to move the measurement to a new position.
- To increase the measurement area, click (or tap) anywhere on the border (do not select ). Draw a line outside the border that connects to another point on the border. This area is added to the measurement.
- To decrease the measurement area, click (or tap) anywhere on the border (do not select ). Draw a line inside the border that connects to another point on the border. This area is removed from the measurement.

**Note**

To increase or decrease the measurement area, the Area Ratio tool must be selected.



## Angle Measurements

### Angle

Click (or tap) and drag to create the first side of the angle (the start of this side will be the vertex). Click (or tap) where you want to place the bottom of the second side of the angle. The two sides are automatically connected. The angle between the two sides is shown.

### Cobb Angle

Click (or tap) and drag to create the first side of the Cobb angle, then drag to create the second side. The two sides are automatically connected. The angle between the two sides is shown.

### Color

Select the color to use for annotations.

### Manage

#### Delete Last, Delete All

Remove the last change or all changes from the current image.

#### Note

Use Reset to remove changes from all images in the series.

### Editing Annotations

You can edit annotations. For example, you can drag to change the annotation's position or size. You can also double-click (or touch and hold) the text in an arrow or text annotation to modify it.

### Deleting Annotations

To remove an annotation, right-click (or touch and hold) the annotation, then select **Delete**.

## Measurements for wide field ophthalmic photography images

NilRead calculates linear and area measurements on wide field ophthalmic photography images. The calculations are done using a 3D geometric model of the eye.

When you apply a linear measurement to a wide field ophthalmic photography image using the ruler tool, the measurement is calculated as the length of the curve representing the line on the 3D surface of the eye. Area measurements are performed on a 3D model of the eye by projecting the 2D shape (ellipse or ROI) from the image to the 3D model. The area measurement is calculated from the enclosed pixels on the 3D model.

If the distance or area cannot be measured, the measurement value will be \*\*\*. If you move a linear or area measurement to a different location on the image, the measurement will be recalculated based on the measurement's new location.

## Key Image



Available for 2D views only. Create a series of key images for a study. This allows you to quickly access important images within a large series of images.

To mark the current image as a key image:

1. Select **Key Image**.
2. Select the arrow beside **Key Image**, then select a label. If you do not select a label, the label selected for the last key image will be used.
3. (Optional) To add a note, select **Show KO description window** and enter your note.
4. Click (or tap) the image. A key icon, the label and your note are added to the top-left corner of the image.



5. The image is added to the key images series.



6. You can keep the Key Images Description window open if you want to apply the same note to another key image. Select Close to close the window.

## Titles



Show or hide image details in all viewports (see “View image details” on page 67).

## Full Quality



View the original, uncompressed image.

## Reset



Remove changes from all images in the series. Changes will only be removed from the current view.

#### Note

Use Annotations > Delete Last/Delete All to remove changes from the current image only.

## Hanging Protocols



Use hanging protocols to customize the image viewing area (see “Select hanging protocols” on page 65).

## Study Layout



Use study layouts to customize the image viewing area (see “Arrange images” on page 57).

## View



Use views to customize the image viewing area (see “Arrange images” on page 57).

## Rendering



Select the rendering mode for the study. Options are MIP (maximum intensity projection), volume rendering and average.

#### Note

Use presets (side panel) to apply common rendering settings (see “Apply presets” on page 47).

## Reference



Show or hide reference lines.

#### Note

Use Relate to change the position of the reference lines (see “Relate” on page 27).

## Thickness



Use the arrows to increase or decrease the plane thickness.

## Clipper



Clippers are used to selectively remove portions of a study from a 3D rendering. This is generally used to expose a part of anatomy or a pathology. Several types of clippers are available: Plane, Box, Ellipsoid and Cylinder.

To use the clipper, select **View Tools** (side panel).

- **Plane** Front plane clipper. Click (or tap) on an image to enable the clipper. Drag to push the plane in and out.
- **Box** Rectangular clipper. Click (or tap) on an image to enable the clipper. Drag a handle on the corner of the box to change the box size. Drag the center of the box to move it.
- **Ellipsoid, Cylinder** Elliptical or cylindrical clipper. Click (or tap) on an image to enable the clipper. Drag the center of the shape to move it.
- **Clear** Remove all clipping from the image.
- **Reset** Reset the currently selected clipper to the default settings.
- **Pin, Unpin** Lock or unlock the clipping changes that have been made to an image. This allows you to retain the current clipping while working with an image (rotating, zooming, etc.). Further clipping cannot be performed until the image is unpinned. Pin is not available for the Plane clipper.

### Note

You can perform other actions, such as rotating the image, while using a clipper. You can also save a clipped image as a bookmarked image (see “Share bookmarked images” on page 152).

## Curved MPR

Curved MPR allows you to define a curve in the volumetric dataset and then view an image along this curve. This is useful for viewing structures such as blood vessels or the spine.

1. Select View.
2. Under MPR Views, select Curved. Three MPR views are shown on the left and a blank viewport is shown on the right.



3. Select View Tools (side panel). The curved reformat tools are shown.

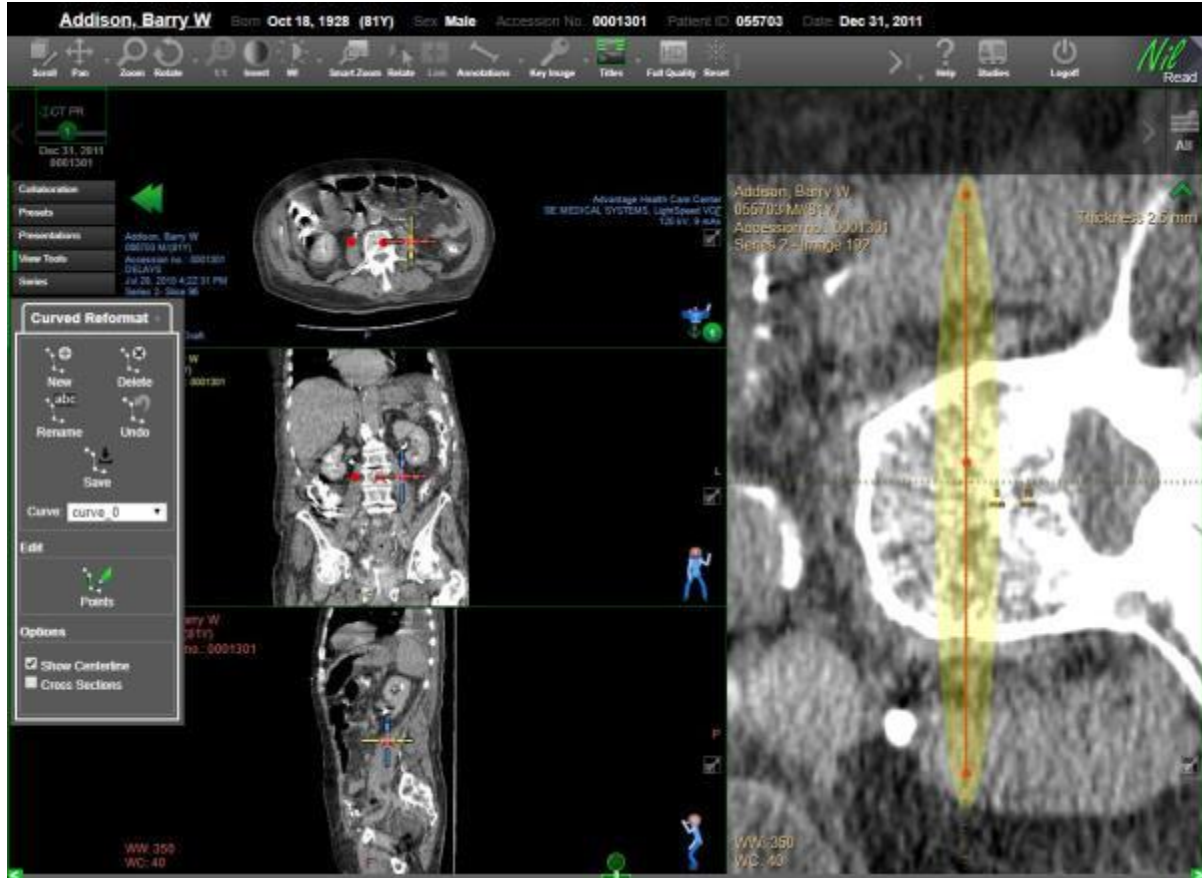


### Create a curved reformat

1. Select **New**.
2. Click (or tap) to add points to the curve reformat. Once you have added at least two points, the curved reformat view is shown in the viewport on the right.  
For MPR images, points are shown as filled circles if the corresponding point is visible in the current MPR or curvilinear view.  
On planar slabs, points are shown as filled circles (when the point is on the reformat plane), ^ (when there is a control point on a plane located closer to the current view) or v (when there is a control point on a plane located further away from the current view). The centerline is not displayed on planar slabs.
3. To set the focus point, right-click a seed, then select **Focus to this Seed**.
4. When done adding points, select **Save**. The curved reformat will be saved in the local database and will be available when the study is reloaded.

### Show Centerline

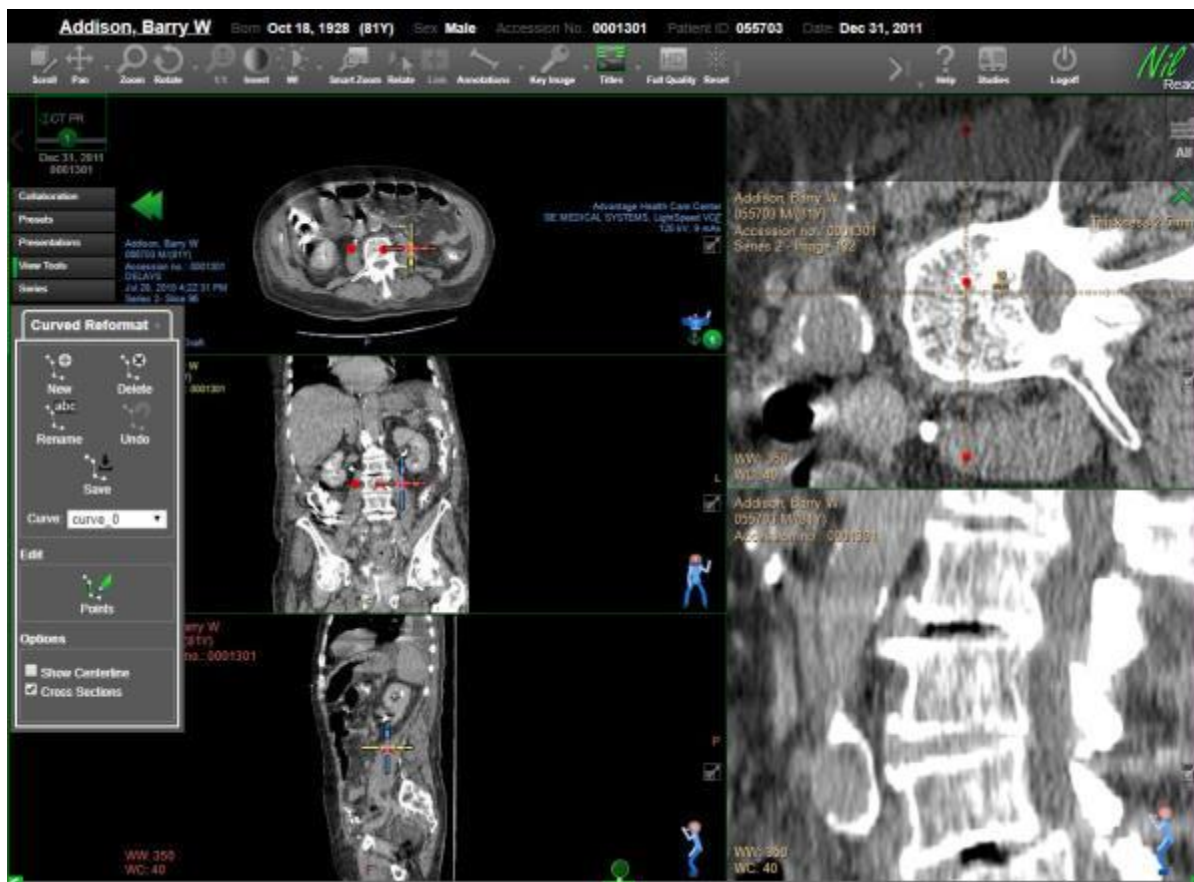
Applies to the curved reformat view (right viewport). Select this option to view a polyline connecting all of the points created for the reformat.





## Cross Sections

Select this option to view a cross-sectional reformatted view perpendicular to the centerline through the focus location. The cross-section is shown in the bottom-right viewport and is a reformat along the plane shown in the top-right viewport.



## Edit a curved reformat

1. In the Edit area, select Points.
2. To edit a point, click (or tap) on the point, then drag the point to a new location. Select Undo to remove the last action you performed.
3. To move through the points, right-click a point, then select Previous Seed Point or Next Seed Point.
4. To delete a point, right-click the point, then select Delete Seed Point.

## Rename a curved reformat

1. Select a curved reformat from the Curve list.
2. Select Rename. Enter a new name, then select OK.

### View a saved curved reformat

To view a different curved reformat, select a curved reformat from the **Curve** list.

### Delete a curved reformat

1. Select a curved reformat from the **Curve** list.
2. Select **Delete**. The curved reformat will be deleted from the local database.

## Segment



Available for 3D views. Use to view and edit tissues.


### Note

Changes made with the Segment tool are not saved when you close the study. However you can save a static screenshot using a secondary capture image (see "Share secondary capture images" on page 153).

To view a tissue:

1. Select a 3D view.
2. Select **Tissue** (side panel). The Tissue panel contains part segmentation results by tissue.
3. Select a tissue from the panel. You can select multiple tissues to view simultaneously.

To edit a tissue:

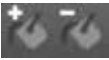
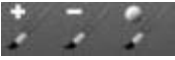
1. In the Tissue panel, select  beside a tissue, then select **Segment**.  
The **Current Tissue** area shows the tissue you are currently editing. This area also contains rendering presets you can apply to the tissue.
2. You can use the **Segmentation** tool to edit the tissue. See the following section for details.
3. Select **Undo** to undo the last change made to the tissue.
4. Select **Reset** to remove all changes made to the tissue.

### Note

If you do not select a tissue, any changes you make with the Segment tool will be saved as a new tissue. You can also create a new tissue based on an existing tissue. If you edit an existing tissue then deselect the tissue in the Tissue panel, the edited tissue will be added as a new tissue. You can only create one new tissue.

### Segmentation Tools (Available on MPR viewports)

These tools select an area in close proximity to the tissue you select, then grow or shrink this area.

1. Select the type of tissue (**Tissue**, **Nodule**, **Lesion**, or **Vessel**).
2. To select an area, use of the following tools:
  -  Hover over the area, then click (or tap) to select the area.
  -  Drag to select the area. The tool will apply color to the area identified as part of the tissue.

## NM Map



Assign a color map to nuclear medicine images.

## Fusion Map



Assign a color map to fusion images.

## Fusion Blend



Adjust the fusion blend level.

## Cine



View the images in a study as a "movie". Use the Cine controls to:

- **Run** Play the cine.
- **Sync Run** Synchronized play of all viewports.
- **Pause** Pause the cine.
- **Speed** Change the desired playback speed. The actual playback speed is shown while the cine is playing.
- **Range** Select the range of images from the series to include in the cine, based on the current image. For example, selecting 40 will include the 20 images before the current image and the 20 images after the current image. You can also choose to include all images in the series.
- **Replay/Yoyo** Replay the cine continuously or yoyo (play forwards then backwards).

## RT Template



Apply a radiation therapy (RT) template to a study. For details, see “View radiation therapy (RT) plans” on page 112.

## First, Previous, Next, Last



Scroll through the series in a study.

## Use additional tools

### Add notes to a study

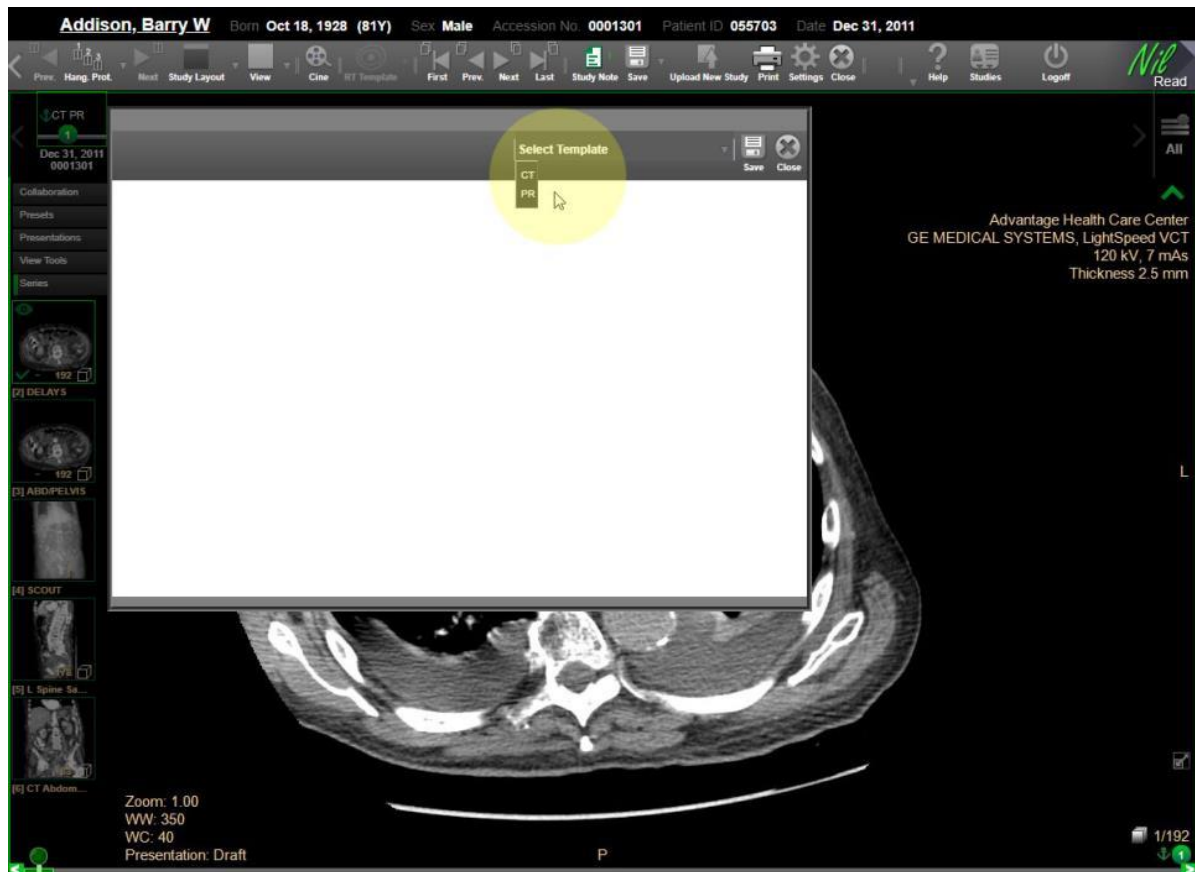
You can add notes as you are reviewing a study. These notes are available until you close the study.

You can also save the notes as a structured report. Structured reports can be accessed the same way as other reports (on the patient timeline and in the Patient Directory).

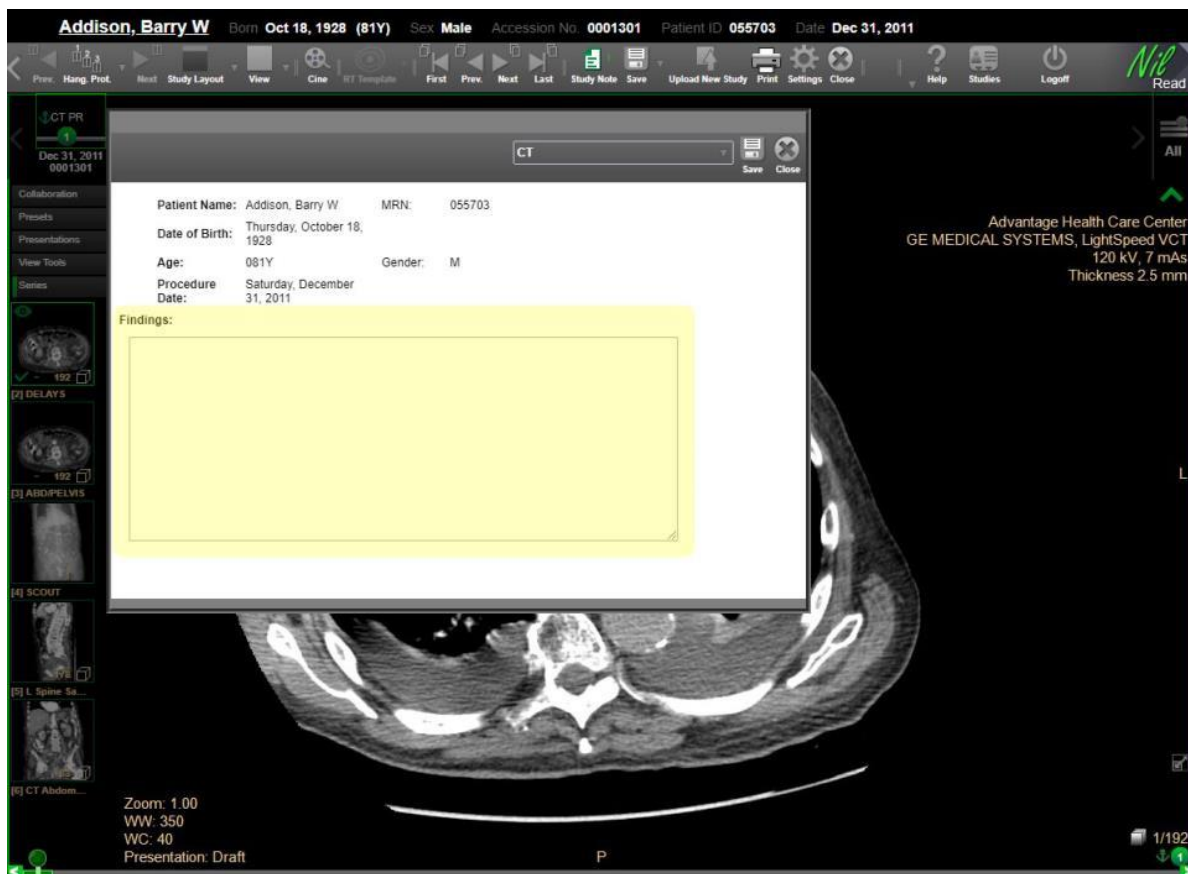
1. Select **Study Note** (toolbar). A new window appears.
2. Select a template. If there is only one applicable template for the study, it is applied automatically.

#### Note

For details on creating templates, see “Manage structured report templates” on page 160.



3. Enter your comments in the Findings area. You can leave the window open as you work with the study. To move the window to a different location on the screen, drag the title bar.



4. To create a structured report, select **Save**, then select **Close**.
5. If you do not want to create a structured report, select **Close**.

## Apply presets

Use a preset to visualize different aspects of a study. For example, a CT study could include a preset to visualize vessels or a preset to visualize bones. The study view, modality and rendering mode determine what presets are available.

- **2D** Presets can change window level.
- **MPR** Presets can change rendering mode and opacity.
- **3D** Presets can change rendering mode and opacity.
- **Sculpting** Presets can change rendering mode and opacity.

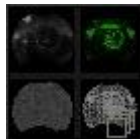
When you apply a preset, any changes you have made to an image will be removed (rotation, annotations, etc.). Any changes you make to a preset are not saved.

1. Select **Presets** (side panel). The presets available for the study are shown below the side panel.
2. Select a preset thumbnail.

For details on modifying presets, see “Change window level presets” on page 174.

## Create a series with all images

NilRead can automatically create a “virtual series” that contains all images in a study in the order they were acquired. The virtual series is added to the side panel and the series icon shows four images side-by-side. For example:



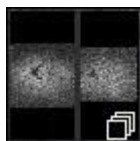
When you hover over the series, the description is **All images**.

You can control whether virtual series are created automatically. You can also choose whether virtual series are created only for studies containing a specific modality.

1. Select **Settings**.
2. Under **Preferences**, select **Modality Preferences**.
3. Enter the following information:
  - **Modality** Select the modality for which you want to set the virtual series preference.
  - **Virtual Series** Select **Yes** to automatically create virtual series for the modality you selected. Select **No** if you do not want to create virtual series for the modality you selected.
4. Select **Save**.

## View stereometric images

If a study contains stereometric images, NilRead automatically creates a series containing all stereometric pairs of images in the study. The series is added to the side panel and the series icon shows two images side-by-side. For example:



- When you hover over the series, the series description is “All stereometric images”.
- When you view images from the series, the 1x2 view is automatically applied and the images in each stereometric pair are shown side-by-side.
- Scrolling through the series will scroll through each pair of images.

## View CAD marks

If a study has an associated computer-aided detection (CAD) report, you can view the CAD marks on the relevant mammography images. CAD marks are also available for DBT mammography images produced by Hologic (if CAD marks are provided by the manufacturer).

### Important

Users are instructed to review all images in the study before enabling CAD marks.

1. Select **View Tools** (side panel). An icon for the CAD report is shown. For example:



2. Hover over the icon to view the following information:
  - **Manufacturer** CAD report manufacturer.
  - **Algorithms** Algorithms used by the CAD software.
  - **Calc** Number of calcification marks.
  - **Mass** Number of mass marks.
  - **Total** Total number of CAD marks in the report.
3. Select **Show CAD** to enable CAD marks on the study images. If an image contains CAD marks, the number of marks is shown on the image.
4. Clear **Show CAD** to hide CAD marks.

## View DBT slice position

When scrolling through slices in a DBT series, an indicator appears in the bottom-left corner:



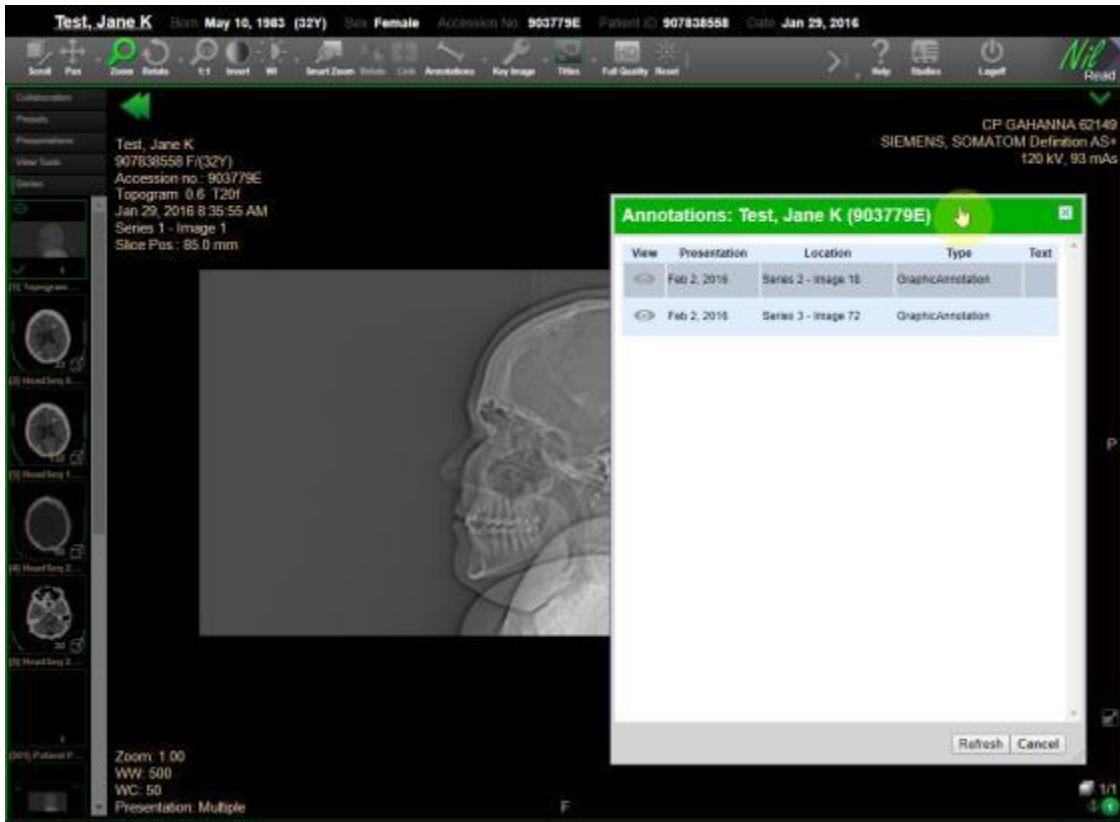
The indicator shows the current slice, total number of slices, and an orientation marker (F = feet, H = head).

## View study annotations

You can quickly find the annotated images in a study (these are annotations added to the source image, not annotations added in NilRead).

1. Select **Annotations** (toolbar), then select **View**.
2. A list of the annotated images in the study appears. You can leave the window open as you work with the study. To move the window to a different location on the screen, drag the title bar.





3. Click (or tap) View beside an image. The image is loaded in the viewer.



4. To check for any new annotated images in the study, select **Refresh**.
5. To close the window, select **Cancel**.

## Edit videos

You can edit a video to remove irrelevant information. The segments of the video you want to retain are saved as a new video. The original video also remains in the study and is not modified.

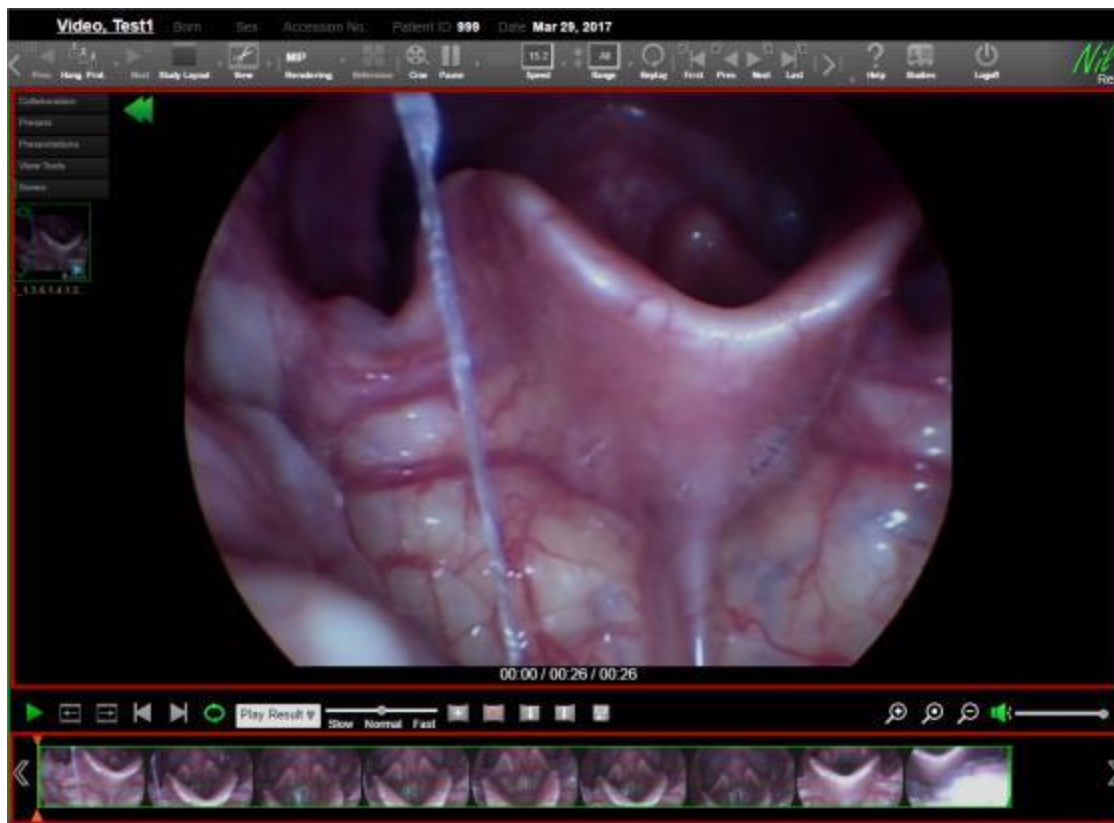
1. In the Patient Study Directory, open a study that contains a video.
2. Select **Series** (side panel) and select a video. The video opens in the image viewer and begins to play. Note that if the first series in the study contains a video, the video will play automatically when the study opens.
3. Select **View** (toolbar), then select **Video Editor**. The video editor opens.

### Note

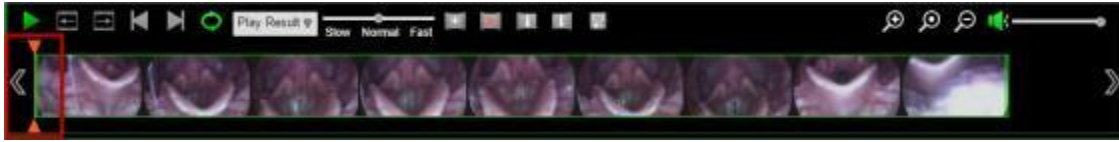
If you open a video from the QC viewer, the video automatically opens in the video editor.

The video editor contains the following sections.

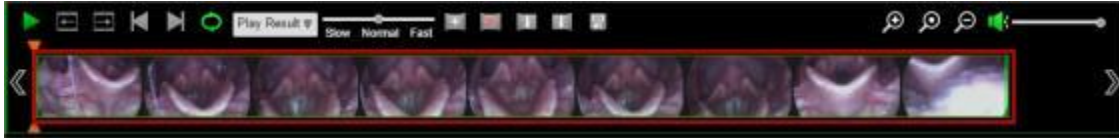
- The **preview window** at the top of the screen shows the location currently selected in the timeline. The **timeline** at the bottom of the screen contains thumbnail images of the video content.



- The **position indicator** shows the current location in the video. When you first open the editor, the position indicator is at the start of the video.



- Use the **selection box** in the timeline to mark the segments you want to include in the edited video. When you first open the editor, the entire video is included in the box.



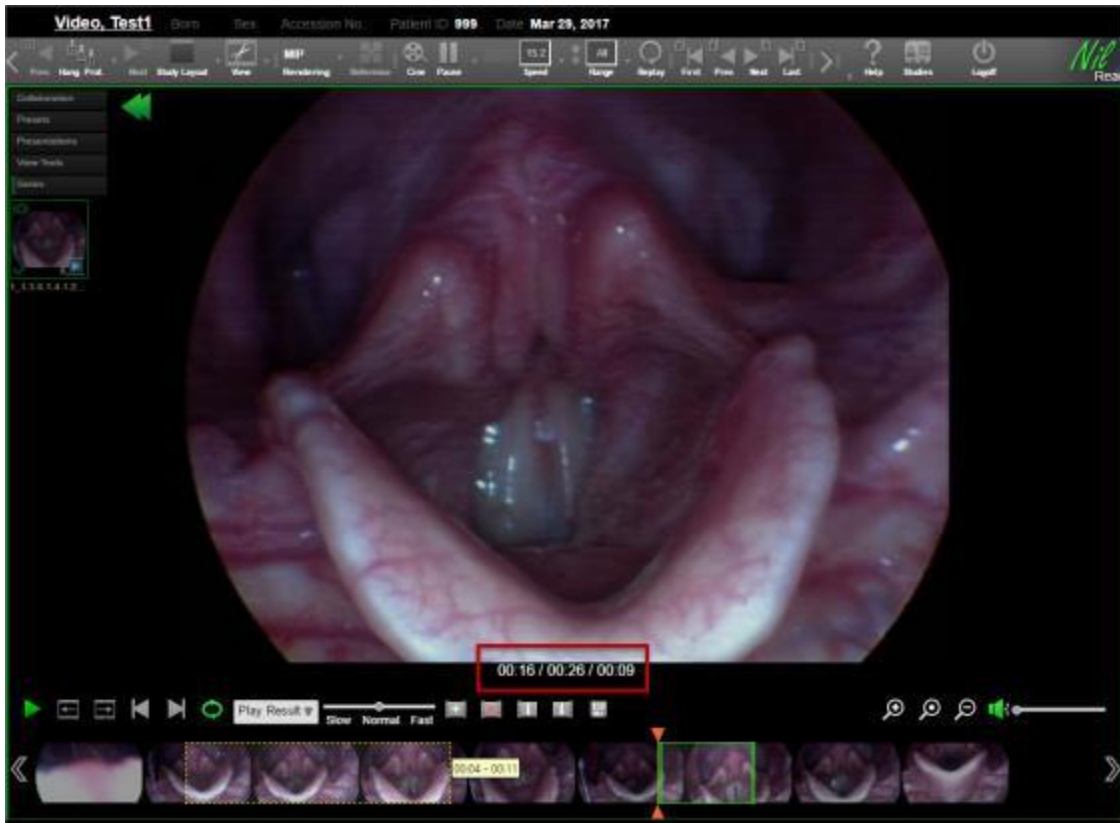
You can resize and move the selection box. You can also add more boxes to the timeline, allowing you to mark segments from different parts of the video. For example, the following timeline contains three boxes. These three segments of the original video will be included in the edited video.



The following information is shown below the preview window.

- The current playback time from the start of the original video.
- The duration of the original video.

- The total duration of the segments that will be included in the edited video.

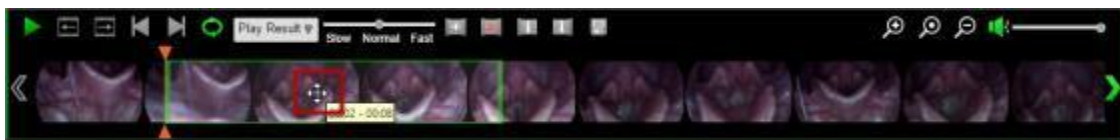



### Modify a selection box

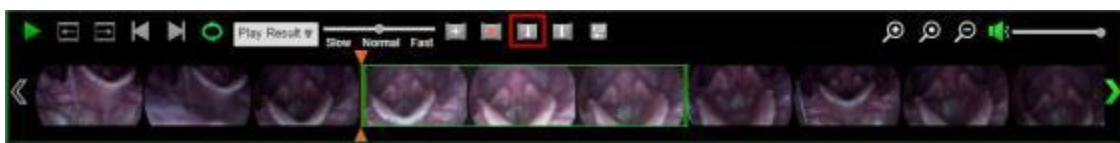
- Drag the ends of the box to resize it.




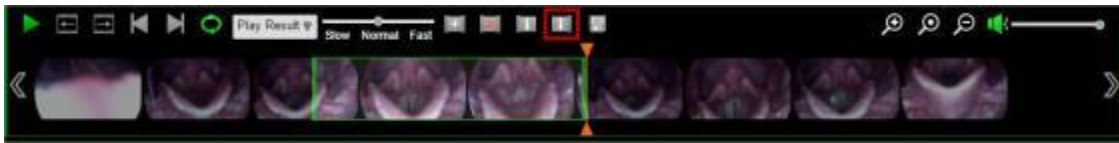
- Drag the box to a new position.



- To set the beginning of the box to the position indicator location, select the box, then select .



To set the end of the box to the position indicator location, select the box, then select .




- Hover over a box to view the timeframe of the original video within the box.



### Add and remove selection boxes

Use multiple selection boxes to mark non-contiguous segments. You can add as many boxes as needed.

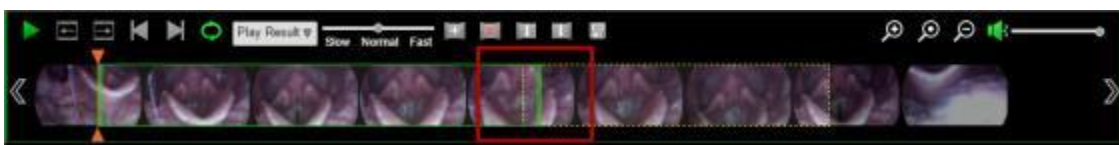
- To add a box, select . A new box appears to the right of the current box. Change the box position and size as needed.



- To remove a box, select the box, then select . Note that you cannot remove all boxes; at least one box must remain on the timeline.



- Note that if boxes overlap, they will be merged together when the edited video is saved.





### View thumbnail images

You may need to use the arrows at each end of the timeline to view all of the thumbnail images. You can also hold SHIFT while dragging the timeline to view additional thumbnails. On touch devices, use a two-finger drag.

Use the following tools to resize the thumbnail images in the timeline.



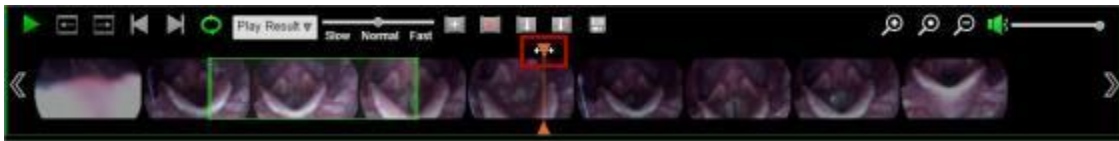
Increase the thumbnail size. This allows you to view the thumbnails more clearly; however, this reduces the number of thumbnails shown on the screen.

	Fit all thumbnails on the screen.
	Decrease the thumbnail size. This allows you to view more thumbnails on the screen.

### Change the position indicator



Move the position indicator to the video location you want to preview.

- Drag the position indicator to a new location on the timeline.





- Click (or tap) above or below the timeline to move the position indicator to a new location.



- To move the position indicator to the start of a selection box, select a box, then select . To move the position indicator to the end of a selection box, select a box, then select .




- Use  and  to move the position indicator forwards or backwards frame-by-frame. You can click (or tap) and hold these icons to continue moving frame-by-frame.








### Preview the edited video

Select the content you want to preview, then select . You can choose from the following options:

- **Play Result** Play the entire edited video.
- **Play Segment** Play one of the segments in the edited video. Select a segment, then select .
- **Play Original** Play the original video.


You can use the following controls while playing a video.

- To skip to the start of the video or segment, select . To skip to the end of the video or segment, select .

- To change the playback speed, select **Slow**, **Normal** or **Fast**. You can also use the slider to change the speed.
- To change the playback volume, use the volume controls above the timeline .
- To loop the playback, select .
- To pause the playback, select . You can also click (or tap) on the preview window to pause and resume playback.

### Save the edited video

The edited video will be saved in a new series.

1. Select .
2. Select the following options:
  - **Encoding Profile** Select the encoding profile for the edited video. The profile determines the video quality and file size.
  - **Audio** Include or exclude audio in the edited video.
  - **Series Description** Enter a description for the new series. Leave this field blank to use the description from the original series.
3. Select **Save**.

### Return to the image viewer

To return to the image viewer and exit the video editor, select **View** (toolbar), then select **Video**.

## 3. Use the image viewing area

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### Arrange images

When you open a study, the study is shown in the NilRead image viewing area. You can change the layout of the image viewing area using study layouts and views.

- **Study Layout** Apply a study layout to the image viewing area. This divides the area into multiple "screens". You can drag a different series into each screen, allowing you to view multiple series simultaneously.
- **View** Apply a view to a screen. A view is a predefined viewport arrangement specific to a clinical scenario. Some views display a single viewport while others display multiple viewports, each with a different type of visualization. You can apply different views to each screen or apply the same view to all screens.

For common uses of layouts and views, see "Sample layouts and views" on page 58.

### Apply a study layout to the image viewing area

1. Select **Study Layout** (toolbar).
2. Select a study layout. The study layout is applied, dividing the image viewing area into multiple screens.

### Apply a view to a screen

1. Click (or tap) a screen, then select **View** (toolbar).
2. To apply the same view to all screens, select **Apply View Mode to Whole Screen**.
3. Select a view. The view is applied to the selected screen (or all screens).

You can drag a different series into each viewport. You can also drag a study from the patient timeline into a viewport.



## Sample layouts and views

The following examples show common ways to arrange images using study layouts and views. Available views depend on your NilRead implementation.

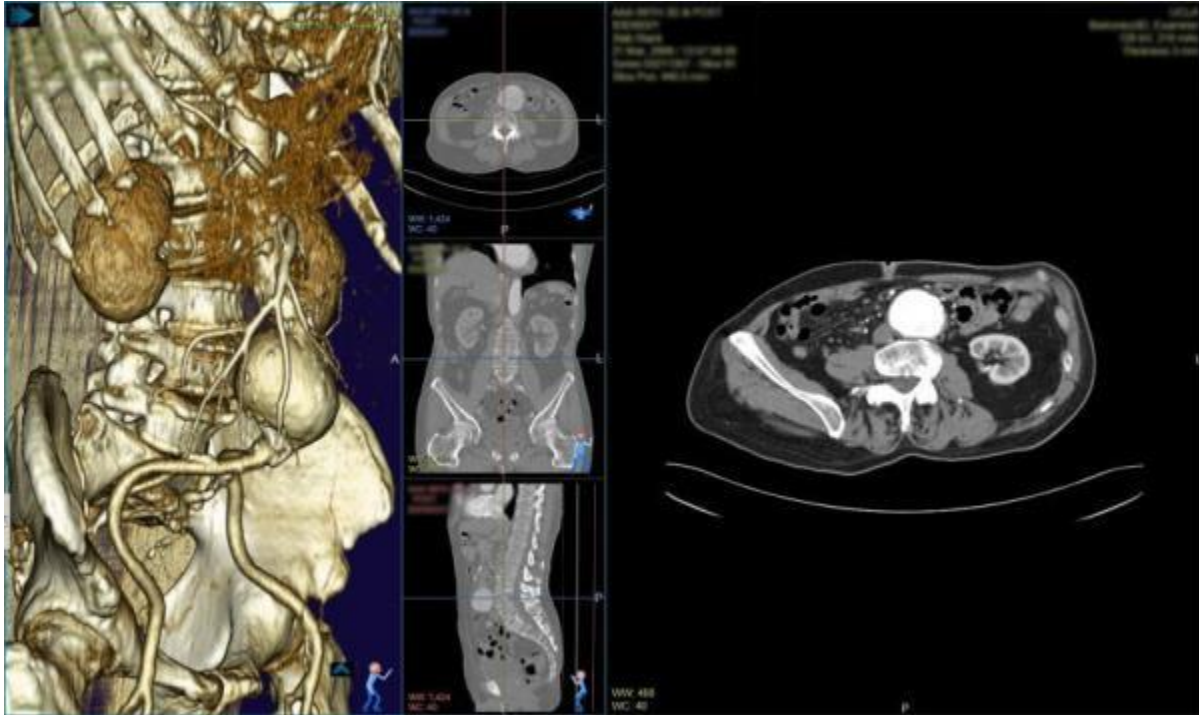
### 1x2 layout

The following example shows a 1x2 study layout. This creates two side-by-side screens with a different series in each screen.



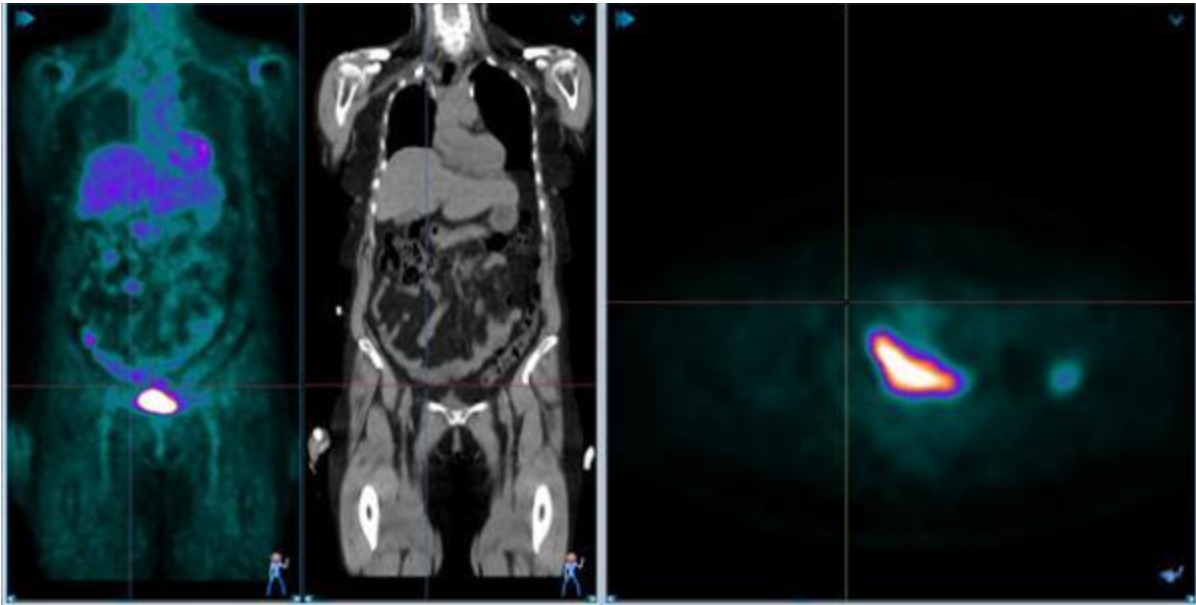
## Multiple viewports

When a view is applied to a screen, the screen may be divided into multiple viewports. In the following example, the MPR 3D view has been applied to the first screen, dividing the screen into four viewports. Note that a different view (or the same view) could also be applied to the second screen.



## Multiple monitors

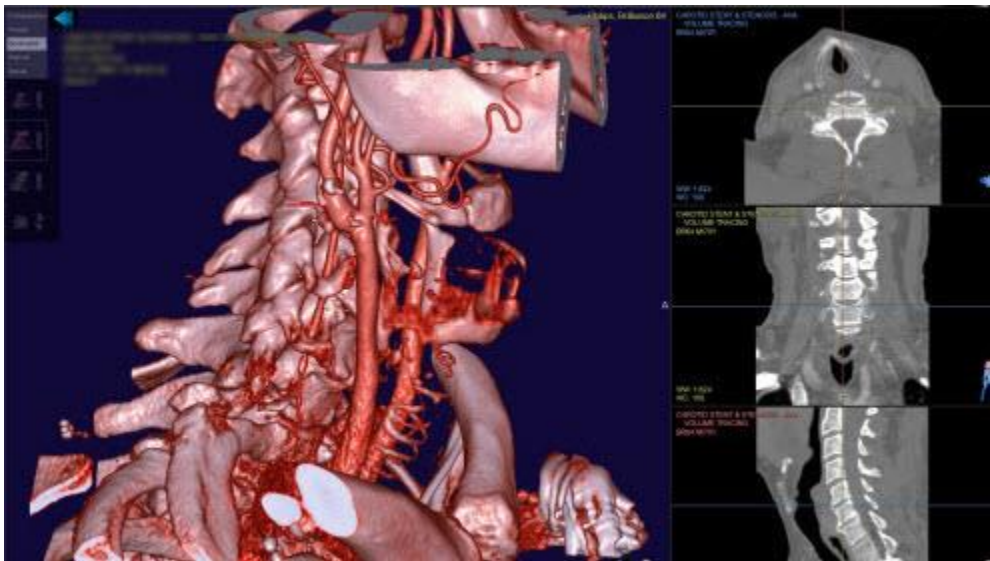
Each monitor can have its own study layout. In the following example, the first monitor displays two coronal MPR views and the second monitor displays an axial MPR.



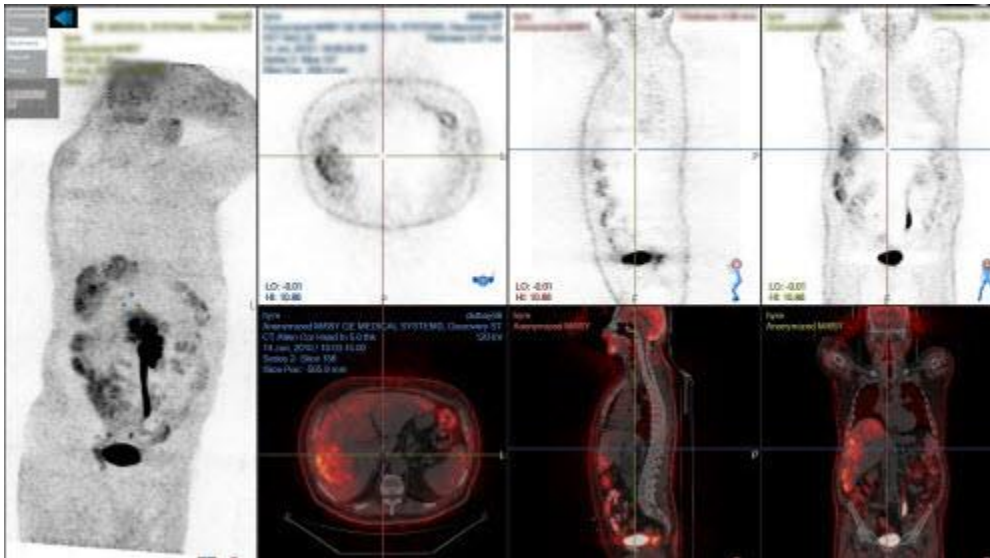
## Side-by-side series comparison (study layout)



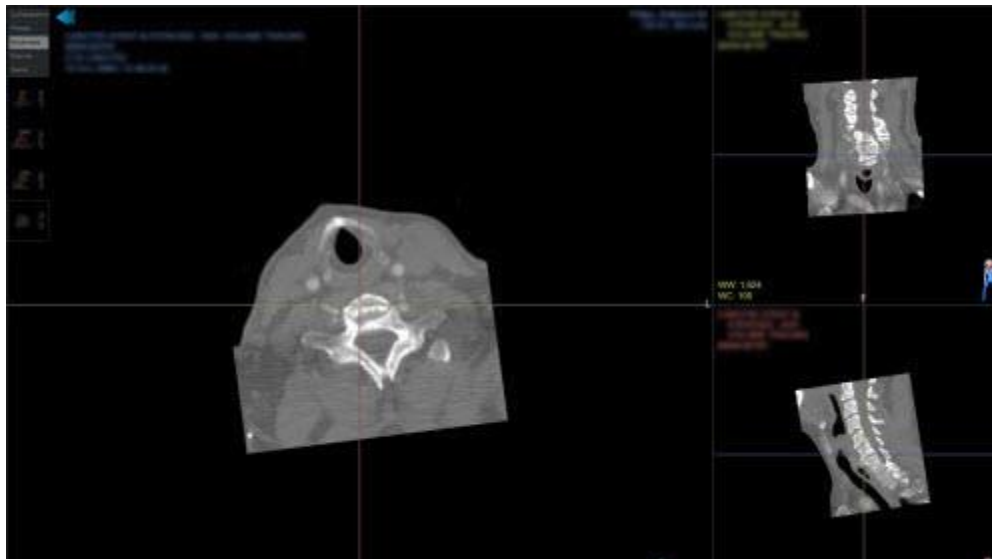
### 3D view



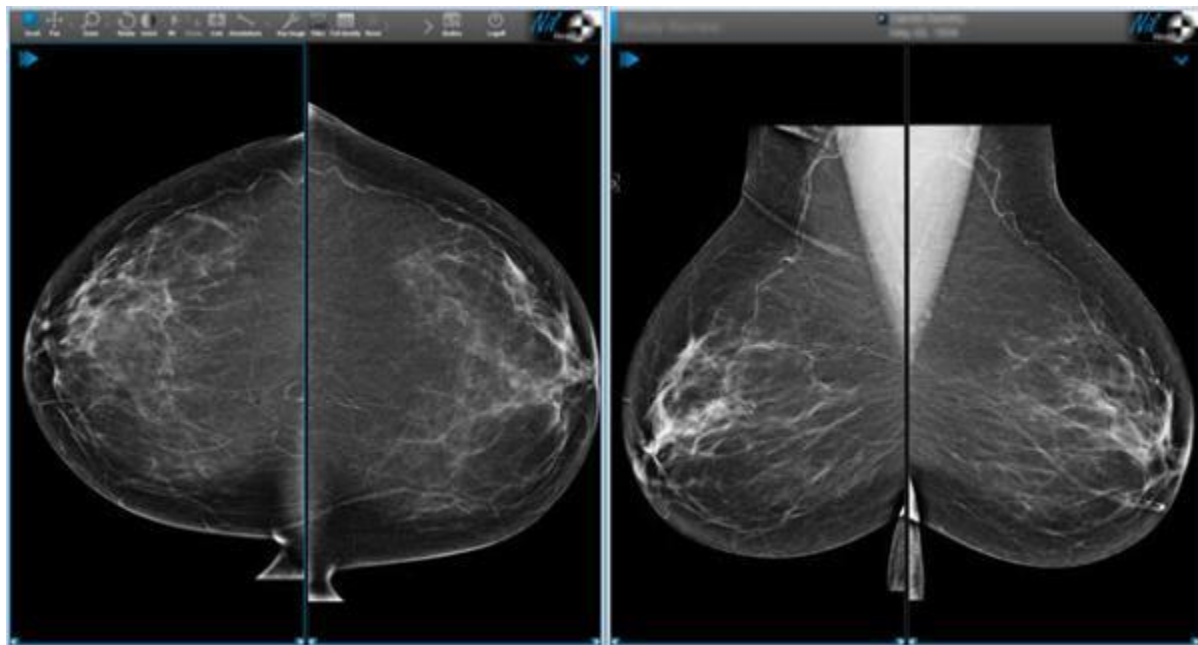
### PET-C fusion view



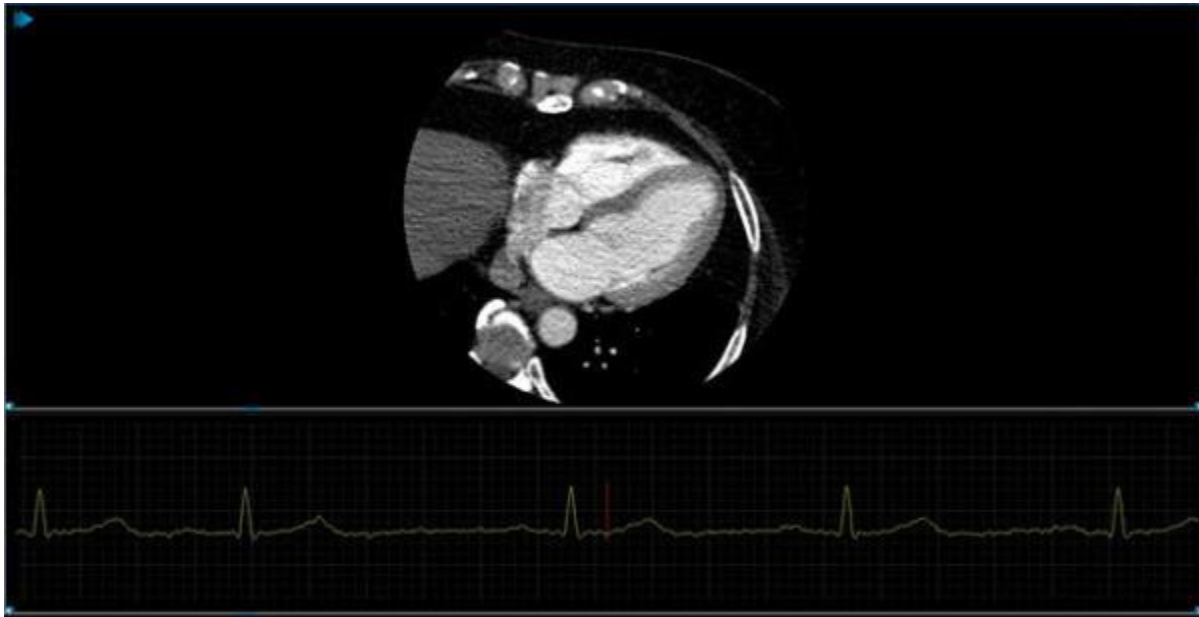
### Slab view



### Multi-monitor auto-aligned mammography hanging protocol

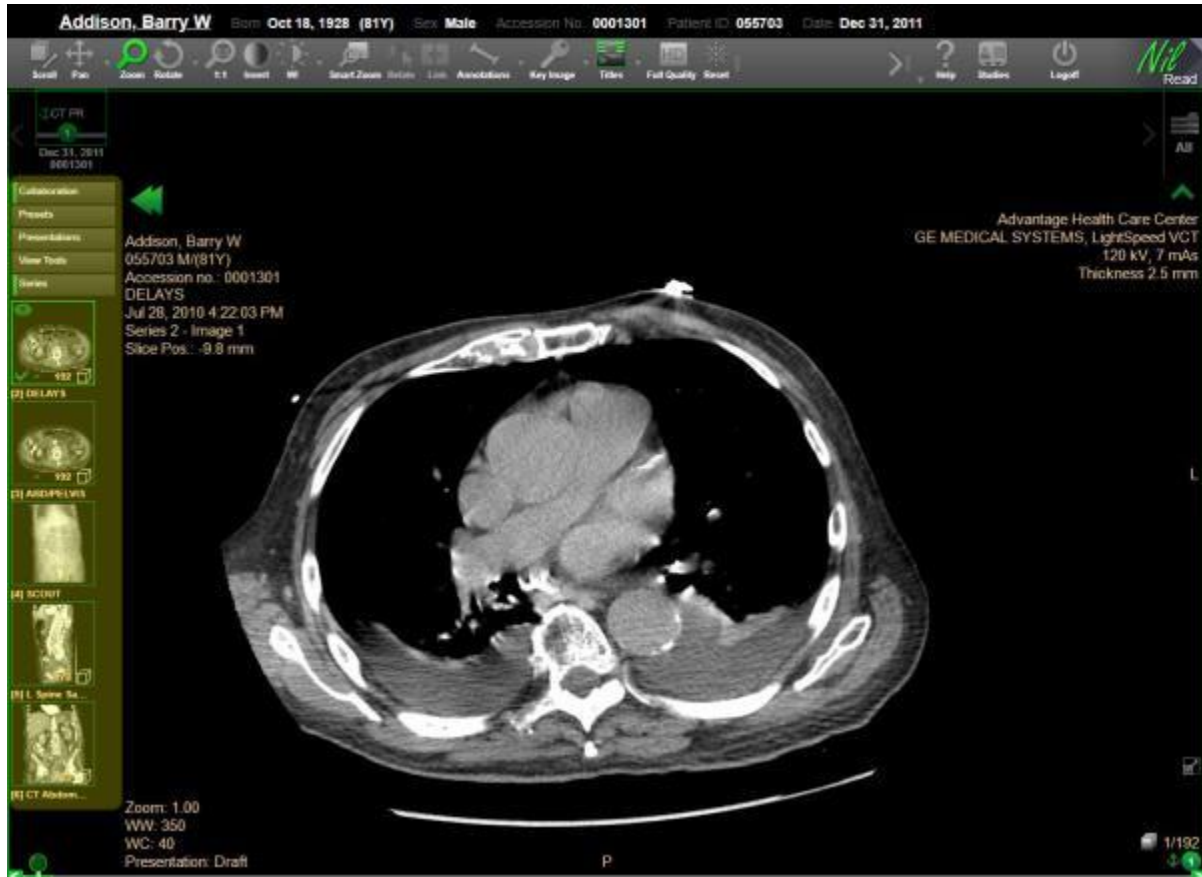


### Non-symmetric 2x1-1/3 study layout with ECG view



## View the side panel

The side panel provides quick access to NilRead features such as presentations and bookmarks. You also use the side panel to select a series.



Use the arrows to hide or view the side panel.




## Select a series

You can view multiple series by dragging series into different viewports.

### Note

For details on enabling multiple viewports, see "Arrange images" on page 57.

1. Select **Series** (side panel). The series in the study are shown below the side panel. A filmstrip icon  is shown on series with a multiframe cine sequence.
2. Hover over a series thumbnail for information (series ID, image count, date, modality, description).
3. Select a series thumbnail to load the series in the viewer. The series is opened in all viewports.  
or  
Drag a series into a viewport.

## Select hanging protocols

The purpose of a hanging protocol is to display the images in a study in a consistent manner. While the term originally referred to the arrangement of physical films in a film box, it now refers to the display of images on a computer monitor. When properly setup, the use of hanging protocols significantly improves reading quality and efficiency.

When opening a study, NilRead analyzes the DICOM attributes of the study and identifies matching hanging protocols. If any candidates are found, the best one is selected and applied automatically.

You can manually select a hanging protocol from the list of matched protocols. You can also create a new hanging protocol based on the current image viewing area.

### Note

See the [Hanging Protocols Handbook](#) for more information about using hanging protocols.

## Apply a hanging protocol

1. Select **Hang. Prot.** (toolbar). Available hanging protocols and the stages within each protocol are shown.
2. Select a stage within a hanging protocol. The image viewing area is updated.
3. Select **Prev H.P.** and **Next H.P.** (toolbar) to move through the stages in the hanging protocol.

## Create a new hanging protocol

You can customize the study layout and presentation state (window level, zoom, etc.) while viewing a hanging protocol, then create a new hanging protocol using these settings. Presentation state is not captured for clinical hanging protocols.

1. Select **Hang. Prot.** (toolbar), then select **Capture**. The Hanging Protocol Editor appears.
2. Change the protocol name and any other customizable information. Customizable areas are underlined and are also highlighted when you hover over them. For details, see "Set up hanging protocols" on page 206.
3. Select **Save**.



## Edit a hanging protocol

You can edit the hanging protocol currently applied to the image viewing area. (You must have the appropriate user privileges to edit hanging protocols.)

1. Select **Hang. Prot.** (toolbar), then select **Edit**. The Hanging Protocol Editor appears.
2. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it. For details, see "Set up hanging protocols" on page 206.
3. Select **Save**.

## Add a stage to a hanging protocol

While viewing a hanging protocol, you can add more stages. You can create a stage based on the current image viewing area or add a blank stage.

1. If desired, customize the image viewing area to use the settings you want for the new stage. For example, select a study layout and view, select the series to be viewed, and adjust the presentation state (window level, zoom, etc.). All of these settings will be automatically entered in the corresponding sections of the hanging protocol. Presentation state is not captured for clinical hanging protocols.
2. Select **Hang. Prot.** (toolbar), then select **Add Stage**. The Hanging Protocol Editor appears. A new stage is added, based on the current settings in the image viewing area.



### Note

You can also select <add stage> to add a blank stage you can customize.

3. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it. For details, see "Set up hanging protocols" on page 206.
4. Select **Save**.

## Use full screen view

You can view an image using the full screen. This hides the toolbar, side panel and other viewports. While in full screen, right-click (or touch and hold) the image to view a list of tools. You can also use keyboard shortcuts to select tools.

1. Select  on a viewport to display the image in full screen view.
2. Select  again to restore the original viewport layout.

## Maximize a viewport

Double-click (or double-tap) a viewport to maximize it and hide other viewports. The toolbar and side panel are still available while the viewport is maximized. This can be useful for mobile devices with smaller screens. Double-click (or double-tap) again to restore the original viewport layout.

## Use reference lines

Reference lines are shown on all series on the current screen that are in the same frame of reference. The intersection of the reference lines represents the corresponding position in all viewports.

## View image details

Details about the study, series and image are shown on an image. The details shown depend on the view mode and image modality. You can hide this information by turning off the image titles (for details, see "Titles" on page 36).

### 2D Images

Modality	Top-Left	Top-Right	Bottom-Left
CT	Patient Name Patient Details Series Description Date and Time Series Number Slice Location Key Image Flag	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width
MR	Patient Name Patient Details Series Description Date and Time (Philips) Scan and Slice Number (Philips) Scan Technique (Philips) MR Echo Repetition (Philips) Flip Angle (Philips) Delay Time (Philips) B Factor Diffusion Direction (Philips) Trigger Delay Time (Philips) Temporal Position Id Slice Location Key Image Flag	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Protocol Name and Receiving Coil Window Center Window Width
NM	Patient Name Patient Details Series Description Date and Time	Hospital Name Equipment Name Voltage And Amperage Slice Thickness	Window Center Window Width

Modality	Top-Left	Top-Right	Bottom-Left
	Series Number Slice Location Key Image Flag	Reconstruction Diameter	
OP	Patient Name Series Description Date and Time Instance Number Columns Rows	Hospital Name Equipment Name Image Laterality	Enhancement Gamma Window Width Window Center Image Compression Presentation
OPT	Patient Name Patient Details Series Description Date And Time Series Instance Number Slice Location Key Image Note	Hospital Name Equipment Name Image Laterality	Enhancement Gamma Window Width Window Center Presentation
PT	Patient Name Patient Details Series Description Date and Time Series Number Slice Location Key Image Flag	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width
Others	Patient Name Patient Details Series Description Date and Time Series Number Slice Location Key Image Flag	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width

## Slab Images

Modality	Top-Left	Top-Right	Bottom-Left
CT	Patient Name Patient Details	Hospital Name Equipment Name	Window Center Window Width

Modality	Top-Left	Top-Right	Bottom-Left
	Series Description Date and Time Series and Instance Number Slice Location	Voltage And Amperage Slice Thickness Reconstruction Diameter	Rendering Preset Name
MR	Patient Name Patient Details Series Description Date and Time Series and Instance Number Slice Location	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Protocol Name and Receiving Coil Window Center Window Width Rendering Preset Name
NM	Patient Name Patient Details Series Description Date and Time Series Number Slice Location	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width Rendering Preset Name
OPT	Patient Name Patient Details Series Description Date And Time Series Instance Number Slice Location Key Image Note	Hospital Name Equipment Name Image Laterality	Enhancement Gamma Window Width Window Center Presentation
PT	Patient Name Patient Details Series Description Date and Time Series Number Slice Location	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width Rendering Preset Name
Others	Patient Name Patient Details Series Description Date and Time Series Number Slice Location	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width

Modality	Top-Left	Top-Right	Bottom-Left
	Key Image Flag		





### 3D Images

Modality	Top-Left	Top-Right	Bottom-Left
CT	Patient Name Patient Details Series Description Date and Time Series and Instance Number Slice Location	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width Rendering Preset Name
MR	Patient Name Patient Details Series Description Date and Time Series and Instance Number Slice Location	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Protocol Name and Receiving Coil Window Center Window Width Rendering Preset Name
NM	Patient Name Patient Details Series Description Date and Time Series Number Slice Location	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width Rendering Preset Name
OPT	Patient Name Patient Details Series Description Date And Time Series Instance Number Slice Location Key Image Note	Hospital Name Equipment Name Image Laterality	Enhancement Gamma Window Width Window Center Presentation
PT	Patient Name Patient Details Series Description	Hospital Name Equipment Name Voltage And Amperage	Window Center Window Width Rendering Preset Name

Modality	Top-Left	Top-Right	Bottom-Left
	Date and Time Series Number Slice Location	Slice Thickness Reconstruction Diameter	
Others	Patient Name Patient Details Series Description Date and Time Series Number Slice Location Key Image Flag	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width

## View image orientation

Applies to MPR and volume viewports. Each viewport contains information regarding the image orientation. The figure in the bottom-right corner of an image represents the image orientation:

	<b>Axial</b> Figure standing on head (feet up)
	<b>Sagittal</b> Figure standing sideways
	<b>Coronal</b> Figure facing forward
	Select the arrow above the orientation figure to change the cardinal orientation or flip the image 180 degrees.

The orientation is also indicated by the letters to the right of and below the image:

F foot

H head

P posterior

A anterior

L left

R right

## View DICOM attributes

You can view the DICOM attributes for an image.

1. Right-click (or touch and hold) a viewport, then select **View DICOM attributes**.
2. Select one of the following options:
  - **View DICOM Attributes** View the DICOM attributes on a new browser tab.
  - **View Presentation Attributes** View the presentation attributes on a new browser tab.
  - **View DICOM Attributes Popup** View the DICOM attributes in a popup window.
3. The DICOM attributes appear.
4. Use your browser to search, print or save the attribute list.

## View study information

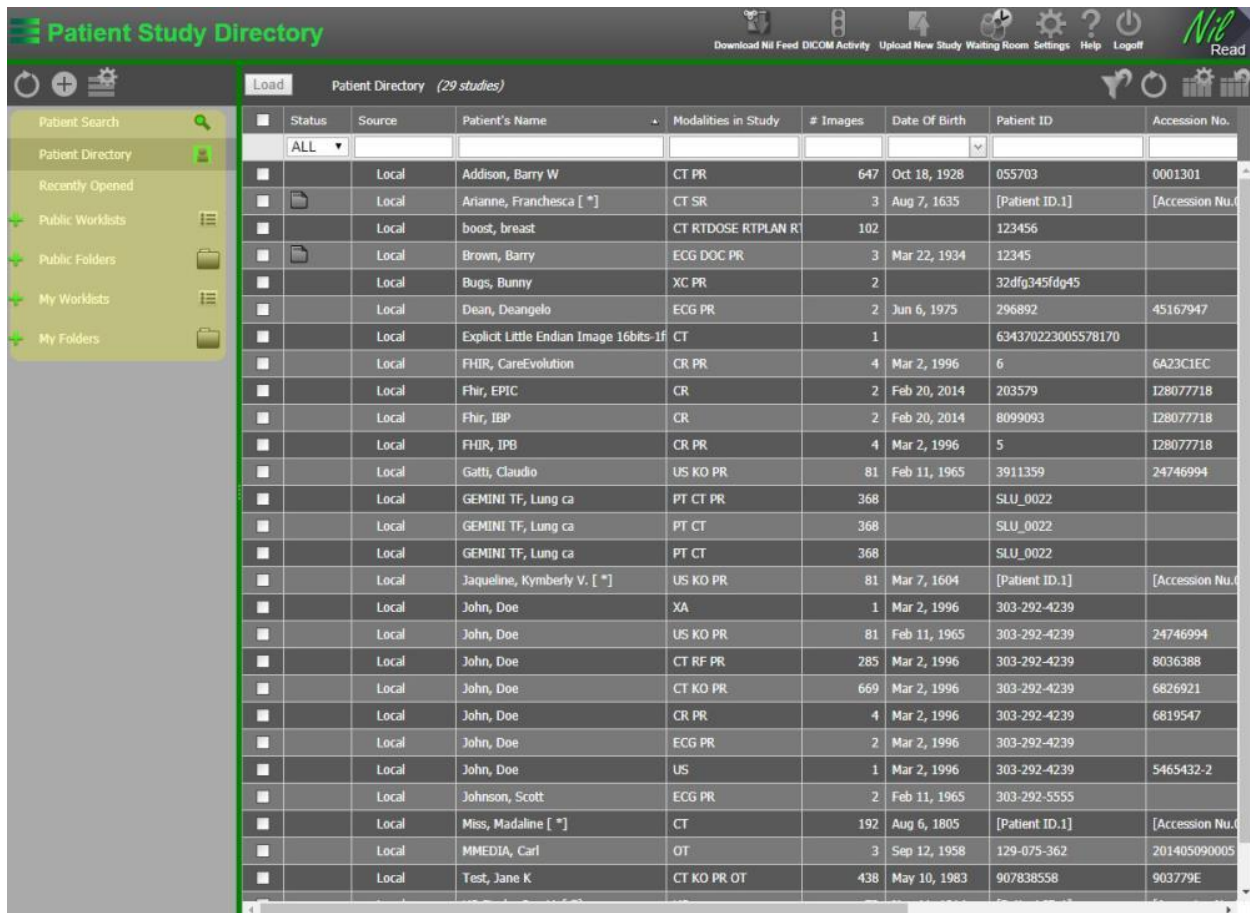
While viewing an image, you can view details about the study.

1. Right-click (or touch and hold) a viewport, then select **View study info**. The study information appears in a new window.
2. Select **OK** to close the window.

## 4. Manage studies


### Access studies

When you first start NilRead, the Patient Study Directory opens. The navigation tree on the left side of the directory opens at the item you used most recently (for example, the Patient Directory or a worklist).



Status	Source	Patient's Name	Modalities in Study	# Images	Date Of Birth	Patient ID	Accession No.
ALL							
■	Local	Addison, Barry W	CT PR	647	Oct 18, 1928	055703	0001301
■	Local	Arianne, Francesca [ * ]	CT SR	3	Aug 7, 1635	[Patient ID.1]	[Accession Nu.0
■	Local	boost, breast	CT RTDOSE RTPLAN R	102		123456	
■	Local	Brown, Barry	ECG DOC PR	3	Mar 22, 1934	12345	
■	Local	Bugs, Bunny	XC PR	2		32dfg345fdg45	
■	Local	Dean, Deangelo	ECG PR	2	Jun 6, 1975	296892	45167947
■	Local	Explicit Little Endian Image 16bits-1f	CT	1		634370223005578170	
■	Local	FHIR, CareEvolution	CR PR	4	Mar 2, 1996	6	6A23C1EC
■	Local	Fhir, EPIC	CR	2	Feb 20, 2014	203579	I28077718
■	Local	Fhir, IBP	CR	2	Feb 20, 2014	8099093	I28077718
■	Local	FHIR, IPB	CR PR	4	Mar 2, 1996	5	I28077718
■	Local	Gatti, Claudio	US KO PR	81	Feb 11, 1965	3911359	24746994
■	Local	GEMINI TF, Lung ca	PT CT PR	368		SLU_0022	
■	Local	GEMINI TF, Lung ca	PT CT	368		SLU_0022	
■	Local	GEMINI TF, Lung ca	PT CT	368		SLU_0022	
■	Local	Jaqueline, Kymberly V. [ * ]	US KO PR	81	Mar 7, 1604	[Patient ID.1]	[Accession Nu.0
■	Local	John, Doe	XA	1	Mar 2, 1996	303-292-4239	
■	Local	John, Doe	US KO PR	81	Feb 11, 1965	303-292-4239	24746994
■	Local	John, Doe	CT RF PR	285	Mar 2, 1996	303-292-4239	8036388
■	Local	John, Doe	CT KO PR	669	Mar 2, 1996	303-292-4239	6826921
■	Local	John, Doe	CR PR	4	Mar 2, 1996	303-292-4239	6819547
■	Local	John, Doe	ECG PR	2	Mar 2, 1996	303-292-4239	
■	Local	John, Doe	US	1	Mar 2, 1996	303-292-4239	5465432-2
■	Local	Johnson, Scott	ECG PR	2	Feb 11, 1965	303-292-5555	
■	Local	Miss, Madaline [ * ]	CT	192	Aug 6, 1805	[Patient ID.1]	[Accession Nu.0
■	Local	MEDIA, Carl	OT	3	Sep 12, 1958	129-075-362	201405090005
■	Local	Test, Jane K	CT KO PR OT	438	May 10, 1983	907838558	903779E

#### Note

To hide the navigation tree, select  in the top-left corner.

The Patient Study Directory contains several options for finding a study.



- **Patient Search** Search for a study on all local and remote repositories. For details, see “Use Patient Search” on page 74.

**Note**

Studies on restricted sites can only be opened through Patient Search. Users must have the appropriate privileges to access restricted sites.

- **Patient Directory** Lists all studies in the local repository. For details, see “Open a study” on page 10.
- **Recently Opened** Lists the studies you have opened most recently. A maximum of 50 studies are listed for each repository you have used.
- **Worklists and Folders** Create a collection of studies that you want to view as a group. For details, see “Use a worklist or folder” on page 75.

**Note**

The studies you can view depend on your privileges in NilRead. You may be given access to specific studies or you may be able to view the full directory.

## Use Patient Search

1. In the Patient Study Directory, select **Patient Search**.
2. In the **Patient Search** area at the top of the screen, enter information about the study. Select **More** to view additional fields.
  - **Accession No.** Study accession number.
  - **Data Sources** DICOM and XDS servers you want to search. You can select multiple servers.
  - **Time Range** Time period during which the study was created.
  - **Patient ID** Patient’s ID.
  - **Patient Name** Patient’s name.
  - **Date of Birth** Patient’s date of birth.
  - **Sex** Patient’s gender.
  - **Modality** Modality in the study.


3. Select **Query**. Studies matching your search criteria are shown.

**Note**




Studies are loaded on demand as you scroll down the page. On mobile devices, you can also swipe to move through the pages.

4. To open a study, click (or tap) anywhere on the directory entry for the study.

To find a study in the search results:

1. Enter information about the study in the blank row below the column headings (patient name, patient ID and so on).
2. To find a study based on status, select one of the following options in the **Status** column:
  - **All** Show all studies.
  - **Available** Show studies containing at least one report.
  - **Not Available** Show studies with no reports.
  - **Approved** Show studies containing at least one approved report.
  - **Locked** Show locked studies.
3. To view all studies again, select **Clear** .

To customize the columns:

- Select **Customize**  in the top-right corner. To add a column, drag a column from the **Customize** list to the location where you want to place it. To remove a column, drag it to the **Customize** list.
- Click (or tap) a column heading to sort the studies. Click (or tap) the column heading again to sort the studies in the reverse order.
- To rearrange the columns, drag a column heading to a new location.
- Select **Reset**  to reset the columns to the default sort order, remove any custom columns and reload all studies.
- Select **Refresh**  to refresh the studies list and view the latest changes made by all users.

## Use a worklist or folder

You can use worklists and folders to create a collection of studies that you want to view as a group.

- The studies in a **worklist** are selected based on the data source and conditions you set. For example, you could create a worklist that includes all studies with a specific modality that originate from a specific data source.
- You select the specific studies you want to include in a **folder**. For example, you can use a folder to group studies that you want to review in a collaboration session with other users.


### Note

For information on creating worklists and folders, see “Manage your preferences” on page 155.

In the Patient Study Directory:

1. Select **+** beside **Public Worklists, Public Folders, My Worklists** or **My Folders** to expand the category and view the available worklists or folders. Select **-** to collapse the category.

**Note**

Select  to refresh the navigation tree and see any new worklists and folders.

2. Select a worklist or folder. The studies in the worklist or folder are shown on the right.
3. Select a study to open it.

## Open multiple studies

You can open multiple studies at once. This allows you to review multiple studies in a single session without having to return to the Patient Study Directory.

1. Use any of the options in the navigation tree to find a study (Patient Search, Patient Directory, Recently Opened, Worklists and Folders). For details, see "Access studies" on page 73.
2. Select the checkbox beside the studies you want to open. You can also select studies from a folder or worklist. To select all studies in a folder or worklist, select the checkbox in the top row.
3. Right-click (or touch and hold) one of the studies and select **Load Studies**. Select one of the following options:
  - **Load as batch** Load the studies separately (as separate patients). You can also select the **Load** button to load studies separately.
  - **Load as priors** Treat the studies as a collection of studies from a single patient. The most recent study will open in the image viewer and older studies will appear as prior studies in the patient timeline.
4. The studies open in the image viewer. If you selected **Load as batch** (or the **Load** button), the number of loaded studies is shown at the top of the image viewer (for example, **1 of 5**).
  - Use the arrows beside the number of loaded studies to navigate through the studies.
  - Click (or tap) the number of loaded studies to select a study.
  - Click (or tap) the patient name to view patient details.

## Use "Break Glass" to find studies

If you are a NilRead guest user, you may be able to use emergency override ("break glass") to find a patient study. Emergency override should only be used to search for studies that you should be authorized to view but are not appearing in the Patient Study Directory.


1. In the Patient Study Directory, select **Break Glass**.

2. Read the privacy rule requirements, then select **I agree** if you agree to comply with the requirements. The Emergency Override page appears.
3. To find a patient study, enter information in the search fields at the top of the page:
  - **Family Name** Patient's last name.
  - **Given Name** Patient's first name.
  - **Soundex** Select this option to also search for names that sound like the **Family Name/Given Name** you have entered.
  - **Accession Number** Study accession number.
4. Select **Find**.

## Lock studies

NilRead automatically deletes older studies from the database when disk space is low. You can lock studies to ensure they are never deleted.

### Note

 appears beside locked studies. The total number of locked studies is shown in the top-right corner of the Patient Study Directory.

In the Patient Study Directory:

1. To lock or unlock a study, right-click (or touch and hold) a study, then select **Lock** or **Unlock**.
2. To lock or unlock multiple studies, select the checkbox beside each study, then right-click (or touch and hold) one of the studies and select **Lock** or **Unlock**.

## Upload studies

NilRead provides multiple ways to upload studies to the database.

### Note

Ensure popups are enabled in your browser settings before uploading studies. Google Chrome supports all of the following upload options; other browsers may not support all options.

### Upload DIOCM files from media

Upload DICOM files from removable media such as a CD, DVD or USB flash drive. The media must contain a DICOMDIR file. The files may be from multiple patients and studies.

1. Select **Upload New Study**.
2. Select **Upload DICOM Media**.

3. Select the folder containing the DICOM files and the DICOMDIR file. Be sure to select the entire folder; NilRead will ignore files that should not be uploaded.
4. Select **Next**. A list of studies to be uploaded is shown.
5. Select **Upload**. A confirmation message appears when the upload is complete.

### Upload zipped DICOM files

Upload a .zip file containing DICOM files. The .zip file must contain DICOM files only. The files may be from multiple patients and studies.

1. Select **Upload New Study**.
2. Select **Upload Zip with DICOM files**.
3. Select the .zip file.
4. Select **Upload**. A confirmation message appears when the upload is complete.

### Upload a folder containing DICOM files

Upload a folder containing DICOM files. The folder must contain DICOM files only. The files may be from multiple patients and studies.

1. Select **Upload New Study**.
2. Select **Upload Folder with DICOM files**.
3. Select the folder containing the DICOM files.
4. Select **Next**. A list of studies to be uploaded is shown.
5. Select **Upload**. A confirmation message appears when the upload is complete.

### Upload individual DICOM files

Upload individual DICOM files. The files must be uploaded from the same location (for example, the same folder) and may be from multiple patients and studies.

1. Select **Upload New Study**.
2. Select **Upload DICOM files**.
3. Select the DICOM files.
4. Select **Next**. A list of studies to be uploaded is shown.
5. Select **Upload**. A confirmation message appears when the upload is complete.

### Upload non-DICOM files

Upload non-DICOM files. The files must be for the same patient and study.

1. Select **Upload New Study**.

2. Select **Upload non-DICOM files**.
3. Select the non-DICOM files.
4. Select **Next**. Enter the study details.
5. Select **Upload**. A confirmation message appears when the upload is complete.

## Create an upload link

Create an encrypted link that other people can use to upload files. The link can be used to upload a .zip file containing DICOM files or to upload individual DICOM and non-DICOM files.

1. Select **Upload New Study**.
2. Select **Create Upload Link**.
3. Determine how long the link will be active. You must select at least one of the following options:
  - **Limit number of upload sessions to X** Number of times the link can be used before it expires.
  - **Link will expire in X days** Number of days until the link expires.
4. Determine if the user must login to NilRead to use the upload link. You must select only one of the following options:
  - **User must login to upload** If selected, the user must login to their NilRead account before using the link. If not selected, the user does not require an account with NilRead to use the link.
  - **User required to enter this password** If you did not select the **User must login to upload** option, enter the password the user must enter to use the link. The password must contain at least eight characters.
5. Determine if the user can upload DICOM files only.
  - **Allow uploading non-DICOM files** If selected, the user can upload DICOM and non-DICOM files. If not selected, the user can only upload DICOM files.
6. Select **Next**.
7. The upload link is shown. Select one of the following options:
  - **Copy link to clipboard** Copy the link. You can now paste the link into an email or instant message.
  - **Click to send link by email** Create an email with the link, using your default email application.
8. When done, click **Close**.

## Attach files to studies or patients

You can attach files to a study or patient. If you attach files to a study, they are saved as a new series. If you attach files to a patient, they are saved as a new study. You can attach files using the Patient Study Directory or when viewing a study.

### Note

Ensure popups are enabled in your browser settings.

1. In the Patient Study Directory, right-click (or touch and hold) a study, then select **Attach files to this study** or **Attach files to this patient**.  
or  
While viewing a study, right-click (or touch and hold) a series (side panel), then select **Upload**. Select **Attach files to this study** or **Attach files to this patient**.
2. Select **Choose Files** and select the files to attach. You can select multiple files if they are located in the same folder.
3. Select the type of files you are attaching (**DICOM** or **Image/Video**).
4. If attaching an image or video file, enter the patient and study information.
5. Select **Upload**.

## Edit or split studies

You can edit information for a study such as the patient name or referring physician. You can apply your changes to all series or to selected series, and you can choose to save the changes in the original study or create a copy of the study.

You can split a study by modifying specific series and moving the modified series to a new study. You can leave the unmodified series in the original study or delete them.

In the Patient Study Directory:

1. Right-click (or touch and hold) a study, then select **Edit Patient/Study**.
2. Make changes to the patient and study information. If you want to retrieve information about the patient from a modality worklist, select **Reconcile**. Enter information about the patient and select **Search**. If a match is found, select the patient and select **Select**.
3. To apply the changes to specific series in the study, select **>**. A list of series appears on the right. Select the series you want to apply the changes to. Note that this option is only available if the **Copy to new study** option is selected.
4. To save your changes in a new study, select **Copy to new study**. To make changes to the original study, do not select this option.

### Note

If you are modifying only some of the series in the study, the modified series will be moved to a

new study. The unmodified series will remain in the original study (unless you choose the **Delete original instances** option).

5. To apply your changes to all studies for this patient, select **Apply changes to all studies for the same patient**.
6. If you are saving your changes in a new study and want to delete the original study, select **Delete original instances**.
7. Select **Save**.

## Download studies, series or images

You can download a copy of a patient study, series, or image.

In the Patient Study Directory:

1. Right-click (or touch and hold) a study, then select **Download Study**.
2. To download non-DICOM files in their original format, select **Download encapsulated documents in the original file format**.
3. To anonymize the study, select **Deidentify**, then select a confidentiality profile. For more information, see "About anonymization" on page 145.
4. Select **Download**.

While viewing a study:

1. Right-click (or touch and hold) an image, then select **Download**.
2. Select **Download Study**, **Download Series** or **Download Image**.
3. To download non-DICOM files in their original format, select **Download encapsulated documents in the original file format**.
4. To anonymize the study, series or image, select **Deidentify**, then select a confidentiality profile. For more information, see "About anonymization" on page 145.
5. Select **Download**.

## Merge patients

You can update patient information in one study to match patient information in another study. You can also update information in all studies for the same patient. This ensures consistent patient information exists across all studies.

In the Patient Study Directory:

1. Select the checkbox beside the study that contains the patient information you want to copy into another study.
2. Select the checkbox beside the study you want to copy the patient information into.



3. Right-click (or touch and hold) one of the studies, then select **Merge Patients**. Information for the selected patients is shown.
4. To update patient information in all studies with the same patient ID, select **Apply changes to all studies for the same patient**.
5. To use the patient information from the study shown on the left, select **Merge to left**. The study on the right will be updated to match the study on the left.
6. To use the patient information from the study shown on the right, select **Merge to right**. The study on the left will be updated to match the study on the right.
7. Select **Continue**. The patient information in the study is updated. If you selected **Apply changes to all studies for the same patient**, the patient information is also updated in all studies with the same patient ID.

## Merge studies

You can combine two studies into a single study. When you merge studies, one of the studies is deleted.

In the Patient Study Directory:

1. Select the checkbox beside the two studies you want to merge.
2. Right-click (or touch and hold) one of the studies, then select **Merge Studies**. Information for the selected studies is shown.
3. To merge the studies into the study shown on the left, select **Merge to left**.
4. To merge the studies into the study shown on the right, select **Merge to right**.
5. Select **Continue**. The studies are merged into the study you selected. The other study is deleted.

## Delete studies, series or images

You can permanently delete a patient study, a series or an image.

To delete a study:

- In the Patient Study Directory, right-click (or touch and hold) a study, then select **Delete**.

To delete a series or image:

1. Open a patient study.
2. Right-click (or touch and hold) a series (side panel), then select **Delete Series**.
3. Right-click (or touch and hold) an image, then select **Delete Image**.

## Delete series containing segmentation results

You can delete series that contain part segmentation results. Part segmentation results are typically created through a data lifecycle activity (see "Manage data lifecycle policies" on page 210).

In the Patient Study Directory:

1. Right-click (or touch and hold) a study, then select **Delete Pre-processed Results**.
2. Select **OK**.

## Export images

You can export a screenshot of the patient study currently loaded in the image viewing area. The screenshot can include one or all viewports and is saved as an image (JPG).

1. (Optional) If you want to export a screenshot of a single viewport, click (or tap) the viewport to select it.
2. Select **Save**, then select **Export** (toolbar).
3. Select the following options for the screenshot:
  - **Save: Viewport/Display** Create a screenshot of the selected viewport (**Viewport**) or all viewports (**Display**).
  - **Titles: Show/Hide** Include (**Show**) or exclude (**Hide**) the information shown on the image (patient name, series number, and so on).
4. Enter a filename in the **Save as** field in the bottom-left of the screen.
5. Select **Download**.
6. When done, select **Close**.

## Print images

You can print the patient study currently loaded in the image viewing area. You can print one or all viewports.

1. (Optional) If you want to print a single viewport, click (or tap) the viewport to select it.
  2. Select **Print** (toolbar).
  3. Select the following options for the screenshot:
    - **Save: Viewport/Display** Print the selected viewport (**Viewport**) or all viewports (**Display**).
    - **Titles: Show/Hide** Include (**Show**) or exclude (**Hide**) the information shown on the image (patient name, series number, and so on).
  4. Select **Print**.
- or

To use a DICOM printer, select **DICOM Print**. Select a printer and the page layout options, then select **OK**.

**Note**

You must first configure a DICOM printer to use with NilRead (see "Manage DICOM services" on page 203).

5. When done, select **Close**.

## View reports

If one or more reports exist for a patient study, a folder icon is shown in the study's Status column in the Patient Study Directory. Reports can be DICOM structured reports or can be provided through DICOM Detached Interpretation. NilRead also supports custom HL7 integration for obtaining reports from a RIS/HIS system.

**Note**

You can also access DICOM embedded PDF reports through the patient timeline when viewing a patient study (see "Use the patient timeline" on page 15).

1. (Optional) In the blank row at the top of the Patient Study Directory, select an option in the **Status** column.
  - **All** Show all patient studies.
  - **Available** Show patient studies containing at least one report.
  - **Approved** Show patient studies containing at least one approved report.
  - **Not Available** Show patient studies with no reports.
2. To view the reports for a study, select the folder icon beside the patient name. The reports in the study appear below the directory. If the study contains multiple reports, use the **Previous** and **Next** arrows in the report area to scroll through the reports.
3. The following options are available when viewing reports:
  - **Delete** Delete the report.
  - **Save** Save a PDF copy of the report.
  - **Print Report** Print the report from your browser.
  - **Vert/Horiz** Place the report area on the right side (**Vert**) or bottom (**Horiz**) of the screen.
  - **Maximize/Restore** View the report area only and hide the directory (**Maximize**) or view both the report area and the directory (**Restore**).
  - **Close** Close the report.

**Note**

To resize the directory and report areas, drag the divider between the two areas.

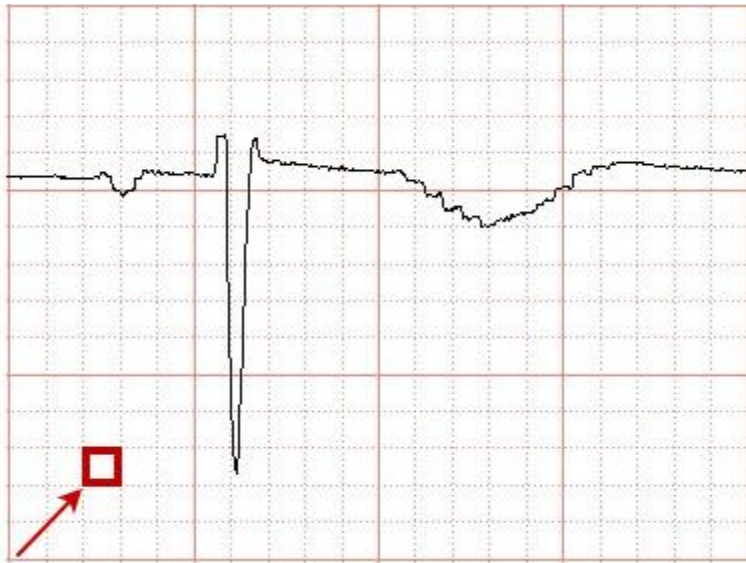
## 5. Review ECG studies

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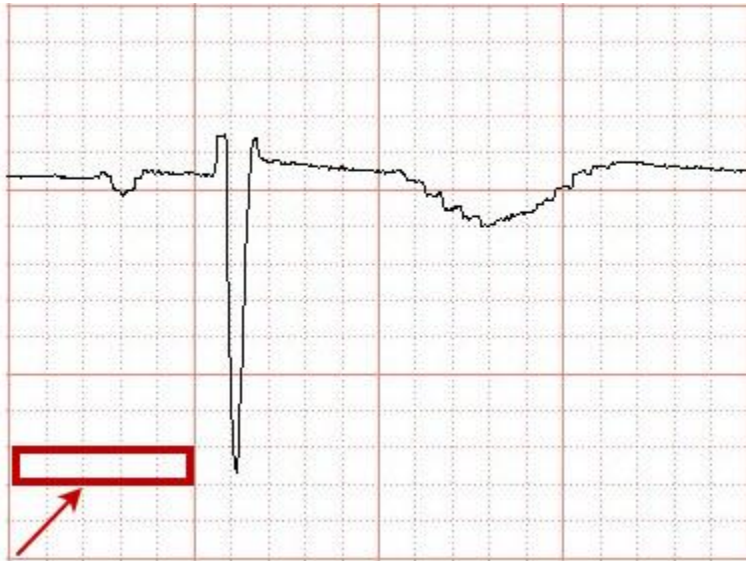
### About ECG paper

ECG graphs are presented on standard ECG paper. ECG paper speed is usually 25 mm/second.

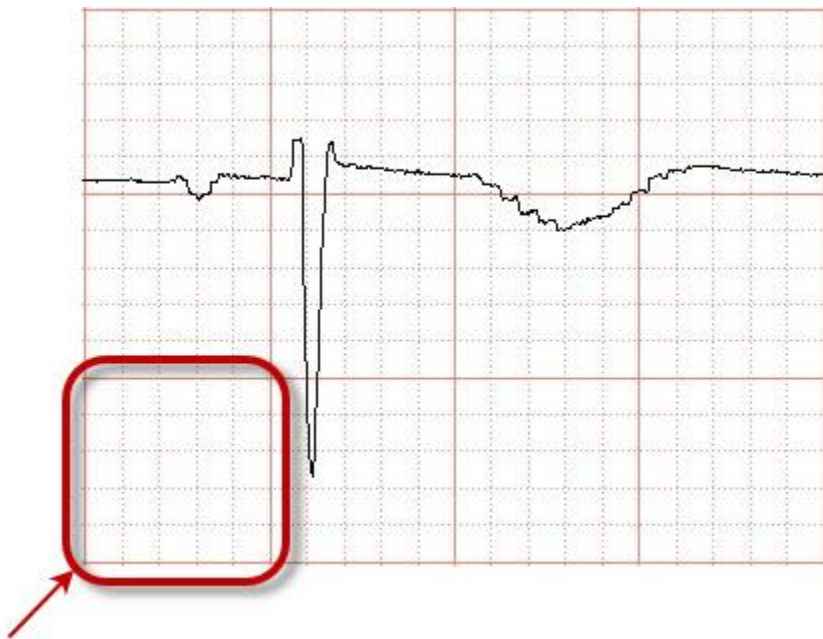
If you zoom in on a graph, you can see that the paper is divided into small boxes. Each box represents a 1 mm interval or 0.04 seconds (40 ms).



A group of 5 horizontal boxes, bordered by a thick line, represents a 5 mm interval or 0.2 seconds (200 ms).



A group of 25 boxes, bordered by a thick line, represents a 25 mm interval or 1 second.



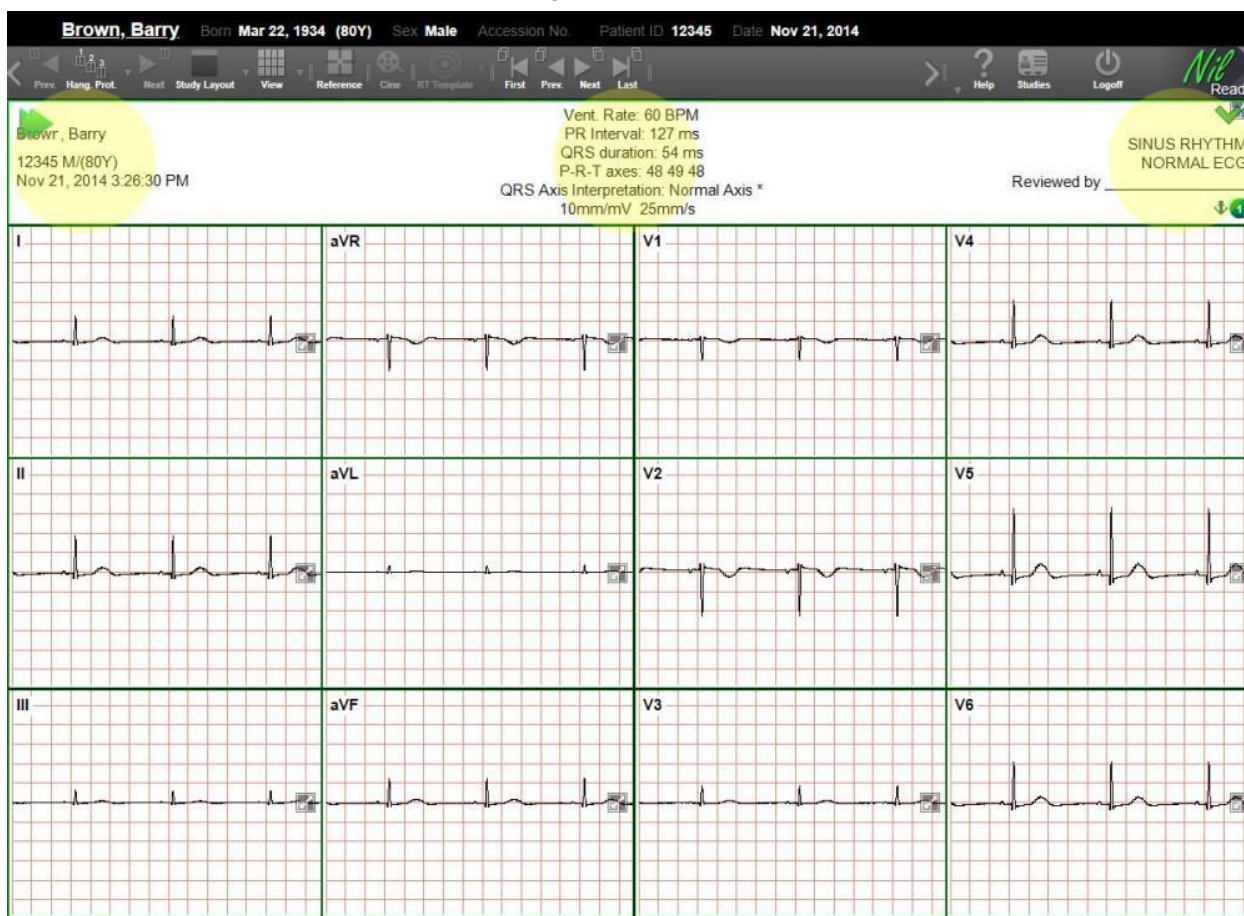
## Use ECG views



NilRead provides several views that can be used to review 12-lead electrocardiogram (ECG) images.

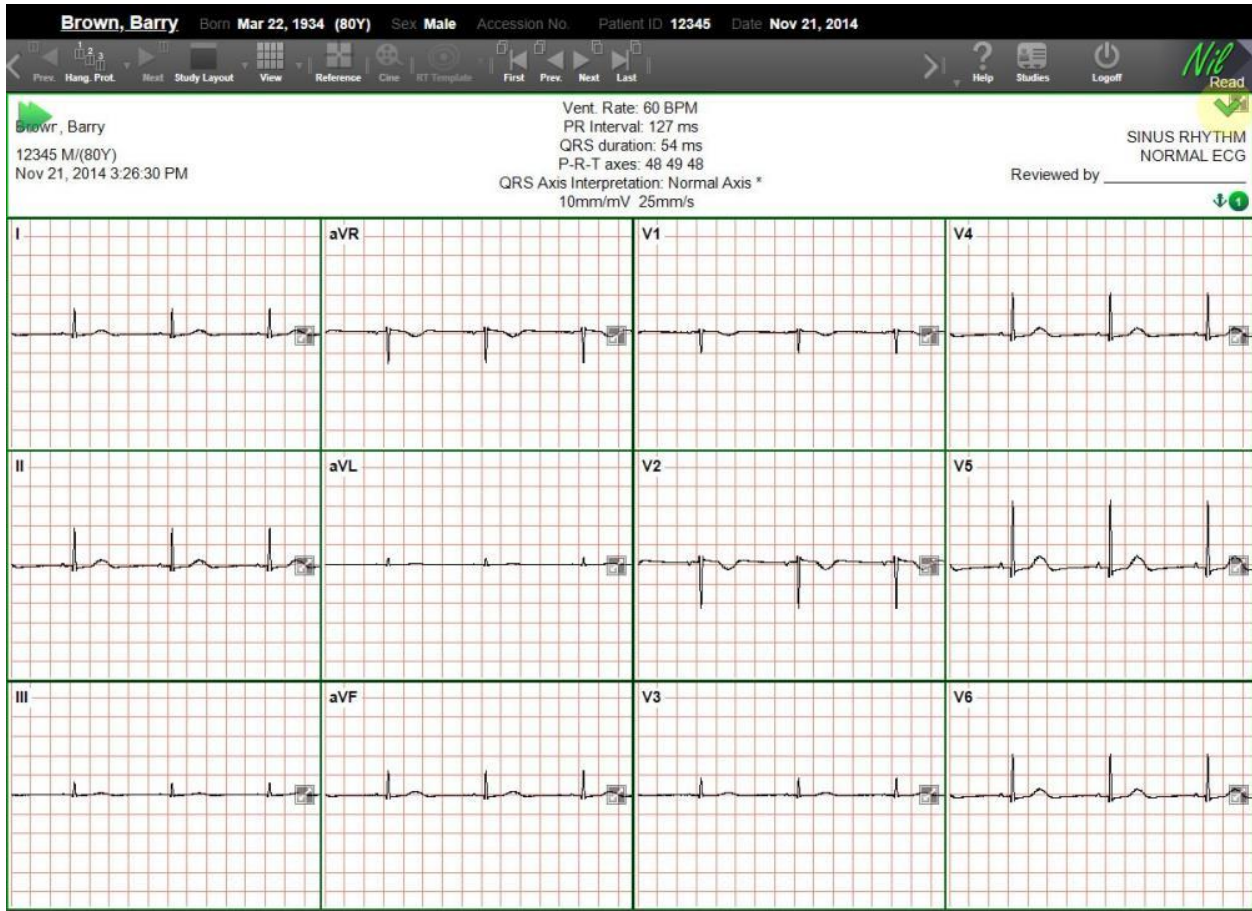
1. Open an ECG study.
2. (Optional) In the **View** menu, select the ECG leads you want to view.
3. In the **View** menu, select an **ECG View**. You can choose from standard views such as Rhythm and 3X4.

The following information is shown in the information bar above the image.

- Patient demographics (patient name, study date, etc.) are shown in the top-left corner.
- Metrics (ventricle rate, PR interval, etc.) are shown in the center. These metrics are taken from the study's DICOM attributes, with the exception of QRS Axis Interpretation, which is calculated by NilRead. For details, see "Understanding QRS Axis Interpretation" on page 90.
- Any comments are shown in the top-right corner.

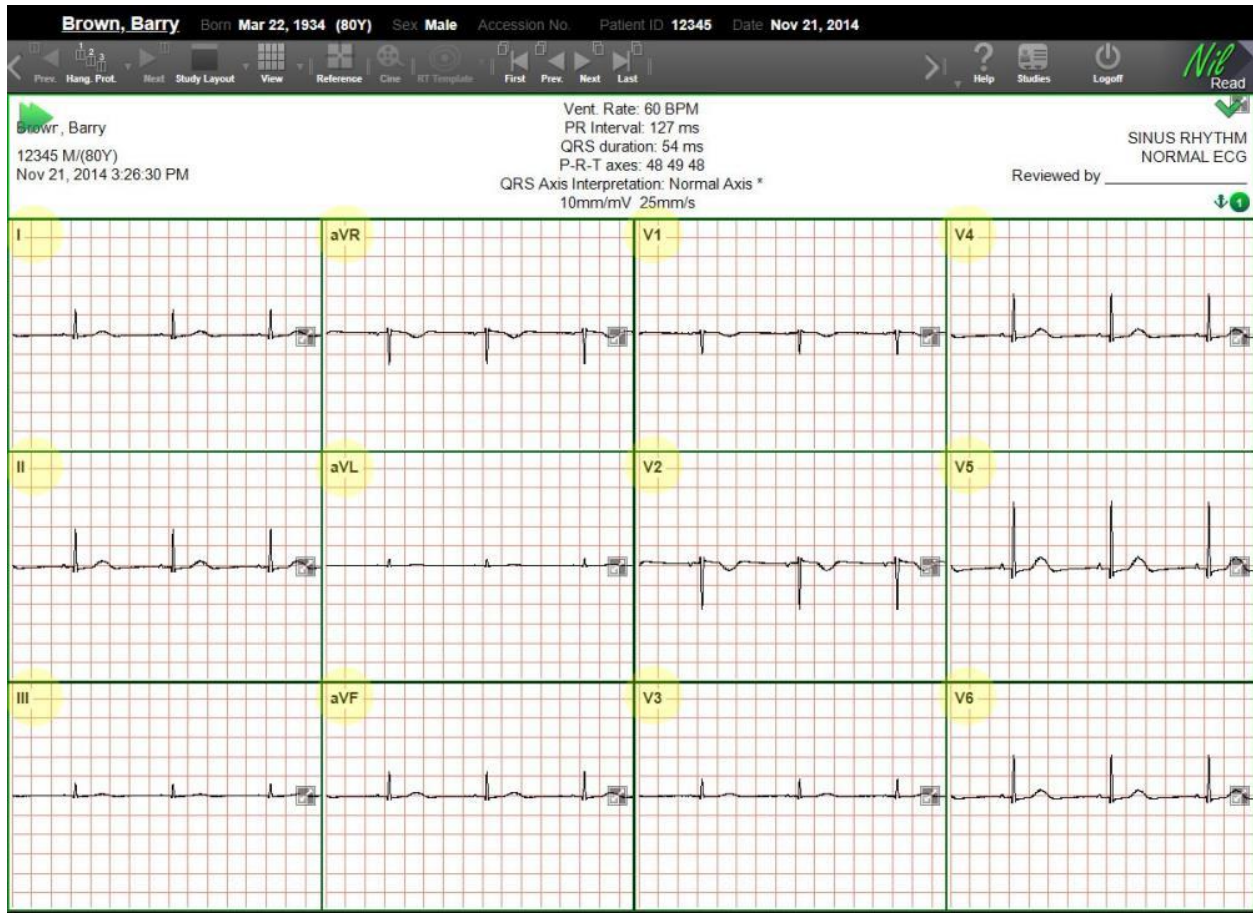


To expand the information bar, double-click the bar or click  in the top-right corner. To return the information bar to its original size, double-click the bar again or click .





The lead name is shown in the top-left corner of each graph.



### Understanding QRS Axis Interpretation

The QRS axis interpretation is calculated using the "Three Lead Analysis (Lead I, Lead II and aVF)" method of ECG axis interpretation. Using this method, the QRS axis is determined to be normal, LAD Physiological, LAD Pathological, RAD, Extreme Axis, or Indeterminate.

The following table summarizes how the QRS axis is calculated.

	Normal Axis 0 to +90°	LAD Physiological 0 to -30°	LAD Pathological -30° to -90°	RAD 90° to 180°	Extreme Axis -90° to -180°	Indeterminate ?
LEAD I	POSITIVE	POSITIVE	POSITIVE	NEGATIVE	NEGATIVE	EQUIPHASIC

	Normal Axis 0 to +90°	LAD Physiological 0 to -30°	LAD Pathological -30° to -90°	RAD 90° to 180°	Extreme Axis -90° to -180°	Indeterminate ?
<b>LEAD II</b>	POSITIVE	EQUIPHASIC	NEGATIVE	POSITIVE	NEGATIVE	EQUIPHASIC
<b>LEAD III or aVF</b>	POSITIVE	NEGATIVE	NEGATIVE	POSITIVE	NEGATIVE	EQUIPHASIC

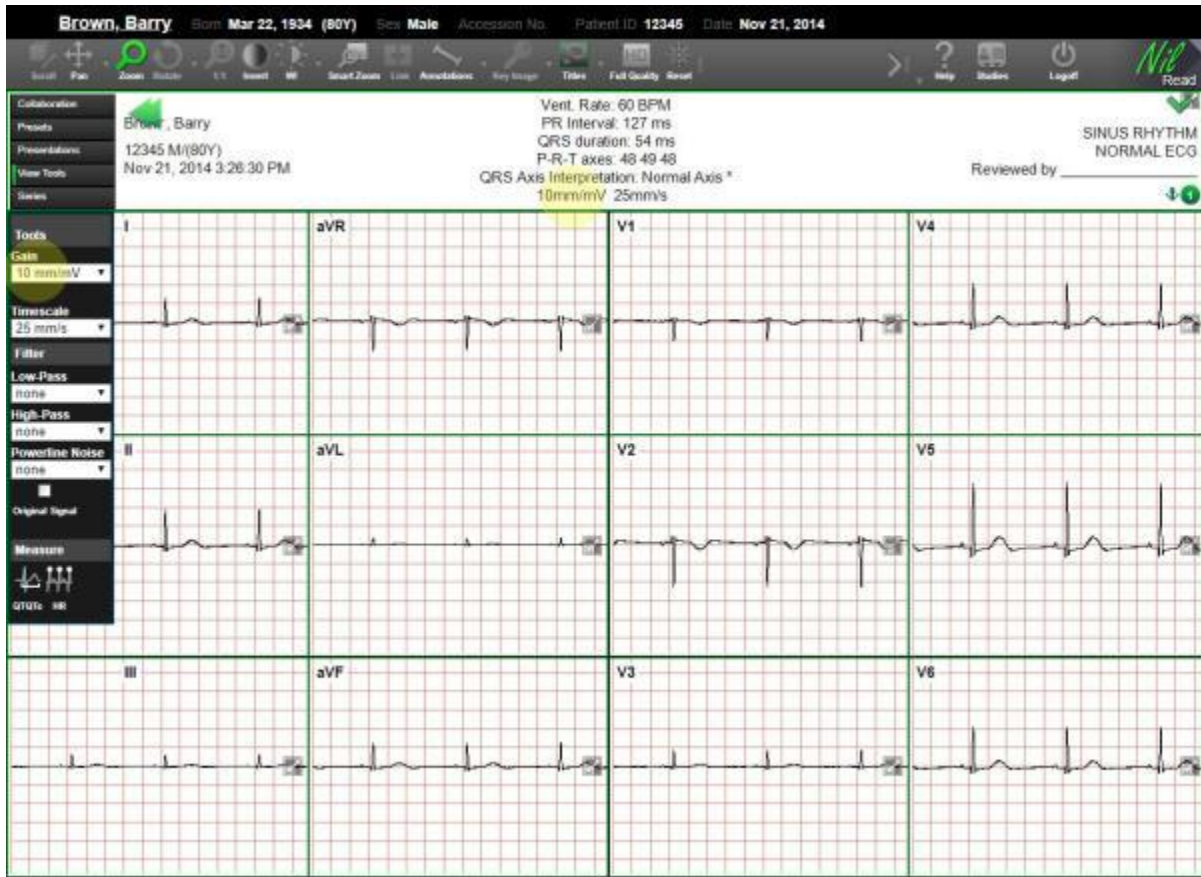
## Use the ECG view tools

NilRead provides several tools that can be used to adjust the visualization of ECG images. To access these tools, select **View Tools** (side panel).

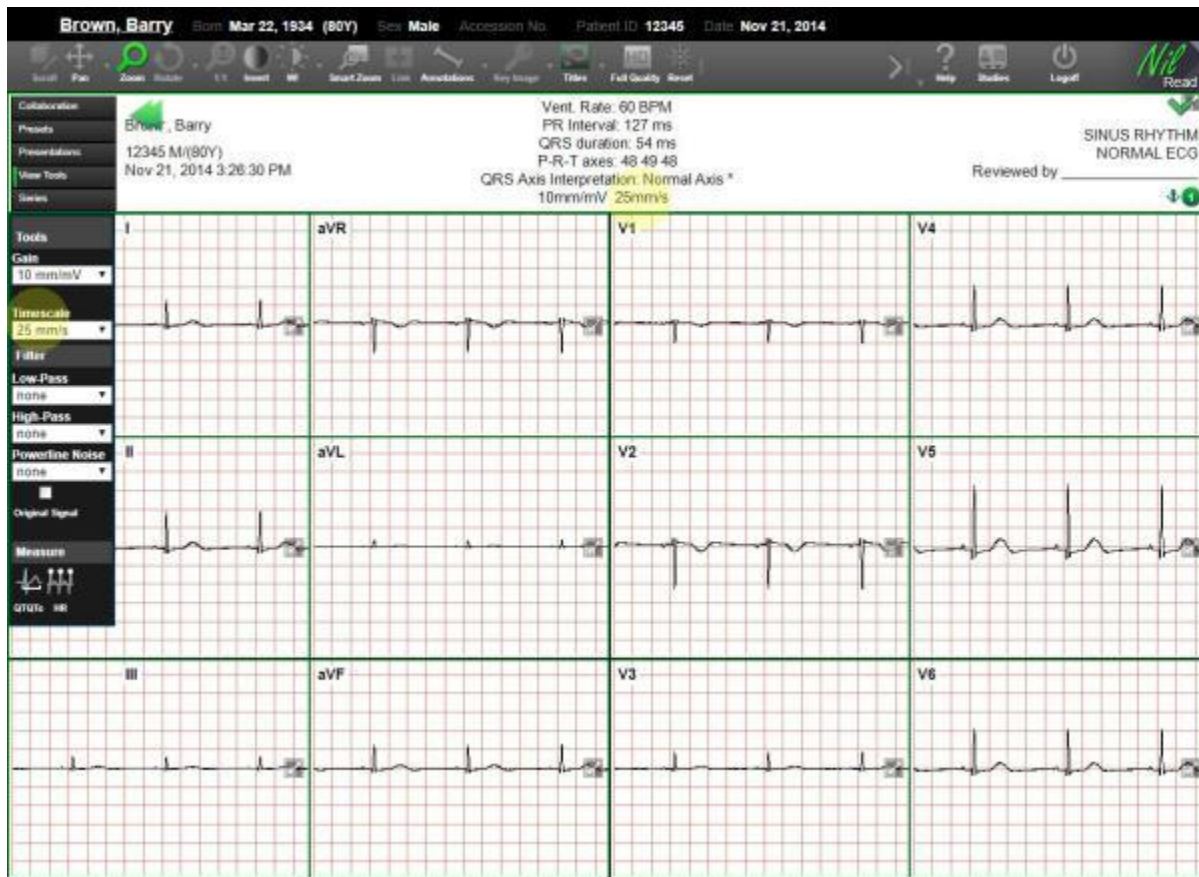
### Gain and Timescale

You can adjust the gain and timescale for the graph to better define the waveforms.

Use Gain to change the height (amplitude) shown on the vertical axis. The current Gain value is shown in the center of the information bar. (Standard calibration for an ECG is 10mm/mV.)



Use Timescale to adjust the timescale shown on the horizontal axis. The current Timescale value is shown in the center of the information bar. (Standard timescale for an ECG is 25 mm/s.)

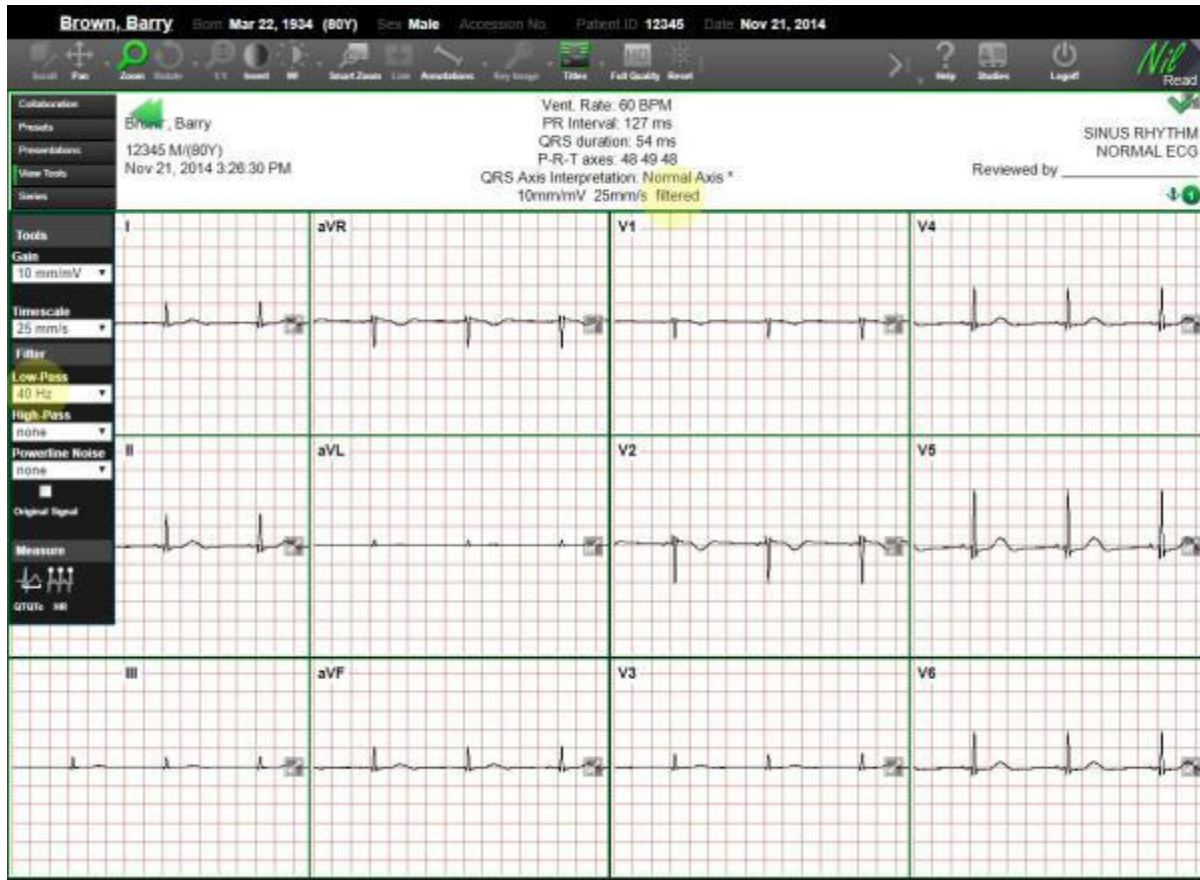


## Filter

Use Filter to remove unwanted artifacts and noise from the ECG recording. You can use the following filters:

- **Low-Pass** Remove high frequency interference.
- **High-Pass** Remove lower frequency interference.
- **Powerline Noise** Remove powerline interference. Powerline interference may result from factors such as electromagnetic interference by power lines or nearby machinery.
- **Original Signal** Show the original signal and the filtered signal at the same time.

If a filter is applied, this is stated in the center of the information bar.



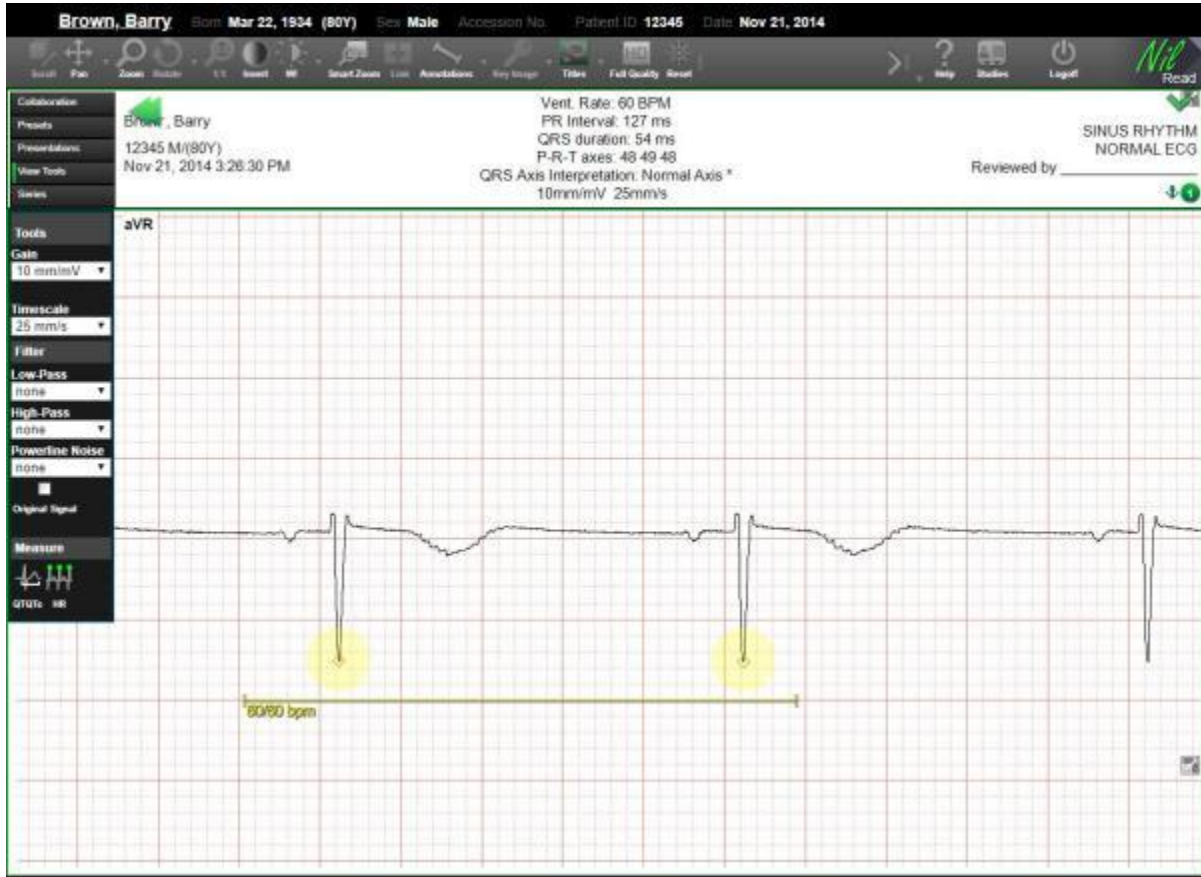
## HR

Use the HR tool to calculate the number of heart beats per minute (bpm) between two points on a graph.

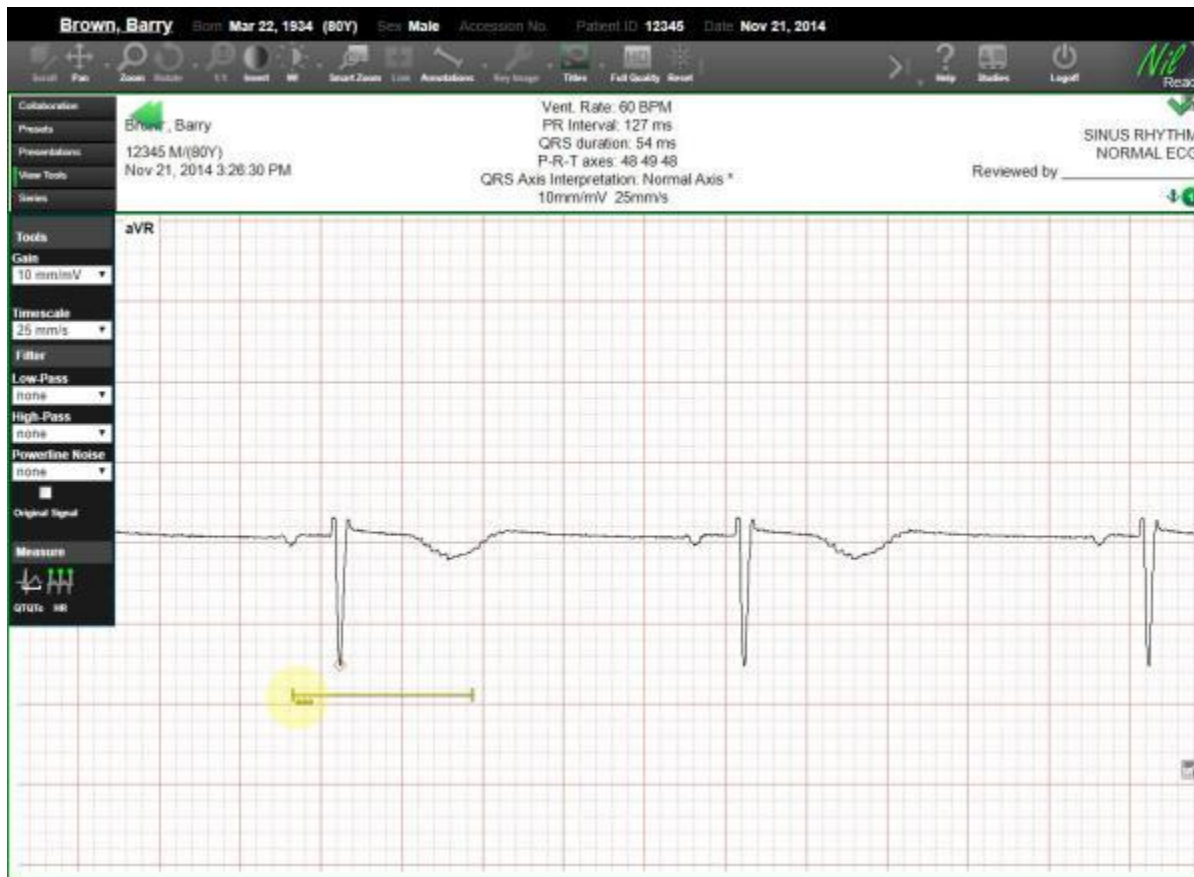
Click (or tap) and drag to create a line. After the line is drawn, the bpm is calculated and displayed. This calculation is based on the wave peaks included in the interval covered by the line. The peaks included in the calculation are circled.

The first number in the calculation represents the number of heart beats in the interval covered by the line. The second number represents the number of heart beats for the entire signal. A regular heartbeat

will have the same values for the interval time and total time (for example: 80/80). An irregular heartbeat will have different values.



At least two peaks are required to calculate the heart rate for an interval. If less than two peaks are included in the interval, \*\*\* will be shown, indicating that the heart rate could not be calculated.

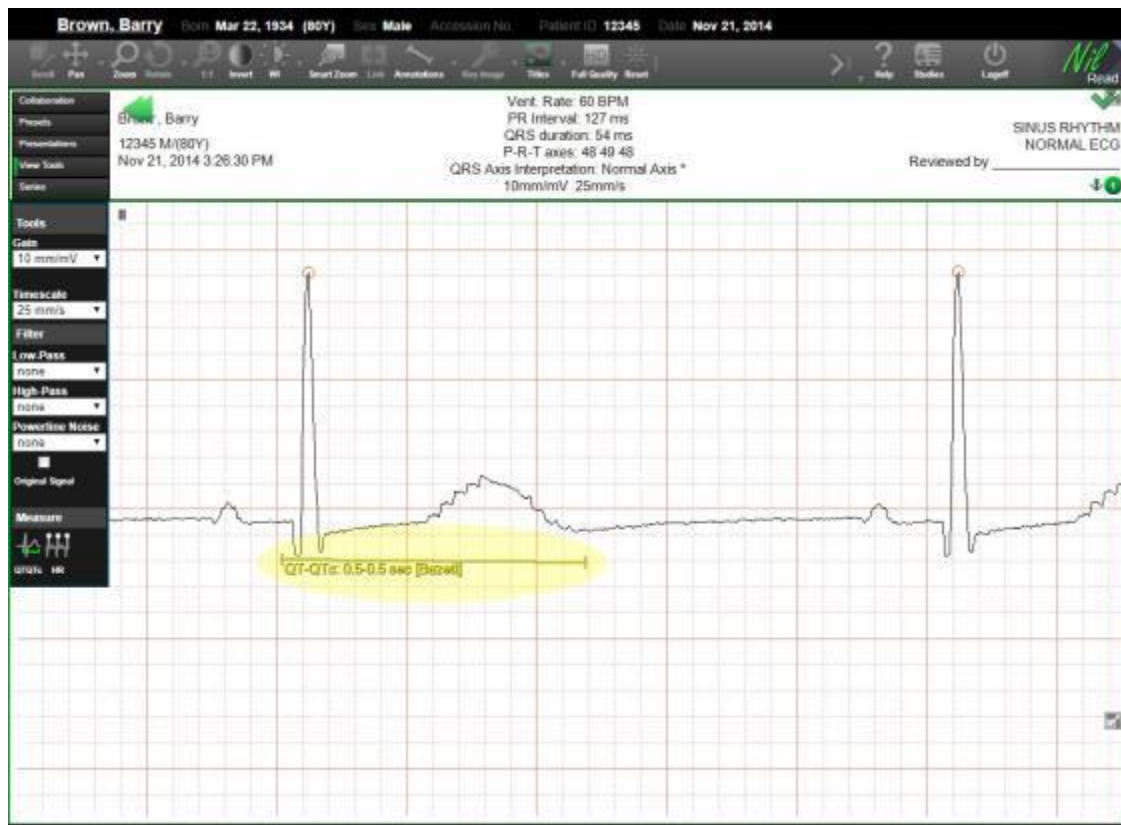


To delete a line, right-click the line, then select **Delete**.

## QTQTc

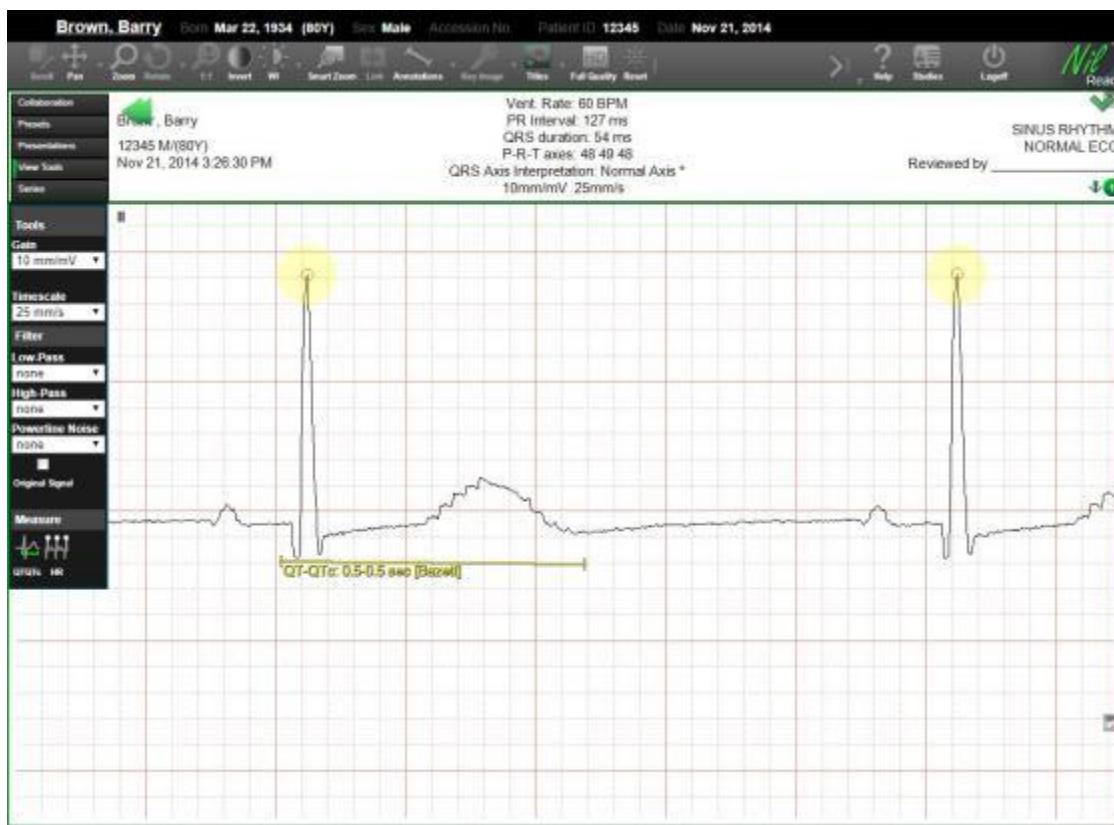
Use the QTQTc tool to measure the QT interval. NilRead also calculates the corrected QT interval (QTc). The QTc is calculated based on Bazett's formula.

1. Using lead II or V5-6, draw a line from the start of the Q wave to the end of the T wave. The QT and QTc are shown.



2. The two R peaks in the QT interval are circled. The first R peak is between the Q and P waves. The second R peak is used as a reference point.





If the line does not cover the required to calculate the QT interval, \*\*\* will be shown, indicating that the QT and QTc could not be calculated.

To delete a line, right-click the line, then select **Delete**.

## Annotation Tools

There are some differences in how measurements are shown when using regular annotation tools with ECG images.

### Linear and Area Measurements

For linear measurement tools (such as the ruler) and area measurement tools (such as the rectangle), horizontal measurements are shown in seconds and vertical measurements are shown in mV.

### Angle

The measurement for an angle shows the time and signal value between the two points.

## Change ECG preferences

You can change the zoom tool behaviour and the image viewer color scheme for ECG images.

#### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

1. Select **Settings**.
2. Under **Preferences**, select **Modality Preferences**.
3. Enter the following information, then select **Save**.

#### Modality

Select **ECG**.

#### Zoom Policy

Determines the zoom behavior.

- **Zoom at center** Zoom in or out from the center of the image.
- **Relative zoom at mouse position** Zoom in or out from the mouse position.

#### ECG Color Scheme

Select the color scheme to use when viewing ECG images (**Dark** or **Traditional**).

## 6. Review pathology studies

### About the pathology viewer

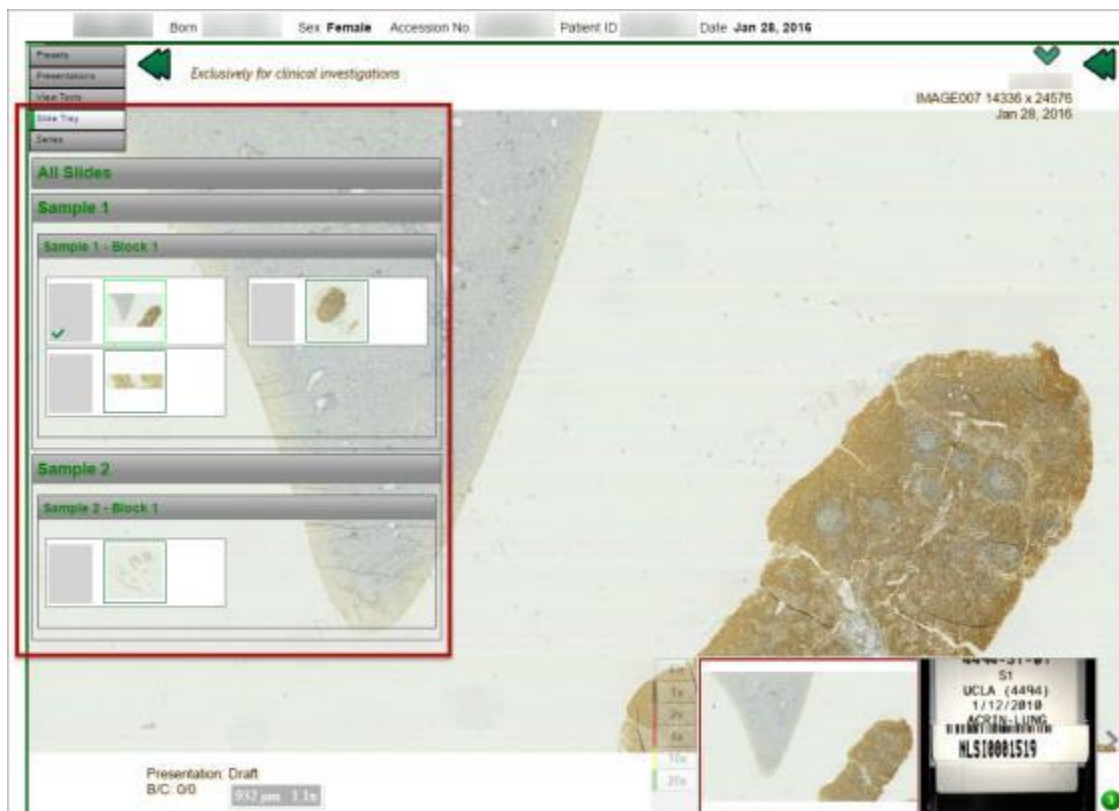
Pathology studies automatically open in a specialized viewer. The viewer has a simplified layout to allow you to focus on the pathology workflow. Note that the pathology viewer is intended for clinical reference viewing only.

The following hardware is recommended when using the pathology viewer:

- Monitor: 4K monitor to facilitate reading at a 5X magnification factor
- Specialized input tool: 3D mouse

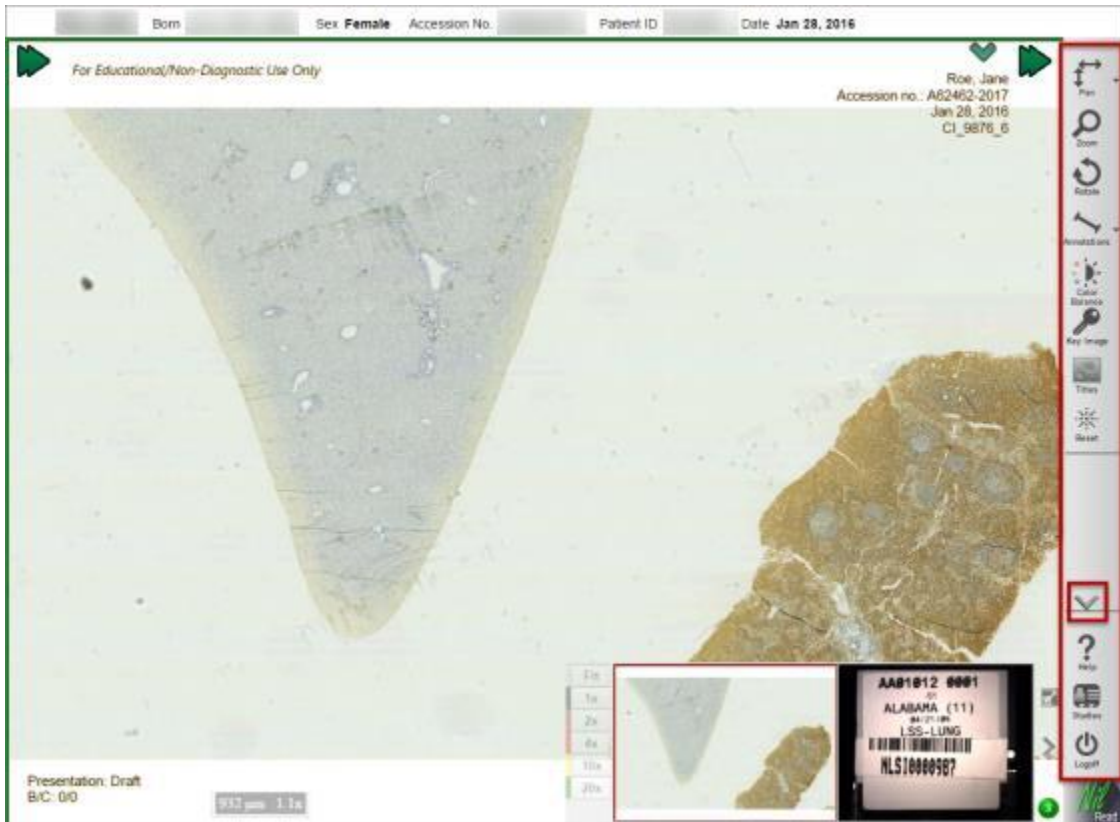
The pathology viewer contains the following features:

- The left side panel contains a Slide Tray with the samples in the study. Select a sample to load it in the viewer.



- The right toolbar contains image visualization tools commonly used to review pathology images, including a color balance tool. The tools are designed to work with a regular mouse or a 3D

mouse, which can be used to perform intricate adjustments. 3D mouse functionality is only available when using Google Chrome. Select the arrow above **Help** to view more tools, such as study layout.



- The slide label is shown on the bottom-right corner of the image. The number of samples in the study is shown to the right of the slide label.



- Magnification options and a navigation map are shown to the left of the slide label.



- To provide the maximum viewing area, the toolbar, side panel and patient timeline (if available) are hidden by default. Use the arrows to hide or view these items.



- You can also hide the slide label, magnification options and navigation map using the arrow in the bottom-right corner.



## Use the slide tray

1. Select Slide Tray (side panel). The samples in the study are shown below the side panel.
  2. Hover over a thumbnail for information about the sample (ID, image count, date, modality, description, stain).
  3. Select a thumbnail to load the sample in the viewer. The sample is opened in all viewports (if you are using multiple viewports).
- or
- Drag a sample into a viewport.

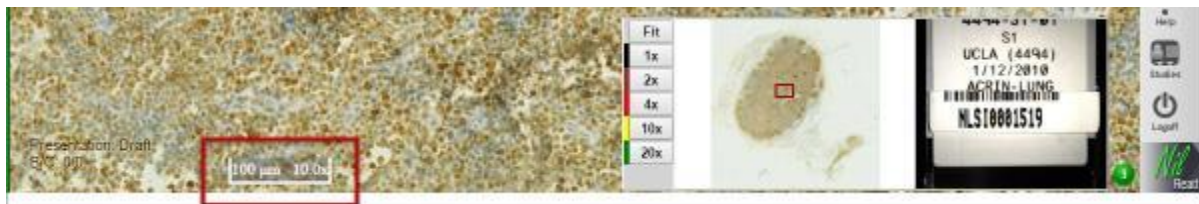
## Use the navigation map and magnification options

The red rectangle in the navigation map indicates the area of the image currently shown in the viewport.



- To focus on a point of interest, click (or tap) in the navigation map with a regular or 3D mouse. You can also use the arrow keys on your keyboard to select an area. The image is repositioned in the viewer to focus on the selected area.
- To change the magnification for the image, select a magnification factor beside the navigation map. You can also use a 3D mouse to change the magnification. Select Fit to fit the entire sample in the image viewer.
- The navigation map is updated when you change the magnification or use tools such as pan and rotate.

The following example shows a sample with a 10x magnification factor applied. The Caliper tool on the bottom-left of the image shows the current magnification factor. You can move the Caliper to a different position on the screen. Double-click (or touch and hold) the Caliper to return it to its original position.



## Use the pathology image visualization tools

The toolbar on the right contains the image visualization tools commonly used to review pathology images.

- Pan (see page 21)
- Zoom (see page 22)
- Rotate (see page 22)
- Annotations, including relevant measurement tools for pathology images (see page 28)
- Color Balance (see the next section)
- Key Image (see page 35)
- Titles (see page 36)
- Reset (see page 36)
- Hanging Protocols (see page 65)
- Study Layout (see page 57)
- Link (see page 27)

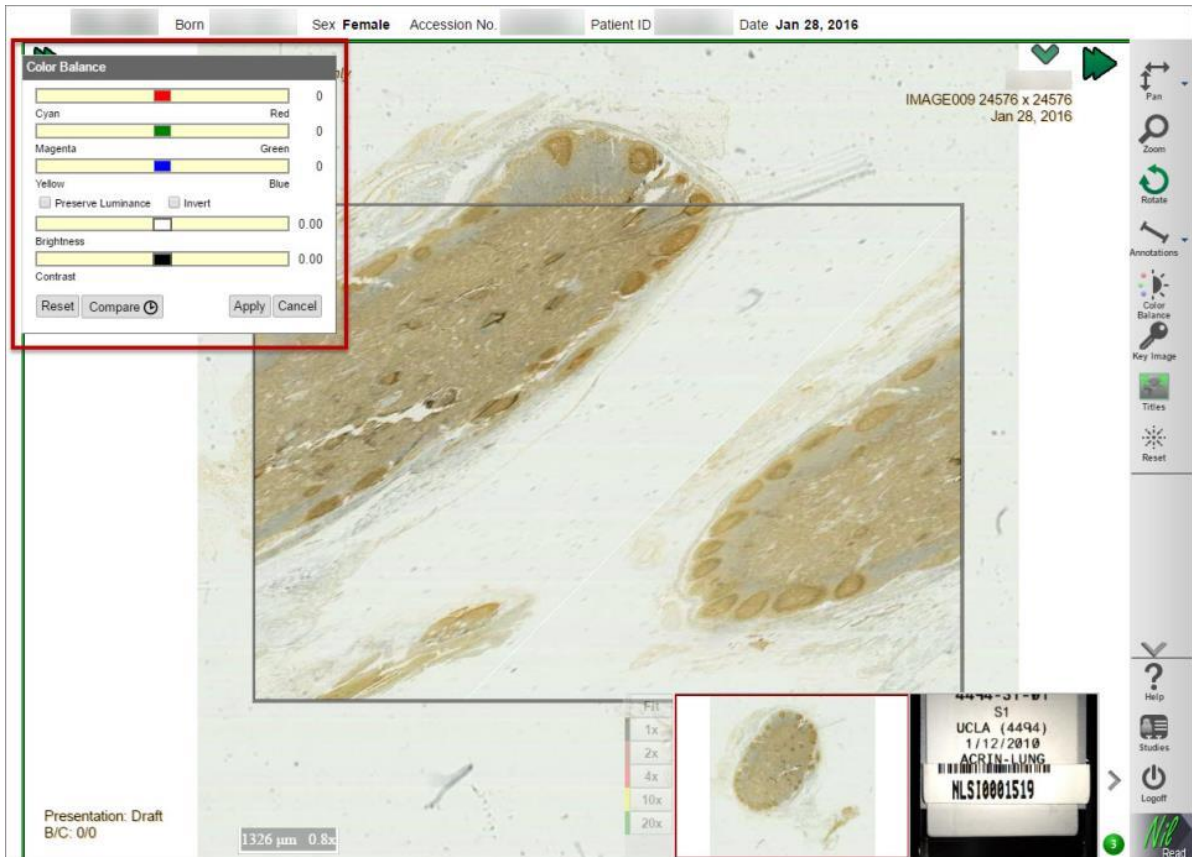
### View annotations

Press PAGE UP and PAGE DOWN to move between the annotations applied to the image. Note that the navigation map will adjust to show the location of the annotation currently being viewed.

## Adjust the color balance

Use the Color Balance tool to adjust the color balance of a sample.

1. Select **Color Balance** (right toolbar). Use the options on the left side of the screen to adjust the color balance.

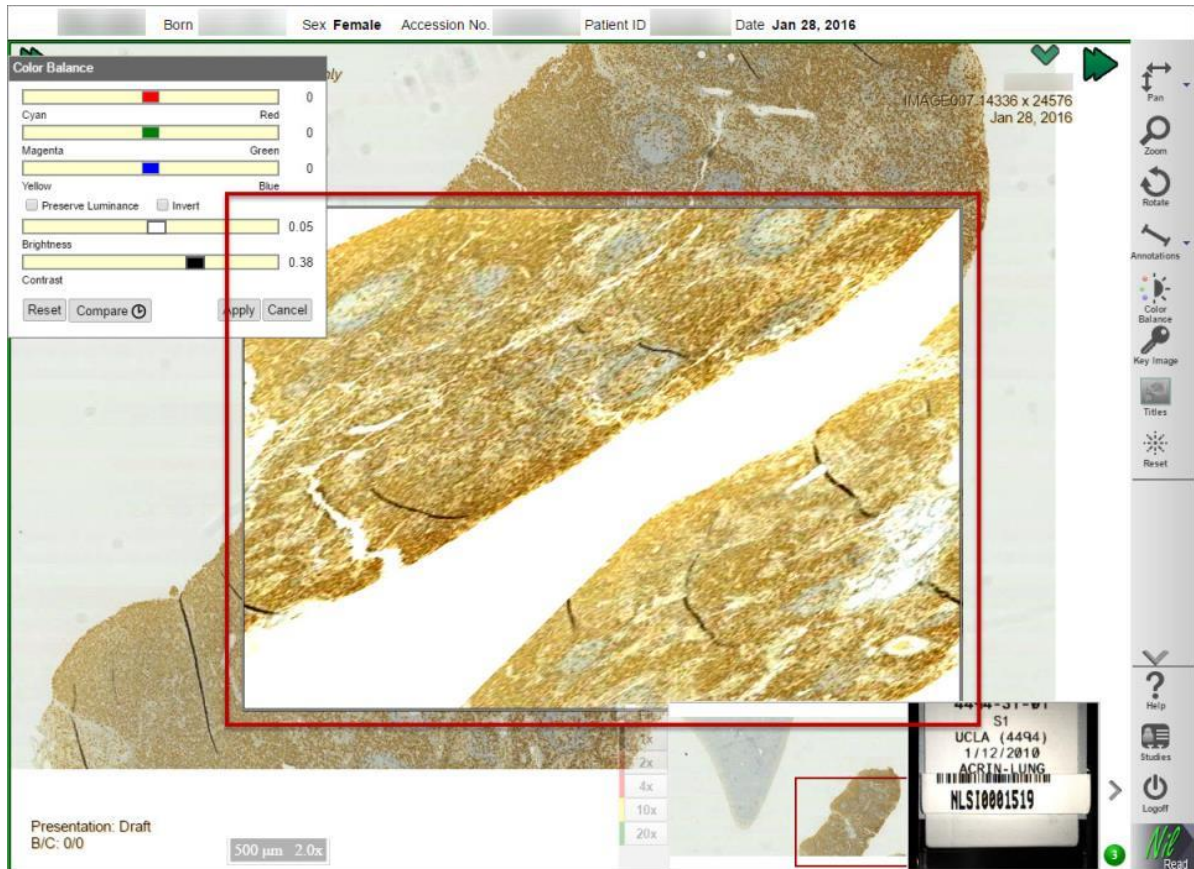


Color balance options include:

- **Red, Green, and Blue Color Channels** Each channel has a primary color (red, green, and blue) and a complementary color (cyan, magenta and yellow). Adjust the slider to increase the amount of the primary or complementary color.
- **Preserve Luminance** Maintain the image luminance while changing the color balance.
- **Invert** Invert the color channels, changing the image from a positive to a negative image.
- **Brightness** Adjust the image brightness.
- **Contrast** Adjust the image contrast.



2. When you make a change in the color balance options, your change is shown in the preview window overlaid on the image.



3. To compare your changes with the original image, click and hold (or tap and hold) Compare. Your changes are temporarily removed from the preview window so you can view the original image.
4. When you are satisfied, select **Apply** to apply your changes to the sample. If you do not want to apply your changes, select **Cancel**.
5. To remove all color balance changes from the sample, select **Reset**.

## 7. Use the vessel tracer

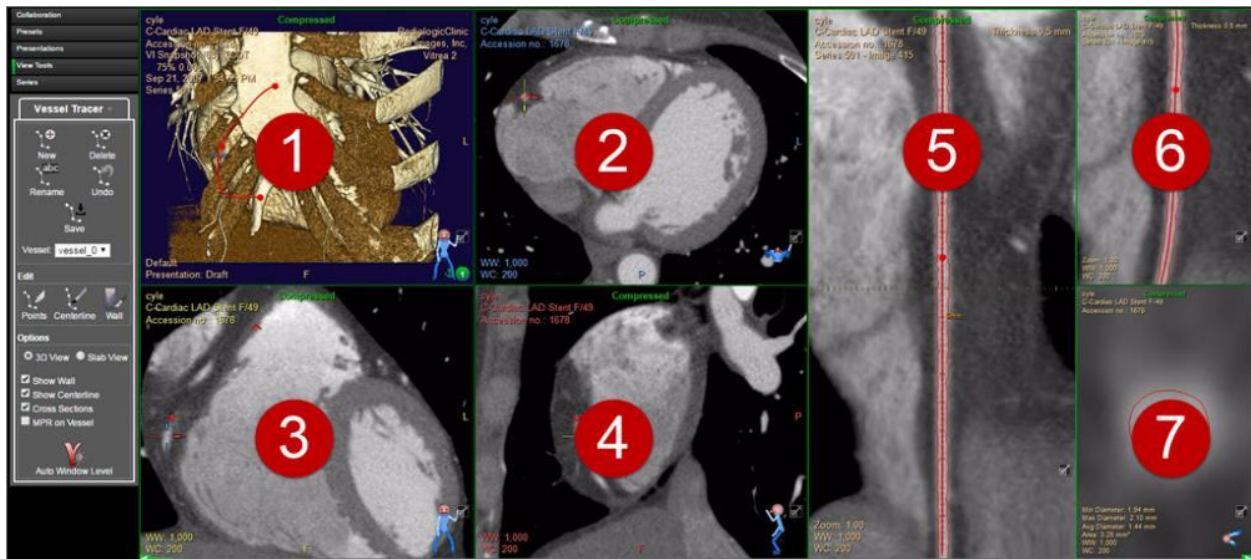
### About the vessel tracer

For CT studies, the vessel tracer tools allow you to extract a vessel from the volumetric data set in order to examine the vessel more closely.

### Use the Vessel Tracer view

To use the vessel tracer tools, first apply the vessel tracer view. Select **View** (toolbar), then select **Vessel Tracer**. (You can also use the Study Layout options to place the vessel tracer view beside an existing view. For details, see "Arrange images" on page 57.)

The default vessel tracer view contains seven viewports.



- By default, viewport 1 contains a 3D shaded rendering of the data. To change the viewport to a thick slab MIP rendering, select the **Slab View** option in the Vessel Tracer tools panel. To switch back to the 3D rendering, select the **3D View** option.
- Viewports 2, 3, and 4 contain MPR views on the three major planes (axial, sagittal and coronal).
- Viewports 5, 6, and 7 contain reformat views of the selected vessel. These views appear once you have created a vessel.
  - Viewport 5 contains a "stretched" ribbon view along the centerline of the vessel. This view has overlays showing the centerline, the intersecting inner wall curve of the vessel and a reference marker which identifies the location of the cross-section in viewport 7. The

reference marker in this view is a pattern of distance ticks. You can edit the vessel in this viewport.

- Viewport 6 contains a curved reformat view of the vessel. This view has overlays showing the centerline, the intersecting inner wall curve of the vessel and a reference marker which identifies the location and orientation of the cross-section in viewport 7. You cannot edit the vessel in this viewport; it is for viewing only.
- Viewport 7 shows an axial cross-section through the vessel at the location of the reference marker along the vessel's centerline. Several cross-section measurements are shown such as the minimum diameter, maximum diameter, average diameter and area of the lumen. Note that you can use the **Cross Sections** option to hide the cross-section view. If the cross-section view is hidden, the curved reformat view is expanded to fill the viewport.

To hide the cross-section view and expand the curved reformat view:

- In the Vessel Tracer tools panel, clear the **Cross Sections** option.

To change the orientation of the MPR viewports according to the direction of the vessel:

- In the Vessel Tracer tools panel, select the **MPR on Vessel** option.

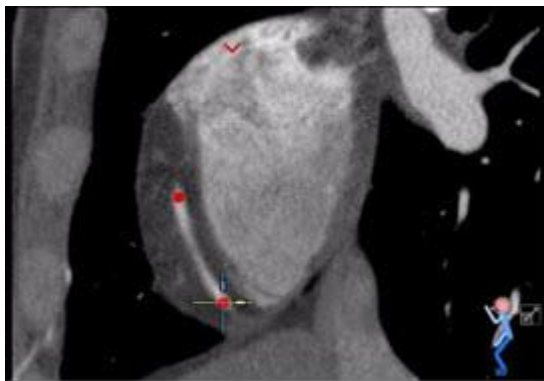
To apply a window level preset that tries to optimize the display of the vessel:

- In the Vessel Tracer tools panel, select **Auto Window Level**.

## Define a vessel

Once you have applied the vessel tracer view, you can identify vessels using seed points. After defining a vessel, you can adjust the seed points, centerline and lumen wall.

1. Select **View Tools** (side panel). The Vessel Tracer tools panel appears below the side panel.
2. Select **New**. A new vessel is added to the **Vessel** list in the side panel. The vessel is given a default name, such as vessel\_0. To change the vessel name, select **Rename**.
3. Note that the **Edit Points** option is now enabled. In one of the MPR viewports (or the 3D viewport), click (or tap) to place seed points within the lumen of the vessel. For example:



Note that if a point appears as an arrow (instead of a dot), this indicates that the seed point is not on the current plane.

If the arrow faces down, scroll down to view the seed point. If the arrow faces up, scroll up to view the seed point. You can also use the **Previous Seed Point** or **Next Seed Point** options that appear when you right-click (or touch and hold) a point.

Note that you can work with points in the ribbon view (5) in addition to the 3D and MPR viewports (1-4).

4. You must place a minimum of two points to define a vessel. Once a vessel is defined, reformat views of the vessel are shown in the ribbon view (5), curved reformat view (6), and cross-section (7).
  - To add more points to the vessel, select **Edit Points** and click (or tap) on the vessel to place a point. You can add (or move) points in any of the MPR, 3D or ribbon viewports.
  - To move a point, select **Edit Points** and drag a point to a new location.
  - To delete a point, right-click (or touch and hold) the point, then select **Delete Seed Point**.
  - To change the focus of the viewports to a specific seed point, right-click (or touch and hold) the point, then select **Focus to This Seed**.
  - To move through the seed points, right-click (or touch and hold) a point, then select **Previous Seed Point** or **Next Seed Point**.
5. In the Vessel Tracer tools panel, select **Save**. This will save all of the vessels that have been defined.

**Note**

Before saving, you can select **Undo** to remove your last change to the vessel.

6. To work with a previously defined vessel, select the vessel from the **Vessel** list.
7. To delete a vessel, select the vessel from the **Vessel** list, then select **Delete**.

## Adjust the centerline and wall

NilRead identifies the vessel centerline and lumen wall based on the seed points you have defined. The user is responsible for reviewing and editing the results shown in the vessel tool. A convenient way to view a vessel is to press the middle mouse button and drag in the cross-section viewport.

The centerline is shown in the ribbon and curved reformat views. The wall is shown in the ribbon, curved reformat and cross-section views. For example:



To adjust the centerline:

1. In the Vessel Tracer tools panel, select **Edit Centerline**.
2. In the ribbon view, drag to draw a new approximation of the centerline.
3. NilRead uses the new centerline to adjust the vessel visualization. NilRead may add more seed points to accommodate the new centerline.
4. In the Vessel Tracer tools panel, select **Save**.

To adjust the wall:

1. In the Vessel Tracer tools panel, select **Edit Wall**.
2. In the ribbon view, drag to draw a new approximation of the wall.
3. In the cross-section view, click (or tap) within the boundaries of the wall. A dotted line appears. Drag the dotted line to draw a new approximation of the wall.
4. NilRead uses the new wall to adjust the vessel visualization.
5. In the Vessel Tracer tools panel, select **Save**.

To hide the centerline or wall:

- In the Vessel Tracer tools panel, clear the **Show Centerline** or **Show Wall** option.

To use the clipper tools in the **Vessel Tracer** view:

- In the Vessel Tracer tools panel, select the arrow beside the **Vessel Tracer** title, then select **Clipper**. The Clipper tools panel appears. To return to the vessel tracer tools, select the arrow, then select **Vessel Tracer**.

## 8. View radiation therapy (RT) plans

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### About RT plans

You can view external beam radiation therapy (RT) plans using any NilRead view. There are also two specific RT views available, RT Graph and DRR.

#### Note

You can use these views to create hanging protocols for RT plans. For details, see “About hanging protocols” on page 206.

### Using the RT Plan panel

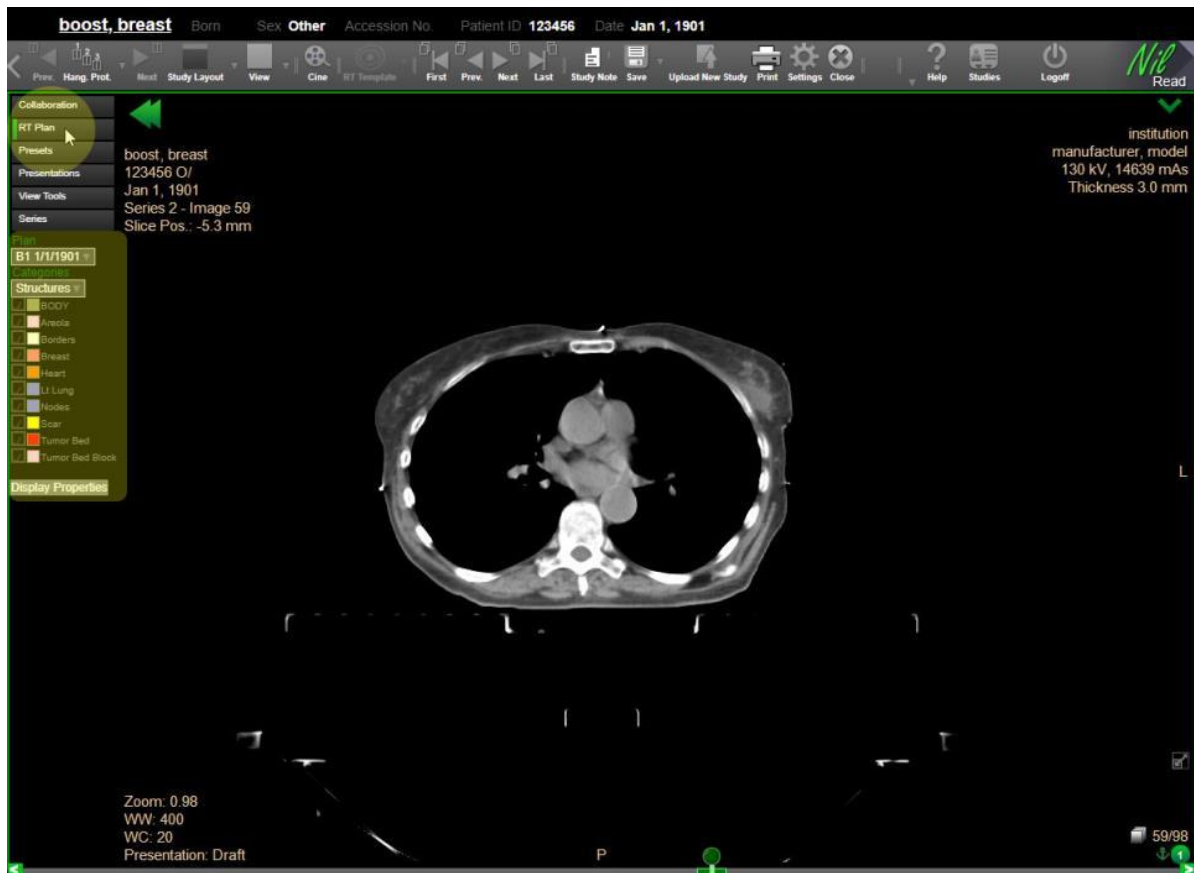
When you load a study containing RT plans, **RT Plan** options are available in the side panel. These options allow you to choose the plan details you want to view.

If the image viewer contains multiple viewports, enable **Link** (toolbar) to apply the RT Plan options to all viewports. If Link is not enabled, the options will be applied to the currently selected viewport only.

#### Note

You can use RT templates to control how information is displayed. For details, see “Manage RT templates” on page 138.

1. Select RT Plan (side panel). The RT Plan options appear below the side panel.





2. Select a plan.

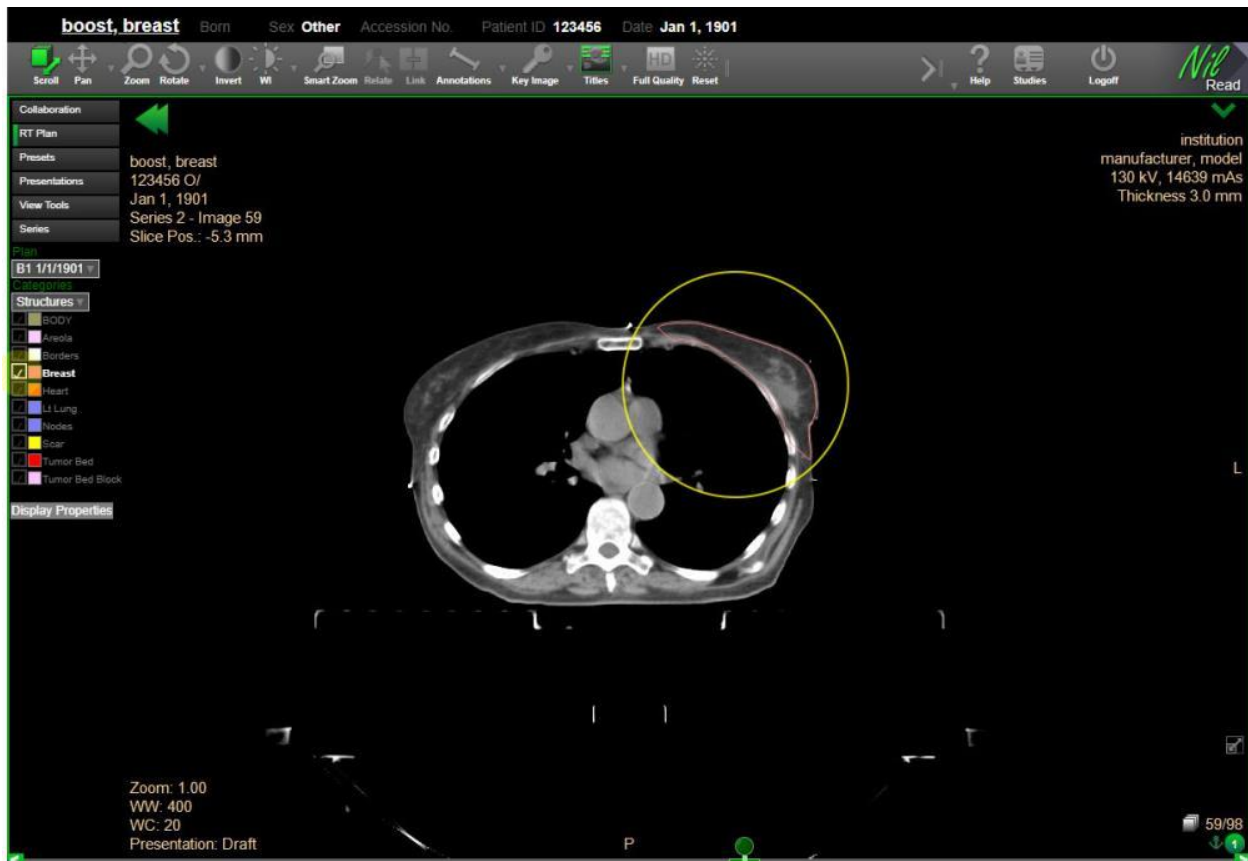


3. Select a category: Structures, Isodoses or Beams.



## Structures

Select the checkbox beside the structures you want to target. The selected structures are contoured.



## Isodoses

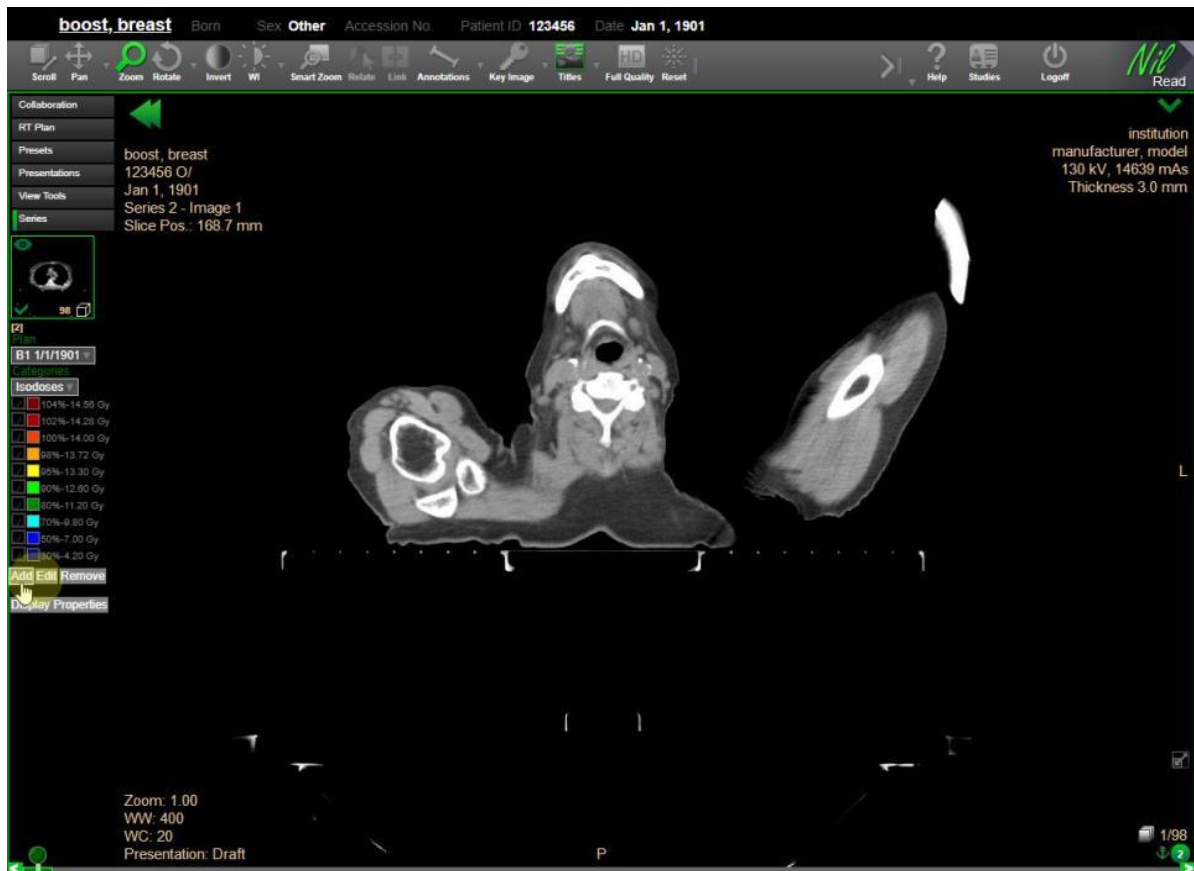
Select the checkbox beside the isodose levels you want to target. The selected levels are contoured.

Isodose levels are shown as a percentage of the prescription dose. The first item in the isodose list is the Maximum isodose level, which represents isodose levels that are above the maximum level. You cannot modify the Maximum isodose level except to change the color.

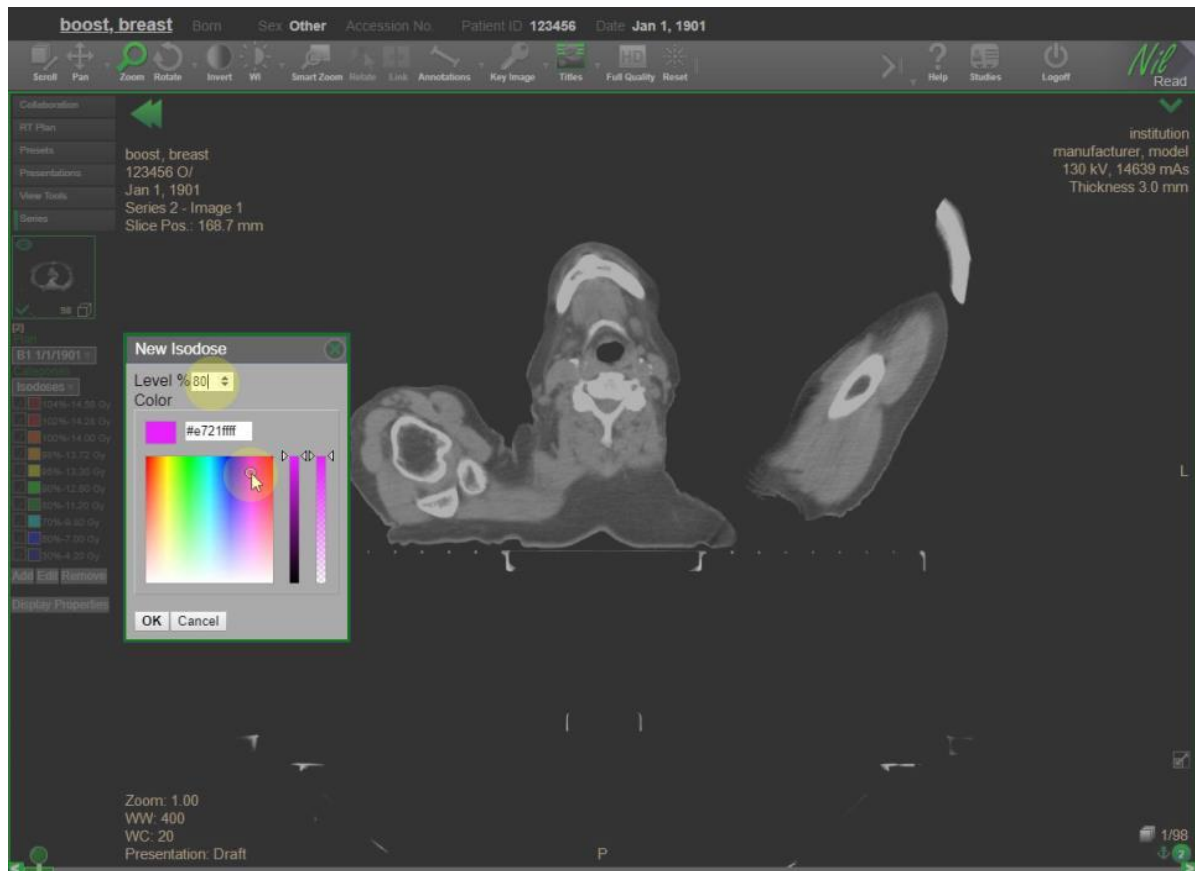


You can add an isodose level.

1. Select Add.



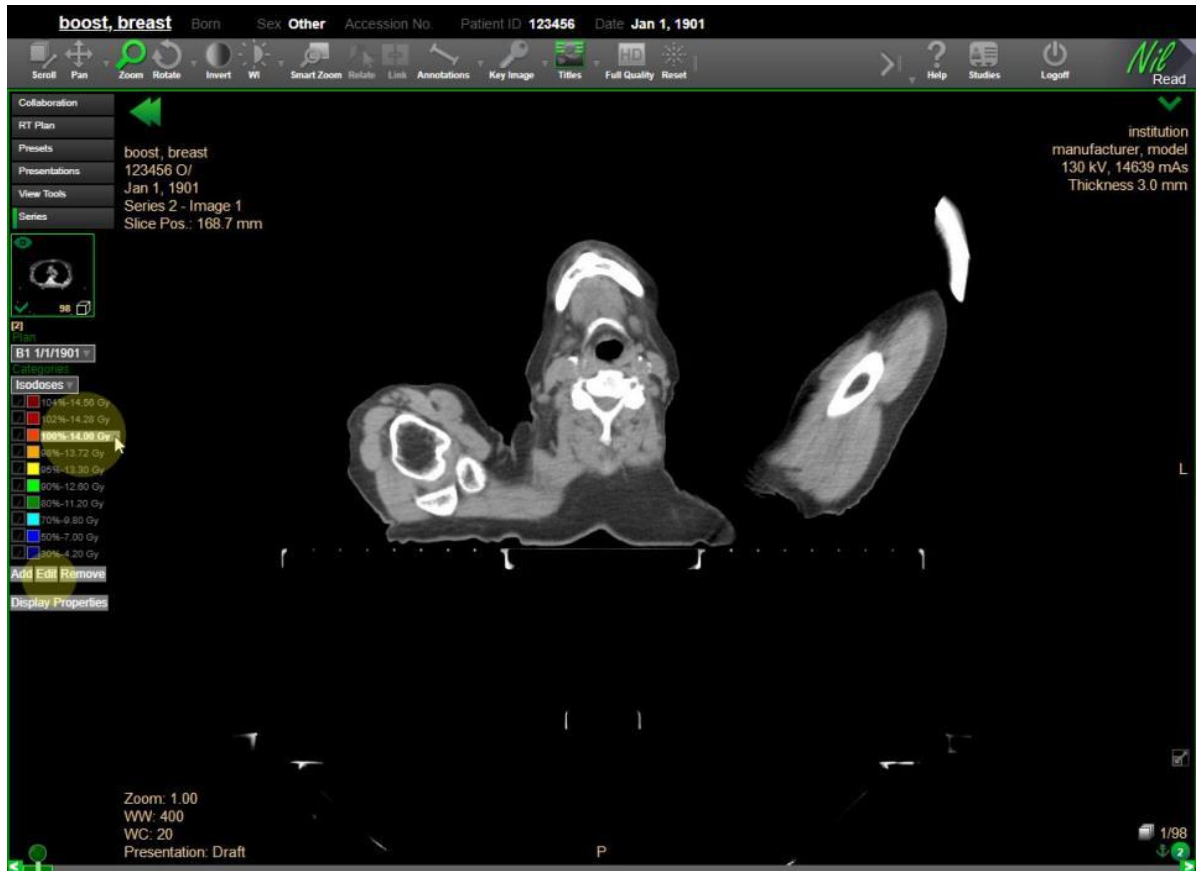
2. Enter the level (as a percentage of the prescription dose) and select a color.



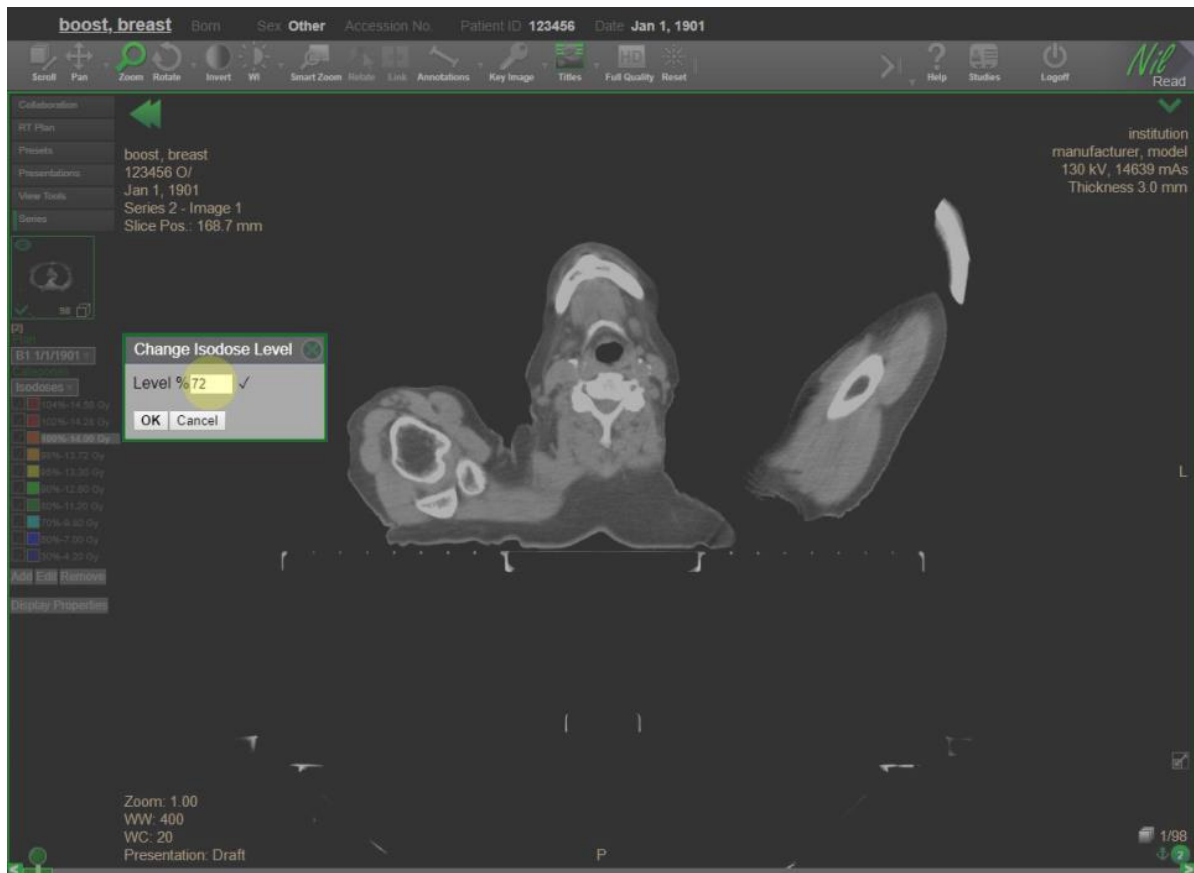
3. Select OK.

You can change the level of an isodose.

1. Select the isodose label, then select Edit.



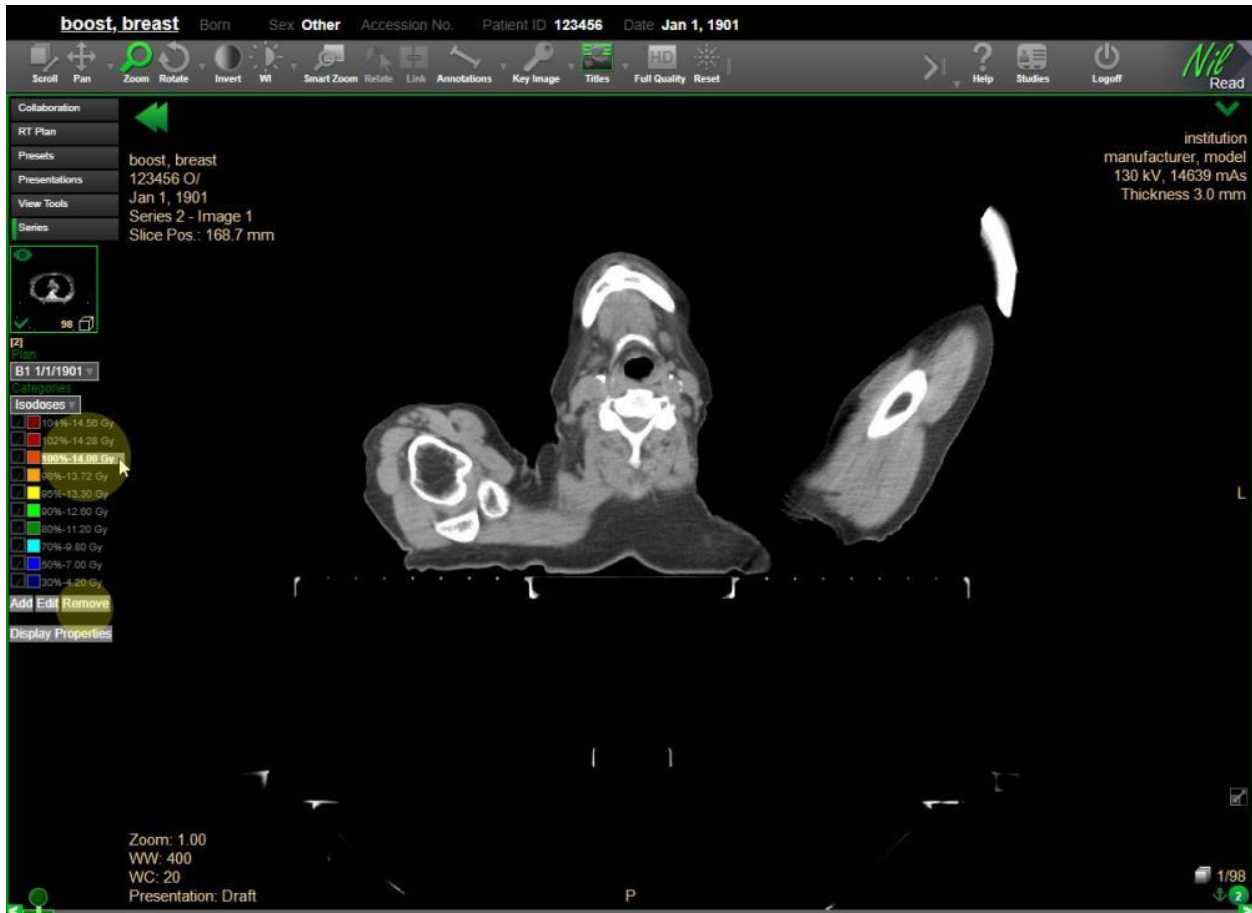
2. Enter the new level (as a percentage of the prescription dose).



3. Select OK.

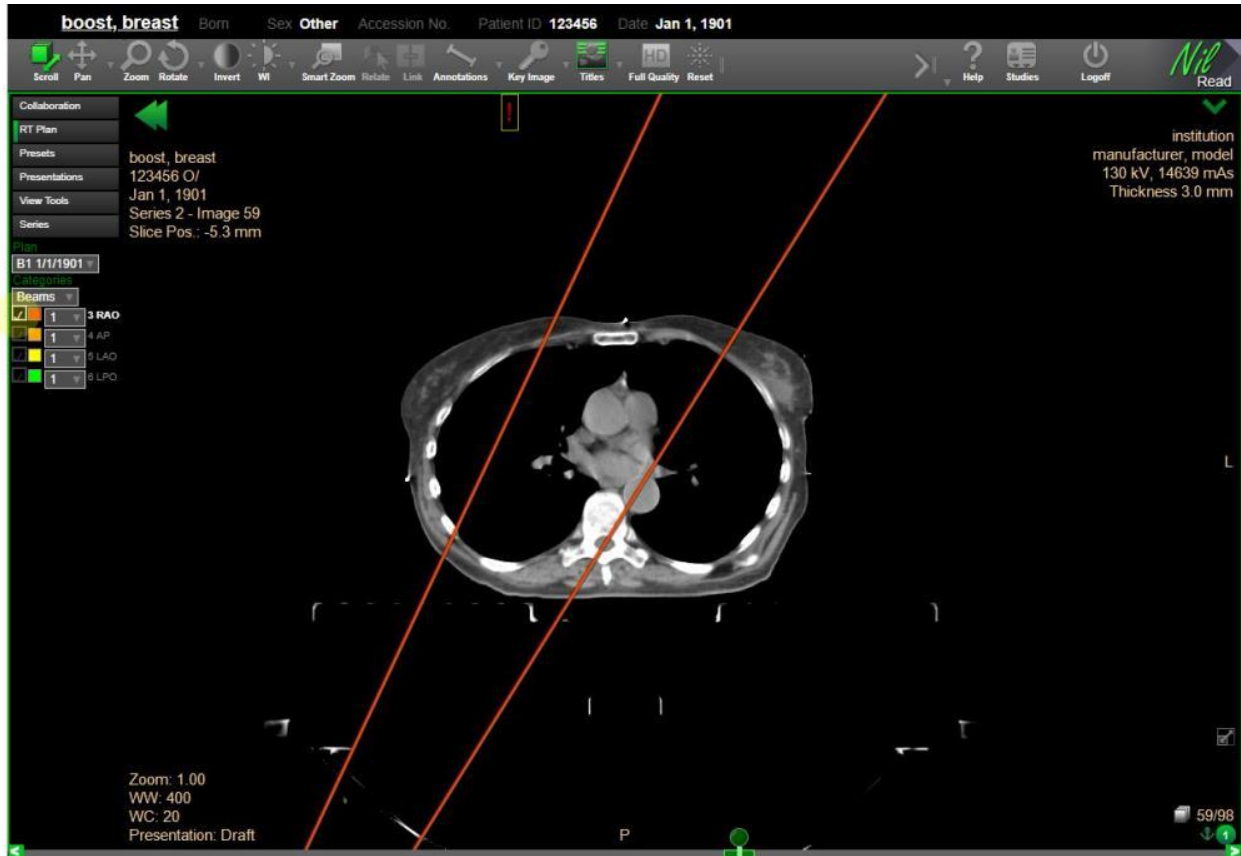


You can delete an isodose. Select the isodose label, then select Remove.

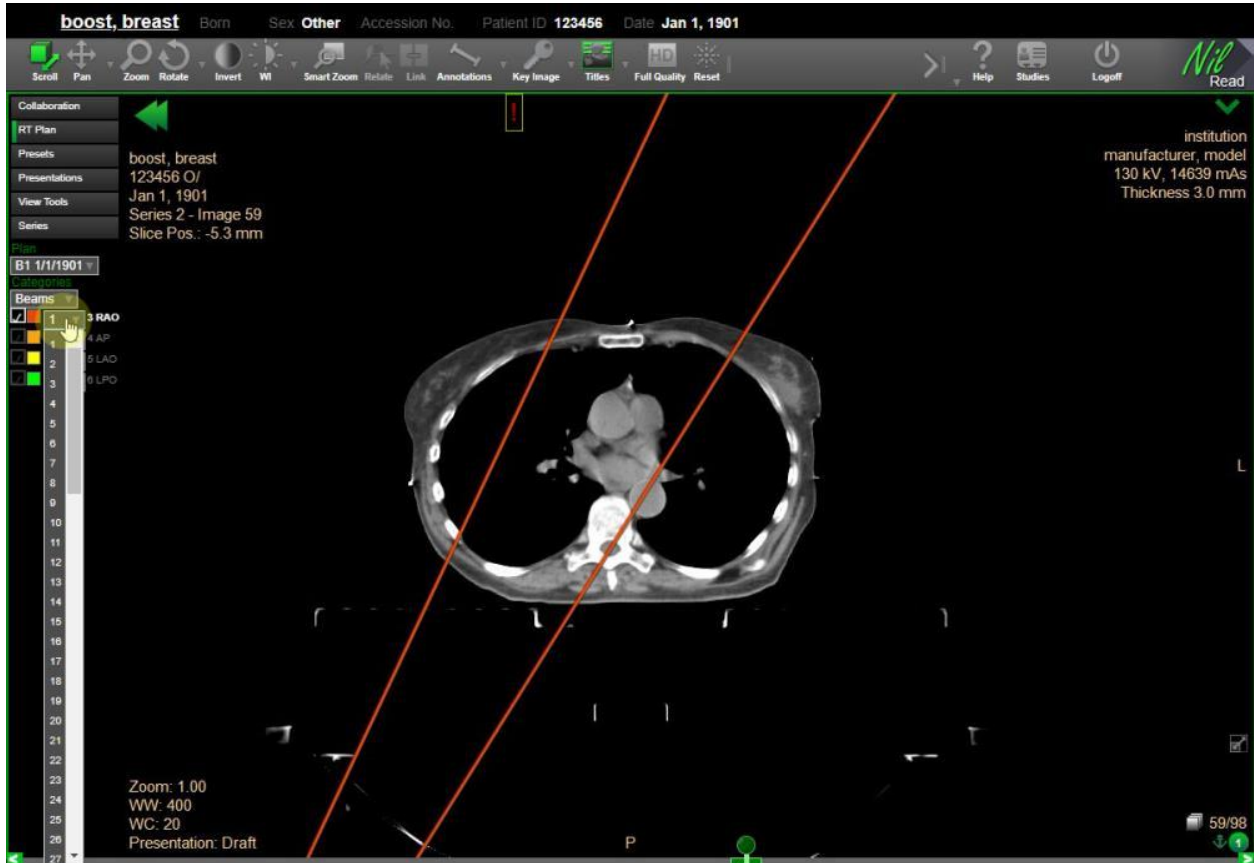


## Beams

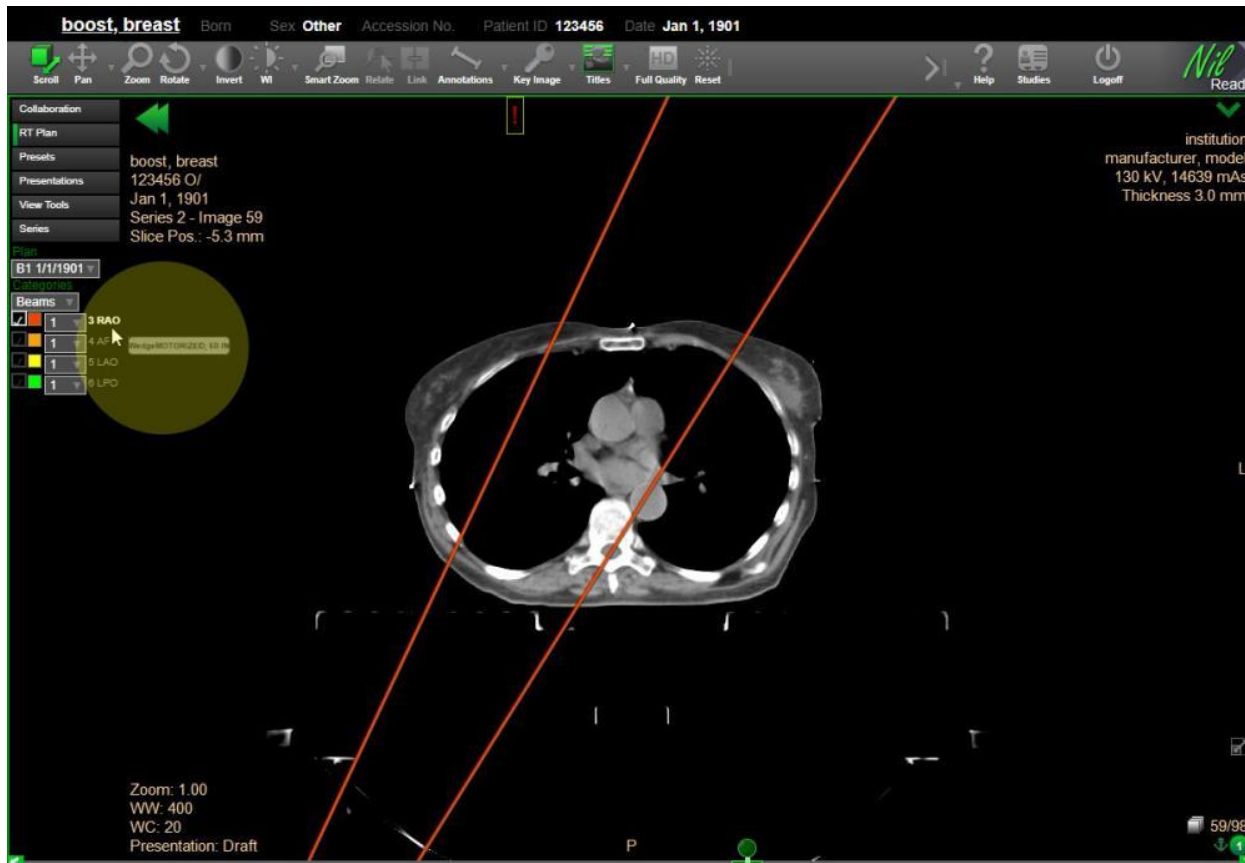
Select the checkbox beside the beams you want to target. The selected beams are shown.



Use the list beside a beam to select the control point you want to visualize. Note that the shape and source of the beam may change between control points.



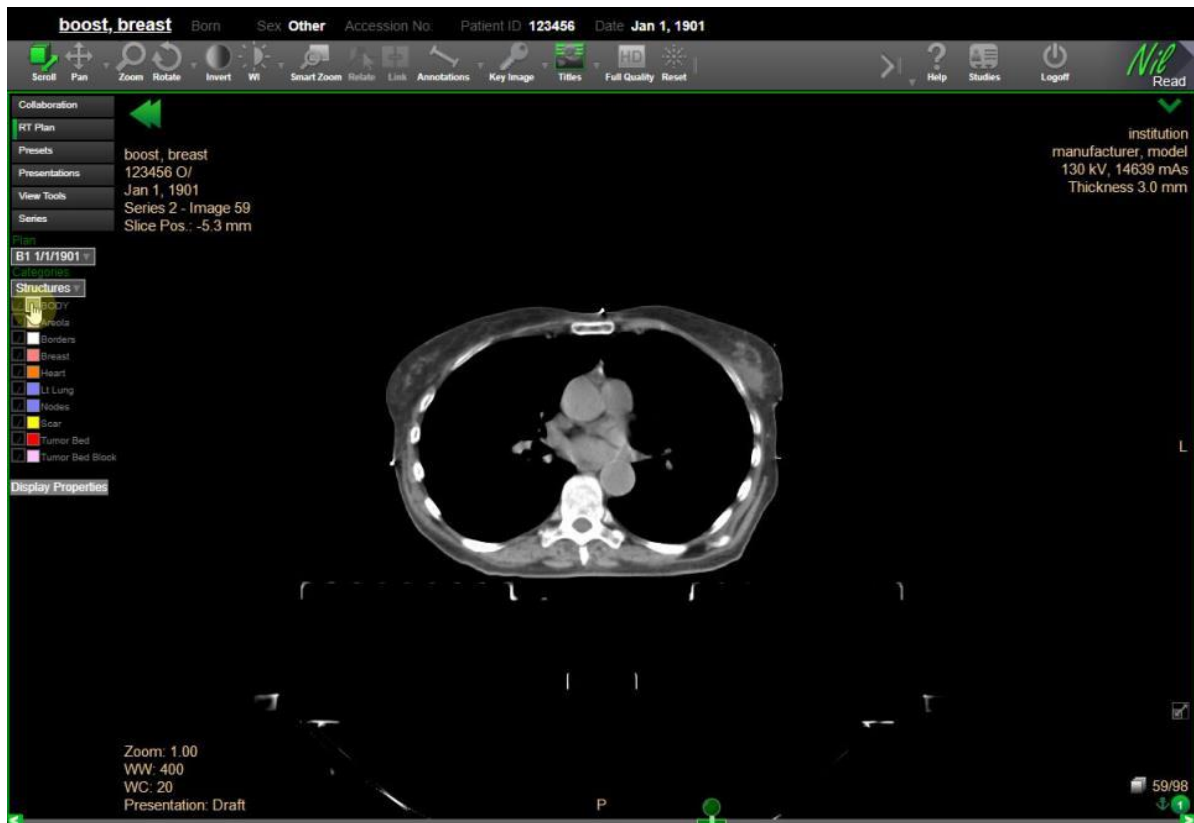
To view information about the wedge associated with the currently selected beam control point (if one exists), hover over the beam label.



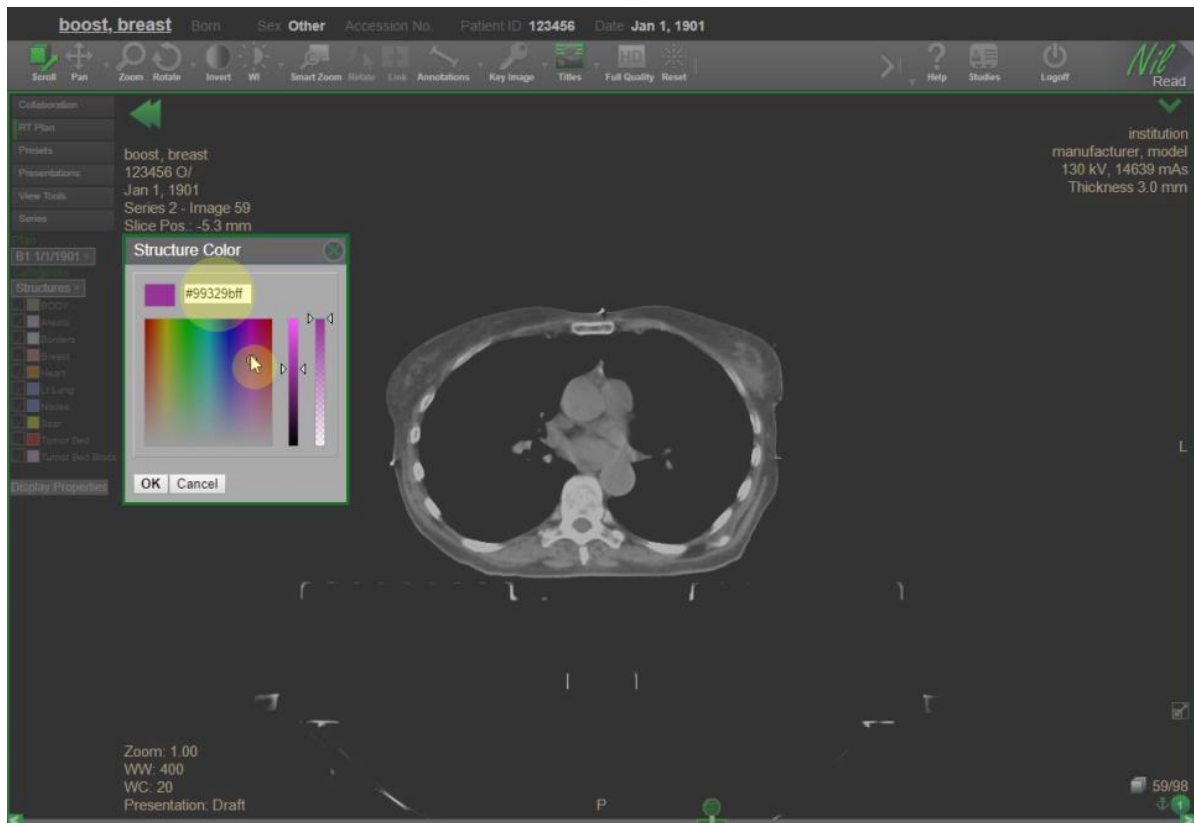
### Color Options

You can change the color used to display a structure, beam or isodose. These changes will last until you close the study. To permanently change the display colors, use an RT template (see "Manage RT templates" on page 138).

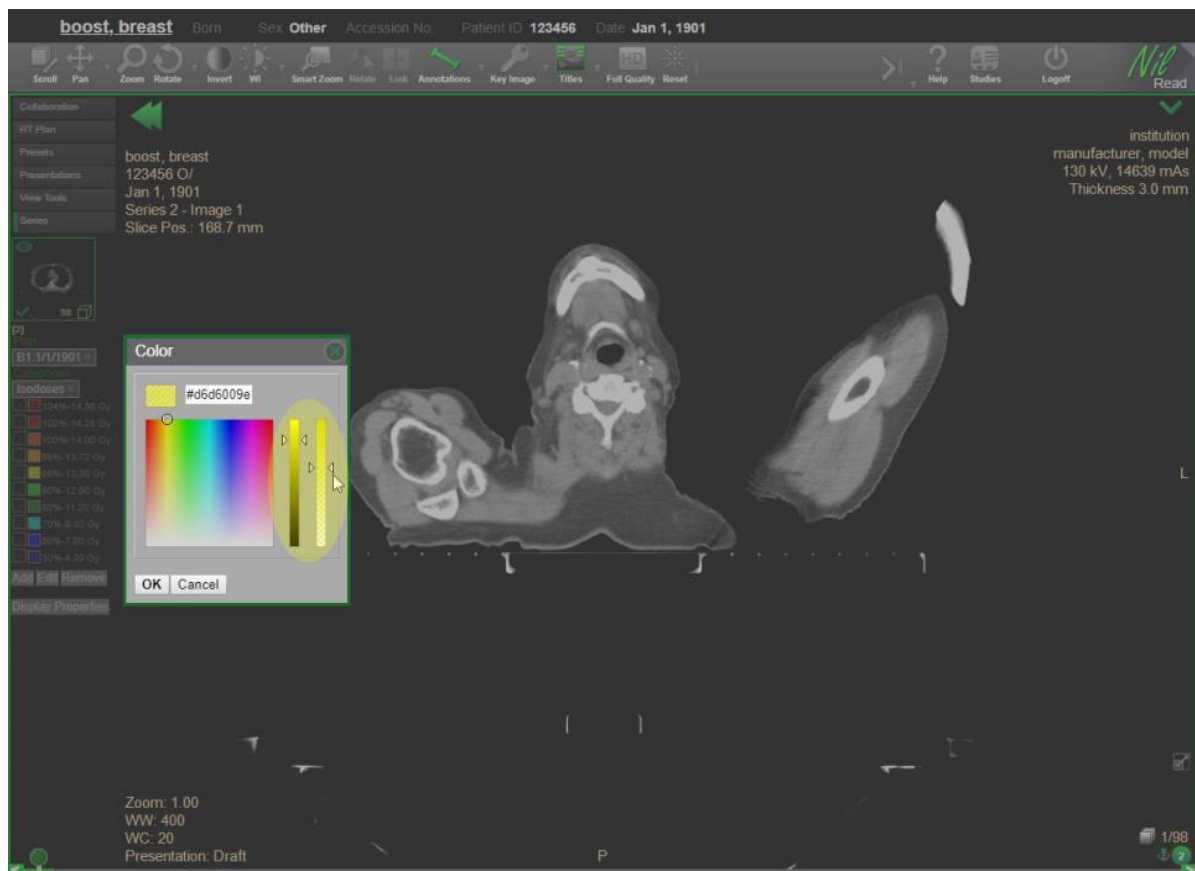
1. Click (or tap) the color box beside the structure, beam or isodose.



2. Select a color by entering the hexadecimal color code or using the color picker.



3. Use the sliders to adjust the color tone and opacity.

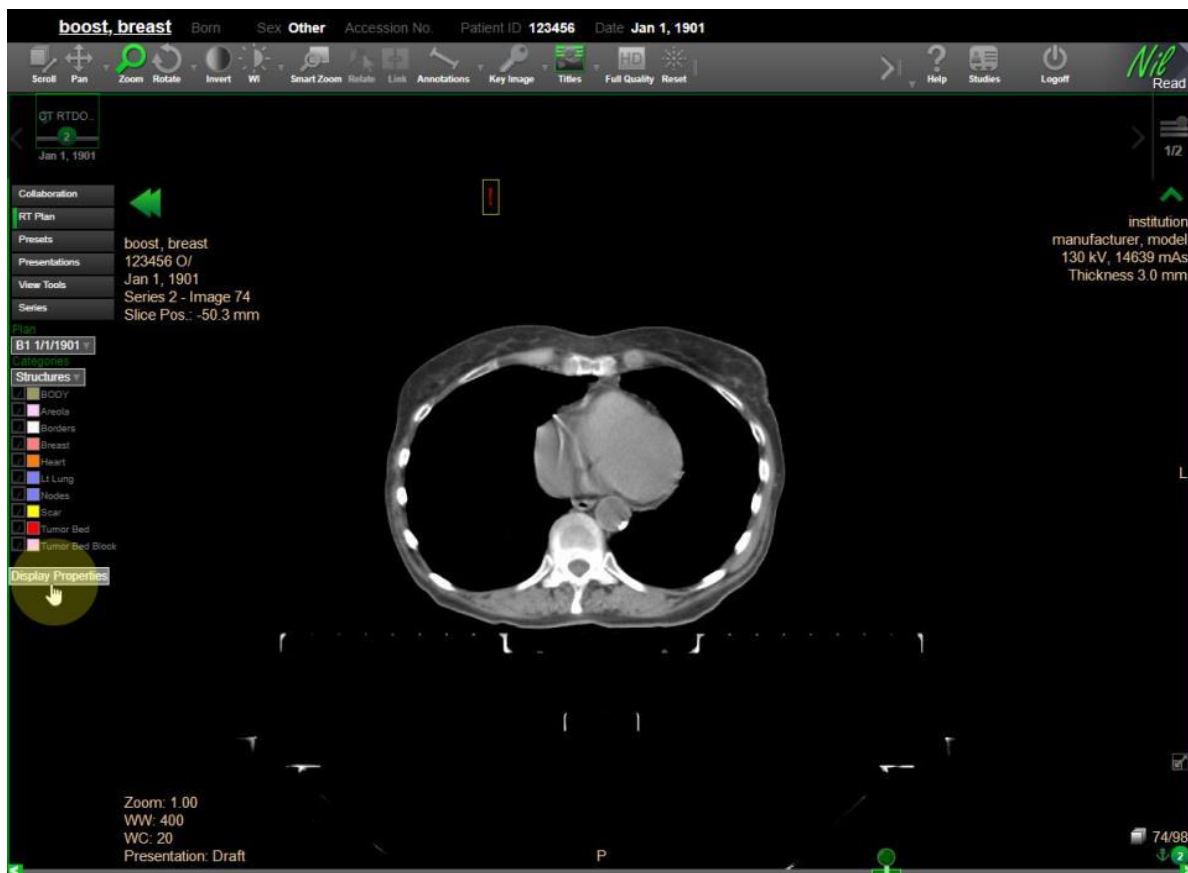


4. Select OK.

### Display Properties

You can change the way structures and isodoses are shown. These changes will last until you close the study. To permanently change the display properties, use an RT template (see “Manage RT templates” on page 138).

1. Select Isodoses or Structures, then select Display Properties.



2. You can change the following options.
  - **Contour width** Select the width of the contour outline. Note that you cannot change the contour width for MPR images.
  - **Display as** Select the type of contour: **Contours** (outline) or **Filled Contours** (shaded).
3. Select OK.

## Using the RT Graph view

The RT Graph view includes a cumulative dose-volume histogram (DVH) relating radiation dose to tissue volume. You can select the structures to include in the histogram.

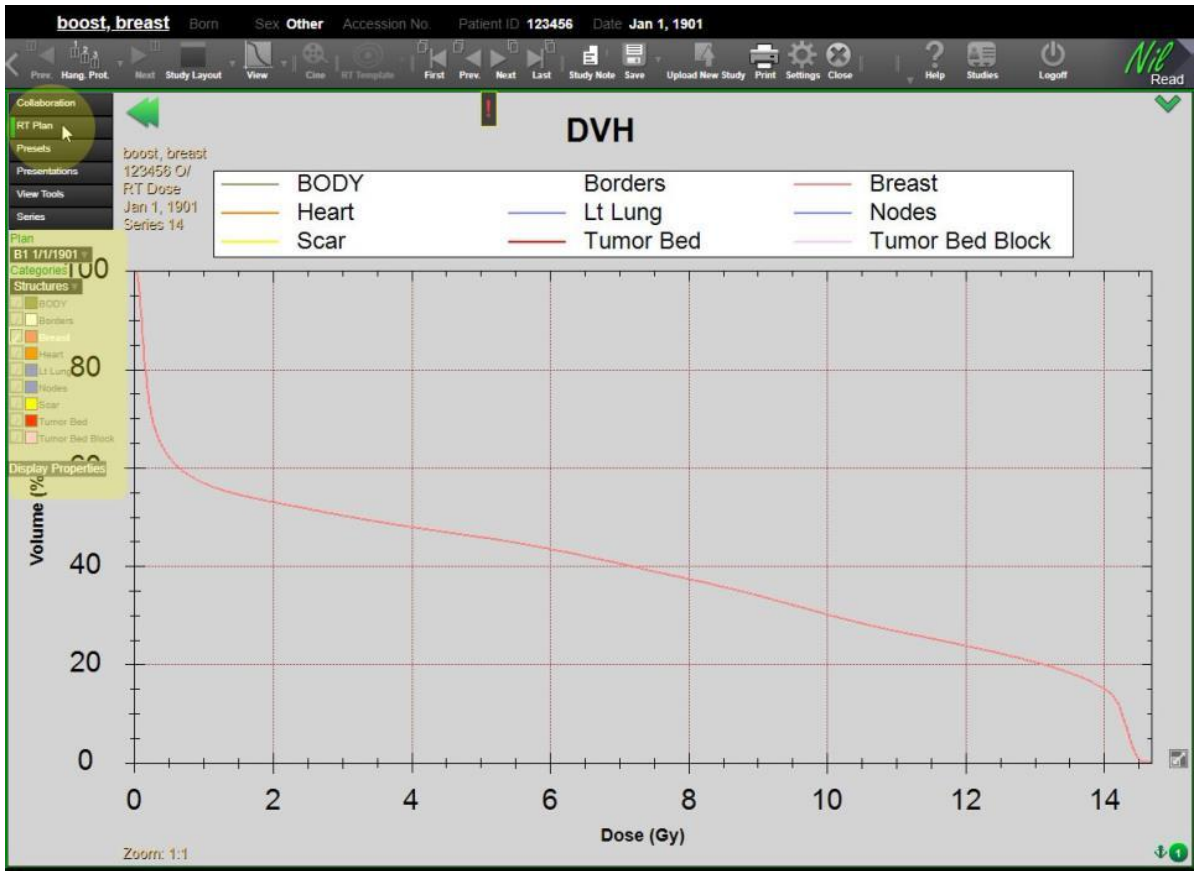
1. Select **View** (toolbar), then select **RT Graph**.

### Note

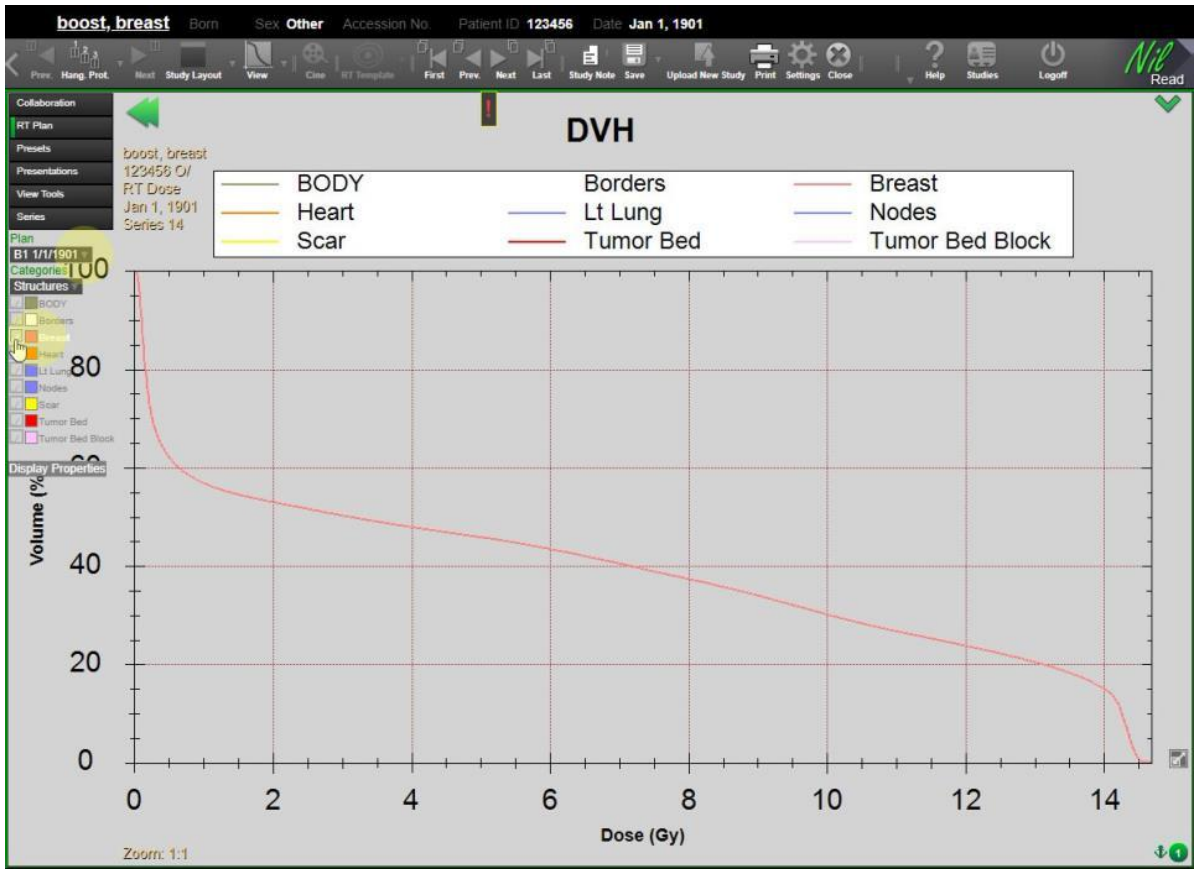
You can also use the study layout options to place the RT Graph view beside an existing view. For details, see "Arrange images" on page 57.



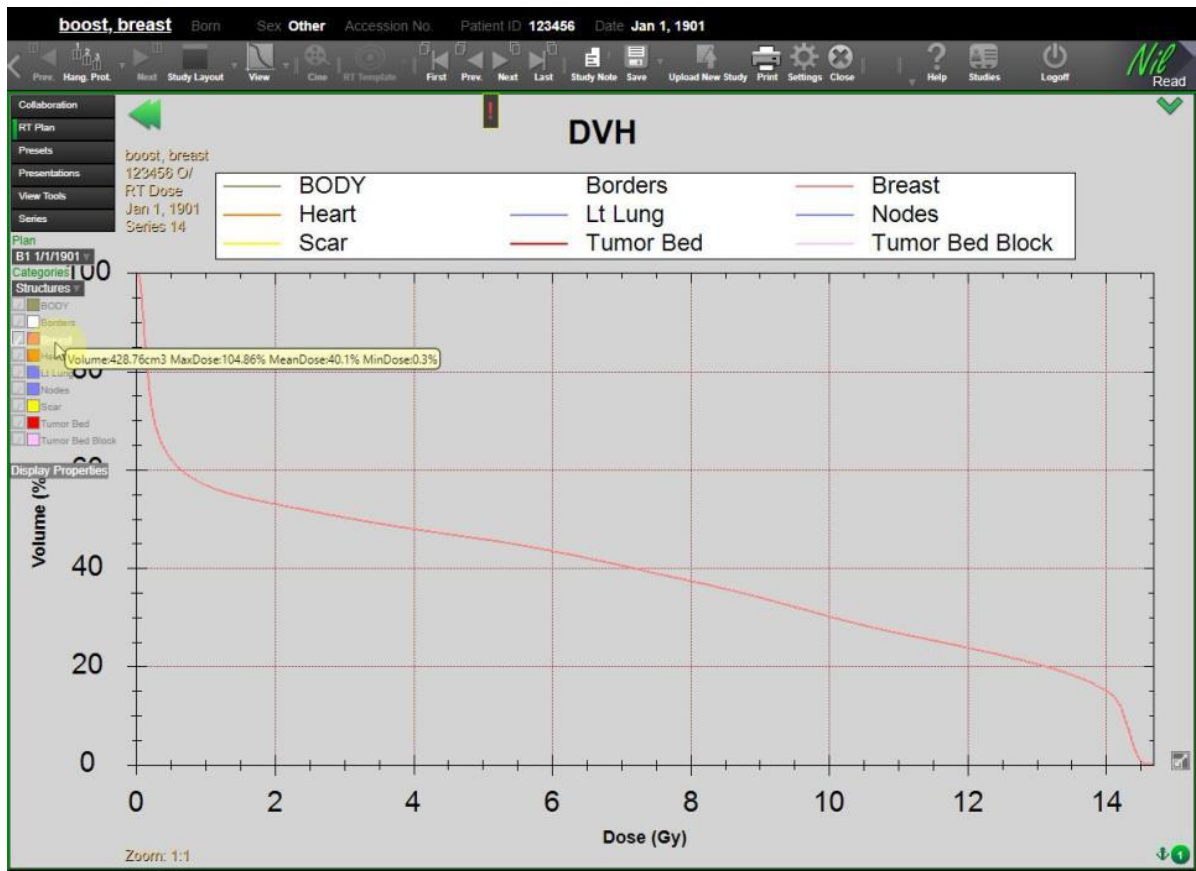
2. Select RT Plan (side panel). The RT Plan options appear below the side panel.



3. Select a plan, then select one or more structures. On the DVH, the radiation dose received for the percentage volume for each structure is shown.



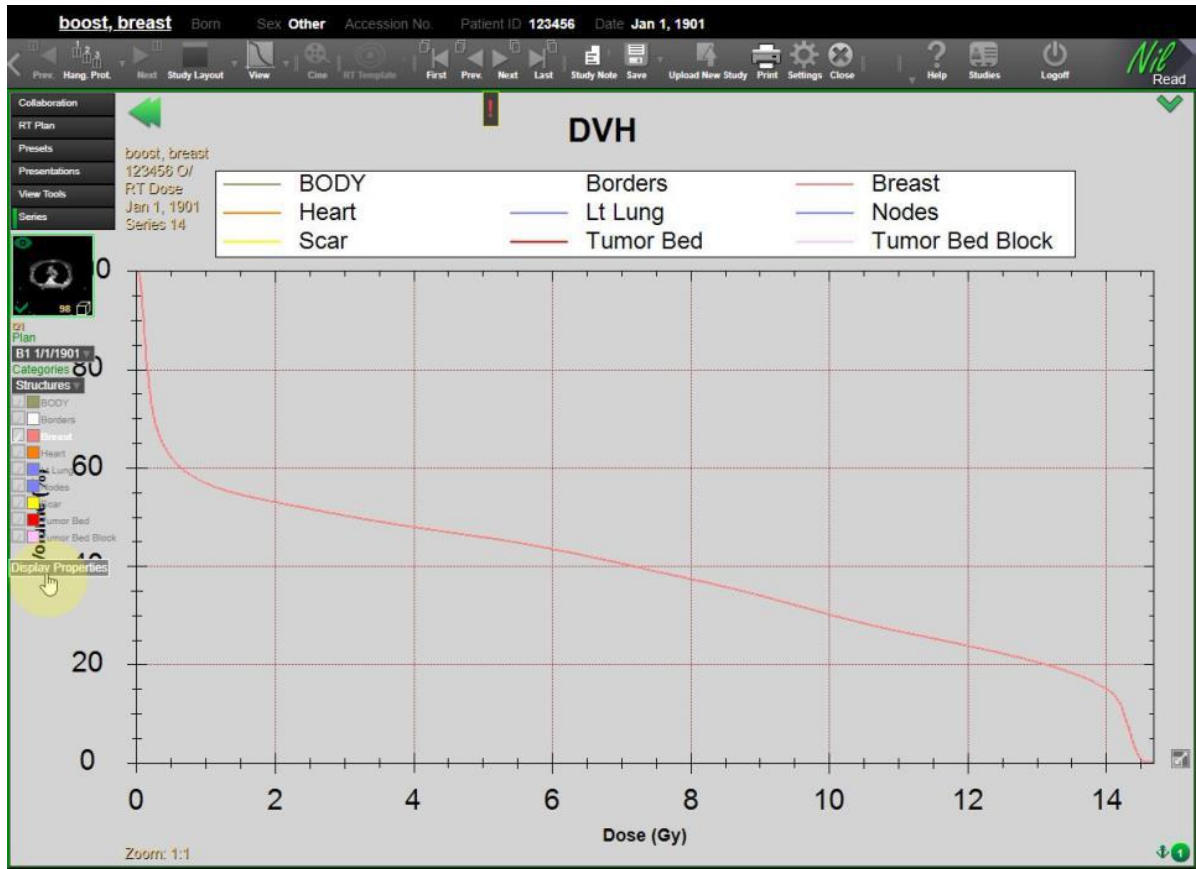
4. Hover over a structure in the side panel to view dose statistics.



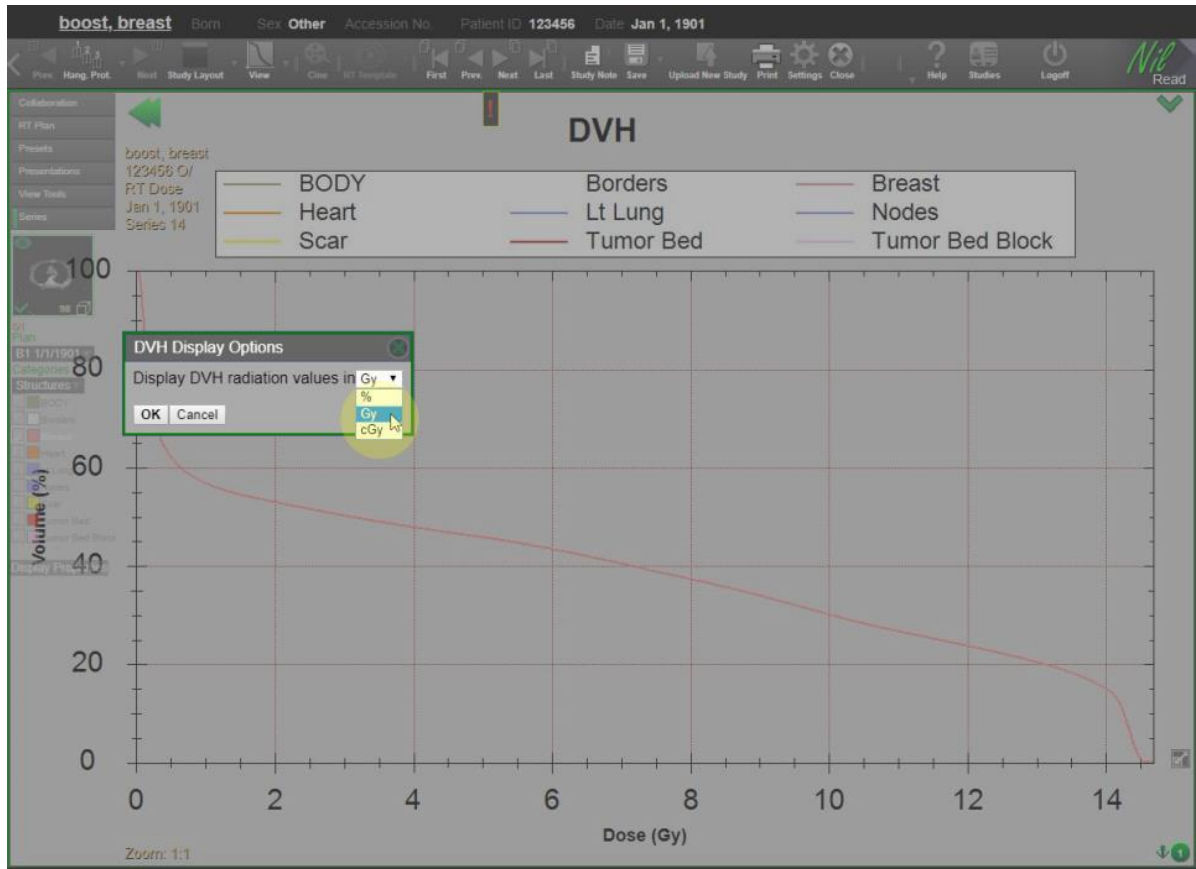
### Display Properties

You can change the dose unit of measurement on the graph.

1. Select Display Properties.



2. Select the unit of measurement for dose values. You can choose cGy, Gy or a percentage of the prescription dose.



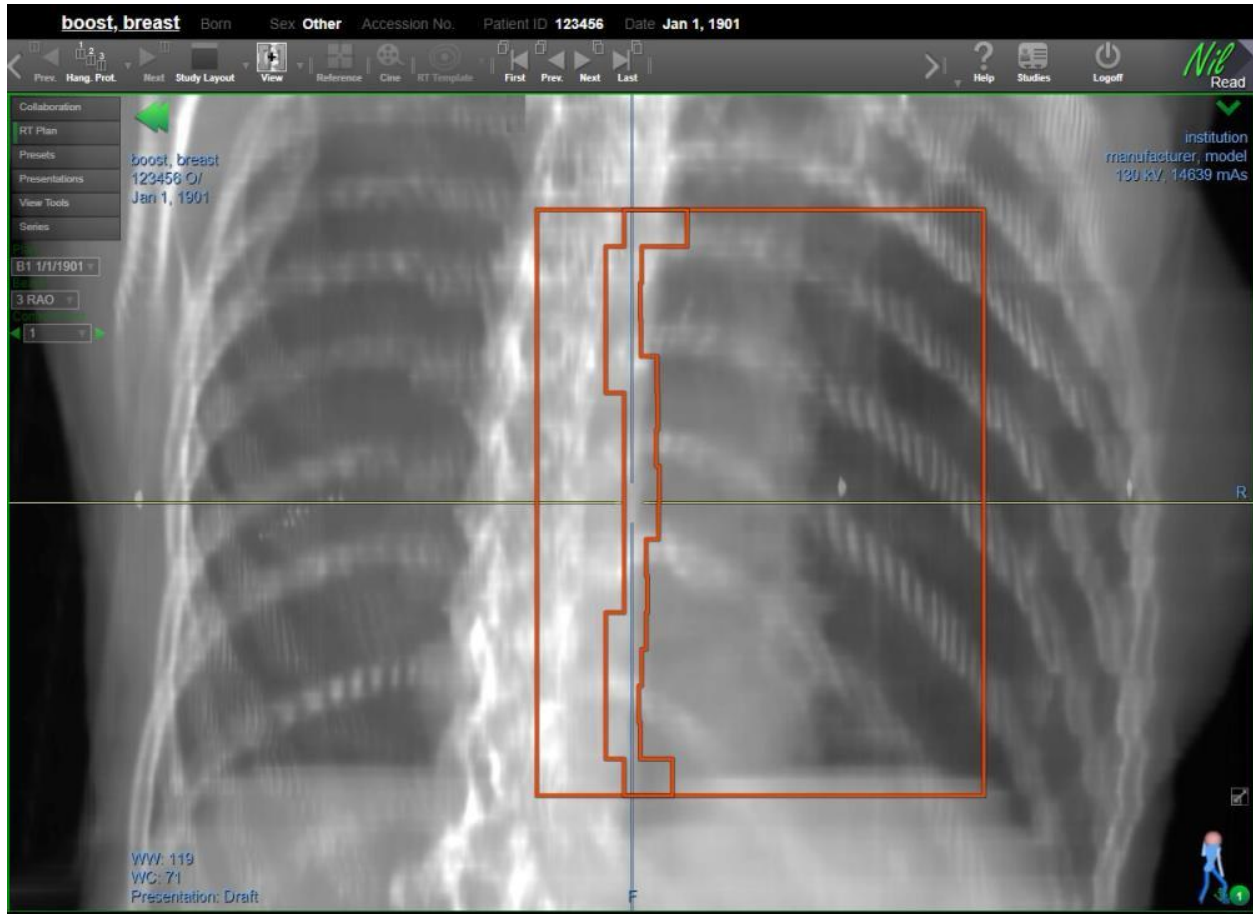
3. Select OK.

### Structure Color Options

You can change the color used for a structure. For details, see “Using the RT Plan panel” on page 112.

## Using the DRR view

The digitally reconstructed radiograph (DRR) view allows you to view the treatment field positions for a beam. The rectangle represents the jaw pairs and the area selected within the rectangle represents the multileaf collimators.

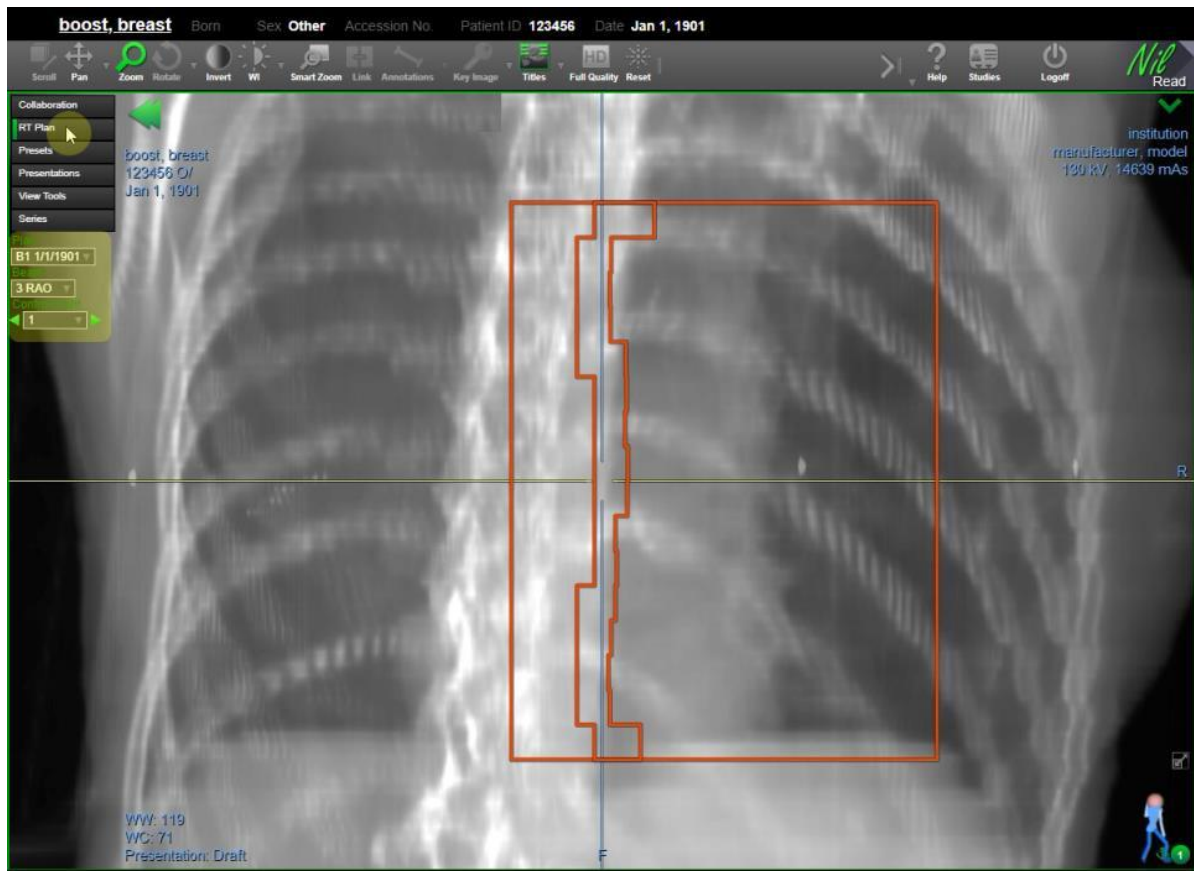


1. Select **View** (toolbar), then select **DRR**.

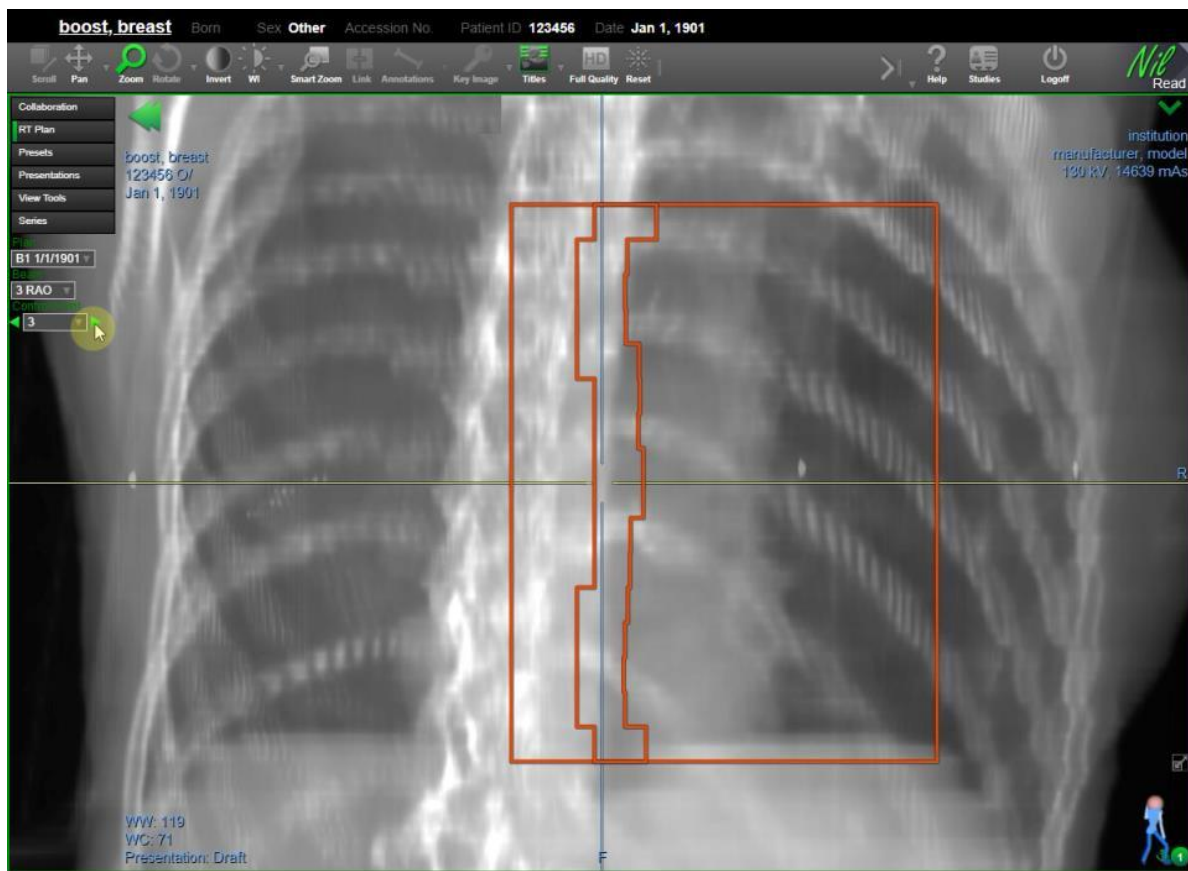
### Note

You can also use the study layout options to place the DRR view beside an existing view. For details, see "Arrange images" on page 57.

2. Select RT Plan (side panel). The RT Plan options appear below the side panel.



3. Select a plan, then select a beam. Optionally, select a beam control point. To switch between control points, select the previous and next arrows beside the control point list.



## Apply an RT template to a study

When you open a study containing RT plans, the appropriate RT template will be applied to the study (if one exists). You can also choose a template while viewing a study.

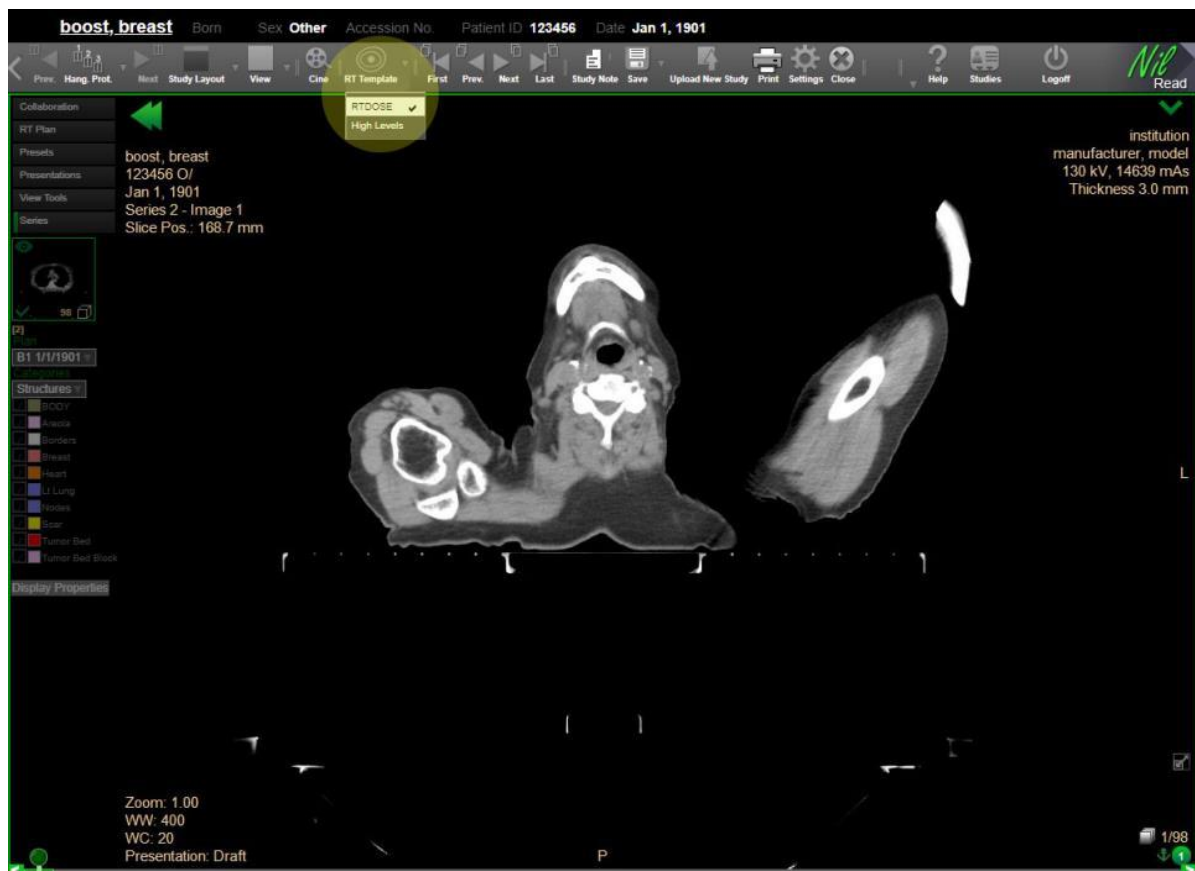
### Note

For details on creating templates, see "Manage RT templates" on page 138.

To apply a template to a study:

1. Select **RT Template** (toolbar). Any available templates for the current study are listed. A checkmark is shown beside the template currently applied to the study.





2. Select a template from the list. The template is applied to all viewports.

## Manage RT templates

You can create radiation therapy templates to control how information is displayed. For example, you can change contour colors, isodose levels, and the isodose unit of measurement.

1. Select **Settings**.
2. Under **Preferences**, select **Radiation Therapy Templates**.
3. A list of radiation therapy templates appears. Select **Refresh** at any time to refresh the list and view the latest changes made by all users.

## Add a template

1. Select **Add**. You can also select an existing template, then select **Clone**.
2. Enter the following information, then select **Save**.

### Template Info

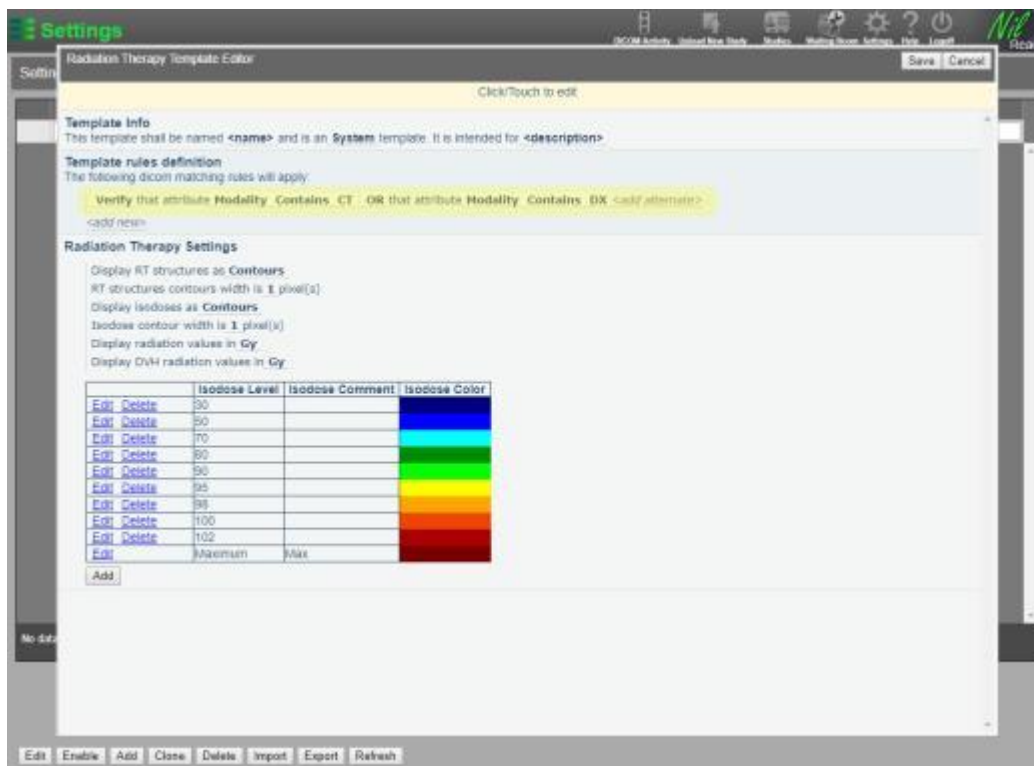
1. Enter a name for the template.
2. Select whether this is a **System**, **Group** or **User** template.  
A system template will be available to all users of NilRead, a group template will only be available to the group you specify, and a user template will only be available to the user you specify.
3. Enter a description for the template.

### Template Rules Definition

You can add rules that determine the types of studies the template applies to. For example, you could state that images must be a specific modality.

If you add multiple rules, the template can only be applied to studies that match all of the rules.

1. Select <add new> to add a new rule.
2. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.
3. Select <add alternate> to add an alternate value to a rule. The template can only be applied to studies that match at least one of these rules. For example, you could list several modalities the template can be used for.



4. To remove a rule, select **Verify** and switch to **Delete**.

### Radiation Therapy Settings

Select the default settings to apply to the study. These settings can be changed while viewing the study.

You can choose the following settings for displaying structures.

- Display as contours (outline) or filled contours (shaded).
- Select the width of the contour outline. Note that you cannot change the contour width for MPR images.

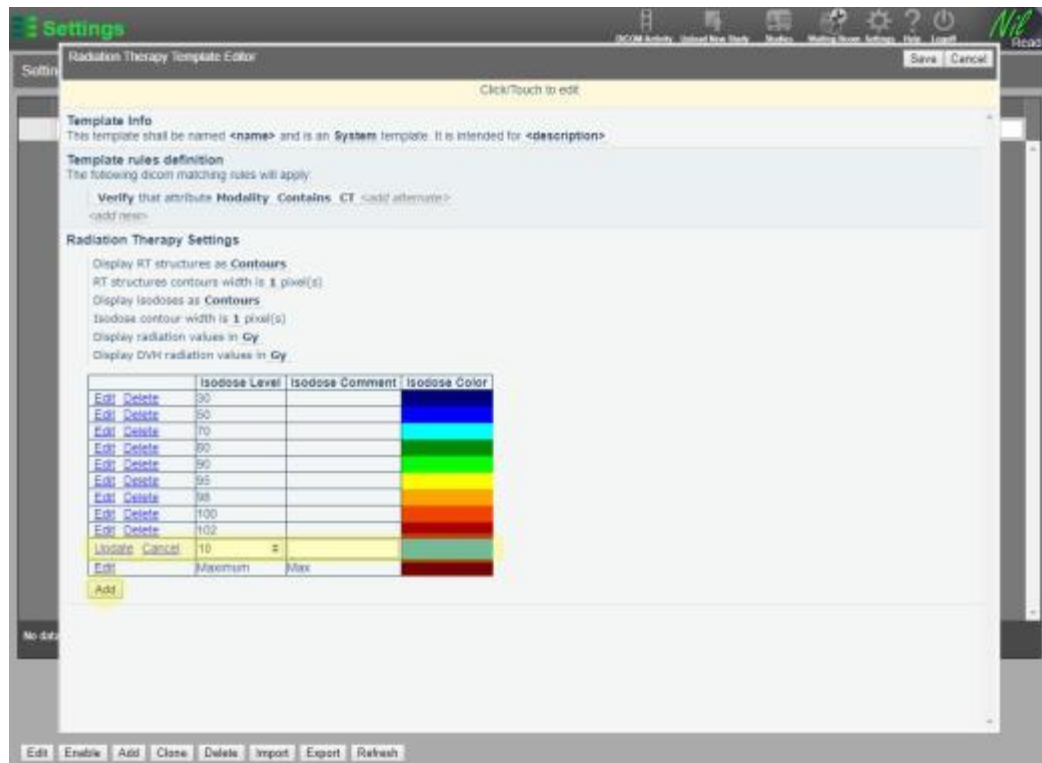
You can choose the following settings for displaying isodoses.

- Display as contours (outline) or filled contours (shaded).
- Select the width of the contour outline. Note that you cannot change the contour width for MPR images.
- Display radiation values as Gy or cGy. This unit of measurement will be used in the list of isodoses.
- Display DVH radiation values as Gy or cGy. This unit of measurement will be used in the RT Graph.

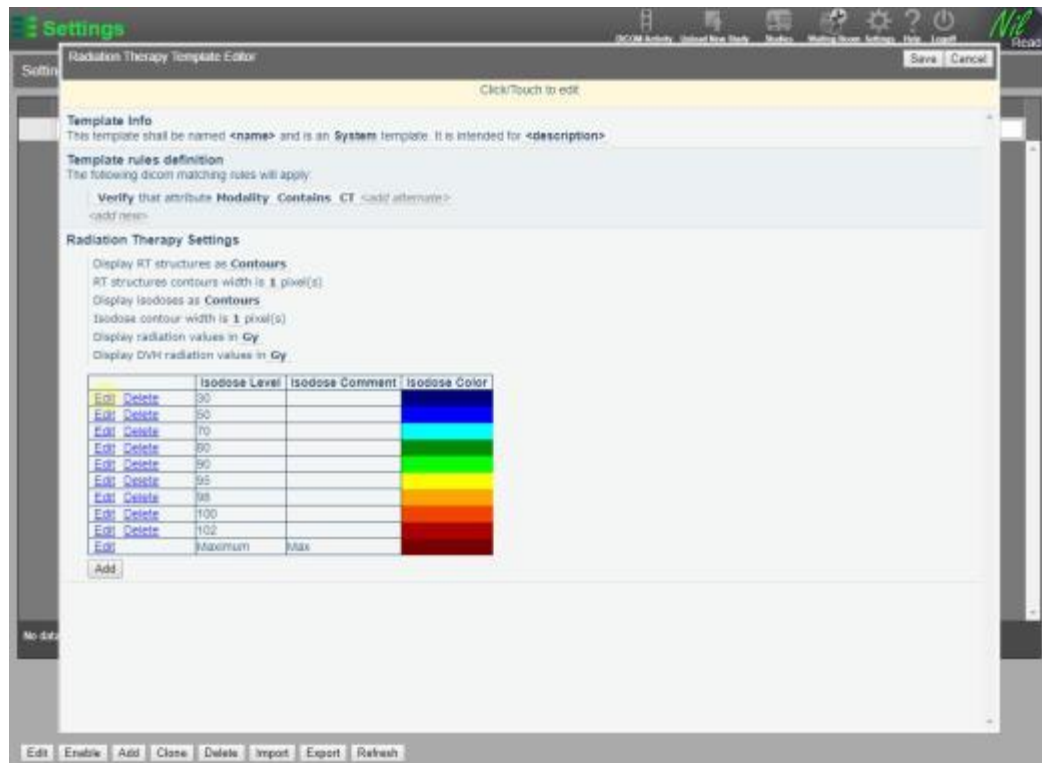
You can add, edit and delete the default isodose levels.

- To add a level, select **Add** below the isodose levels table. Enter the **Isodose Level** and select a color. Select **Update**.

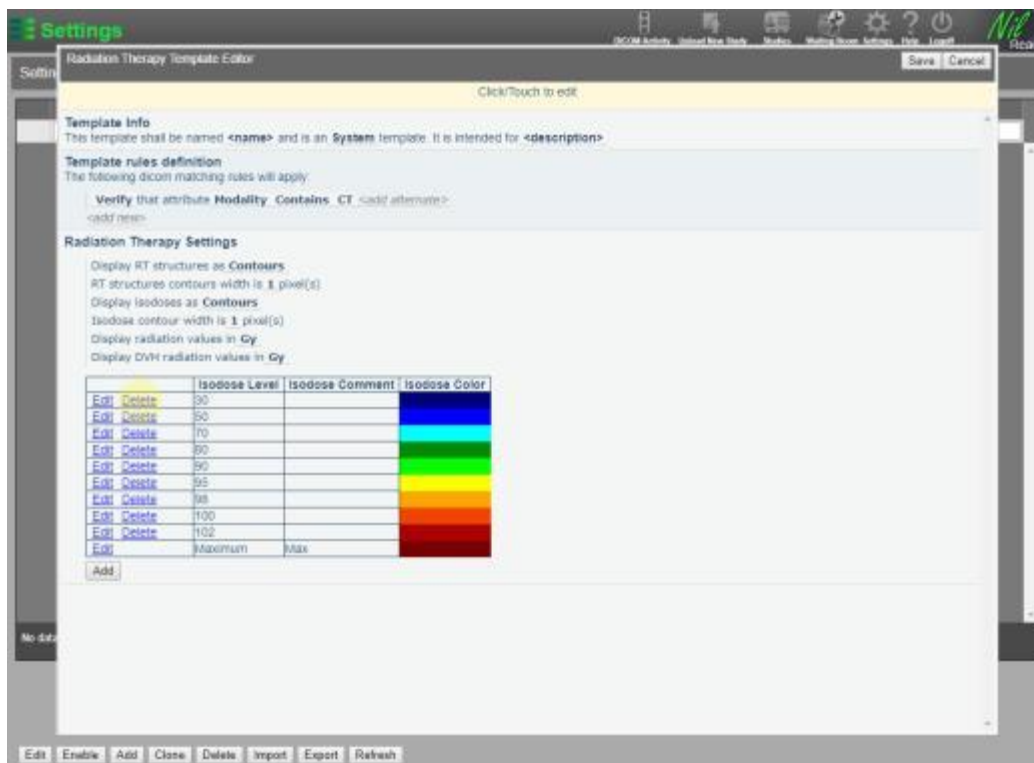
Note that the **Isodose Comment** is reserved for future use and information entered in this field will not appear in NilRead.



- To modify a level, select Edit beside the level. Enter the Isodose Level and select a color. Select Update.



- To delete a level, select Delete beside the level.



You can select a color to use for isodose levels that are above the maximum level set in the isodose levels table.

- Select Edit beside the Maximum level. Select a color, then select Update.

## Edit or delete a template

1. Select a template.
2. Select Edit. Modify the details, then select Save.  
or  
Select Delete.

## Enable a template

You must enable a template to make it available when viewing a study.

1. Select the Enabled checkbox beside a template. You can also select a template, then select Enable.
2. To disable a template, clear the Enabled checkbox beside the template.

## Import and export templates

To import a template:

1. Select **Import**.
2. Select a file to import, then select **OK**.

To export a template:

1. Select a template.
2. Select **Export**, then select **OK**. You will be prompted by your browser to save the file.

## 9. Anonymize patient data

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### About anonymization

NilRead supports anonymization of studies for research, clinical trials or any other workflow which requires patient confidentiality. Anonymization allows you to remove identifying and confidential patient information from studies.

To anonymize studies, do the following:

1. **Create confidentiality profiles** that define how patient data will be anonymized (see “Manage confidentiality profiles” on page 145). You can also use the default confidentiality profile, called Nominal.
2. (Optional) **Create confidentiality masks** that define regions of an image that contain patient data as part of the image. These areas will be redacted to obscure the patient data. Masks are only applied if enabled in the confidentiality profile.
3. **Assign a confidentiality profile to a worklist or folder** (see “Manage worklists” on page 155 and “Manage folders” on page 158). Patient data for studies in the worklist or folder will be anonymized when the study is viewed in the Patient Study Directory or the image viewer. This anonymization is temporary; the original study data is not modified.

#### Note

Studies are only anonymized when opened from a worklist or folder that contains the **Deidentify** option. Regular patient data will appear if a study is opened from the Patient Study Directory.

4. **Create a permanent anonymized copy of a study** by applying a confidentiality profile when downloading a study, series or image (see “Download studies, series or images” on page 81).

### Manage confidentiality profiles

You can create confidentiality profiles that define how patient data will be anonymized based on DICOM attributes. You can also use the default confidentiality profile, called Nominal, which is based on the DICOM standard “PS3.15 Table E.1-1. Application Level Confidentiality Profile Attributes”. For details, see <http://dicom.nema.org/standard.html>.

You can then assign a confidentiality profile to a worklist or folder (see “Manage worklists” on page 155 and “Manage folders” on page 158). Patient data for studies in the worklist or folder will be anonymized when the study is viewed in the Patient Study Directory or the image viewer. This anonymization is temporary; the original study data is not modified.



#### Note

Studies are only anonymized when opened from a worklist or folder that contains the **Deidentify** option. Regular patient data will appear if a study is opened from the Patient Study Directory.

You can also create a permanent anonymized copy of a study by applying a confidentiality profile when downloading a study (see “Download studies, series or images” on page 81).

## Add a confidentiality profile

1. Select **Settings**.
2. Under **Preferences**, select **Confidentiality Profiles**.
3. Select **Add**. You can also select an existing profile and select **Copy**.
4. Enter the following information:
  - **Name** Profile name.
  - **Comment** Profile description.
  - **Enabled** If selected, the profile can be used to anonymize data.

#### Note

To use a profile, you must assign it to a worklist or folder (see “Manage worklists” on page 155 and “Manage folders” on page 158) or select the profile when downloading a study (see “Download studies, series or images” on page 81).

- **Apply Masks** If selected, confidentiality masks may be used to redact patient data (see “Manage confidentiality masks” on page 147).
  - **Options** Anonymization options for the profile. To add options to the profile, select one or more options in the **Disabled** area, then select **Enable**. To remove an option, select an option in the **Enabled** area and select **Disable**.
  - **Details** DICOM attributes that will be anonymized by this profile. The action that will be applied to each attribute is shown. If you do not want to anonymize an attribute, select the **Disabled** checkbox beside the attribute.
5. Select **Save**.

## Edit or delete a confidentiality profile

1. Select **Settings**. Under **Preferences**, select **Confidentiality Profiles**.
2. Select a profile.
3. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Refresh the confidentiality profiles list

1. Select **Settings**. Under **Preferences**, select **Confidentiality Profiles**.
2. Select **Refresh** to view the latest changes made by all users.

## Manage confidentiality masks

In addition to confidentiality profiles, you can create confidentiality masks that define regions of an image that contain patient data as part of the image. These areas will be redacted to obscure the patient data.

If you are using a confidentiality profile that has masks enabled, a confidentiality mask will be applied if a mask exists that matches all of the following study attributes: modality, manufacturer and (optionally) scanner model. See "Manage confidentiality profiles" on page 145.

## Add a confidentiality mask

1. Select **Settings**.
2. Under **Preferences**, select **Confidentiality Masks**.
3. Under the **Masks** area, select **Add**. You can also select an existing mask and select **Copy**.
4. Enter the following information:
  - **Name** Mask name.
  - **Comment** Mask description.
  - **Modality** Modality. The mask will only be applied to images with this modality.
  - **Manufacturer** Manufacturer. The mask will only be applied to images with this manufacturer.
  - **Model Name** (Optional) Scanner model. The mask will only be applied to images with this scanner model name.
  - **Height, Width** Height and width of the image (in pixels).
  - **Enabled** If selected, the mask can be used as part of a confidentiality profile. Clear this checkbox if you do not want NilRead to use this mask.
5. Select **Save**.

You can now define the regions of the image to be redacted (see the following section).

## Add regions to be redacted

You can add multiple regions to a mask.

1. Select **Settings**.
2. Under **Preferences**, select **Confidentiality Masks**.

3. In the **Masks** area, select a mask. The **Mask Regions** area shows the regions defined for the mask.
4. Under the **Mask Regions** area, select **Add**. You can also select an existing region and select **Copy**.
5. Enter the following information:
  - **Top** Top of the region to be redacted (in pixels).
  - **Left** Left side of the region to be redacted (in pixels).
  - **Width, Height** Height and width of the region to be redacted (in pixels).
6. Select **Save**.

### Edit or delete a confidentiality mask or region

1. Select **Settings**. Under **Preferences**, select **Confidentiality Masks**.
2. Select a mask or mask region.
3. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

### Refresh the confidentiality masks or regions list

1. Select **Settings**. Under **Preferences**, select **Confidentiality Masks**.
2. Select **Refresh** to view the latest changes made by all users.

## 10. Share studies

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### Use an online meeting

Online meetings allow you to collaborate with other physicians and interactively review a patient study. Meeting participants all see the same screen and can annotate images at the same time. The person who starts the meeting is the organizer.

#### Note

The displayed screen size may be reduced if a participant uses a small resolution device such as a phone.

### Start a meeting

1. Open a patient study.
2. Select **Collaboration** (side panel). The Collaboration tools appear below the side panel.
3. Select **Share**. The meeting control panel opens. You can drag the control panel to any location on the screen.
4. To invite participants, select **Invite** on the meeting control panel. A new email is created using your default email application. Enter the email addresses for the participants and any additional information, then send the email.

### Join a meeting

If you receive a meeting link by email:

1. Click (or tap) the link. The NilRead Waiting Room will open in your browser.
2. In the Waiting Room, enter the meeting ID and your name. Select **Join**.







If you are logged into NilRead, you can:

- In the Patient Study Directory, select **Waiting Room**. Enter the meeting ID and your name, then select **Join**.
- While viewing a patient study, select **Collaboration** (side panel), then select **Join**. Enter the meeting ID, then select **Join**.

### Use meeting controls

Participants currently in the meeting are shown in **Active Users** (below the side panel). The symbols beside a participant's name indicate if they are the meeting organizer (O) or the presenter currently in control of the meeting (P). \* is shown beside your own name.

You can use the following controls during an online meeting. Some controls are only available to the meeting organizer.




	<p><b>Transfer control</b></p> <p>The organizer can transfer control of the meeting to another participant. Only the participant in control is able to use the NilRead toolbar containing the image tools. To transfer control, select a participant from the <b>Control</b> list. The organizer can regain control by selecting their own name.</p>
	<p><b>Annotate images</b></p> <p>To draw on an image, select <b>Highlighter</b>. To add an arrow and note, select <b>Arrow</b>. Participants can annotate images at the same time. Annotations made by a participant are shown in the same color as the participant name in the <b>Active Users</b> list.</p>
	<p><b>Undo all</b></p> <p>Select <b>Undo all</b> to remove all annotations made by all of the meeting participants.</p>
	<p><b>Undo</b></p> <p>Select <b>Undo</b> to remove the last annotation made by any meeting participant.</p>
	<p><b>Invite others</b></p> <p>Select <b>Invite</b>. A new email is created using your default email application. Enter the recipient's email address and any additional information, then send the email.</p>
	<p><b>End meeting</b></p> <p>Select <b>Quit</b>. This can only be done by the meeting organizer.</p> <p><b>Note</b></p> <p>All annotations are removed from images when the meeting ends. If you want to save the image with annotations, capture the image before ending the meeting (see "Share secondary capture images" on page 153).</p>

## Use Skype

You can use Skype™ calls and instant messaging to communicate with other physicians associated with a study. You can initiate a Skype session at any time when viewing a study, including during an online meeting.

### Note

You can only initiate Skype sessions with physicians who are associated with your user profile (see “Manage your user profile” on page 177). Skype must be enabled in your user preferences (see “Change your user preferences” on page 168). Skype software must also be installed and running on participants’ devices.

1. Open a patient study.
2. Select **Collaboration** (side panel). The names of any physicians associated with both the study and your user profile are listed below  **Settings**.
3. Select  **Settings**. Select the type of Skype session:
  - **Call** Voice call. Note that you can enable video once the Skype session is in progress.
  - **Chat** Instant messaging.
4. To start a Skype session, select a physician below  **Settings**.
5. To search for a physician in the list:
  - a. Enter the physician’s first name, last name or NilRead user name in the **Search Users** field.
  - b. Select **Search**. Any matching physicians are shown below the **Search** button.
  - c. Select a physician to start a Skype session.

## Send study links

Share a patient study with others by sending them a link. Others will see the default view of the study, not the view you are using.

### Note

Depending on your organization’s NilRead configuration, users may require a login name and password for NilRead to view the study.

In the Patient Study Directory:

- Right-click (or touch and hold) a study, worklist or folder, then select **Send Study Link**. A new email is created using your default email application. Enter the recipient’s email address and any additional information, then send the email.

- Right-click (or touch and hold) a study, worklist or folder, then select **Copy Link**. A box appears with the link. Copy the link and paste it into an email or instant message.

## Send series links

Share a series of images with another user by sending them a link. The series specified in the link will open by default; however the entire study is still available to the user. Note that when you send a series link, the user will see the default view of the series, not the view you are using.

### Note

Depending on your organization's NilRead configuration, users may require a login name and password for NilRead to view the study.

1. Open a patient study.
2. Right-click (or touch and hold) a series, then select **Send Series Link**.
3. A new email is created using your default email application. Enter the recipient's email address and any additional information, then send the email.

## Share bookmarked images

Use a bookmark to tag an image in a patient study that you want to find again quickly or that you want to share with others.

### Create a bookmark

Select **Save**, then select **Bookmark** (toolbar). A bookmark is created for the current screen. Bookmarks are saved in the Presentations panel.

### View a bookmark

1. Select **Presentations** (side panel). Presentations and bookmarks for the study are shown below the side panel.
2. Select a bookmark thumbnail.
3. While viewing a bookmark, select **Series** (side panel) to see which series the image belongs to. The series is highlighted.

### Send a bookmark

Share a bookmarked image with others by sending them a link. Others will see the image as you do, including your annotations and visualization changes.

To send a bookmark, you can:

- Right-click (or touch and hold) a bookmark, then select **Email**. A new email is created using your default email application. Enter the recipient's email address and any additional information, then send the email.
- Right-click (or touch and hold) a bookmark, then select **Copy Link**. A window opens with the link text. Select and copy the link text. You can now paste the link into an email or instant message.

#### Note

Depending on your organization's NilRead configuration, users may require a login name and password for NilRead to view the study.

## Delete a bookmark

Right-click (or touch and hold) a bookmark, then select **Delete Bookmark**.

## Share secondary capture images

You can create a series of secondary capture images for a patient study. Secondary capture images are static screenshots and cannot be modified.

### Create a series of secondary capture images

Select **Save**, then select **Capture** (toolbar). A secondary capture image is created for the current screen and is added to a new series. Other secondary capture images created during this NilRead session will be added to the same series.

#### Note

If you create secondary capture images for the same study in a future session, the images will be saved in a new series.

### Share a series of secondary capture images

Share a series of secondary capture images with others by sending them a link.

1. Right-click (or touch and hold) a series thumbnail, then select **Send Series Link**.
2. A new email is created using your default email application. Enter the recipient's email address and any additional information, then send the email.

#### Note

Depending on your organization's NilRead configuration, users may require a login name and password for NilRead to view the study.



## Delete a series of secondary capture images

1. Select **Series** (side panel).
2. Right-click (or touch and hold) a series thumbnail, then select **Delete Series**.

## 11. Manage your preferences

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### Manage worklists

You can use a worklist to create a collection of studies that you want to view as a group. The studies in a worklist are selected based on the data source and conditions you set. For example, you could create a worklist that includes all studies with a specific modality that originate from a specific data source.


Every time you access a worklist, the worklist is automatically updated to include any new studies that meet the worklist conditions. The studies are not actually moved to the worklist; the worklist just provides you with an easy way to access them.

Worklists created by users with no administrative privileges are automatically private. Users with administrative privileges can also create public worklists that can be accessed by all NilRead users or assign worklists to specific users or groups.

#### Note

You can also use folders to create a group of studies (see “Manage folders” on page 158).

### Add a worklist

1. In the Patient Study Directory, select . You can also right-click (or tap and hold) an existing worklist, then select **Copy**.  
or  
Select **Settings**. Under **Preferences**, select **Work Lists and Folders**. Select **Add**. You can also select an existing worklist, then select **Copy**.
2. Enter the following information, then select **Save**.

#### Name

Worklist name.

#### Comment

Worklist description.

#### Default

Administrators only. Allows you to specify a default worklist for new users when logging in for the first time.

#### Folder

Do not select this option. This will create a folder instead of a worklist (see “Manage folders” on page 158).

### Deidentify

If selected, studies in this worklist will be anonymized when viewed in NilRead. Select **Nominal** to use the default anonymization profile or select a profile you have created (see "Manage confidentiality profiles" on page 145).

#### Note

Once the worklist is created, you cannot change the **Deidentify** option.

#### Note

Studies are only anonymized when opened from a worklist or folder with the **Deidentify** option. Regular patient data will appear if a study is opened from the Patient Study Directory.

### Groups

(Administrators only) Select the groups that can access the worklist. Note that this option is not available if no groups are currently defined.

### Users

(Administrators only) Select the users that can access the worklist. Note that if you do not have administrative privileges, any worklists you create will be private worklists that only you can access.

- To create a public worklist that all users can access, do not select any users.
- To create a private worklist for specific users, select one or more users in the **Unassigned** area, then select **Add**. These users will see the worklist in their **My Worklists** area. To remove a user's access, select a user in the **Assigned** area, then select **Remove**.

### Rule

Specify the rule for the worklist by adding one or more conditions. All conditions must be satisfied in order for a study to be included in the worklist.

1. Select **All Data Sources** to search all data sources when selecting studies for the worklist.

or

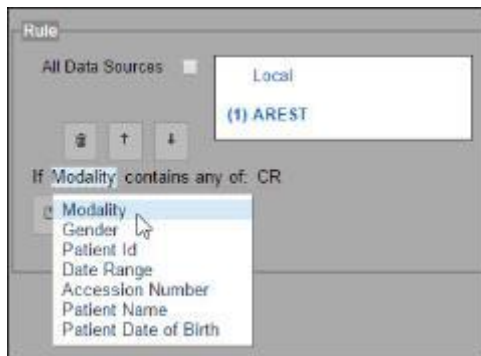
Select a data source from the list to select studies from this data source only.

Note that if a data source has any existing rules (from other worklists), the number of existing rules is shown before the data source name. When you select the data source, the existing rules are shown. In the following example, the data source "AREST" has two existing rules:

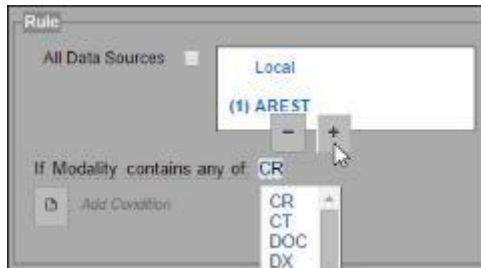



You can delete the existing rules if desired (see step 4).

2. Select **Add Condition**. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.



3. To add an item to a condition, select a customizable area, then select +. To remove an item, select -.



4. To delete a condition, select the first customizable area, then select .
5. To move a condition to a new position, select the first customizable area, then select



## Edit or delete a worklist

In the Patient Study Directory:

1. Right-click (or tap and hold) a worklist.

2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

In Settings:

1. Select **Settings**. Under **Preferences**, select **Work Lists and Folders**.
2. Select a worklist.
3. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Manage folders


You can use a folder to create a collection of studies that you want to view as a group. You select the specific studies you want to include in a folder. For example, you can use a folder to group studies that you want to review in a collaboration session with other users. The studies are not actually moved to the folder; the folder just provides you with an easy way to access them.

Folders created by users with no administrative privileges are automatically private. Users with administrative privileges can also create public folders that can be accessed by all NilRead users or assign folders to specific users or groups.

### Note

You can also use worklists to create a group of studies (see "Manage worklists" on page 155).

## Add a folder

1. In the Patient Study Directory, select . You can also right-click (or tap and hold) an existing folder, then select **Copy**.  
or  
Select **Settings**. Under **Preferences**, select **Work Lists and Folders**. Select **Add**. You can also select an existing folder, then select **Copy**.
2. Enter the following information, then select **Save**.

### Name

Folder name.

### Comment

Folder description.

### Default

Administrators only. Allows you to specify a default folder for new users when logging in for the first time.

### Folder

Select this option. This will create a folder instead of a worklist.

### Deidentify

If selected, studies in this folder will be anonymized when viewed in NilRead. Select **Nominal** to use the default anonymization profile or select a profile you have created (see "Manage confidentiality profiles" on page 145).

#### Note

Once the folder is created, you cannot change the **Deidentify** option.

#### Note

Studies are only anonymized when opened from a worklist or folder with the **Deidentify** option. Regular patient data will appear if a study is opened from the Patient Study Directory.

### Groups

(Administrators only) Select the groups that can access the folder. Note that this option is not available if no groups are currently defined.

### Users

(Administrators only) Select the users that can access the folder. Note that if you do not have administrative privileges, any folders you create will be private folders that only you can access.

- To create a public folder that all users can access, do not select any users.
- To create a private folder for specific users, select one or more users in the **Unassigned** area, then select **Add**. These users will see the folder in their **My Folders** area. To remove a user's access, select a user in the **Assigned** area, then select **Remove**.

## Edit or delete a folder

In the Patient Study Directory:

1. Right-click (or tap and hold) a folder.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

In Settings:

1. Select **Settings**. Under **Preferences**, select **Work Lists and Folders**.
2. Select a folder.
3. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Add studies to a folder

You can add the same study to multiple folders.

In the Patient Study Directory:

1. Right-click (or tap and hold) a study.
2. Select **File Study**, then select a folder.

## Remove studies from a folder

In the Patient Study Directory:

1. Select a folder.
2. Right-click (or tap and hold) a study.
3. Select **Remove from Folder**.

In Settings:

1. Select **Settings**. Under **Preferences**, select **Work Lists and Folders**.
2. Select a folder in the **Work Lists** area. The studies in the folder are shown at the bottom of the screen.
3. Select a study, then select **Remove**.

## Manage structured report templates

You can create different layouts for structured reports using templates.

1. Select **Settings**.
2. Under **Preferences**, select **Structured Report Templates**.
3. A list of structured report templates appears. Select **Refresh** at any time to refresh the list and view the latest changes made by all users.

## Add a template

1. Select **Add**. You can also select an existing template, then select **Clone**.
2. Enter the following information, then select **Save**.

### Template Info

1. Enter a name for the template.
2. Select whether this is a **System**, **Group** or **User** template.  
A system template will be available to all users of NilRead, a group template will only be available to the group you specify, and a user template will only be available to the user you specify.
3. Enter a description for the template.

### Template Rules

You can add rules that determine the types of studies the template applies to. For example, you could state that images must be a specific modality.

If you add multiple rules, the template can only be applied to studies that match all of the rules.

1. Select **<add new>** to add a new rule.
2. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.
3. Select **<add alternate>** to add an alternate value to a rule. The template can only be applied to studies that match at least one of these rules. For example, you could list several modalities the template can be used for.

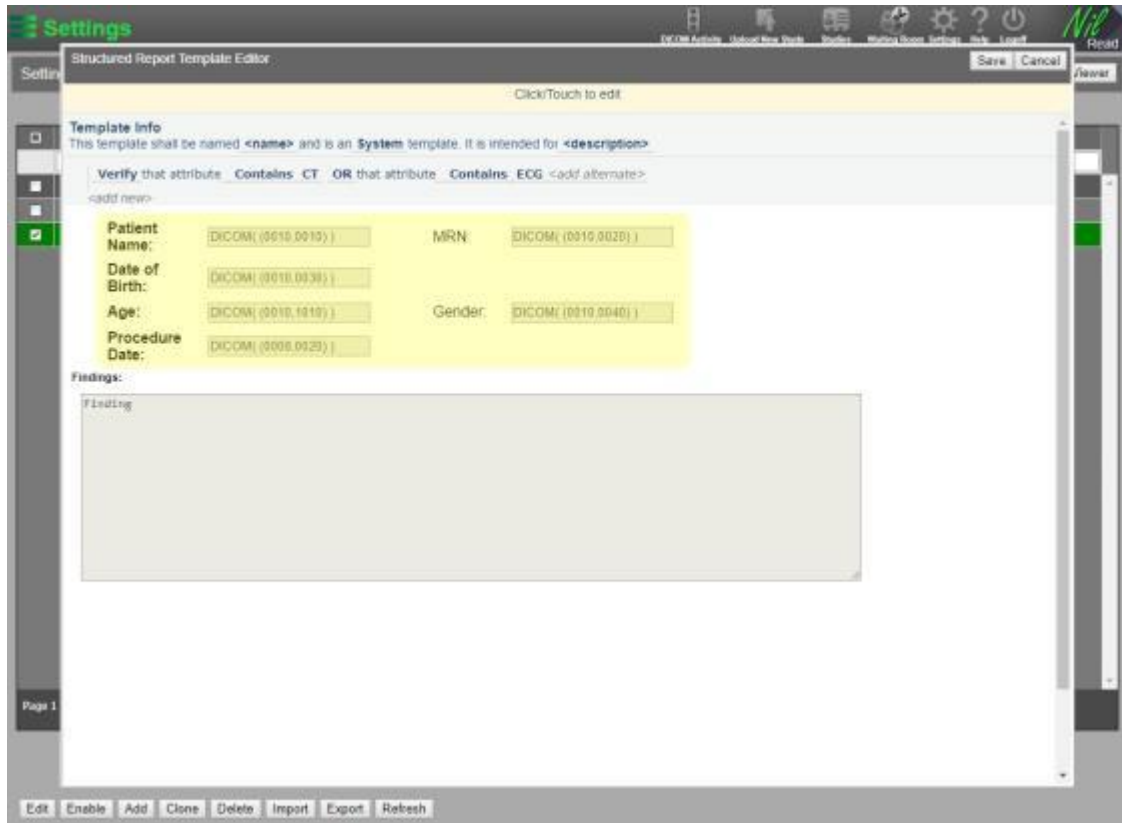
The screenshot shows the 'Structured Report Template Editor' window. At the top, it says 'Settings' and 'Structured Report Template Editor'. Below that, there's a 'Template Info' section with a description: 'This template shall be named <name> and is an System template. It is intended for <description>'. There's a rule: 'Verify that attribute: Contains: CT OR that attribute: Contains: EDG <add alternate>'. Below the rule, there are several fields for patient information: 'Patient Name', 'Date of Birth', 'Age', 'Procedure Date', 'MRN', and 'Gender'. Each field has a dropdown menu with DICOM codes. At the bottom, there's a 'Findings' section with a text area for 'Finding'. The interface includes a 'Save' button and a 'Cancel' button at the top right. At the bottom, there are buttons for 'Edit', 'Enable', 'Add', 'Close', 'Delete', 'Import', 'Export', and 'Refresh'.



4. To remove a rule, select **Verify** and switch to **Delete**.

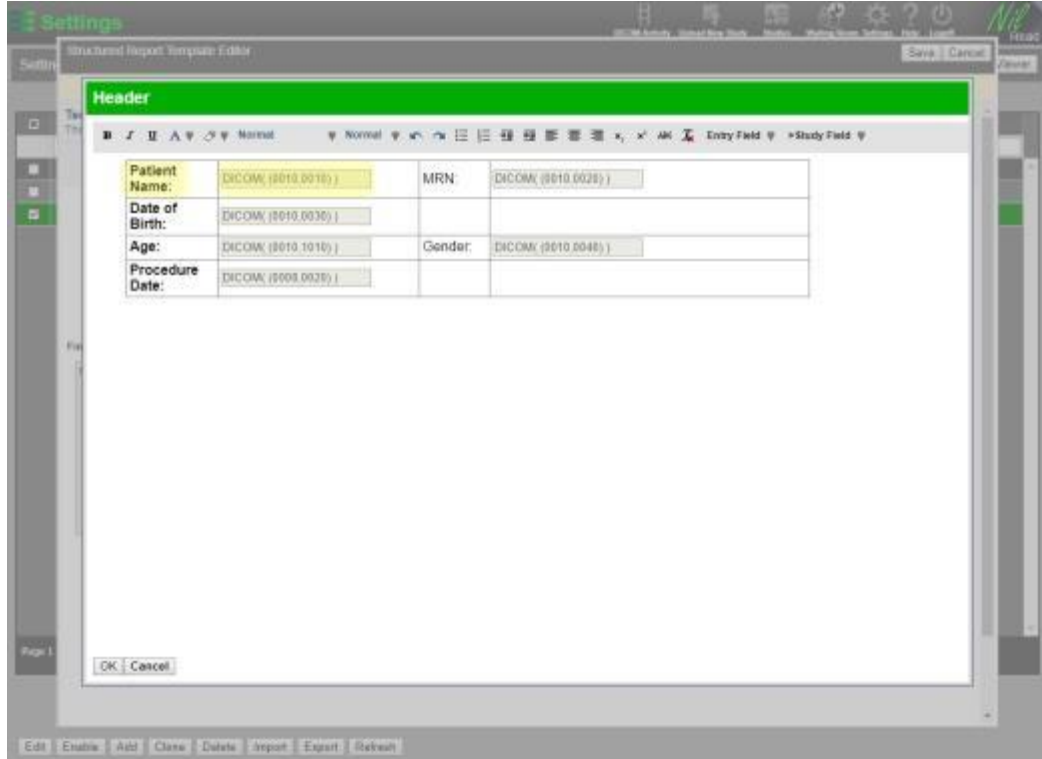
### Study Information Header

You can add study information to the header area at the top of the report. This information is taken from the study's DICOM attributes and cannot be edited in the report. Several default fields are provided by default.



You can add and remove fields in the **Header** area.

1. Click (or tap) the **Header** area. The **Header** window appears.  
The default fields are arranged in a table with the field label on the left and the field value on the right.



2. To add a new label and field:
  - a. Click (or tap) in an empty table cell and type a label.
  - b. Click (or tap) in the adjacent cell. Select **Study Field**, then select a DICOM attribute.
3. To remove a label or field, use the BACKSPACE or DELETE key.
4. You can use the toolbar options to format your text (color, font, etc.).
5. Click OK to save your changes.

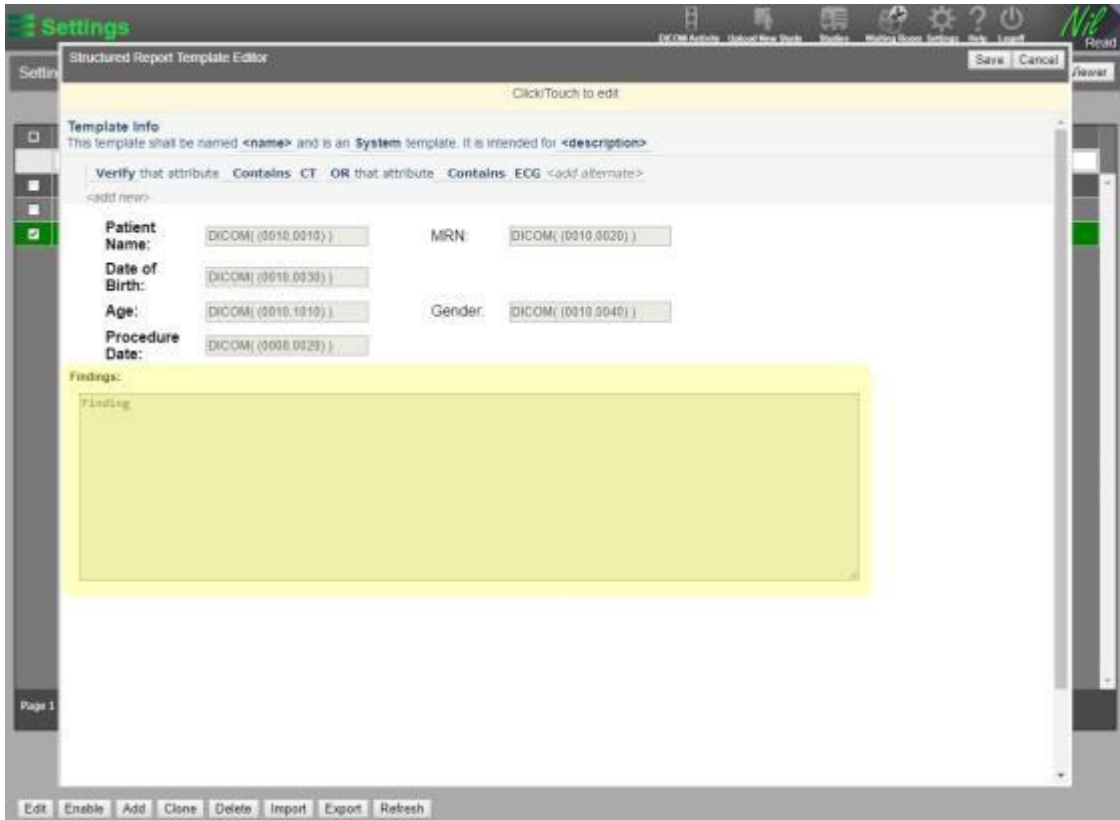
You can add an asset to the **Header** area. An asset is an item you would typically include on all templates, such as your logo. Saving a file as an asset allows you to quickly add it to any structured report template for your site.

For details on creating assets, see [Managing structured report assets](#).

1. To place an asset before the fields table, place your cursor before the table, then press ENTER.  
or  
To place an asset after the fields table, place your cursor after the table, then press ENTER.
2. Select the **Entry Field** list, then select **Asset**.
3. Select an asset, then select **Add to Template**.

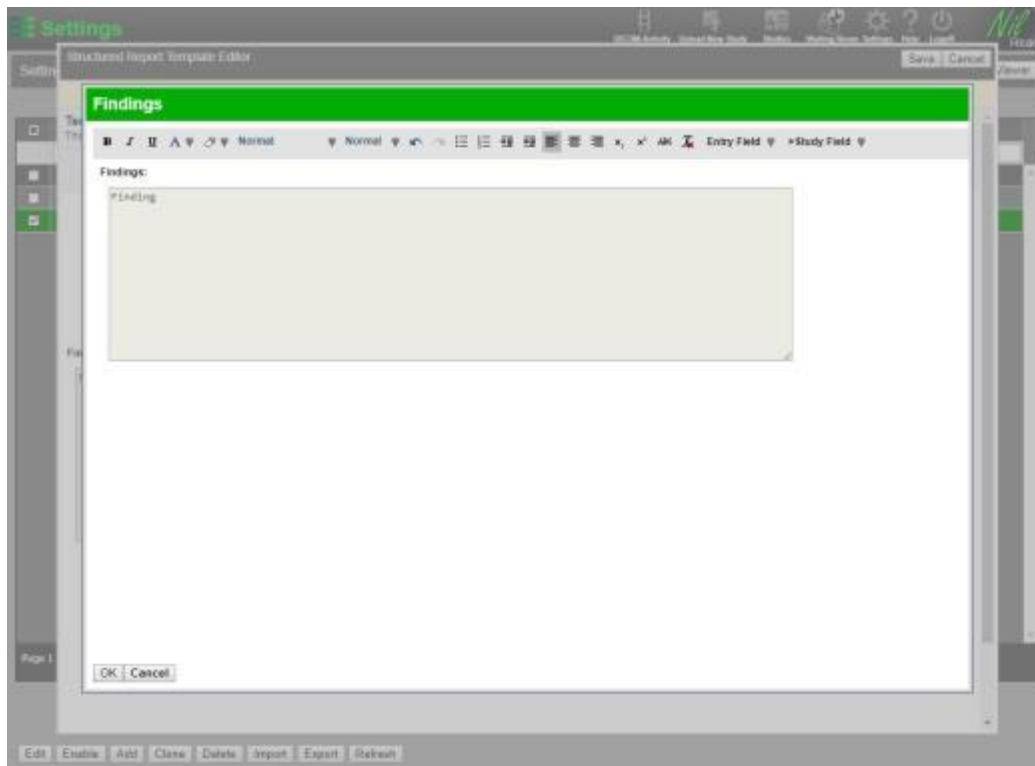
## Findings Area

By default, the Findings area contains a single text box where comments can be entered for the report.



To modify the Findings area:

1. Click (or tap) the Findings area. The Findings window appears.



2. To add an item, select an option from the **Entry Field** list. For example, you can add text entry areas, checkboxes and drop down lists. You can also add an image placeholder which is used to display key images in the study.
3. To remove an item, use the BACKSPACE or DELETE key.
4. You can use the toolbar options to format your text (color, font, etc.).
5. Click OK to save your changes.

## Edit or delete a template

1. Select a template.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Enable a template

You must enable a template to make it available when viewing a study.

1. Select the **Enabled** checkbox beside a template. You can also select a template, then select **Enable**.

2. To disable a template, clear the **Enabled** checkbox beside the template.

## Import and export templates

To import a template:

1. Select **Import**.
2. Select a file to import, then select **OK**.

To export a template:

1. Select a template.
2. Select **Export**, then select **OK**. You will be prompted by your browser to save the file.

## Manage structured report assets

You can add assets to your structured report templates. An asset is an item you would typically include on all templates, such as your logo. Saving a file as an asset allows you to quickly add it to any structured report template for your site.

1. Select **Settings**.
2. Under **Preferences**, select **Assets**.
3. A list of assets appears. Select **Refresh** at any time to refresh the list and view the latest changes made by all users.

## Add an asset

1. Select **Create**. Enter the following information.
  - **Cluster** Leave this field blank.
  - **Name** Name to identify the asset.
  - **Value** You can enter **Text** or select an **Image**.
2. Select **Save**.

## Edit or delete an asset

1. Select an asset.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Change your workstation preferences

You can set preferences for your NilRead workstation.

### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

1. Select **Settings**.
2. Under **Preferences**, select **Workstation Preferences**.
3. Select your preferences, then select **Save**.

### Connection Type

Default connection type to access NilRead. (You can select a different option when logging in.) NilRead uses different compression polices based on the selected connection type to provide both interactive performance and image quality.

- **Internet** Connection speed is under 4 Mbps.
- **Fast Internet** Connection speed is between 4 and 10 Mbps.
- **Local network** Connection speed is over 10 Mbps.
- **Auto detect** Allow NilRead to detect the network connection.

Select **Speed Test** to check your NilRead connection speed.

### Session Settings

Select the session timeout period. You will be logged out if your NilRead session is inactive for this amount of time.

- **Default** Use the default timeout period.
- **Workstation** Select a different timeout period. Select **Workstation**, then select a **Session Timeout** period.

### User Interface Size

View NilRead using the default interface size (100%) or a larger size (150%). If using a larger size, you can also choose to enlarge the patient directory.

### Image view controls

Whether the patient timeline and side panel are always visible in the image viewer. If this preference is enabled, the option to hide these items will be hidden.

### Desktop Touch UI

Whether the NilRead desktop touch interface is enabled. Select this option if you are using a desktop operating system with touch features.

### Viewer Monitor Type

Whether you are using a color or grayscale monitor.

### Monitors

Virtual monitor layout. Select a layout based on the number of monitors you are using. Using multiple monitors allows you to display the Patient Study Directory on one monitor and the image viewing area on the remaining monitors. Note that this option is not available for all browsers.

## Change your user preferences

You can set your preferences for using NilRead.

### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

1. Select **Settings**.
2. Under **Preferences**, select **User Preferences**.
3. Select your preferences, then select **Save**.

### Series Navigation

Behaviour when scrolling through the series in a study.

- **Move By One** Update the selected viewport only.
- **Move By Group** Update all viewports.

### Magnify Glass

Default magnifying glass size and zoom factor for smart zoom (see "Smart Zoom" on page 26).

### Skype Enabled

Whether other meeting participants can contact you using Skype.

### Skin

NilRead skin (dark or light).

### Preferred Language

Language to use for the NilRead application.



### Measurement Settings

Default settings for measurement tools (see "Annotations and measurements" on page 28).

- **Microscopy Measurement Units** Units used for microscopy measurements. Applies to all measurement tools.
- **Ruler label placement** Placement of the label on the ruler measurement tool.
- **Cursor Options** Information to show for the cursor tool. You can choose to show the cursor location and pixel value.
- **Angle Between Rulers** Whether to show the angle between two intersecting lines created with the ruler measurement tool.
- **ROI Threshold Default (SUV)** Default threshold value for ROI threshold measurements.

### Measurement Patterns

Pre-defined patterns for the area measurement tools (see “Annotations and measurements” on page 28). You can also create new patterns.

1. Select **Add Pattern**.
2. To customize the pattern, select any of the underlined areas and choose an option. (Customizable areas are highlighted when you hover over them.)
3. To delete a pattern, select the first customizable area, then select .
4. To move a pattern to a new position, select the first customizable area in the pattern, then select . The patterns will be shown in the Annotations and Measurement tool in the order defined here.

## Change mouse and keyboard preferences

You can assign NilRead tools (such as zoom and scroll) to mouse buttons, keyboard shortcuts and touch gestures. This allows you to quickly access tools you use frequently.

Customizing mouse, keyboard, and touch actions involves two steps:

1. Create templates that define the tools assigned to mouse buttons, keyboard shortcuts and touch gestures.
2. Select the mouse, keyboard and touch templates you want to use when working in NilRead.

### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

### Add a template

1. Select **Settings**.
2. Under **Preferences**, select **Mouse, Keyboard and Tools**.



3. Select the **Templates** tab.
4. Select **Add**. You can also select an existing template, then select **Clone**.  
The Mouse, Keyboard and Tools Template Editor opens. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.
5. Enter the following information, then select **Save**. The template is added to the **Templates** tab.

#### Template Info

1. Enter a name for the template.
2. Select whether this is a **Mouse**, **Keyboard** or **Touch** template.
3. Enter a description for the template.

#### Template Rules Definition

Select the tools you want to assign. Depending on the type of template, you can assign tools to the mouse buttons and scroll wheel, create keyboard shortcuts, or assign tools to gestures.

Default tools are already assigned. To change a tool:

1. Click (or tap) the tool. A list appears with available tools you can choose from.
2. Select a tool from this list or search for a tool.

### Edit or delete templates

1. On the **Templates** tab, select a template.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

### Select a template to use in NilRead

Create definitions that specify the templates you want to use in NilRead. For example, you could create different definitions for mouse, keyboard and touch gestures. You can also use different keyboard shortcuts for different devices.

1. Select the **Definition** tab.
2. Select **Add**. You can also select an existing definition, then select **Clone**.  
The Mouse, Keyboard and Tools Template Editor opens. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.
3. Enter the following information, then select **Save**. The definition is added to the **Definition** tab and is enabled by default, meaning it will be applied to NilRead. To disable the definition, clear the **Enabled** checkbox.

### Protocol Info

1. Enter a name.
2. Select whether this is a **System**, **Group** or **User** protocol. A system protocol will be applied to all users of NilRead. A group protocol will only be applied to the group you specify (enter the group name). A user protocol will only be applied to the type of user you specify (enter **Admin**, **User**, or **Guest**).
3. Select whether this is a **Mouse and Touch** protocol or a **Keyboard** protocol.
4. Select the view mode and modality the protocol applies to.

### Mouse

1. Select <add new>.
2. Select <pick> and select a mouse template.
3. You can select <add new> again and add additional mouse templates.
4. To remove a mouse template, select **Cycle** to switch to **Delete**.

### Touch

Select <pick> and select a touch template.

### Keyboard

1. Select which devices these keyboard assignments apply to.
2. Select <pick> and select a keyboard template.

## Edit or delete definitions

1. On the **Definition** tab, select a template.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Change tool preferences

You can customize the tools that appear in the toolbar, Annotations menu and image viewer context menu. This allows you to quickly access tools you use frequently.

Customizing tools involves two steps:

1. Create templates that define the tools assigned to the toolbar, Annotations menu and image viewer context menu.
2. Select the tool templates you want to use when working in NilRead.

#### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

## Add a template

1. Select **Settings**.
2. Under **Preferences**, select **Mouse, Keyboard and Tools**.
3. Select the **Templates** tab.
4. Select **Add**. You can also select an existing template, then select **Clone**.  
The **Mouse, Keyboard and Tools Template Editor** opens. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.
5. Enter the following information, then select **Save**. The template is added to the **Templates** tab.

### Template Info

1. Enter a name for the template.
2. Select **Tools** template.
3. Enter a description for the template.

### Template Rules Definition

a) Customize the placement of the tools in the toolbar.

Note that tools must be placed in a group. The tools in a group will be placed beside each other in the toolbar. To add a new group, select **Add Group** below the **Fixed Controls** or **Scrolling Controls** box.

To add or rearrange tools in the toolbar, drag a tool or a group of tools to the **Fixed Controls** or **Scrolling Controls** box.

- **Fixed Controls** contains tools that will also be visible on the left side of the toolbar and will not scroll. Note that if you have too many fixed controls, you may not be able to see all of the tools if your browser window size is reduced.
- **Scrolling Controls** contains tools that will scroll if there is not enough room to display all of the tools at once.

To remove a tool from the toolbar, drag the tool to the **Unassigned Controls** box.

b) Customize the annotations tools.

- To rearrange the annotation tools, drag a tool to a new position in the **Active Annotations** box.
- To remove an annotation tool, drag the tool to the **Available Annotations** box.
- To add an annotation tools, drag the tool to the **Active Annotations** box.

c) Customize the image viewer context menu. This menu appears when you right-click (or touch and hold) an image.

- To rearrange the menu items, drag a menu item to a new position in the **Context Menu Items** box.
- To remove an item from the menu, drag the item to the **Unused Menu Items** box.
- To add an item to the menu, drag the item to the **Context Menu Items** box.
- To add a submenu, select **Add Submenu**. Enter a name and select **OK**. Drag the submenu from the **Unused Menu Items** box to the **Context Menu Items** box. You can now drag other menu items into the submenu list.
- To delete a submenu, right-click (or touch and hold) the submenu, then select **OK**.
- To add a separator line, select **Add Separator**. Drag the separator from the **Unused Menu Items** box to the **Context Menu Items** box.
- To remove a separate line, drag the line to the **Unused Menu Items** box.

## Edit or delete templates

1. On the **Templates** tab, select a template.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Select a tool template to use in NilRead

Create definitions that specify the tool templates you want to use in NilRead for different devices.

1. Select the **Definition** tab.
2. Select **Add**. You can also select an existing definition, then select **Clone**.  
The Mouse, Keyboard and Tools Template Editor opens. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.
3. Enter the following information, then select **Save**. The definition is added to the **Definition** tab and is enabled by default, meaning it will be applied to NilRead. To disable the definition, clear the **Enabled** checkbox.

### Protocol Info

1. Enter a name.
2. Select whether this is a **System**, **Group** or **User** protocol. A system protocol will be applied to all users of NilRead. A group protocol will only be applied to the group you specify

(enter the group name). A user protocol will only be applied to the type of user you specify (enter **Admin**, **User**, or **Guest**).

3. Select **Tools**.

#### Tools

1. Select which devices this toolbar configuration applies to.
2. Select **<pick>** and select a tools template.

### Edit or delete definitions

1. On the **Definition** tab, select a template.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Change window level presets

You can change the window level presets for different modalities. These presets appear in the **Presets** side panel when viewing a study.

#### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

1. Select **Settings**.
2. Under **Preferences**, select **Modality Preferences**.
3. Enter the following information, then select **Save**.

#### Modality

Select the modality that you want to set preferences for.

#### Window Level Presets

In the **Scope** area, select the presets you want to modify.

- **SiteDefaults** Default site presets. Select this option if you want to modify the default presets for all users of the site.
- **User** Your presets. Select this option if you want to modify your presets only.

You can modify the values for a preset.

1. Select **Edit** beside the preset.

2. Change the values, then select **Save** beside the preset. Select **Cancel** to discard your changes.

You can change the order of the presets in the side panel.

- Select the up or down arrow beside a preset to move the preset to a new position in the list.

## Change modality preferences

You can change NilRead settings for different modalities.

### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

1. Select **Settings**.
2. Under **Preferences**, select **Modality Preferences**.
3. Enter the following information, then select **Save**.

### Modality

Select the modality that you want to set preferences for. The changes you make on the Modality Preferences page will only affect studies containing this modality. Select **All** to apply the changes to all modalities. Note that if you set a preference for an individual modality, this will override the same preference set for all modalities.

### Series Navigation

Determines the behavior of the Scroll tool for the modality you selected. By default, the Scroll tool will scroll through images in the current series only.

- **None** Scroll through the current series only.
- **Single Frame Only** Scroll through all of the series in the study. When advancing to the next series, scroll through single frame images only (omit multiframe images).
- **All** Scroll through all of the series in the study. When advancing to the next series, scroll through all images (single frame and multiframe).

### Virtual Series

Determines whether a virtual series is automatically created for a study (see "Create a series with all images" on page 48).

- Select **Yes** to automatically create virtual series for the modality you selected.
- Select **No** if you do not want to create virtual series for the modality you selected.

### Zoom Policy

Determines the behavior of the Zoom tool for the modality you select.

- **Zoom at center** Zoom will be applied at the center of the viewport, regardless of where you click (or tap) on the image with the Zoom tool.
- **Relative zoom at mouse position** Zoom will be applied at the point where you click (or tap) on the image with the Zoom tool. This is the default setting for mammography images.

### Old Study Warning

A warning is displayed in the viewport if an image is older than the specified number of days. The default value for mammography images is 365 days. The default value for other modalities is 0, meaning a warning will not be displayed.

### Cine Sequence

Determines whether cine sequences are played automatically when the cine sequence is loaded in the viewport.

## 12. Manage your account



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### Manage your user profile

You can manage information in your user profile. You cannot change information such as your username and privileges.

#### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

1. Select **Settings**.
2. Under **User Management**, select **Profile**.
3. Change information in the **Account** area.
  - **User Name** Username to login to NilRead. This information cannot be modified.
  - **Role** NilRead role (Admin, User, Guest). This information can be modified by Administrators only. By default:
    - Guests have no privileges.
    - Users have basic privileges, such as accessing the Patient Study Directory.
    - Administrators have full privileges. Only Administrators can manage users.
  - **Email** Email address.
  - **Skype ID** Skype ID. Allows the user to participate in Skype sessions.
  - **Phone** Phone number.
  - **Facility, Department, Job Description** User's facility and job information.
  - **Notify on Study Arrival** User will receive an email when a new study containing one of the user's DICOM person name matches is added to the database.
  - **Last Name, First Name, Middle Name, Prefix, Suffix** User's name.
  - **Expiry Date** Date the user's access to NilRead will expire. This information can be modified by Administrators only.
    - Select  and select an expiry date. Select whether the user's account will be locked or deleted on the expiry date.
    - Select  to remove the expiry date and set the user's access to **Unlimited**.
4. Change your password.
  - a. Select **Change Password**.
  - b. Enter your current password (**Old**). Enter your new password (**New, Confirm**).



- c. Select OK.
5. The **Groups** area contains the groups you belong to. This information cannot be modified.
6. The **Privileges** area contains your privileges. This information cannot be modified.
7. Select OK.

## Change your password

You can change the password you use to login to NilRead.

### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

1. Select **Settings**.
2. Under **User Management**, select **Profile**.
3. Select **Change Password**.
4. Enter your password:
  - a. **Old** Enter your current password.
  - b. **New, Confirm** Enter your new password.
  - c. Select OK.
5. Select OK.

## 13. Manage users

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### About user privileges

#### ADMINISTRATORS ONLY

You can manage NilRead user privileges at several levels. This allows you to tightly control user access to NilRead features and the Patient Study Directory. A user's privileges are initially based on their role and group assignment; these are both assigned in the user's account. The user's privileges can then be customized through their account.

#### Note

Users must be assigned the StudyListAccess privilege in order to access the Patient Study Directory. For details, see "Privilege descriptions" on page 180.

#### Role

Users are assigned default privileges based on their role (Admin, User or Guest). This role is assigned in the user's account.

- **Administrators** typically have full privileges for NilRead use and configuration; only Administrators can manage NilRead users. By default, Administrators have full privileges.
- **Users** are regular NilRead users. Users typically have access to the entire Patient Study Directory.
- **Guests** are occasional NilRead users, such as external referring physicians. Guests can typically only see studies for their own patients. Guests can access emergency override ("break glass"). By default, Guests have no privileges.

For more information, see "Manage user accounts" on page 183.

#### Group

Users are also assigned the default privileges of the group to which they belong. This group is assigned in the user's account. For details on setting up groups, see "Manage user groups" on page 182.

#### Account

User privileges can be customized in the user's account. The default privileges inherited from the user's role and group can be changed and additional privileges can be assigned. For more information, see "Manage user accounts" on page 183.

## Profile

**Administrators** can manage their privileges using their profile. **Guests** and **Users** can only change settings such as their name, email address and password. For more information, see “Manage your user profile” on page 177.

## Privilege descriptions

### ADMINISTRATORS ONLY

The following privileges can be assigned to a group or user.

- **AutoEnroll** Automatically create NilRead user accounts for members of a Windows group on their first login.
- **BookmarkSaveSend** Create and share a bookmark.
- **Collaboration** Access collaboration tools.
- **CreateAccounts** Create new NilRead user accounts.
- **ContentDownload** Download DICOM files using NilFeed.
- **ContentUpload** Upload DICOM files using NilFeed.
- **DicomClearLogs** Remove logs from the DICOM Activity page (see “Monitor DICOM patient study transfers” on page 203).
- **DicomConfig** Manage DICOM services (see “Manage DICOM services” on page 203).
- **DicomConfigEdit** Edit DICOM configuration.
- **DicomDelete** Remove DICOM services from the database (see “Manage DICOM services” on page 203).
- **DicomPrint** Manage DICOM printers.
- **DicomQueryRetrieve** Access the Search tab in the Patient Study Directory and retrieve patient studies from a DICOM server (see “Retrieve studies to the local database” on page 201).
- **DicomRT** Enables protocol support and tools for DICOM RT studies.
- **DicomStore** Access the DICOM store features.
- **EditAnonTemplates** Create, modify and delete anonymization profiles and masks.
- **EditHangingProtocols** Create, modify, delete and enable/disable user hanging protocols.
- **EditPatientStudy** Edit patient-level and study-level DICOM attributes.
- **EditSystemHangingProtocols** Create, modify, delete and enable/disable system hanging protocols.
- **EditWorkItems** Create, modify and delete worklists and folders.
- **EmergencyOverride** Use emergency override (“break glass”) to access patient studies (see “Use “Break Glass” to find studies” on page 76). NilRead guest users typically have limited access to

the Patient Study Directory. However, guests may be given access to emergency override ("break glass") which allows them to search for studies based on patient name and study accession number. For example, a referring physician may only have access to studies containing his own name. If the referring physician's name is misspelled or missing from a study, he will be unable to access the study using the Patient Study Directory. However, the referring physician can search for the study if he has been granted the emergency override privilege.

- **GuiAdvanced** Access all user interface features. (The user's role and privileges may limit the features they can view.)
- **GuiBasic** Access basic user interface features. Only a single study can be reviewed in the image viewing area. Advanced features, such as measurement tools and hanging protocols, will not be available. (The user's role and privileges may limit the features they can view.)
- **GuiIntermediate** Access intermediate user interface features. For example, basic measurement tools, screen layouts and cross-correlation between series are available. Multiple studies can be reviewed in the image viewing area at the same time. Advanced features, such as advanced measurement tools and hanging protocols, will not be available. (The user's role and privileges may limit the features they can view.)
- **GuiPatient** Access simple user interface features. Intended for patient use.
- **LifecycleManagement** Enable and modify data lifecycle options (see "Manage data lifecycle policies" on page 210).
- **MprProtocols** View Slab views.
- **OverrideLosslessModalities** Override system settings that specify that images from specific modalities are always shown as lossless, uncompressed images. If a user has this privilege, the user is able to turn off Full Quality for images, regardless of the default system settings (see "Full Quality" on page 36).
- **PatientDirectory** View all studies in the local database.
- **PersistentAnnotations** Allow persistent annotations and measurements across review sessions.
- **RestrictedSiteAccess** Access sensitive data on restricted sites.
- **SaveEvidence** Save secondary capture images, key images and bookmarks.
- **SecondaryCaptureCreation** Create secondary capture images (see "Share secondary capture images" on page 153).
- **ShowBookmark** Display a list of bookmarks in Presentations (see "Use presentations" on page 12).
- **SkypeIntegration** View Skype controls in the Collaboration panel.
- **StudyListAccess** Access the Patient Study Directory.
- **ThreeDProtocols** View 3D views.
- **VesselTrace** Access the Vessel Trace view.
- **ViewAnalytics** View Analytics (see "View analytics" on page 223).

- **ViewPublicWorkItems** Access public (unassigned) worklists and folders created by administrators.
- **XdsAccess** Access XDS repositories.

## Manage user groups

### ADMINISTRATORS ONLY

You can use groups to assign NilRead privileges to users (see “Privilege descriptions” on page 180). If NilRead is part of a domain, you can also add Active Directory groups to NilRead. If changes are made to an Active Directory group, such as adding users, the changes are automatically applied in NilRead as well.

#### Note

You can also manage privileges for individual users (see “Manage user accounts” on page 183).

### Access group settings

1. Select **Settings**.
2. Under **User Management**, select **Groups**.

See the next sections for details on managing groups.

### Create an application group

An application group is specific to NilRead and is not linked to an Active Directory group.

1. In the **Group** field (below the **Application Groups** area), enter the group name.
2. Select **Create**.
3. Select the type of group (Admin or User).
4. The **Granted Privileges** area lists the default privileges assigned to the group. By default, User groups have basic privileges (such as accessing the Patient Study Directory) and Admin groups have full privileges. To add or remove privileges from the group:
  - **Add a privilege** Select a privilege in the **Revoked Privileges** area, then select **Grant**.
  - **Remove a privilege** Select a privilege in the **Granted Privileges** area, then select **Revoke**.
5. In the **Session Timeout** field, select the session timeout period. A user’s session will end if they are inactive for this amount of time.

### Add an AD group to NilRead

You can add Active Directory groups to NilRead.

1. In the **AD Groups** area, select a group, then select **Add**.
2. Enter the following information, then select **OK**.
  - **Name** Name of the LDAP server.
  - **URL** URL for the LDAP server.
  - **Username, Password** Credentials for connecting to the LDAP server. Leave blank to connect using the credentials of the IIS application pool.
  - **Simple Bind** Use simple bind authentication when connecting to an LDAP provider. Typically used with ADAM and other non-Microsoft servers.
  - **SSL** Use a secure connection when using simple bind authentication.
3. In the **CN** field, enter the name of the Active Directory group you want to add, then select **Search**. Groups matching your search criteria are shown in the **AD Groups** area.
4. In the **AD Groups** area, select the group you want to add, then select **Add**. The group is added to the **Application Groups** area.
5. The **Granted Privileges** area lists the default privileges assigned to the group. To add or remove privileges from the group:
  - **Add a privilege** Select a privilege in the **Revoked Privileges** area, then select **Grant**.
  - **Remove a privilege** Select a privilege in the **Granted Privileges** area, then select **Revoke**.

### Edit or delete a group

1. In the **Application Groups** area, select the group, then select **Delete**.
2. In the **AD Groups** area, select the group, then select **Remove**.
3. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Manage user accounts

### ADMINISTRATORS ONLY

A user account defines the NilRead user's username, role, and group assignment. The user's privileges are shown in the user's account and can be modified. You can also lock user accounts and reset user passwords.

#### Note

Users can manage some of their account information through their profile (see "Manage your user profile" on page 177).

1. Select **Settings**.

2. Under **User Management**, select **Accounts**. Existing NilRead user accounts are shown.
3. If you have included Active Directory groups in NilRead, select **Refresh** to update the **Accounts** tab with any changes to Active Directory user accounts.



See the next sections for details on managing user accounts.

## Add an account

1. Select **Add**.
2. In the **Account** area, enter the user's information.
  - **User Name** Username to login to NilRead.

### Note

The user receives an automatic email with their NilRead password when their NilRead user account is created.

- **Role** NilRead role (Admin, User, Guest). By default:
    - Guests have no privileges.
    - Users have basic privileges, such as accessing the Patient Study Directory.
    - Administrators have full privileges. Only Administrators can manage users.
  - **Email** Email address.
  - **Skype ID** Skype ID. Allows the user to participate in Skype sessions.
  - **Phone** Phone number.
  - **Facility, Department, Job Description** User's facility and job information.
  - **Notify on Study Arrival** User will receive an email when a new study containing one of the user's DICOM person name matches is added to the database.
  - **Last Name, First Name, Middle Name, Prefix, Suffix** User's name.
  - **Password** Password to login to NilRead.
  - **Expiry Date** Date the user's access to NilRead will expire.
    - Select  and select an expiry date. Select whether the user's account will be locked or deleted on the expiry date.
    - Select  to remove the expiry date and set the user's access to **Unlimited**.
3. (Optional) In the **Groups** area, select the group to which the user belongs. Guests cannot be assigned to groups.
    - **Add a user to a group** Select a group in the **Not Member** area, then select **Add**.
    - **Remove a user from a group** Select a group in the **Members** area, then select **Remove**.

4. The privileges assigned to the user are shown in the **Privileges** area (see “Privilege descriptions” on page 180). These privileges are initially based on the user’s role and group but can be modified.
  - **Grant a privilege to a user** Select a privilege in the **Revoked** area, then select **Grant**.
  - **Remove a privilege from a user** Select a privilege in the **Granted** area, then select **Revoke**.
5. Select **OK**.

### Edit or delete an account

1. Select the user account. To find an account, enter account information in the blank row at the top of the tab.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

### Lock an account

1. Select the user account. To find an account, enter account information in the blank row at the top of the tab.
2. Select **Lock**. The user’s Locked status changes to True.
3. To unlock an account, select **Lock**. The user’s Locked status changes to False.

### Reset a user’s password

If you reset a user’s password, the user will receive an email with a new auto-generated password.

1. Select the user account. To find an account, enter account information in the blank row at the top of the tab.
2. Select **Reset**.



## 14. Manage data quality control

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### About data quality control

The NilRead data quality control (QC) tools allow you to make adjustments to data. You can use the QC tools to:

- Modify DICOM attributes for a patient, study, series or image.
- Redact areas on images.
- Add and hide labels on images.
- Split a series into multiple series.

The QC tools are available in the QC viewer. See the next section for details on accessing the viewer.

### Add studies to the data QC viewer

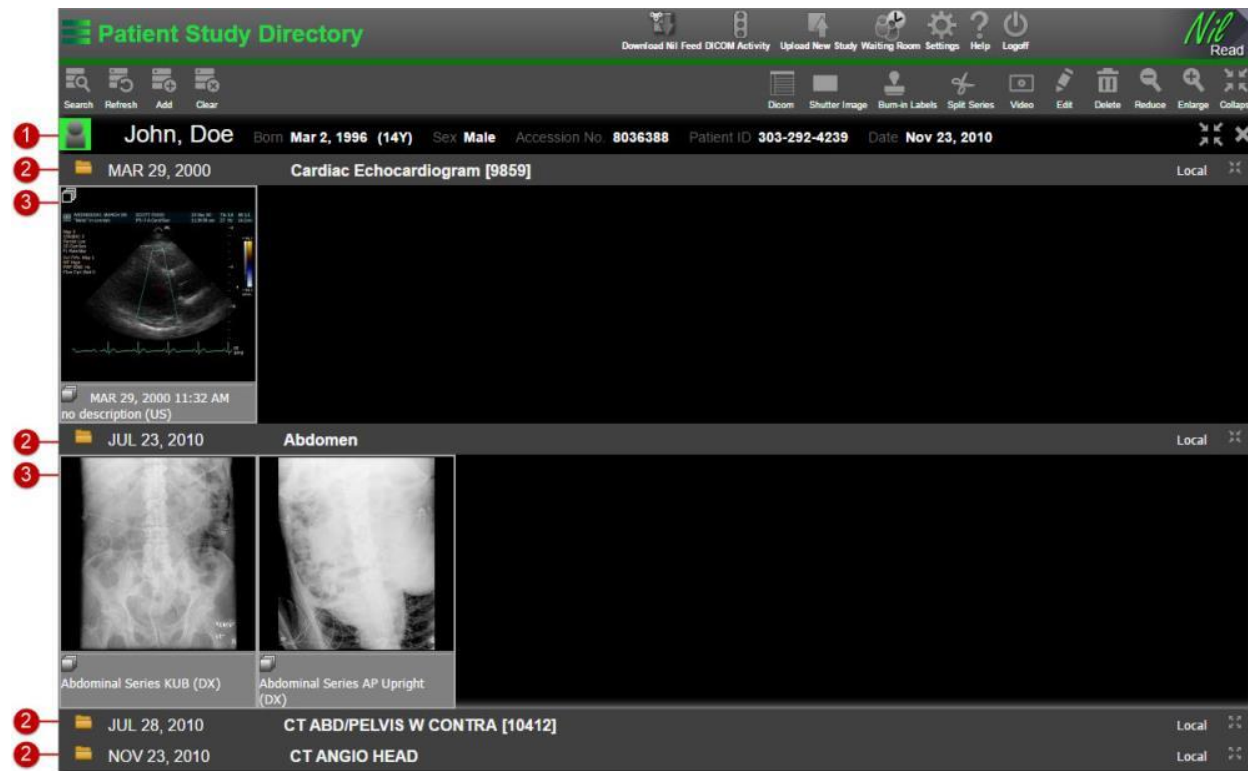
To use the data quality control tools on a study, add the study to the QC viewer. You can add studies for one or more patients to the viewer.

1. Use any of the options in the navigation tree to find a study (Patient Search, Patient Directory, Recently Opened, Worklists and Folders).
2. Right-click (or touch and hold) a study, then select **Advanced QC**. To add multiple studies, select the checkbox beside the studies, then select **Load**. To add all studies in a worklist or folder, right-click (or touch and hold) the worklist or folder name, then select **Advanced QC**.
3. The QC viewer opens with the study (or studies) you selected.
4. To add more studies to the QC viewer:
  - a. Select **Add** in the top-left corner.
  - b. Use the Patient Search page to find the study you want to add (for details, see "Use Patient Search" on page 74).
  - c. To add a study to the QC viewer, click (or tap) the study. To add multiple studies, select the checkbox beside the studies, then select **Load**.
5. To remove a patient from the QC viewer, select **X** on the patient row.
6. To remove all patients from the QC viewer, select **Clear** in the top-left corner.
7. To update the studies in the QC viewer with the latest changes made by all users, select **Refresh** in the top-left corner.

The following information is shown for the studies in the QC Viewer. The studies are organized by patient.





1. The patient information is shown first. Click (or tap) the patient name to view details.
2. The patient's studies are listed by date. Each study is shown on a separate row. Click (or tap) the study title to view details.
3. Thumbnails for the series in the study are shown. Series can be color-coded according to the type of series.

The following example shows one patient with four studies. The last two studies have been collapsed so that only the study date and title are shown.



## Optimize the QC viewer display

You can change the amount of information displayed in the viewer and the size of the series thumbnails. This can be useful when using a device with a small screen.

- To view the patient rows only, select **Collapse** (toolbar). The study and series rows are hidden. Select **Expand** to view the rows.
- To collapse a specific patient row, select  on the patient row. The patient's studies are hidden. Select  again to view the studies.
- To collapse a study row, select  on the study row. The series in the study are hidden. Select  again to view the series.




- To reduce the size of the series thumbnails, select **Reduce** (toolbar). To enlarge the thumbnails, select **Enlarge**. Note that you can select **Reduce** or **Expand** multiple times until the minimum or maximum size is reached.

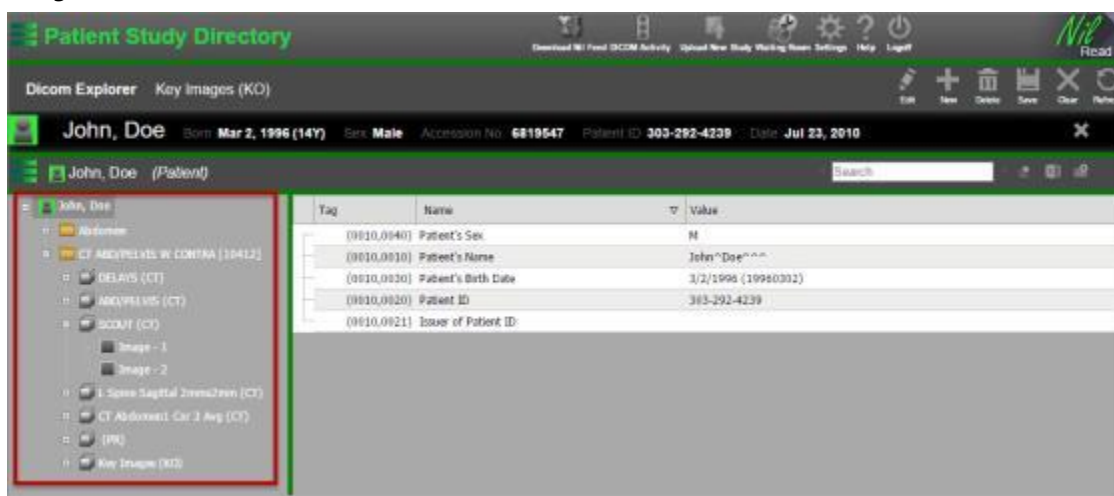
## View and modify DICOM attributes

You can modify DICOM attributes for a patient, study, series or image. For example, you may need to correct a patient's name. You can also add and delete attributes.

### Note

Changes to attributes, including additions and deletions, will not be permanently applied until you select **Save**.


1. Select **DICOM** (toolbar).
2. Select  on a patient row. This opens the DICOM attributes starting at the patient level (patient, studies, series and images).  
or  
Select  on a study row. This opens the DICOM attributes starting at the study level (study, series and images).  
or  
Click (or tap) a series. This opens the DICOM attributes starting at the series level (series and images).
3. The DICOM Explorer opens in a new browser tab. The left pane shows the hierarchy of DICOM attributes (patient, study, series, images). Note that the icon  is shown for multiframe images.



Tag	Name	Value
(0010,0040)	Patient's Sex	M
(0010,0010)	Patient's Name	John^Doe^^
(0010,0030)	Patient's Birth Date	3/2/1996 (19960302)
(0010,0020)	Patient ID	303-292-4239
(0010,0021)	Issuer of Patient ID	


4. Select an item in the left pane. The item's DICOM attributes are shown in the right pane. For example, select a patient to view the patient's attributes. If you select an image, all of the attributes related to the image are shown (patient, study, series and image).



5. To reload the DICOM attributes and view the latest changes made by all users, select **Refresh**. Any unsaved changes you have made will be lost.
6. To customize the columns in the right pane:
  - Select **Customize**  in the top-right corner. To add a column, drag a column from the **Customize** list to the location where you want to place it. To remove a column, drag it to the **Customize** list.
  - Click (or tap) a column heading to sort the attributes. Click (or tap) the column heading again to sort the attributes in the reverse order.
  - To rearrange the columns, drag a column heading to a new location.

## Find an attribute

If there is a long list of attributes in the right pane, use the **Search** box to find an attribute.

1. Enter your search text in the **Search** box and press ENTER.
2. Attributes matching your search text are highlighted. Use the arrows on each side of the **Search** box to go to the next or previous match.
3. Select  beside the **Search** box to clear your search text and the highlighted matches.

## Modify an attribute

1. Select an attribute in the right pane, then select **Edit**.

2. The Edit DICOM Tag window appears. The DICOM Tag area shows the DICOM tag information. The DICOM Value area contains the values you can modify. Make your changes, then click OK.

**Edit DICOM Tag**

**DICOM Tag**

Group: 0010  
Element: 0010  
Type: PN  
Description: Patient's Name

**DICOM Value**

Last Name: John  
First Name: Doe  
Middle Name:  
Prefix:  
Suffix:

OK Cancel

3. The modified attribute is shown in red in the right pane. The item the attribute belongs to (patient, study, series or image) is shown in red in the left pane.

**Patient Study Directory**

Download Nil Read DICOM Activity Upload New Study Working Areas Settings Help Logout

**Dicom Explorer** Key Images (KO)

**John, Doe** born: Mar 2, 1996 (14Y) Sex: Male Accession No: 6819547 Patient ID: 303-292-4239 Date: Jul 23, 2010

**John, Doe (Patient)**

Tag	Name	Value
(0010,0020)	Patient's Name	John, Doe, Richard
(0010,0020)	Patient ID	303-292-4239
(0010,0021)	Issuer of Patient ID	
(0010,0030)	Patient's Birth Date	3/2/1996 (19960302)
(0010,0040)	Patient's Sex	M

## Add an attribute

1. Select a patient, study, series or image in the left pane.

2. Select **New**. The **Add DICOM Tag** window appears.



3. Select **<click to select attribute>** and select the attribute you want to add. To search for an attribute, type all or part of the attribute name in the **Search** box.
4. When you select an attribute, the **DICOM Tag** area shows the DICOM tag information. The **DICOM Value** area contains the values you can modify. If the attribute already exists, the current values are shown in the **DICOM Value** area and can be modified.
5. Make your changes, then click **OK**. The new attribute is shown in red in the right pane. The item the attribute belongs to (patient, study, series or image) is shown in red in the left pane.

## Delete an attribute


Select an attribute in the right pane, then select **Delete**.

## Save attribute changes

To save your changes, select **Save**. Attribute changes, additions and deletions will be saved.

If you do not want to save your changes, select **Clear**.

## Save attributes in a spreadsheet

Select an item (patient, study, series or image) in the left pane, then select  in the top-right corner. Follow your browser instructions to save the file.

## Return to the QC viewer

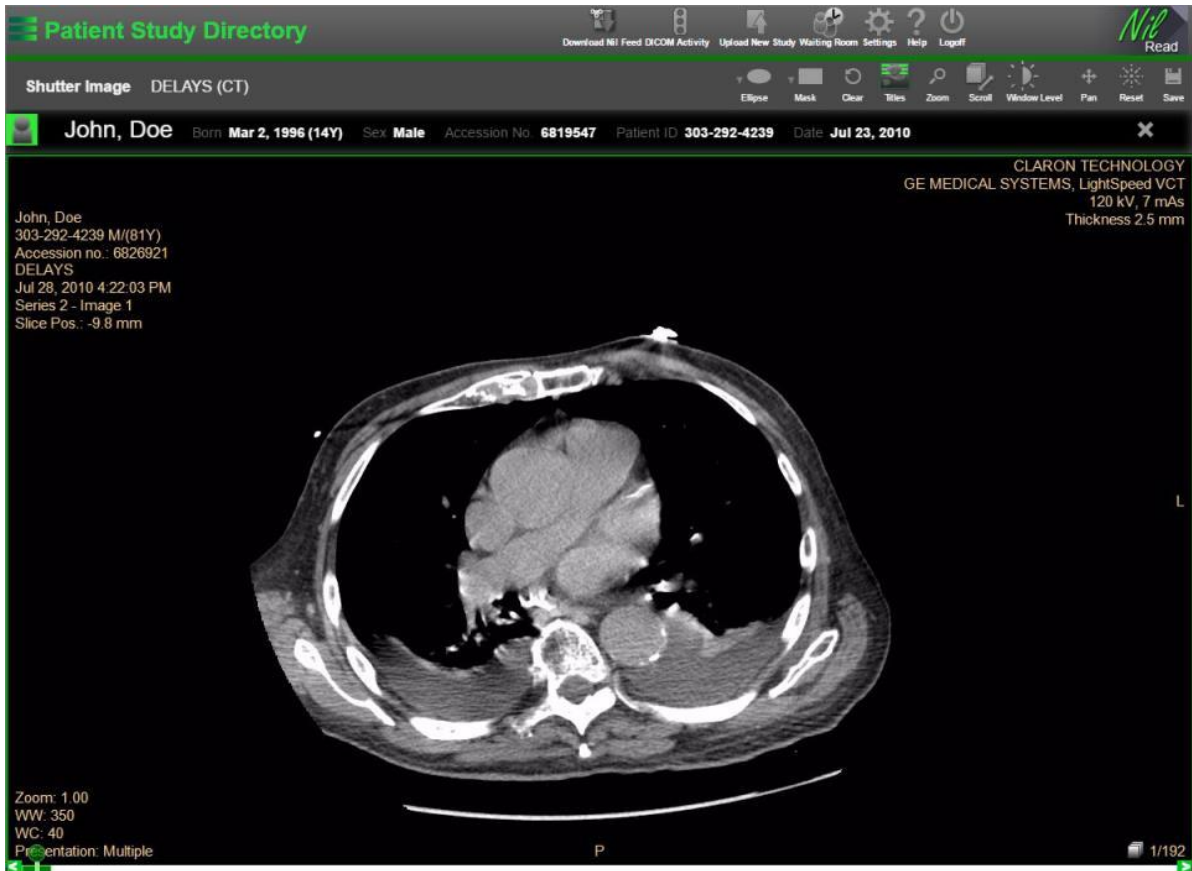
To return to the QC viewer, select **X** in the top-right corner (beside the patient information).

## Redact areas on images

You can redact areas on an image. For example, you may want to anonymize a study by removing patient information. When you make redactions to an image, the changes are applied to all images in the series.

NilRead provides two methods to redact an image. You can add masks to cover the areas you want to redact, or you can use shutters to identify the areas you want to retain. You can also hide the image titles for all images in the series.

1. In the QC viewer, select **Shutter Image** from the toolbar.
2. Select a series. You can only select a series containing images eligible for redaction. If the study contains one or more multiframe series, the **Select Instance** window appears with all series selected by default. To select one or more specific series, clear the **Select All** checkbox, then click (or tap) the series you want to select. Click **OK**.
3. The first image in the series opens.



4. Use **Scroll** or the scroll bar at the bottom of the window to select a different image. You can also use tools such as zoom, window level, and pan to adjust the image.

## Apply a mask

1. Select **Mask** from the toolbar.
2. Select a shape from the toolbar (**Rectangle, Square, Ellipse, Circle**).
3. Draw shapes over the areas you want to redact. The areas covered by shapes will be blocked out on all images in the series.
4. To resize a shape, drag a corner of the shape. To move a shape, drag the shape to a new position.
5. To remove all shutters and masks, select **Clear**.

## Apply a shutter

1. Select **Shutter** from the toolbar.
2. Select a shape from the toolbar (**Rectangle, Square, Ellipse, Circle**).
3. Draw shapes over the areas you want to retain. Only the areas covered by shapes will be visible; the rest of the image will be redacted.
4. To resize a shape, drag a corner of the shape. To move a shape, drag the shape to a new position.
5. To remove all shutters and masks, select **Clear**.

## Hide titles

1. Select **Titles** from the toolbar. The image details are removed from all images in the series.
2. To display the image details, select **Titles** again.

## Save redactions

Redactions will be applied to all images in the series. The modified images will be saved as a new series in the original study unless you choose to save the series in a new anonymized study. You can also choose whether or not to remove the images from the original series.

### Note

If you do not want to save your changes, select **Clear**.

1. Select **Save** from the toolbar.
2. To remove the images from the original series, select **Delete original instances**.  
or  
To keep the images in the original series, clear **Delete original instances**.
3. To save the series in a new anonymized study, select **Deidentify**, then select a confidentiality profile (for details, see "About anonymization" on page 145). The anonymized series will only contain the series that have been redacted.
4. Enter a **Series Description** and **Series Number** for the new series.



5. Select Save.

## Return to the QC viewer

To return to the QC viewer, select X in the top-right corner (beside the patient information).

## Add and correct labels

You can add missing labels to an image or correct labels that have been burned into an image, such as an incorrectly placed label. To correct a label, first hide the incorrect label, then add a new label.

1. In the QC viewer, select **Burn-in Labels** from the toolbar.
2. Select a series. You can only select a series containing images that can be labelled.
3. The first image in the series opens.



4. Use Scroll or the scroll bar at the bottom of the window to select a different image. You can also use tools such as zoom, window level, and pan to adjust the image.

## Hide a label

1. Select the arrow beside **Left** in the toolbar, then select **Mask**.
2. Draw a shape over the label you want to hide.
3. To resize a shape, drag a corner of the shape. To move a shape, drag the shape to a new position.
4. To remove all shapes, select **Clear**.

## Add a label

1. Select a label (**Left, Right, Head, Foot, Anterior, Posterior**) from the toolbar.
2. Draw a label on the image.
3. To resize a label, drag a corner of the label. To move a label, drag the label to a new position.
4. To remove all labels, select **Clear**.

## Save labels

The modified images will be saved as a new series. You can also choose whether or not to remove these images from the original series.

### Note

If you do not want to save your changes, select **Clear**.

1. Select **Save** from the toolbar.
2. To remove the images from the original series, select **Delete original instances**.  
or  
To keep the images in the original series, clear **Delete original instances**.
3. Enter a **Series Description** and **Series Number** for the new series.
4. Select **Save**.

## Return to the QC viewer

To return to the QC viewer, select **X** in the top-right corner (beside the patient information).

## Split a series

You can divide a series of images into multiple series. This can be useful if the images need to be reviewed by different specialists.

1. In the QC viewer, select **Split Series** from the toolbar.
2. Select a series. You can only select a series that can be divided.

3. The series editor opens.

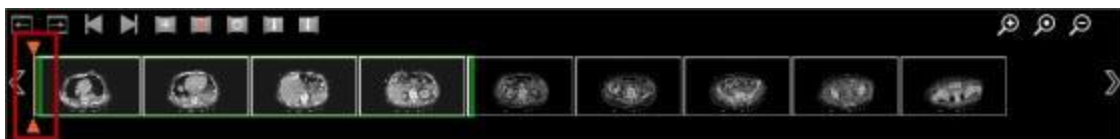
The series editor contains the following sections.

- The preview window at the top of the screen shows larger versions of the images in the series. You can select a 1x1 or 1x3 layout for the preview window using the toolbar. The timeline at the bottom of the screen contains thumbnail images for the entire series.

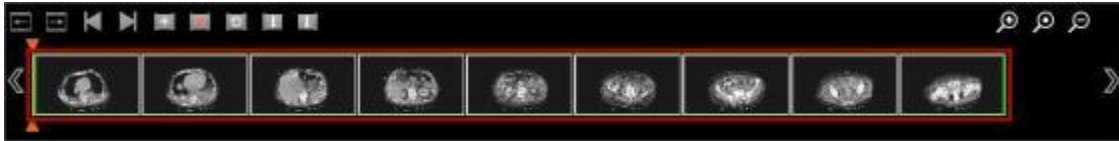


Icons are shown on the images in the preview window to indicate if they will be included in the new series.

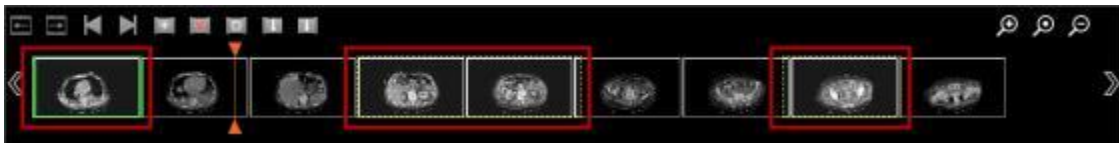
- Green scissors indicate the first image to be included in the new series.
  - A checkmark indicates the image will be included in the new series.
  - A red X indicates the image will not be included in the new series.
- The position indicator shows the current location in the series. When you first open the editor, the position indicator is at the first image in the series.



- Use the selection box in the timeline to select the images you want to include in the new series. When you first open the editor, all of the images are selected.

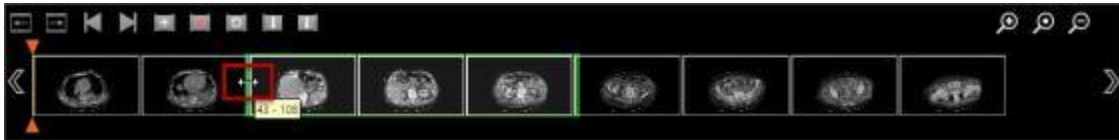


You can resize and move the selection box. You can also add more boxes to the timeline, allowing you to select images throughout the series. For example, the following timeline contains three boxes. These three groups of images will be included in the new series.

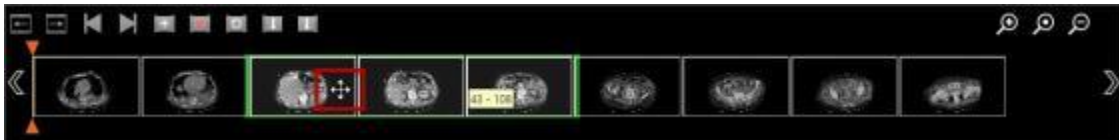



### Modify a selection box

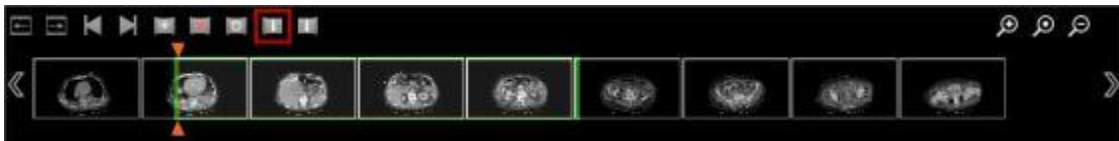
- Drag the ends of the box to resize it.



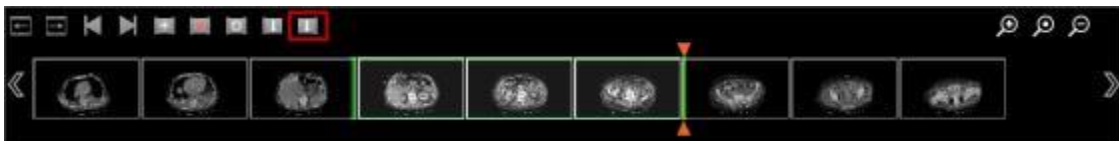
- Drag the box to a new position.



- To set the beginning of the box to the position indicator location, select the box, then select .



To set the end of the box to the position indicator location, select the box, then select .




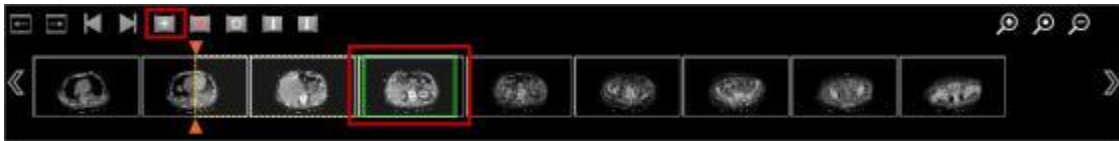
- Hover over a box to view the range of images within the box.



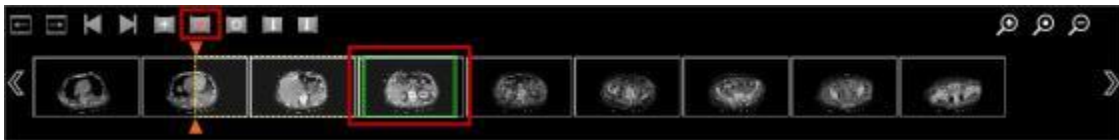
## Add and remove selection boxes

Use multiple selection boxes to select non-contiguous images. You can add as many boxes as needed.

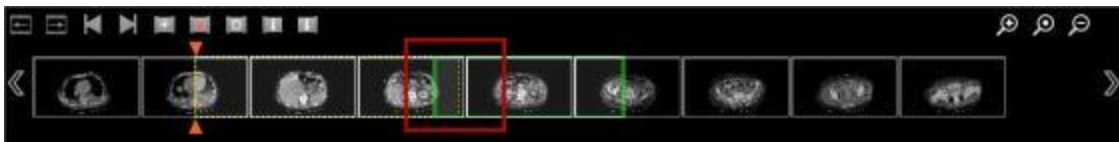
- To add a box, select . A new box appears to the right of the current box. Change the box position and size as needed.



- To remove a box, select the box, then select . Note that you cannot remove all boxes; at least one box must remain on the timeline.





- Note that if boxes overlap, they will be merged together when the new series is saved.



## View thumbnail images

You may need to use the arrows at each end of the timeline to view all of the thumbnail images. You can also hold SHIFT while dragging the timeline to view additional thumbnails. On touch devices, use a two-finger drag.

Use the following tools to resize the thumbnail images in the timeline.

	Increase the thumbnail size. This allows you to view the thumbnails more clearly; however, this reduces the number of thumbnails shown on the screen.
	Fit all thumbnails on the screen.

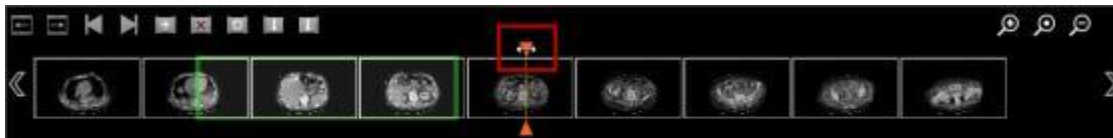


Decrease the thumbnail size. This allows you to view more thumbnails on the screen.

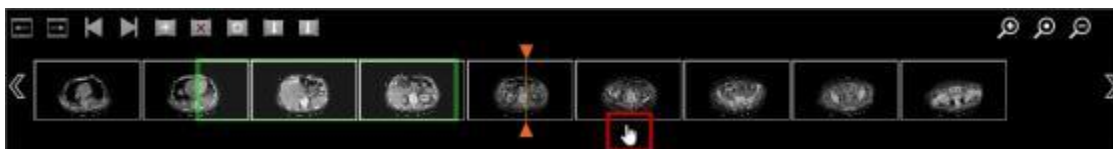
## Change the position indicator

Move the position indicator to the image you want to preview.

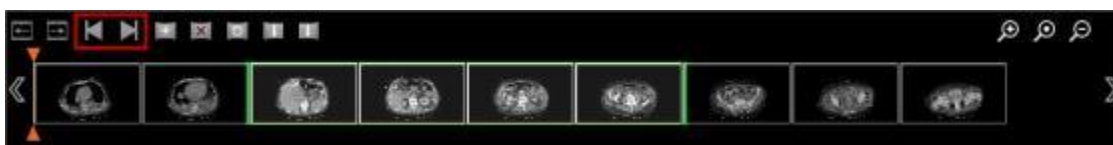
- Drag the position indicator to a new location on the timeline.



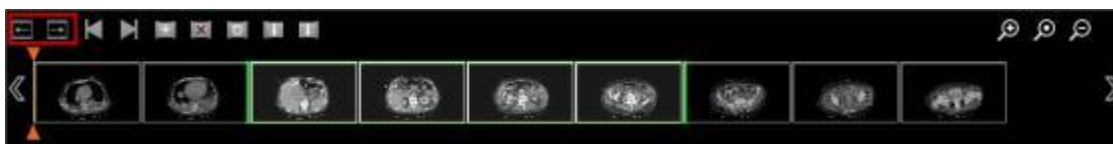
- Click (or tap) above or below the timeline to move the position indicator to a new location.



- To move the position indicator to the start of the series, select . To move the position indicator to the end of the series, select .



- Use and to move the position indicator forwards or backwards frame-by-frame. You can click (or tap) and hold these icons to continue moving frame-by-frame.



## Save the new series

The images you have selected will be saved as a new series. You can choose whether or not to remove the images from the original series.

1. Select **Save** from the toolbar.
2. To remove the images from the original series, select **Delete original instances**.

or

To keep the images in the original series, clear **Delete original instances**.

3. Enter a **Series Description** and **Series Number** for the new series.
4. Select **Save**.

## Return to the QC viewer

To return to the QC viewer, select **X** in the top-right corner (beside the patient information).


## Edit a video

You can edit a video from the QC viewer.

1. Select **Video** from the toolbar, then select a series containing a video. For more information, see "Edit videos" on page 51.
2. To return to the QC viewer, select **X** in the top-right corner (beside the patient information).


## Edit a patient, study or series

You can quickly edit key DICOM attributes for a patient, study or series in the QC viewer. Your changes will be saved in a new instance.

1. Select **Edit** from the toolbar.
2. Select  beside a patient or study, or click (tap) a series.
3. Make changes to the patient, study or series attributes. If you want to retrieve information about the patient from a modality worklist, select **Reconcile**. Enter information about the patient and select **Search**. If a match is found, select the patient and select **Select**.
4. To delete the original instance, select **Delete original instances**.
5. Select **Save**.

## Delete a patient, study or series

You can permanently delete a study, series or image using the QC viewer.

1. Select **Delete** from the toolbar, then select a study, series or image.
2. Select  beside a patient or study, or click (tap) a series.
3. Click **OK**.

## Exit the QC viewer

To close the QC viewer and return to the Patient Study Directory, select **Search** in the top-left corner.

## 15. Manage NilRead


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### Customize the navigation tree

#### ADMINISTRATORS ONLY

By default, the navigation tree in the Patient Study Directory shows only worklists and folders that are public or belong to the current user.

You can add worklists and folders belonging to specific groups and users to the navigation tree, making these items available to all NilRead users.

1. In the Patient Study Directory, select  above the navigation tree.
2. Select groups and users. All NilRead users will be able to view the worklists and folders for these groups and users.
  - **Groups** To add groups, select one or more groups in the **Hidden** area, then select **Show**. To hide groups, select one or more groups in the **Shown** area and select **Hide**.
  - **Users** To add users, select one or more users in the **Hidden** area, then select **Show**. To hide users, select one or more users in the **Shown** area and select **Hide**.
3. Select **OK**.

### Manage patient search results

You can set the maximum number of studies that are returned on the Patient Search page in the Patient Study Directory.

1. Select **Settings**.
2. Under **Devices**, select **DICOM**.
3. In the **Patient Search** area, click **Edit**.
4. Enter the maximum number of query results, then click **Save**.

### Manage DICOM study transfers

#### Retrieve studies to the local database

Use Patient Search to find patient studies on a remote DICOM server and retrieve the studies to the local database. You can also choose to load a study (open it in NilRead) immediately after retrieving it.

#### Note

Your user privileges determine whether you can retrieve studies to the local database. Your



DICOM settings for Query/Retrieve Service Class Providers also determine whether you are able to retrieve studies (see “Manage DICOM services” on page 203). If retrieve mode is not enabled, you can load studies from a remote server but the studies are not saved in the local database.

**Note**

You can monitor patient study transfers using the DICOM Activity page (see “Monitor DICOM patient study transfers” on page 203).

1. In the Patient Study Directory, select **Patient Search**.
2. Find the study or studies you wish to retrieve (see “Access studies” on page 73).

You can now transfer studies to the local database. You can also choose to open studies in NilRead after they are transferred.

**View a study**

Click (or tap) a study in the search results. You can also right-click a study, then select **Load Studies**.

The study is opened in NilRead. Depending on the retrieve mode that has been configured for the remote DICOM server, the study may also be transferred to the local database (if it is not already in the directory).

**View multiple studies**

Select the checkbox beside each study. Right-click (or touch and hold) one of the studies and select **Load Studies**.

The studies are opened in NilRead. Depending on the retrieve mode that has been configured for the remote DICOM server, the studies may also be transferred to the local database (if they are not already in the directory).

**Transfer one or more studies**

Select the checkbox beside each study. Right-click (or touch and hold) one of the studies and select **Retrieve Studies**. The studies are transferred to the local database (if they are not already in the directory).

## Send studies, series or images to a DICOM server

You can send a patient study, series or image to a remote DICOM server. The study, series or image remains in NilRead as well.

In the Patient Study Directory:

- Right-click (or touch and hold) a study, select **Send to Device**, then select a remote device.

While viewing a study:

1. To send a series, right-click (or touch and hold) a series (side panel), then select **Send Series**.
2. To send an image, right-click (or touch and hold) an image, then select **Send Image**.

## Monitor DICOM patient study transfers

Monitor patient studies transfers between the local database and remote DICOM servers. You can view current, completed, and failed transfers.

In the Patient Study Directory:

1. Select **DICOM Activity**.
2. The **Current**, **Completed** and **Failed** tabs contain the following areas. Click (or tap) a column heading to sort the column in ascending or descending order.
  - **Inbound Associations** Studies received by NilRead from a remote DICOM server.
  - **Outbound Associations** Studies sent from NilRead to a remote DICOM server.
  - **Retrievals** Studies retrieved by NilRead from remote DICOM servers (see "Retrieve studies to the local database" on page 201).
3. The **Deleted** tab lists the studies that have been purged from the local database.
4. To update a tab with the latest activities, select **Refresh**.
5. To remove the activities list from a tab, select **Clear**. You cannot clear the **Current** tab.

## Manage DICOM services

Configure your NilRead server and the remote DICOM servers on the network. You can use several types of DICOM services:

- **Local Application Entity Configuration** Refers to NilRead. NilRead is a Storage Service Class Provider that can receive patient studies from remote DICOM servers.
- **Streaming Service** NilRead DICOM Query/Retrieve Service Class User service, which incrementally retrieves DICOM data and loads it directly to the NilRead viewer without caching in the file system.
- **Repository** Refers to a data directory path which can be used to store imported DICOM data.
- **Acuo VNA Providers** Acuo VNA repositories that NilRead has direct access to.
- **Storage Service Class Providers** Remote DICOM servers that can receive patient studies from NilRead.
- **Storage Commitment Service Class Providers** Remote DICOM servers that support the DICOM storage commitment service. Used to confirm that data has been permanently stored by a server to ensure it is safe to delete the data locally.
- **Query/Retrieve Service Class Providers** DICOM servers that NilRead can query and retrieve patient studies from.
- **Modality Worklist Service Class Providers** Facilitate the communication of patient and scheduled acquisition procedure information to imaging modalities.
- **Instance Availability Notification Service Class Providers** NilRead can notify the configured IAN DICOM AE of the availability of the replacement instances. The notification contains the AE titles of the replacement instances, from which the replacement instances can later be retrieved.
- **Detached Interpretation Management Service Class Providers** Provide detached reports and notifications associated with studies.

- **Print Service Class Providers** Remote DICOM servers which support DICOM printing.
- **RESTful Dicom Service Providers** Remote DICOM servers which support DICOM QIDO-RS, WADO-RS, and STOW-RS protocols.

### Access DICOM configuration settings

1. Select **Settings**.
2. Under **Devices**, select **DICOM**.

See the next sections for details on configuring your services.

### Configure the NilRead DICOM Storage Service

1. In the **Local Application Entity Configuration** area, select **Edit**.
2. Modify the service details.
  - **AE Title** NilRead DICOM server's DICOM Application Entity Title.
  - **Host** IP address of the TCP/IP network endpoint that the NilRead DICOM server listens at.
  - **Port** Port number of the TCP/IP network endpoint that the NilRead DICOM server listens at.
  - **Maximum Inbound Associations, Maximum Outbound Associations** Maximum number of DICOM associations that the DICOM server will execute concurrently. This controls system resources utilization of the DICOM server (CPU, Disk I/O, etc.).
3. Select **Save**.

### Configure Streaming Service

1. In the **Streaming Service** area, select **Edit**.
2. Modify the service details.
  - **AE Title** NilRead streaming service's DICOM Application Entity Title.
  - **Port** Port number of the TCP/IP network endpoint that the NilRead streaming service listens at.
  - **Maximum Inbound Associations, Maximum Outbound Associations** Maximum number of DICOM associations that the DICOM streaming service will execute concurrently. This controls system resources utilization of the DICOM server (CPU, Disk I/O, etc.).
  - **Enabled** Indicates whether the DICOM streaming service is enabled.
3. Select **Save**.

### Configure Repository Information

1. In the **Repository** area, select **Edit**.
2. Modify the repository details.
  - **Repository path** Path to the data repository.

- **Free disk space watermark** Drag to select the low and high watermark settings used to trigger the purging service.
- **Critical disk space watermark** Drag to select the watermark settings that will trigger the DICOM storage SCP service to enter suspended mode. The service will remain in suspended mode until enough free disk space is available.
- **CPU idle watermark** Drag to select the CPU idle threshold when purging can be performed.
- **Number of protected studies** Auto-purging will stop if the number of studies in the database is equal to or less than this number.
- **Free disk space check interval (seconds)** Interval (in seconds) to check for free disk space. Also triggers purging if all purging criteria are met.
- **Number of studies to delete per batch** Number of studies to delete when the system performs an automatic data purge (performed when disk space is reaching capacity).
- **Dicom activity retention period (days)** Number of days to retain DICOM activity logs. Logs will be deleted after this period.
- **Email notification address** Email address to send notifications when the critical disk space watermark is reached.

3. Select **Save**.

### Configure patient search results

In the Patient Search area:

- **Maximum number of query results** Enter the maximum number of studies that are returned on the Patient Search tab in the Patient Study Directory.

### Add a remote DICOM server

1. In the Remote AE Configuration area, select a DICOM services type. The existing servers are shown.
2. Select **New**.
3. Enter the server details.
4. Select **Update**.

### Edit or delete settings for a remote DICOM server

1. In the Remote AE Configuration area, select a DICOM services type. The existing servers are shown.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Manage hanging protocols

### About hanging protocols

The purpose of a hanging protocol is to display the images in a study in a consistent manner. While the term originally referred to the arrangement of physical films in a film box, it now refers to the display of images on computer monitors. When properly set up, the use of hanging protocols significantly improves reading quality and efficiency.

When opening a study, NilRead analyzes the DICOM attributes of the study and identifies matching hanging protocols. If any candidates are found, the best one is selected and applied automatically. You can also choose a hanging protocol when viewing a study (see “Select hanging protocols” on page 65).

Depending on your NilRead license, you will have access to either clinical or advanced hanging protocols.

- **Clinical hanging protocols** allow you to quickly create protocols based on the study modality. You can also include studies based on the series description.
- **Advanced hanging protocols** have additional anchor study matching options. They also include the ability to select prior studies for comparison, load prior studies in specific viewports, and apply presentation settings (window level, invert greyscale, zoom, and orientation).

The Hanging Protocols page has two tabs:

- **Protocols** Contains a list of all hanging protocols in NilRead (see “Set up hanging protocols” on page 206). You can add, edit, clone, delete, enable/disable, import and export protocols.
- **Rules templates** Contains a list of rules templates you can optionally use when creating a hanging protocol (see “Set up hanging protocol rules templates” on page 209). Rules templates make it easy to apply a standard set of rules to multiple hanging protocols. If you make changes to a rules template, the changes will also be applied to all protocols using the template.

#### Note

See the [Hanging Protocols Handbook](#) for more detailed information about using hanging protocols.

### Set up hanging protocols

1. Select **Settings**.

#### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

2. Under **Preferences**, select **Hanging Protocols**.
3. Select the **Protocols** tab.

See the next sections for details on adding, modifying, deleting, and enabling hanging protocols.

## Add hanging protocols

1. Select **Add**. You can also select an existing protocol, then select **Clone**.

The **Hanging Protocol Editor** appears. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.

### Note

See the **Hanging Protocols Handbook** for more detailed information about using hanging protocols.

2. Enter the following information, then select **Save**. The hanging protocol is added to the **Protocols** tab and is enabled by default, meaning it will be available in NilRead. To disable the hanging protocol, clear the **Enabled** checkbox.

### Protocol Info

1. Enter a name for the protocol.
2. Select whether this is a **System** or **User** protocol. A system protocol will be applied to all users of NilRead. A user protocol will only be applied to the type of user you specify (Admin, User, or Guest).
3. Select the type of users, based on job description, for this protocol.
4. Enter a **description** for the protocol.

### Anchor study matching

Define the type of studies the protocol will apply to.

1. To add a new DICOM rule, select **<add new>**. Customize the rule. For example, you could state that images must be a specific modality. For clinical hanging protocols, attribute options include Modality and Series Description only.
2. To add a rules template, select **<add new ruleset>**. Select **<pick>** and select a template. If you are using clinical hanging protocols, any attributes in the template that are not applicable to clinical hanging protocols will be shown in red and will be ignored.
3. To remove a rule or ruleset, select **Verify** to switch to **Delete**.

### Comparison study matching

Select whether the hanging protocol includes prior studies. This section is not available for clinical hanging protocols.

1. By default, prior studies are not included. To include prior studies, select **will not be** to switch to **will be**.
2. Select **<add new>** or **<add new ruleset>** and add the same rules as the **Anchor study matching** section.

### Relevant Patient History

Define filters to determine which prior studies are shown in the patient timeline for this hanging protocol.

1. Be default, all prior studies are shown. To define filters, select **all** to switch to **these**.

2. You can enter filters based on modality, keywords, and the study age. Keywords are words that will be searched in a few common DICOM attributes such as body part examined, region of interest, and study description.

### Monitors and protocol stages

Define the image placement.

1. On the **Stage 1** tab, the number of screens is shown under **Monitors and screen layouts**. The default number of screens is 1x1. If desired, select 1x1 and select a different number of screens.
2. In the **Protocol layouts** section, define the rules for each screen. Presentation state settings are not available for clinical hanging protocols (window level, invert greyscale, zoom, orientation).
3. If desired, select <add stage> and add additional stages to the hanging protocol. Define the screen layout for each stage.

### Application preferences

1. Select whether the side panel is visible or hidden.
2. Select whether the patient timeline is visible or hidden.

## Edit or delete hanging protocols

1. Select a protocol.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Enable a hanging protocol

You must enable a hanging protocol to make it available in NilRead. You can disable protocols that you do not want to make available to NilRead users.

1. Select the checkbox beside a protocol. You can also select a protocol, then select **Enable**.
2. To disable a protocol, clear the checkbox beside the protocol.

## Import and export hanging protocols

To import a hanging protocol:

1. Select **Import**.
2. Select a file to import, then select **OK**.

To export a hanging protocol:

1. Select a protocol.
2. Select **Export**.
3. Under **Export Range**, choose whether to export the selected protocol only or export all protocols.

4. You will be prompted by your browser to select a location to save the file.

## Set up hanging protocol rules templates

You can create rules templates to use in hanging protocols. If you make changes to a rules template, the changes will also be applied to all protocols using the template.

1. Select **Settings**.

### Note

If you access **Settings** while viewing a study, select **Back to Viewer** to return to the image viewing area.

2. Under **Preferences**, select **Hanging Protocols**.
3. Select the **Rules Templates** tab.

See the next sections for details on adding, modifying and deleting rules templates.

## Add rules templates

1. Select **Add**. You can also select an existing template, then select **Clone**.

The **Hanging Protocol Template Editor** appears. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.

### Note

See the **Hanging Protocols Handbook** for more detailed information about using hanging protocols.

2. Enter the following information, then select **Save**.

### Template Info

1. Enter a name for the protocol.
2. Enter a description for the protocol.

### Template rules definition

1. Select **<add new>** to add a new DICOM rule. Customize the rule. For example, you could state that images must be a specific modality.
2. To remove a rule, select **Verify** to switch to **Delete**.

## Edit or delete rules templates

1. Select a template.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.



## Manage data lifecycle policies

Use data lifecycle policies to manage the lifecycle of any series imported into NilRead or created in NilRead. A data lifecycle policy is defined in terms of conditions and activities. If a series meets all of the policy conditions, the lifecycle activities defined in the policy are applied to the series. For example, a policy could state that all data imported from a specific institution (condition) will be retained in NilRead for six months before being moved to a new storage location (activity).

### Note

NilRead automatically verifies series against your data lifecycle policies. You can also choose to apply a policy to a study. This is useful if you created a new policy or modified your existing policies after the study was imported to the database.

### Note

See the [Data Lifecycle Management Handbook](#) for more detailed information about creating policies.

## Set up data lifecycle policies

1. Select **Settings**.
2. Under **Devices**, select **Data Lifecycle**.

See the next sections for details on configuring policies and endpoints.

## Add a policy

The **Policies** area contains a list of all existing data lifecycle policies.

1. In the **Policies** area, select **Add**.
2. Enter the following information, then select **Save**. The policy is added to the **Policies** area.

### Name

Policy name.

### Comment

Policy description.

### Enabled

If selected, the policy can be applied to NilRead data.

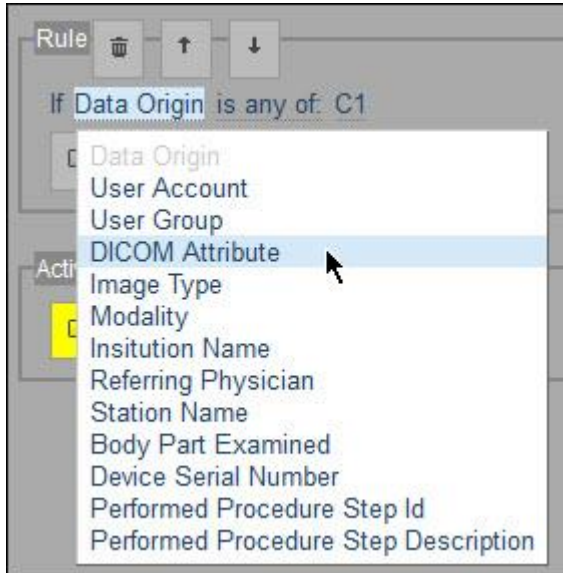
### Training

If selected, the policy will be run in a “training” mode. The activities will be logged but will not be applied to data.

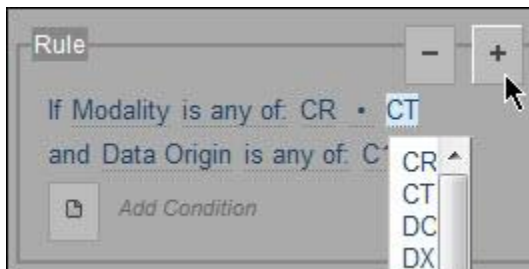
## Rule


Specify the rule for the policy by adding one or more conditions. All conditions must be satisfied in order for the policy to be applied to a study.

1. Select **Add Condition**.
2. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.



3. To add an item to a condition, select a customizable area, then select +. To remove an item, select -.



4. To delete a condition, select the first customizable area, then select .
5. To move a condition to a new position, select the first customizable area, then select



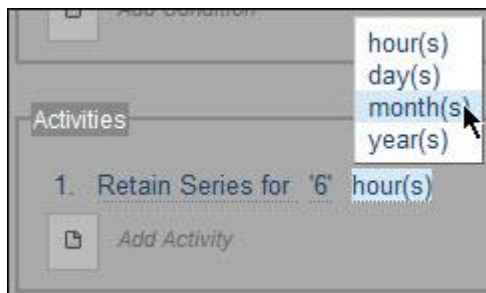
## Activities

Specify the activities that will occur if the policy rule is satisfied. You can use a series of activities to manage data. For example, you could retain series for six months before moving them to a storage location; you could then move the series to an offline storage location after two years.

Activities are executed in the order listed in the policy.


1. Select **Add Activity**.

2. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.



You can use activities to:

- **Retain** Specify how long to retain data in the database. Typically used in conjunction with another activity, such as moving data to a storage location.
- **Route** Move data to a DICOM server.
- **Relocate** Copy data to a storage location (defined by a Storage Tier endpoint).
- **Recycle** Delete data.
- **Email** Send an email to a specified email address.
- **Tiff Move** Move TIFF pathology images to a storage location (defined by a TIFF Import endpoint).
- **Tiff Convert** Convert TIFF pathology images to DICOM format.
- **Notify Study Import** Receive a notification when a study is imported.

3. To delete an activity, select the activity, then select .
4. To move an activity to a new position, select the first customizable area, then select



## Add an endpoint

The **Endpoints** area contains a list of non-DICOM endpoints (storage tiers and data pickup folders) that can be used for data lifecycle management.

1. In the **Endpoints** area, select **Add**.
2. Enter the endpoint information, then select **Save**.
  - **Name** Endpoint name.
  - **Type** Endpoint type:
    - **Storage Tier** Storage location used to store NilRead data.
    - **TIFF Import** Storage location used to retrieve Tiff pathology images to be imported to NilRead.
    - **EventSink** Remote endpoint capable of receiving NilRead study import event notifications.
  - **Path** Path to the endpoint location (for example, c://storage1).

## Edit or delete a policy or endpoint

1. In the **Policies** area, select a policy.  
or  
In the **Endpoints** area, select an endpoint.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Correct or abort an activity

You can view a log of recent activities performed on series based on lifecycle policies.

1. Select **Settings**.
2. Under **Devices**, select **Data Lifecycle**.
3. Activities are shown in the **Lifecycles** area. The **Status** column indicates whether the activity was performed successfully.
  - **OK** The activity is executing successfully and is not yet complete.
  - **Waiting** The workflow is waiting for a condition in order to proceed.
  - **Faulting** The activity failed to execute successfully. You can correct or abort the activity.
  - **Completed** The activity executed and completed successfully.
  - **Aborted** The activity was aborted.
  - **Failed** The activity failed to execute successfully. The activity cannot be corrected or aborted.

If an activity has a **Faulting** status, you can correct the activity workflow and rerun the activity.

1. In the **Lifecycles** area, select an activity, then select **Correct**.
2. Modify the workflow.
3. Select **Save**.

You can abort an activity that has not yet completed (**OK**, **Waiting**, or **Faulting** status).

- In the **Lifecycles** area, select an activity, then select **Abort**.

## Apply a data lifecycle policy to a study

NilRead automatically verifies series against your data lifecycle policies. You can also manually apply a policy to a study. There may be cases when you need to manually apply activities associated with a data lifecycle policy to a particular study, either to bypass the policy rule conditions or to apply the policy to a series that was already in NilRead before you created (or modified) the policy.

In the Patient Study Directory:

1. Select the checkbox beside each study to which you want to apply the policy.
2. Right-click (or touch and hold) one of the studies and select **Apply Policy**, then select a data lifecycle policy. After the activities are applied, a message will appear with the results.

## Manage prefetch settings

NilRead can be configured to retrieve archived images from external sources in advance of a scheduled patient visit. This ensures prior exams are available for comparison.

Prefetch is controlled by user-defined policies. Each policy is defined in terms of triggers and actions. Triggers specify conditions on which prefetch should be performed while actions specify the prefetch details. NilRead can be configured to query multiple MWL service class providers for scheduled workflow items associated with a specific modality, station name, and AE title. Alternatively, prefetch can be triggered by an imported study based on a study modality, data source, or age.

If a trigger condition is satisfied, priors will be prefetched based on the configured number of studies, age, modality, data source, and patient matching. For example, a policy could state that when a CR acquisition is scheduled on a specific device (or when a CR study is imported from a specific DICOM server), NilRead will prefetch a maximum of three CR studies, not older than six months, from a specific data source, and the studies will be selected by matching the patient name.

### Note

Prefetch activities are logged and can be reviewed on the DICOM Activity page (see “Monitor DICOM patient study transfers” on page 203).

## Set up prefetch

1. Select **Settings**.
2. Under **Devices**, select **Prefetch**.

See the next sections for details on configuring prefetch.

## Prefetch settings

1. In the **Services** area, define the prefetch settings.
  - **Enable** If selected, prefetch is enabled.
  - **Modality Worklist Poll Period** Frequency (in hours) to check the modality worklist. Select **Poll** to check the worklist immediately.
  - **Query Modality Worklist Items not older than** Age (in days) of modality worklist items to include when checking the worklist.
  - **Prefetch Activation** Frequency to run prefetch (check the modality worklist and fetch data). You can activate prefetch immediately or schedule it to run between specific hours. When **immediate** is selected, prefetch actions will be executed immediately when a worklist item is scheduled or a study is imported to NilRead which matches a policy trigger; otherwise, prefetch actions will be executed within the configured time range.
  - **Keep prefetch request records for** Period (in days) to retain scheduled prefetched requests. If data cannot be accessed within this period, the requests will be removed from the system.
2. Select **Save**.

**Note**

Select **Reset** to restore the default settings.

### Add a prefetch policy

1. In the **Policies** area, select **Add**.
2. Enter the following information, then select **Save**.

**Name**

Policy name.

**Comment**

Policy description.

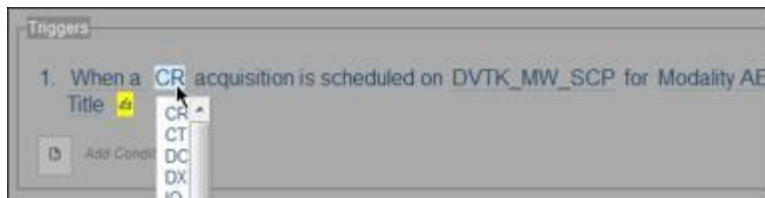
**Enabled**

If selected, the policy will be applied to NilRead data.

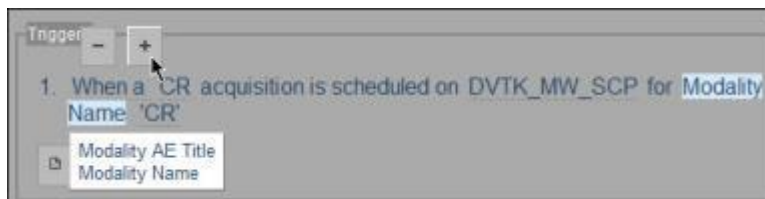
**Triggers**

Specify the triggers for the policy by adding one or more conditions. The policy actions will be triggered if any of the trigger conditions are satisfied.


1. Select **Add Condition**.
2. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.



3. To add an item, select a customizable area, then select **+**. To remove an item, select **-**.



4. To delete a condition, select the first customizable area, then select .

5. To move a condition to a new position, select the condition, then select .

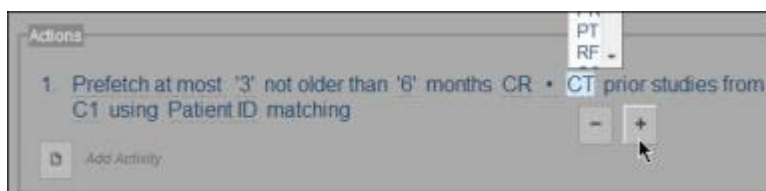
**Actions**

Specify the actions that will occur if any of the policies triggers are satisfied. Actions are executed in the order listed in the policy.

1. Select **Add Activity**.
2. Customizable areas are underlined and are highlighted when you hover over them. Click (or tap) a customizable area to edit it.



3. To add an item, select a customizable area, then select +. To remove an item, select -.



4. To delete an action, select the action, then select .

5. To move an action to a new position, select the action, then select .

### Edit or delete a prefetch policy

1. In the **Policies** area, select a policy.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Manage XDS settings

The XDS and XDS-I profiles (defined by Integrating the Healthcare Enterprise, or IHE) provide standards-based cross-enterprise document sharing among healthcare organizations. NilRead can be configured to use these profiles to obtain patient data from multiple healthcare organizations, allowing physicians to build comprehensive patient histories. NilRead XDS configuration requires the following steps.

- **XDS registry** Registry that stores meta-data for documents located in multiple XDS repositories (e.g. at multiple healthcare institutions).
- **Master Patient Index** Database that maintains a unique index for every patient registered at a healthcare organization. Alternatively, Patient Identity Domains can be specified instead of using the MPI.
- **XDS endpoints** Repositories that store patient documents.

## Add an XDS server configuration

You can create configurations for different XDS servers.

1. Select **Settings**.
2. Under **Devices**, select **XDS**.
3. In the **XDS Context** area, select **Add**.
4. Enter a name for the configuration, then select **Save**. The configuration has been created.
5. To enter the XDS server configuration settings, select **Edit**.
6. Enter information in the following sections, then select **Save**.

### XDS Content

- **Disable** Disable this XDS server. For example, you may want to exclude a server while it is undergoing maintenance.
- **MPI** Use the Master Patient Index (MPI) with this XDS server.
- **Reports** Select the report types to include (Approved, Submitted, Deprecated).

### XDS Registry

- **Address** XDS registry address.

If you selected MPI, enter the following additional information:

- **Application** XDS registry application name.
- **Facility** XDS registry facility name.

### Master Patient Index

This section is shown if you selected MPI. The MPI contains two integration profiles: PDQ (Patient Demographics Query) and PIX (Patient Identifier Cross Referencing).

- **Application** MPI application name.
- **Facility** MPI facility name.
- **PDQ Address** IP address (including port) of the TCP/IP network endpoint that NilRead XDS queries for MPI resolution.
- **PIX Address** IP address (including port) of the TCP/IP network endpoint that NilRead XDS queries for MPI resolution.

### Patient Identity Domain

This section is shown if you did not select MPI and allows you to enter patient identity domains manually.

1. In the **Patient Identify Domain** area, select **Add**. (To edit a domain, select the domain, then select **Edit**.)
2. Enter the following information, then select **Save**.
  - **Disable** Disable this patient identity domain.
  - **UID** Unique IHE identifier for the domain supplied by the issuer of the patient ID.



- **Domain** Patient identity domain (typically ISO).
3. To delete a domain, select the domain, then select **Delete**.

### XDS Endpoints

1. In the **XDS Endpoints** area, select **Add**. You can also select an existing endpoint, then select **Copy**. (To edit an endpoint, select the endpoint, then select **Edit**.)
2. Enter the following information, then select **Save**.
  - **Name** A unique friendly name to identify the endpoint.
  - **UID** Unique identifier supplied by the endpoint provider.
  - **Type** Endpoint type:
    - **XDS Repository** Endpoint supplying XDS documents.
    - **RAD 69 (Retrieve Imaging Document Set)** Endpoint supplying images over the RAD 69 protocol.
    - **RAD 55 (WADO Retrieve)** Endpoint supplying images over the RAD 55 protocol.
  - **Address** Web service address (URL) of the network endpoint that NilRead XDS queries for document or image resolution.
3. To delete an endpoint, select the endpoint, then select **Delete**.

## Manage IOCM

Image object change management (IOCM) manages the synchronization of changes applied on existing imaging objects between NilRead and remote servers. IOCM uses rejection notes (DICOM key object selection documents) to ensure that remote servers are notified when studies, series or images are deleted on the NilRead server, and that the NilRead server is notified when these items are deleted on a remote server.

Replacement instances can be sent to the remote server through the NilRead data lifecycle services (for details, see “Manage data lifecycle policies” on page 210). Alternatively, NilRead can send instance availability notifications (IAN) to remote application entities (AE). The notification contains the AE titles of the replacement instances, from which the replacement instances can later be retrieved. For details, see “Manage DICOM services” on page 203.

### NilRead rejection notes

If a study, series or image is deleted from the NilRead server, a rejection note is created with a list of the rejected (deleted) instances. Rejection notes are used to notify remote servers to delete these rejected instances. You can configure which remote servers receive NilRead rejection notes.

Rejection notes are created in the following scenarios:

- a user deletes a study from the Patient Study Directory
- a user edits a study and deletes the original study
- a user deletes a series from a study

- a user deletes an image from a study

By default, rejection notes generated by NilRead use the following title:  
(113039, DCM, "Data Retention Policy Expired")

## Received rejection notes

NilRead can also accept rejection notes from remote servers. If a study, series or image is deleted on a remote server and NilRead receives a rejection note, the rejected instances will be deleted on the NilRead server as well.

## Configure IOCM settings

1. Select **Settings**.
2. Under **Devices**, select **IOCM**.
3. Enter the following information, then select **Save**.
  - **Enable** Allow NilRead to send and receive rejection notes. If this option is disabled, NilRead will not create rejection notes. NilRead will still receive rejection notes from remote servers but the notes will not be applied.
  - **Accept rejection notes from** Select the types of sources that NilRead will accept rejection notes from.
  - **Send Nil rejection notes to** Select the remote application entities (AE) that NilRead will send rejection notes to.
  - **Generate rejection notes when delete** You can choose to create rejection notes when a study is deleted (**Study**) and when a series or images is deleted (**Series/instances**).
  - **Keep rejection notes for XX days** Number of days to keep rejection notes. Notes older than the retention period will be deleted the next time a scheduled data purge occurs. To remove older notes immediately, select **Purge** at the bottom of the page.

The **Rejection Notes** list contains the notes NilRead has sent and received. Rejection notes received from a remote server are applied automatically (check the timestamp in the **Applied** column to verify that a note has been applied). To apply a rejection note immediately, select the note, then select **Apply**. To delete a rejection note, select the note, then select **Delete**.

NilRead ignores all instances that have been rejected. If the rejected instances must be reimported, delete the corresponding rejection notes and resend the rejected instances to NilRead.

### Note

Rejection notes are also shown on the **DICOM Activity** page.

## Manage FHIR settings

NilRead can be configured to access FHIR® reports on a FHIR resource server. FHIR (Fast Healthcare Interoperability Resources) is a next generation standards framework created by HL7. FHIR reports can be accessed the same way as other reports in NilRead (on the patient timeline and in the Patient Directory).

NilRead FHIR configuration requires the following steps.

1. Enable FHIR reports for the site.
2. (Optional) Modify the FHIR report templates for the site.
3. For each FHIR service you want to use:
  - a. Register with the FHIR service.
  - b. Add an endpoint for the FHIR service. This contains the settings that allow NilRead to access the FHIR resource server.
  - c. Add a device for the FHIR service. This is required in order to load FHIR reports from the service.

## Enable FHIR reports for the site

To enable FHIR reports for the site, add the highlighted parameter to the `configs/Nil.config` file within your NilRead site folder (for example: `C:\inetpub\wwwroot\Nil\Nil-4.3.22.95194-Site\configs\Nil.config`).

```
<setting name="DicomBeReportSources" serializeAs="Xml">
  <value>
    <ArrayOfString xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
      xmlns:xsd="http://www.w3.org/2001/XMLSchema">
      <string>Claron.Nil.DicomBE.DataProvider.FhirReportSource, Claron.Nil.DicomBE.DataProvider</string>
    </ArrayOfString>
  </value>
</setting>
```

## Modify FHIR report templates

NilRead uses XSL transformation (XSLT) templates to render FHIR reports. You can change the appearance of FHIR reports for your site by modifying these templates. For example, you could add a logo to the reports.

The FHIR report templates are located in the `App_Data/DicomSRTemplates` folder within your NilRead site folder (for example: `C:\inetpub\wwwroot\Nil\Nil-4.3.22.95194-Site\App_Data\DicomSRTemplates`). This folder contains two XSLT templates you can modify: `FhirReportNarrativeTemplate` and `FhirReportTemplate`.

Some FHIR reports have a built-in narrative. To render FHIR reports with the built-in narrative (when available), add the following parameter to the `configs/Nil.config` file within your NilRead site folder. Set the value to `False` to use the NilRead report templates. Set the value to `True` to use the built-in narrative (the NilRead report templates will be used if a built-in narrative is not available).

```
<setting name="FhirDiagnosticReportShowNarrative" serializeAs="String">
  <value>True</value>
</setting>
```

## Register with a FHIR service

Register with each FHIR service you want to use. See the FHIR service web site for details on registering and creating an app to use with NilRead.

## Add an endpoint

Add an endpoint for the FHIR service resource server. The endpoint configuration is based on the SMART on FHIR open specifications.

1. Select **Settings**. Under **Devices**, select **FHIR**.
2. In the **Endpoints** area, select **Create**.
3. Enter the FHIR endpoint information. This information will depend on the service you registered with. For example, the service will require you to use a specific authorization grant type. The required endpoint fields will change based on the authorization grant type you select.
4. Select **Verify** to test the configuration settings.
5. Select **Save**.

## Add a device

Add a device for the FHIR endpoint resource you want to use for reports.

1. Select **Settings**. Under **Devices**, select **FHIR**.
2. In the **Devices** area, select **Create**.
3. Enter the following information.
  - **Name** Name for the device.
  - **Endpoint** Endpoint to use with the device.
  - **Resource Type** Type of resource to retrieve. Select **DiagnosticReport** to create a report.
  - **Filter, Patient Identifier Filter** Search filters to use when querying the FHIR service. Use `$(DicomTagName)` to specify the query values NilRead should use. For example, NilRead will replace `$(AccessionNumbers)` with the actual accession number from the study when submitting the query.
4. Select **Enabled** to allow NilRead to query the FHIR service and retrieve reports.
5. Select **Verify** to test the configuration settings.
6. Select **Save**.


## Edit or delete an endpoint or device

1. Select an endpoint or device.
2. Select **Edit**. Modify the details, then select **Save**.  
or  
Select **Delete**.

## Check the status of a FHIR endpoint

You can check if NilRead is currently authorized to access a FHIR endpoint. You may need to refresh the FHIR endpoint connection periodically if the authorization period has expired. Depending on the authorization type, you may be prompted to log into the FHIR service in order to access the endpoint.

The message "Check FHIR endpoint status" will appear on a FHIR report if NilRead is not able to access the FHIR endpoint. This message will also appear in the image viewing area if the study contains an FHIR report and NilRead is not able to access the FHIR endpoint.

1. Select **Settings**. Under **Devices**, select **FHIR**. In the **FHIR Status** section, select **Check FHIR endpoint status**.  
or  
Click (or tap) the "Check FHIR endpoint status" message in a report or the image viewing area.
2. The **FHIR Endpoint Status** window appears. Endpoints that NilRead is currently authorized to access are shown in green.
3. To refresh all endpoints, select **Refresh**. To refresh a specific endpoint, select  beside the endpoint.
4. If prompted, log into the FHIR service.
5. Select **Close**.

## Manage system preferences

### ADMINISTRATORS ONLY

You can manage system settings, such as the region where NilRead is deployed.

1. Select **Settings**.
2. Select **System**. You can change the following settings:
  - General
  - Launch
  - Patient Search
  - Patient Search Panel
  - Collaboration
  - Login
  - Timeline
  - Timeline Reports
  - Image Display
  - Third Party Applications

## View the dashboard

Use the dashboard to view system information and counters regarding NilRead components and operational environment. The Dashboard is only available for single tenant configurations of NilRead.

1. Select **Settings**.
2. Select **Dashboard**. The dashboard contains the following areas:
  - **Server Status** NilRead server system level information including the server name, build version, current CPU utilization, available RAM, and current number of users. Select the number of users to view statistics for the users currently logged into NilRead.
  - **DICOM Statistics** NilRead DICOM service counters, including CPU utilization, inbound throughput, and total number of imported studies and images.
  - **User Statistics** Statistics for the users currently logged into NilRead, including the user account name, current session start time, and recent inactivity time.
  - **Database** Database information, including the database server name, database name, current database size, and database capacity usage.
  - **Licensing** NilRead licensing information, including the maximum number of concurrent users, expiration time, and enabled NilRead features.
  - **Network** NilRead server network interface card information, including the adapter name, network utilization, link speed, and operational status.

## View analytics

Use the NilRead analytics to view detailed information including audit trails, user activity, study access and load-balancing statistics.

1. Select **Settings**.
2. Select **Analytics**. You can view the following information:
  - Patient audit trail
  - User activity
  - Event audit trail
  - Patients accessed by user
  - Top users by patient access
  - Study access by modality
  - User login load-balancing across servers
  - Study review load-balancing across servers
  - Study review distribution over time
  - Login distribution over time

## View federation statistics

ADMINISTRATORS ONLY

Federation statistics are only available for single tenant configurations of NilRead.

1. Select **Settings**.

2. Select **Federation**. You can view the following information:

- Status
- Archiving & Backup
- Software Updates
- Network Utilization