Hyland

NilRead

User Guide

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Trademarks

Contact Us

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

Direct: 913-227-7030

Customer Portal: **https://community.hyland.com**

Manufacturer

Hyland Software Canada ULC

111 Peter Street, Suite 540

Toronto, Ontario, M5V 2H1

Canada

NilRead_info@hyland.com (for Vigilance reporting only)

Intended use

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**). For hardware requirements and supported browsers, see **Hardware requirements**. Please also review the **Warnings and precautions**.

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**).

⚠ View additional regulatory information including warnings and precautions.

Version number

The NilRead version number can be viewed at **Setting** -> **Product information** -> **NilRead**.

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

WARNING	⚠	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.
CAUTION	❗	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

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

⚠ 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**). 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. The diagnostic quality image is presented at the end of the manipulation, as part of a progressive refinement display. Lossless images are marked with an HD label.

❗ NilRead has been qualified on a variety of operating system and browsers (see **Device specifics**). 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.

⚠ The stitched image is created to allow accurate measuring of distances and angles by qualified medical practitioners. Any incidental clinic findings that are seen on the source of stitched images should be verified or further evaluated by additional diagnostic methods.

⚠ A misconfigured Auto Reconciliation can have a direct impact on patient safety, including incorrect diagnosis due to the patient information/image mismatch and/or delay in diagnosis due to images not being available in the patient record. The system administrators shall ensure that sufficient parameters (such as First name, last name, DOB, Gender) are configured.

⚠ The data upload may result in illegal or inappropriate images being ingested into the system that can potentially introduce cybersecurity risks. The hospitals are responsible to implement the cybersecurity best practices.

⚠ The uploading/Patient portal can only be activated under the consensus of hospital and/or the healthcare provider, and distributed under this consensus.

⚠ Non-compliant Dicom data can have a direct impact on patient safety including the incorrect or delayed diagnosis. The hospitals are responsible to monitor and ensure Dicom compliance of connected entities.

⚠ Referential Pathology Studies are not intended for diagnostic image review. The use of this feature is intended for information purposes such as multidisciplinary patient management meetings or patient consultation.

⚠ When using the option to Auto-load and visually merge studies with the same Accession Number, the system will group together series, annotations, labeling, and other artifacts from multiple independent studies under a single view in various areas of the software and can result in incorrect diagnosis. Please ensure that the data is suitable for this option and that users receive adequate training.

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.

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 “Compressed” 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 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 and breast tomosynthesis. NilRead also allows users to collaborate by sharing application sessions.

Lossy compressed mammographic images are not intended for diagnostic review. Mammographic images should only be viewed with a monitor approved by FDA for viewing mammographic images. For primary diagnosis, post process DICOM “for presentation” images must be used.

On mobile platforms, this device is not intended for diagnostic use.

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® Edge® (81.0)
- Mozilla® Firefox® (75.0 and higher)
- Google Chrome™ (81.0 and higher)
- Apple® Safari® (8.0 and higher)

Mobile devices

NilRead is verified to work for clinical reference only on the following mobile devices:

- Apple® iPhone® (iOS 12.0 and higher)
- Apple® iPad®
- Android™ devices (11.0 and higher)
- Microsoft® Surface™ (Windows 10)

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 mobile devices, images are displayed for informational purposes only — NilRead is not for diagnostic use on mobile devices.

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**
- **Canadian Association of Radiologists 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.

Touch gestures

You can use touch gestures in the image viewer. The default actions for each gesture are shown below. For details on customizing touch gestures, see **Change mouse, keyboard and touch preferences**.

- **Pan and Zoom** Pinch-to-zoom.
- **Scroll** Touch and drag.
- **Window Level** Three finger drag.
- **Reset** Shake the device.
- **Maximize a viewport** Double-tap.

Reading environment verification

NilRead provides a reading environment verification tool to assist the user in adjusting device settings (such as brightness) on mobile platforms. It is recommended that users keep mobile screens clear of thumbprints and dirt and that they disable the auto brightness adjustment.

Follow these steps to perform a reading environment verification.

1. Select **Settings**. Under **Preferences**, select **Reading environment verification**.
2. A low contrast pattern is shown in the viewport. Note that in the following example, the contrast has been highlighted for demonstration purposes.

Touch the low contrast patch to verify the reading environment

Verification not completed

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. 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 viewing images on a mobile device. 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.

Studies

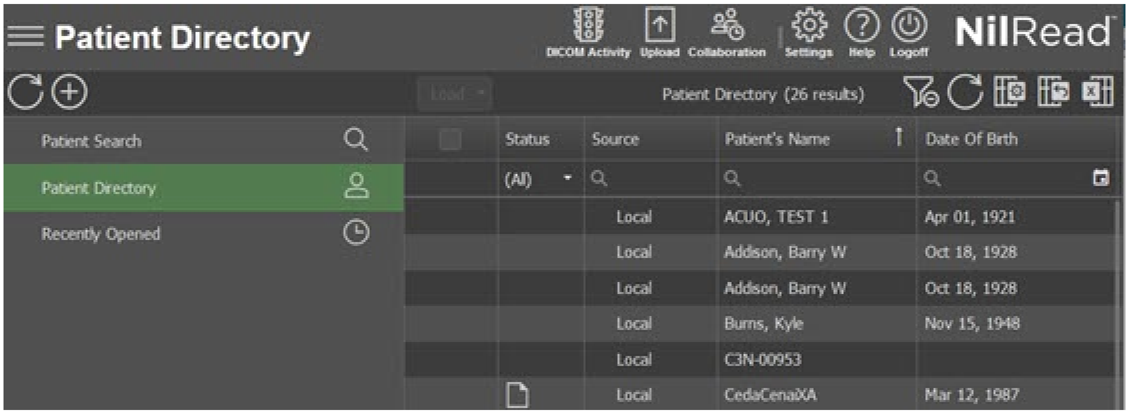
Open a study

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

Notes

- 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.
- 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**.
- 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**.

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



Patient Directory (26 results)

☐	Status	Source	Patient's Name	Date Of Birth
	(All)			
		Local	ACUO, TEST 1	Apr 01, 1921
		Local	Addison, Barry W	Oct 18, 1928
		Local	Addison, Barry W	Oct 18, 1928
		Local	Burns, Kyle	Nov 15, 1948
		Local	C3N-00953	
	🗋	Local	CedaCenaXA	Mar 12, 1987

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.

Preview a series

Prerequisites

You must activate the **Show series preview on single click** option in the **Settings**. For more information, see **Manage preview settings**.

To preview a series in the Patient Directory:

1. In the **Patient Directory**, click on a study row.
   The thumbnails of the series appear in the bottom pane.
2. To hide the preview, click the hamburger icon on the left above the series preview.
3. To view the reports for a study, select the folder icon left to the patient name.
   For more information, see **View reports**.

Note
The series preview and the report are synchronized to always display the data for the selected study.

Use presentations

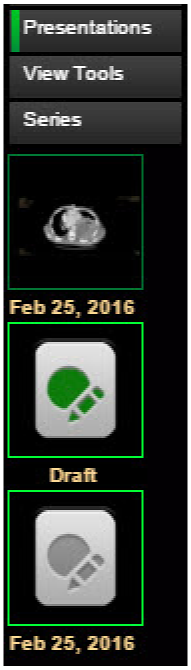
The measurements and annotations you apply to an image are saved in a presentation.

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**.

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 create annotations and measurements but your changes will not be saved.

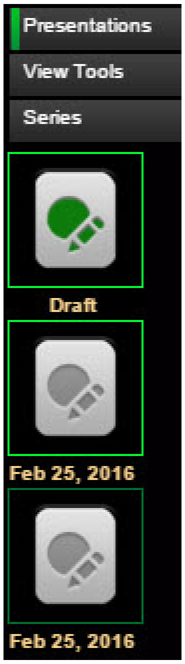
Select presentations

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.

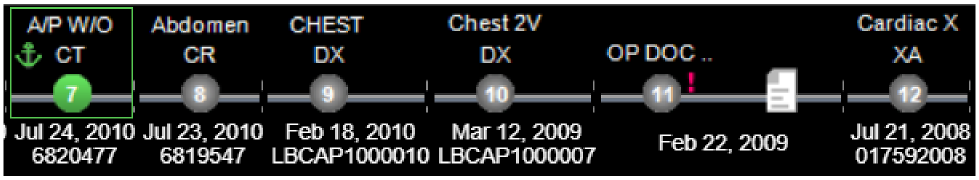
If you choose to allow transient in-session overlays, the Presentations label in the bottom-left corner of the image will contain the word “Transient”, indicating that your changes will not be saved.

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.



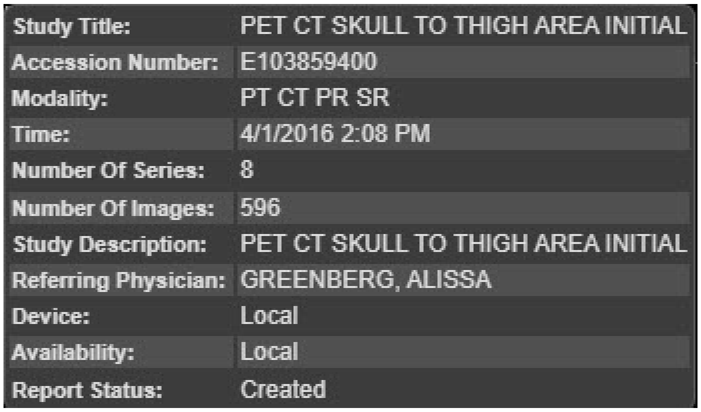
> **Note**
>
> The timeline is only shown if enabled by the system administrator.

The following information is shown on the timeline:

- Prior studies and DICOM embedded PDF reports are shown in chronological order.
- Anchor indicating this is the current study.
- If the **Auto-load and visually merge with the same Accession Number** option is active, a plus sign next to the number indicates that the studies are displayed merged.
- Exclamation mark to identify if a warning exists for a study or report.
- Number of studies including the modality.
- Date of the report
- Accession number
- Study description

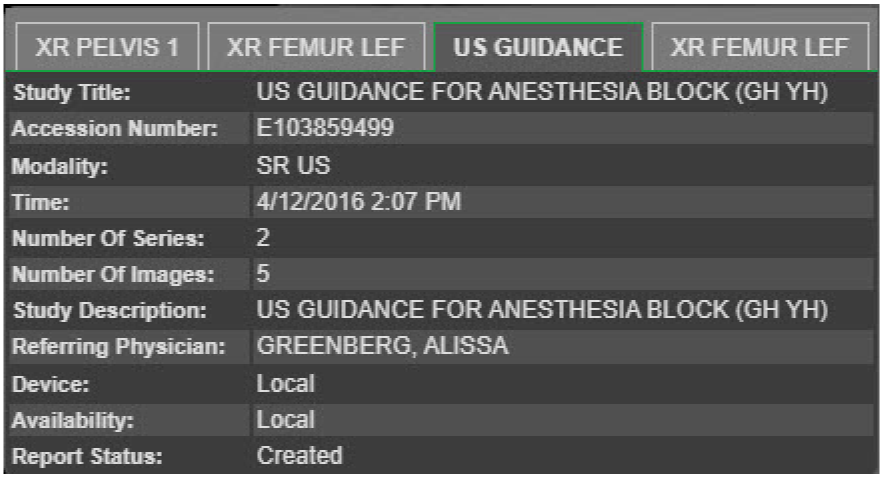
View study or report details

Hover over a study or report in the timeline to view more detailed information.



Study Title:	PET CT SKULL TO THIGH AREA INITIAL
Accession Number:	E103859400
Modality:	PT CT PR SR
Time:	4/1/2016 2:08 PM
Number Of Series:	8
Number Of Images:	596
Study Description:	PET CT SKULL TO THIGH AREA INITIAL
Referring Physician:	GREENBERG, ALISSA
Device:	Local
Availability:	Local
Report Status:	Created

If the **Auto-load and visually merge with the same Accession Number** option is active, the tooltip displays all studies with the same accession number in chronological order.



Study Title:	US GUIDANCE FOR ANESTHESIA BLOCK (GH YH)
Accession Number:	E103859499
Modality:	SR US
Time:	4/12/2016 2:07 PM
Number Of Series:	2
Number Of Images:	5
Study Description:	US GUIDANCE FOR ANESTHESIA BLOCK (GH YH)
Referring Physician:	GREENBERG, ALISSA
Device:	Local
Availability:	Local
Report Status:	Created

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.

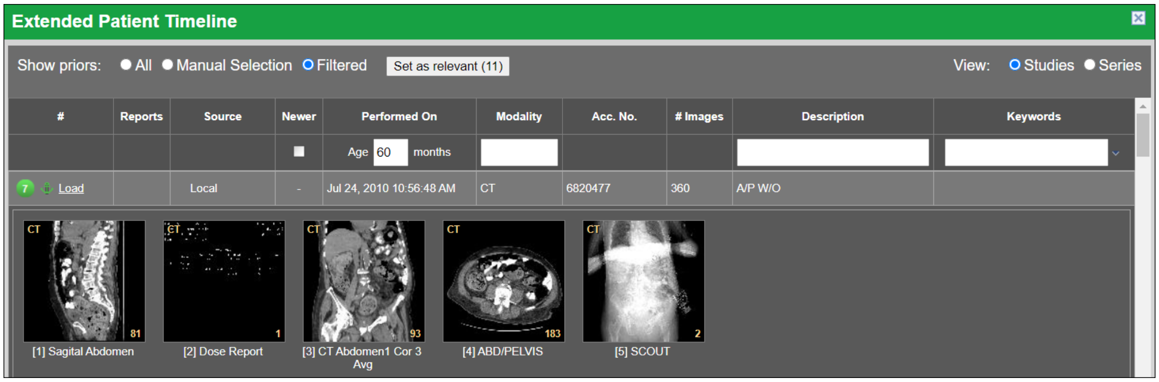
Select priors to include in the timeline

You can select the priors to include in the timeline.

1. Select the **Filter icon** located at the right side of the timeline. The number under the icon indicates how many studies are displayed in the timeline (for example, All or 2/3).

   The **Extended Patient Timeline** dialog box is displayed.

   Extended Patient Timeline

   Show priors: ● All ● Manual Selection ○ Filtered Set as relevant (11) View: ○ Studies ● Series

#	Reports	Source	Newer	Performed On	Modality	Acc. No.	# Images	Description	Keywords
			☐	Age 60 months					
7 Load		Local	-	Jul 24, 2010 10:56:48 AM	CT	6820477	360	A/P W/O	

2. Select **Set as relevant**. The selected prior studies are shown in the timeline.
3. To filter the available priors, select one of the following options beside **Show priors**:

   All. Include all priors.

   Manual Selection. Select the check box for the prior to include.

   Filtered. Enter search information in the blank row below the column headings. You can select priors based on **Age**, **Modality**, **Description** and **Keywords**.

4. To load a prior in the image viewer, select the prior study, then select **Load** link.

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 behavior is only available for priors located on dicom devices using a ‘cache’ retrieve mode.

Filter the timeline using one-click

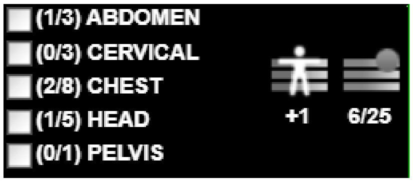
When viewing a patient's timeline, you can filter the studies according to keyword(s) associated with that study.

In order to see keywords, you must have the following options enabled:

- **Enable study keyword tagging** enabled through **Settings | System | Timeline** (option available to system administrators only).
- Matching Hanging Protocols Templates configured through **Settings | Hanging Protocols | Rules Templates**.

To filter the timeline using one or more keywords:

1. At the far right of the timeline, select the checkbox(es) for the applicable keyword(s). The number in parentheses indicates the number of studies shown, All matching studies are displayed in the timeline.



☐ (1/3) ABDOMEN
☐ (0/3) CERVICAL
☐ (2/8) CHEST
☐ (1/5) HEAD
☐ (0/1) PELVIS

If no keywords have been associated with a study, the text "no keywords found" is displayed inside of the keyword list.

2. To see what keywords are associated with a particular study, hover over the study to display the keyword information.

3. To update the timeline and remove any previously selected keywords, select the checkbox for the applicable keyword(s).

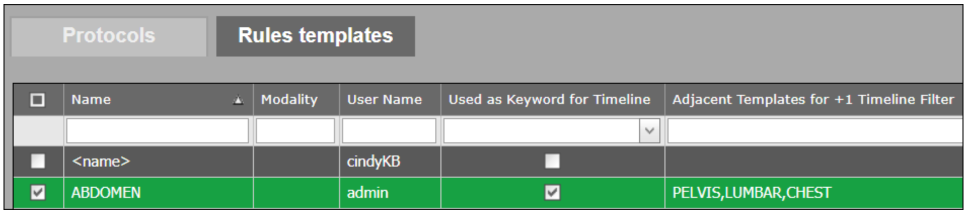
> **Note**
> It is possible to filter the timeline entries only by keywords, ignoring any other existing timeline filters. This option is available by enabling the **Available Keyword Matching Only** option through **Settings** | **User Preferences** | **Patient History**.

Filter the timeline using Plus One (+1)

The Plus One (+1) feature expands the studies in the timeline based upon the adjacent keyword relationship as defined in the **Rules Templates**. This allows you to append the current study type with other relevant studies, allowing for easier and quicker viewing of related material.

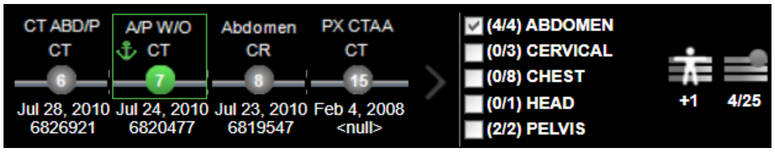
Example scenario

- The Rules templates for **ABDOMEN** includes the adjacent templates **PELVIS, LUMBAR and CHEST** (as these are body parts adjacent to the ABDOMEN).

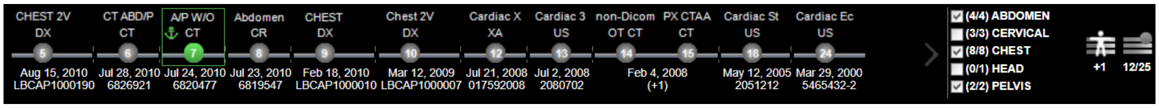


☐	Name	Modality	User Name	Used as Keyword for Timeline	Adjacent Templates for +1 Timeline Filter
☐	<name>		cindyKB	☐	
☑	ABDOMEN		admin	☑	PELVIS,LUMBAR,CHEST

- On the timeline, the **ABDOMEN** keyword is selected, and the timeline looks like this:



- When the **+1 icon** is selected, the keyword(s) defined as adjacent to the ABDOMEN in the Rules templates are automatically selected; for example, CHEST and PELVIS. The timeline is updated and shows all the relevant studies by date.



- If you continue to click the **+1 icon**, more adjacent keywords are selected, and more studies are shown based. For example: The ABDOMAN, CHEST and PELVIS keywords are selected. When you select **+1 icon**, the adjacent keywords for CHEST - CERVICAL and HEAD - are selected, and the timeline is appended with the relevant studies.
- If all keywords are selected and you select the **+1 icon**, all the keyword selections are cleared.

Timeline display options

The timeline display can be changed in several ways:

- Hovering over the image area to bring the timeline to the foreground.
- Using the collapse/expand arrow widget to hide the timeline.
- Changing the **Workstation Preferences | Image viewer controls | Always show timeline** to **Yes** so that the timeline displays a separate area, and not overlapping the image.

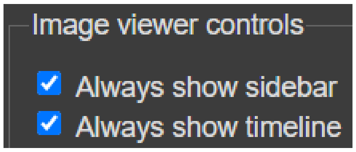
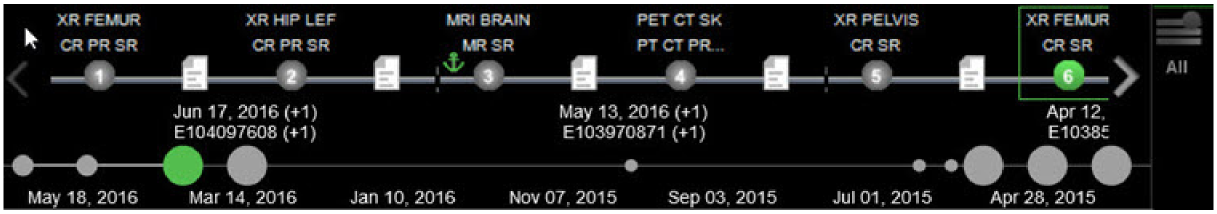


Image viewer controls
☑ Always show sidebar
☑ Always show timeline

Use the timeline heatmap

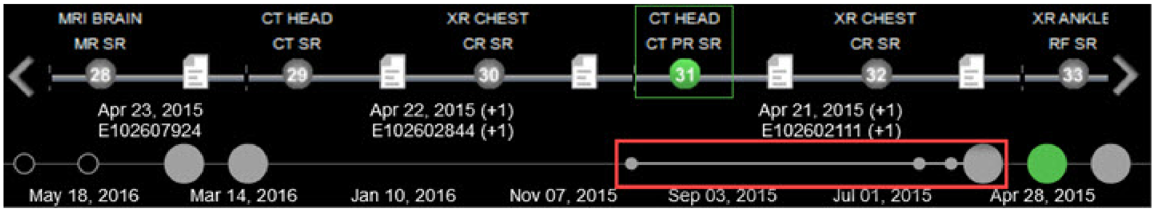
The timeline heatmap is displayed below the patient timeline and shows the entries on a proportional time scale to provide a better overview of the patient's history.



The heatmap provides the following information:

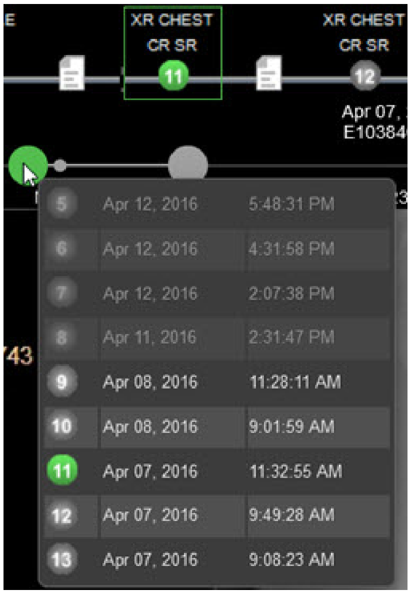
- Each circle on the heatmap represents a set of studies, where the size of the circle is proportional to the number of studies in the time slot - 1, 2, 3, and 4 or more studies.
- The currently selected set is displayed as a green circle.
- Sets containing only filtered out studies are displayed as hollow circles: .

- In contrast to the patient timeline, the timeline heatmap is always displayed entirely and adjusts to fit the available space.
  The currently displayed part of the patient timeline is represented by a slightly thicker line on the heatmap.



To view the set of studies represented by a circle:

1. Hover over the circle. The list of studies appears as a tooltip, with filtered out studies grayed out.



5	Apr 12, 2016	5:48:31 PM
6	Apr 12, 2016	4:31:58 PM
7	Apr 12, 2016	2:07:38 PM
8	Apr 11, 2016	2:31:47 PM
9	Apr 08, 2016	11:28:11 AM
10	Apr 08, 2016	9:01:59 AM
11	Apr 07, 2016	11:32:55 AM
12	Apr 07, 2016	9:49:28 AM
13	Apr 07, 2016	9:08:23 AM

2. To open a study, select it in the tooltip list.

Display the timeline heatmap

To display the timeline heatmap for all instances of the system:

1. Select **Settings**.
2. Under **System**, select **Timeline**.
3. In the **System - Timeline** pane, select **Show heatmap**.
4. Click **Save**.

> **Note**
> This setting is available to administrators only.

Users who do not have administrator privileges can display the timeline heat map for their own account:

1. Select **Settings**.
2. Under **Preferences**, select **Viewer Preferences**.
3. In the **Preferences - Viewer Preferences** pane, below **Patient History**, select **Show heatmap**.
4. Click **Save**.

Image stitching

Use image stitching to assemble several images into a larger, more cohesive image. This can be useful to produce an image containing a larger area or an entire body part to which measurements can be applied.

> **Important**
> The images will be stitched in the order you select them. **For the best results, stitch images sequentially from top to bottom.**

1. Open a study.
2. In the side panel, select the first image in the sequence.
3. Select **View** (toolbar), then select **2D View > Stitch Editor**.

4. In the side panel, continue to select the images you want to stitch together. The images will be stitched in the order you select them. **For the best results, stitch images sequentially from top to bottom.**
5. To remove an image from the stitched image, right-click (or touch and hold) the image, then select **Delete**.
6. To fine-tune the stitched image, zoom in and drag the images to align them more precisely. To zoom in on the stitch areas, select **View Tools** (side panel), then select **Zoom on Stitch** to view the first stitch area. Select **Zoom on Stitch** again to view the next stitch area. To view the entire image again, select **Fit View**.
7. When done, select **Save** from the **View Tools** panel. The stitched image is saved in a new series.

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).

Add notes to a study

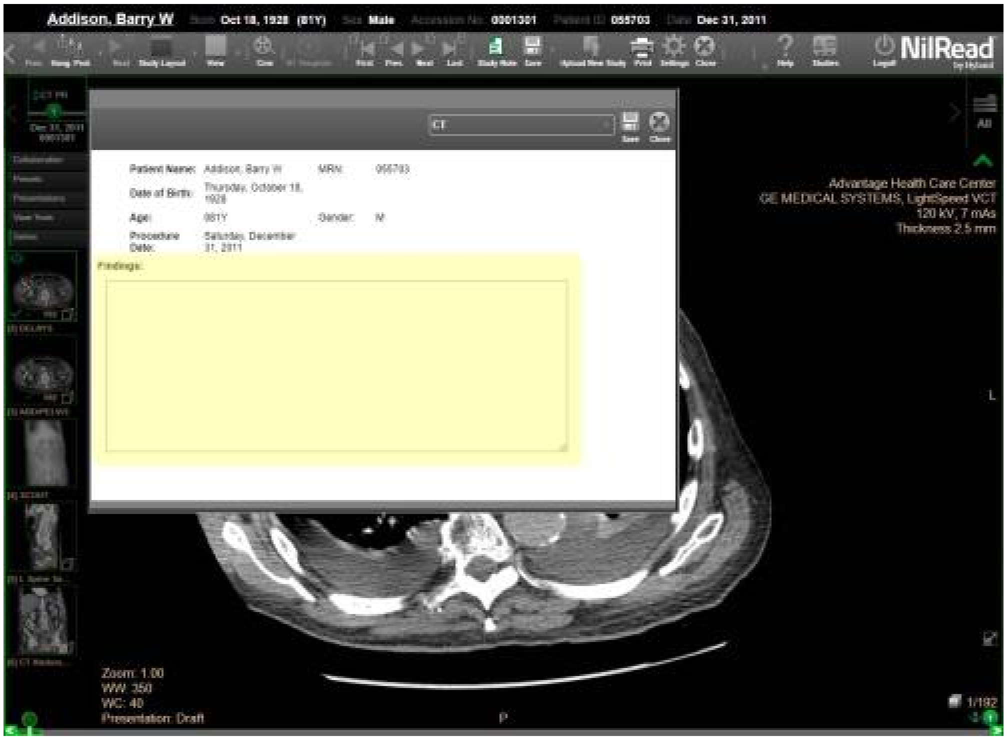
You can add notes as you are reviewing a study. These notes are available until you close the study.

You can also save the notes as a report. The report 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 study note templates**.

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.



Patient Name: Addison, Barry W
MRN: 055703
Date of Birth: Thursday, October 18, 1928
Age: 081Y
Gender: M
Procedure Date: Saturday, December 31, 2011
Findings:

4. To create a report, select **Save**, then select **Close**.
5. If you do not want to create a 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 only change window level.
- **3D** Presets can change rendering mode and opacity.
- **Sculpting** Presets can change rendering mode and opacity.

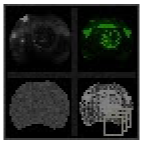
When you apply a preset, any changes you have made to an image will be removed (rotation, annotations, etc.). Any changes you make to a preset are not saved.

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**.

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:



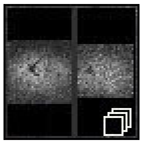
When you hover over the series, the description is **All images**.

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.

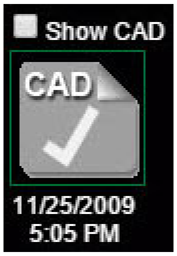
- Scrolling through the series will scroll through each pair of images.

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. Deselect **Show CAD** to hide CAD marks.

Use implant masks to reduce brightness

NilRead applies a mask to implants in mammography images to reduce their brightness. You can choose to remove this mask when viewing an image.

- To remove implant masks for the current image, select **Titles** (toolbar), then deselect **Implant Masks**.
- To reapply implant masks for the current image, select **Titles** (toolbar), then select **Implant Masks**.

View DBT slice position

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

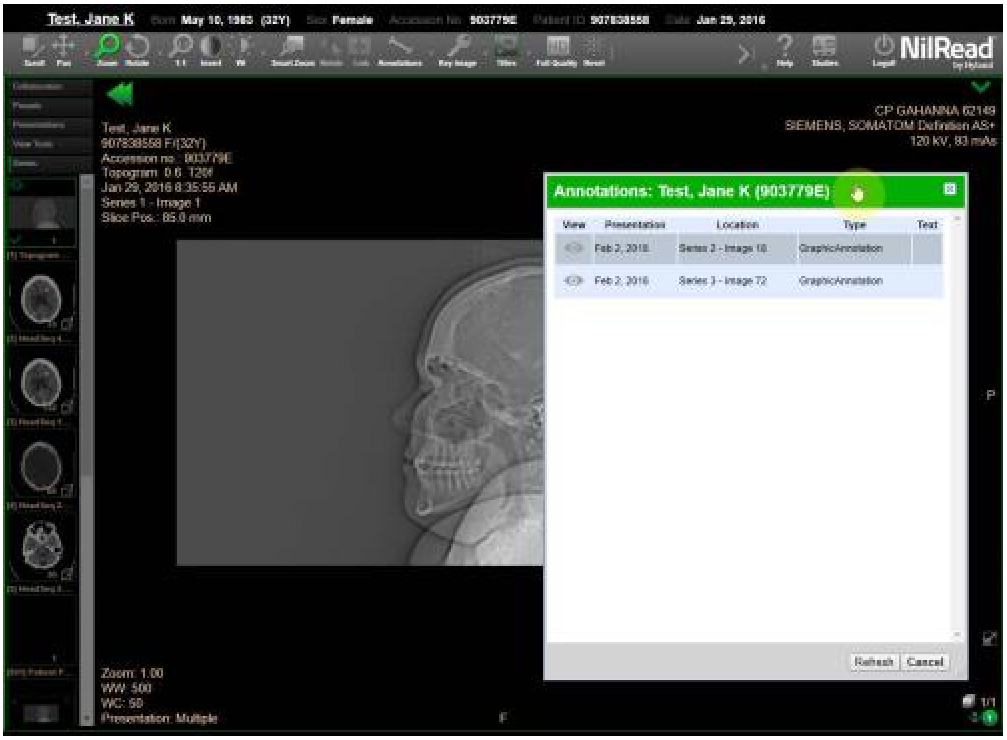
The indicator shows the current slice, total number of slices, and an orientation marker (F = feet, H = head).

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.



Annotations: Test, Jane K (903779E)

View	Presentation	Location	Type	Text
	Feb 2, 2016	Series 2 - Image 10	GraphicAnnotation	
	Feb 2, 2016	Series 3 - Image 72	GraphicAnnotation	

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

Annotations: Test, Jane K (903779E)

View	Presentation	Location	Type	Text
	Feb 2, 2016	Series 2 - Image 18	GraphicAnnotation	
	Feb 2, 2016	Series 3 - Image 72	GraphicAnnotation	

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

Edit videos

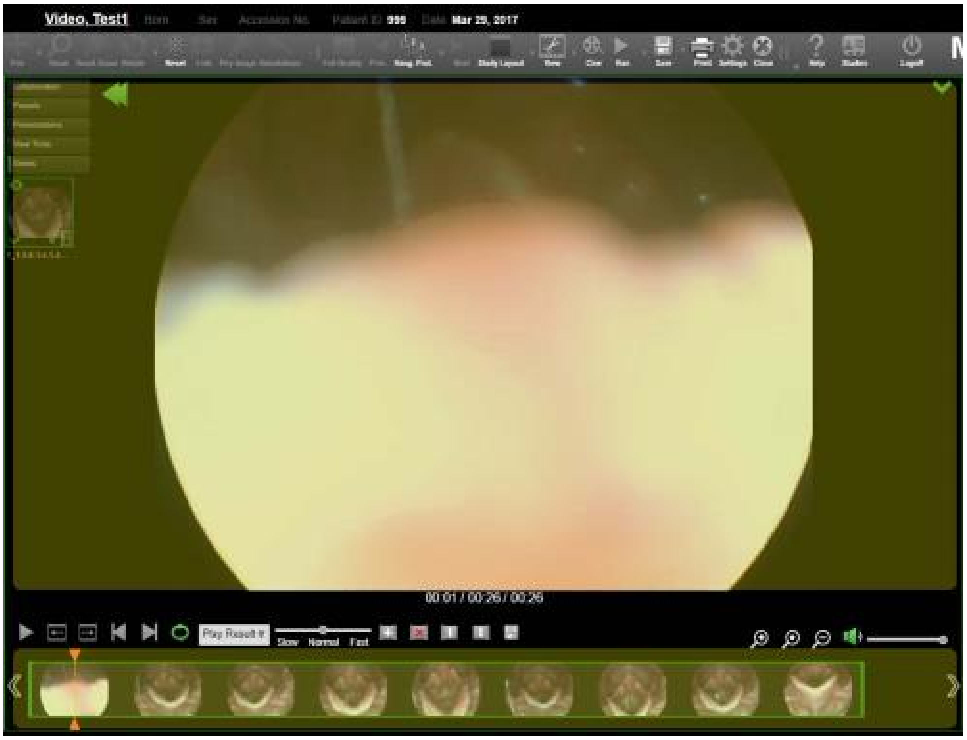
You can edit a video to remove irrelevant information. The segments of the video you want to retain are saved as a new video. The original video also remains in the study and is not modified.

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.

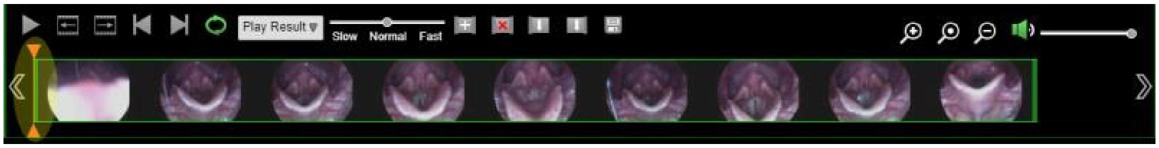
> **Note**
> If you open a video from the QC viewer, the video automatically opens in the video editor.

The video editor contains the following sections.

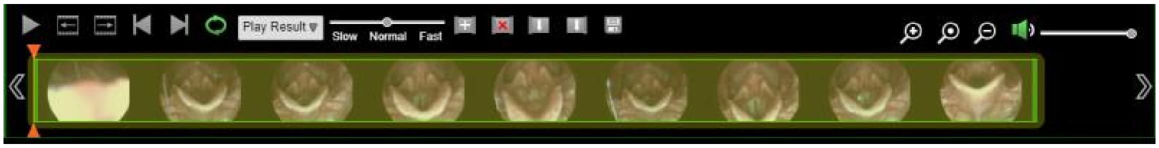
- The **preview window** at the top of the screen shows the location currently selected in the timeline. The **timeline** at the bottom of the screen contains thumbnail images of the video content.



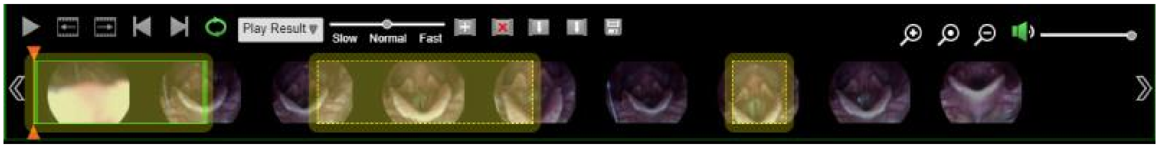
- The **position indicator** shows the current location in the video. When you first open the editor, the position indicator is at the start of the video.



- 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.



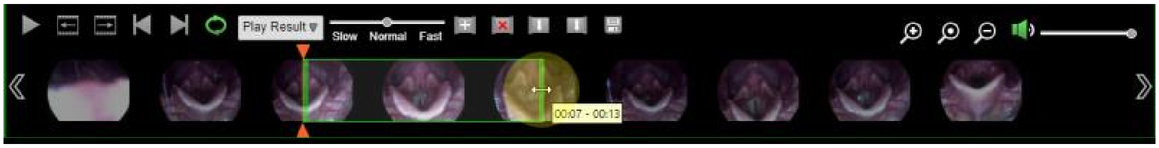
The following information is shown below the preview window.

- 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.

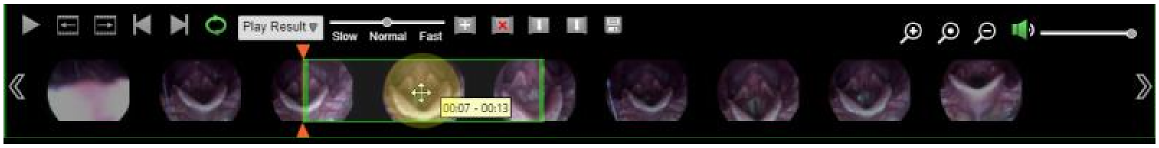
Video, Test1 Born Sex Accession No. Patient ID **999** Date **Mar 29, 2017**

Modify a selection box

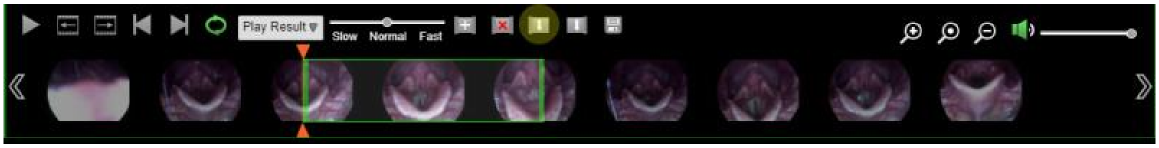
- Drag the ends of the box to resize it.



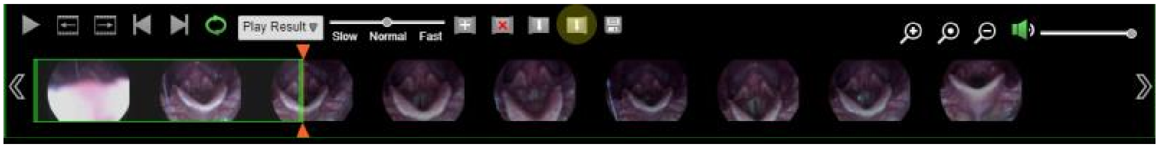
- Drag the box to a new position.



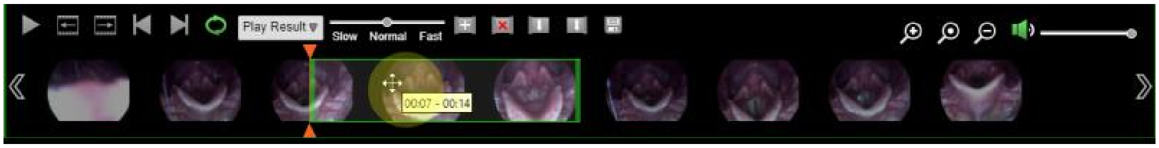
- To set the beginning of the box to the position indicator location, select the box, then select ⬇.



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



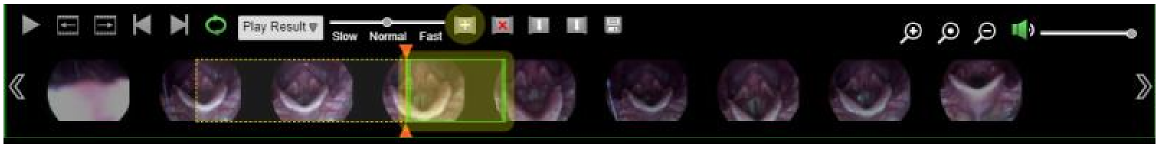
- Hover over a box to view the timeframe of the original video within the box.



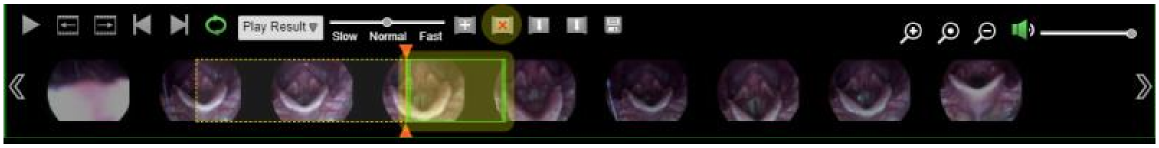
Add and remove selection boxes

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

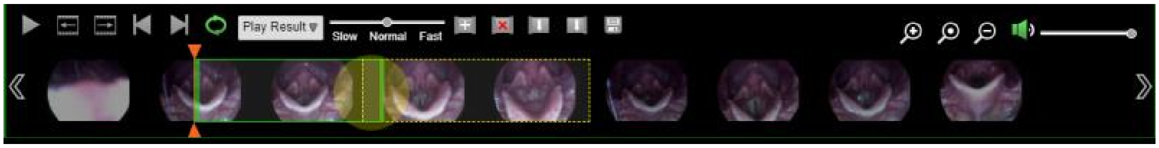
- To add a box, select +. A new box appears to the right of the current box. Change the box position and size as needed.



- 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.

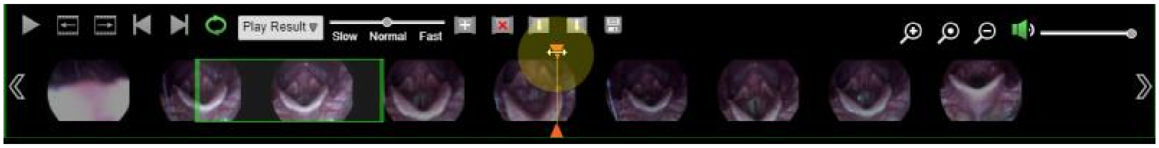
🔍	Increase the thumbnail size. This allows you to view the thumbnails more clearly; however, this reduces the number of thumbnails shown on the screen.

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

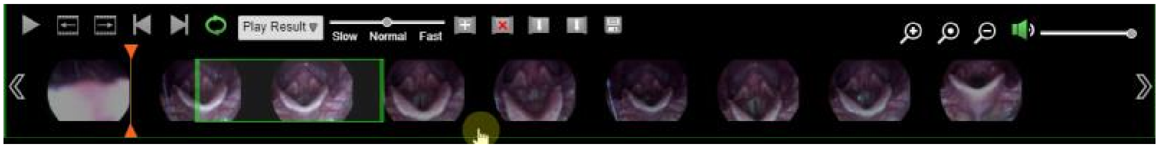
Change the position indicator

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

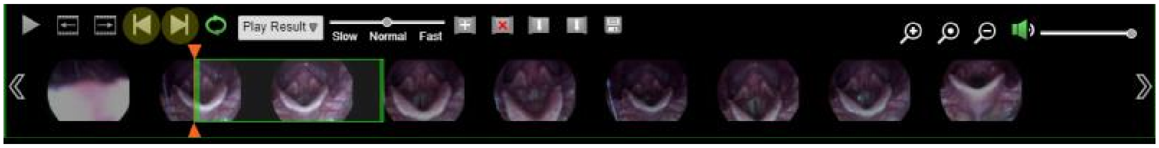
- Drag the position indicator to a new location on the timeline.



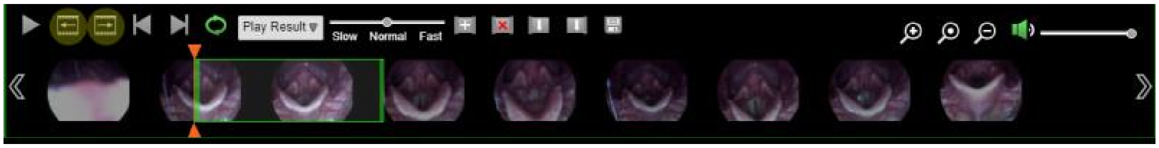
- Click (or tap) above or below the timeline to move the position indicator to a new location.



- 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**.

Track review status

You can use folders to track whether studies have been reviewed. A typical example is to group studies that require review in a **For Review** folder, then move these studies to a **Reviewed** folder once they have been reviewed.

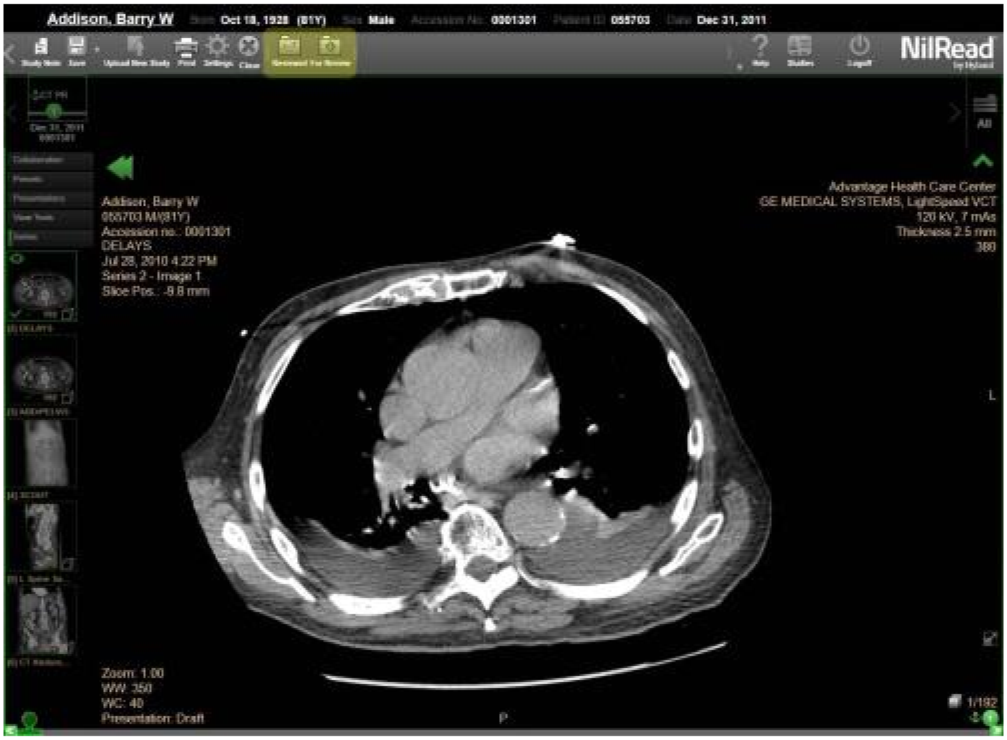
Organize studies in review folders

The folders used to review studies (such as **For Review** and **Reviewed**) must be created by an administrator. The administrator will grant access to these folders to authorized users who can then add studies to the folders. Note that you can use more than two folders for the review process and can use any name for the folders. Contact your NilRead administrator to discuss your review folder requirements.

Manage reviewed studies

When viewing a study in the image viewer, icons for the review folders are shown in the toolbar. The highlighted icon indicates which folder the study currently belongs to. For example, the following study is in the **For Review** folder. Once the study has been reviewed, select the **Reviewed** icon to move the study to the **Reviewed** folder.

Note
These are example icons. In general, click a folder icon to move the study to the folder.

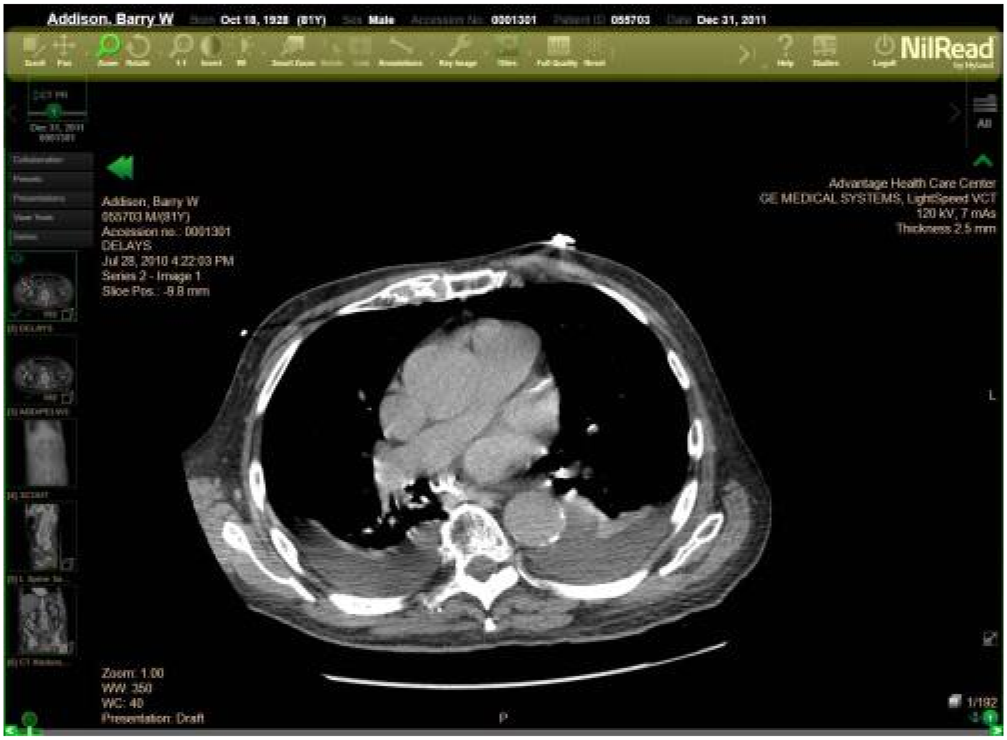


Note

The review folder icons must be created by an administrator. For more information, see **Set up review folders**.

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**) and assign tools to mouse buttons, keyboard shortcuts and touch gestures (see **Change mouse, keyboard and touch preferences**).

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

Note

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**).

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

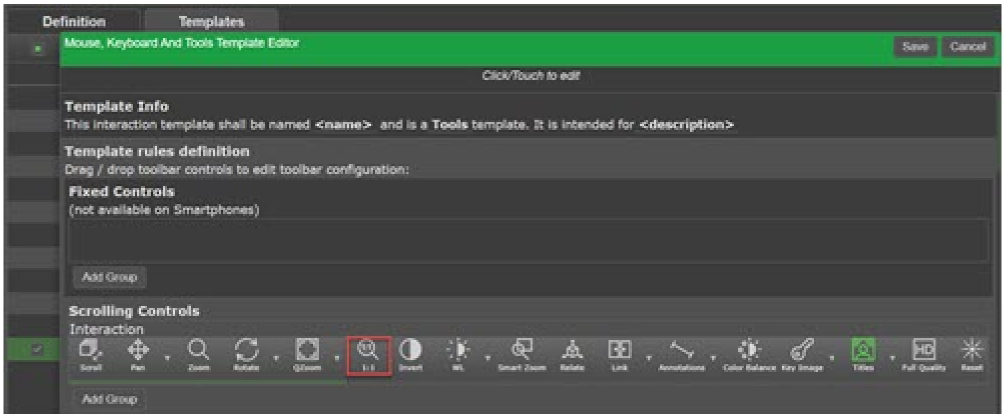
Check the following display settings for your monitor.

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**.



Template Info
This interaction template shall be named **<name>** and is a **Tools** template. It is intended for **<description>**

Template rules definition
Drag / drop toolbar controls to edit toolbar configuration:

Fixed Controls
(not available on Smartphones)

Scrolling Controls
Interaction

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.

Gamma

γ

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**).
- 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.

Note

Measurement units are set in your user preferences.

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 plumblines 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.

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.

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.

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.

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.

Cobb Multi-Angle

Click (or tap) and drag to create the first line of the Cobb angle, then drag to create each additional line. When done adding lines, right-click (or touch and hold) the image. The angle between each set of lines 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.

GEMINI TF, Lung ca
SLU_0022 F(63Y)
Transverse Body-Low Dose CT 11/9/2009 8:38:33 PM
Aug 23, 2007 8:45:28 AM
Series 2218 - Image 113
Quality issue: Image quality insufficient.

Philips, EBW NM
140 kV, 66 mAs
Thickness 5.0 mm

Quality Issue

Key Images Description: Image quality insufficient.

Close

Zoom: 1.00
WW: 350
WC: 35
Presentation: Draft

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

GEMINI TF, Lung ca (63Y) Sex Female Patient ID SLU_0022 Date Aug 23, 2007

GEMINI TF, Lung ca
SLU_0022 F(63Y)
Transverse Body-Low Dose CT 11/9/2009 8:38:33 PM
Aug 23, 2007 8:45:28 AM
Series 2218 - Image 113
Quality Issue: Image quality insufficient.

Philips, EBW NM
140 kV, 66 mAs
Thickness 5.0 mm

Quality Issue
Key Images Description
Image quality insufficient.

Zoom: 1.00
WW: 350
WC: 35
Presentation: Draft

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 information such as image details, image orientation and annotations. This affects all viewports.

To show or hide all information, select **Titles**. Use the arrow beside **Titles** to select specific information to show or hide.

- **Hide All** Show/hide all information.
- **Image Titles** Show/hide **image details**.
- **Image Orientation** Show/hide **image orientation information**.
- **Annotations** Show/hide **annotations**.

- **Dicom Overlays** Show/hide DICOM overlays.
- **Image Shutters** Show/hide image shutters.
- **Reference Lines** Show/hide **reference lines**.
- **CAD Overlay** Show/hide **CAD marks** on mammography studies.
- **Implant Masks** Show/hide implant masks.
- **Image Rulers** Show/hide image rulers. Rulers can only be displayed when the underlying meta-data provides known and consistent pixel spacing and image geometry is flat. To customize the ruler behaviour, see **Change modality preferences**.

Full Quality

HD

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.

Reset Current

↩

In contrast to **Reset**, this tool removes only the changes for the interaction currently selected on the toolbar.

Example

You have used various tools in the current view, such as **Zoom**, **Pan**, and **Rotate**, and now you want to reset only the changes you made with the **Pan** tool.

- On the toolbar, select **Pan**, then select **Reset Current**.
  Only the changes you made with the **Pan** tool are reset, while the changes you made with the

Zoom and **Rotate** tools are preserved.

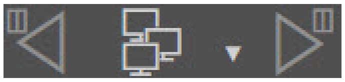
This feature is available for the following interactions:

- Zoom
- Pan
- Rotate/Flip
- WL
- Color Balance
- Opacity (3D)
- Gamma
- Enhance
- Fusion Blend
- Color Balance
- RG/RGB Blend (optomap)
- Green Tint (optomap)
- Pan

Keyboard Shortcut

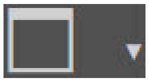
The corresponding shortcut is **Reset Current Interaction**.

Hanging Protocols



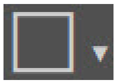
Use hanging protocols to customize the image viewing area (see **Select hanging protocols**).

Study Layout



Use study layouts to customize the image viewing area (see **Arrange images**).

View



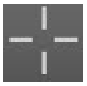
Use views to customize the image viewing area (see **Arrange images**).

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.

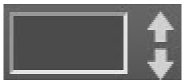
Reference



Show or hide reference lines.

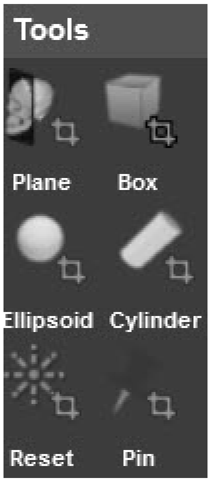
> **Note**
>
> Use **Relate** to change the position of the reference lines.

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**).

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

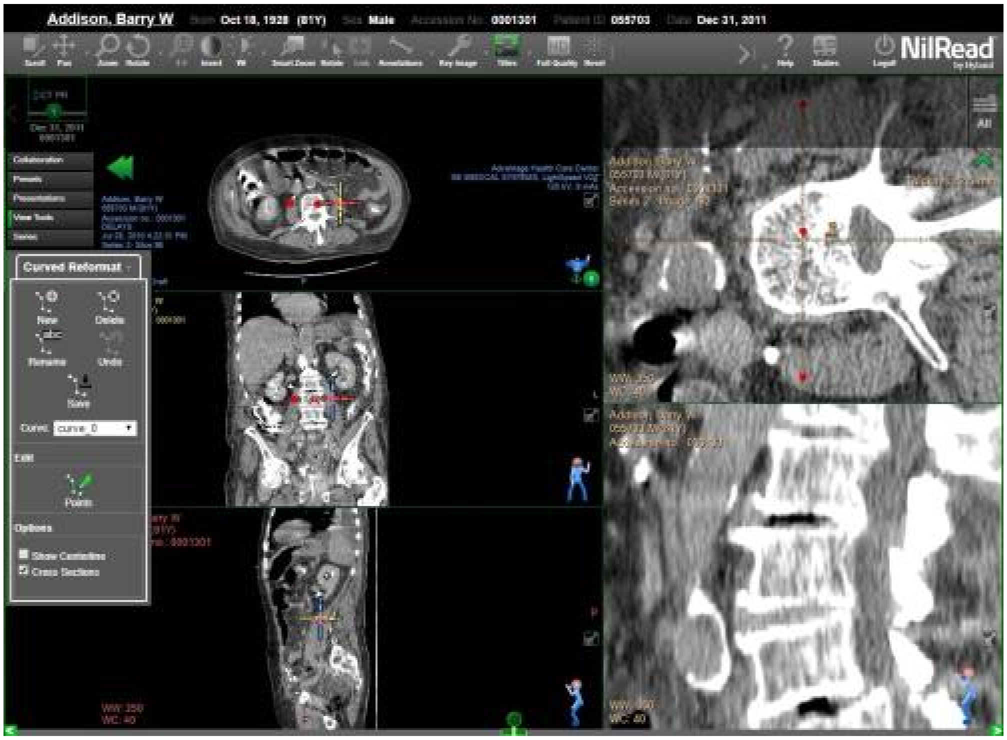
Applies to the curved reformat view (right viewport). Select this option to view a polyline connecting all of the points created for the reformat.

Curve: curve_0

☑ Show Centerline
☐ Cross Sections

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**).

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/Next** Replay the cine continuously, yoyo (play forwards then backwards), or select **Next** to autoplay multiple cine runs (when the current cine run is finished, the next cine run will begin automatically).

> **Important**
>
> Users should pay attention to the screen while the cine is playing automatically.

> **Note**
>
> Cine **Replay/Yoyo/Next** settings can be specified in hanging protocols. For details, see **Set up hanging protocols**.

RT Template

Apply a radiation therapy (RT) template to a study. For details, see **View radiation therapy (RT) plans**.

First, Previous, Next, Last

Scroll through the series in a study.

Use the image viewing area

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**.

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

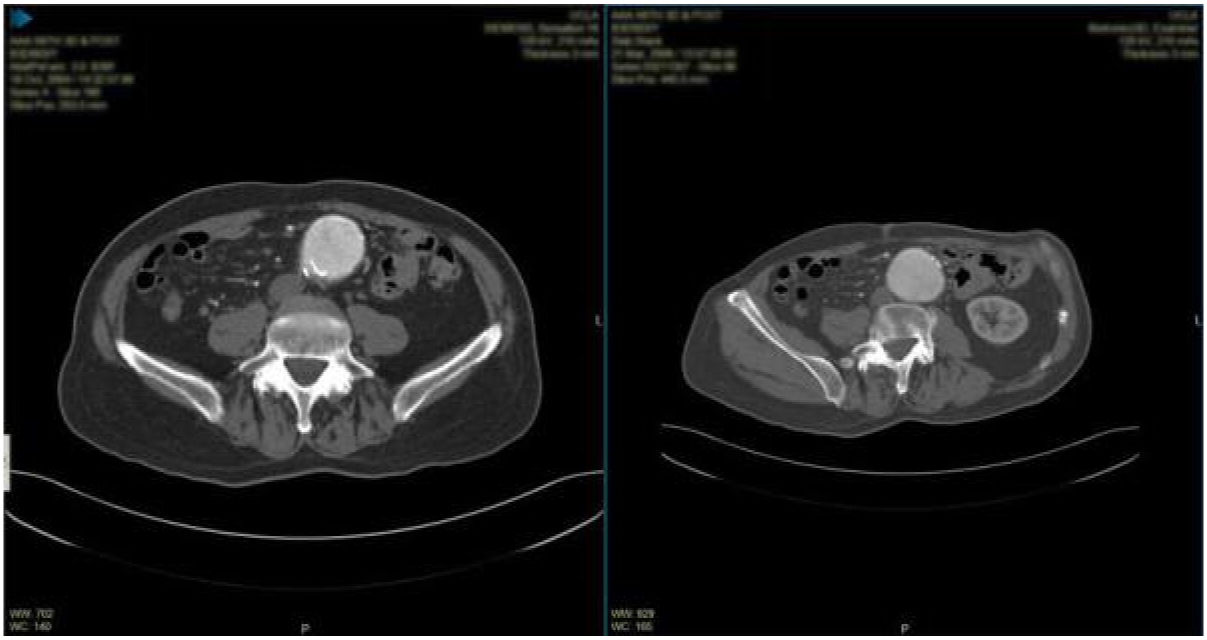
1. Click (or tap) a screen, then select **View** (toolbar).
2. To apply the same view to all screens, select **Apply View Mode to Whole Screen**.
3. Select a view. The view is applied to the selected screen (or all screens).

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.

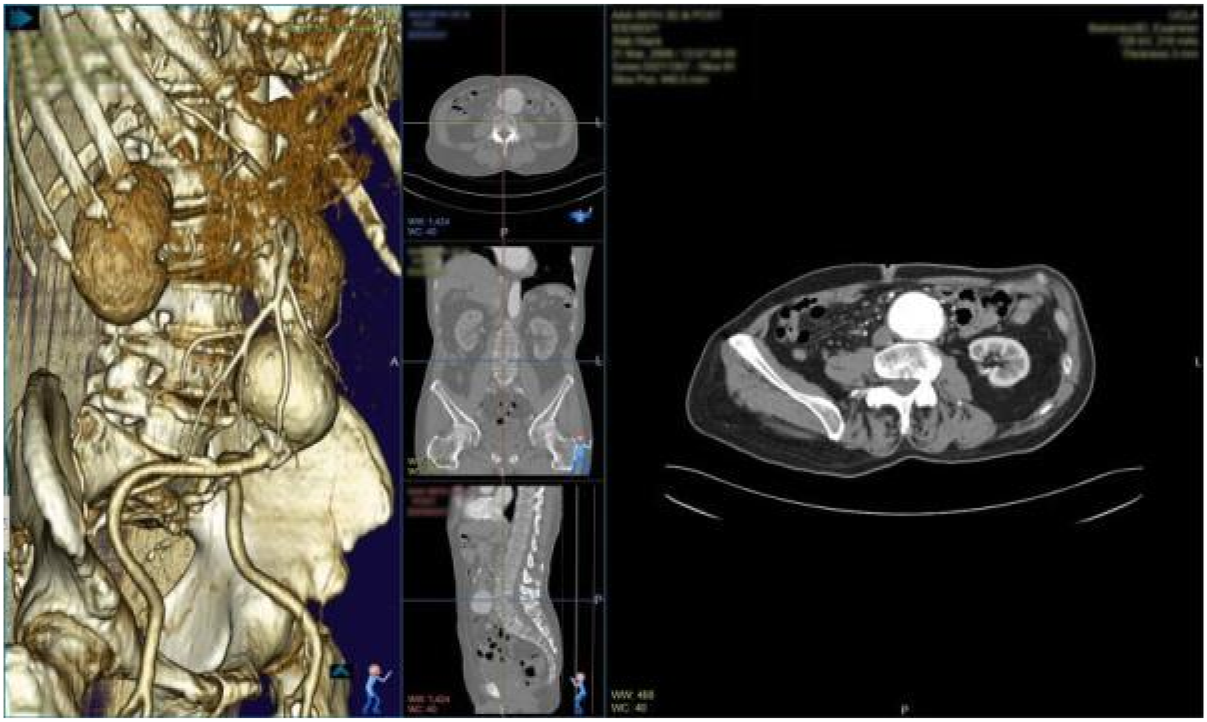
1x2 layout

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



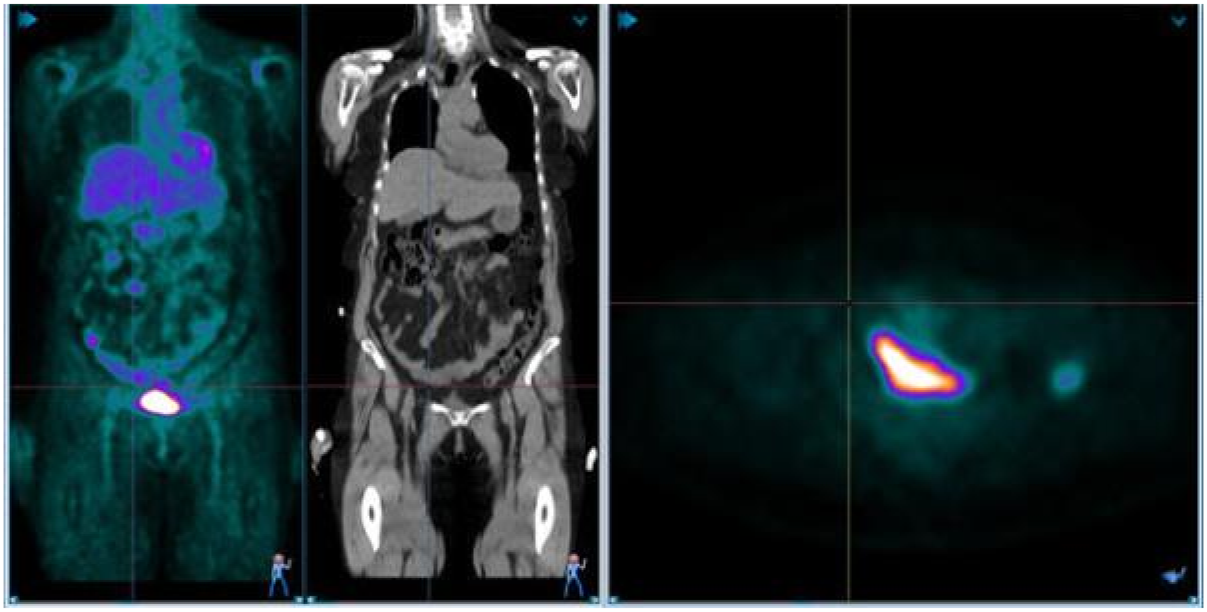
Multiple viewports

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.



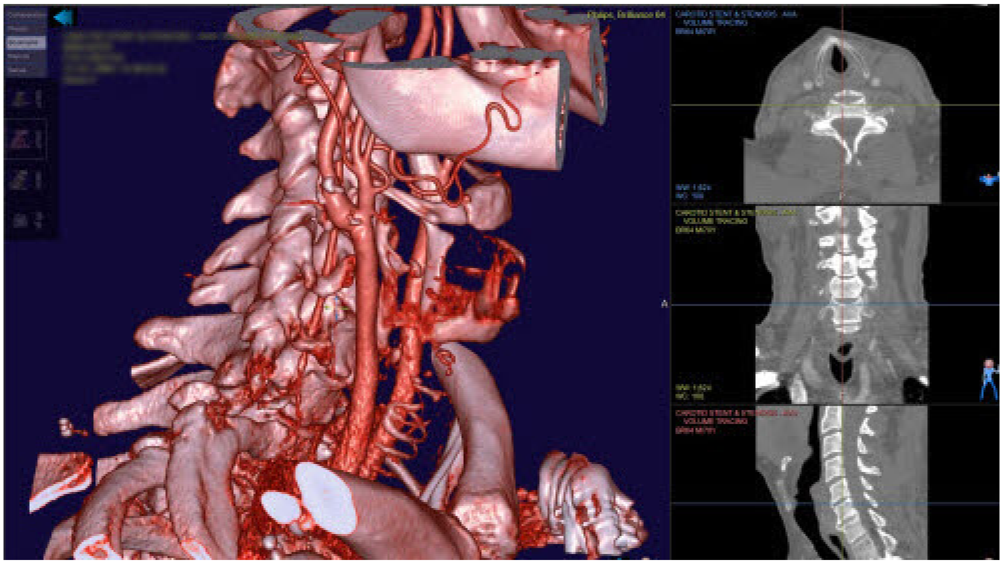
Multiple monitors

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.

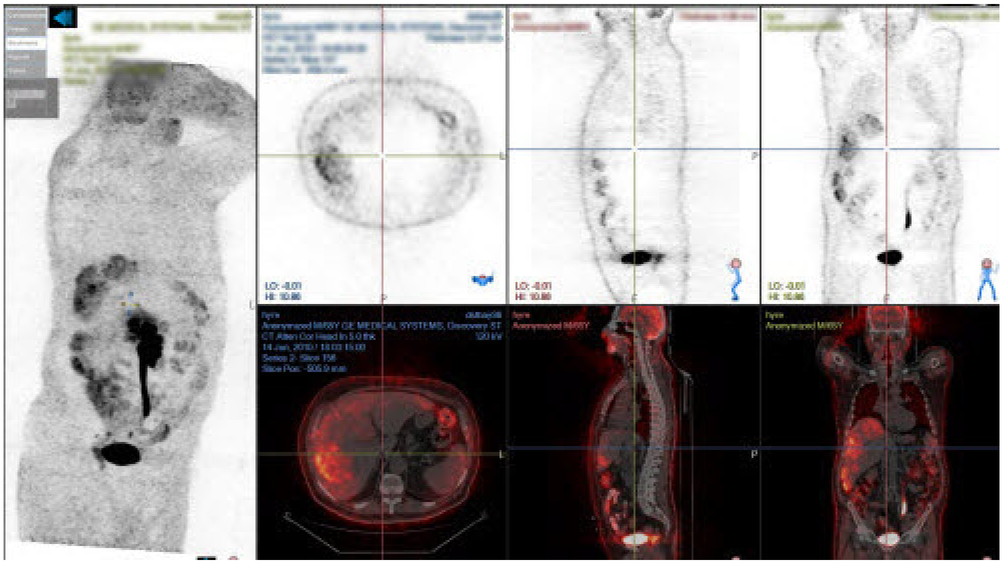


Side-by-side series comparison (study layout)

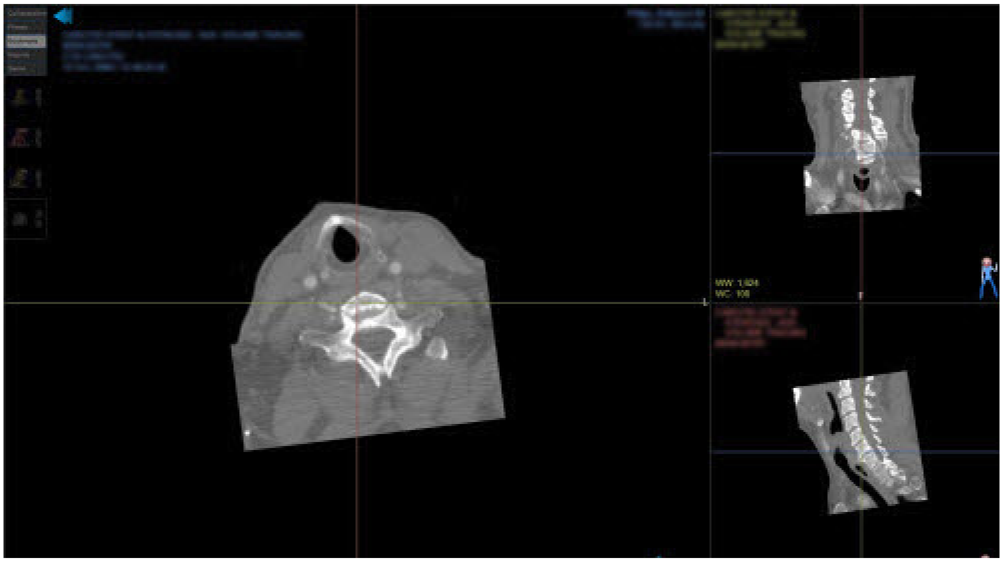
3D view



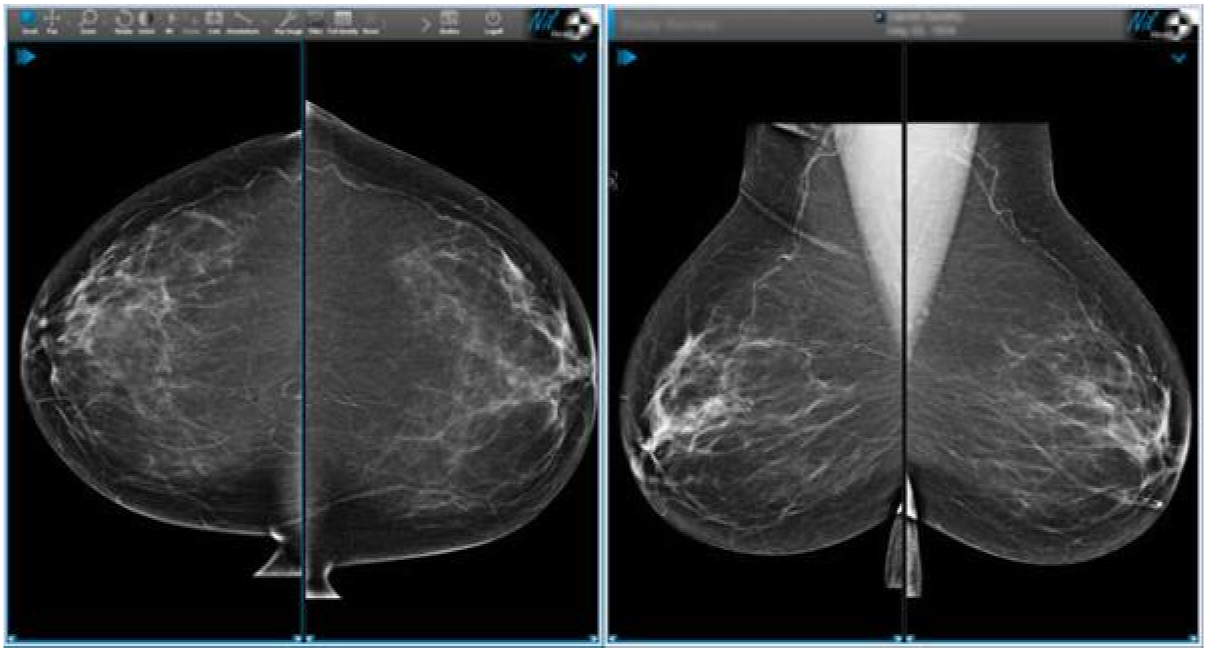
PET-C fusion view



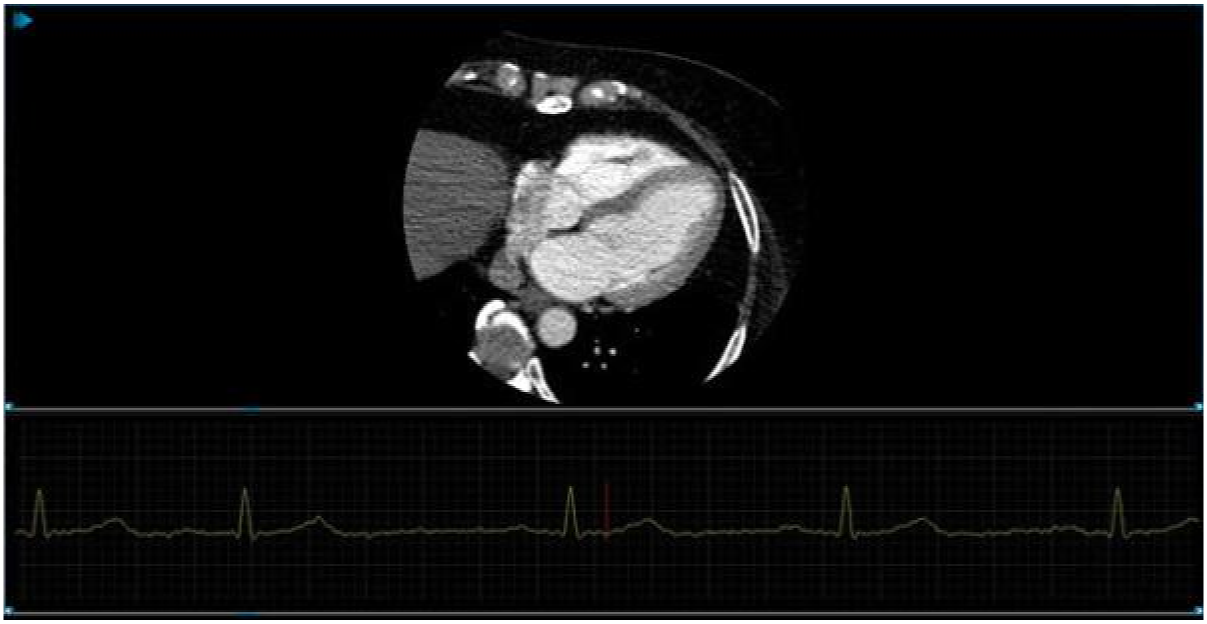
Slab view



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**.

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.

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**.
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**.
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**).

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

Modality	Top-Left	Top-Right	Bottom-Left
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 Series Number Slice Location Key Image Flag	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width

Modality	Top-Left	Top-Right	Bottom-Left
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

Modality	Top-Left	Top-Right	Bottom-Left
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 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

Modality	Top-Left	Top-Right	Bottom-Left
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

Modality	Top-Left	Top-Right	Bottom-Left
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 Key Image Flag	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width

3D Images

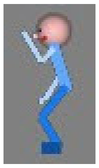
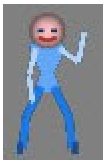
Modality	Top-Left	Top-Right	Bottom-Left
CT	Patient Name Patient Details Series Description Date and Time Series and Instance Number Slice Location	Hospital Name Equipment Name Voltage And Amperage Slice Thickness Reconstruction Diameter	Window Center Window Width Rendering Preset Name
MR	Patient Name 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

Modality	Top-Left	Top-Right	Bottom-Left
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

Modality	Top-Left	Top-Right	Bottom-Left
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:

	**Axial** Figure standing on head (feet up)
	**Sagittal** Figure standing sideways
	**Coronal** 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.

Use worklists and folders

About worklists and folders

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

Worklists

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.

For more information, see **Manage worklists**.

Folders

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.

For more information, see **Manage folders**.

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.

> **Note**
> You can also use folders to create a group of studies (see **Manage folders**).

Add a worklist

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

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.

Category

You can use categories to organize your worklists in the navigation tree. To place this worklist in a category, enter the category name. Note that the category will be created if it does not already exist.

Comment

Worklist description.

Default

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

Disabled

If selected, the worklist will be hidden in the navigation tree.

Folder

Do not select this option. This will create a folder instead of a worklist (see **Manage folders**).

De-identify

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**).

> **Note**
> Once the worklist is created, you cannot change the **De-identify** option.

> **Note**
> Studies are only anonymized when opened from a worklist or folder with the **De-identify** 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.

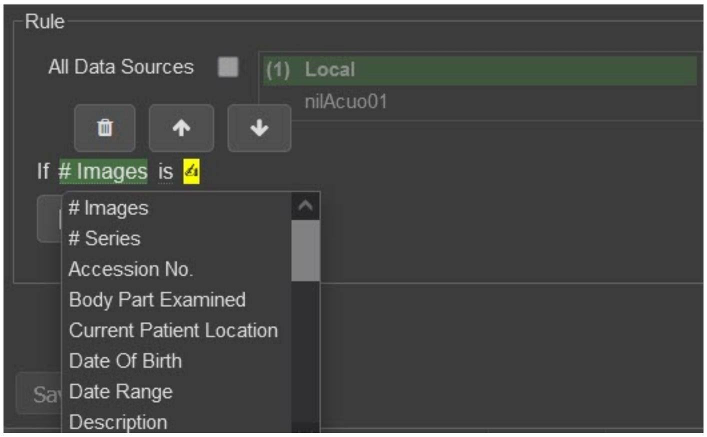
1. Select **All Data Sources** to search all data sources when selecting studies for the worklist.

   or

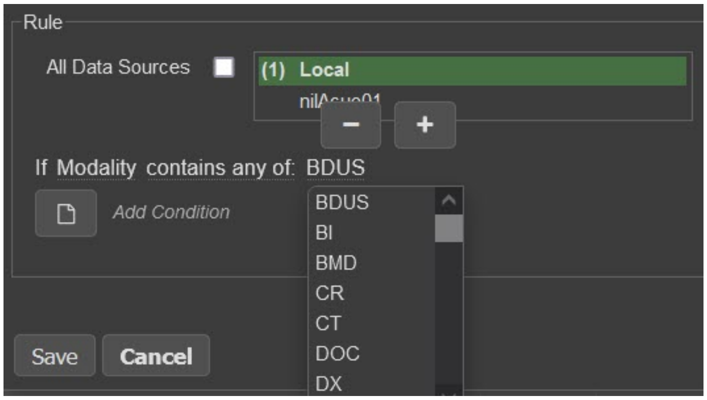
   Select a data source from the list to select studies from this data source only.

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. 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.

> **Note**
> You can also use worklists to create a group of studies (see **Manage worklists**).

Add a folder

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

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.

Category

You can use categories to organize your folders in the navigation tree. To place this folder in a category, enter the category name. Note that the category will be created if it does not already exist.

Comment

Folder description.

Default

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

Disabled

If selected, the folder will be hidden in the navigation tree.

Folder

Select this option to create a folder (instead of a worklist). To create this folder inside another folder, select the parent folder.

> **Note**
> An alternate way to create a subfolder is available in **Settings > Preferences > Work Lists and Folders**. Select an existing folder, then select **Add Sub-Folder**.

Add Notes

If selected, users will be able to add notes when adding studies to a folder.

De-identify

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**).

> **Note**
> Once the folder is created, you cannot change the **De-identify** option.

> **Note**
> Studies are only anonymized when opened from a worklist or folder with the **De-identify** 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**.

Manage the studies in a folder

You can use a folder to create a collection of studies that you want to view as a group. For more information, see **Manage folders**.

Add studies to a folder

Note that you can add the same study to multiple folders.

In the Patient Study Directory:

1. Select the checkbox beside one or more studies, then drag the studies on top of the folder.

   or

   Right-click (or tap and hold) a study. Select **File to Folder**, then select a folder.
2. If notes are enabled for the folder, you can add a note with details about why the study has been added to the folder. Enter the note, then select **File to Folder**. The note is not saved as part of the study.

View and edit folder notes

You can view and edit the notes that were created when the studies were added to the folder.

1. To view the folder notes, select **Customize** in the top-right corner. Drag the **Folder Notes** column from the **Customize** list to the location where you want to place it.

2. To edit a note, right-click (or touch and hold) a study, then select **Edit Folder Note**.

Organize studies by date

You can organize studies by the date they were added to the folder.

1. Select **Customize** in the top-right corner.
2. Drag the **Filed to Folder** column from the **Customize** list to the location where you want to place it.
3. Click this column to sort the studies by the date the studies were added to the folder.

Move studies to another folder

You can move studies between folders.

In the Patient Study Directory:

1. Select one or more studies in a folder.
2. Right-click (or tap and hold) the studies.
3. Select **Move to Folder**, then select a folder.

Remove studies from a folder

You can remove a study from a folder.

In the Patient Study Directory:

1. Select one or more studies in a folder.
2. Right-click (or tap and hold) the studies.
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**.

Open a study in a worklist or folder

You can use worklists and folders to create a collection of studies that you want to view as a group. For more information, see **About worklists and folders**.

In the Patient Study Directory:

1. Select **+** beside **Public Worklists**, **Public Folders**, **My Worklists**, **My Folders** or a custom category. The available worklists or folders are shown. Select **–** to collapse the category.

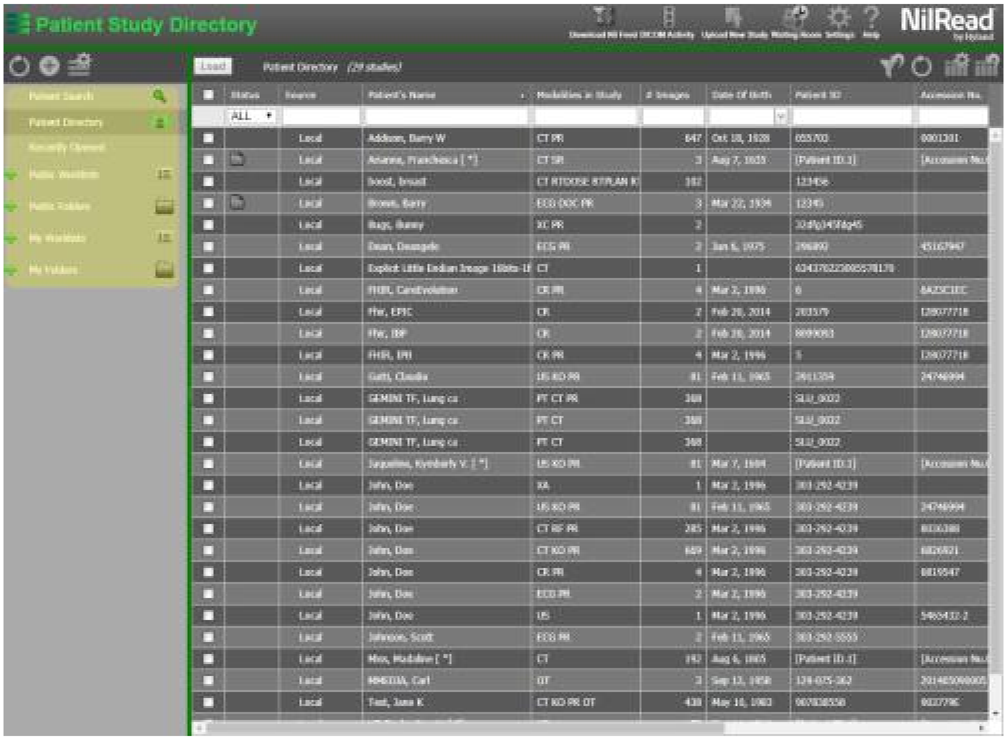
   > **Note**
   >
   > Select ↻ to refresh the navigation tree and see any new worklists and folders.

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

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).



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**.

  > **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**.
- **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 **Open a study in a worklist or folder**.

> **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.

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**.

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 diskspace 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.

1. In the Patient Study Directory, right-click (or touch and hold) a study, then select **Download Study**.
   or
   While viewing a study, right-click (or touch and hold) an image, then select **Download**.
2. You can select the following options.
   - **Download encapsulated documents in the original file format** Download non-DICOM files in their original format.
   - **Download as DICOM CD** Download an ISO CD image containing the studies and a DicomDir file which you can view with a DICOM viewer. You can burn this image to CD using standard CD burning software. You can also mount the CD image (for example, as a virtual clone drive) which allows you to view the files without creating a CD. Depending on your NilRead configuration, the CD image may also contain a DICOM viewer.
   - **Create DicomDir file** Create a catalog of the downloaded studies to be used with a DICOM viewer.
   - **Deidentify** Anonymize the study. Select a confidentiality profile (for more information, see **About anonymization**).
3. 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**).

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**).

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**).

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 to the right of 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

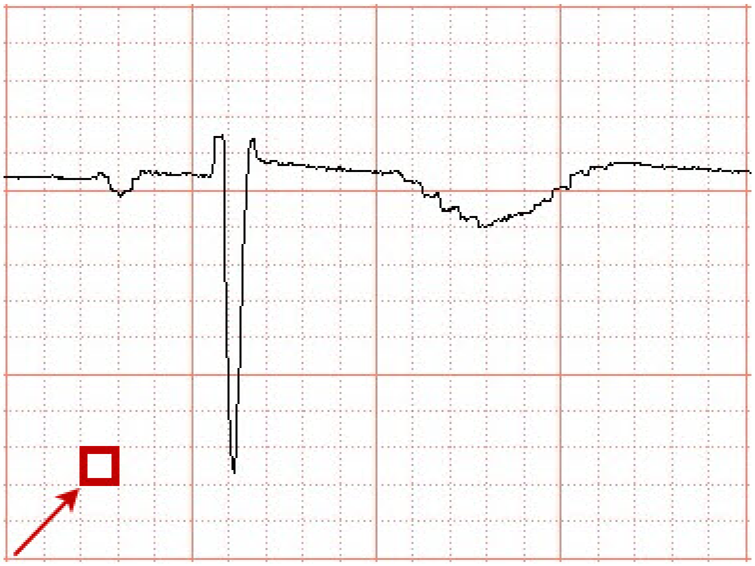
To resize the directory and report areas, drag the divider between the two areas.

Review ECG studies

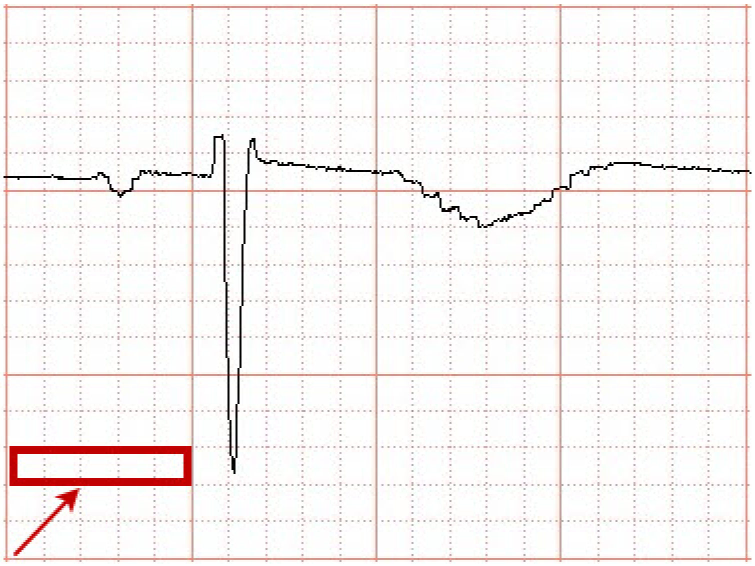
About ECG paper

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

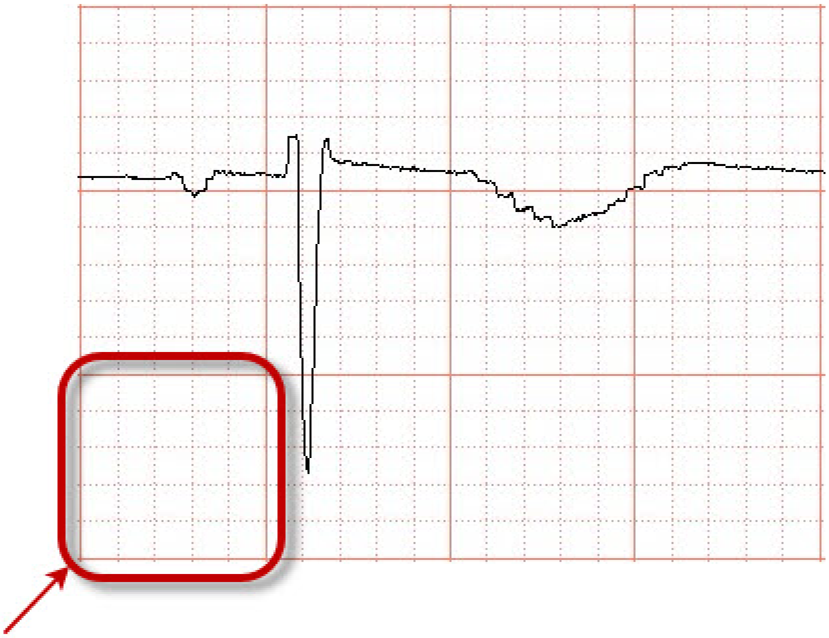
If you zoom in on a graph, you can see that the paper is divided into small boxes. Each box represents a 1 mm interval or 0.04 seconds (40 ms).



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.

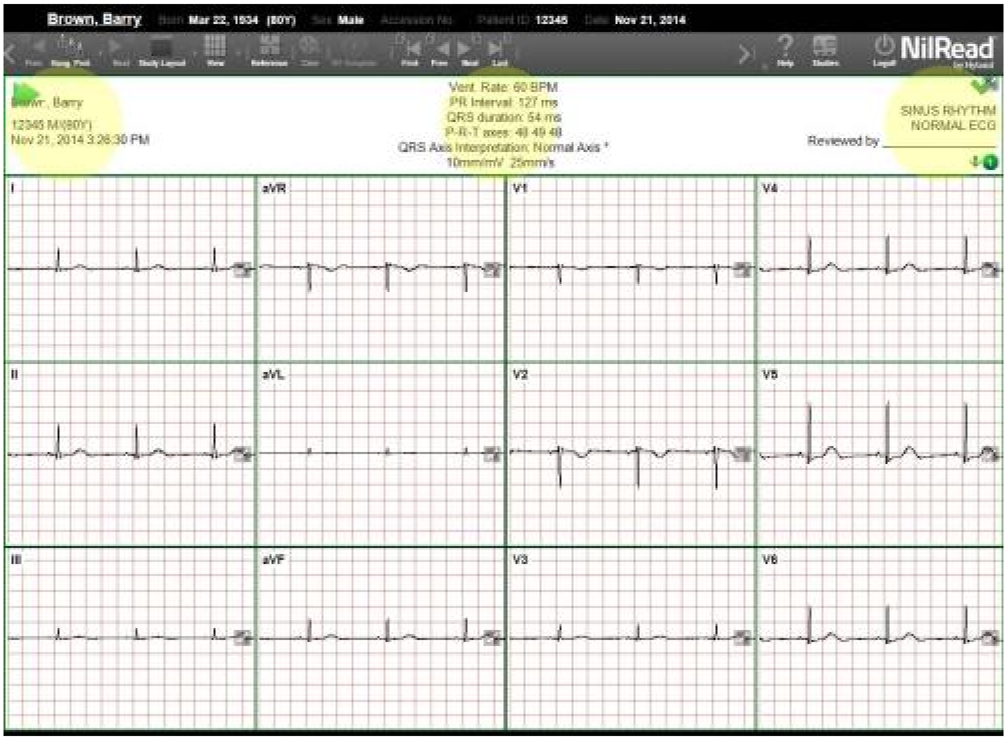


Use ECG views

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.



Brown, Barry Born Mar 22, 1934 (80Y) Sex Male Accession No Patient ID 12345 Date Nov 21, 2014

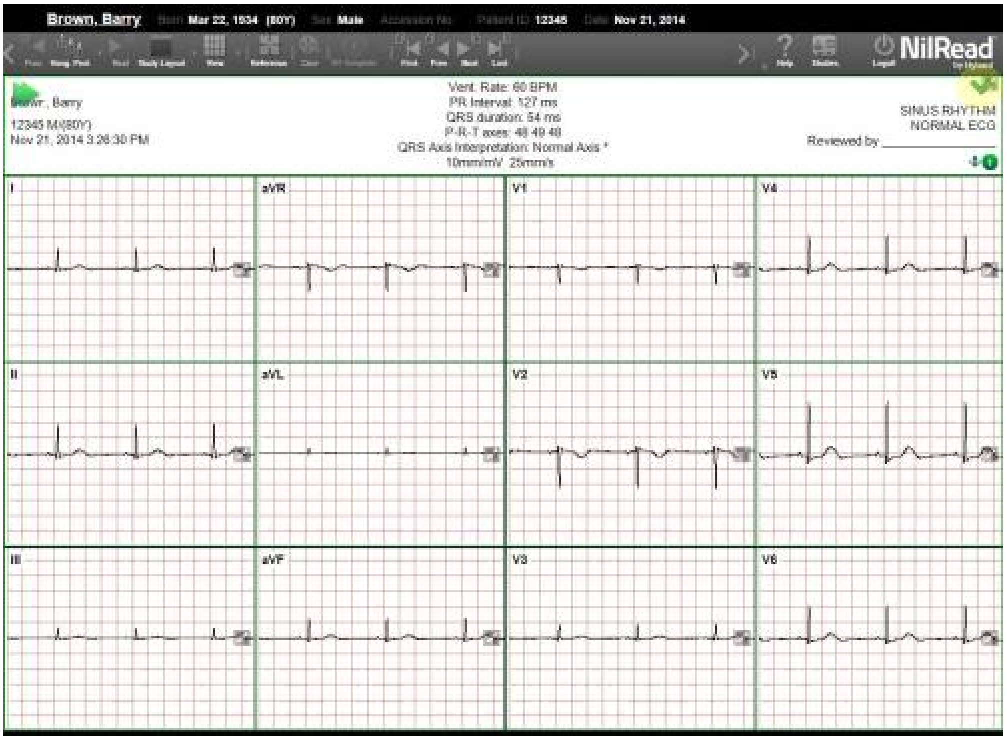
Brown, Barry
12345 M(80Y)
Nov 21, 2014 3:26:30 PM

Vent. Rate: 60 BPM
PR Interval: 127 ms
QRS duration: 54 ms
P-R-T axes: 48 49 48
QRS Axis Interpretation: Normal Axis *
10mm/mV 25mm/s

SINUS RHYTHM
NORMAL ECG
Reviewed by

- 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**.
- 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 .



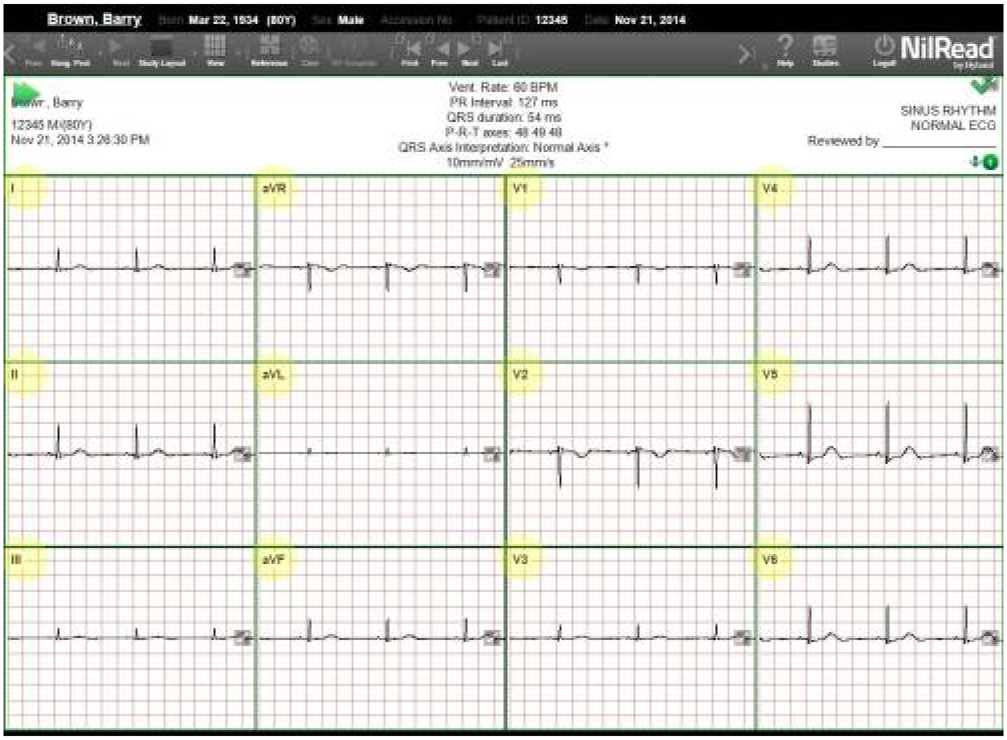
Brown, Barry Born Mar 22, 1934 (80Y) Sex Male Accession No Patient ID 12345 Date Nov 21, 2014

Brown, Barry
12345 M(80Y)
Nov 21, 2014 3:26:30 PM

Vent. Rate: 60 BPM
PR Interval: 127 ms
QRS duration: 54 ms
P-R-T axes: 48 49 48
QRS Axis Interpretation: Normal Axis *
10mm/mV 25mm/s

SINUS RHYTHM
NORMAL ECG
Reviewed by ____________

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



Brown, Barry Mar 22, 1934 (80Y) Male 12345 Nov 21, 2014

Vent. Rate: 60 BPM
PR Interval: 127 ms
QRS duration: 54 ms
P-R-T axes: 48 49 48
QRS Axis Interpretation: Normal Axis *
10mm/mV 25mm/s

12345 M(80Y)
Nov 21, 2014 3:26:30 PM

SINUS RHYTHM
NORMAL ECG
Reviewed by ____________

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
LEAD II	POSITIVE	EQUIPHASIC	NEGATIVE	POSITIVE	NEGATIVE	EQUIPHASIC
LEAD III or aVF	POSITIVE	NEGATIVE	NEGATIVE	POSITIVE	NEGATIVE	EQUIPHASIC

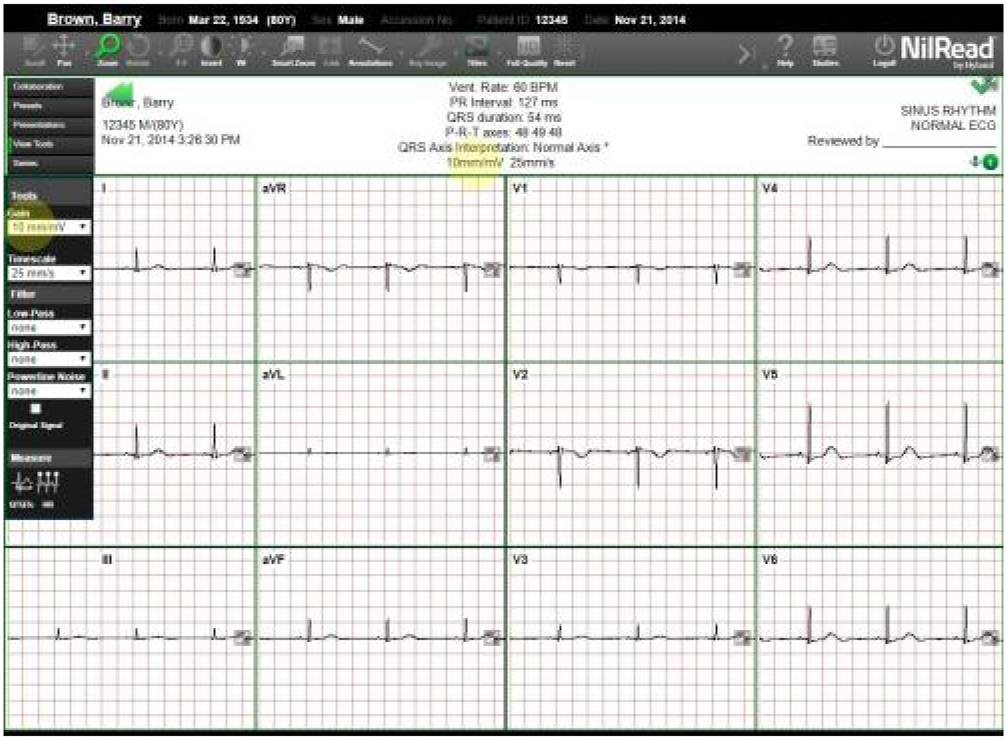
Use the ECG view tools

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.)



Brown, Barry Mar 22, 1934 (80Y) Male 12345 Nov 21, 2014

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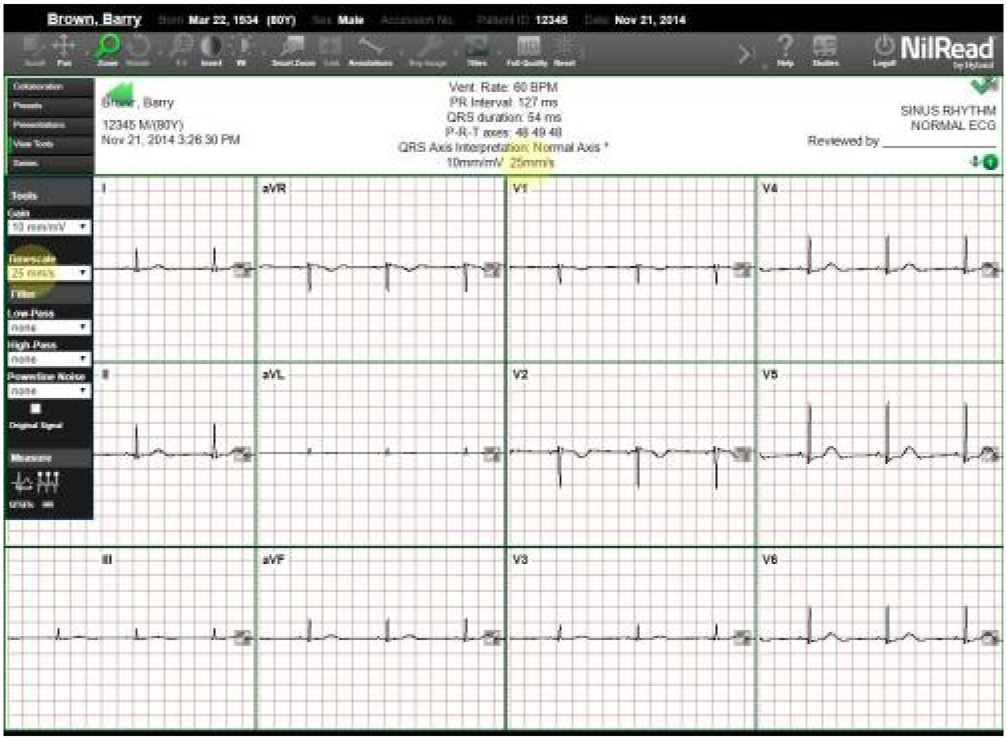
P-R-T axes: 48 49 48
QRS Axis Interpretation: Normal Axis *
10mm/mV 25mm/s

SINUS RHYTHM
NORMAL ECG
Reviewed by ______________

Gain: 10 mm/mV
Timescale: 25 mm/s
Low-Pass: none
High-Pass: none
Powerline Noise: none

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.)



Brown, Barry Mar 22, 1934 (80Y) Male 12345 Nov 21, 2014

Vent. Rate: 60 BPM
PR Interval: 127 ms
QRS duration: 54 ms
P-R-T axes: 48 49 48
QRS Axis Interpretation: Normal Axis *
10mm/mV 25mm/s

SINUS RHYTHM
NORMAL ECG
Reviewed by ____________

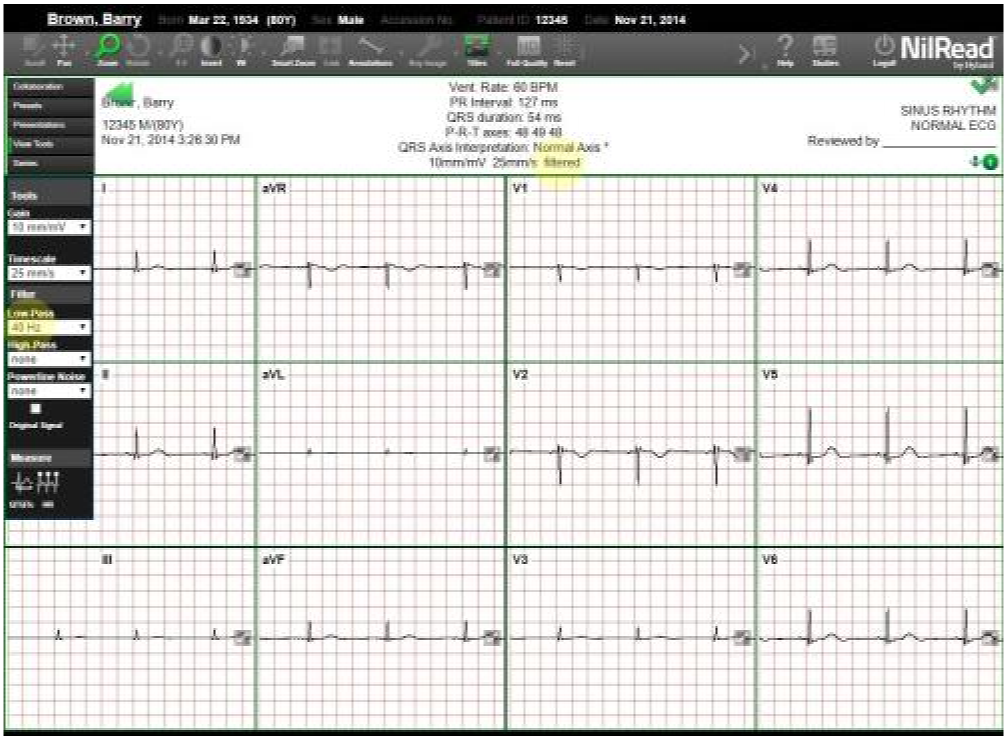
Timescale: 25 mm/s

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.



Brown, Barry Mar 22, 1934 (80Y) Male 12345 Nov 21, 2014

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12345 M(80Y)
Nov 21, 2014 3:26:30 PM

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P-R-T axes: 48 49 48
QRS Axis Interpretation: Normal Axis *
10mm/mV 25mm/s filtered

SINUS RHYTHM
NORMAL ECG
Reviewed by ____________

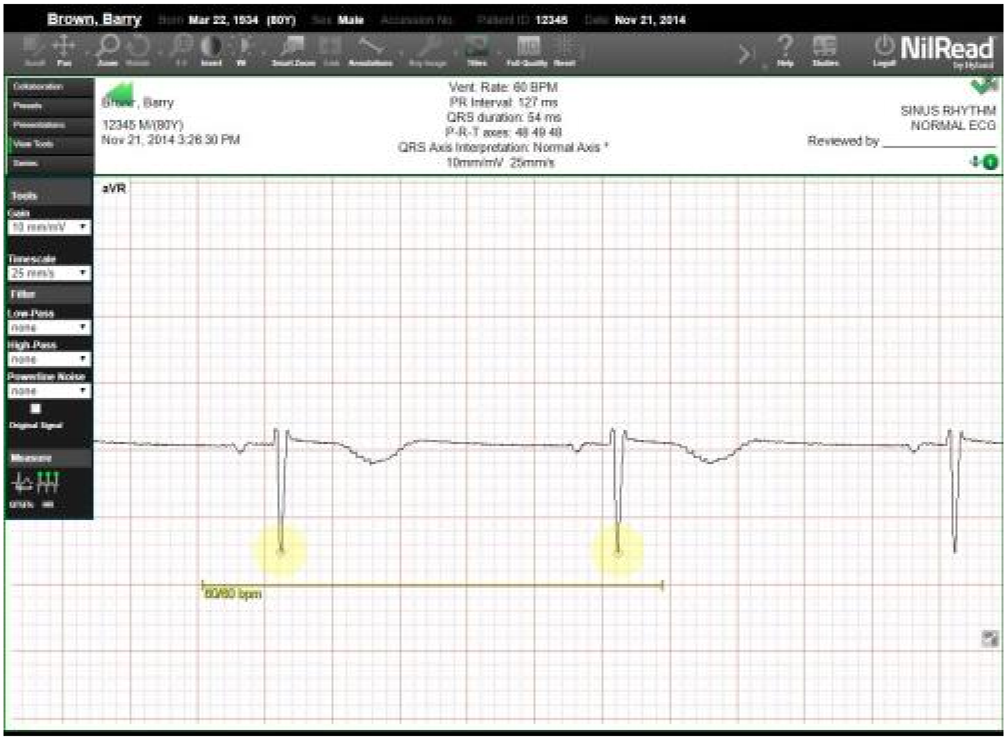
Tools
Gain: 10 mm/mV
Timescale: 25 mm/s
Filter
Low Pass: 40 Hz
High Pass: none
Powerline Noise: none

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.


Brown, Barry Mar 22, 1934 (80Y) Male 12345 Nov 21, 2014

Barry
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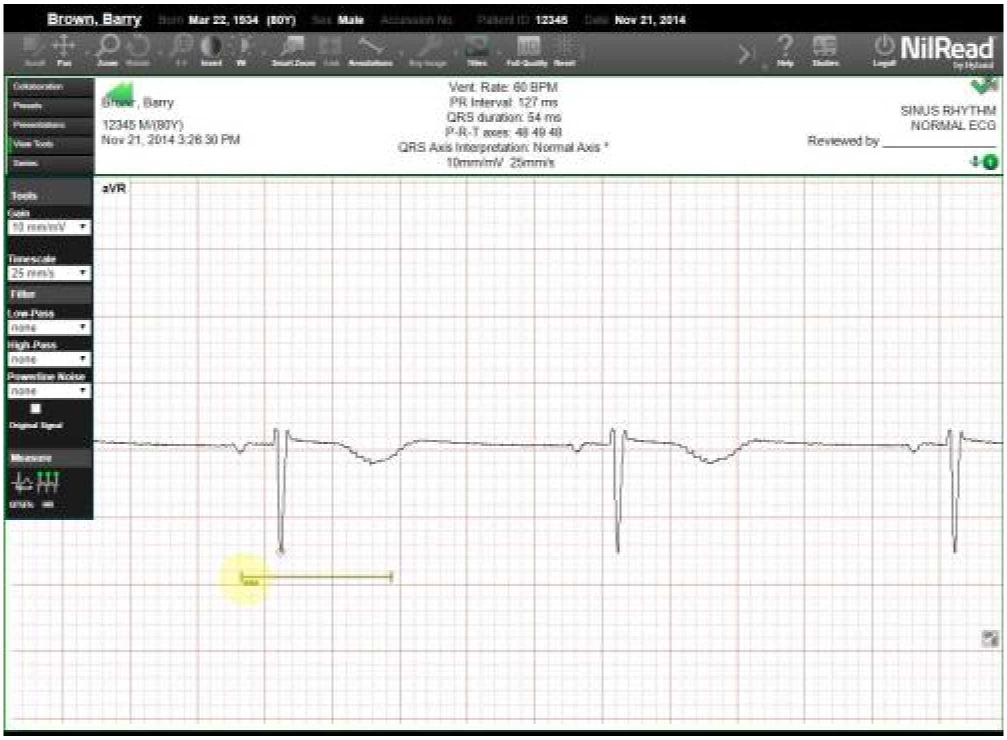
QRS Axis Interpretation: Normal Axis *
10mm/mV 25mm/s

SINUS RHYTHM
NORMAL ECG
Reviewed by ____________

Gain: 10 mm/mV
Timescale: 25 mm/s
Low-Pass: none
High-Pass: none
Powerline Noise: none

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.



Brown, Barry Mar 22, 1934 (80Y) Male 12345 Nov 21, 2014

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Nov 21, 2014 3:26:30 PM

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PR Interval: 127 ms
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P-R-T axes: 48 49 48
QRS Axis Interpretation: Normal Axis *
10mm/mV 25mm/s

SINUS RHYTHM
NORMAL ECG
Reviewed by ____________

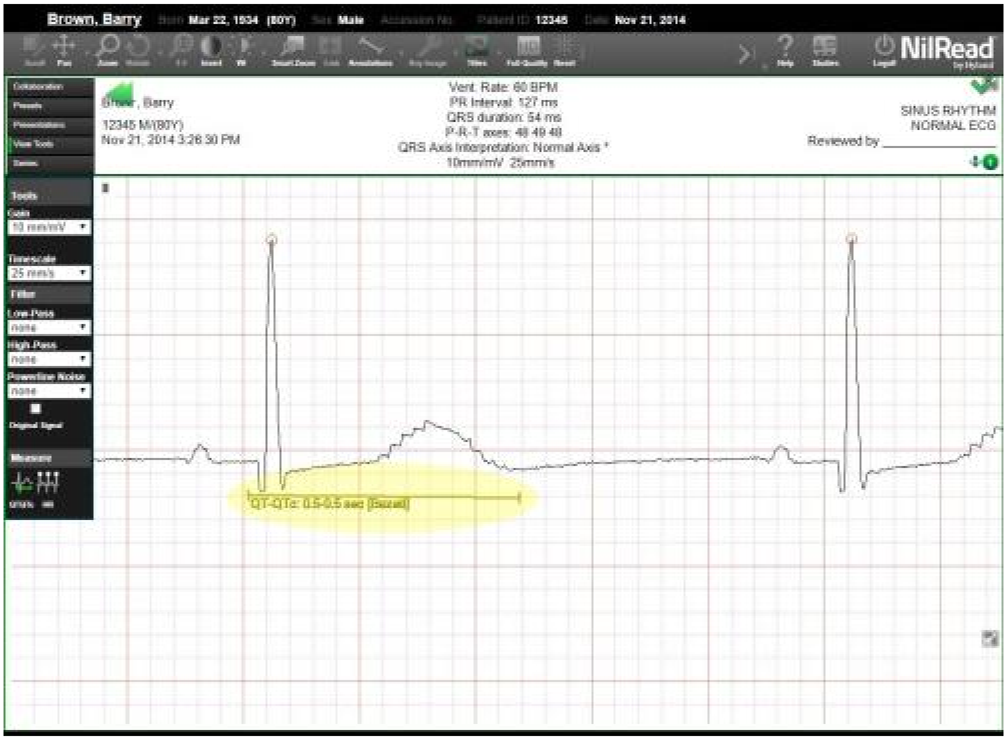
Gain: 10 mm/mV
Timescale: 25 mm/s
Low-Pass: none
High-Pass: none
Powerline Noise: none

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.



Brown, Barry Mar 22, 1934 (80Y) Male 12345 Nov 21, 2014

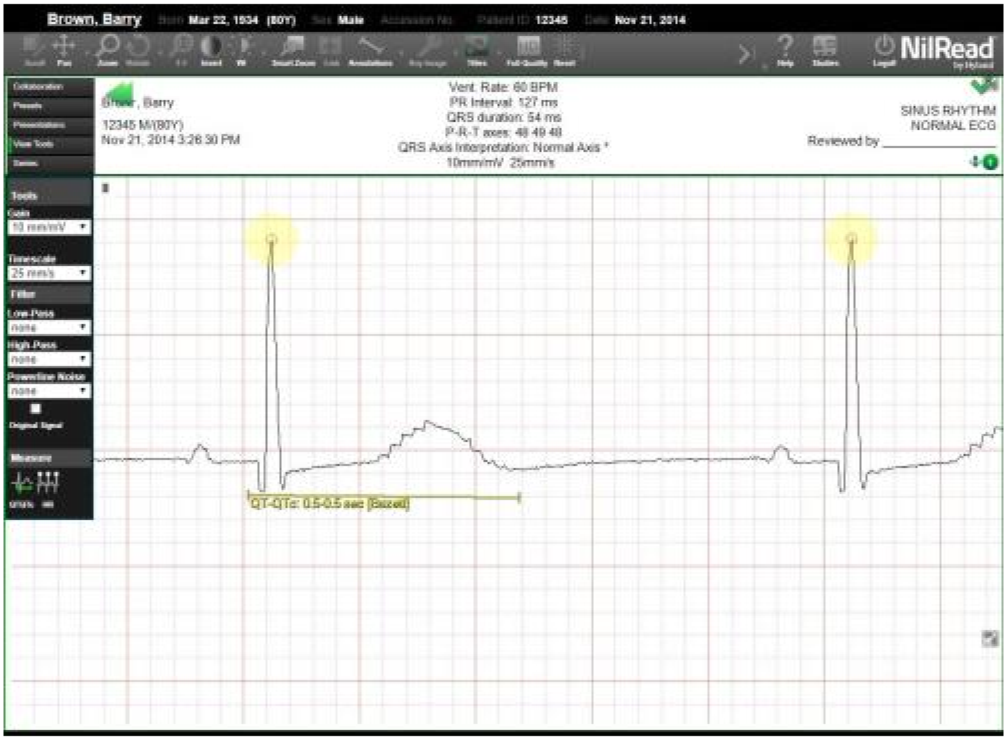
Vent. Rate: 60 BPM
PR Interval: 127 ms
QRS duration: 54 ms
P-R-T axes: 48 49 48
QRS Axis Interpretation: Normal Axis *
10mm/mV 25mm/s

12345 M(80Y)
Nov 21, 2014 3:26:30 PM

SINUS RHYTHM
NORMAL ECG
Reviewed by ______

Gain: 10 mm/mV
Timescale: 25 mm/s
Low-Pass: none
High-Pass: none
Powerline Noise: none

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**).

Use the vessel tracer

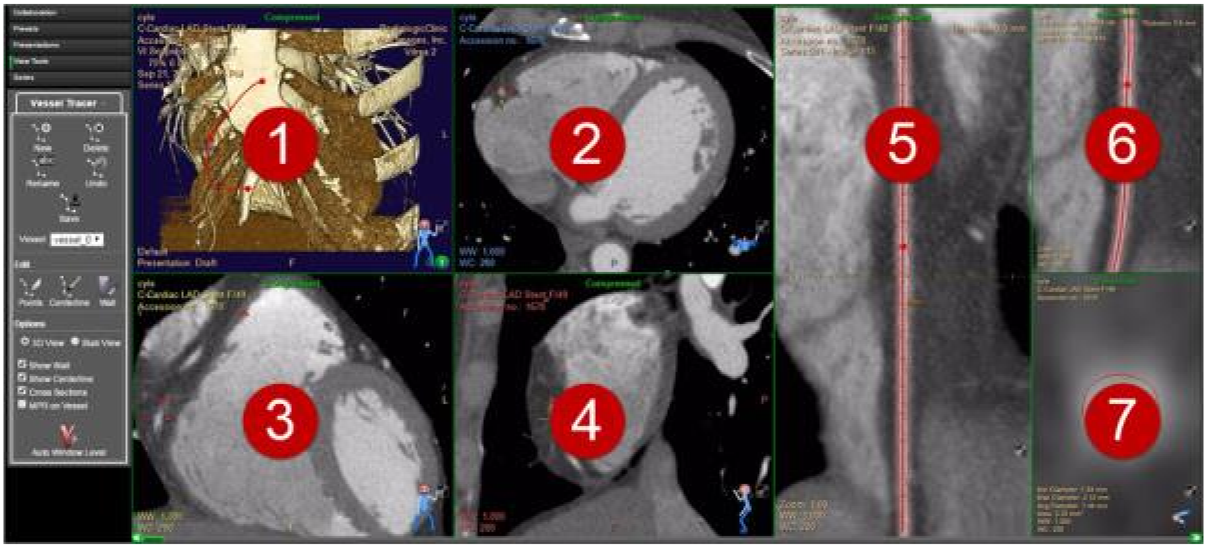
About the vessel tracer

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**.)

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, deselect 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.

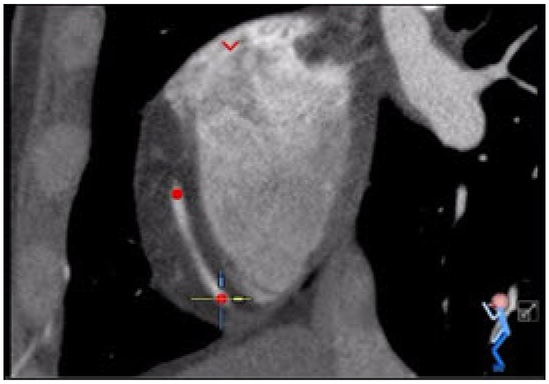
To apply a window level preset that tries to optimize the display of the vessel:

- 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:

taha
Anonymized M/079Y
Accession no.: 302314063
Series 8 - Image 981
Thickness 0.5 mm
Zoom: 1.00
WW: 400
WC: 40

taha
Anonymized M/079Y
Accession no.: 302314063
Series 8 - Image 981
Thickness 0.5 mm
Zoom: 1.00
WW: 400
WC: 40

taha
Anonymized M/079Y
Accession no.: 302314063
Min Diameter: 4.38 mm
Max Diameter: 4.75 mm
Avg Diameter: 3.23 mm
Area: 16.39 mm²
WW: 400
WC: 40

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, deselect 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**.

View radiation therapy (RT) plans

Using the RT Plan panel

When you load a study containing RT plans, when you select a series containing RT plans, **RT Plan** options are available in the side panel.

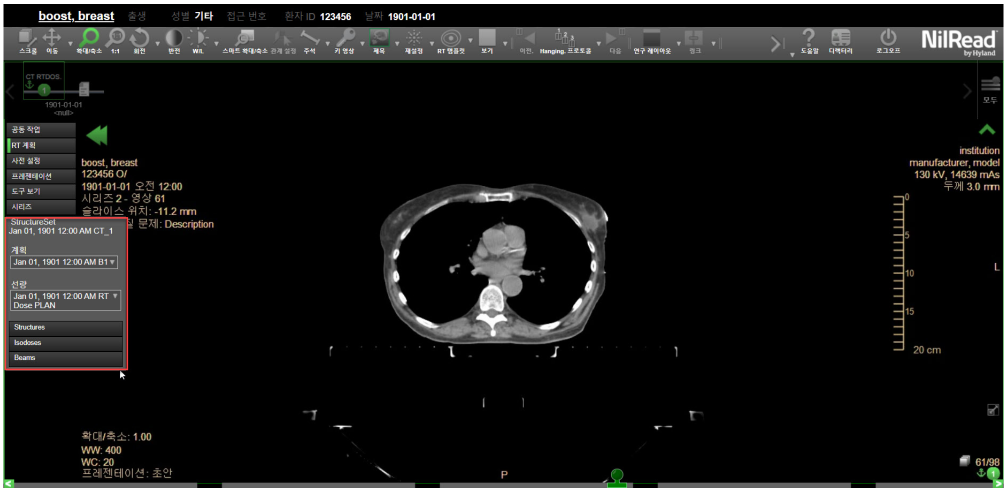
Studies that contain RT plans are marked with an **RT** icon in their thumbnails.

RT plan 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**.

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



StructureSet
Jan 01, 1901 12:00 AM CT_1

계획
Jan 01, 1901 12:00 AM B1

선량
Jan 01, 1901 12:00 AM RT Dose PLAN

The **RT Plan** panel allows you to select RT Objects associated with the series.

2. Select a **StructureSet**. The list contains the structure sets associated with the current image series. After you select the structure set, the list of plans is populated with the RT plans that ref-

erence the selected structure set.

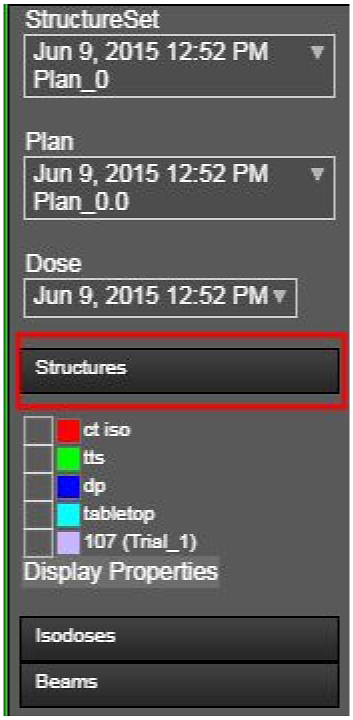
3. Select a **Plan**. After you select a plan, the list of doses is populated with the doses that reference the selected plan.

4. Select a **Dose**. Doses can be one of several Summation Types. If the Summation Type of a dose is BEAM, a composite dose is computed from all available BEAM type doses and added to the list of selectable doses. The Summation Type for this composite dose is PLAN.

5. With a dose selected, you can view the following categories: **Structures**, **Isodoses**, and **Beams**.

Structures

To view options related to structures, click **Structures** to expand the **Structures** section.



StructureSet: Jun 9, 2015 12:52 PM Plan_0

Plan: Jun 9, 2015 12:52 PM Plan_0.0

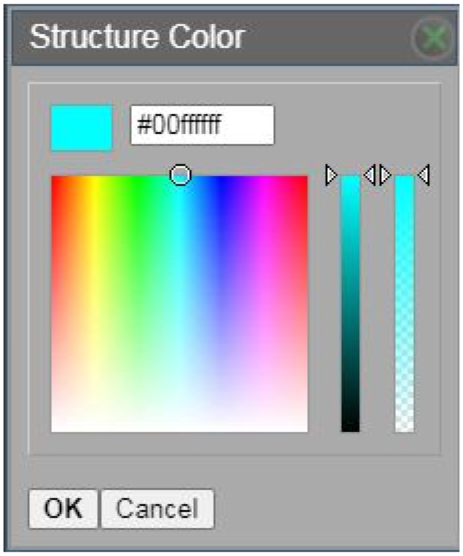
Dose: Jun 9, 2015 12:52 PM

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

To focus on a structure, select the structure label. (This will also select the structure if it is not already selected.) For 2D views, the viewport is updated to show the first image containing the structure. For slab images, the viewport is updated to show the first location where the structure is visible.

Changing Structure Colors

To change the color of a structure, click the color box beside the structure label. The **Structure Color** dialog is displayed.

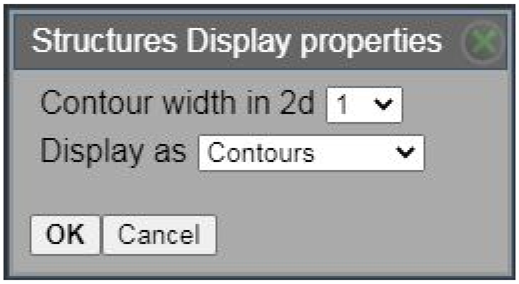


Choose a color by entering the hexadecimal color value or using the color picker. Click **OK** when finished.

Structure Display properties

You can change the way structures 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**).

1. To change the display properties of a structure, click **Display Properties**. The **Structures Display properties** is displayed.



Contour width in 2d 1
Display as Contours

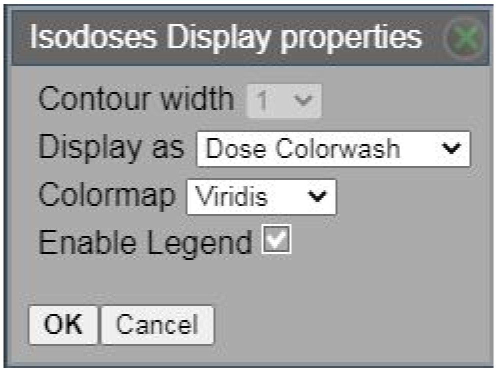
2. You can change the following options.
   - **Contour width in 2d** Select the width of the contour outline. Note that you cannot change the contour width for MPR images.
   - **Display as** Select the type of contour: **Contours** (outline) or **Filled Contours** (shaded).
3. Select **OK**.

Isodoses

Display properties

You can change the way 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**).

1. Select **Isodoses**, then select **Display Properties**. The **Isodoses Display properties** dialog is displayed.



Isodoses Display properties

Contour width 1

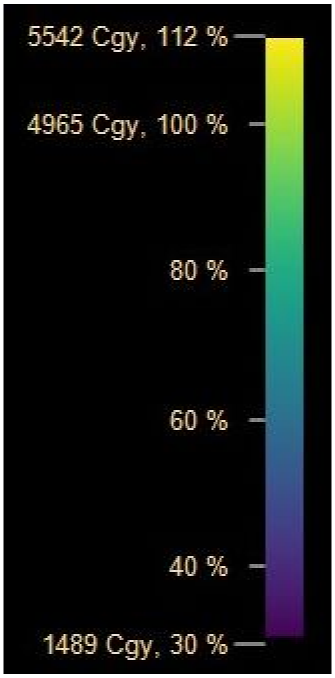
Display as Dose Colorwash

Colormap Viridis

Enable Legend ☑

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 display: **Contours** (outline), **Filled Contours** (shaded), **Dose Colorwash**, or **Isodose Colorwash**.
   - **Colormap** Select the type of colormap: **Rainbow**, **Plasma**, or **Viridis**.

- **Enable Legend** If this option is selected, the colormap legend is displayed in the viewport.



3. Select **OK**.

Contours and Filled Contours

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.

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

Jun 9, 2015 12:52 PM

Max: 5542.61 cGy

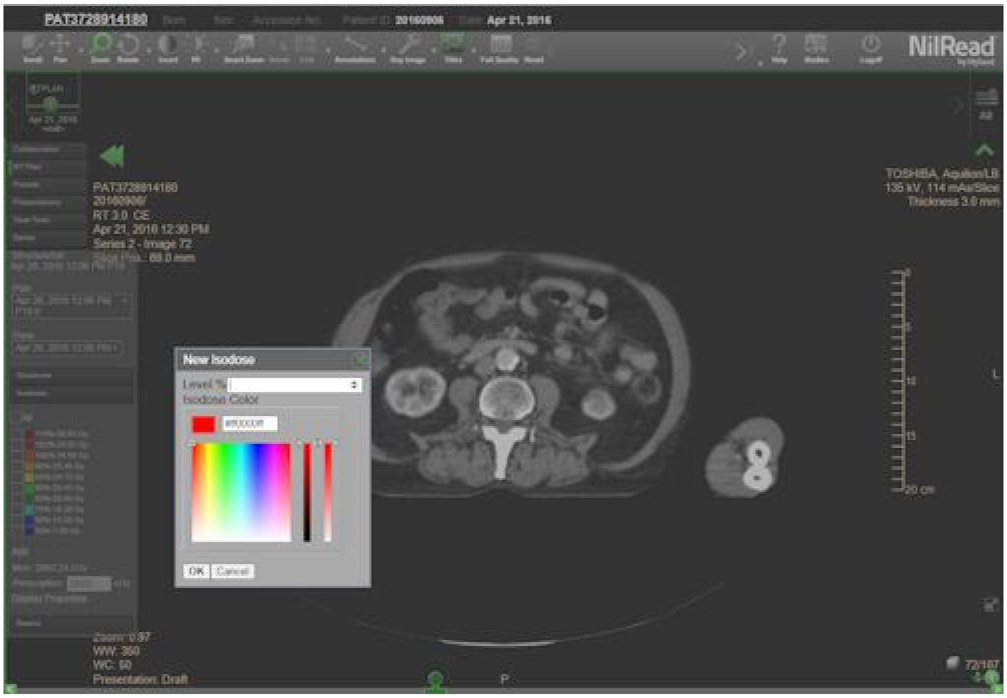
Prescription: 4965 cGy

To focus on an isodose, select the isodose label. (This will also select the isodose if it is not already selected.) For both 2D views and slab images, the viewport is updated to focus on the centroid of the isodose.

You can add an isodose level.

1. Select **Add**.

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

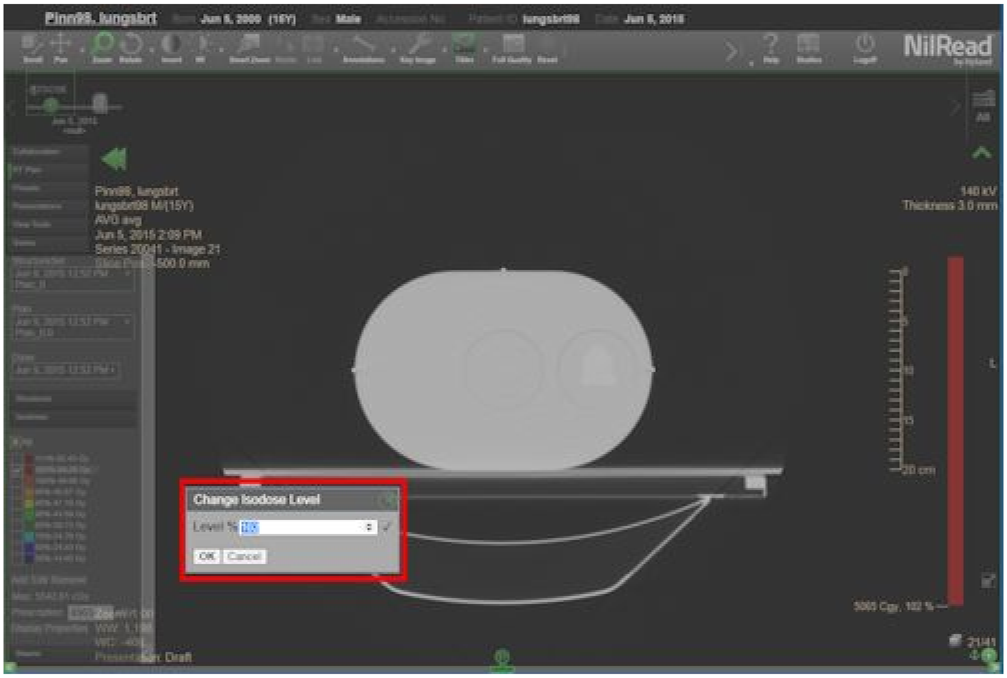


3. Select **OK**.

You can change an isodose level.

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 level. Select the isodose label, then select **Remove**.

Color options for contours and filled contours

You can change the color used to display an isodose. These changes will last until you close the study. To permanently change the display colors, use an RT template (see **Manage RT templates**).

1. Click (or tap) the color box beside the 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**.

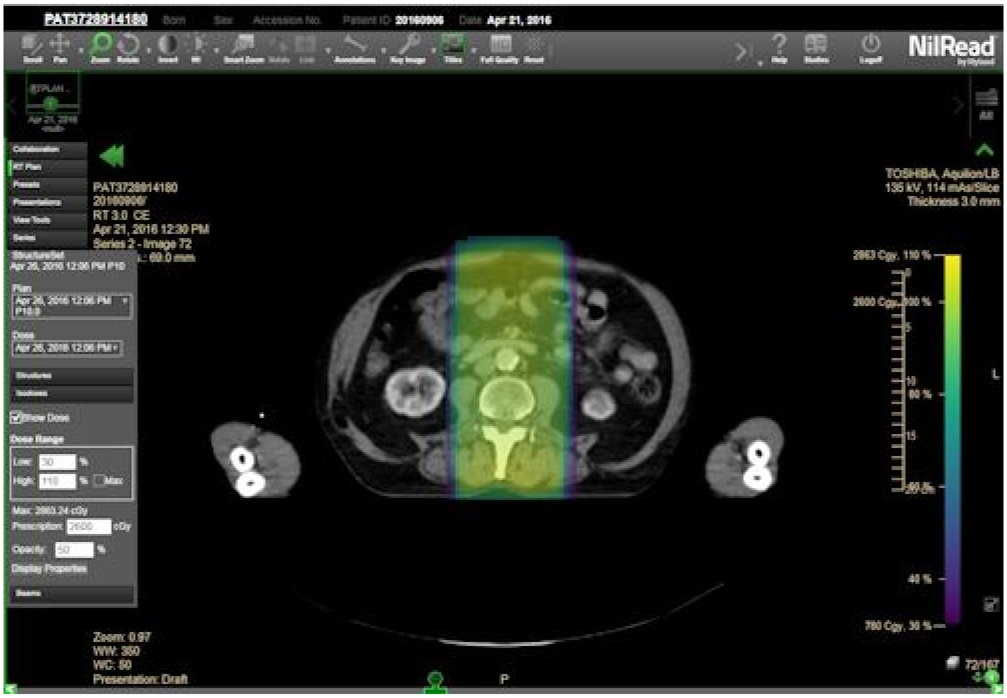
Dose Colorwash and Isodose Colorwash

The colorwash modes show the original, not resampled RT dose blended with the image series. Before blending, the dose data is colored by applying a color lookup table to the dose values.

The Dose Colorwash applies the LUT to a contiguous set of dose values within a range of minimum and maximum dose values, that is a percentage of the prescription.

The Isodose Colorwash applies the LUT to isodose regions and as a result the blended image may appear pixelated depending on the resolution of the dose data.

To show the colowash dose, select **Show Dose**.



PAT3728914180
20160906/
RT 3.0 CE
Apr 21, 2016 12:30 PM
Series 2 - Image 72

☑ Show Dose

Dose Range

Low: 30 %

High: 110 % ☐ Max

Max: 2863.24 cGy

Prescription: 2600 cGy

Opacity: 50 %

Zoom: 0.97
WW: 350
WC: 50
Presentation: Draft

You can enter the dose range to view the affected areas.

- In the **Low** field enter the minimum value of the range you want to view.
- In the **High** field enter the maximum value of the range you want to view. If you want to set the maximum value to be equal to the maximum dose, select the **Max** option.

You can change the value of the prescription dose in the **Prescription Dose** field.

You can change the percentage of the opacity of the colorwash in the **Opacity** field.

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 focus on a beam, select the beam label. (This will also select the beam if it is not already selected.) For both 2D views and slab images, the viewport is updated to focus on the location of the current beam control point.

You can display all the beams for the dose by selecting **All for Dose**.

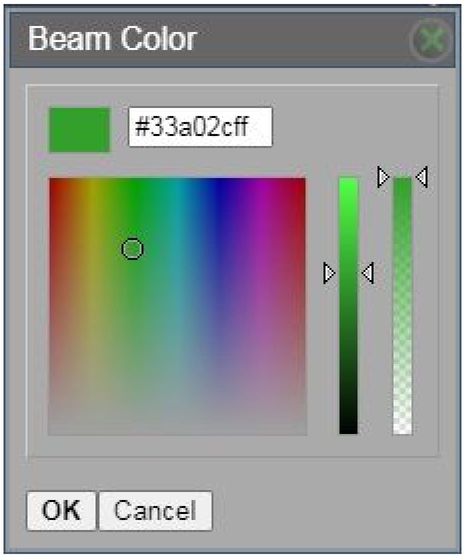
You can specify whether the isocenter is displayed by selecting **Show Isocenter**.

Color options

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

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.



#33a02cff

3. Use the sliders to adjust the color tone and opacity.
4. Select **OK**.

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**.

Using the RT Graph view

The RT Graph view includes a dose-volume histogram (DVH), representing the distribution of a dose within a structure. You can choose to view a cumulative DVH or a differential DVH. You can also select the structures to include in the histogram.

1. Select **View** (toolbar). Under **RT Views**, 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**.

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

3. Under **Histogram Type**, select **Cumulative** or **Differential**.

4. Select a dose, then select one or more structures.

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

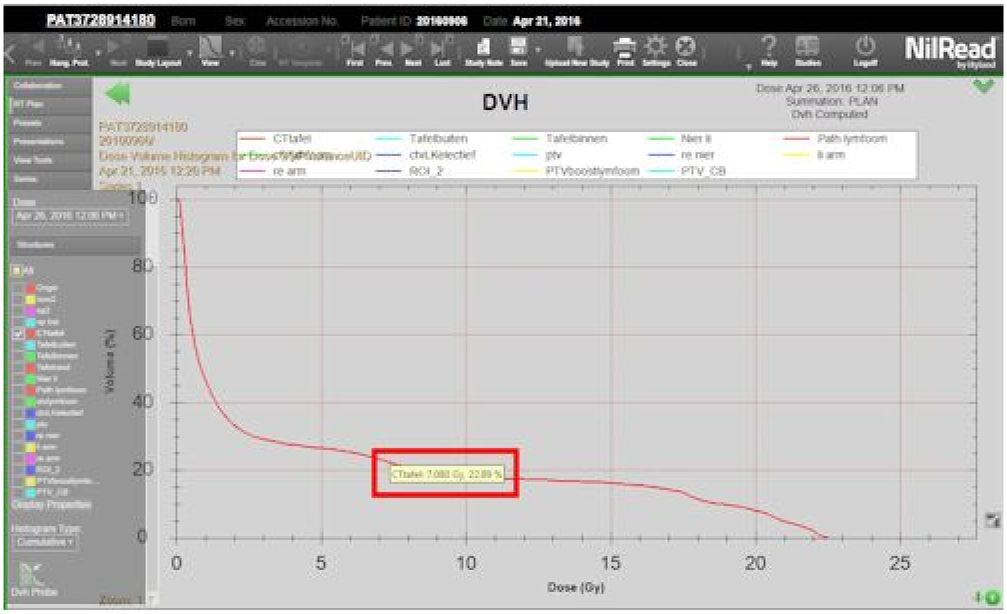
6. You can use **Zoom** (toolbar) to zoom in and out on the graph. You can also use **Pan** (toolbar) to pan the graph horizontally.

Using the DVH Probe

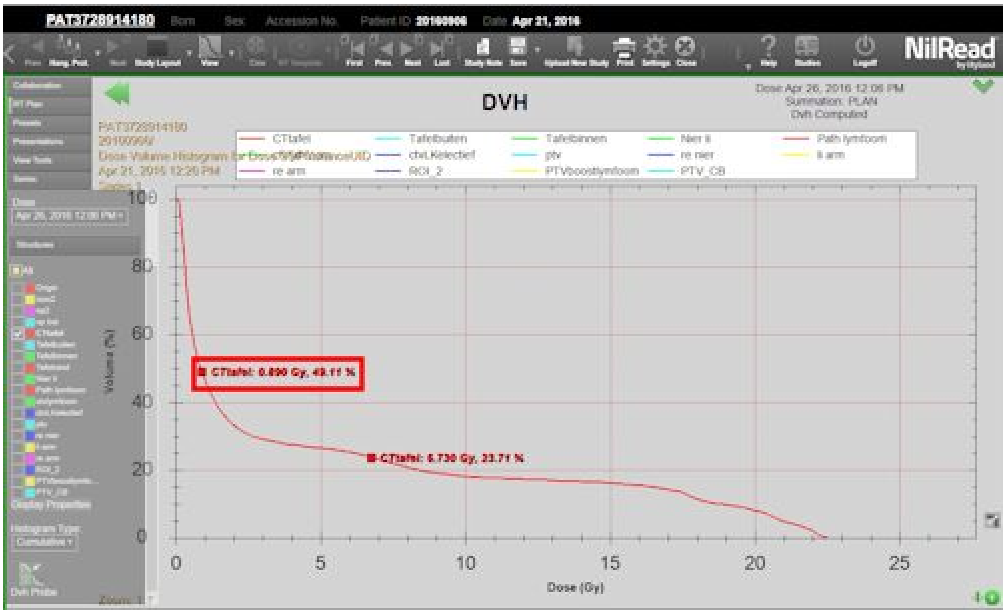
You can use the **DVH Probe** to view values for a point on a curve.

1. Select **DVH Probe**.

2. Hover over a point on a curve. The dose and volume are shown.



3. Click (or tap) a point on a curve. A marker is shown on the curve along with the dose and volume. You can select multiple points. To remove a point, click (or tap) the point on the curve.

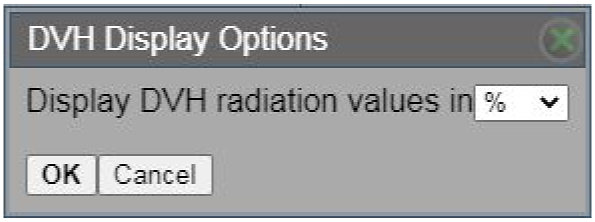


Display properties

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.



DVH Display Options

Display DVH radiation values in %

3. Select **OK**.

Structure color options

You can change the color used for a structure. For details, see **Using the RT Plan panel**.

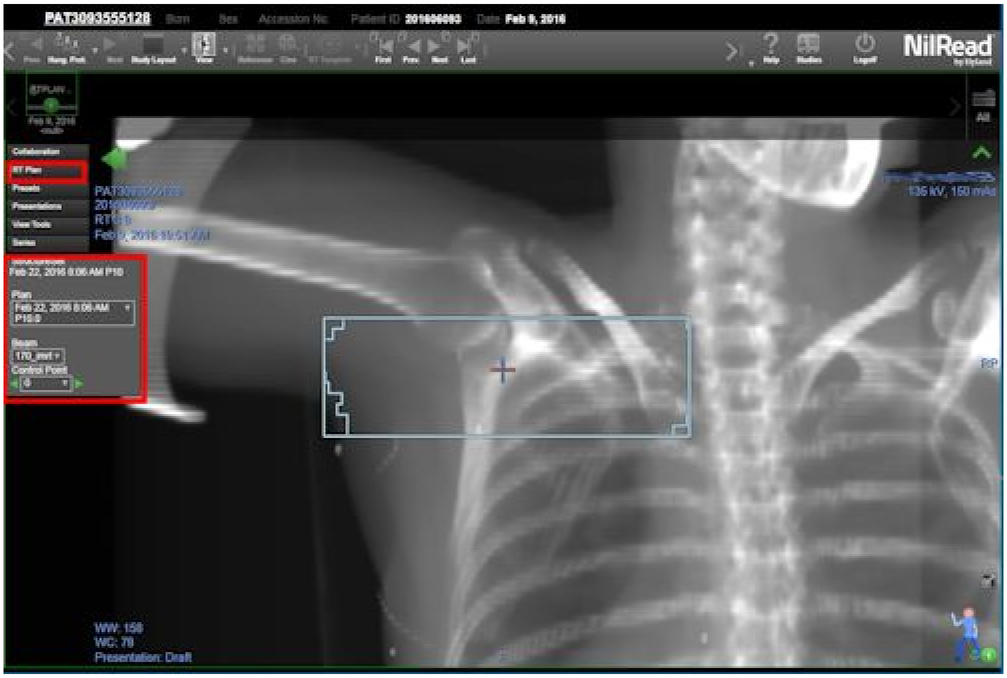
Using the DRR view

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.

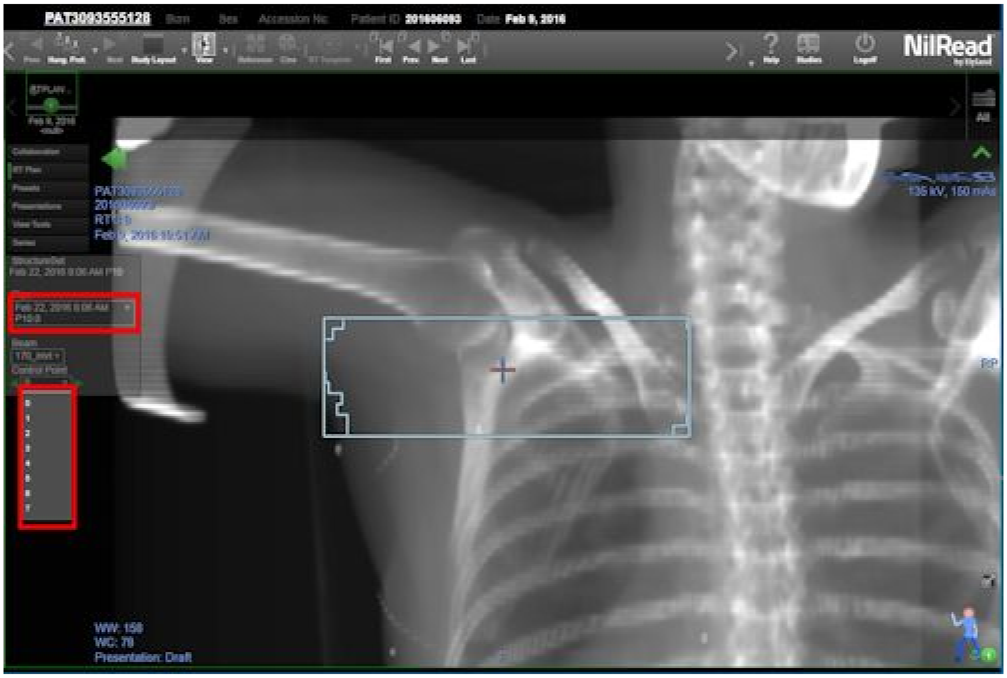
1. Select **View** (toolbar). Under **RT Views**, select **DRR**.

> **Note**
> You can also use the study layout options to place the DRR view beside an existing view. For details, see **Arrange images**.

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, or click the control point list and select a control point from the drop-down list.

4. 

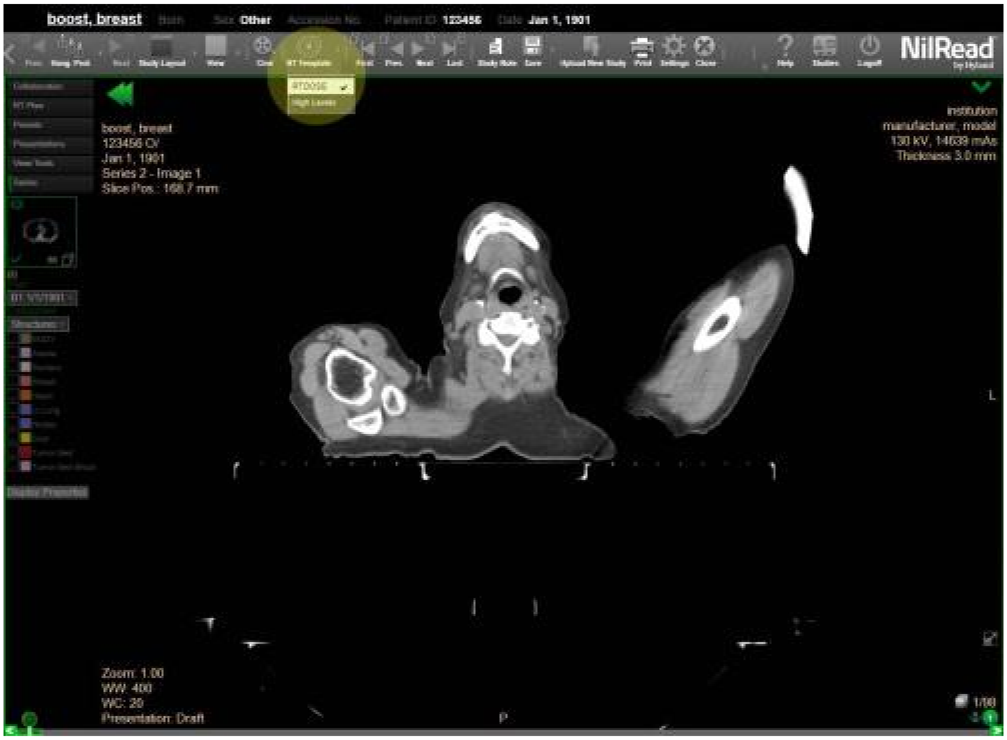
Apply an RT template to a study

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**.

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. 

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.

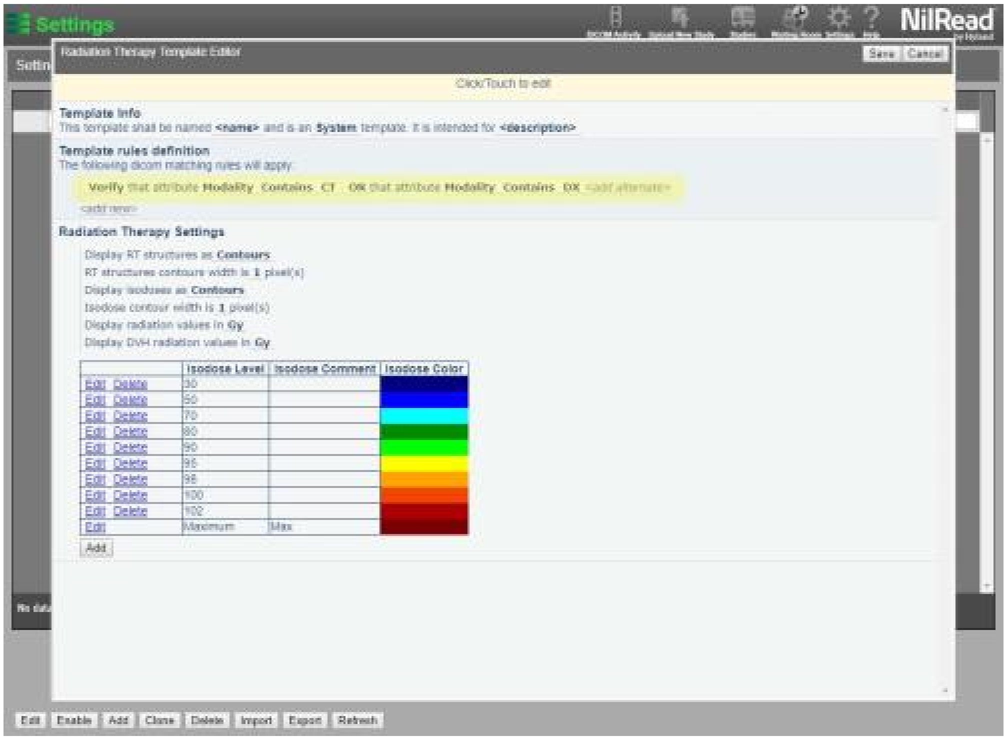
   A system template will be available to all users of NilRead, a group template will only be available to the group you specify, and a user template will only be available to the user you specify.
3. Enter a description for the template.

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.



Template Info

This template shall be named **<name>** and is an **System** template. It is intended for **<description>**

Template rules definition

The following dicom matching rules will apply:

Verify that attribute **Modality** **Contains** **CT** **OR** that attribute **Modality** **Contains** **DX** <add alternate>

<add new>

Radiation Therapy Settings

Display RT structures as **Contours**

RT structures contours width is **1** pixel(s)

Display isodoses as **Contours**

Isodose contour width is **1** pixel(s)

Display radiation values in **Gy**

Display DVH radiation values in **Gy**

	Isodose Level	Isodose Comment	Isodose Color
Edit Delete	30		🟦
Edit Delete	50		🟦
Edit Delete	70		🟦
Edit Delete	80		🟩
Edit Delete	90		🟩
Edit Delete	95		🟨
Edit Delete	98		🟧
Edit Delete	100		🟧
Edit Delete	102		🟥
Edit	Maximum	Max	🟥

Add

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.

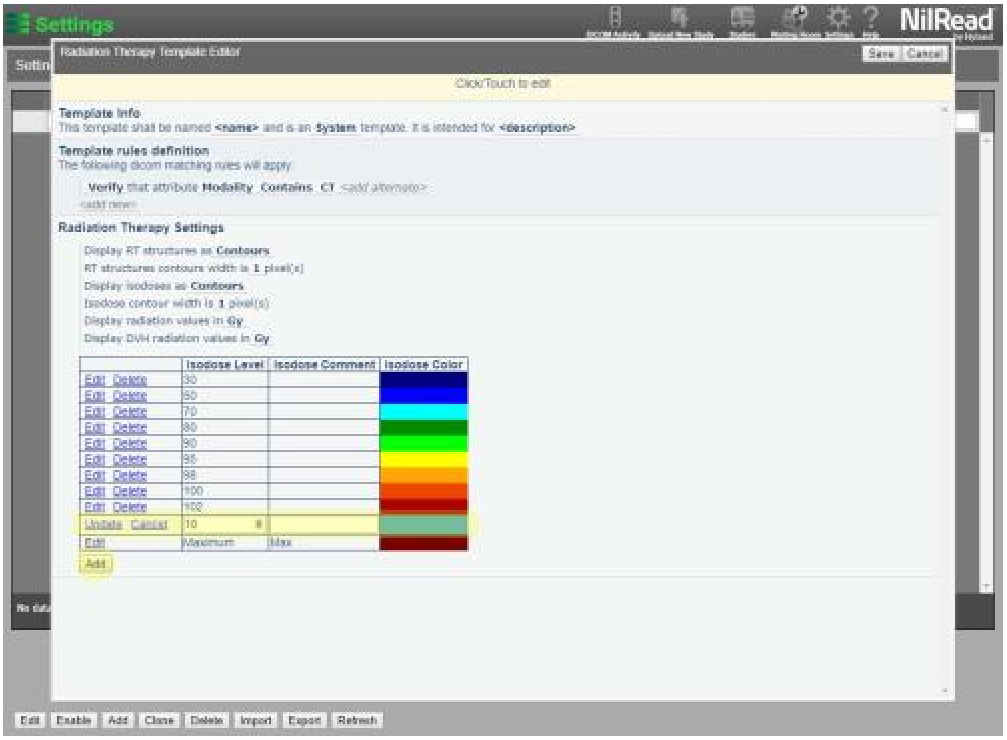
- Select one of the following options: contours (outline), filled contours (shaded), dose colorwash, or isodose colorwash.
- Select the width of the contour outline. Note that you cannot change the contour width for MPR images.

- 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.



Template Info
This template shall be named **<name>** and is an **System** template. It is intended for **<description>**

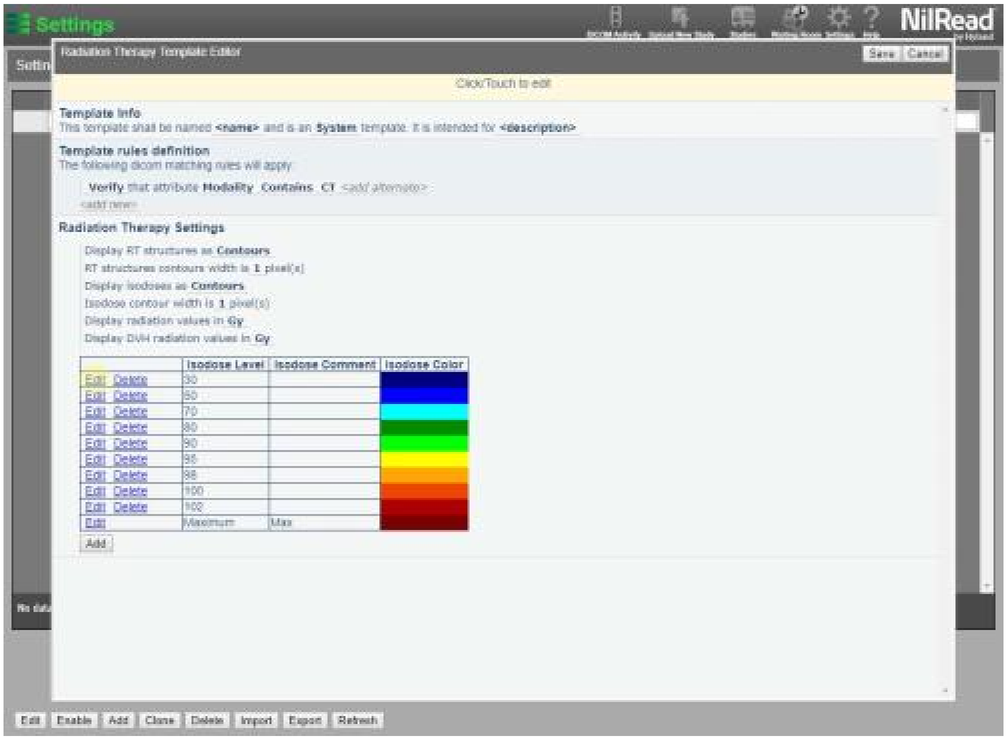
Template rules definition
The following dicom matching rules will apply:
Verify that attribute **Modality** **Contains** **CT** <add alternate>
<add new>

Radiation Therapy Settings
Display RT structures as **Contours**
RT structures contours width is **1** pixel(s)
Display isodoses as **Contours**
Isodose contour width is **1** pixel(s)
Display radiation values in **Gy**
Display DVH radiation values in **Gy**

	Isodose Level	Isodose Comment	Isodose Color
Edit Delete	30		🟦
Edit Delete	50		🟦
Edit Delete	70		🟦
Edit Delete	80		🟩
Edit Delete	90		🟩
Edit Delete	95		🟨
Edit Delete	98		🟧
Edit Delete	100		🟥
Edit Delete	102		🟥
Update Cancel	10		🟩
Edit	Maximum	Max	🟥

Add

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



Template Info
This template shall be named **<name>** and is an **System** template. It is intended for **<description>**

Template rules definition
The following dicom matching rules will apply

Verify that attribute **Modality** **Contains** **CT** *<add alternate>*
<add new>

Radiation Therapy Settings

Display RT structures as **Contours**
RT structures contours width is **1** pixel(s)
Display isodoses as **Contours**
Isodose contour width is **1** pixel(s)
Display radiation values in **Gy**
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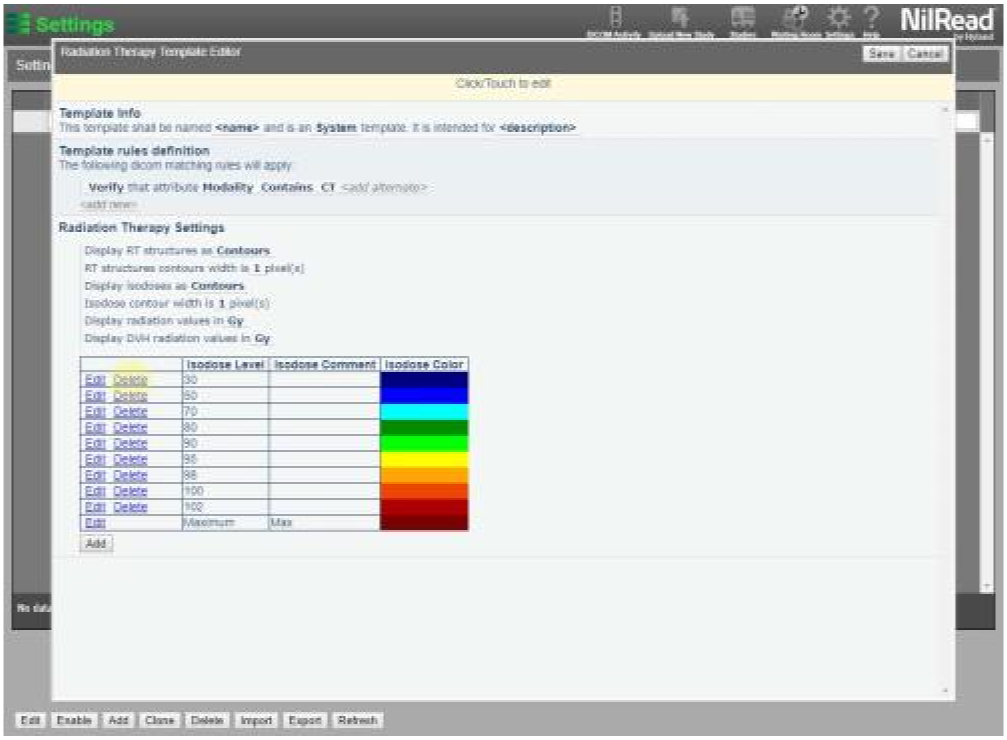
	Isodose Level	Isodose Comment	Isodose Color
Edit Delete	30		🟦
Edit Delete	50		🟦
Edit Delete	70		🟦
Edit Delete	80		🟩
Edit Delete	90		🟩
Edit Delete	95		🟨
Edit Delete	98		🟧
Edit Delete	100		🟧
Edit Delete	102		🟥
Edit	Maximum	Max	🟥

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



Template Info
This template shall be named **<name>** and is an **System** template. It is intended for **<description>**

Template rules definition
The following dicom matching rules will apply
Verify that attribute **Modality** **Contains** **CT** *<add alternate>*
<add new>

Radiation Therapy Settings
Display RT structures as **Contours**
RT structures contours width is **1** pixel(s)
Display isodoses as **Contours**
Isodose contour width is **1** pixel(s)
Display radiation values in **Gy**
Display DVH radiation values in **Gy**

	Isodose Level	Isodose Comment	Isodose Color
Edit Delete	30		🟦
Edit Delete	50		🟦
Edit Delete	70		🟦
Edit Delete	80		🟩
Edit Delete	90		🟩
Edit Delete	95		🟨
Edit Delete	98		🟧
Edit Delete	100		🟥
Edit Delete	102		🟥
Edit	Maximum	Max	🟥

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, deselect 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.

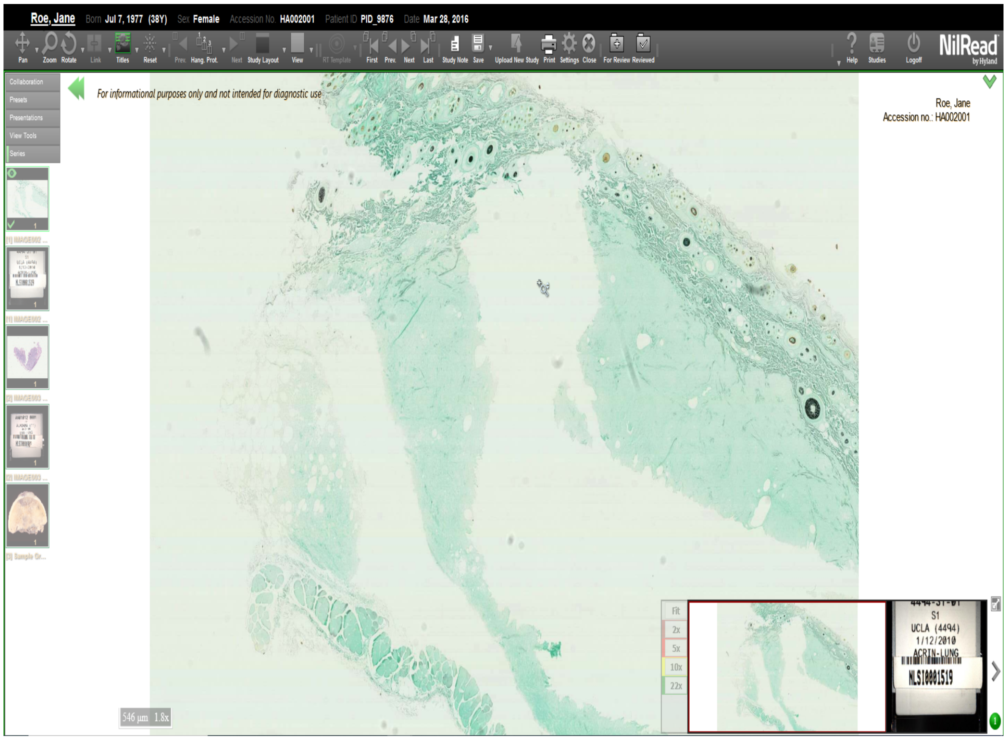
Referential pathology studies

View referential pathology studies

Referential pathology studies automatically open in a specialized viewer. The viewer has a simplified layout to allow you to focus on the referential pathology workflow.

> **Note**
> This functionality is only available if the *referentialPathology* license is present.

The viewer offers most of the typical tools available for the other modalities.

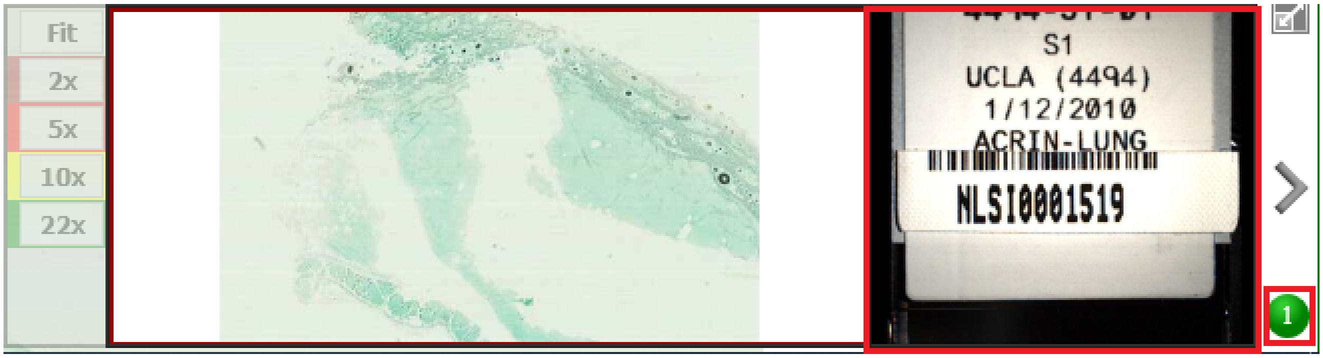

Roe, Jane Born Jul 7, 1977 (38Y) Sex Female Accession No. HA002001 Patient ID PID_9876 Date Mar 28, 2016

For informational purposes only and not intended for diagnostic use

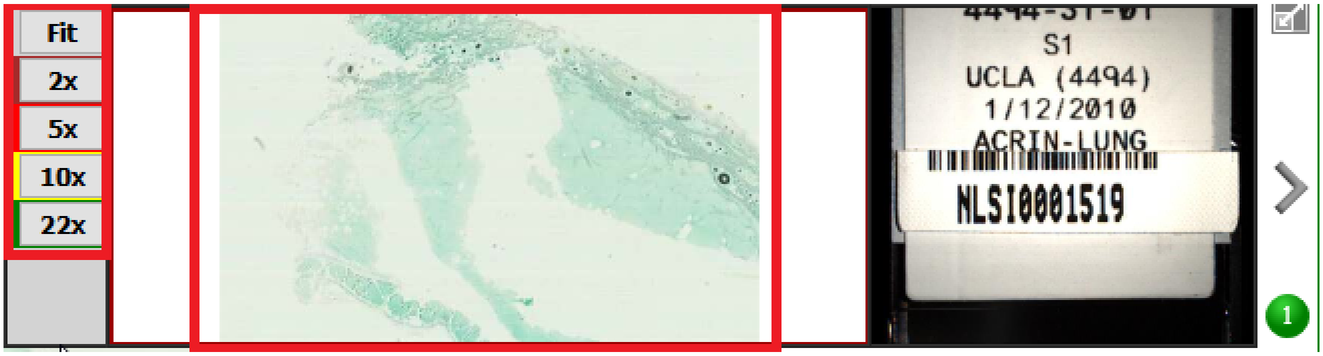
Roe, Jane
Accession no.: HA002001

In addition, the viewer provides the following functionality:

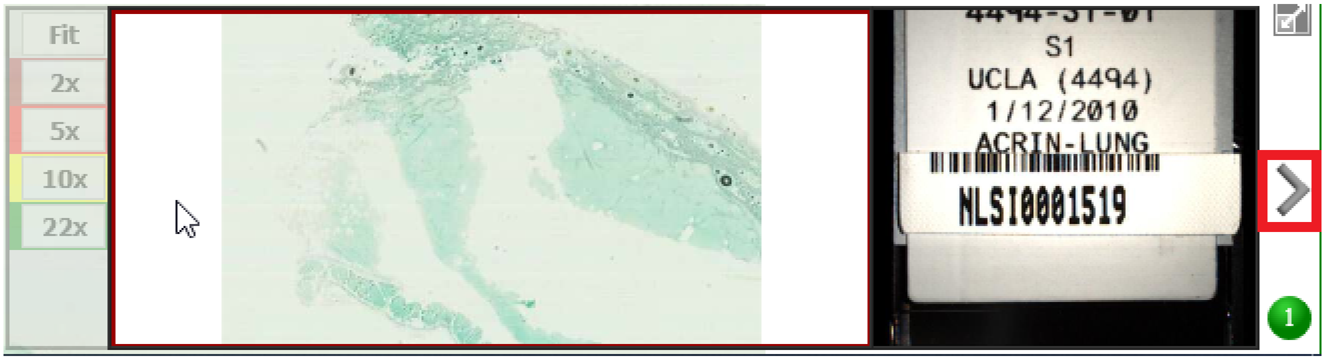
- The slide label is shown on the bottom-right corner of the image. The number of samples in the study is shown to the right of the slide label.



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

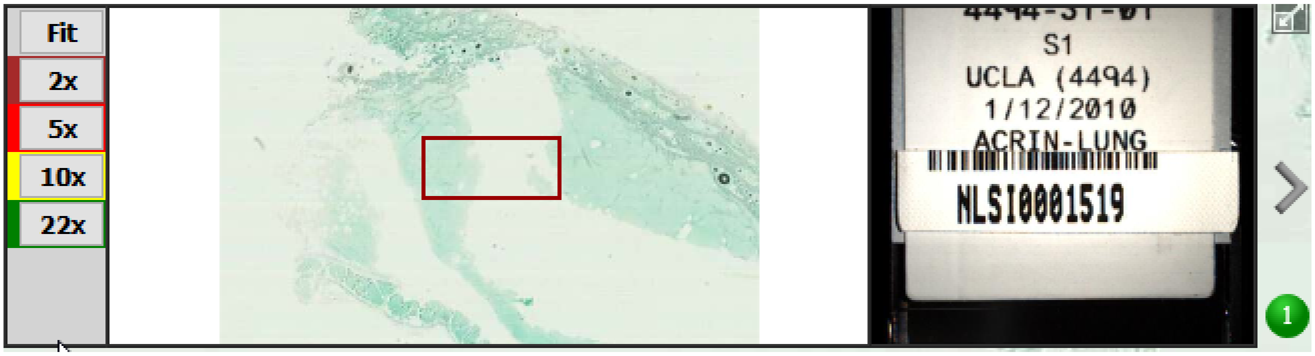


- You can also hide the slide label, magnification options and navigation map using the arrow in the bottom-right corner.



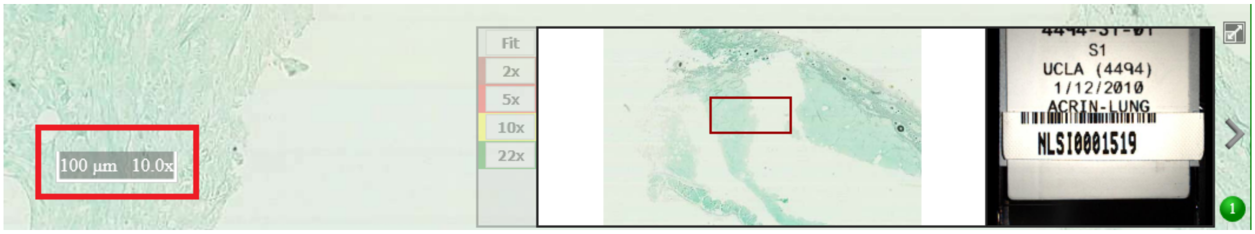
Use the navigation map and magnification options

The red rectangle in the navigation map indicates the area of the image currently shown in the view-port.



- 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 differentposition on the screen. Double-click (or touch and hold) the Caliper to return it to its original position.



Anonymize patient data

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**). 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** and **Manage folders**). 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**).

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** and **Manage folders**). 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**).

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** and **Manage folders**) or select the profile when downloading a study (see **Download studies, series or images**).

    - **Apply Masks** If selected, confidentiality masks may be used to redact patient data (see **Manage confidentiality masks**).
    - **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**.

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. Deselect 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.

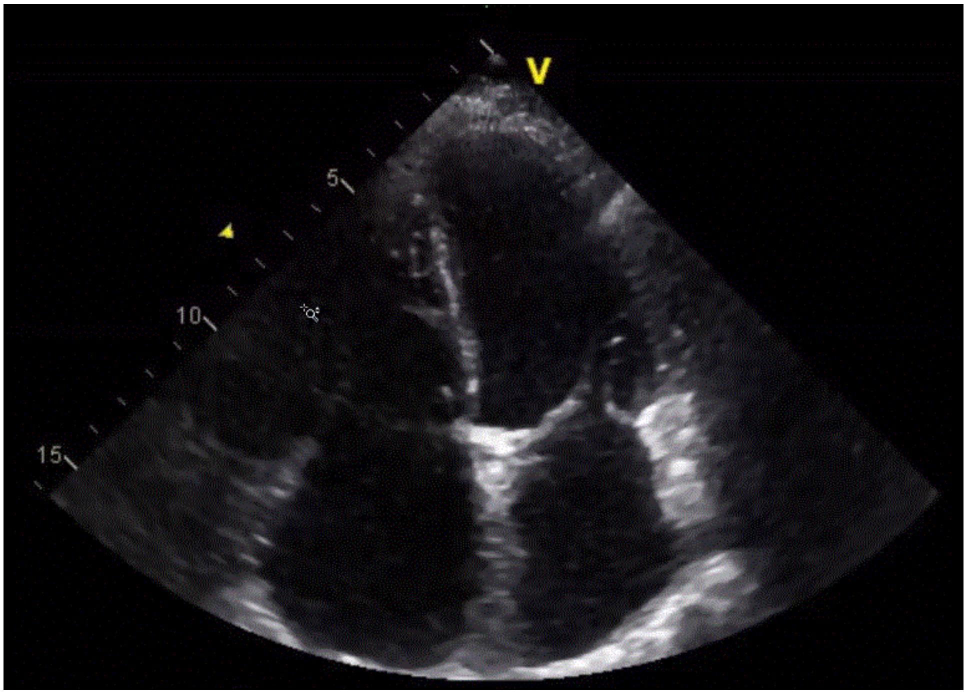
Left Ventricle Ejection Fraction (LVEF)

The Left Ventricle Ejection Fraction (LVEF) function is used to estimate the volume of blood pumped out by the left ventricle of the heart.

The LVEF measurement is based on estimation of the volume of left ventricle at two different states: End Diastole (when the left ventricle is at its maximum volume) and End Systole (when the left ventricle is at its minimum volume). The volume of the left ventricle is estimated using the Simpson method on cardiac ultrasound images in Apical 4 Chamber (A4C) and Apical 2 Chamber (A2C) views.

> **Note**
> It is more convenient to perform this measurement in 1x1 view. Switch to 1x1 view if the current view is different.

1. Begin the measurement by loading an ultrasound series with an Apical 4 Chamber view of the heart.
2. If Cine is playing, stop it by selecting the **Cine Stop** button on the toolbar.



Finding diastole

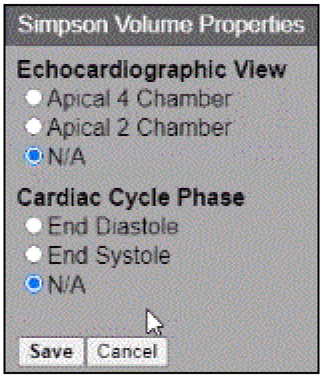
Find the image of end diastole inside the series by using the ECG signal as an aid, or visually locating the image with maximum relaxation of the left ventricle.

Finding systole

With the current series still selected, locate and open the image of end systole by using the ECG signal as an aid, or visually locating the image with maximum contraction of the left ventricle.

Measuring the volume using the Simpson method

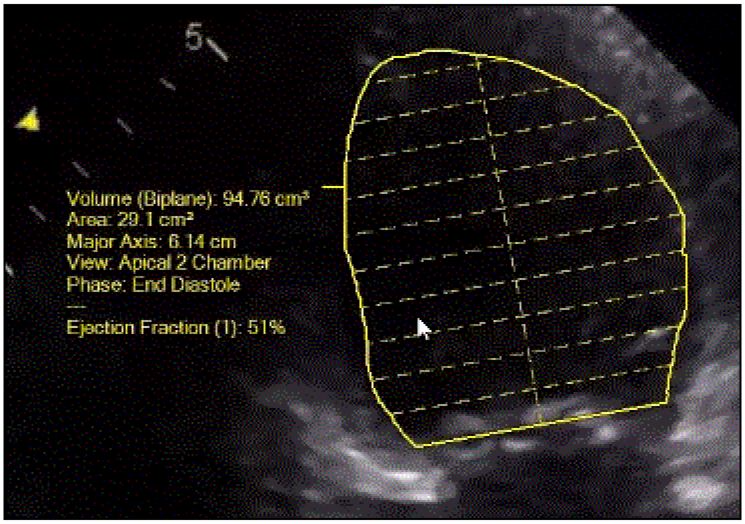
1. From the menu bar, select **Annotation | Cardiology | Simpson Volume**.
2. To start marking the area of the left ventricle, click in the corner at one end of the mitral valve annulus, and drag the mouse around to the other end of the annulus, encapsulating the entire chamber. When the mouse is released, the Simpson Volume Properties dialog box is displayed.


Simpson Volume Properties

Echocardiographic View
○ Apical 4 Chamber
○ Apical 2 Chamber
● N/A

Cardiac Cycle Phase
○ End Diastole
○ End Systole
● N/A

3. Under **Echocardiographic View**, select the type of the view in this image.
4. Under **Cardiac Cycle Phase**, select the phase to which this cycle corresponds.
5. Click **Save**. An information box displays on the image and contains the measurement details including volume, area, major axis, view, and phase. If an end systole measurement has not been performed, the Ejection Fraction information is not shown.


Volume (Biplane): 94.76 cm³
Area: 29.1 cm²
Major Axis: 6.14 cm
View: Apical 2 Chamber
Phase: End Diastole
—
Ejection Fraction (1): 51%

Notes

The Ejection Fraction value will be displayed only after volumes for both End Diastole and End Systole phases are measured. The Biplane label on volume measurement means that the measurement uses biplane Simpson method, which requires performing the measurement on both Apical 4 Chamber and Apical 2 Chamber views as will be explained further below.

You can adjust the position and direction of the major axis of the ventricle by moving the apex point along the ventricle contour. Specifically, you can:

- Adjust end points of the contour by moving them slightly
- Adjust direction of the major axis by moving the apex point along the ventricle contour
- Adjust part of the contour by redrawing only this portion, beginning at some position on the contour
- As you make the adjustments, measurement values will be updated

Selecting the end systole

1. With the current series still selected, locate and open the image of end systole by using the ECG signal as an aid, or visually locating the image with maximum contraction of the left ventricle.
2. Repeat steps 1-6 outlined in the previous section.

The measurements made are automatically saved. In addition, after the Simpson Volumes are measured for end diastole and end systole, the ejection fraction value is computed and displayed on each of the measurements.

Improving precision using biplane Simpson volume

If the study contains a series of Apical 2 Chamber views, additional measurements can be performed on this view to improve precision of the left ventricle volume and ejection fraction.

1. Select the series with the Apical 2 Chamber view.
2. Measure the Simpson Volumes at the end diastole and end systole points, as done for the Apical 4 Chamber view.

3. From the menu bar, select **Annotation | Cardiology | Simpson Volume**.
4. In the Simpson Volume Properties dialog box, select **Apical 2 Chamber**.
5. Select the appropriate **Cardiac Cycle Phase**.

The following occurs:

- The values of the volumes are computed using biplane Simpson method.
- The value of ejection fraction will be updated.
- The values are updated on the measurements of the Apical 4 Chamber view as well.

Viewing all volumes used for ejection fraction calculation

There are two methods for viewing the calculation volumes:

Method 1:

Right-click on any of the Simpson volumes and select **Show Related volumes**.

Method 2:

1. Right-click on any image in the study.
2. Select **View Study Annotations**.
3. Select the ejection fraction measurement.
4. Click the **View** icon.

Replacing one volume with another

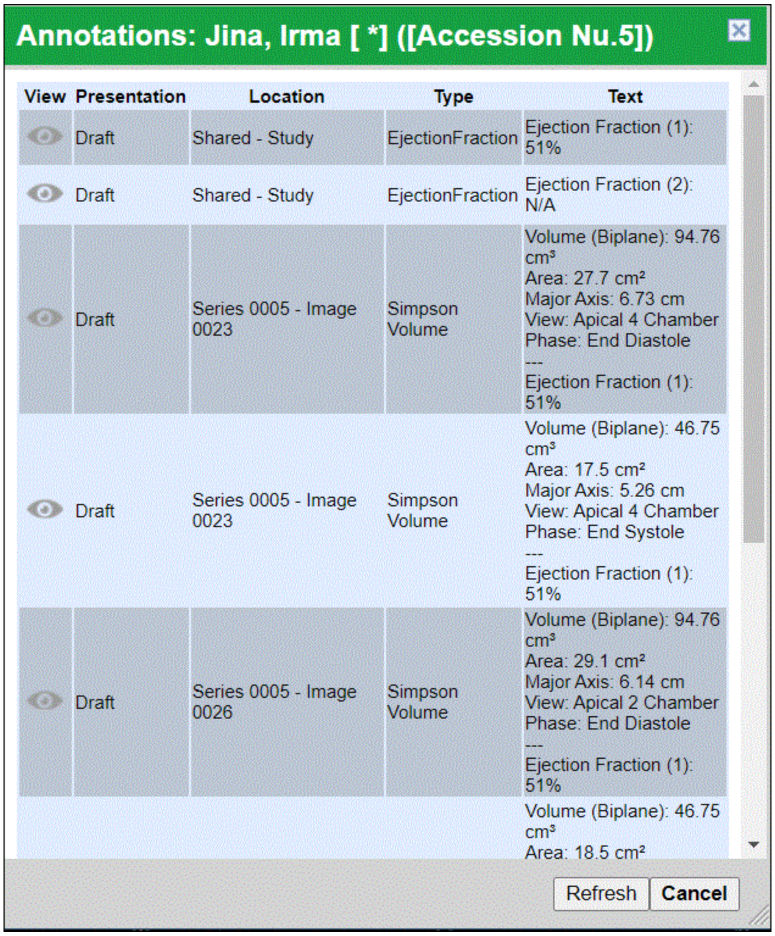
It is possible to recompute the existing ejection fraction measurement by again measuring a volume with particular cardiac view and phase. This can be useful if a better image is found, and would like to use that image instead.

1. Measure the Simpson Volume on a new image as described under **Measuring the volume using the Simpson method**. The Warning dialog box is displayed.
2. Select **Overwrite** to replace a previously measured Simpson Volume with the new one. The ejection fraction value will be recomputed, and the values will be updated on all other Simpson Volume measurements in the study.

Performing another ejection fraction measurement in the same study

It is possible to measure ejection fraction more than once using a different set of images.

1. Select an image with A4C view.
2. Start with measuring the Simpson Volume at end diastole point (as described previously). The Warning dialog box is displayed.
3. Select **New** to add the new volume measurement and start a new ejection fraction measurement. The previous ejection fraction measurement remains unchanged and becomes immutable and cannot be updated.
4. Continue measuring additional Simpson Volumes (as described above) to complete this ejection fraction measurement.
5. To view all measured Simpson Volumes and ejection fractions, right-click on any image.
6. From the menu, select **View study annotations**. The Annotations dialog box is displayed and contains information about an annotation, and includes a View icon, which can be selected to open the image with selected measurement.



View	Presentation	Location	Type	Text
👁	Draft	Shared - Study	EjectionFraction	Ejection Fraction (1): 51%
👁	Draft	Shared - Study	EjectionFraction	Ejection Fraction (2): N/A
👁	Draft	Series 0005 - Image 0023	Simpson Volume	Volume (Biplane): 94.76 cm^3 Area: 27.7 cm^2 Major Axis: 6.73 cm View: Apical 4 Chamber Phase: End Diastole --- Ejection Fraction (1): 51%
👁	Draft	Series 0005 - Image 0023	Simpson Volume	Volume (Biplane): 46.75 cm^3 Area: 17.5 cm^2 Major Axis: 5.26 cm View: Apical 4 Chamber Phase: End Systole --- Ejection Fraction (1): 51%
👁	Draft	Series 0005 - Image 0026	Simpson Volume	Volume (Biplane): 94.76 cm^3 Area: 29.1 cm^2 Major Axis: 6.14 cm View: Apical 2 Chamber Phase: End Diastole --- Ejection Fraction (1): 51%
				Volume (Biplane): 46.75 cm^3 Area: 18.5 cm^2

Collaborate

Use online meetings

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 an small resolution device such as a phone.

Create a meeting for a folder

You can start a meeting based on a folder. All of the studies in the folder are opened in the image viewer separately (as separate patients) when the meeting starts. Users with access to the folder can quickly join the meeting. You can also invite participants using **Invite** on the meeting control panel.

Start a meeting for a folder

Right-click (or touch and hold) a folder, select **Meeting**, then select **Start Meeting**.

Send the meeting link to participants

You can copy the meeting link.

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

You can create an email with the meeting link.

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

Join a meeting for a folder

If you have access to the folder, right-click (or touch and hold) the folder, select **Meeting**, then select **Join Meeting**. You can also use the meeting link, if one is provided by the meeting organizer.

Create a general meeting

You can start a meeting and invite participants.

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.

admin *PO ▼	**Transfer control** 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 **Control** list. The organizer can regain control by selecting their own name.
✎ ↘	**Annotate images** To draw on an image, select **Highlighter**. To add an arrow and note, select **Arrow**. 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 **Active Users** list.
⟲	**Undo all** Select **Undo all** to remove all annotations made by all of the meeting participants.
↶	**Undo** Select **Undo** to remove the last annotation made by any meeting participant.
@	**Invite others** Select **Invite**. A new email is created using your default email application. Enter the recipient’s email address and any additional information, then send the email.

⊗	**End meeting** Select **Quit**. This can only be done by the meeting organizer. **Note** 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**).

Send secure study links

Share a patient study with others by sending them a secure link. The link is temporary and does not contain any identifying information about the study.

Send a secure link by email

In the Patient Study Directory:

1. Right-click (or touch and hold) a study, worklist or folder, then select **Send Link**.
2. End users are responsible for complying with privacy regulations and ensuring that study links are only provided to authorized users. Users cannot disable a study link once it has been sent. To indicate that you understand this, select the checkbox beside **Note: authorization cannot be removed once the secure link is sent.**

   > **Note**
   > The site's NilRead administrator is able to revoke a study link. However, the recipient may receive and use the link before it is revoked.

3. Choose the security options you want to use. Depending on your organization's NilRead configuration, some of the following options may not be available.
   - **Send via email to** If you want to send an email with the study link, select this option and enter the user's email address.
   - **Limit number of uses to** To limit number of times the user can use the link to access the study, select this option and enter the number of uses.

- **Link will expire in** To set an expiry date, select this option and enter the number of days and/or hours until the link expires.
- **User must login to see images** Select this option if the user must login to their NilRead account before using the link. If this option is not selected, the user does not require a NilRead account to use the link.
- **Require user to enter this password** If the user does not have a NilRead account and you want to create a password for the link, select this option and enter the password. You must give this password to the user; for security reasons, it is not sent to them automatically.
- **Display this password hint** Select this option to display a password hint to the user. Enter a password hint in the provided field.
- **Require confirmation via email** Select this option to use a two-step verification process. The user will receive an email with a link to confirm they are the intended recipient. When the user clicks the link, they will be sent a second email with the study link. Note that this option is only available if your organization uses an IIS SMTP mail server.

4. Select **Get Link**.
5. In the **Send Link** dialog box, choose how to send the link.
   - **Copy link to clipboard** Copy the link and paste it into an email or instant message.
   - **Click to send link by email** Automatically create a new email using your default email application. The user’s email address is entered automatically. Add any additional information, then send the email.
   - **Show QR code to send the link** This option displays a QR code that you can scan with your cell phone.
     Ensure that you have entered a valid email address in the **Send via email to** field and then complete the following substeps:
     1. Select **Show QR code to send link**.
        The QR code is displayed on the screen.
     2. Scan the QR code using the camera application of your cell phone.
        Your cell phone prompts you to send the email. The exact message depends on your phone type and operating system.

   3. Tap on the message on your cell phone.
      An email is created using the previously entered email address and the URL link in the body.
   4. Send the email.
      You can optionally add comments before sending or copy the URL to use it in another messaging application.
   5. Click anywhere on the screen to return to the previous dialog box.
6. Select **Close**.

Copy a link

In the Patient Study Directory:

1. Right-click (or touch and hold) a study, worklist or folder, then select **Copy Link**.
2. 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. End users are responsible for complying with privacy regulations and ensuring that study links are only provided to authorized users. Users cannot disable a study link once it has been sent. To indicate that you understand this, select the checkbox beside **Note: authorization cannot be removed once the secure link is sent**.

> **Note**
> The site's NilRead administrator is able to revoke a study link. However, the recipient may receive and use the link before it is revoked.

4. Choose the security options you want to use. Depending on your organization's NilRead configuration, some of the following options may not be available.
   - **Send via email** If you want to send an email with the study link, select this option and enter the user's email address.
   - **Limit number of uses to** To limit number of times the user can use the link to access the study, select this option and enter the number of uses.
   - **Link will expire in** To set an expiry date, select this option and enter the number of days and/or hours until the link expires.
   - **User must login to see images** Select this option if the user must login to their NilRead account before using the link. If this option is not selected, the user does not require a NilRead account to use the link.
   - **Require user to enter this password** If the user does not have a NilRead account and you want to create a password for the link, select this option and enter the password. You must give this password to the user; for security reasons, it is not sent to them automatically.
   - **Display this password hint** Select this option to display a password hint to the user. Enter a password hint in the provided field.
   - **Require confirmation via email** Select this option to use a two-step verification process. The user will receive an email with a link to confirm they are the intended recipient. When the user clicks the link, they will be sent a second email with the study link. Note that this option is only available if your organization uses an IIS SMTP mail server.
5. Select **Get Link**.
6. Choose how to send the link.
   - **Copy link to clipboard** Copy the link and paste it into an email or instant message.
   - **Click to send link by email** Automatically create a new email using your default email application. The user's email address is entered automatically. Add any additional information, then send the email.

7. Select **Close**.

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:

1. Right-click (or touch and hold) a bookmark, then select **Email**.
2. End users are responsible for complying with privacy regulations and ensuring that study links are only provided to authorized users. Users cannot disable a study link once it has been sent. To indicate that you understand this, select the checkbox beside **Note: authorization cannot be removed once the secure link is sent**.

> **Note**
> The site's NilRead administrator is able to revoke a study link. However, the recipient may receive and use the link before it is revoked.

3. Choose the security options you want to use. Depending on your organization's NilRead configuration, some of the following options may not be available.
    - **Send via email** If you want to send an email with the study link, select this option and enter the user's email address.
    - **Limit number of uses to** To limit number of times the user can use the link to access the study, select this option and enter the number of uses.
    - **Link will expire in** To set an expiry date, select this option and enter the number of days and/or hours until the link expires.
    - **User must login to see images** Select this option if the user must login to their NilRead account before using the link. If this option is not selected, the user does not require a NilRead account to use the link.
    - **Require user to enter this password** If the user does not have a NilRead account and you want to create a password for the link, select this option and enter the password. You must give this password to the user; for security reasons, it is not sent to them automatically.
    - **Display this password hint** Select this option to display a password hint to the user. Enter a password hint in the provided field.
    - **Require confirmation via email** Select this option to use a two-step verification process. The user will receive an email with a link to confirm they are the intended recipient. When the user clicks the link, they will be sent a second email with the study link. Note that this option is only available if your organization uses an IIS SMTP mail server.
4. Select **Get Link**.
5. Choose how to send the link.
    - **Copy link to clipboard** Copy the link and paste it into an email or instant message.
    - **Click to send link by email** Automatically create a new email using your default email application. The user's email address is entered automatically. Add any additional information, then send the email.

6. Select **Close**.

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. End users are responsible for complying with privacy regulations and ensuring that study links are only provided to authorized users. Users cannot disable a study link once it has been sent. To indicate that you understand this, select the checkbox beside **Note: authorization cannot be removed once the secure link is sent**.

   > **Note**
   > The site’s NilRead administrator is able to revoke a study link. However, the recipient may receive and use the link before it is revoked.

3. Choose the security options you want to use. Depending on your organization's NilRead configuration, some of the following options may not be available.
   - **Send via email** If you want to send an email with the study link, select this option and enter the user's email address.
   - **Limit number of uses to** To limit number of times the user can use the link to access the study, select this option and enter the number of uses.
   - **Link will expire in** To set an expiry date, select this option and enter the number of days and/or hours until the link expires.
   - **User must login to see images** Select this option if the user must login to their NilRead account before using the link. If this option is not selected, the user does not require a NilRead account to use the link.
   - **Require user to enter this password** If the user does not have a NilRead account and you want to create a password for the link, select this option and enter the password. You must give this password to the user; for security reasons, it is not sent to them automatically.
   - **Display this password hint** Select this option to display a password hint to the user. Enter a password hint in the provided field.
   - **Require confirmation via email** Select this option to use a two-step verification process. The user will receive an email with a link to confirm they are the intended recipient. When the user clicks the link, they will be sent a second email with the study link. Note that this option is only available if your organization uses an IIS SMTP mail server.
4. Select **Get Link**.
5. Choose how to send the link.
   - **Copy link to clipboard** Copy the link and paste it into an email or instant message.
   - **Click to send link by email** Automatically create a new email using your default email application. The user's email address is entered automatically. Add any additional information, then send the email.
6. Select **Close**.

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**.

Preferences

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.
   - **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**.

Manage study note templates

You can use templates to create different study note layouts.

1. Select **Settings**.
2. Under **Preferences**, select **Study Note Templates**.

3. A list of 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.

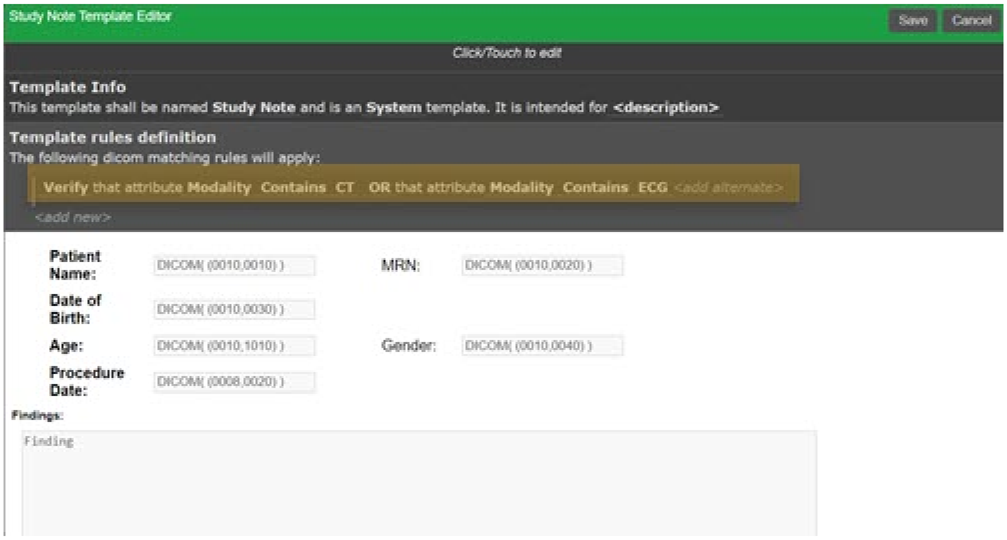
   A system template will be available to all users of NilRead, a group template will only be available to the group you specify, and a user template will only be available to the user you specify.
3. Enter a description for the template.

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 values. For example, you could list several modalities the template can be used for.



Click/Touch to edit

Template Info
This template shall be named **Study Note** and is an **System** template. It is intended for **<description>**

Template rules definition
The following dicom matching rules will apply:

Verify that attribute **Modality** **Contains** **CT** **OR** that attribute **Modality** **Contains** **ECG** *<add alternate>*

<add new>

Patient Name:	DICOM((0010,0010))	MRN:	DICOM((0010,0020))
Date of Birth:	DICOM((0010,0030))		
Age:	DICOM((0010,1010))	Gender:	DICOM((0010,0040))
Procedure Date:	DICOM((0008,0020))		

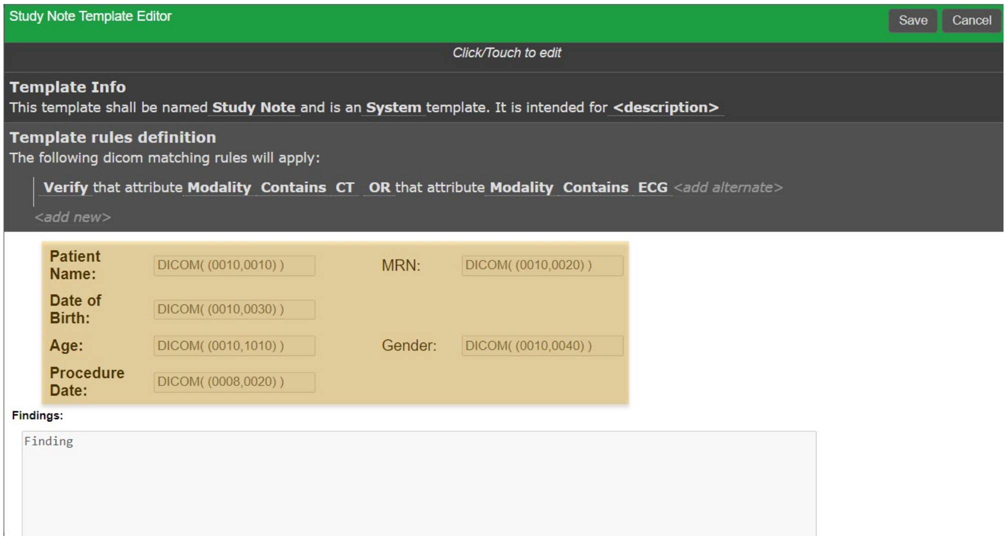
Findings:

Finding

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.



Click/Touch to edit

Template Info
This template shall be named **Study Note** and is an **System** template. It is intended for **<description>**

Template rules definition
The following dicom matching rules will apply:

Verify that attribute **Modality** **Contains** **CT** **OR** that attribute **Modality** **Contains** **ECG** *<add alternate>*

<add new>

Patient Name:	DICOM((0010,0010))	MRN:	DICOM((0010,0020))
Date of Birth:	DICOM((0010,0030))		
Age:	DICOM((0010,1010))	Gender:	DICOM((0010,0040))
Procedure Date:	DICOM((0008,0020))		

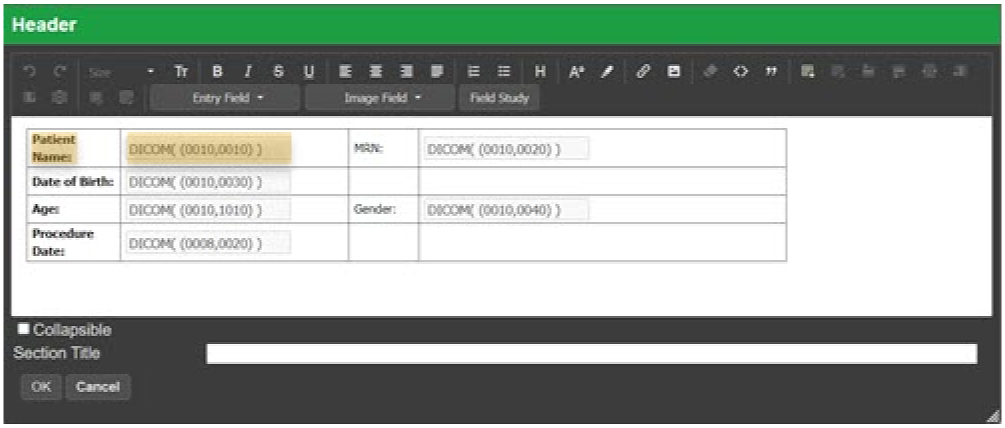
Findings:

Finding

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.



Patient Name:	DICOM((0010,0010))	MRN:	DICOM((0010,0020))
Date of Birth:	DICOM((0010,0030))		
Age:	DICOM((0010,1010))	Gender:	DICOM((0010,0040))
Procedure Date:	DICOM((0008,0020))		

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 the text (color, font, and so on).
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 study note template for your site. For details on creating assets, see **Manage assets**.

1. To place an asset before the fields table, place your cursor before the table, then press ENTER.

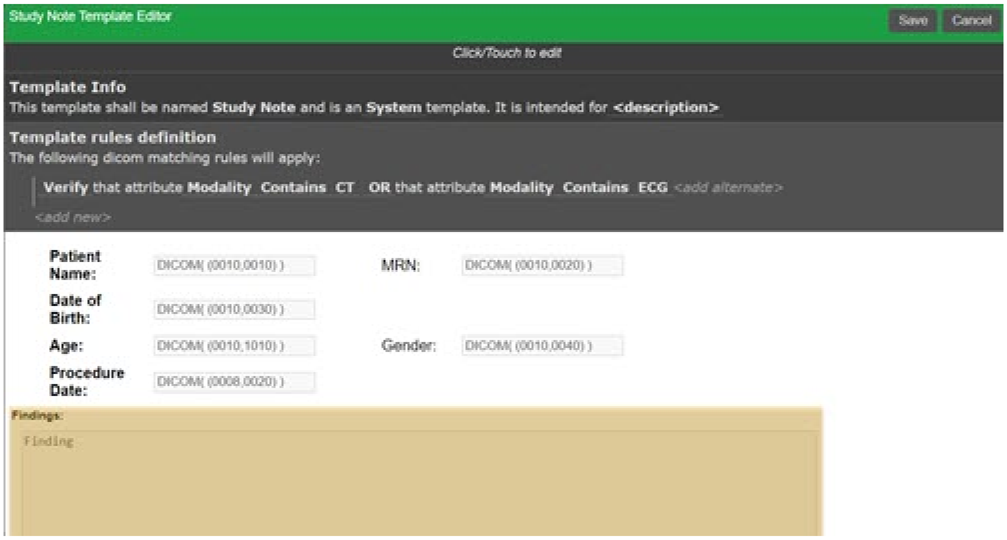
   or

   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.



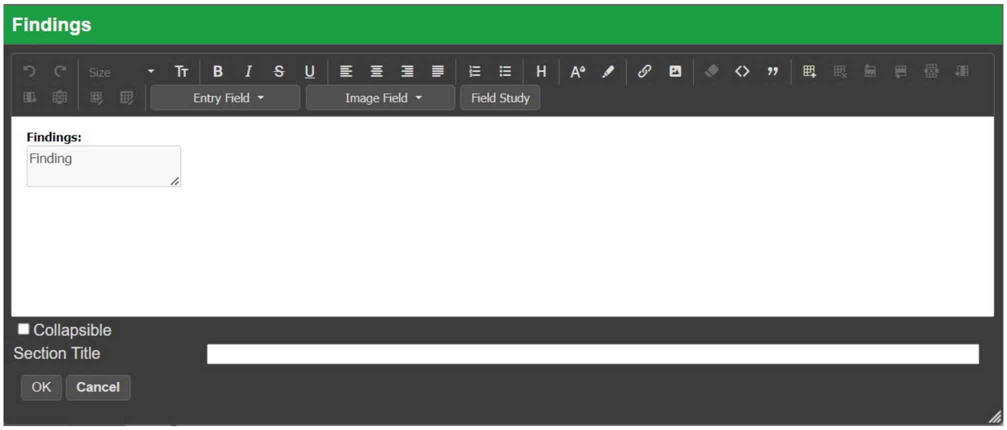
Template Info
This template shall be named **Study Note** and is an **System** template. It is intended for **<description>**

Template rules definition
The following dicom matching rules will apply:
Verify that attribute **Modality** **Contains** **CT** **OR** that attribute **Modality** **Contains** **ECG**

Patient Name: DICOM((0010,0010))
MRN: DICOM((0010,0020))
Date of Birth: DICOM((0010,0030))
Age: DICOM((0010,1010))
Gender: DICOM((0010,0040))
Procedure Date: DICOM((0008,0020))

To modify the **Findings** area:

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



2. To place an item before the Findings text box, place your cursor before the box, then press ENTER.

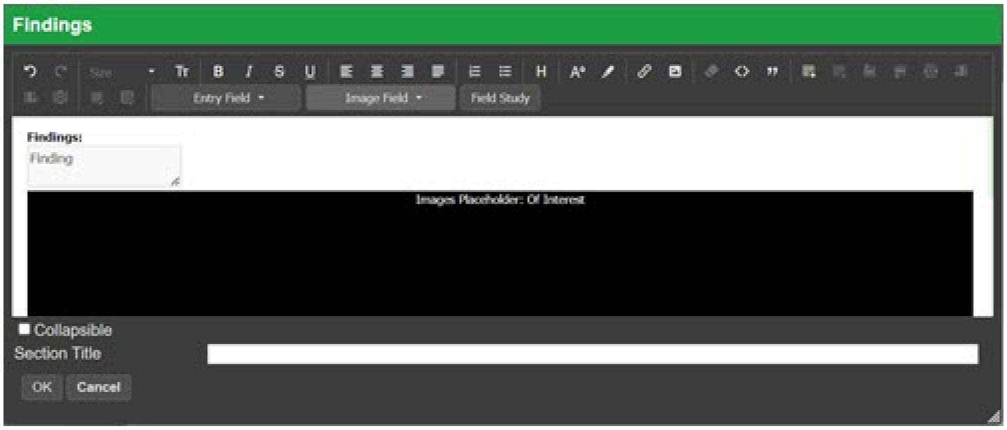
   or

   To place an item after the Findings text box, place your cursor after the box, then press ENTER.
3. Select the **Entry Field** list, then select an option. For example, you can add text entry areas, checkboxes and drop down lists.
4. To remove an item, use the BACKSPACE or DELETE key.
5. You can use the toolbar options to format the text (color, font, and so on.).
6. Click **OK** to save your changes.

Include images

You can include images in the study note report. You can choose to include key images, secondary capture images, or all images.

1. Click (or tap) the **Header** or **Findings** area.
2. Click to place your cursor where you want to insert the images. You would typically place the images after the Findings box so that the images would appear at the end of the report. For example:



3. Select **Image Field**, then select one of the following options.
   - **Of Interest** Include **key images** for the study.
   - **All Secondary Capture** Include all **secondary capture images** for the study.
   - **All Study Images** Include all of the study images.
4. 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, deselect 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 assets

You can add assets to your study note 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 study note 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 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.

Patient History

Specifies how filtering is done on the patient timeline.

- **Available keyword matching only**. Sorts the **timeline** based upon keyword types; for example, head, chest, and so forth.
- **All study filters**. Displays all prior studies even if **hanging protocols** are not in place.

Magnify Glass

Default magnifying glass size and zoom factor for smart zoom (see **Smart Zoom**).

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**).

- **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.

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 mouse, keyboard and touch 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.

Step 1: 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 NilRead 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 touch 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**.

Step 2: 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, deselect 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 a device (**Desktop**, **Tablet** or **Smartphone**).
2. Select **<pick>** and select a keyboard template for this device.

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.

Step 1: 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**.

Step 2: 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, deselect 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. 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.

   > **Note**
   > Window level presets are not available for all modalities.

   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. 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.

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

Zoom Policy

Determines the behavior of the Zoom tool.

- **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.

Window level presets

(Available for some modalities only) You can change the window level presets for different modalities. For details, see **Change window level presets**.

Image Ruler Options

(Available for some modalities only) Determines how the image ruler size is controlled. Rulers can only be displayed when the underlying meta-data provides known and consistent pixel spacing and image geometry is flat.

- **Scope** (Administrators only) Choose whether the settings apply to the entire site (**Site Defaults**) or to your account (**User**).
- **Basis** Choose how the ruler size is controlled. **Viewport** basis constrains the ruler to fit in the viewport (typically 60%). Different ruler lengths can be chosen while zooming the image. **Image** basis keeps the ruler size constant independent of zoom; however, the ruler may extend beyond the viewport size under certain zoom factors.

> **Note**
> NilRead users can use **Titles** to show or hide a ruler for an image (see **Titles**). Administrators can choose whether rulers are shown by default (see **Ruler display settings**).

Admin

Manage data quality control

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.
- Redact areas on images.
- Add and hide labels on images.
- Split a series into multiple series.
- Merge patients, studies and series.
- Delete a patient, study or 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

Add the studies you want to edit to the QC viewer. You can add studies for one or more patients.

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, right-click (or touch and hold) one of the studies, then select **Advanced QC**.

   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**).
   c. Click (or tap) a study to add it to the QC viewer. 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.

Overview of the QC viewer

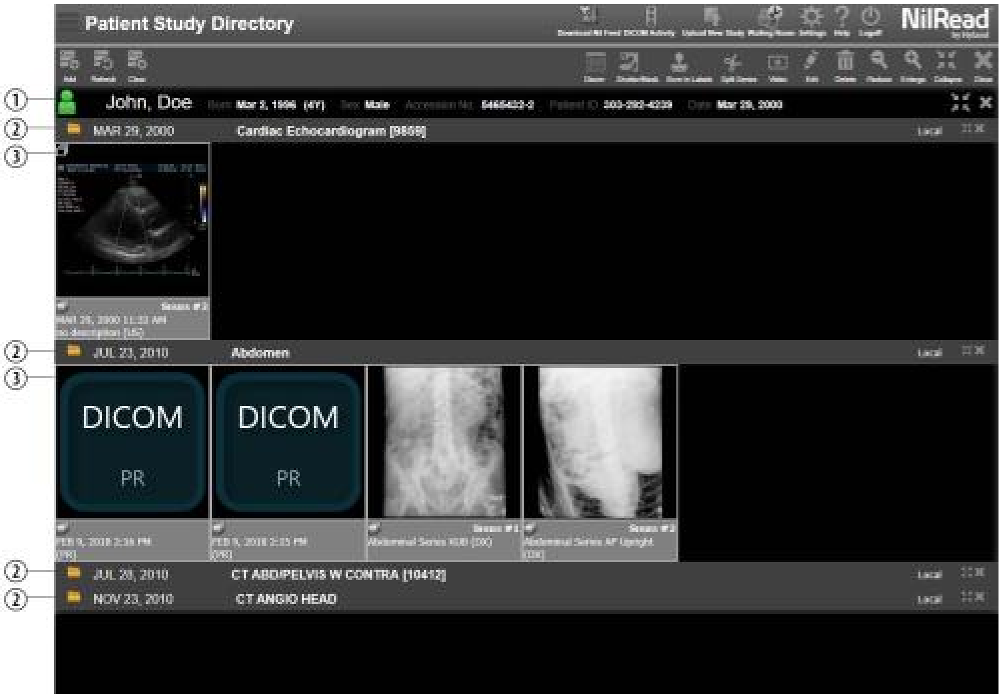
The following information is shown for the studies in the QC Viewer. The studies are organized by patient.

① **Patient** Patient information is shown first. Click (or tap) the patient name to view details.

② **Studies** 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 **Series** Thumbnails for the series in the study are shown. Series can be color-coded according to the series type.

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.

Edit key DICOM attributes

You can quickly edit key DICOM attributes for a patient, study or series. Your changes will be saved in new SOP instances.

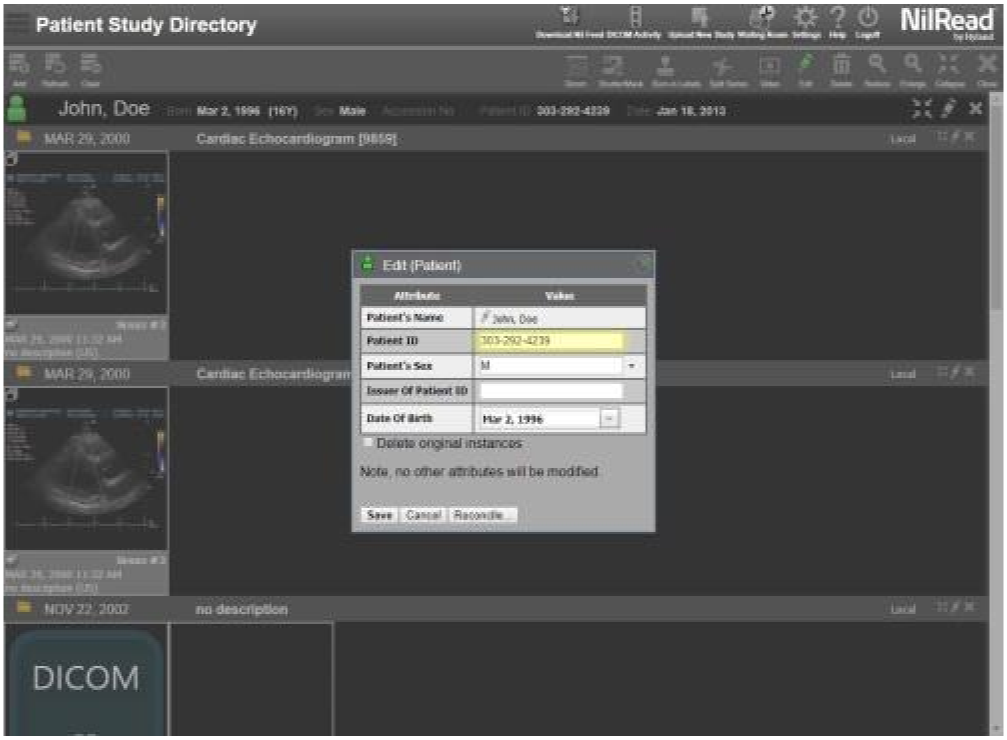
DICOM attributes conform to the following hierarchy: (1) patient, (2) study and (3) series. When you edit key DICOM attributes at one of these levels, you also have access to the higher level attributes. For example, if you edit attributes for a study, you can also edit the patient attributes. If you edit attributes for a series, you can also edit the study and patient attributes.

> **Note**
> You cannot edit image attributes using the **Edit** tool. To modify DICOM attributes in more detail, including image attributes, see **Manage DICOM attributes**.

1. Select **Edit** from the toolbar, then do one of the following.
   - Select ✎ on a patient row. This opens the patient attributes.
   - Select ✎ on a study row. This opens the study and patient attributes.
   - Click (or tap) a series. This opens the series, study and patient attributes.

   or

   Right-click (or touch and hold) a patient, study or series, then select **Edit**.
2. Make changes to the DICOM attributes. For most attributes, you can type directly in the **Value** field.



Edit (Patient)

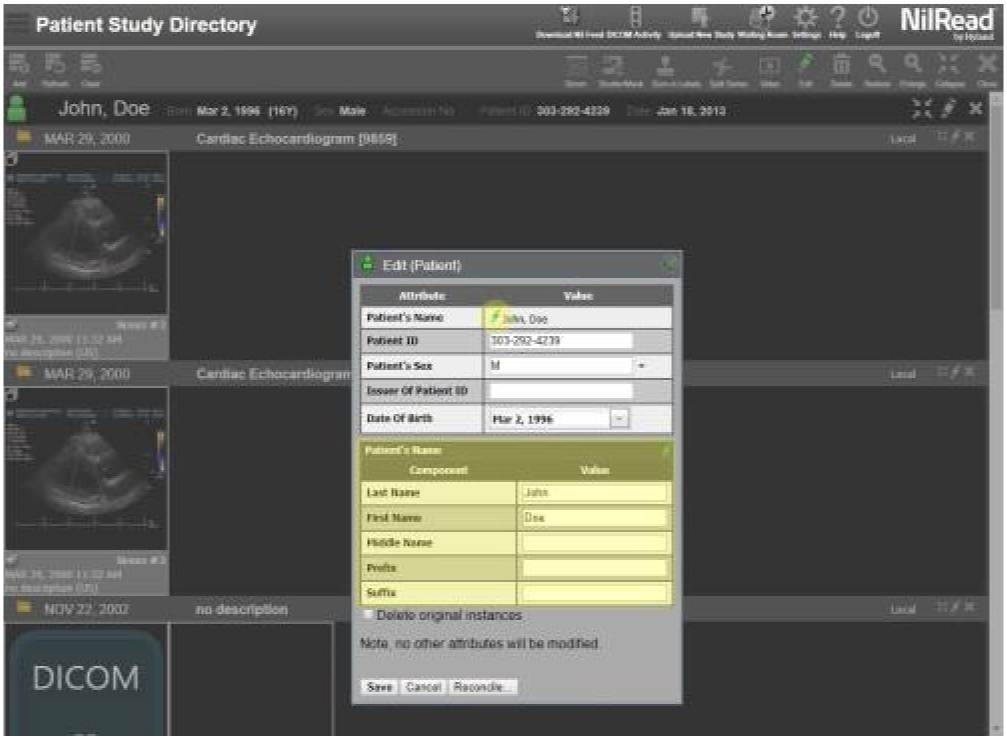
Attribute	Value
Patient's Name	John, Doe
Patient ID	303-292-4239
Patient's Sex	M
Issuer Of Patient ID	
Date Of Birth	Mar 2, 1996

☐ Delete original instances

Note, no other attributes will be modified.

Save | Cancel | Reconcile...

For person name (PN) attributes, click ✎. Additional fields appear that you can edit.



Edit (Patient)

Attribute	Value
Patient's Name	John, Doe
Patient ID	303-292-4239
Patient's Sex	M
Issuer Of Patient ID	
Date Of Birth	Mar 2, 1996

Patient's Name

Component	Value
Last Name	John
First Name	Doe
Middle Name	
Prefix	
Suffix	

☐ Delete original instances

Note, no other attributes will be modified

3. When editing series attributes, select **Copy to new study** to save your changes in a new study. To make changes to the original study, deselect **Copy to new study**.
4. To delete the original SOP instances, select **Delete original instances**.
5. When editing patient attributes, you can retrieve information about the patient from a modality worklist. Select **Reconcile**, enter information about the patient, then select **Search**. If a match is found, select the patient and select **Select**.
6. Select **Save**.

Manage 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**.

DICOM attributes conform to the following hierarchy: (1) patient, (2) study and (3) series. When you choose to edit DICOM attributes at one of these levels, attributes at the other levels are available for editing as well.

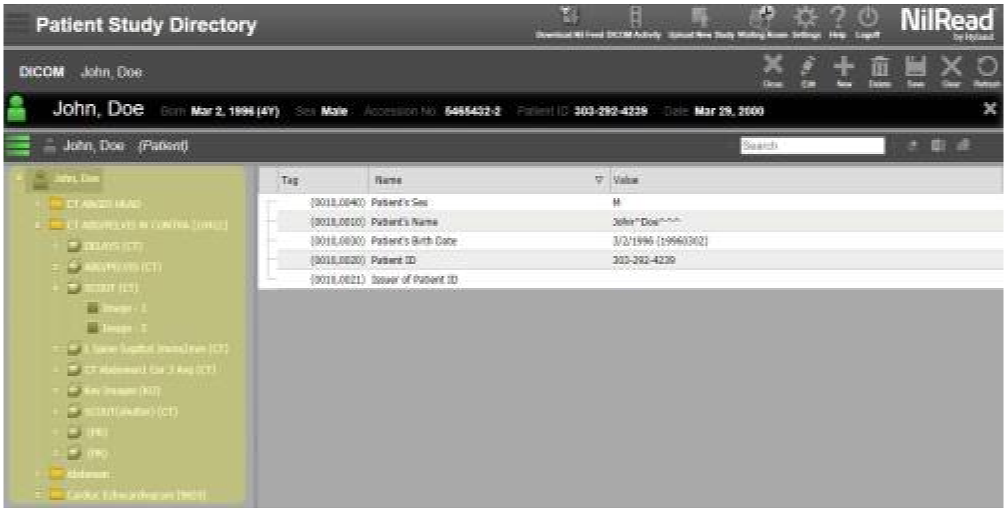
1. Select **DICOM** (toolbar).
2. Select ▤ on a patient row. This opens the DICOM attributes with the patient selected.

   or

   Select ▤ on a study row. This opens the DICOM attributes with the study selected.

   or

   Click (or tap) a series. This opens the DICOM attributes with the series selected.
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.

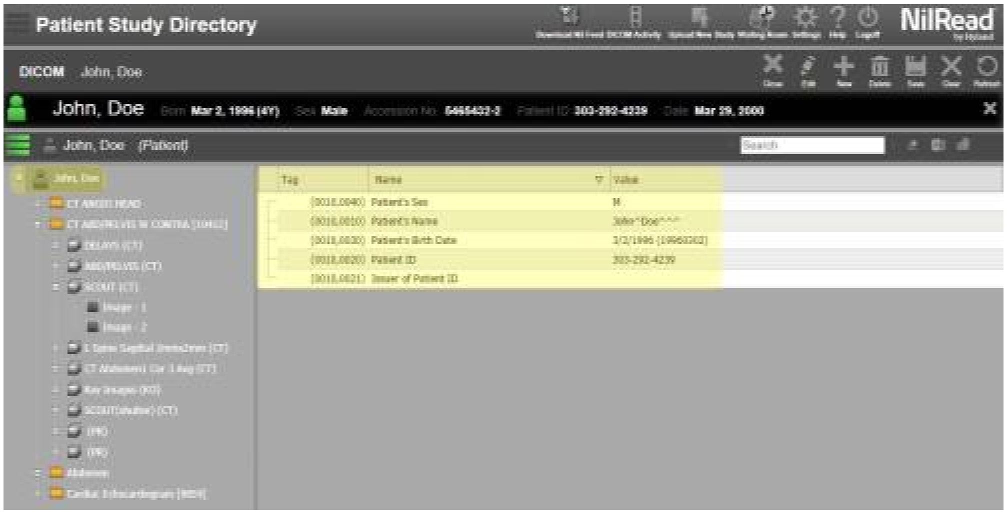


John, Doe Born Mar 2, 1996 (4Y) Sex Male Accession No 6465432-2 Patient ID 303-292-4239 Date Mar 29, 2000

John, Doe (Patient)

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).



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	

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.

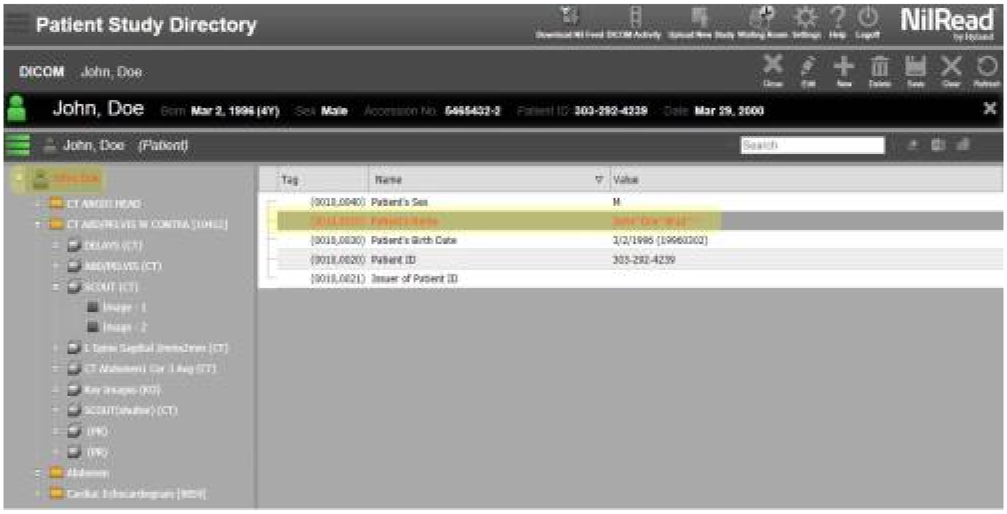
1. Enter your search text in the **Search** box and press ENTER.
2. Attributes matching your search text are highlighted. Use the arrows on each side of the **Search** box to go to the next or previous match.
3. Select **Clear** beside the **Search** box to clear your search text and the highlighted matches.

Modify an attribute

1. Select an attribute in the right pane, then select **Edit**. You can also right-click (or touch and hold) the attribute, 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.**

Group: 0010
Element: 0010
Type: PN
Description: Patient's Name
Last Name: John
First Name: Doe
Middle Name:
Prefix:
Suffix:

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.



John, Doe Born Mar 2, 1996 (4Y) Sex Male Accession No. 6466432-2 Patient ID 303-292-4239 Date Mar 29, 2000

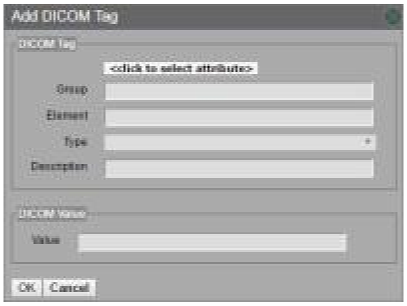
Tag	Name	Value
(0010,0040)	Patient's Sex	M
[illegible]	[illegible]	[illegible]
(0010,0030)	Patient's Birth Date	3/2/1996 (19960302)
(0010,0020)	Patient ID	303-292-4239
(0010,0021)	Issuer of Patient ID	

4. To save your changes, select **Save**. All attribute changes, additions and deletions you have made will be saved. If you do not want to save your changes, select **Clear**.

Add an attribute

You can add a DICOM attribute to a patient, study, series or image.

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 select **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.
6. To save your changes, select **Save**. All attribute changes, additions and deletions you have made will be saved. If you do not want to save your changes, select **Clear**.

Delete an attribute

1. Select an attribute in the right pane, then select **Delete**. You can also right-click (or touch and hold) the attribute, then select **Delete**.
2. To save your changes, select **Save**. All attribute changes, additions and deletions you have made 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 **Export** 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 images

You can redact areas on an image. For example, you may want to anonymize a study by removing patient information. You can choose to apply the redactions to the current image or to all images in the series.

NilRead provides two methods to redact an image.

- You can add **masks** to cover areas you want to redact.
- You can use **shutters** to identify the areas you want to retain.

You cannot use both methods on the same image.

1. In the QC viewer, select **Shutter/Mask** from the toolbar.
2. Select a series. You can only select a series containing images eligible for redaction.

   If the series contains at least one multiframe instance, the **Select Instance** window appears, allowing you to choose the instances you want to edit. To edit all instances, select **OK**. To edit specific instances, deselect the **Select All** checkbox, click (or tap) the instances you want to edit, then select **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 use standard tools such as titles, zoom, window level, pan, and reset to adjust the image.
5. If the study contains multiple series, they are shown in a side panel.

Apply a mask

Use masks to cover areas you want to redact.

1. Select **Mask** from the toolbar.
2. Select a shape from the toolbar (**Ellipse**, **Rectangle**, **Square**, **Circle**).
3. Draw shapes over the areas you want to redact. The areas covered by shapes will be blocked out on the image.
4. To edit a shape, right-click (or touch and hold) the shape, then select **Edit**. Change any of the following options, then select **Save**.

- **Shape** Type (**Rectangle**, **Square**, **Ellipse**, **Circle**).
- **Color** Fill color.
- **Border** Border color.
- **Top, Left** Location on the image.
- **Width, Height** Width and height.

5. To resize a shape, drag a corner of the shape.
6. To move a shape, drag the shape to a new position.
7. To delete a shape, right-click (or touch and hold) the shape, then select **Delete**.
8. To remove all shutters and masks from the image, select **Clear**.

Apply a shutter

Use shutters to identify the areas you want to retain.

1. Select the arrow beside **Mask** in the toolbar, then select **Shutter**.
2. Select a shape from the toolbar (**Ellipse**, **Rectangle**, **Square**, **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 edit a shape, right-click (or touch and hold) the shape, then select **Edit**. Change any of the following options, then select **Save**.
    - **Shape** Type (**Rectangle**, **Square**, **Ellipse**, **Circle**).
    - **Color** Fill color for the redacted area. By default, the redacted area is black. To change the color, edit the color for the first shutter applied to the image. This color will be used for the redacted area. If the first shutter is deleted, the color for the second shutter will be used.
    - **Top, Left** Location on the image.
    - **Width, Height** Width and height.
5. To resize a shape, drag a corner of the shape.
6. To move a shape, drag the shape to a new position.
7. To delete a shape, right-click (or touch and hold) the shape, then select **Delete**.
8. To remove all shutters and masks from the image, select **Clear**.

Reverse masks and shutters

You can change the masks applied to an image to shutters. You can also change shutters to masks.

- To change the masks on an image to shutters, select **Shutter** from the toolbar.
- To change the shutters on an image to masks, select **Mask** from the toolbar.

Save redactions

The redacted image (or 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 choose to apply the redactions to the current image or to all images in the series. You can also choose to remove the redacted 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 redacted images from the original series, select **Delete original instances**.
   or
   To keep a copy of the images in the original series, deselect **Delete original instances**. The images will remain in their original state in the original series.
3. To save the series in a new anonymized study, select **Deidentify**, then select a confidentiality profile (for details, see **About anonymization**). The anonymized study will only contain the series that has been redacted.
4. Enter a **Series Description** and **Series Number** for the new series.
5. To apply the redactions to the current image only, select **Apply to image**.
   or
   To apply the redactions to all images in the series, select **Apply to series**.
6. 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 use standard tools such as titles, zoom, window level, pan and reset to adjust the image.
5. If the study contains multiple series, they are shown in a side panel.

Hide a burn-in label

1. Select the arrow beside **Left** in the toolbar, then select **Mask**.
2. Draw a mask over the label you want to hide.

3. To edit a mask, right-click (or touch and hold) the mask, then select **Edit**. Change any of the following options, then select **Save**.
   - **Top, Left** Location on the image.
   - **Width, Height** Width and height.
4. To resize a mask, drag a corner of the mask.
5. To move a mask, drag the mask to a new position.
6. To delete a mask, right-click (or touch and hold) the mask, then select **Delete**.
7. To remove all masks from the image, select **Clear**.

Add a label

1. Select a label (**Left**, **Right**, **Head**, **Foot**, **Anterior**, **Posterior**) from the toolbar. Note that you can change the label text after adding the label to the image.
2. Draw a label on the image.
3. To edit a label, right-click (or touch and hold) the label, then select **Edit**. Change any of the following options, then select **Save**.
   - **Text** Label content.
   - **Template** Label appearance. By default, labels are transparent. You can choose to make the label opaque or translucent.
   - **Top, Left** Location on the image.
   - **Width, Height** Width and height.
4. To resize a label, drag a corner of the label.
5. To move a label, drag the label to a new position.
6. To delete a label, right-click (or touch and hold) the label, then select **Delete**.
7. To remove all labels from the image, select **Clear**.

Save labels

The modified images will be saved as a new series. You can choose to apply the labels to the current image or to all images in the series. You can also choose to remove the modified 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 a copy of the images in the original series, deselect **Delete original instances**. The images will remain in their original state in the original series.
3. Enter a **Series Description** and **Series Number** for the new series.
4. To apply the redactions to the current image only, select **Apply to image**.
   or
   To apply the redactions to all images in the series, select **Apply to 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).

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 Split Series window opens. If the study contains multiple series, they are shown in the side panel.

The Split Series window contains the following sections.

Preview window

The **preview window** at the top of the screen shows previews of the images in the series. You can select different layouts for the preview window (such as 1x1 or 5x5) using the toolbar.

To scroll through the images in the series, use the **Scroll** tool in the preview window. You can also use standard tools such as titles, zoom, window level, pan and reset to adjust the images.

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.
- **Red scissors** indicate the last image to be included in the new series.

You can use the preview area to quickly select a range of images for the new series. For details, see **Quickly select a range of images**.

Segment editor

The **segment editor** at the bottom of the screen contains thumbnail samples across the entire series.

Use the following tools to change the number of samples shown in the segment editor.

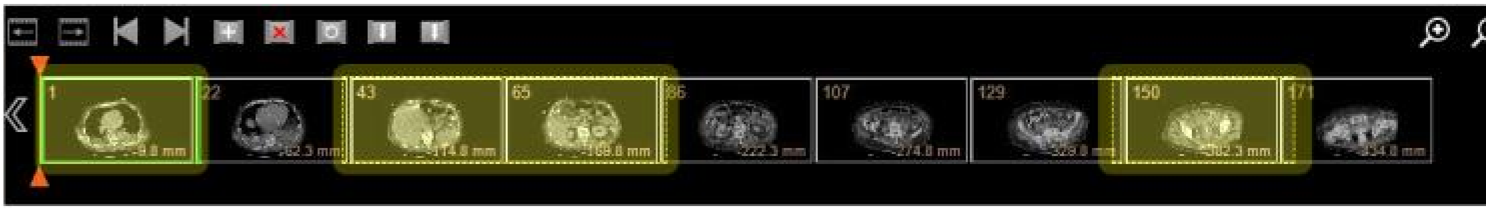
⊕	Generate more samples across the entire series.
⊙	Generate the most samples that will fit in the segment editor.
⊖	Generate less samples across the entire series.

If you have generated more samples, use the arrows at each end of the segment editor to scroll through the samples. You can also hold SHIFT while dragging the editor. On touch devices, use a two-finger drag.

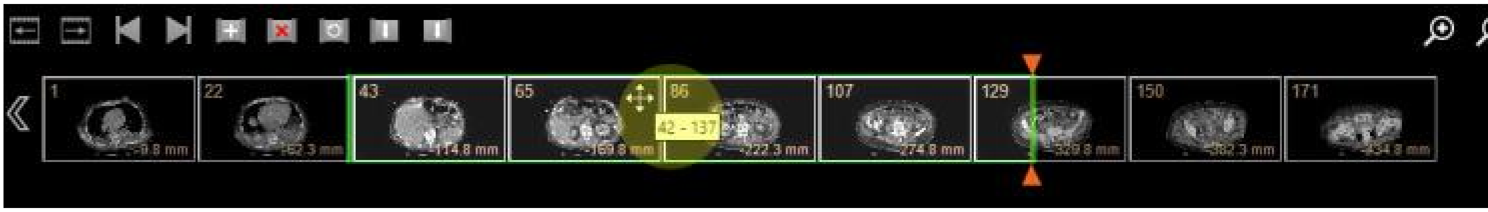
Segment Box

Use the **segment box** in the editor to select the images you want to include in the new series. By default, all of the images are included.

You can resize and move the segment box. You can also add more boxes, allowing you to select images throughout the series. The following example contains three boxes. These three groups of images will be included in the new series.



Hover over a box to view the range of images within the box.

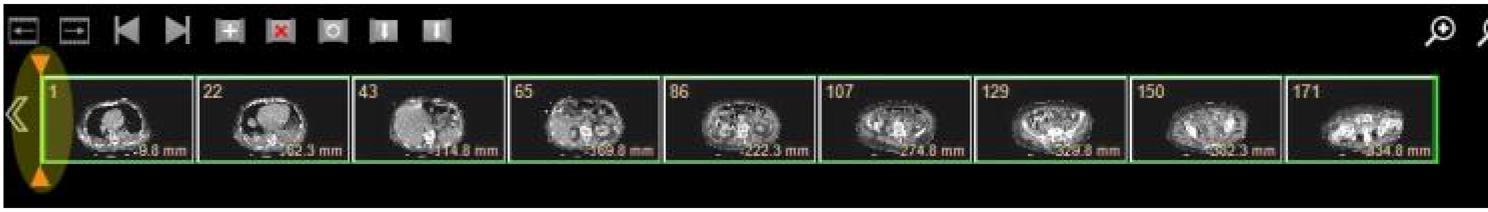


Position Indicator

The **position indicator** in the editor is synchronized with the preview window.

- When you select an image in the preview window, the position indicator moves to the corresponding location in the editor.
- When you move the position indicator in the editor, the preview window is updated to the same location. For more information, see **Move the position indicator**.

By default, the position indicator is located at the start of the series.



Quickly select a range of images

Use the preview window to quickly select a range of images to include in the new series.

1. Change the preview layout to display more images (for example, 3x3 or 5x5).
2. In the preview window, find the **first** image in the range (use **Scroll** to move through the images). Click (or tap) the image, then select **Set Segment Start**.

In the segment editor, the segment box is adjusted to start at this image. The position indicator is moved to this location as well.

3. In the preview window, find the **last** image in the range (use **Scroll** to move through the images). Click (or tap) the image, then select **Set Segment End**.

John, Doe Born Mar 2, 1996 (16Y) Sex Male Accession No. Patient ID 303-292-4239 Date Jan 18, 2013

In the segment editor, the segment box is adjusted to end after this image. The position indicator is moved to this location as well.

4. The range of images is now selected in the segment editor.

5. If desired, use additional segment boxes to select more images. For details, see **Select non-contiguous images**.
6. When done selecting images, save the images as a new series. For details, see **Save the new series**.

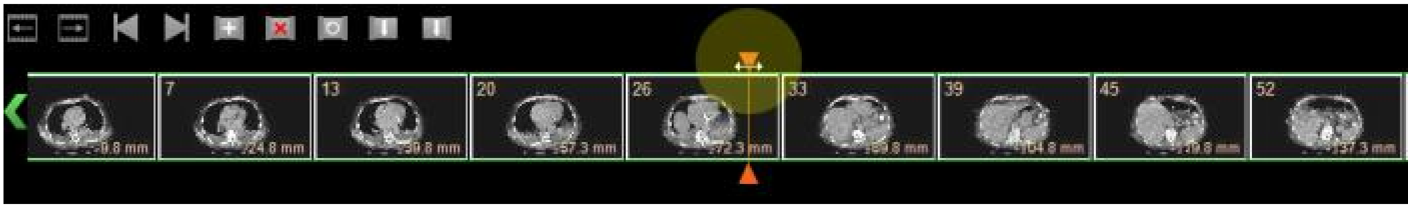
Move the position indicator

Use the position indicator to locate images and display them in the preview window. You can also use the position indicator to select images (for details, see **Select images**).

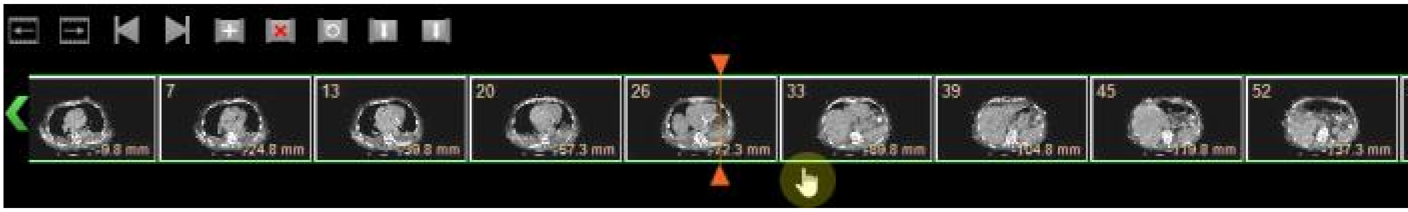
Use the following methods to move the position indicator.

- Click (or tap) an image in the preview window. The position indicator moves to the image location.

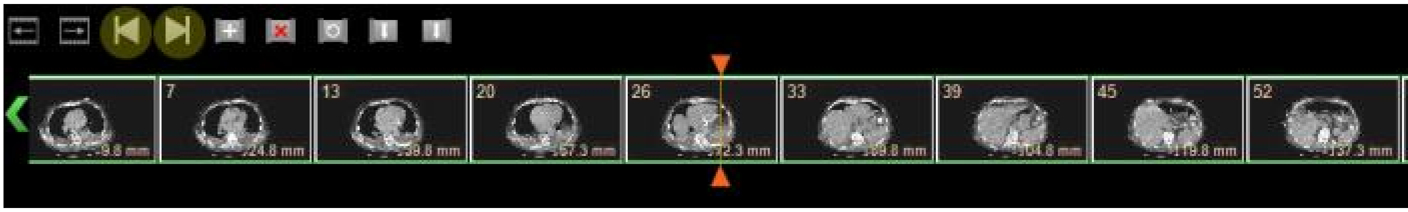
- Drag the position indicator to a new location on the editor.



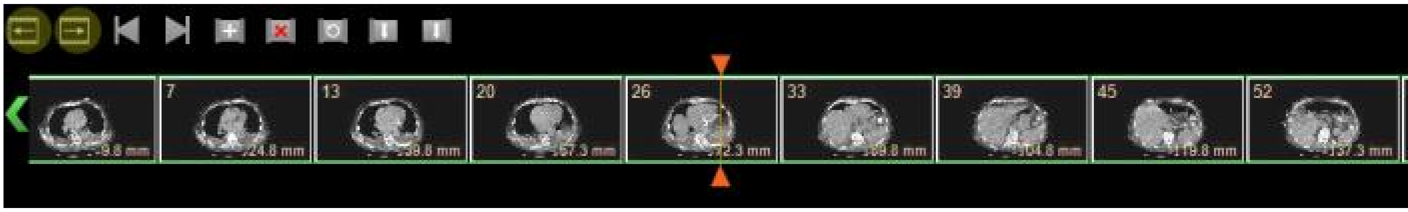
- Click (or tap) above or below the thumbnails to move the position indicator to that location.



- 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.



Select images

Use the following methods to change the range of images included in a segment box.

Edit a segment box

1. Right-click (or touch and hold) the box, then select **Edit**.
2. The first and last images included in the box are shown. Hover over an image to view detailed information about the image attributes.

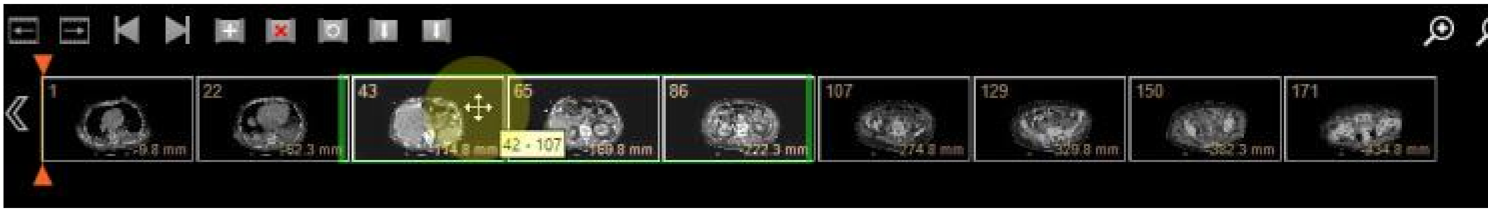
3. Use the arrows to change the first and last images. Click (or tap) and hold an arrow to quickly scroll through the images in the series.
4. Select **OK**.

Resize a segment box

Drag the ends of the box to resize it.

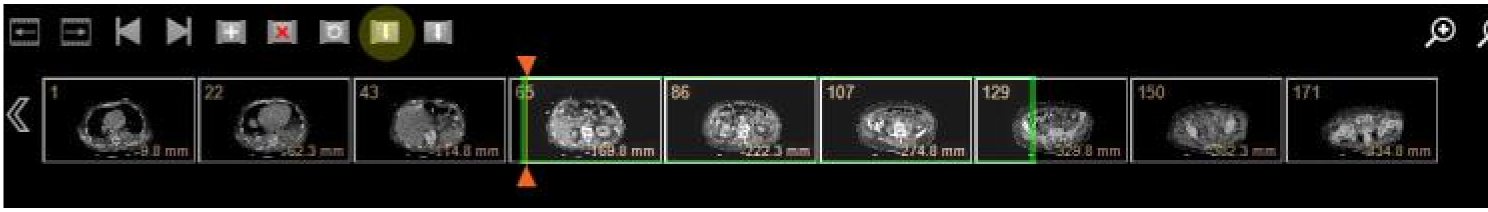
Move a segment box

Drag the box to a new position.



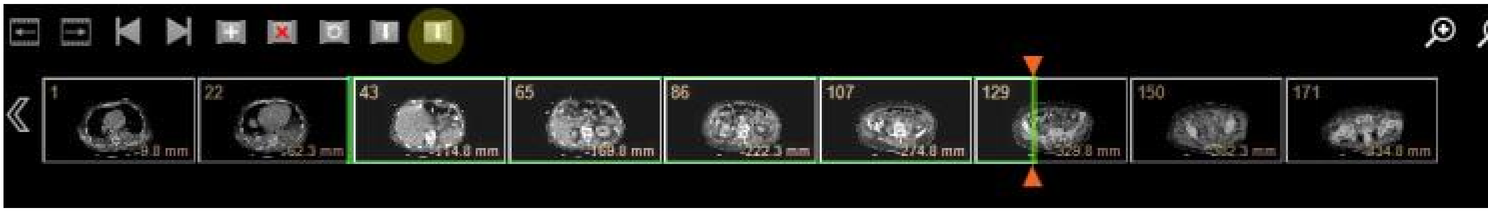
Set the start of a segment box to the position indicator

To set the start of the box to the position indicator location, select the box, then select **Set Segment Start**.



Set the end of a segment box to the position indicator

To set the end of the box to the position indicator location, select the box, then select **Set Segment End.**

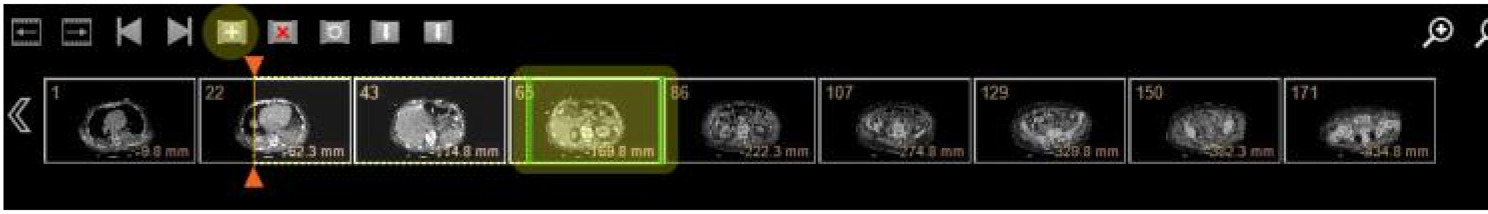


Select non-contiguous images

You can use multiple segment boxes to select non-contiguous images. You can add as many boxes as needed.

Add a segment box

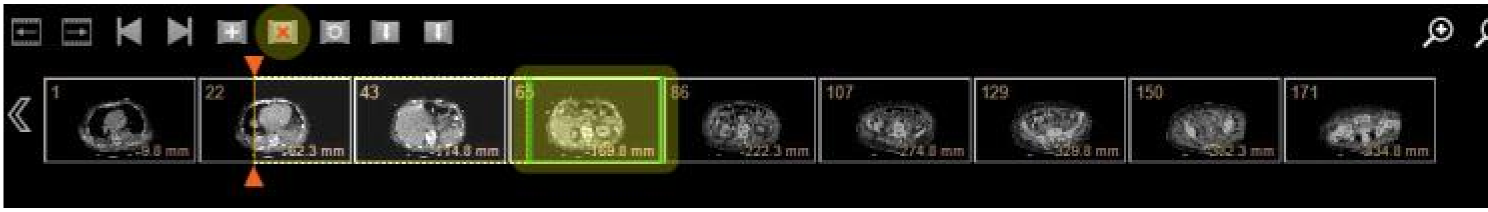
To add a box, select +. A new box appears to the right of the position indicator. (If a box already exists at the position indicator, the new box appears to the right of the existing box.) Change the box position and size as needed.



Note that if boxes overlap, they will be merged together when the new series is saved.

Remove a segment box

To remove a box, select the box, then select ✕. Note that you cannot remove all boxes; at least one box must remain in the editor.



Save the new series

The images you have selected (using segment boxes) will be saved as a new series. You can also choose 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 a copy of the images in the original series, deselect **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).

Merge patients, studies and series

You can use the QC viewer to merge patients or studies. You can also move a study to a different patient or move a series to a different study.

Merge two patients

You can move studies from one patient to another patient.

1. Drag-and-drop **the patient row** for one patient (e.g. patient A) onto **the patient row** for another patient (e.g. patient B).

   All of the studies loaded in the QC viewer for patient A will be moved to patient B. Note that any studies for patient A that are not currently loaded in the QC viewer will not be affected.
2. To remove the studies from the original patient (patient A), select **Delete original studies**.

   or

   To keep a copy of the studies for the original patient (patient A), deselect **Delete original studies**.
3. Select **OK**.

Merge two studies

You can merge two studies together.

1. Drag-and-drop **the study row** for one study (e.g. study 1) onto **the study row** for another study (e.g. study 2). The studies can belong to the same patient or different patients.

   Study 1 will merged into study 2.
2. To remove the original study (study 1), select **Delete original study**.

   or

   To keep a copy of the original study (study 1), deselect **Delete original study**.
3. Select **Save**.

Move a study to a different patient

You can move a study to a different patient.

1. Drag-and-drop **the study row** for a study from one patient (e.g. patient A) onto **the patient row** for another patient (e.g. patient B).

   The study will be moved to patient B.
2. To remove the study from the original patient (patient A), select **Delete original study**.

   or

   To keep a copy of the study for the original patient (patient A), deselect **Delete original study**.
3. Select **OK**.

Move a series to a different study

You can move a series to a different study.

1. Drag-and-drop **a series** onto **the series row** for another study. The study can belong to the same patient or a different patient.

   The series will be moved to the study.
2. To remove the series from the original study, select **Delete original series**.

   or

   To keep a copy of the series in the original study, deselect **Delete original series**.
3. Select **OK**.

Delete a patient, study or series

You can permanently delete a patient, study or series using the QC viewer.

1. Select **Delete** from the toolbar, then do one of the following.
   - Select 🗑 on a patient row. All studies for the patient loaded in the QC viewer will be deleted. Note that any studies for the patient that are not currently loaded in the QC viewer will not be affected.
   - Select 🗑 on a study row. The study will be deleted.
   - Click (or tap) a series. The series will be deleted.

   or

   Right-click (or touch and hold) a patient, study or series, then select **Delete**.
2. Click **OK**.

Edit a video

You can edit a video from the QC viewer.

1. Select **Video** from the toolbar. This tool is not available if the QC viewer does not contain a series with a video.
2. Select a series containing a video.
3. The video opens in the video editor. Edit the video as required. For more information, see **Edit videos**.
4. To return to the QC viewer, select **X** in the top-right corner (beside the patient information).

Exit the QC viewer

To close the QC viewer and return to the Patient Study Directory, select **Close** ✖ (toolbar).

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**). 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**).

1. In the Patient Study Directory, select **Patient Search**.
2. Find the study or studies you wish to retrieve (see **Access studies**).

   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**).
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**).

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. 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. 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, deselect 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>**.
3. 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, deselect 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.

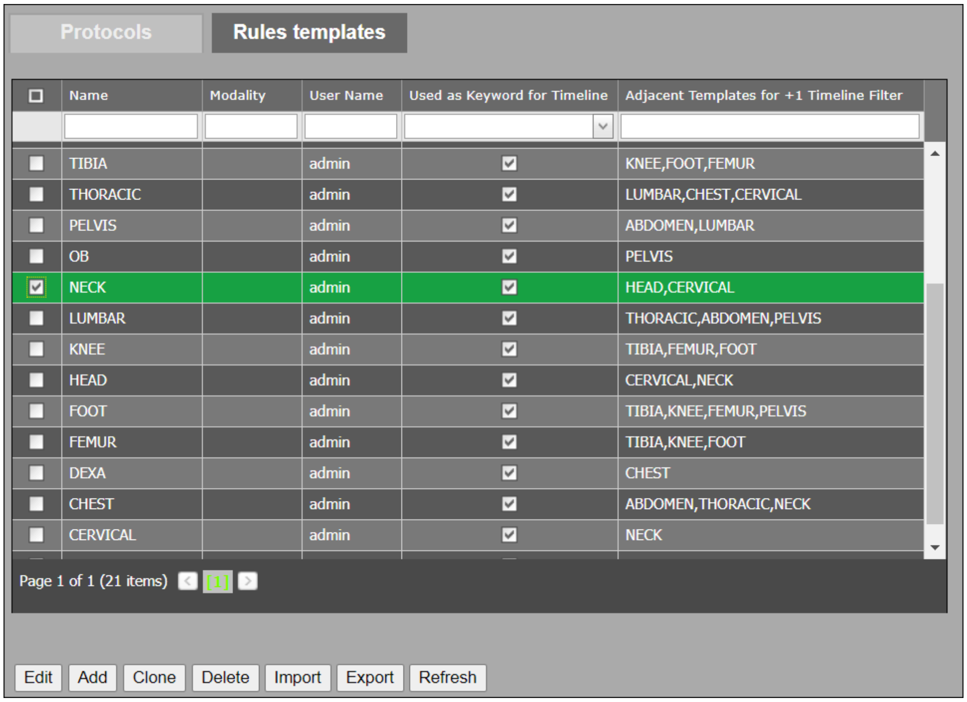
Set up hanging protocol rules templates

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 that template.

> **Note**
> For more information about hanging protocols, refer to the **Hanging Protocols Handbook**.

1. From the menu bar, select **Settings**.
2. Under **Preferences**, select **Hanging Protocols**.

3. Select **Rules templates**.



☐	Name	Modality	User Name	Used as Keyword for Timeline	Adjacent Templates for +1 Timeline Filter
☐	TIBIA		admin	☑	KNEE,FOOT,FEMUR
☐	THORACIC		admin	☑	LUMBAR,CHEST,CERVICAL
☐	PELVIS		admin	☑	ABDOMEN,LUMBAR
☐	OB		admin	☑	PELVIS
☑	NECK		admin	☑	HEAD,CERVICAL
☐	LUMBAR		admin	☑	THORACIC,ABDOMEN,PELVIS
☐	KNEE		admin	☑	TIBIA,FEMUR,FOOT
☐	HEAD		admin	☑	CERVICAL,NECK
☐	FOOT		admin	☑	TIBIA,KNEE,FEMUR,PELVIS
☐	FEMUR		admin	☑	TIBIA,KNEE,FOOT
☐	DEXA		admin	☑	CHEST
☐	CHEST		admin	☑	ABDOMEN,THORACIC,NECK
☐	CERVICAL		admin	☑	NECK

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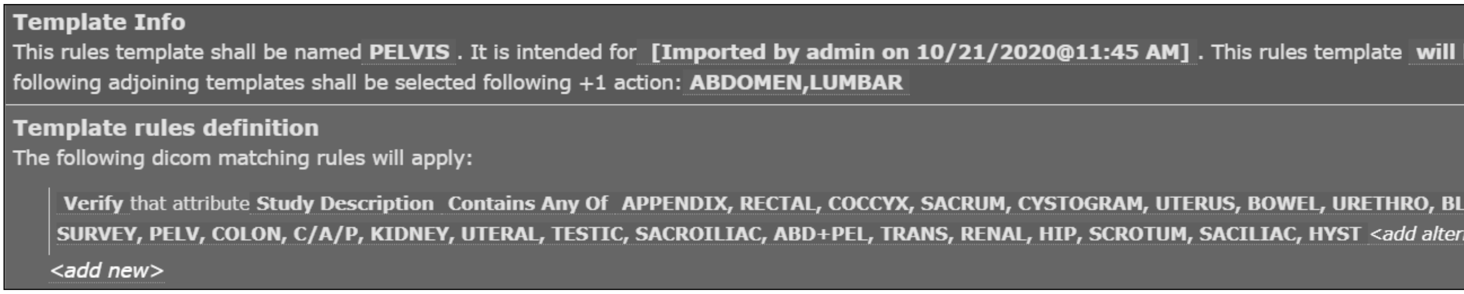
See the next sections for details on adding, modifying and deleting rules templates.

Add rules templates

1. Select **Add**. The **Hanging Protocol Template Editor** is displayed. Customizable areas are shown as between brackets < >, and underlined.



Template Info

This rules template shall be named PELVIS . It is intended for [Imported by admin on 10/21/2020@11:45 AM] . This rules template will
following adjoining templates shall be selected following +1 action: ABDOMEN,LUMBAR

Template rules definition

The following dicom matching rules will apply:

Verify that attribute Study Description Contains Any Of APPENDIX, RECTAL, COCCYX, SACRUM, CYSTOGRAM, UTERUS, BOWEL, URETHRO, BL
SURVEY, PELV, COLON, C/A/P, KIDNEY, UTERAL, TESTIC, SACROILIAC, ABD+PEL, TRANS, RENAL, HIP, SCROTUM, SACILIAC, HYST *<add alter*

<add new>

2. Under **Template Info**, enter a <**name**> and <**description**> for the protocol.
3. If the rules template will be used for study keyword tagging, change <will not be> to <**will be**>, and add the **+1 action** (such as ABDOMEN and LUMBAR).

4. Under **Template rules definition**, select <**add new**> to add a new DICOM rule. Then customize the rule, as applicable. For example, you can indicate what is associated with a Study Description.
5. To remove a rule, click the **Verify** text at the beginning of the rule definition, and select **Delete**.
6. When all rules are entered, click **Save**.

Edit a rules template

1. In the **Hanging Protocol Template Editor**, select an existing template.
2. Select the **Edit** button.
3. Modify the details, as necessary.
4. Select **Save**.

Delete a rules template

1. In the **Hanging Protocol Template Editor**, select an existing template.
2. Select the **Delete** button.

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

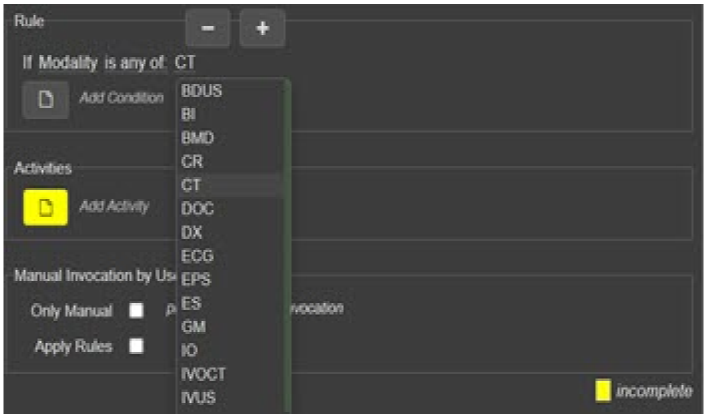
If selected, the policy will be run in a “training” mode. The activities will be logged but will not be applied to data.

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.
   - **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.
        - **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 FHIR settings

Access FHIR reports

NilRead can be configured to access FHIR® diagnostic 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 report configuration requires the following steps.

1. Enable FHIR reports for the site.
2. (Optional) Modify the FHIR report templates for the site.
3. Complete the following steps for each FHIR service you want to use to access diagnostic reports.
   a. Register with the FHIR service.
   b. Add an endpoint for the FHIR service. This allows NilRead to access the FHIR resource server.

c. Add a diagnostic report for the FHIR service. This is required to load FHIR reports from the service.

Enable FHIR reports for the site

Use the **Timeline Reports** settings to enable FHIR reports for the site.

1. Select **Settings**. Under **System**, select **Timeline Reports**.
2. Enter the following information.

   Enable reports access Select this option to enable FHIR reports for the site.

   Report search adapters Select **Fhir** in the **Excluded** list, then select **Add**. **Fhir** is moved to the **Included** list.
3. Select **Save**.

Modify FHIR report templates

NilRead uses XSL transformation (XSLT) templates to render FIHR 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 **FHIR 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.

   The NilRead Authorization Code Flow redirection URL is **[base url]/FhirRedirect.aspx**.
4. Select **Verify** to test the configuration settings.
5. Select **Save**.

Add a diagnostic report resource

Add a diagnostic report resource for the FHIR endpoint you want to use for reports.

1. Select **Settings**. Under **Devices**, select **FHIR**.
2. In the **Resources** area, select **Create**.
3. Enter the following information.
   - **Name** Name to identify the diagnostic report.
   - **Endpoint** Endpoint to use with the diagnostic report.
   - **Resource Type** Type of resource to retrieve. Select **DiagnosticReport**.
   - **Filter, Patient Identifier Filter** Search filters to use when querying the FHIR service. Use the format {DicomTagName} to specify the query values NilRead should use. For example, NilRead will replace {AccessionNumber} with the accession number from the study when submitting the query.
4. Select **Enabled** to allow NilRead to query the FHIR service and retrieve information.

5. Select **Verify** to test the configuration settings.
6. Select **Save**.

Edit or delete an endpoint or resource

1. Select an endpoint or resource.
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 **Remote FHIR Resources** section, select **Remote 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**.

Configure NilRead as a FHIR patient resource service

NilRead can be configured as a FHIR patient resource service. This allows authorized NilRead users to query or update patient information using FHIR. NilRead provides a token endpoint for authorization and authentication. NilRead users must have the FhirAccess privilege to obtain an access token to query the patient information and the FhirUpdate privilege to use the access token to update patient information.

NilRead FHIR service configuration requires the following steps.

1. Enable and configure the NilRead FHIR service.
2. Grant the FhirAccess and FhirUpdate privileges to users that need access to the NilRead FHIR token and patient endpoints.

Enable and configure NilRead FHIR service settings

You can configure general settings for the token endpoint and patient resource endpoint. Note that the FhirConfig privilege is required to access the FHIR settings page.

1. Select **Settings**. Under **Devices**, select **FHIR**.
2. In the **FHIR Services** area, select **Enable**.
3. Enter information in the following sections, then select **Save**.

Token

- **Address** Token endpoint provided by NilRead.
- **Authentication**:
  - **Authorization grant type** NilRead uses the Client Credentials grant type.
  - **Client authentication type** Authentication method.
- **Access token life span** Length of authentication period in minutes.

Patient

- **Address** Patient resource endpoint provided by NilRead.
- **Search**:
  - **Max number of results** Maximum number of patient records to return.
  - **Default patient identifier assigner** Value to return if the patient record does not contain a patient identifier assigner.

  - **Overwrite patient ID issuer** Overwrite the existing patient identifier issuer with the value specified for the **Default patient identifier assigner**.
- **When update patient, delete original studies** Whether to delete the patient's original studies after the patient information is updated.

Grant users access to the NilRead FHIR service

Assign the following privileges to each user that is allowed to access the NilRead FHIR service. For details on assigning privileges, see **Manage users**.

- **FhirAccess** Acquire access tokens from the NilRead token endpoint and query patient information on the patient endpoint.
- **FhirUpdate** Modify patient information using the patient endpoint with the access token.

Example of a client application with the NilRead FHIR service

The following code shows a simplified example of updating patient information in NilRead using the FHIR-Net-API library. For more information, see the FHIR specification and the FHIR-Net-API documentation.

```
var client = new FhirClient("[NilRead base URL]/fhir");


var pat = client.Read<Patient>("Patient/1");

pat.Resource.Name.Add(HumanName.ForFamily("John").WithGiven("Doe"));


client.Update<Patient>(pat);
```

Reconcile patient demographics with FHIR patient resources

NilRead can reconcile patient demographics with FHIR patient resources on a FHIR resource server. This allows a FHIR resource server to be used as a data reconciliation source when updating patient information using the NilRead edit patient/study feature (for details, see **Edit or split studies**).

Complete the following steps for each FHIR patient resource you want to use as a reconciliation source.

1. Register with the FHIR service.
2. Add an endpoint for the FHIR service. This allows NilRead to access the FHIR resource server.
3. Add a patient resource for the FHIR service. This is required to use the FHIR patient resource as a reconciliation source.

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 **FHIR 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.

   The NilRead Authorization Code Flow redirection URL is **[base url]/FhirRedirect.aspx**.
4. Select **Verify** to test the configuration settings.
5. Select **Save**.

Add a patient resource

Add a patient resource for the FHIR endpoint you want to use for reconciliation.

1. Select **Settings**. Under **Devices**, select **FHIR**.
2. In the **Resources** area, select **Create**.
3. Enter the following information.
   - **Name** Name to identify the diagnostic report.
   - **Endpoint** Endpoint to use with the diagnostic report.
   - **Resource Type** Type of resource to retrieve. Select **Patient**.

- **Filter, Patient Identifier Filter** Search filters to use when querying the FHIR service. Use the format {DicomTagName} to specify the query values NilRead should use. For example, NilRead will replace {AccessionNumber} with the accession number from the study when submitting the query.

4. Select **Enabled** to allow NilRead to query the FHIR service and retrieve information.
5. Select **Verify** to test the configuration settings.
6. Select **Save**.

Edit or delete an endpoint or resource

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

Manage FHIRcast settings

NilRead can be configured to use FHIRcast. FHIRcast synchronizes healthcare applications in real time to show the same clinical content to a common user.

> **Note**
> This functionality is only available if the **NuanceConnector** license is present.

Prerequisites

- A Nuance PowerScribe® One server
  A Nuance PowerScribe® One Client running on the workstation
- A Nuance Powercast connector

NilRead FHIRcast configuration requires the following steps.

Create the Nuance authentication endpoint

Nuance uses the Auth0 authentication.

To create an endpoint for the Nuance authentication:

1. Select **Settings**. Under **Devices**, select **FHIR**.
2. In the **FHIR Endpoints** area, select **Create**.

3. In the **FHIR endpoint** dialog box, enter the following information:
   - **Name**: NuanceAuth0
   - **Authorization grant type**: ClientCredentials
   - **Authorization endpoint**: URL to the authorization endpoint
   - **Token endpoint**: URL to the token endpoint
   - **Audience**: URL to the PowerCast hub
   - **Resource endpoint**: URL to the resource endpoint
   - **Scope**: Enter a single space.
   - **Client authentication type**: PostForm
   - **Client Id** and **Client secret**: These values are provided by Nuance.
   - Select **Search with HTTP POST**.
4. Select **Verify** to test the configuration settings.
5. Select **Save**.

Enable FHIRcast

To enable the FHIRcast feature:

1. Select **Settings**. Under **Devices**, select **FHIR**.
2. In the **FHIRcast** section, select **Enable**.
3. In the **Powercast Connector** field, enter the PowerCast Connector URL provided by Nuance.

   Example

   `http://localhost:9292/configuration`
4. For **Mode**, select **Active** to make NilRead drive the workflow and ignore the open and close events sent by other applications or select **Passive** to when the workflow is driven by other applications.
5. From the **Endpoint** drop-down list, select the Nuance authentication endpoint previously created.
6. To test the configuration, select **Subscribe**.

   On success, the message **Subscription confirmed** is displayed next to **Subscribe**.
7. Select **Save**.

FHIRcast status information

When the user opens a study and NilRead is successfully connected to the Nuance Powercast connector, the FHIRcast icon is displayed in the upper left corner.

The icon flashes if the connection could not be established.

Additional information

- When a connection is established, NilRead sends **diagnosticreport-open** and **diagnosticreport-close** events to the PowerScribe® One Hub when a user opens or closes a study in NilRead.
- When a user adds, modifies, or deletes annotations in NilRead, NilRead sends a **diagnosticreport-update** event with the verbs **post**, **put**, or **delete** to the PowerScribe® One Hub.
- When a user selects annotations in NilRead, NilRead sends a **diagnosticreport-select** event to the PowerScribe® One Hub.
- When NilRead receives a **diagnosticreport-update** event with the verb **delete**, NilRead deletes the corresponding annotation.
- When NilRead receives a **diagnosticreport-select** event, NilRead navigates to the corresponding annotation.

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 polices. 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 associate 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**).

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.

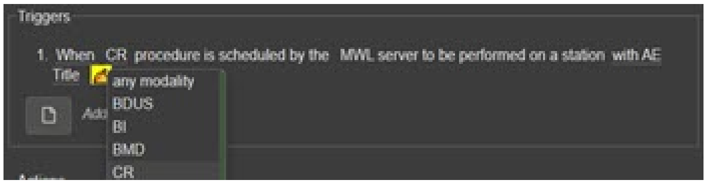
Enabled

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.


1. When CR procedure is scheduled by the MWL server to be performed on a station with AE Title

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

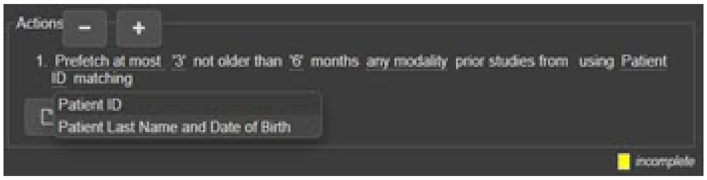
1. When CR procedure is scheduled by the MWL server to be performed on a station with AE Title

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.



1. Prefetch at most '3' not older than '6' months any modality prior studies from using Patient ID matching

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**). 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**.

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 users

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**.

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**.

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**.

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**.

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**.

Privilege descriptions

ADMINISTRATORS ONLY

The following privileges can be assigned to a group or user.

- **Assets** Manage site-level assets.
- **AssignWorkItems** Assign work items to other users and groups. Make work items public.
- **AutoEnroll** Automatically create NilRead user accounts for members of a Windows group on their first login.

- **BookmarkSaveSend** Create and share a bookmark. Note: The user must also have the SaveEvidence privilege and the EnableSaveMenu configuration option must be set to true.
- **Collaboration** Access collaboration tools.
- **ContentDownload** Download DICOM files. Note: The user must also have the GuiPatient privilege in order to access the Download option in the image viewer context menu.
- **ContentUpload** Upload DICOM files.
- **CreateAccounts** Create, modify, and delete NilRead user accounts.
- **CreateSecureLinks** Create and send secure study links.
- **DicomClearLogs** Remove logs from the DICOM Activity page (see **Monitor DICOM patient study transfers**).
- **DicomConfig** Manage DICOM services (see **Manage DICOM services**). Note: The DICOM Activity button is only enabled if the patient directory provider implements the **IDicomPatientDirectoryProvider** interface.
- **DicomConfigEdit** Edit DICOM configuration.
- **DicomDelete** Delete saved presentation state information. Note: The user must also have the GuiPatient privilege in order to access the Delete Image option in the image viewer context menu. The user must also have the SaveEvidence privilege in order to delete persistent curved reformat centerline data.
- **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**). Note: The DICOM Activity button is only enabled if the patient directory provider implements the IDicomPatientDirectoryProvider interface.
- **DicomRT** Enables protocol support and tools for DICOM RT studies.
- **DicomStore** Access the DICOM store features. Note: The DICOM Activity button is only enabled if the patient directory provider implements the IDicomPatientDirectoryProvider interface.

- **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. Note: The Edit Image Header option requires the ImageHeaderEditorEnabled configuration setting to be set to true.
- **EditSystemHangingProtocols** Create, modify, delete and enable/disable system hanging protocols. Note: The user must also have the EditHangingProtocols privilege.
- **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**). 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.
- **EmergencyOverrideRestrictedContent** Use emergency override (“break glass”) to view XDS content.
- **FhirAccess** Provides read-only access to FIHR patient and imaging study resources. Allows the user to acquire access tokens from the NilRead token endpoint and query patient information on the patient endpoint.
- **FhirConfig** Edit FHIR configuration.
- **FhirUpdate** Modify patient information using the patient endpoint with the access token.
- **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. Note: This privilege cannot be applied to administrator users or members of administrator groups.
- **IOCM** Edit IOCM configurations.
- **LifecycleManagement** Enable and modify data lifecycle options (see **Manage data lifecycle policies**). Enable and modify prefetch option (see **Manage prefetch settings**).
- **MprProtocols** View MPR views.
- **OverrideLosslessModalities** This privilege has been replaced by the AlwaysLosslessModalities configuration setting. Previously, this privilege allowed a user to override system settings that specify that images from specific modalities are always shown as lossless, uncompressed images.
- **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 presentations and key images. Save secondary capture images (the user must also have the SecondaryCaptureCreation privilege). Save bookmarks (the user must also have the BookmarkSaveSend privilege and the EnableSaveMenu configuration option must be set to true). Print images from the image viewer. Access the Link option in the image viewer context menu. Access the Axial, Coronal, and Sagittal options in the MPR Views menu. Access the 1+1 and 3D Only options in the 3D Views menu. Generate, save, and delete persistent curved reformat data (the user must also have the DicomDelete privilege).
- **SecondaryCaptureCreation** Create secondary capture images (see **Share secondary capture images**). Note: The user must also have the SaveEvidence privilege.

- **ShowBookmark** Display a list of bookmarks in Presentations (see **Use presentations**).
- **Spinemapper** View Spine Layout views.
- **StudyListAccess** Access the Patient Study Directory from the directory and the image viewer.
- **StudyNoteCreation** Create study notes.
- **ThreeDProtocols** View 3D views.
- **VesselAnalysis** Access Vessel Analysis views.
- **VesselTrace** Access the Vessel Trace tool. Note: The user must also have the ThreeDProtocols privilege.
- **ViewAnalytics** View Analytics (see **View analytics**).
- **ViewPublicWorkItems** Access public (unassigned) worklists and folders created by administrators.
- **ViewRestricted Content** View restricted content from XDS repositories.
- **XdsAccess** Access XDS repositories.

Manage user groups

ADMINISTRATORS ONLY

You can use groups to assign NilRead privileges to users (see **Privilege descriptions**). 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**).

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**).

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.
   - **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**). 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**.

Manage NilRead

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**.

Set up review folders

ADMINISTRATORS ONLY

NilRead users can use folders to track whether studies have been reviewed. A typical example is to group studies that require review in a **For Review** folder, then move these studies to a **Reviewed** folder once they have been reviewed. For more information, see **Track review status**.

In order to set up the review workflow, you must create the review folders and add folder icons to the image viewer toolbar. See the next sections for details.

Create review folders

Create the folders used to review studies (such as **For Review** and **Reviewed**) and grant access to these folders to authorized users. Note that you can use more than two folders for the review process and can use any name for the folders. For details on creating folders, see **Manage folders**.

Create review folder toolbar icons

Create icons for the review folders on the image viewer toolbar. Users will be able to use these icons to easily move studies from one folder to another.

1. Select **Settings**.
2. Under **System**, select **Third Party Applications**.
3. For each icon, select **Add** and enter the following settings.
    - **Application** Icon label.
    - **Target** Select **API**.

- **Method** Select **POST**.
- **Shortcut** (Optional) Keyboard shortcut to launch a third-party application or make a web API call.
- **Launch URL** URL to launch the NilRead web API:

  `api/nil/relay/$token$/nil-move-study/$vp$`
- **Data** API parameters that define the source and destination folders. For example:

  “For Review” folder:

  `{"fromItemId":"1159","toItemId":"1158"}`

  “Reviewed” folder:

  `{"fromItemId":"1158","toItemId":"1159"}`
- **Icon URL** Icon images to indicate the study state (in the folder and not in the folder). The following icons are provided:

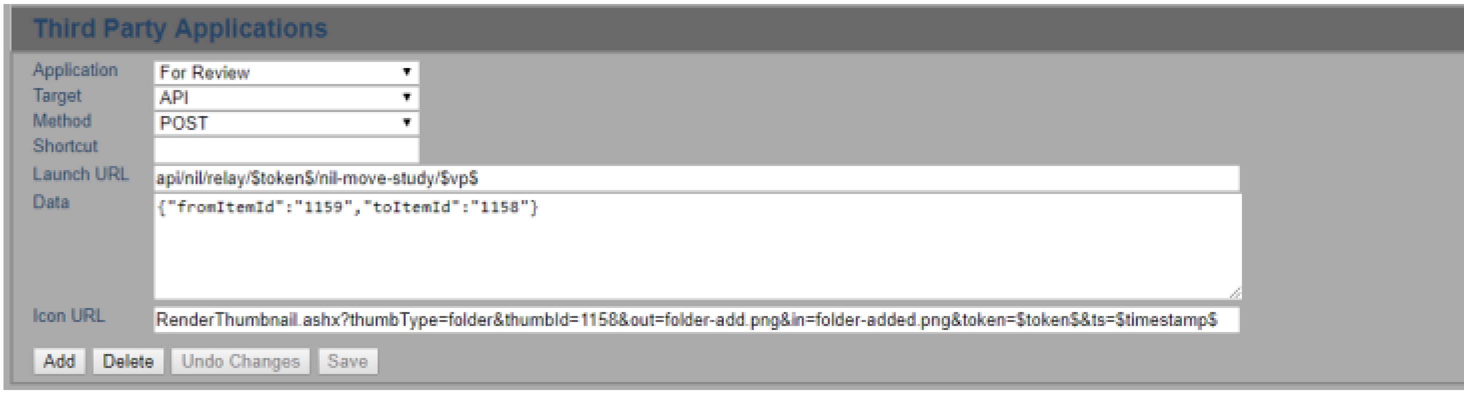
  “For Review” folder:

  `RenderThumbnail.ashx?thumbType=folder&thumbId=1158&out=folder-add.png&inn=folder-added.png&token=$token$&ts=$timestamp$`

  “Reviewed” folder:

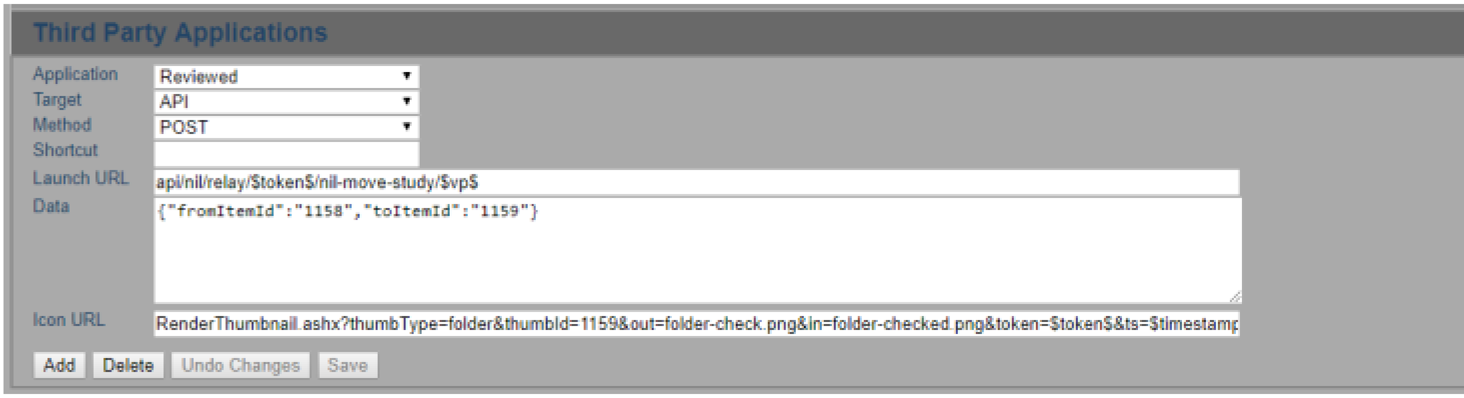
  `RenderThumbnail.ashx?thumbType=folder&thumbId=1159&out=folder-check.png&in=folder-checked.png&token=$token$&ts=$timestamp$`

The following example shows two toolbar icons (Review and Reviewed) that allow users to move studies between two folders.



Third Party Applications

Application	For Review
Target	API
Method	POST
Shortcut	
Launch URL	api/nil/relay/$token$/nil-move-study/vp
Data	{"fromItemId":"1159","toItemId":"1158"}
Icon URL	RenderThumbnail.ashx?thumbType=folder&thumbId=1158&out=folder-add.png&in=folder-added.png&token=$token$&ts=$timestamp$



Application: Reviewed
Target: API
Method: POST
Shortcut:
Launch URL: api/nil/relay/$token$/nil-move-study/vp
Data:

```
{"fromItemId":"1158","toItemId":"1159"}
```

Icon URL: RenderThumbnail.ashx?thumbType=folder&thumbId=1159&out=folder-check.png&in=folder-checked.png&token=$token$&ts=$timestamp

4. Select **Save**.

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 secure study links

ADMINISTRATORS ONLY

Secure link settings

You can select the available security options that users can choose when sending secure study links (see **Send secure study links**). You can customize these settings for each site.

1. Select **Settings**.
2. Under **System**, select **Shared Links**.
3. Select the security options that users can select when sending a study link, then select **Save**.

Email Options

- Select **Show Email Fields** to show a field that allows users to enter the recipient's email address.

Limit Number of Uses

- Select **Show Use Limit** to show a field that allows users to limit the number of uses for the study link.
- To specify a use limit that cannot be changed by the user, deselect **Use limit** and enter the limit in the **Default value** field.
- To specify a default value that can be changed by the user, select **Use limit** and enter the default value in the **Default value** field.

Time Limitations

- Select **Show Time Limitations** to show a field that allows users to set an expiration period for the study link.
- Select **Expiration Time Hours** to show a field that allows users to set an expiration time in hours. You can also enter a **Default value** that can be changed by the user. To specify an expiration period that cannot be changed by the user, deselect **Show Expiration Time Hours** and enter a **Default value**.
- Select **Expiration Time Days** to show a field that allows users to set an expiration time in days. You can also enter a **Default value** that can be changed by the user. To specify an expiration period that cannot be changed by the user, deselect **Show Expiration Time Days** and enter a **Default value**.

Login

- Select **Show Require Login Option** to show a field that allows users to require the recipient to log into their NilRead account before using the link.
- To select this option by default but allow the user to change it, select **Login Option** and select the **Default value** checkbox.
- To always require recipients to log into their NilRead account before using the link, deselect **Login Option** and select the **Default value** checkbox.

Password

- Select **Show Password Option** to show a field that allows users to specify a password the recipient is required to enter in order to use the link.

Two Step Confirmation

- Select **Show Two Step Confirmation Option** to show a field that allows users to use a two-step verification process. The recipient will receive an email with a link to confirm they are the intended recipient. When the recipient clicks the link, they will be sent a second email with the study link. Note that this option is only available if your organization uses an IIS SMTP mail server.
- To select this option by default but allow the user to change it, select **Two Step Confirmation** and select the **Default value** checkbox.
- To always require users to use a two-step verification process, deselect **Two Step Confirmation** and select the **Default value** checkbox.

Send Link Options

- Select **Show Copy to clipboard button** to show the **Copy link to clipboard** button to the user for use when sending the link.
- Select **Show email button** to show the **Click to send link by email** button to the user for use when sending the link.

Standalone Link Server Configuration

A standalone server can be configured to send secure links instead of the main server.

- To use a standalone server to serve links, select the **Use Standalone Server(s) to serve links** option.
- To specify the domain prefix for the configured standalone link server, enter the prefix in the **Link Server Domain Prefix** field.
- To specify another encryption key, enter the key in the **Overwrite Encryption Key** field.

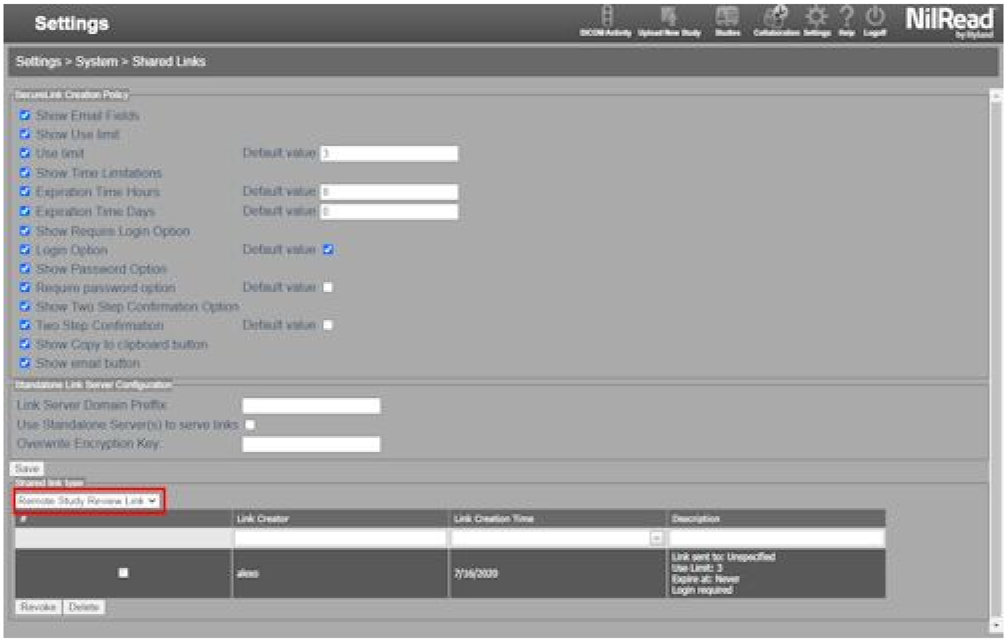
Edit the secure link email template

You can modify the template used to create emails for secure links. The template is located in **\App_Data\Templates**.

View and revoke shared links

You can view an audit trail of study links that have been created. You can also revoke a study link so it is no longer active.

1. Select **Settings**.
2. Under **System**, select **Shared Links**. Shared links are shown in the Shared link type area. You can view **Remote Study Review Links** (study links sent by users) and **Remote Study Upload Links** (links that allow third-party users to upload studies to NilRead).



Settings > System > Shared Links

SecureLink Creation Policy

☑ Show Email Fields
☑ Show Use limit
☑ Use limit — Default value 3
☑ Show Time Limitations
☑ Expiration Time Hours — Default value
☑ Expiration Time Days — Default value
☑ Show Require Login Option
☑ Login Option — Default value ☑
☑ Show Password Option
☑ Require password option — Default value ☐
☑ Show Two Step Confirmation Option
☑ Two Step Confirmation — Default value ☐
☑ Show Copy to clipboard button
☑ Show email button

Standalone Link Server Configuration

Link Server Domain Prefix:
Use Standalone Server(s) to serve links ☐
Overwrite Encryption Key:

Save

Shared link type: Remote Study Review Link

#	Link Creator	Link Creation Time	Description
☐	alex	7/16/2020	Link sent to: Unspecified Use-Limit: 3 Expire at: Never Login required

Revoke Delete

3. To revoke a link so it is no longer active, select the checkbox beside the link, then select **Revoke**.
4. To remove a link from the list, select the checkbox beside the link, then select **Delete**.

Ruler display settings

ADMINISTRATORS ONLY

You can determine whether image rulers are shown by default. This setting will affect all sites. Rulers can only be displayed when the underlying meta-data provides known and consistent pixel spacing and image geometry is flat.

> **Note**
> To customize the ruler behaviour, see **Change modality preferences**.

Note

NilRead users can use **Titles** to show or hide a ruler for an image (see **Titles**).

1. Select **Settings**.
2. Under **System**, select **Image Display**.
3. To show image rulers by default, select **When a ruler can be drawn, show it on initial display**. Deselect this option if you do not want to show rulers by default.
4. Select **Save**.

Merge studies with the same Accession Number

ADMINISTRATORS ONLY

You can determine whether studies are displayed merged in the timeline and the side panel when the following merging rules apply:

- Same accession number
- Same device
- Same patient
- Same MRN
- Maximum 14 days older than the anchor study

1. Select **Settings**.
2. Under **System**, select **Image Display**.
3. To merge studies with the same Accession Number , select **Auto-load and visually merge with the same Accession Number**. Deselect this option if you do not want to display the studies merged.
4. Select **Save**.

When this option is active:

- A plus sign next to the study number in the timeline and the series list in the side panel indicates that the studies are displayed merged.
- The series list in the side panel displays all series of all studies with the same accession number.

Configure DICOM CD images

ADMINISTRATORS ONLY

NilRead users can download studies as an ISO CD image (see **Download studies, series or images**). If you want to include a DICOM viewer in these CD images, place the DICOM viewer files in the **App_Data\CDViewer** folder. The files will be automatically added to the ISO CD image.

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
   - Extended Study Properties
   - Patient Search
   - Patient Search Study Table
   - Patient Search Query Panel
   - Collaboration
   - Login
   - Timeline
   - Timeline Reports
   - Image Display
   - Third Party Applications
   - **Shared Links**

Manage preview settings

You can configure the settings to display the thumbnails of a series in the lower pane when selecting a study in the **Patient Directory**.

1. Select **Settings**.
2. Under **System**, select **Patient Search Study Table**.
3. From the **Load Study Mode** drop-down list, select **double click on study row**.

4. Select **Show series preview on single click**.
5. Click **Save**.

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

Manage Automatic Reconciliation

About Automatic Reconciliation

The NilRead Automatic Reconciliation functionality is a QC feature allowing automatic reconciliation of MRN and other DICOM attributes of outside studies against a site's patient records.

⚠ These configuration options have a direct impact on patient safety and can result in hazards such as incorrect diagnosis due to images being associated with the wrong patient or delay in diagnosis due to images not being available in the patient record.

⚠ This feature may result in data being ingested into the system which can introduce cyber-security risks, or contain illegal or inappropriate images.

It is recommended to only use this feature when reconciliation cannot be done effectively by a trained QC technician or when existing VNA or PACS systems (the primary repositories of studies) cannot provide reconciliation capabilities.

Make sure that the provided functionality is well understood and to perform a hazard analysis of the whole system and not only the NilRead automatic reconciliation feature.

For other warnings, please refer to **Warnings and precautions, General usage**.

> **Note**
> This functionality is only available if the automaticReconciliation license is present.

Configure automatic reconciliation

1. Select **Settings**.
2. Under **System**, select **MRN Reconciliation**.
3. Select the desired options and click **Save**.
4. Read and agree to the warning message that is displayed.

See the next sections for details on configuring each option.

Enable reconciliation

When this option is enabled, all ingested instances go through the automatic reconcilation process before they are stored in the local cache.

MRN source

The **MRN Source** drop-down list allows you to specify which system contains the correct MRN to be associated with a particular patient. The drop-down list contains all of the configured connections which support demographic queries.

In addition, you can specify to reconcile based on private DICOM attributes injected by an API initiated upload. To specify this, select **Tag (0A57, 1091)** in the drop-down list. When this option is used, instead of performing a demographics query, NilRead uses these attributes directly for reconciliation.

Origins

The **Origins** option allows you to define which ingestion sources should be evaluated for reconciliation. You can select any options that apply.

> **Note**
> In the majority of cases, only **nilfeed** should be used. **Nilfeed** corresponds to the NilRead uploader and NilFeed product data sources.

Tags to match

The **Tags to Match** option defines which demographic DICOM attributes present in the ingested data should be used to query the configured MRN source to obtain the site specific MRN.

If the MRN source is the private **Tag (0A57, 1091)** then the above demographics from the data set are verified against API injected tags for additional hazard reduction.

If the matching fails, the ingested data is marked with a configured fallback MRN, to be processed later by a trained QC technician. For more details, see the **Fallback MRN** section.

> **Note**
> It is recommended to use and ensure the availability of the minimum industry standard attributes such as patient's name, data of birth, and patient's sex for matching.

Tags to apply

The **Tags to Apply** option defines the tags that are modified after a successful match. It is recommended to apply only the **Patient ID** and **Issuer of Patient ID** tags to reduce the overall risk of hidden patient data mismatch.

Fallback MRN

The **Fallback MRN** option allows you to configure a specific MRN to be used for marking ingested data if it fails to find a match.

Fallback MRN issuer

The **Fallback MRN Issuer** option allows you to define the Issuer of Patient ID to be used for marking a study as a failed match.

This option supports the ability of preserving the original MRN. To preserve the original MRN, add Outside - {0} where {0} is the placeholder for the original MRN. In a failed match, this configuration results in the Issuer of Patient ID field containing the value "Outside - [Original MRN]". For example, Patient 12345 fails reconciliation, the Issuer of Patient ID field will contain ‘Outside - 12345’.

Query timeout

The **Query Timeout** option allows you to define a timeout in seconds for the demographics query of the selected data source to complete.

The ingestion performance is directly dependent on the query performance. However, it may be necessary for busy systems to control how long the software will wait before closing the connection.

Manage data post automatic reconciliation

Once the data is stored in the local cache, it is recommended to manage the system by performing the following actions:

- Use a Data Lifecycle management activity to automatically send successfully-reconciled data to the final destination system. This destination system should send image availability notifications as needed upon ingestion of the data received from NilRead.
- Periodically check the local cache for failed studies and manually correct them by a trained QC technician. You can configure a worklist to select studies that are marked with the configured fallback MRN, using built-in QC tools.
- Periodically audit and verify that the system is functional and safe.