3Dnet Medical

User's Manual

HTML5 Platform - Software Version 2.15



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Warnings: Please always keep your browser and operation system up-to-date by installing the latest updates.

Note: All the patient names or study identifiers used in this user manual are not real and they are not linked to a real person.

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1 Introduction

3Dnet™ Medical is a DICOM 3.0 compliant, cloud-computing solution for scheduling of medical examinations, medical image archiving, distribution and advanced visualization. 3Dnet Medical enables radiologists and clinicians to access images at anytime and anyplace using a zero-footprint client for advanced visualization and image processing.

3Dnet Medical runs in a browser and does not require download and installation of any software to the user device. All the processing is performed on the server and the images are sent on demand to the client device using progressive streaming. The data is not downloaded to the local hard drive and it is only stored in the browser memory during the visualization session. Upon closing the browser, no patient data is left behind on the client device.

3Dnet Medical zero-footprint client offers coverage of the whole lifecycle of radiologic images, from the scheduling to the reporting, with a full set of advanced diagnostic tools, including: predefined layouts, hanging protocols, 3D reformatting such as MIP, MPR or volume rendering, bone and table removal for angio CT, stenosis analysis, lung nodules segmentation, support for 4 monitors at the same time, measurements and annotations, reporting module with integrated text editor and digital dictation or speech recognition.

Being developed on HTML5 technology, the 3Dnet Medical client runs on any platform (Mac, Windows, Linux) and supports all the modern web browsers: Chrome, Firefox, Safari, Edge, Internet Explorer, etc.

Images and patient records coming from systems outside the radiology department (Cardiology, Oncology, Gastroscopy, etc..) can be archived and displayed as long as they are in supported formats (DICOM, JPEG, TIFF, PDF, WORD, AVI, MBP, etc) or DICOM incapsulated.

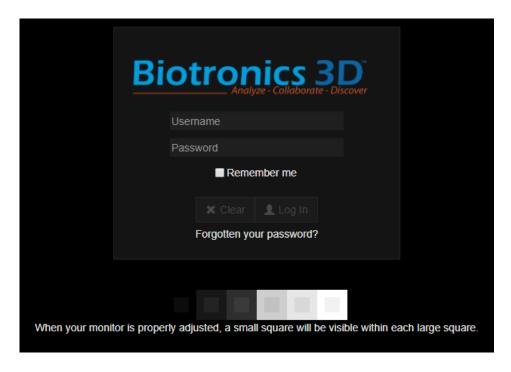
Server Recommendations

Concurrent users	10	5	2
CPU	20 Cores	10 Cores	4 Cores
Memory	48 Gb	32 GB	16 GB
Hard Disk	2 x 300 GB 7.2K RPM SATA, NLSAS or SAS		
Operating System	Mi	crosoft® Windows Serve	er
Database Software		Microsoft® SQL	

2 User account

2.1 Log in

On the main page enter your **username** and **password** then click **Log In**.



Login page. Note the contents of this box regarding your monitor setup.

2.2 User profile

Click on **Profile** in the upper left menu to change your password, edit personal information and application settings.



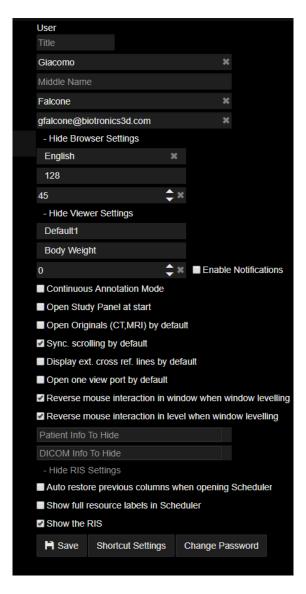
Edit profile information, including passwords and viewer settings.

Click on the **Show Browser Settings** tab to choose the prefered languange for the user interface and how many studies will be listed in the worklist at the same time.

Click on the **Show Viewer Settings** tab to configure the graphical user interface and the viewer according to your preferences. Here you can, among other options:

- Inverse the W/L in the diagnostic viewer
- Hide selected patient information from the viewports in the viewer
- Hide selected DICOM tags from the viewports in the viewer
- Always display cross reference lines by default
- Use a continuous annotaiton mode (eg. Select measurement tool, measure multiple times without deselecting the tool, manually deselect the tool to stop measuring)

Click on the **Show Ris Settings** tag to configure the preferences for the RIS, if it is enabled. From here, if you are an Admin, you can enable/disable RIS.

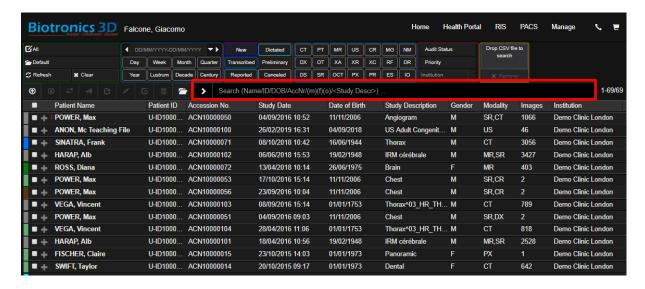


Browser, Viewer and RIS settings.

3 Study browser

3.1 Worklist

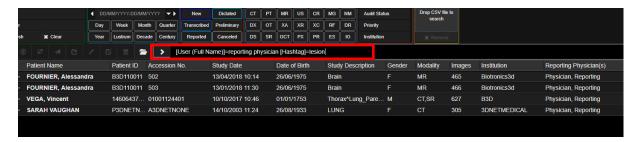
Click on the **PACS** tab located in the upper part of the welcome page to display the study list. This worklist displays studies currently available in the PACS system, showing the patient last name, first name, Patient ID, Accession Number, Modality, Study Description, Referring Physician, Number of images, etc.



Study browser with tools for study searching, filtering and sorting.

To find a patient, type in the Patient Search box located in the middle part of the screen any information related to that study, such as: Patient Name, Patient ID or Accession Number, Body Part, Study Satus, Date, Institution or Referring Physician. To order the patient list, for example by study date or patient name, click on the respective column head in the study list. The study browser also offers quick filters to display patients from Today, Week, from a certain period of time, or display only CT or MR studies. To display only the Reported studies or the Unreported studies click on the respetive buttons located in the upper menu of your screen.

The Omnisearch Tool allows users to do more complex queries in the database, see picture below:



Click on the > icon to show all the possible search criterias.

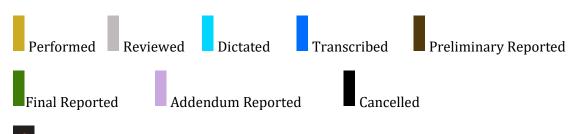
In this example, the user is searching the database for all the studies assigned to a specific user (User full name ="reporting physician", which is a test user created to simulate a reporting

physician), and that have also been marked with the Hashtag "lesion". In the picture below, see the possible search criterias. To add a new criteria, click on the > icon and select it from the list. Each time a new one is selected, it will be added to the searchbar.



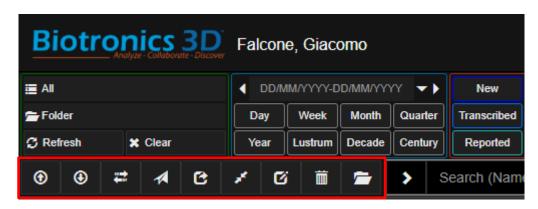
All the possible search criterias.

The colored stripe on the left of a study indicates the status of that study, as follows:



- A red exclamation mark indicates that the priority of the study is CRITICAL.
- A yellow exclamation mark indicates that the priority of the study is URGENT.

In the study browser, the user can perform the following operations with studies, accessible from the upper horizontal menu:



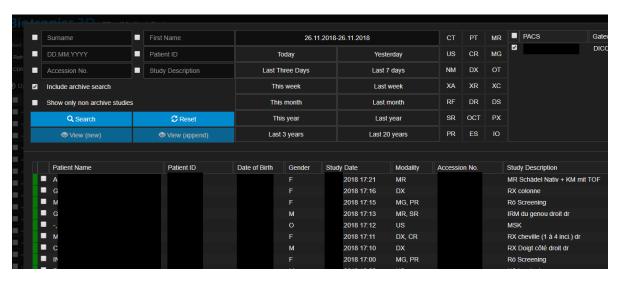
- Upload: import a study into the PACS archive
- **Download**: export a study from the PACS archive using the DICOMDIR format. This feature also allows exporting patient DICOM images and DICOM viewer on CDs or USB flash drives. Anonymization option available.

- Export: DICOM send send study to another PACS system or any other DICOM node, such as modality workstation or DICOM compliant CD/DVD publisher.
- Send To: move study to a different folder within the 3Dnet Medical PACS archive
- Share: share a study via email
- Merge: merge a patient who has been added to the system twice; merging the two IDs for the same patient also merges the studies into one file record for that patient
- **Assign**: allows users to make changes to the study information i.e. assign a reporting physician, change the priority of a study, etc.
- **Delete**: delete study
- Query Retrieve: Query retrieve

First check the box on the left of a study and then click on the button to perform the desired operation as described above.

3.2 Import study from another PACS

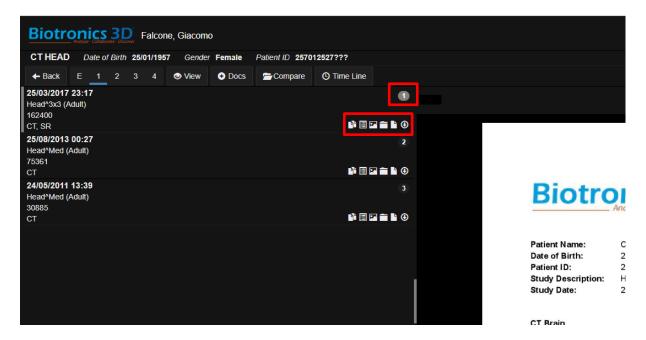
A user can query/retrieve a PACS target to import a study in 3Dnet Medical. Using the tool displayed in the following picture, it's possible to search a database using multiple search parameters (name, last name, accession number, patient id, study time, modality, etc.). A list of records that answer to the query will be displayed. Select the study you want to import and the stripe next to those studies will begin to blink – this means the study is transferred. The user has the options to import them to the database or simply view them in the viewer.



Query retrieve tool accessible from the main PACS page.

3.3 Unified patient record: images, reports, documents, prior studies

Right mouse button click on a study opens the viewer with the images. Left mouse button click on a study sends the user to another page where one can find all the information related to that study: patient history (previous studies), reports, documents, snapshots and images. All the studies of that patient found in the PACS database are displayed automatically by the system and listed in the upper left side of the viewer. For example the patient in the figure below has three studies. The study matching is done automatically by looking at Patient ID, Patient Name and Date of Birth (DOB). If any of these do not match, the system will not match the studies. However, it is possible to relax the matching criteria from the organization settings.



Instant view of the report and patient history. 3 studies of the same patient shown on left side.

For each study, the user can access the series, the snapshots in the study (see the Snapshots section of this user manual), the documents received via HL7 ORM order messages or uploaded manually (referral letters or other relevant medical documents) and reports written dirrectly in 3Dnet system or received via HL7 ORU messages in PDF or text format.

- Notes allows the user to check the notes and tags added to that study by the user itself or other users.
- Series panel displays the list of the series from the selected study.
- Snaps panel images, reconstructions or measurements saved for future reference.
- Docs panel documents, images or movies.
- Reports panel radiological reports.

Series download – allows the user to download selected series from the study.

To download a series from the study, the user will have to open the Series panel, select the series to download, then click on Series download.

The user is able to set the number of monitors (maximum four) used to display images at the same time, by clicking on the desired number. E = 1 - 2 - 3 - 4. Choose the E option if one desires the viewer to open in the same browser window or select E to open images simultaneously on four monitors (four browser instances). Press the **Back** button to the study list.

Click on the button to access the web form used to upload non-DICOM files, such as documents, images or movies, as shown in the figures below (with drag&drop). Supported formats are: PDF, JPEG, BMP, TEXT, WORD, AVI.



Attach, store and visualize non-DICOM files to a study using drag & drop.



Order form manually uploaded by a user and attached to the patient examination in 3Dnet Medical PACS. The same order form can be accepted in 3Dnet Medical via HL7 ORM order message from the HIS/RIS.

Click on the button to search and select another study to be compared with the loaded study in the same viewer (useful for situations where patient info differs from one study to another).

4 The viewer

4.1 Study panel

To open the viewer with images, click on the View button (or directly from the study list with the right mouse button). The viewer is split into two main sections: 1) the studies panel on the left; 2) the main visualization area. The studies panel displays all the studies of a patient, in chronological order, and the series as thumbnail images. The active study is marked with the blue dot. To expand or collapse a study, click on the Study Description. To display the study in the main visualization area, click on the Study Date.

At the top of the study panel, the user can find a modality filter tool (red highlight box). This will filter through modality in the prior examinations of that patient, to make the search easier in the case of a patient will multiple priors.

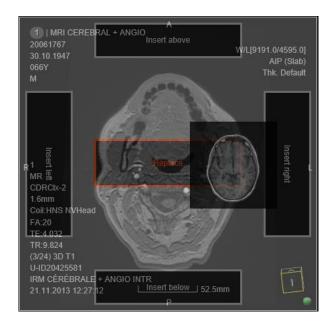


The viewer with the studies panel on the left (collapsed view).



Viewer with the study panel on the left (expanded).

The image in the viewport can be changed with LMB clicking on a sequence in the study panel. RMB clicking on a thumbnail series will add that series in a new viewport, in chronological order. Also, the thumbnail series on the left can be brought into the visualization area (viewport) with drag&drop. The new series can be inserted to the left, right, above or below of an existing viewport or can replace the image in that viewport.



Drag & drop the new series to the main visualization area, with the following available options: insert left, insert below, insert right, insert above, replace.

In order to perform a comparative analysis between two or more studies of the same patient, first, from the **Windows** button select the 1 row x 2 columns layout. Then drag & drop the desired series from the studies panel into the viewports, as shown in the figure below.



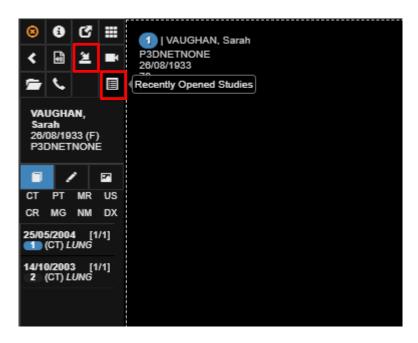
The viewer showing two studies of the same patient for comparative analysis with synchronized scroll between the series. The series from both studies are displayed in the series panel as thumbnails.

In the image above, the prior study is differentiated with the red font to avoid confusion. Click on the two viewports with the left mouse button (LMB) and then press J on the keyboard to link the two series for synchronous scrolling.

Click on the to hide the studies panel (shortcut <**P>**).

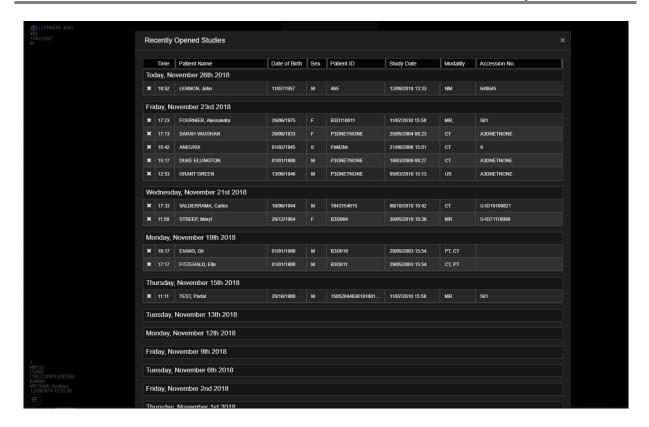
4.2 Suspend study

The presentation state of the viewer is automatically saved after every action. This enables the user to temporarily switch to another study in the middle of a reporting session if he so desires. The user can simply open the new study, analyse it, and close it. At this point he can open the study which was put on hold and restore the state of the viewer. The software will display the same screen layout with processed images, measurements, etc. that were on the screen when study was suspended.



To load the latest saved cached study when opening a patient again, click on "Load cached study session". To open up a list of all the recent studies, click on "Recently opened studies".

This feature is useful to easily switch to a different reporting session, enabling users to easily check pictures from a different scan/patient without losing their progress. The user can use the recently opened studies tool to view a complete list of all the patients recently opened and select the one to go back to.



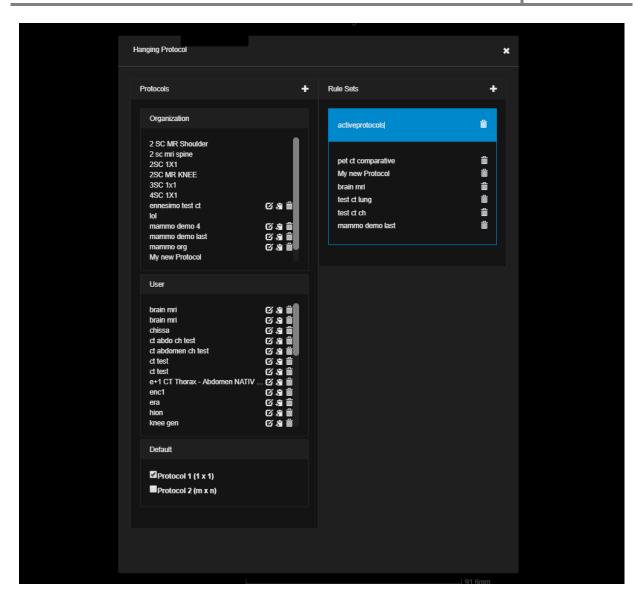
Recently opened studies tool. Displays each study opened day by day.

By clicking on a study, the viewer will switch to the latest saved state for that patient. To delete a cached saved state, simply click on the cross next to the patient name. The list will keep memory of patients opened in the past, as shown in the picture. If no studies were opened on a specific day, that day tab will be empty. It's possible to collapse and expand each day tab to explore it.

4.3 Hanging protocols

A hanging protocol (HP) is the series of actions performed to arrange images for optimal softcopy viewing. The goal is to present specific types of studies in a consistent manner, and to reduce the number of manual image ordering adjustments performed by the radiologist. With 3Dnet Medical, the appropriate HP is automatically applied based on the characteristics of the study being loaded, characteristics which are found in the DICOM header (e.g.: modality, body part, study or series description, image orientation, patient positioning, etc.). To create a hanging protocol, one must first open the viewer and arrange the images in the desired layout. Once the

screen arrangement is done, click on the button in the upper left corner of the viewer to save the layout as a hanging protocol, as shown in the picture below.



Save the current layout in the viewer as a hanging protocol.

This action will open the auto-populated HP editor, where the user is able to edit, modify or apply new rules to the desired HP.

In the left column the user can click on the Plus icon to save a new protocol (this will open the window demonstrated in the picture below, more on this later).

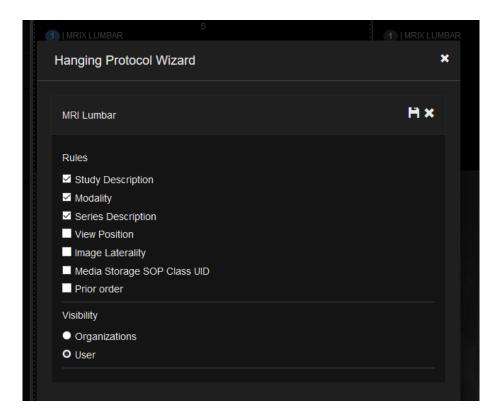
From this menu, it is already possibly to view the entire protocols currently available (left column) and applied to the user (right column, in the ruleset box). It is also possible to select the default behaviour of the viewer if a protocol is not selected:

The Default box in the left column has 2 possible options.

- Protocol 1: the viewer will open with a (1 x 1) matrix
- Protocol 2: the viewer will open with a (m x n) matrix. This means that by default all the images in the study will open at the same time in the viewer.

4.3.1 Saving a new protocol

Every protocol can be set as available for the whole Organization or just for the user who created it. A user can then, if he/she likes one or more of the available protocols, drag and drop said protocol in the right hand side column, in the active protocols folder (Rule Sets column, the blue highlighted folder). A user can have multiple rulesets folders, but only the active ruleset folder (highlighted in blue) will trigger protocols if the conditions apply.



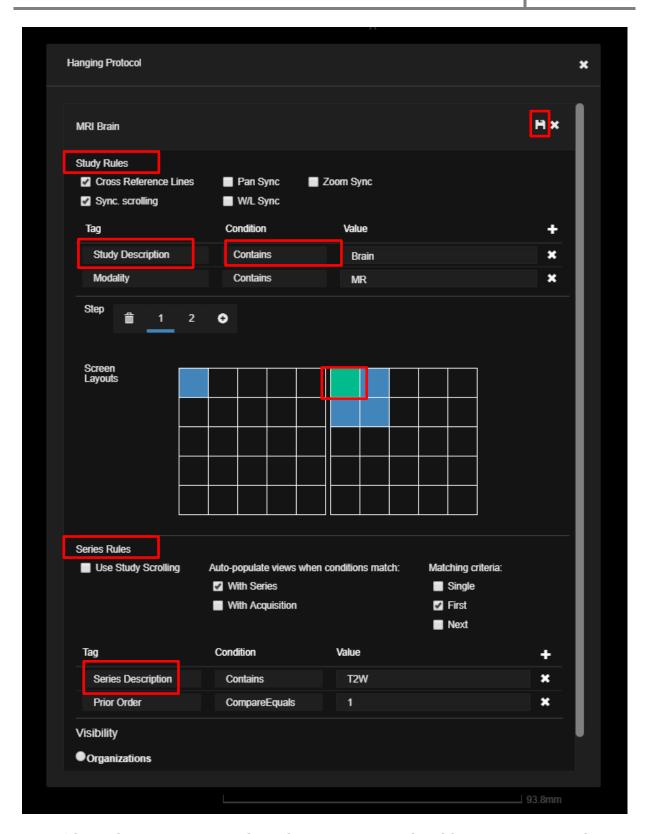
Hanging protocol editor: define visibility of the protocol; define the number of monitors (up to four); define the number of steps; define the study rules.

In the image above, tick Study Description, Modality or Series Description to instruct the HP to trigger every time a study with the same Study Description, Modality or Series Description is loaded. The HP can be made available per User or per Organization (being a hospital or an imaging centre).

4.3.2 Editing a saved protocol: Study Rules

Once the protocol is saved, the user can access more advanced options to further fine tune the protocol. See image below.

In the advanced HP options menu, the user can use logics such as "contains, excludes, match, is not empty, etc" and apply them to DICOM tags such as study description, series description, modality, body part, patient orientation, prior order etc. These options can be set for each individual viewport, for every step (page) of the protocol.



Advanced options in HP wizard. Use these options to tweak and fine tune your protocol.

At the top of the previous picture is the Protocol Name field. Followed by the Study Rules tab. Here the user can enable or disable options such as cross reference lines, synchronized scrolling, synchronized zoom/pan/window level. At this level users can add rules for DICOM tags modality and study description (exclude, match, contains, etc).

Further down users will find a matrix depicting the layout in each screen and the number of steps (or pages) that are saved in the protocol. It is also possible to modify the number and positioning of enabled viewports per screen from the editor itself, clicking with the right mouse button on the blue and green tiles on the displayed matrix (when a tile is green, it means it is selected and the filter tags displayed at the bottom are related to that specific viewport).

4.3.3 Editing a saved protocol: Series Rules

The Series Rules tab is used to add tags and conditions to individual viewports on the screen. This will bring changes to the Diagnostic Viewer layout on a series level (series description, laterality, body part, etc).

For example, in the picture above, the protocol will trigger if:

- the DICOM field study description contains the word "Brain"
- the modality field contains "MR"
- the highlighted viewport (green) contains "T2W" in the study description tag
- it is a prior for the current examination (Prior order = 1)

The tile highlighted in green (right screen, top left position) will display a series that contains "T2W" in the series description and is also a prior (prior equals 1).

All the conditions and tags added must be true at the same time. Missing tags or conditions that are not fulfilled will result in the protocol not working correctly.

Another set of rules that we can apply to the protocol at the Series level is the matching criteria. These criteria will inspect the series list of the study you opened and allocate the correct series to the correct viewport depending on the option you selected among Single, First, Next.

- Single: the HP will trigger if and only if the selected series rules apply to one and only one series. Two or more positive matches will result in the protocol not triggering.
- First: the First series that matches with the Series Rules will be displayed.
- Next: if there is more than one series matching with the Series Rules, the selected viewport will display the one that is not already displayed somewhere else in the Diagnostic Viewer. See the example below.



Series Rules panel

Using as an example the protocol described in a picture above, for a Brain MRI with the following series:

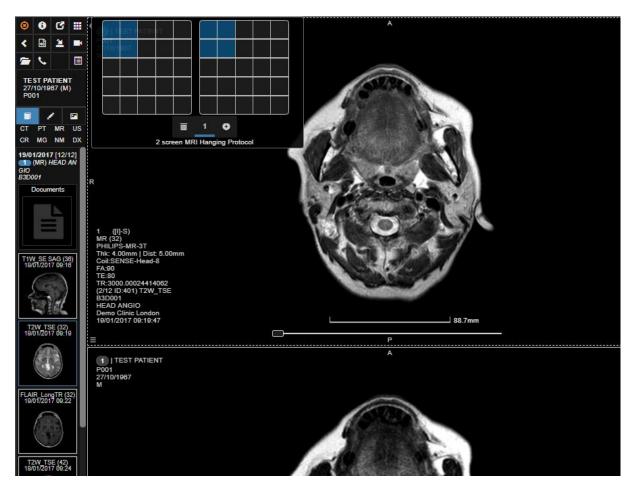
- Localizer
- Sagittal T2 Weighted series

- Sagittal T1 Weighted image
- Axial T2 Weighted image

Looking at the picture above (Edit of a Hanging Protocol) we can see that we applied to the selected (green) viewport tile a series-level rule (DICOM tag Series Description CONTAINS"T2 W"). The study contains two series with the string"T2 W" in the series description (Sag T2 and Axial T2). Keeping this in mind, we will get three different results by using Single, First, Next. Below a description:

- When Single is selected for the active viewport: the software will inspect the series list for this study. In our case, there are two sequences that match with "T2 W" (Sag T2 and Axial T2). The protocol will not trigger.
- When First is selected for the active viewport: the first matching sequence will be displayed in the viewport. (in our case Sag T2)
- When Next is selected for the active viewport: if the first matching sequence (Sag T2) is already displayed in another viewport, this viewport will display the Next matching sequence (in our case Axial T2).

Users can check which HP triggered in the following way. See picture below.



Click on the highlighted icon in the top left. The name of the triggered Hanging Protocol will show at the bottom of the screen matrix representation.

4.4 Series filters

From the Study Panel, the user can filter the series in the study and display all of them with one click. With this tool, users can quickly display all the diagnostic series or all the CT thin slices series, etc. Depending on the modality of the study, the user can access different filters, for example:

CT:

- Thinslices
- Thickslices/Recon
- A1

MR:

- Diagnostic
- Localizers
- All

In the picture below the available filters for CT studies are highlighted. Clicking with the left mouse button on one of the three filters will filter the series accordingly in the study panel. A click with the right mouse button will display in the viewer all the series corresponding to the filter selected. In the picture below, the selected filter for "Thinslices" highlighted 6 series in the study panel. Clicking with the right mouse button on the filter will display them all at the same time in the viewer.



Series filters for CT studies.

5 General Diagnostic - image visualization and processing features

5.1 Operations with series

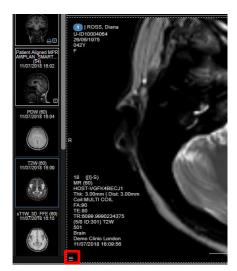
3Dnet Medical offers advanced functionalities for series and image manipulation in the viewing area. Below are some of the operations that can be performed to help the radiologist diagnose a case quicker:

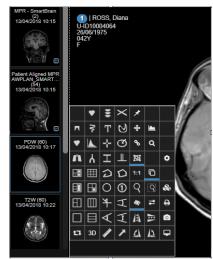
- To **add** series into the viewing area:
 - o Click on it in the study panel on the left

- Right click on a series in the study panel will add that series to the vizualization area, keeping the newest series to the right (in chronological order)
- Drag & Drop the series to the desired viewport. The user has the options to replace
 the series or insert the new series to the right, left, above or below the active
 viewport.
- To swap series between two viewports, press the <Alt> key and Drag & Drop the active series into the desired viewport. The available options are: swap, copy, move, insert below/above/left/right.
- To **activate** a viewport, click on it.
- To **maximize** a viewport, double click on it, if the *"maximise viewport on double-click"* option in the user profile is enabled.
- To scroll through a series use the wheel on your mouse or move the mouse to the right or bottom part of the viewport and drag it on the screen (see the Hot Spot section of this User Manual). You can also scroll by using the slide bar positioned in the lower part of each viewport
- To **navigate** through the series of a study in the active viewport, press the left and right arrows from the keyboard or page up/down.
- To **delete** a viewport press the **<Y>** key.

5.2 Tools menu

In the lower left corner of an active viewport there is a burger button which opens a set of tools for image visualization, processing and measurements (as shown in the images below). If the user hovers the mouse over an item, a tooltip appears describing the function of that button. The same menu can be opened by right clicking and releasing anywhere inside a viewport.





Hide/shows overlays – patient/study information (shortcut I) Maximize viewport - basic layout (one image on the screen) 3D – Volume Rendering layout MPR vertical layout MPR horizontal layout MPR layout MPR & VR layout MPR horizontal & VR layout MPR & VR VOI layout CT Lung module T Vascular module Show cross-reference lines Plane link (for synchronous scrolling of similar series) Magnifying glass Rectangle zoom Quality settings for image streaming (lossless or lossy compression) Window snapshot (W) Link two series from different studies for synchronous scroll

Viewport snapshot (C)

Use study scrolling (S) – scrolls through all the series sequencially in the same viewport ASC (axial, coronal, sagittal) Rotate left Rotate right Hip displacement measurement Point measurement Polygon TT-TG distance (tibial tuberosity trochlear groove distance) Flip horizontally Flip vertically Ruler O Circle Polyline Vertebra labeling Angle Open angle Cobb angle Wiberg angle (hip) Region growing segmentation

Multiple actions (enables repetitive measuremeants)

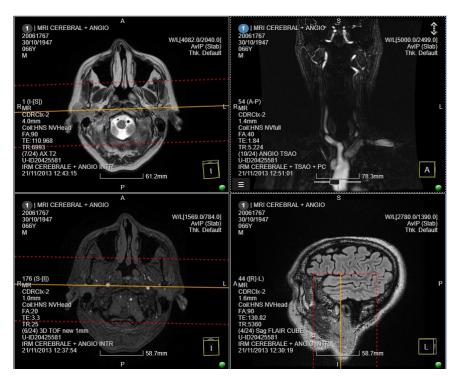
- T Text
- Free Hand Draw
- DICOM Print
- Calcium scoring module
- KiM module
- Spine labeling tool
- Export reformation
- Nouble line
- CT Dental Module
- Ct Colonography Module



The tool box menu.

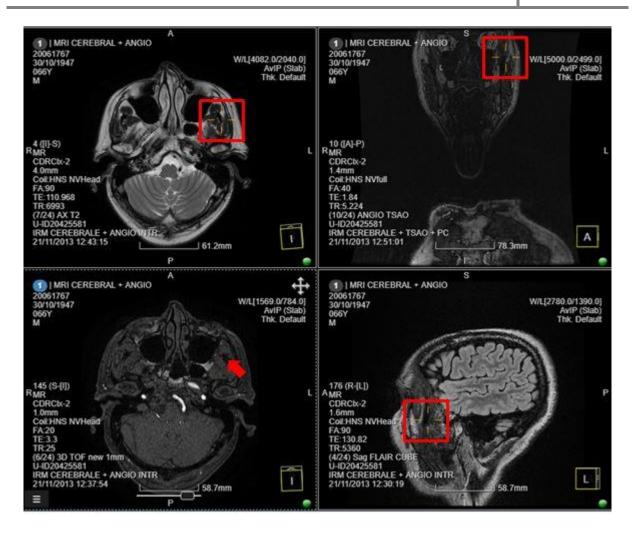
5.3 Synchronized navigation

To display the cross-reference lines between axial, sagittal and coronal views click on the "Show/Hide reference lines" from the viewport menu (burger menu).



Cross-reference lines and synchronized navigation.

3D localization of the cursor is achieved by clicking the left mouse button on an image. The position of the cursor will synchronize on all views and will be shown with an orange cross as in the image below.



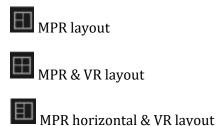
Mouse cursor 3D localization on axial, sagittal and coronal images (shown with orange cross on images).

To link two series from two different studies of the same patient, displayed side-by-side, click sequentially on the first and second viewport and then press the <J> key or click on the button from the tools menu.

5.4 Screen layouts

From the viewport toolset, the user can choose a desired layout by clicking on the following buttons:

- basic layout (one image on the screen)
- 3D Volume Rendering layout
- MPR vertical layout (axial, sagittal, coronal)
- MPR horizontal layout



MPR & VR VOI layout

5.5 Measurements and annotations

The measurements and annotations tools are located in the viewport toolset and include: ruler, angle, Cobb angle, open angle, circle, polygon, polyline, arrow, pixel HU or intensity, hip displacement, vertebra labeling, TT-TG distance (tibial tuberosity trochlear groove distance),

Wiberg angle. To perform repetitive measurements, click on the pin symbol which enables multiple actions. For example, vertebra labeling is achieved by presing and then clicking on each vertebrae. Double click to stop the numbering.

All the measurements and annotations performed on images will be listed in the Annotations panel on the left side of the screen as shown in the figure below (click on the Pen tab). The "eye" symbol hides/displays the measurement in the active viewing area. The color can be selected by clicking on the colored brush next to each measurement.

The user can delete a measurement by clicking on the trash can icon or by clicking on the measurement in the viewport and and pressing the **Delete**> key.



The Measurement panel shows all the measurements performed on images (image showing vertebra labelling).

5.6 Snapshots

The Snapshot function in 3Dnet Medical is similar to the DICOM Key Image concept. It is available in the toolset located in the left lower corner of each viewport (or accessible by right clicking inside a viewport). This function allows the user to save a 'snapshot' of an image (with annotations, measurements, specialized reconstructions, etc) that can then be stored in the PACS archive for future reference, can be attached to a report, sent to a printer or saved as JPEG, BMP, PNG, etc. on your local computer. Snapshots are not just a a"screen capture" but a full blown cached saved state for the study in the moment where the snapshot was taken. Users are able to load a snapshot and resume scrolling, add annotations, measure structures and use advanced picture analysis tools. Snapshot can thus also be used as a presentation state save.

Process:

- Make the changes to the image (measurements, arrows, text, reconstructions)
- Click on the Viewport Snapshot button to capture an image
- Open the Snapshots tab by clicking on the in the study panel

In the figure below, the Snaps panel is shown on the left. The user can easily browse through the snapshots. To save a snapshot to the local drive as PNG, BMP or JPG, click on the button. This will open the Windows Save As dialog box, in which the user can give a name to the file, select the format of the file and select the location where the file will be saved.

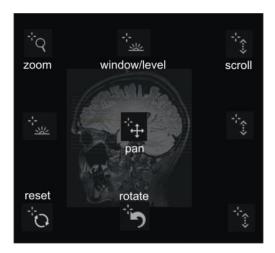


In the Snapshots panel, click on the circle with the arrow pointing down to save a snapshot as an image (PNG, BMP, JPG) to the local hard drive. It will open the Window Save As dialog box.

These images can be saved and stored in PACS as key images and will also work as a presentation state.

5.7 Scroll, window/level, zoom, pan, rotate

In order to keep the mouse closer to images for the sake of efficiency, 3Dnet Medical uses the concept of "hot spots" inside a viewport. A hot spot is a region of the viewport where the LMB takes a certain function. In our software, the viewport is divided in nine hot areas (3x3 matrix), as described in the figure below, which cover the following functionalities: zoom (cell 1x1), window/level (cells 1x2, 2x1), scroll (cells 1x3, 2x3, 3x3), pan (cell 2x2), reset image (cell 3x1), free rotation **<Ctrl>+LMB** (cell 3x2). Just click in one of the nine regions and drag the mouse over in order to perform the operation desired.



Hot spot regions in a viewport showing the left mouse button functions.

For example, if the user places the mouse cursor in the upper left corner of the viewport and clicks the left mouse button, the system will perform zoom. Series Free Rotation is achieved by moving the mouse to the bottom of a vieport and pressing the **<Shift>** key. Double click in the lower left corner resets the image to the initial grayscale and size. Window/Level can also be performed anywhere on the image with the righ mouse button.

One has several options to scroll through a stack of images:

- 1. Use the mouse wheel;
- 2. Use the Up and Down arrows on the keyboard to scroll through images;
- 3. Left and Right arrows will nagivate through the series of that study;
- 4. Use the slide bar in the lower part of the viewport;
- 5. Use the small CINE display menu in the lower part of the viewport. Here the user can modify the frame rate (speed), direction or to jump directly to the first or last image in that series.



Slide bar for stack navigation and CINE menu with speed controls.

Image rotation and flip can be achieved by clicking on the and and and are respectively, in the viewport toolset.

The user has several options to perform zoom. First, position the cursor in the upper left corner and drag it on the image for zoom in/out. Secondly, click on to display a magnifying glass like in the image below. The magnifying area can be resized with the mouse by dragging the edges of the rectangle. Another possibility is zoom inside a rectangle. And finally, one can display a 1 to 1 magnification by selecting the



Zooming operations: magnifying glass, rectangle ROI and 1:1.

To invert the grayscale of an image, click on the W/L text in the upper right corner of the viewport and select the Inv. Gray. This will display the image in negative mode.



Display the negative of an x-ray image.

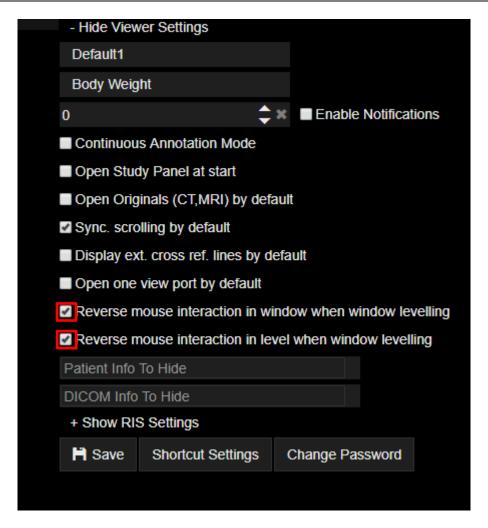
By clicking on the W/L text, the user can also select a Window/Level pre-set for different organs/tissues in case of CT images. The users are also able to add their own prefered pre-sets by entering the Window Width (WW) and Window Level (WL) values, typing a name in the Preset text box and then click on the + button. Window/Level pre-sets are also available using

keyboard shortcuts (keys: 1,2,3,4...)

1) | JEAN-PIERRE 20255951 06.10.1929 084Y 36 Tissue M Soft Tissue 40 Abdomen 1 60 180 Colormap Gray CT ANA cdrcct03 mAs:28 | 1460ms kVP:120 2.5mm mA:150 (3/13) CEREBRAL NATIF U-ID20432953 CT CÉRÉBRAL + TSAO J 43.7mm 20.02.2014 10:52:28

Selecting CT Hounsfield units pre-sets for Window/Level.

It is possible to invert the window/level while levelling while holding the **<Right mouse button>**. Users can access this option from the profile page, under the tab Viewer settings. Users can tick the last two checkboxes in the list below to individually enable the window or the level.



Click on the checkboxes to select the options.

5.8 Mammo tools

For mammography a few other tools are available when loading the images, as described below:

synchronized window/level (when changing the W/L on a mammo image all the other images are changing accordingly)

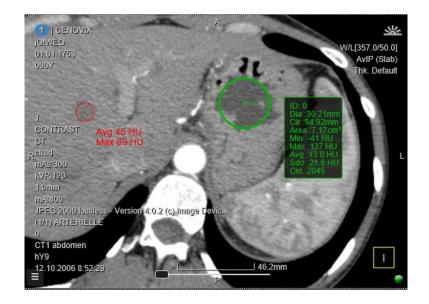
- synchronized zoom
- synchronized pan



Mammo tools: synchronized window/level, zoom and pan.

5.9 Hounsfield units and ROI densities

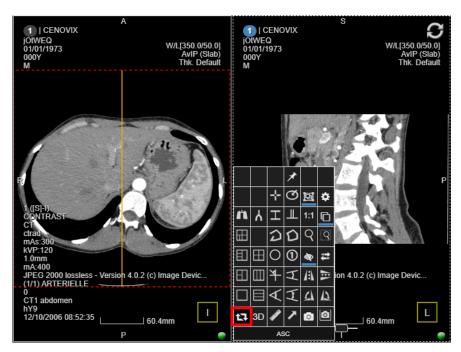
Press the **<U>** key on your keboard to show the Hounsfield unit for each pixel on mouse movement over an image or press the **<O>** key to probe densities inside a circle. The HU value is displayed with red next to the mouse cursor. Use the **<Shift>** key and the mouse wheel to resize the circle. HU densities can also be inspected using the Circle tool from the toolset menu. The software displays information about geometrical measurements as well as HU statistics (min, max, average and standard deviation).



Hounsfield units ROI densities

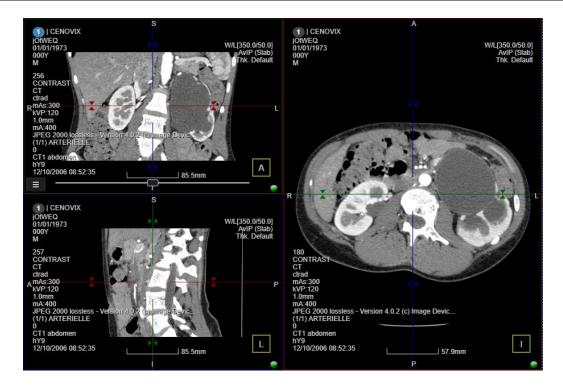
5.10 Multiplanar reformatting (MPR)

MPR views (coronal and sagittal) can be quickly generated and displayed next to the axial view by clicking on the ASC button (Axial, Sagittal, Corronal) as shown in the image below.



Sagittal view created using the ASC tool.

To analyze images using double-oblique multiplanar reconstructions (MPR) open the toolset by right clicking in the viewport, or click on the burger button and select an MPR layout.. Also, a quick way to go to MPR layout is by pressing the **<Q>** key.

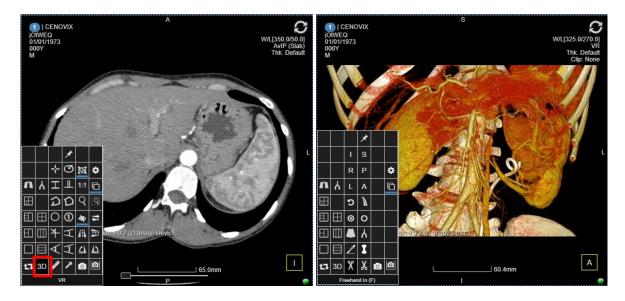


MPR views.

To reposition the cross-hair, click on the intersection of the two perpendicular lines and drag the mouse on the screen. To generate double-oblique MPRs, click on the small triangles positioned on the lines and drag it up and down. In the MPR mode, the position synchronization of the cross-hair on all three views (sagittal, coronal and axial) is achieved by clicking the LMB on the image. To maximize a viewport press <T>.

5.11 Volume rendering (VR)

Like all the other image processing techniques in 3Dnet Medical, Volume Rendering is also performed directly on the server and only the result is streamed to the client computer. As such, VR is accessible on any computer connected to a 3Dnet server, without the need of specialized hardware resources. To generate a Volume Rendering image, click on the 3D button as shown in the figure below. With the <Q> key, the user can switch between base mode (axial view) to MPR and to VR views.



Volume rendering (VR button framed with red on the left).

The following image is generated by default, showing the vessels, kidenys and bones from a CT angiography study. The user has the possibility to rotate the image, zoom it or pan it with the regular tools, using the mouse. In the VR mode, there are several specific tools, as shown on the right image above:



Knife sculpting



Freehand sculpting (in)



Freehand sculpting (out)

The other specific buttons are covered in the CT Vascular chapter of this user guide.

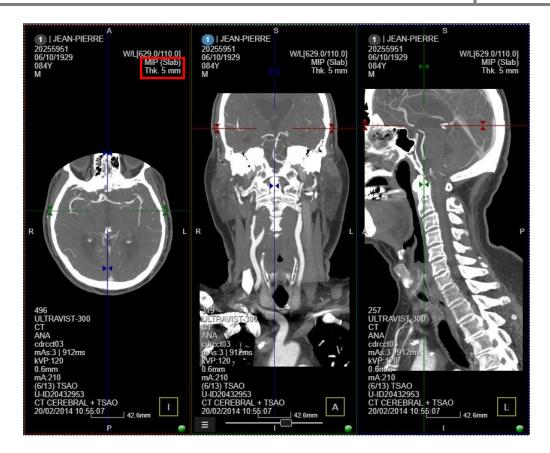
If one clicks on the W/L text in the upper right corner, the viewer displays the presets and filters for the VR transfer function. Use these presets and filters to hide or show different part of tissues or organs. As shown in the image below, a user is able to change the parameters of a VR images by modifying the WW/WL, Opacity, Ambient Light, Add/Remove Shading, Colormap or by selecting presets for various tissues or organs.



In the VR mode it is possible to modify various parameters of the VR rendering in order to show or hide certain anatomical structures.

5.12 Maximum intensity projection (MIP)

To quickly go to a MIP view press the **<Z>** key. The viewer will display by default a thick MIP view with a 5 mm thickness of the slab. The other possibility is the select with the mouse the MIP mode from the upper right side of the viewport. Here, the user can also select average IP (avIP) and minimum IP (minIP). To go back to the original image, double click the left mouse button with **<Ctrl>** and **<Shift>** keys pressed at the same time.



Slab MIP showing cerebral and neck vessels on an angio CT study.

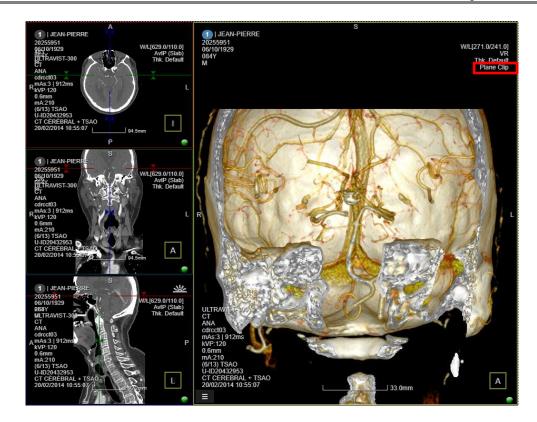
5.13 Sculpting tools

For better visualization, sometimes it is required to remove unwanted structures from the image, such as bones for example. This can be achieved in several ways, using the following tools:

Clipping with elliptical shape or with a plane. This button is available in the upper right side of the VR viewport (see the third figure below)

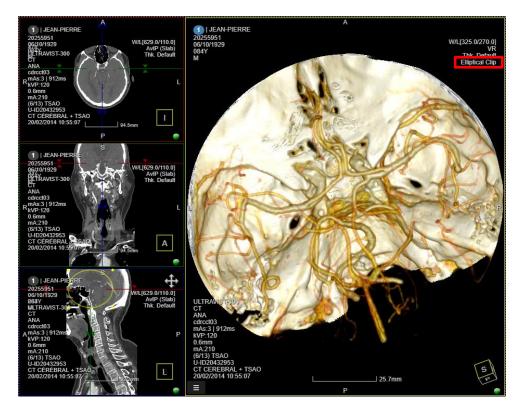
- Freehand in: removes what is inside the shape drawn with this tool
- Freehand out: removes what is outside the shape drawn with this tool
- Knife: draw a line and then double click on the side you want to remove from the image

The clipping tools are available from the upper right corner of the viewer in the VR mode. Select the plane clip and move the cross-hair in the MPR views to the desire location.

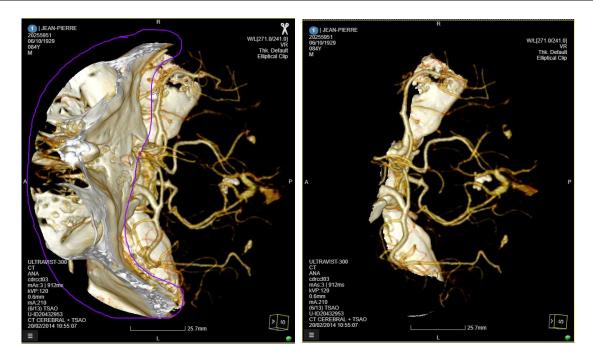


Plane clipping showing a cut through the VR image.

Select the Elliptical clip and resize/reposition the yellow ellipse on the axial, coronal and sagittal views.



Elliptical clip helps at isolating and better visualizing a volume of interest (VOI), such as the Circle of Willis.



Freehand sculpting tool helps remove the cranium bones to reveal the cerebral vessels.

To undo a cut, go to the Annotations panel and remove the sculpting operation. The viewer will show the initial image.

5.14 DICOM print on film

In the Diagnostic Viewer, users user can access the DICOM Print tool in multiple different ways:

1) through the burger menu, or 2) clicking with the RMB on the viewport, and selecting the DICOM Print tool icon; otherwise 3) from the same icon in the study panel on the left side of the screen.

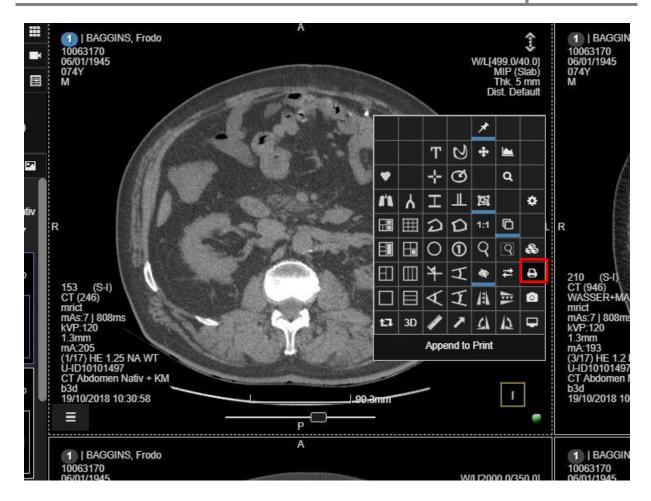
Using the icon in the study panel will show the DICOM print volume selection tool, as in the picture below.



Click on the printer icon on the left to display this menu. The user can set the volume to append for printing use the From/To slider. Adjust W/L and set more options in the drop down menus below.

When finished, click on Append to Print to launch the DICOM Printer layout manager.

It's also possible to add to the printing queue a single slice or image selecting it from the current layout: use the burger menu or RMB tool menu to access the Append to DICOM Print tool. This will add the single slice selected to the queue. It is also possible to quickly add the slice to the queue by pressing **<Ctrl+P>** on the keyboard.



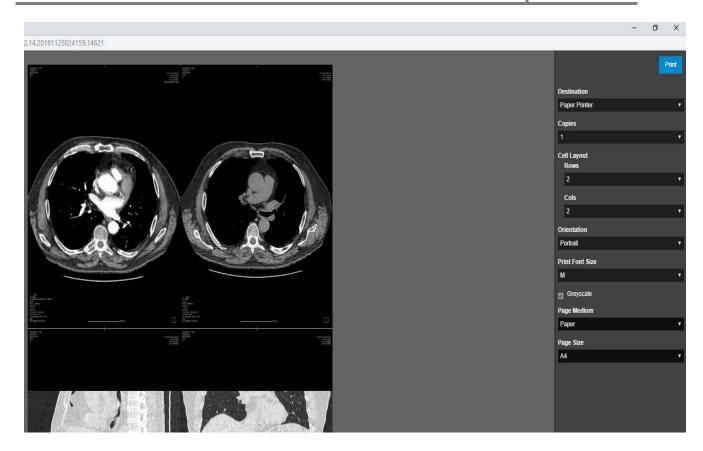
Append a single slice or image to the printing queue.

Once the user clicks on "append to print" the following printer menu will be displayed.

Here the user can set which printer to use, the number of rows and columns, print medium (paper, film, blue film etc), medium size (A4, A3, 14in x17in, etc), number of copies etc.

To delete an image, move the mouse on the picture and look for the X icon in the top left of each image. Scrolling down will show all the images that have been selected for printing. Click on the blue Print icon in the top right to print the file.

Printers can be setup from the Manage page, under the Gateways tab. See manual paragraph 13, 3Dnet Gateways.



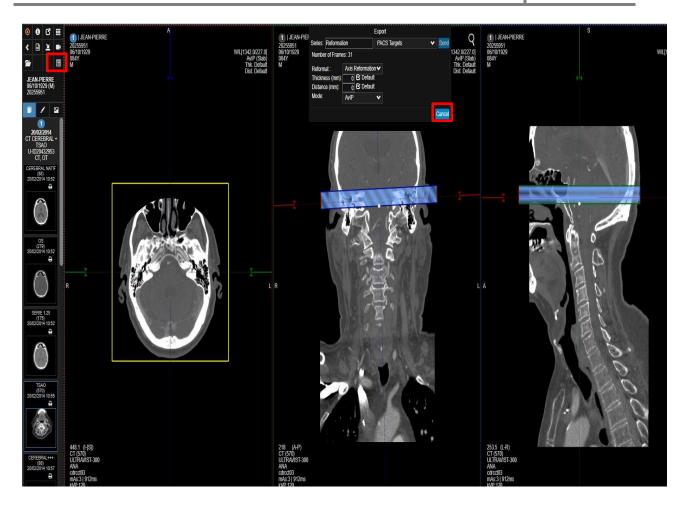
DICOM Print menu. Here the user can set printing layout and medium.

5.15 Create reformatted series

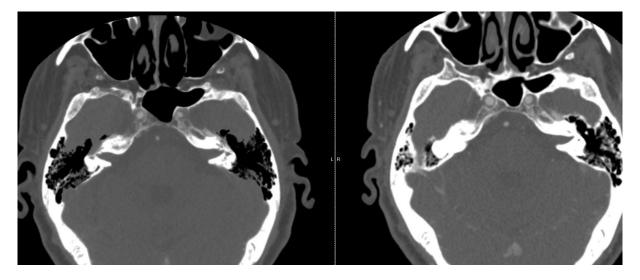
Using the Export tool (accessible through burger menu or RMB click) the user can create and save a reformat to PACS from a native acquisition. This enables the user to create and save a reformat in a new plane (coronal or sagittal from native axial, for example) or save a whole 3D MPR reconstruction starting from the native series.

Once the tool is selected, the following menu will be showed to the user. Use the slider to select From/To, set thickness, distance and mode (MiP, minIP, AvIP). Select a PACS target to send the reformat to.

In the following picture is a practical example. From a native axial CT series we applied the Three MPR Vertical layout. Then we used the reformation tool to create a new series showing a MIP reconstruction of the Mastoids. We tilted slightly the volume on the coronal view to have the perfect visualization of the anatomy on the axial view.



Export Menu.

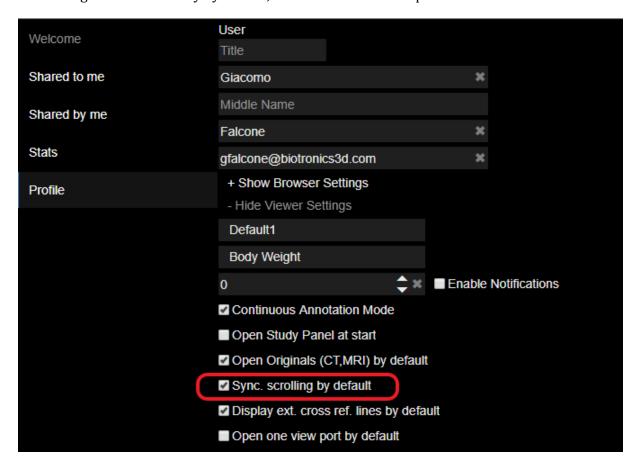


On the left side the Mastoid reformation (clear visualization of the anatomical structure). On the right, native acquisition with suboptimal visualization of the structure.

Once the reformation is sent to PACS, the "recently opened studies" icon in the top left of the viewer will flash intermittently. This means the series has successfully sent to pacs. Clicking with the RMB on the Recently opened studies icon will refresh the viewer and the new series will be available in the study panel on the left side.

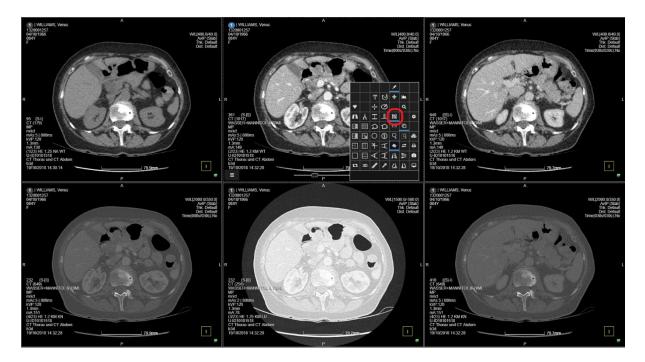
5.16 Synchronize studies in the viewer

3Dnet allows users to synchronize scrolling and reference lines on separate viewports. It is possible to enable synchronization in the scrolling between all series that share the same plane and belong to the same study by default, from the user viewer options.



Click on the highlighted tick box to enable automatic syncing between series in the same study.

The result will be the following:



All the series in the study are linked.

The synchronization for series with the same Frame of Reference will allow the user to scroll on one viewport and automatically have all the viewports synchronized. To enable this (if not enabled by default in the viewer settings) click on the "Linking On/Off" icon in the burger menu (or RMB button). Users can also overwrite the automatic sync and manually sync two acquisitions. To do this, follow these steps (assuming sync is already ON as a starting point):

- Scroll two series (sync is ON)
- Press **<L>** on the keyboard or Plane Link icon in the context menu to remove sync
- Scroll one of the two series to the desired level
- Press <J> on the keyboard or Link Series/FoR icon in the context menu to apply the new manual sync

This feature is useful when, within the same examination (same Frame of Reference), users want to apply a slight offset between two series (eg: series without contrast compared to series with contrast agent. User want to apply offset to balance patient movement occurred at the time of contrast medium injection).

By default there is no automatic linking between series sharing the same plane but belonging to different studies (current study against a prior for example). To enable this user can simply apply the Linking for these types of series as demonstrated below.



On the left: current Brain MRI T2W sequence; on the right: prior Brain MRI T2W sequence, highlighted by the red name in the top left of the viewport.

Enable linking by clicking on "Series Link" icon in the toolbox menu or by pressing <J> on your keyboard after selecting with the LMB the series you want to link (in the example: click with left mouse button on left viewport, click with left mouse button on right viewport and then press J on the keyboard. Start scrolling to see the images scroll in sync). Now the series will be scrolling, synchronized at the slice level selected manually by the user. This allows the best synchronization between series taken in different times that might not share the same starting point or other coordinates.

5.17 Synchronized image manipulation

3Dnet Medical features syncing tool for image manipulation. Other than scrolling, the user can sync Pan , Zoom , adjust W/L...

In order to toggle these tools on, the user can click on the corresponding icon in the burger menu. Synchronizing series will make the action propagate to other viewports, if in those viewports are displayed images taken in the same study/same plane/same study description DICOM tag.

The user can also adjust edges, sharpen or soften a picture and apply a denoise filter. See pictures below. These tools can be accessed from the drop-down menu in the top right corner of each viewport.

5.18 Select and add series in a new viewer page

It is possible to select two or more series that are already displayed on the screen and compare them in a separate page of the viewer. To do this, hold **<Ctrl+Shift>** and left click on the series to compare.



Arrows pointing at the edges of the viewports selected with the tool. Edges are highlighted in blue when selected.

When a viewport is selected, the edges will be highlighted in blue. Now that the selection is done, the user can release **<Ctrl+Shift>**, the selection will stay. Now, if the user presses **<S>** on the keyboard, a new page will be created, showing only the series contained in the viewports selected.



Comparative of viewports selected.

Now the user can analyse the images in a comparative view. Once done, to go back to the previous page, the user can press **<E>** on the keyboard. The page will be removed and the user will be taken back to the original view and layout.

5.19 Spine Labelling tool

The Spine Labelling tool can be accessed from the RMB tool menu, clicking on the highlighted icon.



The spine labeling tool.

To start labeling, click once on the first vertebra, then move the cursor to the following one and click again. Repeat this process until you reach the last one. To stop labeling, double click anywhere in the screen with the LMB. Users can edit the labeling already done by double clicking on the labels (entering editing mode, now the labels are blue instead of orange), deleting or moving a point or by changing the label for each point. To do this, move to cursor on the label and use the mouse wheel to change the label.

Labeling moving the cursor towards the bottom part of the screen causes the numbering in the label do increment. The opposite happens using the labeling tool and moving the mouse towards the top of the screen. In this case the number in the laber will decrement. (If a user starts labeling form the top, the labeling tool will start counting from C1. If the labeling is starting from the bottom of the picture, apply the first label (C1), position the cursor on the label, scroll once upwards and the labeling will switch to Co5. Following clicks going towards the top of the screen will progress as follows: Co5, Co4, Co3,... S5, S4, S3, L5, L4, L3... etc).

Hovering with the mouse on the labels will highlight the curve of the line that goes through each individual point.

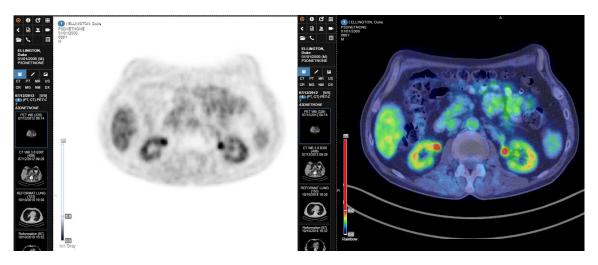


Label curvature.

5.20 PET-CT Fusion

Positron emission tomography (PET-CT) is a technique that combines PET images with CT images. Clinicians can analyse the functional imaging (PET dataset) and morphological imaging (CT dataset) together, to greatly improve clinical outcomes. 3Dnet Medical offers easy methods to perform PET-CT fusion, both manually and automatically (using a Hanging Protocol).

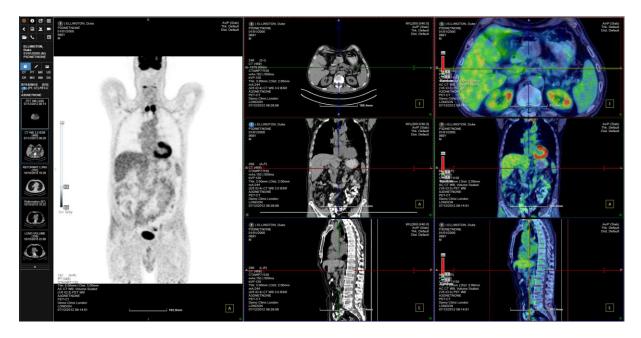
To manually perform the fusion, populate the Diagnostic Viewer with a CT acquisition. Find in the study panel the correlated PET acquisition, move the mouse on top of that series thumbnail and click using **<Shift+Left Mouse Button>**. The fusion will be performed in the viewer between the two series selected. The process works in the same way if first the user populates the Diagnostic Viewer with the PET acquisition, then uses **<Shift+Left Mouse Button>** on the CT thumbnail in the study panel.



On the left: user populated the Diagnostic Viewer with the PET acquisition; on the right: effect of the <Shift+Left Mouse Button> click on the CT acquisition thumbnail in the Study Panel (Fusion performed). The process works in the opposite way if the user populates the Viewer with the CT acquisition first, then clicks on the PET image in the Study Panel.

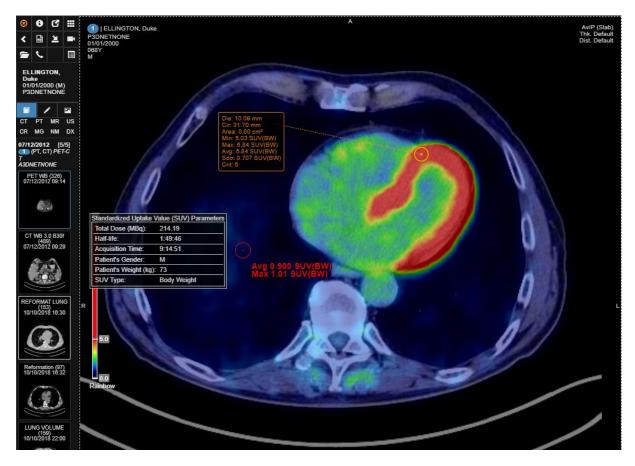
Users can also set Hanging Protocols to automatically perform the fusion whenever PET and CT images are available for the same study. To set this up, manually perform the fusion in the

Viewer, then locate and select the Hanging Protocol tool clicking on the button in the top left. Once the protocol has been saved, the layout saved will be replicated (with fused images) for future studies.



Hanging Protocol example: on the left, a coronal view of the PET acquisition; in the centre, a Vertical MPR layout of the CT acquisition; on the right, Vertical MPR layout of the fused (PET-CT) images.

In the example above, the Hanging Protocol is saving both the fusion and the layout (including the MPR layout) and recreating the same layout for every subsequent patient.



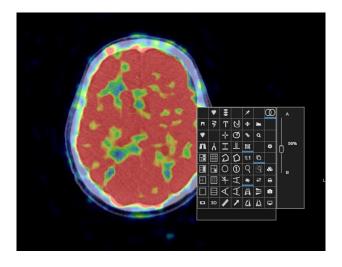
The picture above demonstrates: SUV parameters tab; SUV values in ROI attached to mouse movement (red circle and annotation); SUV values in ROI in a static location (orange tab).

Once the fusion is performed, users can adjust the slider on the left of the viewport to change the fusion threshold. At the top of the slider is an icon : click it to display the SUV parameters tab. In this tab, users will find: Total Dose (MBq), Half Life, Acquisition Time, Patient's Gender, Patient's Weight (kg), SUV Type. At the bottom of the slider users can select which colormap to use (Greyscale, Rainbow, etc).



Adjust the slider to modify the fusion threshold. Click on the icon on top to open the SUV Parameter tab. Click on the text at the bottom to change the colormap (Rainbow in the example).

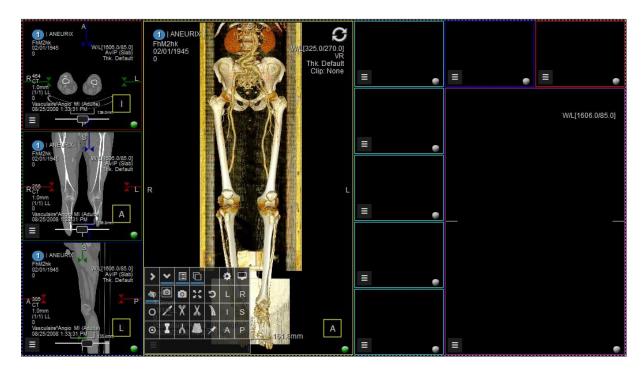
Use the Circle Annotation tool to draw a static ROI and get information about the SUV in that area of interest. Use the keyboard shortcut <0> to display the SUV values in a ROI (resize the ROI by holding <shift+Mouse Scroll Wheel>). Use the keyboard shortcut <U> to display SUV values in a pixel. <U> and <Q> shortcuts will display the SUV values where the user is currently pointing the cursor (opposed to static Circle Annotation). To adjust the fusion overlay, use the icon in the context menu and click on the vertical slider.



Click on the fusion icon in the top right of the context menu, then drag the slider to change the fusion overlay.

6 CT Vascular

CT vascular is an advanced clinical application module. To launch this module, click on the button in the burger menu. The software launches a slightly different user interface, as shown in the image below:

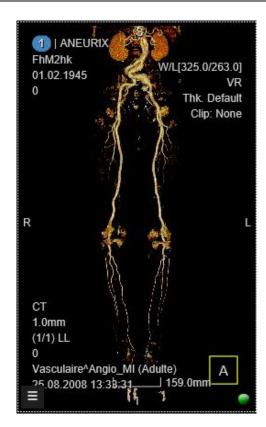


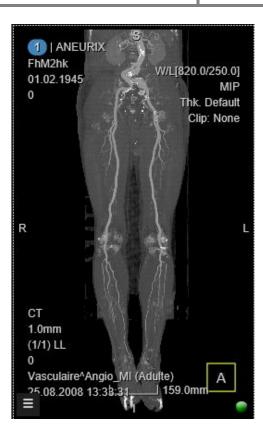
CT Vessel module.

As one can notice, the burger menu contains a different set of tools, among which we have:

- Bone segmentation and removal tool
- Vessel segmentation tool
- Table segmentation and removal tool
- Vessel tracker tool: extract the centerline of a vessel for stenosis analysis.

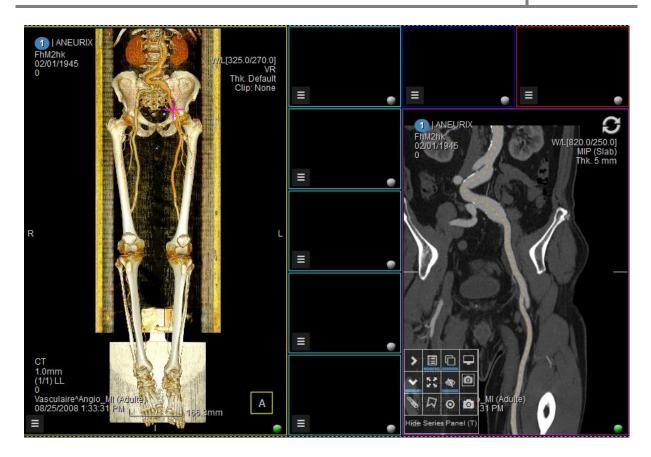
To remove the table and the bones on a CT VR image, select the appropriate tool and click repetitively on the table and on the bone respectively, until these structures are removed completely. The end result is shown in the figure below.





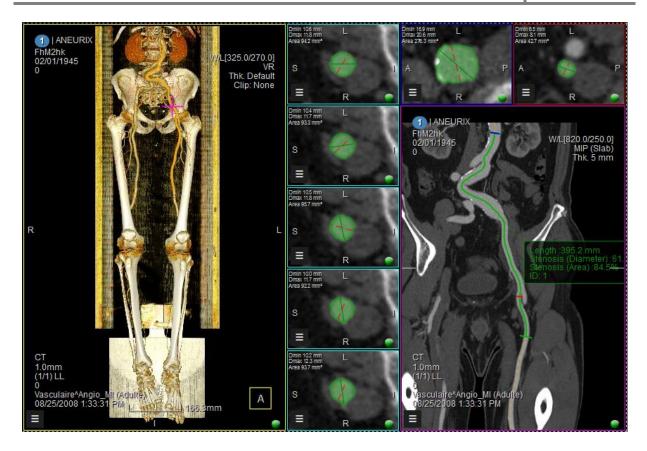
Left: VR image without bones and table. Right: MIP image without bones and table.

The vessel tracker tool is used to segment the vessel and extract the centerline. Click on the start of the vessel and drag the mouse over to the end of the vessel and then release the left mouse button. After computing the centerline, the software display a stretched CPR image.



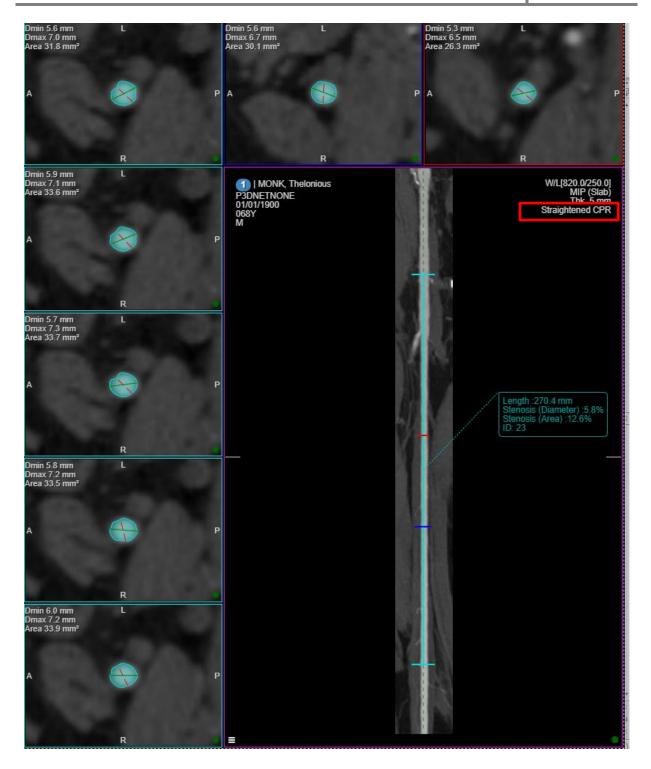
Centre line extraction and stretched CPR display.

To perform the stenosis analysis, enter the burger menu, click on the stenosis tool and then, with the left mouse button pressed, draw a line on the vessel segment under analysis and release the mouse. The software will automatically identify the thinnest part part of the vessel (depicted with red line in the image below) with reference to the blue line level (the reference). The stenosis ratio is computed and displayed, together with the vessel cross-sectional diameters and surface area.



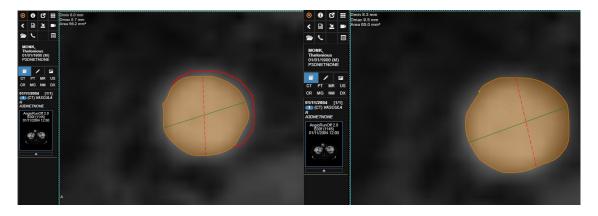
Stenosis analysis: the stenotic part is depicted with the red line, while the reference is depicted with blue on the stretched CPR image.

From this view, the user can select between Stretched (as in the picture above) or Straightened CPR (see next picure).



From the highlighted menu the user can switch between Straightened and Stretched CPR.

Using the Contour Correction tool, users can manually correct the automatic contouring performed by the software. Select the tool from the context menu by clicking on the Correction icon. It is possible to operate the manual correction from the viewports with the cross section of the vessel (around the CPR viewport). Users can also double click on one cross section viewport to maximise it and better display the contoured surface area, as displayed in the picture below.



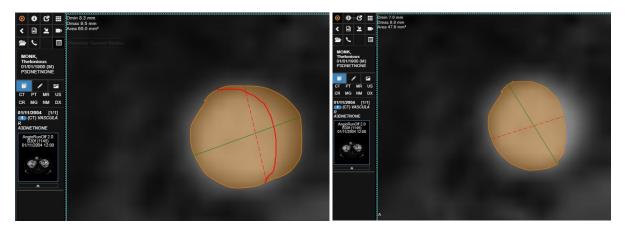
Maximed cross section viewport demonstrating the contour. The orange circle displays the surface area automatically highlighted by the software. In the left picture: the user manually traced a corrected contour (red curve line outside the orange area); In the right picture: new contour obtained by double clicking on the orange area. In this example the user increased the contour area by drawing an additional portion and adding it to the area.

To correct the automatic contour, select the tool then draw on the orange cirle (or outside). To modify the automatic contour, double click on the side you wish to keep. In the example above:

- Draw a curve line around the default automatic contour to highlight a portion of the vessel to add to the counterd area
- Double click on the side you wish to keep

To reduce the contour, follow the steps below:

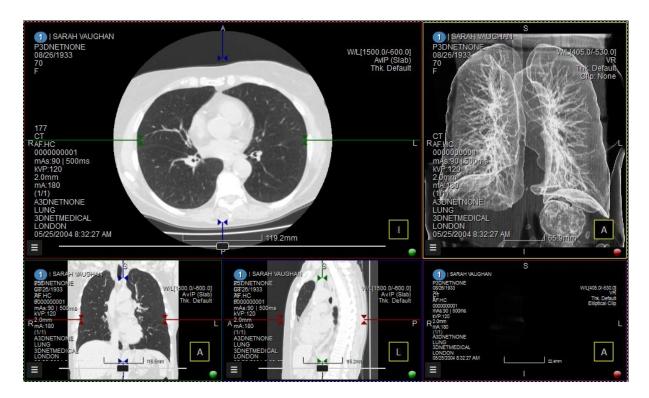
- Draw a curve line inside the orange area to highlight a portion to exclude
- Double click on the side you wish to keep (in the case demonstrated in the pictures below, click on the left portion of the orange area identified by the red curve line)



Picture on the left: draw the new border for the contour within the orange area (automatic surface detected by the software); Picture on the right: double click on the portion you wish to keep (user double clicked on the left portion). See new corrected contour.

7 CT Lung

The CT Lung advanced module is used for pulmonar nodule segmentation and measurement. This module is launched by selecting the Lung module button from the burger menu.



CT Lung user interface.

When a nodule is found, this can be segmented by using the region growing segmentation tool from the tools menu. With the left mouse button pressed, draw an ellipse around the nodule and then release the mouse. The software segments out the nodule and reports the size and HU statistics, as shown in the image below.



Nodule segmentation.

After using the Region Growing tool, a chart will appear. This chart carries valuable information regarding the lesion contoured (Volume, Diamenter, Surface Area, Doubling Time, etc).



Region Growing segmentation tool, zoomed in.

8 DCE MRI

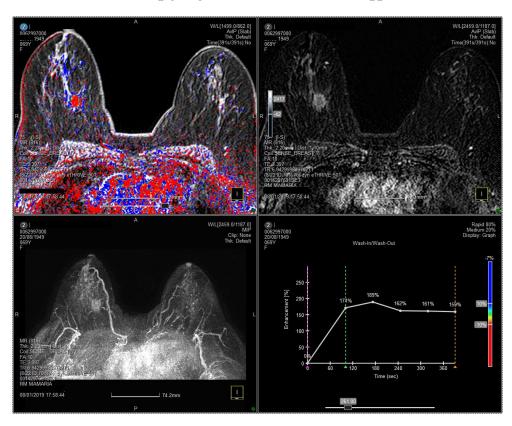
The technique of dynamic contrast enhanced (DCE) magnetic resonance imaging has been widely used in clinical practice. In this technique, multiphase MRI scans are taken following the intravenous injection of a contrast agent. It measures T1 changes in tissues over time, after bolus administration of gadolinium.

Analysing and quantifying the contrast enhancement over time is the major goal of DCE imaging. As a general principle, the degree of contrast enhancement depends on regional blood flow, the size and number of blood vessels quantified by their surface area per unit mass of tissue, and their leakiness or permeability.

To access this module, click on the KiM (Kinetic Modelling) icon in the tool box menu.



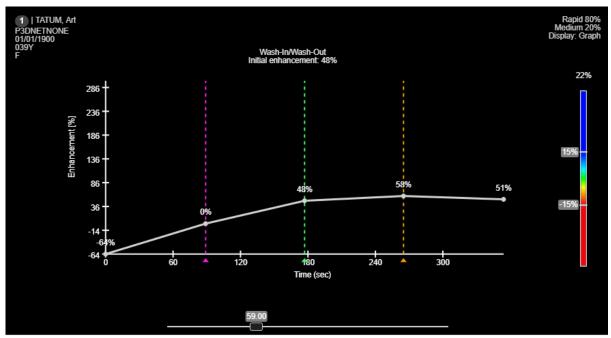
Click on the Kinetic Modelling (KiM) icon in the tool menu to trigger the DCE MRI module.



This is the default layout that triggers when clicking on the KiM icon.

Clicking on the KiM icon triggers this 2x2 layout.

- Top left: view parametric map of the enhancement patterns
- Top right: dynamic images with the baseline subtraction
- Bottom left: MIP Volume Rendering of the subtraction
- Bottom right: graph of the enhancement curve (wash-in/wash-out) for the pixel in which you are focusing. When instead a ROI is drawn, this viewport will display a table with information regarding the voxels in that ROI (more on this later)



In the bottom right viewports, users can manually set a baseline, early enhancement and late enhancement markers

- Use the Purple line to set a baseline value for subtraction
- The Green line is used to set the end of the early enhancement time (initial phase)
- The Yellow line represents the end of the late phase

Below the intensity curves is a slider that is used to set the background noise level. The higher the background noise threshold, the higher the minimum level of SI needed in order to be taken into consideration for the calculations. Pixels with signal intensity values lower than this threshold will not be coloured in the upper left image and will not be included in the analysis.

Curves in the graph will change on the fly, describing the values of each individual voxel where the cursor stops. Alternatively, users can select a fixed spot using the KiM Tracking (<Ctrl+A> shortcut). The graph will display a curve related to that single spot, even if the cursor is moved.

The colour bar to the right of the graph represents the following:

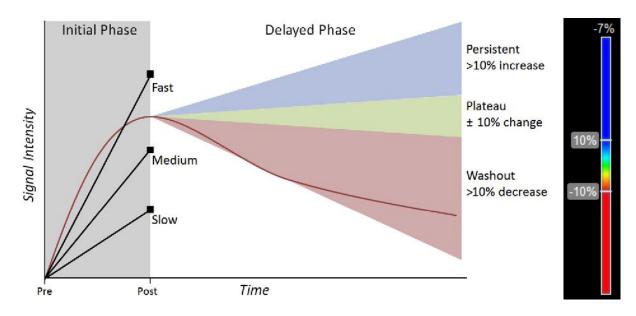
- Blue: persistent
- Red: wash-out
- Between blue and red: plateau

Users can manually change the thresholds for what will be considered Persistent, Wash-out and Plateau with the sliders on the coloured bar. This module can also keep track of the rate at which SI is increasing or decreasing: users can manually set a threshold for what we want to consider Rapid change in the SI or Medium change in the SI. This can be done manually through a drop down menu in the bottom right viewport.



Change the enhancement thresholds for what will be considered fast and medium initial phase.

In our example, increases between 20-80% will be considered Medium rate of change; values over 80% will be considered Rapid. Changes in the threshold will be reflected on the table chart (more on this below) and visually in the coloured overlay in the top left viewport (the quicker the change in SI, the more intense the blue or red will be).



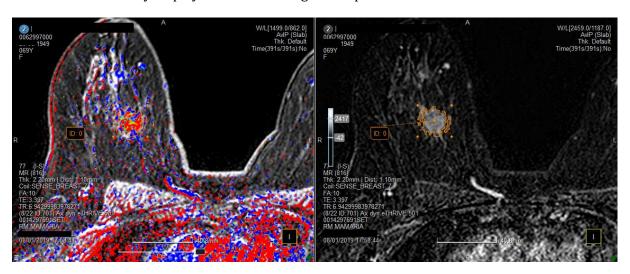
Left: Definition of semi-quantitative variables (taken from Rahbar et al., Multiparametric MR Imaging of the Breast, Magnetic Resonance Imaging of North America, 2016. Right: slidebar in 3Dnet Medical for changing the persistent and wash-out thresholds.

The curve annotated with Slow represents a pixel that did not increase to level of significant enhancement on immediate contrast-enhanced series. This pixel would not be coloured in the parametric map and will not be included in the analysis, regardless of pixel value on delayed contrast-enhanced series. Medium and Fast curves are those which increase faster than 20% or 80% respectively (as it is set up in our analysis), compared with the baseline, in the initial phase (early post-contrast).

Pixels that did increase to level of significant enhancement and continued to increase on delayed series to a value more than 10% higher than its value on immediate contrast-enhanced series will be coloured blue to represent persistent enhancement.

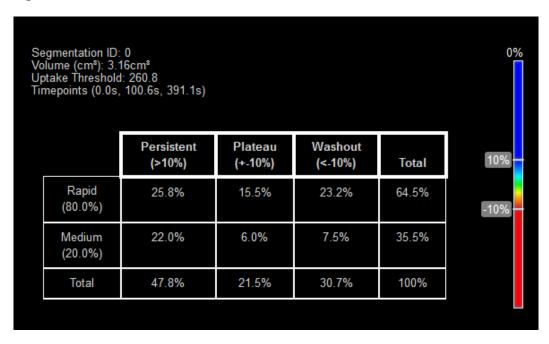
Pixels that increased to level of significant and then decreased by more than 10% on delayed contrast-enhanced series will be coloured red to represent significant and washout enhancement.

Use the KiM Region tool to draw a ROI and measure these changes in that ROI. Drawing this ROI will automatically display in the bottom right viewport a table with the values in that area.



Breast lesion segmentation for enhancement patterns analysis.

Once the ROI has been calculated, the bottom right viewport will display a chart similar to the following.



This chart is referring to the ROI that was drawn in the top left viewport.

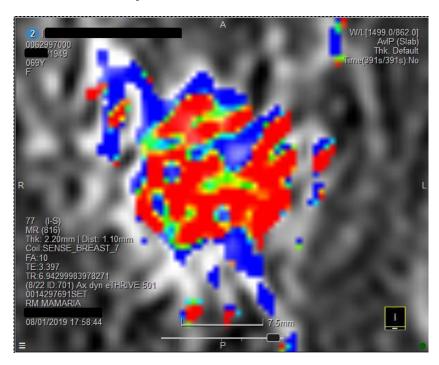
This viewport displays:

- Segmentation ID: number of the segmentation. The first ROI that is drawn will be number 0. The following, number 1, etc
- Volume: sum of the areas of all the voxels contoured by the ROI
- Uptake Threshold: value of the uptake threshold
- Timepoints: the timepoints registered in the DICOM tags. Each timepoint is corresponding to the beginning of an acquisition
- The chart (see below)

If we inspect this change in percentage, using 80% as a threshold for Rapid change and 20% as threshold for Medium increase, we see the following results:

- 47.8% is Persistently changing (growing). Of this:
 - o 25.8% Rapid rate (manual threshold set to 80%)
 - o 22.0% Medium (manual threshold set to 20%)
- 21.5% is Plateauing. Of this:
 - o 15.5% Rapid in the initial phase
 - 6.0% Medium in the initial phase
- 23.2% is Washing-out. Of this:
 - o 23.2% Rapid in the initial phase
 - o 7.5% Medium in the initial phase

The faster is the enhancement in the early post-contrast phase the more opaque will be the colour in the parametric map for that pixel, as shown in the image below. For example, a pixel shown with transparent blue depicts a medium enhancement, while a fully opaque one exhibits fast initial phase. Similar is for red pixels.



Zoom in shows lesion having significant initial enhancement (bright colours, opaque pixels) and mixed pattern of washout, plateau and persistent delayed enhancement.

9 ADC Map creation

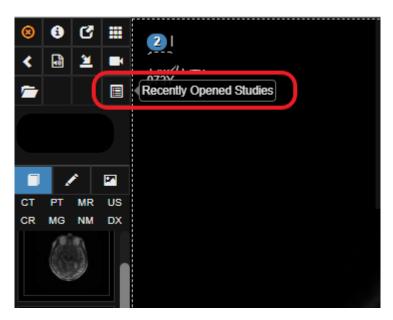
3Dnet Medical allows users to create ADC Maps from diffusion images. This is done in the viewer, by loading on the screen a diffusion image and using the Export Tool in the RMB tool menu or burger menu. Once the tool is selected, a menu like the one in the picture below will appear.



From this menu the user can create the ADC Map by setting the B value range and the name for the new series.

In the image above, it is possible to see the image that has been selected ("AX DIFFUSION") from the study panel and the Export menu. The user can customize the new series that is going to be created: series description (name) can be set in the Series field (in the example, it is "Reformation"); select which DICOM target this series will be sent to (a default PACS target in the image); a range of B Values; a Threshold to optimize the noise in the picture; option to include an exponential ADC Map in the reformation (doing this will create two separate series).

Once the new sequence is completely set up and ready to be exported, click on the blue "Send" icon. Processing of the map will start. Once the processing is completed and the new series reached the PACS target, the icon "Recently Opened Studies" in the top left of the screen will start flashing in white. By right clicking the icon, the viewer will re-load, showing the new series in the Study Panel.



Once the processing is done, RMB click on the highlighted icon to reload the viewer and see the new series in the study panel.

10 Calcium Scoring

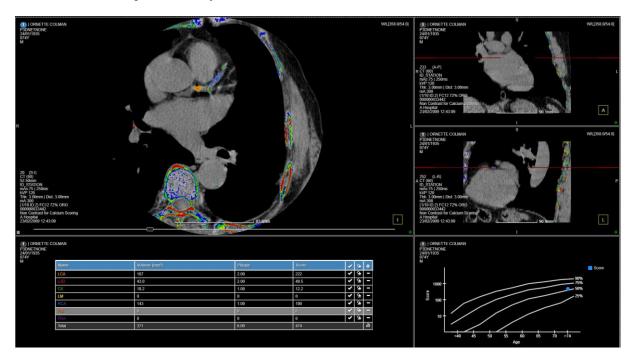
Assessment of coronary calcium burden is widely used as a prognostic risk indicator of a cardiac event. 3Dnet Medical CT Calcium Scoring allows accurate visualization and easy quantification of calcified coronary plaques.

Lesions are highlighted with a coloured overlay on a non-contrast enhanced series. Scoring is performed by contouring the lesion in one of the main coronary branches using the corresponding label (picked from the table at the bottom of the screen). The score table automatically updates when a new lesion is contoured. It provides a comprehensive analysis of: number of plaques, calcium volume, calcium mass and the correlated score.

This module is triggered by selecting the Calcium Scoring icon from the context menu. By default the layout will display:

- Three MPR views of the acquisition
- Score table
- Risk graph

See below an example of this layout.



Default Calcium Scoring Layout: 3 MPR views; Scoring table; Risk graph.

Select a coronary branch label to enable the contouring for that specific branch. Manually draw a circle around the lesions. The information regarding value (mm³), number of plaques and score will be immediately updated in the table.

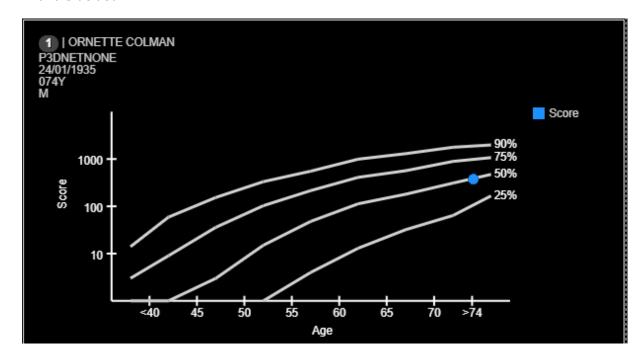
If an entire coronary branch does not present any lesion, use the $\stackrel{\checkmark}{}$ icon to set the score to zero for that branch. If not all the coronary branches present lesions, users can contour lesions in each branch, then use the blue tick icon $\stackrel{\checkmark}{}$ to set all the remaining rows to zero. This is useful

when only a limited number of branches show plaques, while the rest of the branches appear clean. To reset the whole table to default value (empty cell), use the Clear Table icon .

Name	Volume (mm²)	Plaque	Score	4	<u>\$</u>	+
LCA	167	2.00	222	~	<u>•</u>	
LAD	0	0	0	✓	<u>◆</u>	
CX	197	3.00	262	✓	<u>◆</u>	
LM	0	0	0	✓	<u>•</u>	
RCA	18.2	1.00	12.2	~	<u>◆</u>	
RM	1.95	1.00	0.651	✓	<u>\$</u>	_
PDA	0	0	0	~	<u>•</u>	
Total						#

Risk table. This table is automatically updated every time a new plaque is contoured.

To calculate the risk factor using the values in the table, click on the Update Graph icon in the bottom right corner of the table. This will display, as a result, the risk factor in the risk graph with a blue dot.



Risk graph that plots the Score vs. Age of a patient. The blue dot individuates the Risk factor.

Once the graph is drawn, it automatically updates when a contour is performed on a new lesion.

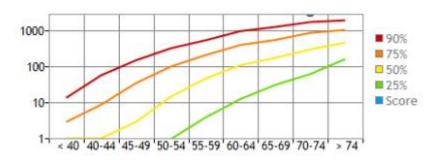
The Coronary Artery Calcium score is calculated based on the number of plaques, area of plaques and peak tomographic density for each plaque. CAC score in each coronary artery is equal to the sum of all lesions for that artery and the total CAC score is equal to the sum of the score of each artery. This score is then adjusted according to patient's age and gender. Based on this, a percentile of risk is assigned.

Score = Area x Weighting x (slice Separation / mm).

- Weighting = 1, HU within [130, 100]
- Weighting = 2, HU within [200, 299]
- Weighting = 3. HU within [300, 399]

• Weighting = 4, HU over 400

Percentile Rank and Mean EBCT Coronary Artery Calcium Scores in Asymptomatic Males



Reproduced from Hoff et al. The Am. J of Cardiology 2001; 87(12):1335-1339.

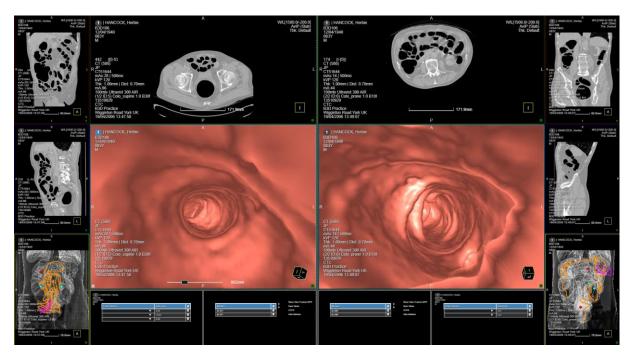
Percentile Rank and Mean EBCT CAC scores.

11 CT Colonoscopy

3Dnet Medical offers a complete CT Colonoscopy Advanced Visualization module that features a range of automated and manual tools to perform colon segmentation, centreline extraction and navigation, tracking and measurement of clinical findings, etc. A CAD pre-processing Module can be added to the standard CT Colonoscopy application.

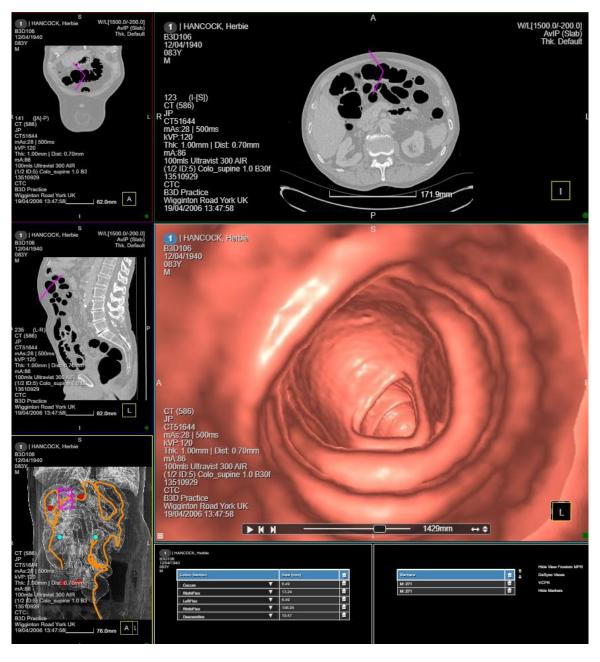
Select the CT Colonoscopy Module from the context menu using the dedicated Colonoscopy icon Clicking on the icon will trigger the Colonoscopy layout in the active viewport. Users can load the Colonoscopy Module in multiple viewports (useful to display a supine and prone acquisition side by side for a direct comparative). In the following screenshot, a supine (left hand side of the screen) and prone (right hand side of the screen) acquisitions are opened in two separate instances of the CTC Module, side by side, for immediate comparative. The Colonoscopy Module displays:

- Three MPR views of the volume acquired
- A fly-through endoluminal VR
- A visualization of the centreline extracted with display of colon segmentation. This
 viewports also displays reference points for lesions measured (red dots) and points of
 interest (blue dots; these markers indicate formations that require further analysis;
 these might be lesions and measured at a later stage). If the CAD pre-processing is
 activated, this viewport will also display markers for the CAD findings (green dots)
- A measurements table, that displays the length of the lesion measured and the colon segment in which it is located
- A markers table, that collects and displays all the points of interest saved



Two CT Colonoscopy instances are open side by side (left: supine; right: prone) for easy and effective comparative. Each instance presents MPR views, fly-through VR, colon segmentation with display of the extracted centreline, measurements/markers table.

The centreline and segmentation is automatically performed and presented to the user. Press **Spacebar>** on your keyboard or click with the **Right Mouse Button>** to start the fly-through in the VR viewport. By default, when the fly-through is paused, a crosshair will be displayed in the three MPR views to precisely locate the point in space. The crosshair will fade after a few seconds to give the user a clear visualization of the anatomy. The crosshair is not visible in the MPR views during the fly-through (with default settings). To enable this behaviour, users can switch on the Sync Views feature from the Markers Viewport: when this feature is enabled, a crosshair will be displayed on all MPR views and its position will be updated on the fly, following the movements of the fly-through. Clicking on a point in space in one of the MPR viewports will synchronize the position of the other MPR views, as well as present that point in the VR viewport (fly-through).



View of the CTC module: clicking on a measurement or marker will synchronize the position in MPR viewports and fly through viewport. Use the control bar in the fly through viewport to paly/pause, jump to end/start, reverse and adjust speed.

Users can follow the fly-through end to end, jump to Start/End, reverse the direction and adjust the speed using the control bar at the bottom of the VR viewport. The control bar displays a number that represents the distance (in mm) from the starting point. If a suspicious formation or a lesion is spotted, users can:

- mark it using the Colon Point tool using the icon in the context menu (this will create a new entry in the Markers table at the bottom of the screen)
- measure it with the Colon Ruler tool in the context menu (this will create a new entry in the Measurements table; users can manually select the colon segment)

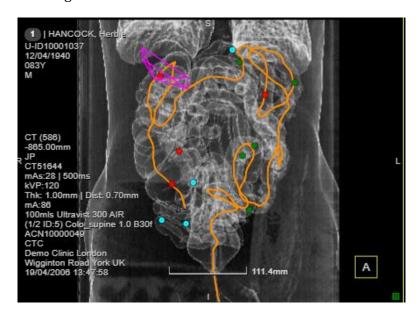
Once the measurements and markers are set, users can check them one by one selecting each entry in the Measurements tab and in the Markers tab. Select an entry from these two tables and display that marker or measurement in all viewports for quick and effective analysis.



Measurement and Markers table. Click on each row of these two tables to find that point in space in all viewports. Left hand side: measurements table; Right hand side: markers table.

In the Markers viewport (image above, right hand side) users can access a list of options:

- Show Frustum MPR: displays frustum on MPR views
- Sync views: on the fly synchronization of the crosshair in MPR view following the movement of the fly-through
- VCPR: enables the VCPR view (more on this later)
- Hide Markers: hides markers from the centreline and segmentation view
- Hide CAD (only available if CAD pre-processing is enabled): hides CAD from the centreline and segmentation view



Measurements, markers and CAD findings are displayed as red, blue, green dots.

In this viewport users can see the extracted centreline and segmentations (orange line). The dots displayed represent measurements (red), markers (blue), CAD (green). Click on colon segments to display the centreline for that segment. Users can enable the VCPR feature to switch to VCPR view.

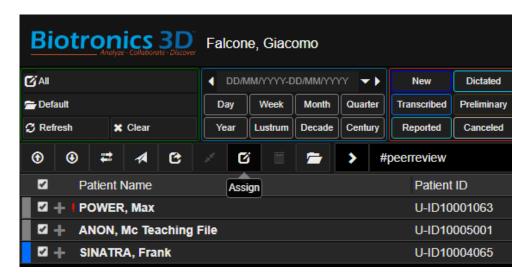


VCPR view: run the fly through to inspect the endoluminal space in VCPR visualization.

The VCPR viewport will displays a VCPR image, cutting the endoluminal space in two halves and displaying it in a 2D plane. The VCPR viewport will be synchronized with the movement in the fly-through in the central VR viewport. Running the fly-through will cause the VCPR view to roll towards the beginning or end of the segmentation, depending on the direction followed by the fly-through.

12 Peer Review

Peer review is a key tool to improve and maintain the level of medical outcomes. 3Dnet Medical offers features and tools to enable this workflow. A list of studies can be assigned either via HL7 or manually to one or more specific users in charge of peer reviews (usually senior level Reporting Physicians). To manually assign studies to a peer reviewer, click on the Assign icon at the top of the study list, then select the field "Peer Reviewer" and select the preferred user. In the example, the user performed a search for all the studies marked with the #peerreview.



Select and Assign studies for Peer Reviewing.

Once the studies are assigned, the designated user will be able to access a dedicated Peer Review Worklist/Folder or simply filter the study list using the Peer Review column. Clicking on a reported study in the study list will display the following layout.



Peer Review layout. Users can read relevant clinical history documentation on the left hand side, read the report in the middle part of the screen and use the comments section on the right hand side to write notes. Users can also select one of the suggested options (customisable per Organisation) to express an opinion on the outcome.

On the left hand side, the Peer Reviewer finds all the information regarding the clinical history of the patient: study and prior browser, attached documents, notes, snapshots, interactive notes (chat). The middle part of the screen is dedicated to the report that was created by the colleague. On the right hand side is an area used to pick one of the options suggested (in the example: 1. Concur with interpretation; 2. Discrepancy in interpretation, understandable miss; 3. Discrepancy in interpretation, misinterpretation.) and add comments. The options suggested can be customised per Organisation and presented in different ways (custom number of options, custom ordering of the options, custom text for each option). Save and Submit at the bottom of the screen when the review is completed.



Peer Review managing tab.

Above is a screenshot taken from the Peer Review managing tab. Create new entries such as the ones demonstrated to give the Peer Reviewer more options. Click on each row to enter the settings for each entry, to change the title, description and ordering in the list.

13 Image streaming and compression

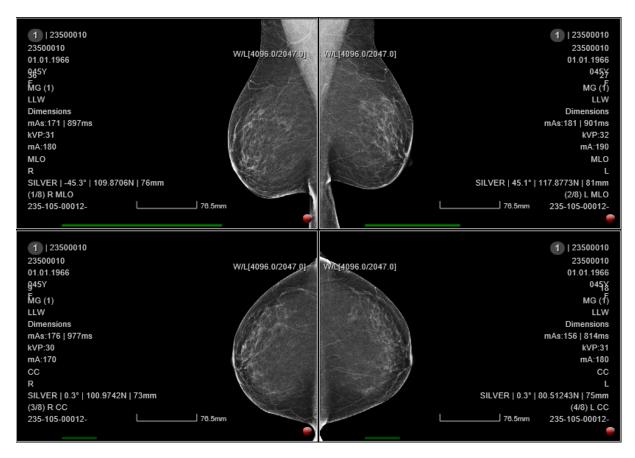
As mentioned before, 3Dnet Medical uses streaming to serve clients with the requested images. The images can be streamed uncompressed, lossless compressed or with lossy compression. The streaming is done progressively, until full resolution is displayed on the client computer. Note the green or red dot in the lower right corner of all viewports. If the dot is red, it means that the image has not been transferred at full resolution yet. If the green dot is displayed, the streaming is complete and the image is displayed at full diagnostic quality.

To facilitate teleradiology on low network bandwidths, 3Dnet allows the user to configure the application to compress the images before sending them from the server to the client workstation. The compression algorithm is JPEG with a compression rate up to 144:1 (lossless and lossy compression). Click on the gearwhell tool from the viewport toolset (burger menu or right click in the viewport). This will open a compression slider. Select Lossless if lossless compression is desired or click on Lossy and then adjust the compression rate with the slider. The picture below shows a compressed CT image with a JPEG compression quality Q=5. Increase the quality gradually from the slider until the image is improved.



Compressed image with very low quality. Note the pixelated aspect of the CT image.

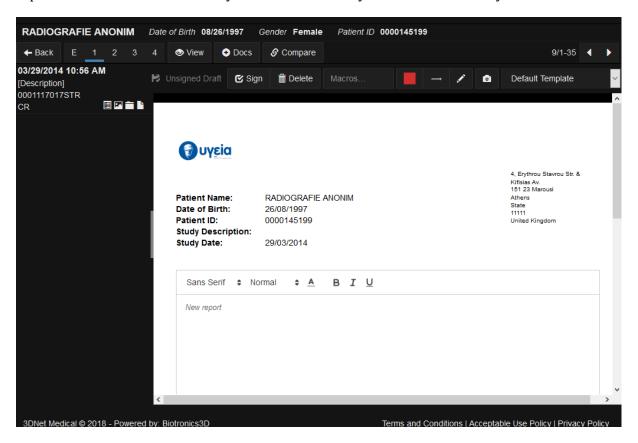
For large images, such as MG or DX/CR, the transmission is performed using progressive streaming (refinement). First, a low resolution image is sent to the client for fast visualization, while the rest of the content is sent in the background, until the full resolution is displayed. The process usually takes 1-5 seconds, depending on the size of the image and network bandwidth. A slide bar is displayed in the viewport to show the progress of the streaming.



Progressive refinement of mammography images. Note the green bars in each of the four viewports denoting different stages of transmission in progress.

14 Reporting module

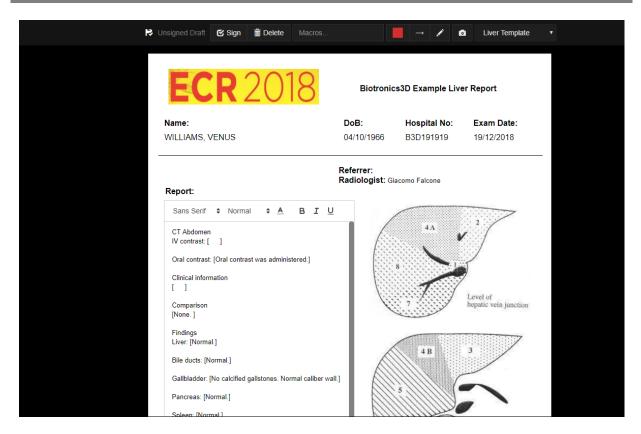
3Dnet Medical has a built-in reporting module with an integrated text editor used to type in the report. This editor is automatically loaded when a study is clicked in the study list.



Text editor for typing the report, with option to add images or to select the desired template.

To select a certain template, go to the Template button and pick the desired report template. It is also possible to include a predefined text from the Macros box. Macros are blocks of text set up in order to offer users the ability to quickly add a standard text in the reporting textbox. Macros can be assigned to a specific Modality or Study Description, so that only macros relevant to the currently opened study are displayed (only MRI macros for MRI studies, only CT macros for CT

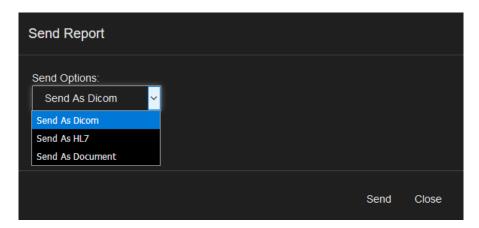
macros, etc). Click the Unsigned Draft button to save the result, or the to add images to the report. The images can be selected from the snapshots in the Snapshot panel, or they can be loaded from the local disk.



An example of report template for liver MRI.

After the text and/or images are inserted, click the **Sign** button to sign the report preliminary or final. For preview, click the **View as PDF button**.

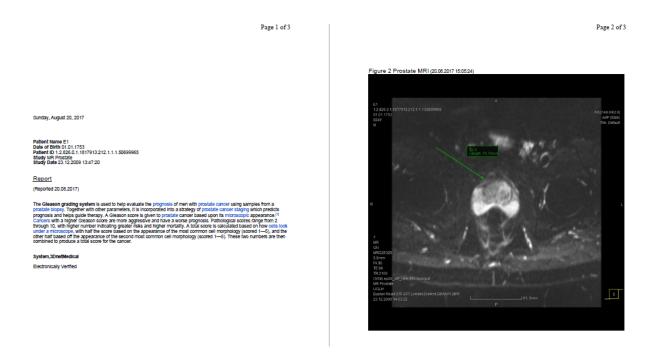
The report can be sent to a HIS/RIS system or to a DICOM system by clicking on the **Send** button as shown below. Here the user has the following sending options: a) HL7 (send the report with a HL7 ORU message); b) SendAsDICOM (encapsulate the report as a DICOM file); c) send as document. The system can also be configured to forward the report automatically via HL7 ORU messages. The sending process is triggered by the final signature event.



Sending a report on demand, from the web interface of 3Dnet Medical, to a 3rd party software system via HL7 or DICOM.

Below it is shown a typical report generated by 3Dnet Medical, with a key image added to it. The header of the report is generated automatically and contains metadata information from the

study DICOM header. Any information from the DICOM header can be added to the report. Click **Print** button to print the report on an office paper printer.

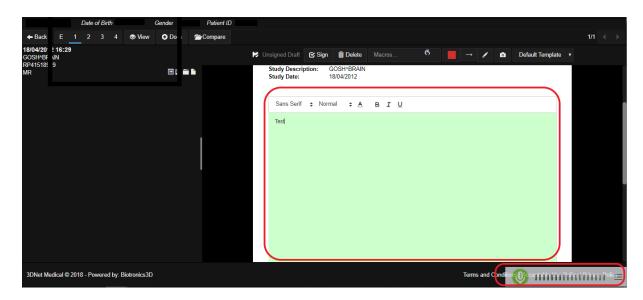


A final report with image attached to it, in PDF format (2 page display).

14.1 Voice recognition

3Dnet Medical users can report using a full zero-footprint web Voice Recognition. Our software fully integrates with Nuance Speechkit dictation.

This integration makes it easy for clinicians to efficiently and quickly report a higher number of examinations in a shorter time, enabling users to take advantage of powerful features such as adding a pre-defined block text, linking actions to specific words ("full stop, next line" etc,), sign report as finalized with a button press on the speech mic, open next patient with a button press on the speech mic, etc.

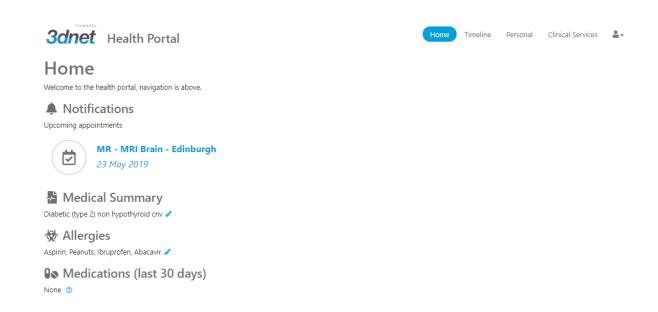


Voice Recognition interface while the tool is in function.

The interface overlay in the bottom right corner indicates the VR is enabled. The volume bars will light up when the microphone senses speech. The report interface turns green when the user is talking, and text will appear on the screen on the fly. Users will be able to easily report and perform many actions without having to click on the screen. This tool is user profile based, so users can carry their profile options across workstations.

15 3Dnet Health Portal

The 3Dnet Health Portal can be used by patients on their computers or or their mobile devices (tablets or cell phones). There is no need to download and install any software application on your device. Just open your preferred web browser and type your username and password. This portal empowers patients to see their images and results online through a secure login, thus eliminating the production of CDs or films for the Organization. The interface is intuitive and easy to use.



Home page of the mobile HTML5-based portal.

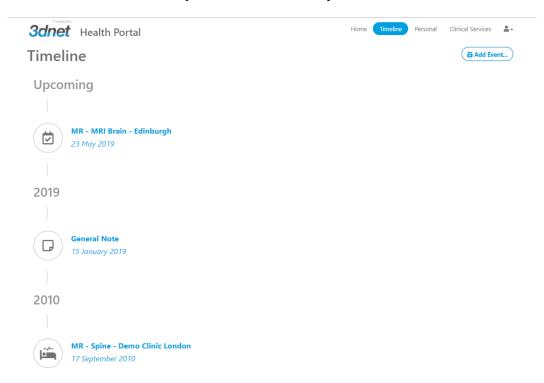
Mobile device view below.



The portal runs on tablet PCs and smart phones.

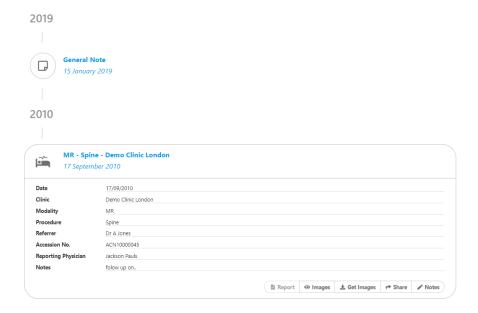
On logon patients will see the Home Page, that highlights Notifications, Upcoming Appointments, Medical Summary, Allergies, Medications. Notifications will alert the patient that the images (and report, if the Organization allows it) are ready to be seen, downloaded or shared (for a

second opinion, specialist review, beginning of treatment, etc). In the top right of the screen users will find labels for the remaining pages of the Health Portal. Click on Timeline to display all the recorded events related to the patient's clinical history.



Health Portal Timeline. Events recorded are presented in a chronological order, starting with the most recent at the top and going backwards as the user scrolls down.

Click on each event to expand it and see more information.



Click on an event to expand it and reveal more information. Use the functions in the bottom right of the event box to see the report, see the images, download images (Get Images), Share, add Notes.

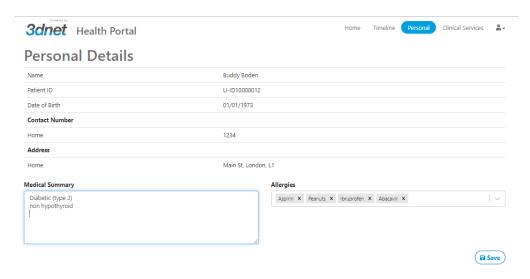
Patients will be able to access their images through our Diagnostic Viewer (click on Images), download the study to the local hard drive as a compressed folder (Get Images), Share the study

or add a Note. Reports can be made available to the patient or hidden, depending on the local workflow.



Patient portal: image visualization. The portal displays the original DICOM images and offers basic post-processing tools such as: scroll, pan, zoom, window/level.

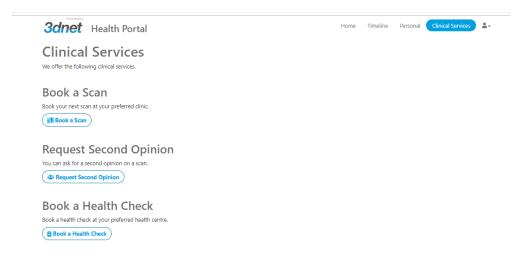
Users can add an event to the timeline by clicking on the Add Event icon in the top right of the Timeline screen. Events that can be added are: Blood Test, General Note, Hospitalisation, Medication, Outpatient Appointment, Scan. Add information such as time, date, location, type of scan (if adding a scan), name and dosage of a medication, etc.



Personal tab. Add or edit personal details, allergies and medical summary.

Click on the Personal tab to view or edit personal details, such as address, telephone number, Medical Summary (summary of the most notable medical conditions, blood type etc), and allergies. Use the Profile icon in the top right corner of the screen to access the payment methods, settings (language and password reset), logout.

Patients using the Health Portal will be able to access a selection of great Clinical Services by clicking on the corresponding icon in the top right corner.

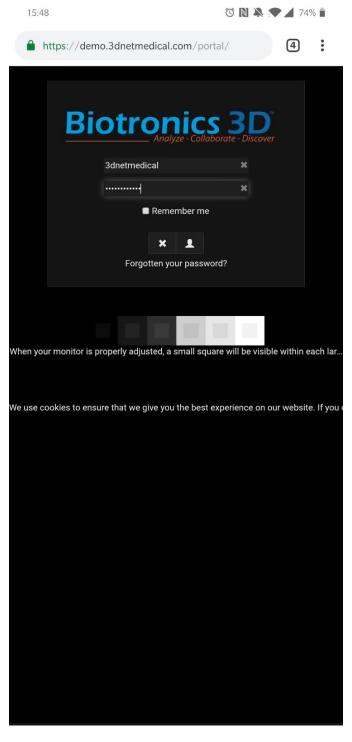


Select one of the services from the list. Services must be setup and agreed upon by the Organization.

Services such as Book a Scan, Request Second Opinion, Book a Health Check, etc. are part of our selection of third party integrations that is available through the 3Dnet Marketplace. Only the enabled services will be available for the patient.

16 3DNet Mobile App

3Dnet users can easily access their work from a mobile device such as a tablet or mobile phone. Users will be able to get the same settings, customisations and worklists/folders through the Mobile App, as in the desktop version of our Portal.



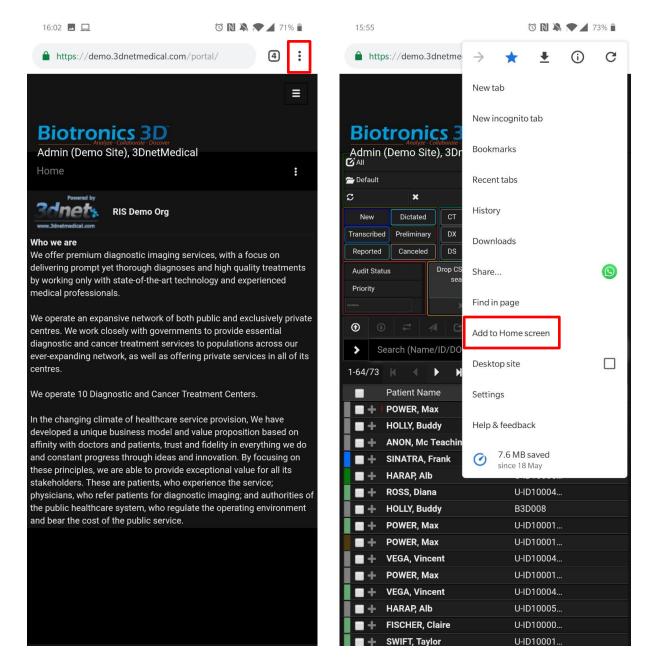
Mobile Login. Enter username/password combination.

16.1 Create a Home Screen shortcut

To create a homescreen shortcut, find the borwser options, then select "Add to Home Screen".

Follow these steps on Android devices (chrome Browser):

- Find the three dots button in the top right to display the page options
- Select "Add to Home Screen"



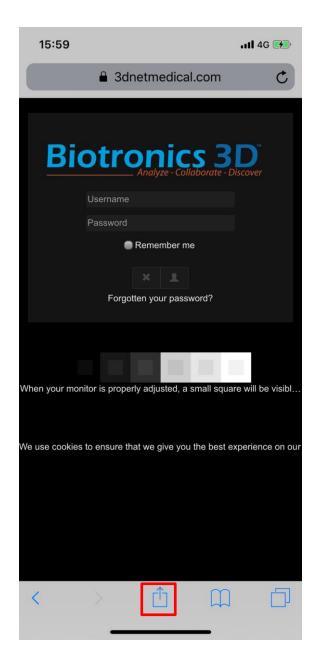
Left picture: select option button; right picture: select Addo to Home Screen. Android devices.

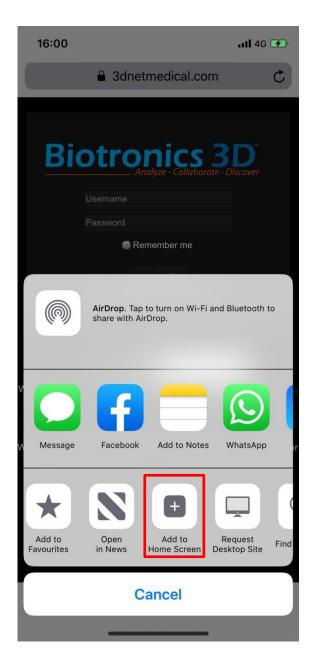
An icon will be added to your Home Screen.

On iOS devices (iPhone, iPad), follow these steps:

• Select the highlighted icon

Select "Add to Home Screen"



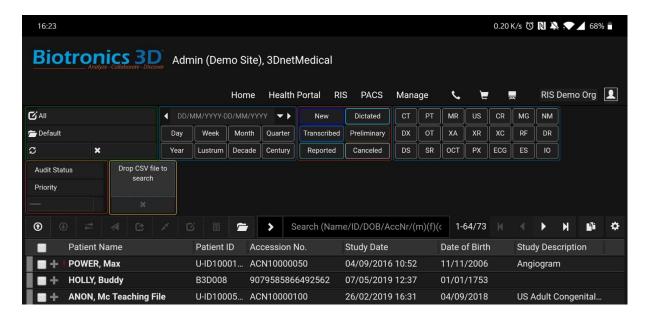


Left picture: select the options button; right picture: select Add to Home Screen. iOS devices.

Once the icon on the Home Screen is created, users will be able to quickly access the 3Dnet Mobile App with one tap.

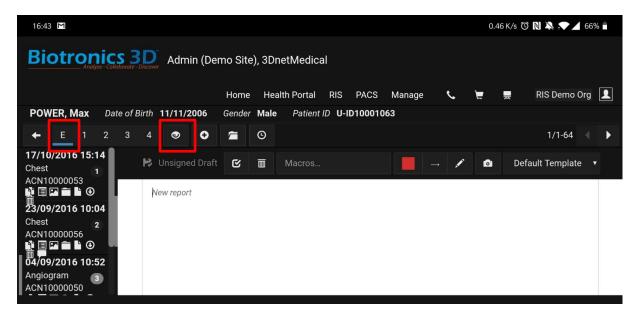
16.2 Navigation in the app

The HTML5 portal layout will resize according to resolution of the device. Users can rotate their device to switch between portrait and landscape mode (if enabled in their device).



Example of the 3Dnet Mobile App in landscape mode.

Use your finger to tap on icons and buttons. Use the keyboard on your device to type information. Select a study from the study list to access the Patient Information Page.



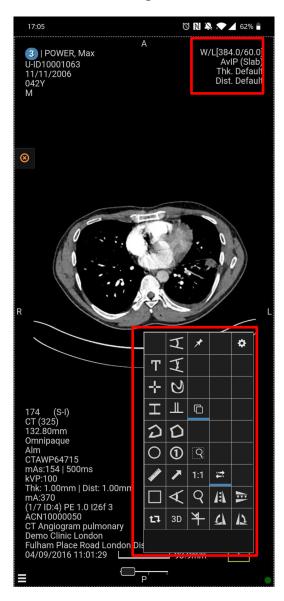
Landscape mode view of the Patient Information Page.

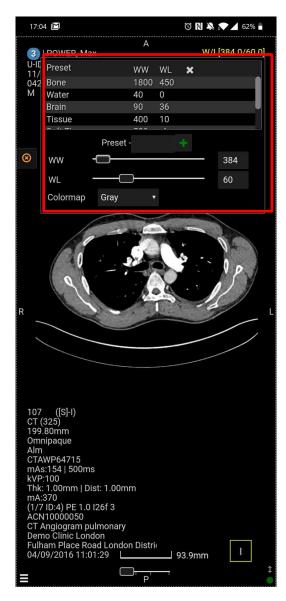
In this page users will find all the relevant information regarding the patient: demographics, clinical history (priors), all the uploaded documentation, etc. Chose the Embedded icon () to open the Diagnostic Viewer into an embedded view. Click on the Eye icon to view images .

16.3 Mobile Diagnositc Viewer

Clicking on the Eye icon will open the Diagnostic Viewer, which presents some slightly different interaction inputs compared to the regular Diagnostic Viewer.

- Pinch the screen with two fingers to zoom in/out
- Slide one finger Up/Down or Left/Right to scroll through the pictures (or use the slider at the bottom of the screen)
- Long press with one finger and release to open the context menu (or use the burger menu in the bottom left corner of the screen)
- Touch the screen with two fingers and slide them across the screen to adjust the W/L (or use the W/L Preset menu in the top right corner of the screen)
- Click on the orange cross icon on the left hand side of the screen to return to the Patient Information Page and close the viewer





Left picture: Mobile Diagnositc Viewer context menu (long press with one finger and release); right picture: Preset and W/L menu (the colormap menu allows users to invert colormap).

Users can access quick tools in the top right hand side of the screen:

- W/L Presets and W/L scroll bars to adjust W/L
- MiP/minIP/AvIP selection button
- Slice thickness menu

• Gap distance menu

The tools displayed in the Toolbox menu work in the same way as their counterparts in the regular Diagnostic Viewer: select a tool and tap on the screen to use it.

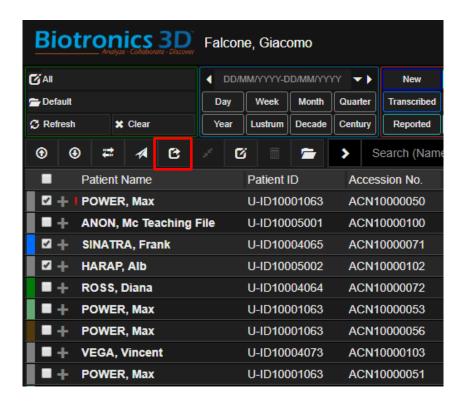
17 Collaborative tools

3Dnet Medical supports several software tools which enable data sharing and collaboration:

- 1. Sharing a study
- 2. Assigning a study
- 3. Folders
- 4. Creating patient CDs

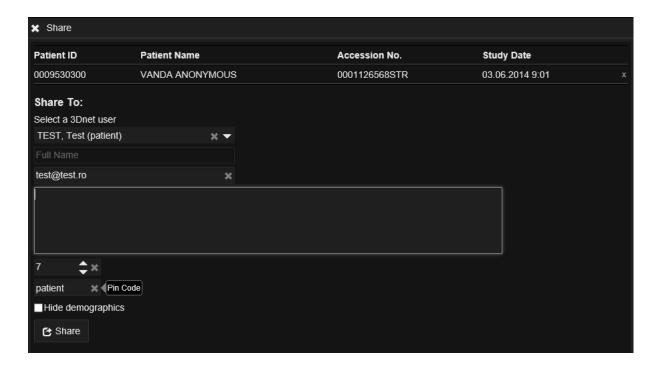
17.1 Study share

Using the "Share Study" feature, a radiologist, or a user in general, can share a study with his colleagues for second opinion or can offer access to the same study to a specialist doctor (e.g. surgeon, neurologist, etc.). The feature is also useful to offer patient access to their studies. The tool is easily accessible from the Study Browser top tool bar, by pressing the **Share** button (the study must checked first).



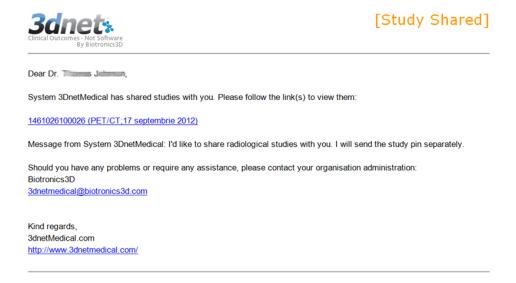
Share study button in the Study browser.

The application displays a dialog box like in the figure below, where the user is required to enter the Name of the recipient, his Email, Username (if he already has one), a Pin number. There is an option to anonymize the study by ticking "Hide Demographics" box.



Share study dialog window.

After all the information is entered, press the Share button. The recipient will receive an email with a URL link, as shown below.



Clicking on the study will launch the following 3Dnet window requesting for the PIN Code. If the recipient already has an account with 3Dnet system will check "Yes, I am already a user" if not, then he must tick the box "no, I will create a new account". As an existing user, the recipient will be requested to introduce the username and password, in addition to the PIN code. As new user, the recipient will be requested to create an account by introducing his Username, First Name,

Last Name, Password. Once the account is created, the recipient can access 3Dnet by typing his username and password on the login page. The system will display the following page with a list of studies shared with him.



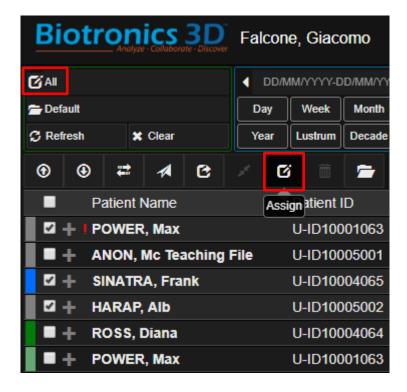
To open a study, the user clicks on eye symbol located on the right. To see the report of a study, the user clicks on the document symbol on the right.

17.2 Worklists

The worklists are accessible from the upper left corner of the Study Browser. This feature is useful for creating worklists for Reporting Physicians and Referring Physicians. The study assignment to a certain user can be done in two ways:

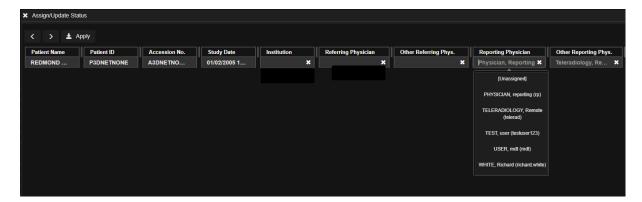
- 1) Manual (as described below)
- 2) Automatically, by reading physician information in the DICOM tags of the study or by reading HL7 ORM/ORU messages.

The manual assignment process in 3Dnet is very simple. First, the worklist must be set up by the Admin user (see the System administration section). Then, click on a study in the Study Browser and press the button Assign.



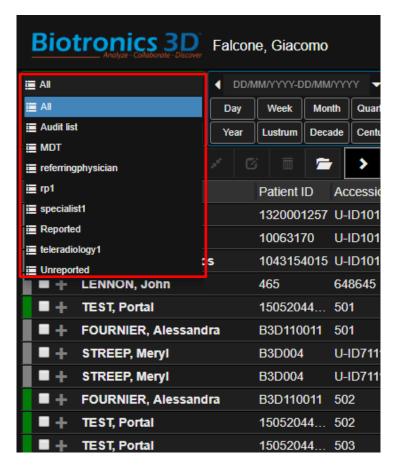
Update button used to assign a study to a user.

A new window opens where the user can assign a study to a Reporting Physician or to a Referring Physician. There can be maximum 2 Reporting Physician assignments per study and 2 Referring Physician assignments per study.



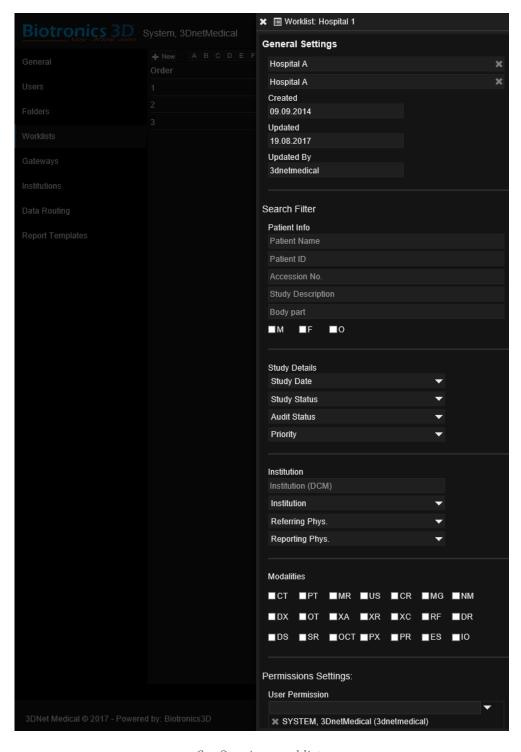
Assign a study to a reporting physician.

The worklist concept can also be used to configure the PACS system in the grid mode for multisite organizations in order to offer users easy access to studies from all the sites of that organization in one window and using a single logon. For example, an organization with three hospitals, with 3Dnet Medical servers in each hospital configured in the grid mode, will have four worklists. One worklist will show all the studies from all the sites, while the other three worklists will display the studies from each hospital, separately.



Worklists configured for an organization: All shows all the studies from all the hospitals.

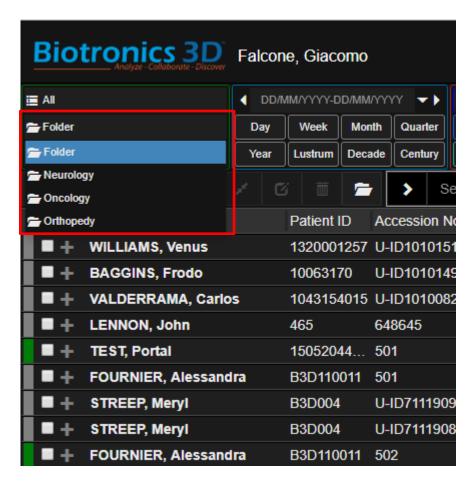
Note that 3Dnet Medical only shares meta-data information between the sites. It does not copy the DICOM images between the servers. The images remain in the hospital where they originated from. The worklist configuration is achieved from the **Manage/Worklist** tab only by users with Administrator permission. The filtering criteria available are: **Patient Info, Study Details, Institution** or **Modality**. For each worklist it can be defined which users will have access to it, from the **Permission Settings/User Permission**.



Configuring worklists.

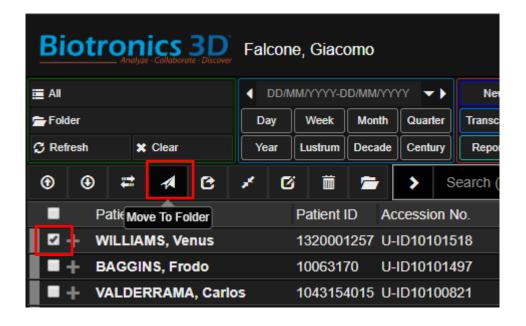
17.3 Folders

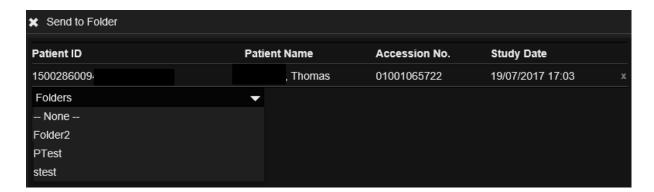
The Folder concept is used by 3Dnet to logically separate studies manually or based on some pre-defined criteria. For example, like in the case of worklists, an organization with several imaging centres in grid mode configuration can choose to set up in 3Dnet a folder for each imaging centre. Another example may be a hospital which desires to use folders to separate studies associated with different hospital sections: a folder for Orthopedy patients, a folder for Neurology patients and so on so forth. The folders can be accessed from the Study Browser directly, as shown below. Users can see only folders which are granted access to by the system administrator.



Accessing different folders in the system containing patients sent to radiology from different sections in the hospital.

If a patient is transferred from one section to another section in the hospital, the study can be transferred between the associated folders by clicking on the Move To Folder button.





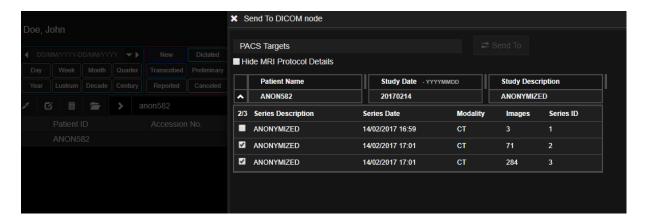
Transfer study from one folder to another.

17.4 Patient CDs

3Dnet Medical can be configured to export DICOM data together with a portable DICOM viewer. This package can then be burned on a CD or DVD and hand in to the patient. The viewer launches automatically when the CD is inserted in the CD/DVD unit and includes many visualization features: measurements and annotations, zoom, pan, rotate, flip, invert, synchronized scroll, cross-reference lines, window/level (pre-sets), comparative mode, cine mode, MPR, MIP.

The portable viewer is developed using JAVA programming language and therefore will run on any operating system: Windows, Mac, Linux.

Check the desired study in the study browser and click the **Download** button in the study browser. The study can be anonymized before download by checking the **Anonymize** checkbox as shown in the image below:



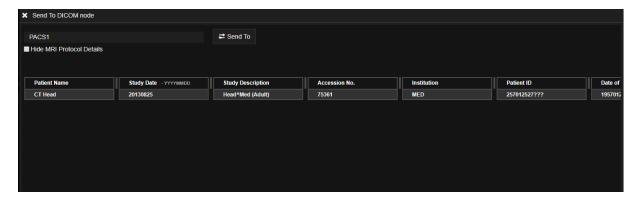
Select the DICOM Target (in this case a CD Burner). Select which series to send. Click "Send To".

Users can select which series to send to the target CD/DVD Burner (or PACS target). Simply use the tickbox next to each series to select or deselect a series.

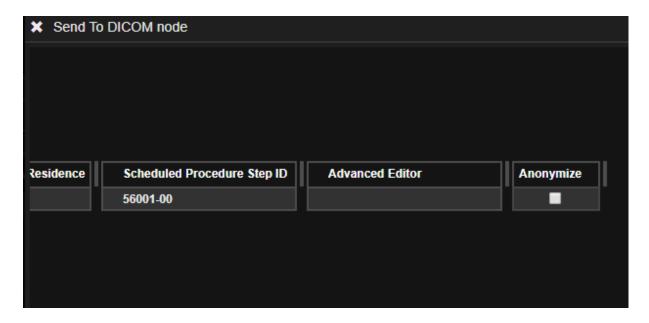
17.5 Send a study to another PACS target

Using the same tool as above (Send To), users can select from a drop down menu all the PACS targets currently connected to our PACS. This target can be a CD Burner or another image database. Before sending the study, users can edit the DICOM tags of this study from the user interface. Users can edit selected DICOM tags or simply click on Anonymize to fully anonymize the study.

In this case, the software will apply a default anonymization of pre-selected DICOM tags. The tags that need anonymization can be set up via config.



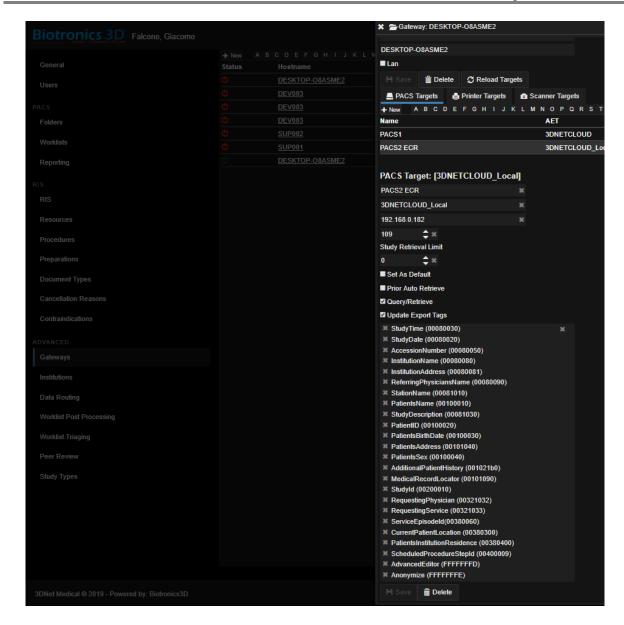
Manually change the info in each DICOM tag that will appear. A list of the DICOM tags that a user can edit can be found in the manage page.



Scrolling all the way to the left, the user will find the Anonymize checkbox.

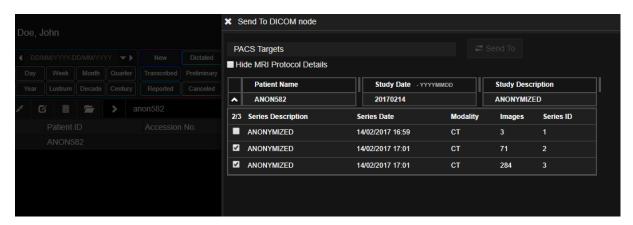
Click on Anonymize to send the patient as anonymous study. The next picture shows which are the DICOM tags that can be edited using this tool. The list can be found from the Gateway management page, after selecting the correct Gateway and PACS target (Update Export Tags).

Users can add and remove DICOM tags from the list below.



This menu is found by clicking on Manage, then Gateways. Select the correct Gateway and then the correct PACS target. Click on Update Export Tags to select DICOM tags.

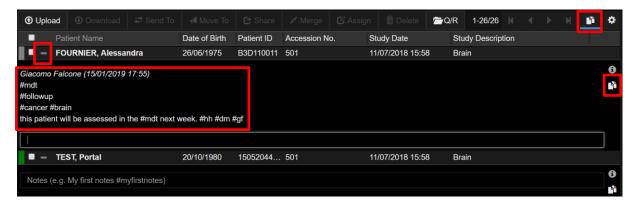
Users can select which series to send to the target CD/DVD Burner (or PACS target). Simply use the tickbox next to each series to select or deselect a series.



Select which series to Send to the DICOM Target by using the tickbox next to each series.

17.6 Study Tagging (MDT and Collaboration Tool), Notes and Lesion Tagging

In 3Dnet Medical, users can add notes and tag studies for clinical meetings or to create ad hoc worklists for selected studies, on the fly. Notes and tags can be added using the Note Tool in multiple ways. These notes and tags can also be used to tag lesions or key images.

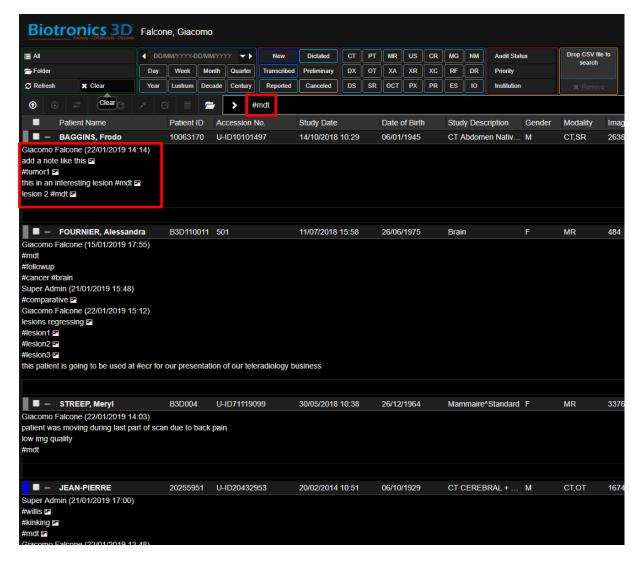


Add and check notes and tags from the worklist.

Notes and tags can be viewed by clicking on the Notes icon in the top right of the worklist. This will expand every study, exposing notes that might have already been added to that patient. To add a new note or tag, use the text box at the bottom of every expanded patient record line.

In the example, the patient Fournier Alessandra has multiple tags. Common tags such as #mdt can be very useful when trying to organize a Multidisciplinary Team meeting. Users can search for any tag in the search bar. The search result will show studies that present the requested tag.

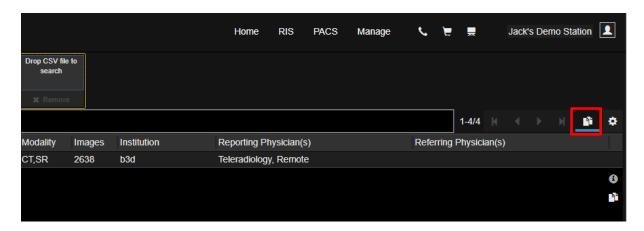
The following picture shows how the search for "#mdt" comes up with all the studies that have been tagged as #mdt. This will make it very easy for user to create ad hoc worklists for presentations, MDT meetings, tag patients as interesting or useful for teaching.



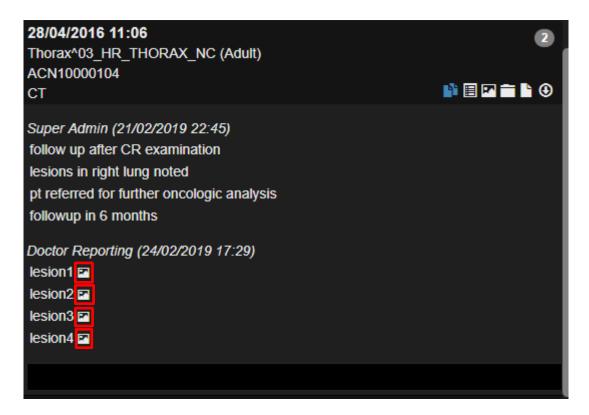
Search result for #mdt. This will highlight every patient marked with a specific tag.

Notes can be very useful to leave a quick comment to a study and enhance the collaborative potential of your workflow. Notes are not only just a text file attached to the examination, but are saved as a complete presentation state to go along with the written annotation. In this way, a user can arrange the images on the display, perform advanced analysis, add a note to comment what he sees and this note will also save the presentation state in which the user took the note. This will allow the same user, or other users, to load the same presentation state in which the note was taken to analyse the same pictures in the same way.

To display all notes for every patient in the worklist, click on the notes icon on the right of the screen.



Clicking this icon will open the notes tab for each patient. Click again (the icon will not be highlighted in blue) to collapse the patient records and hide notes.



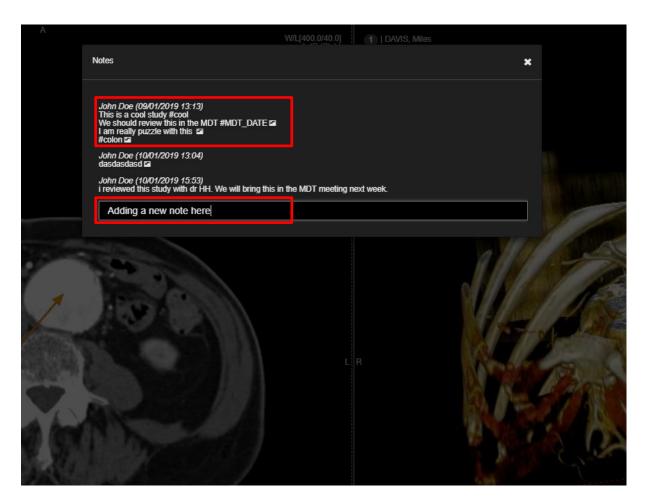
Notes in the Patient Information Page.

Notes can also be accessed from the Patient Information Page (left click on a study in the worklist to access this page). Users can tag lesions (#lesion1, #lesion2, etc.) and key images adding a note with the correlated presentation state. In the picture above, we can see some of the notes left by users in the previous days. Clicking on the picture icon will load the viewer in the presentation state in which the note was saved. The user can also add another note using the textbox at the bottom. It is also possible to add a note during a reporting session inside the diagnostic viewer.

To do this, right click on the study description to make the Notes History pop up in the middle of the screen. Users can read notes and add new ones, as shown in the pictures below.



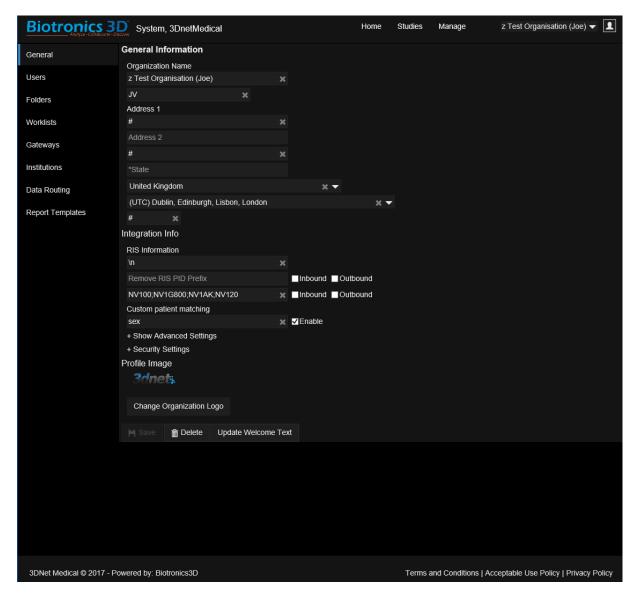
To open the Notes History, <RMB Click> on the study description.



Adding a note from the diagnostic viewer. This window will show after using the right mouse button on the study description in the study panel.

18 System administration

System administration tools are accessible only for users granted with administrator permission, from the **Manage** tab on the right upper side of your screen.

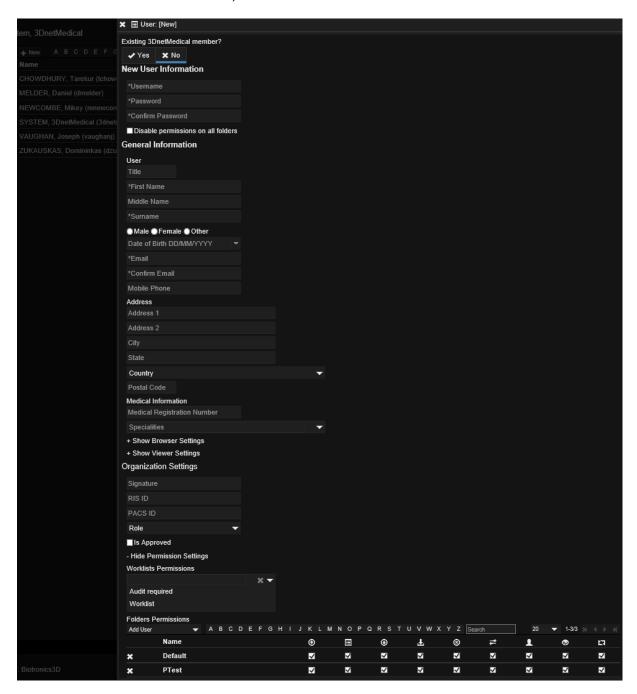


Manage tab showing the general information for an organization.

In this section, the organization admin can modify general information about his organization, manage users, folders or worklists, configure gateways, rules for automatic study forwarding, or configure report templates

18.1 Manage users

In this panel, the system admin can create/edit/remove user accounts by accessing the **Users** tab. To create a new user accounts, click on the **New** button.



Adding users and configuring user permissions.

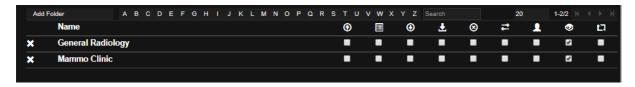
All users are assigned a role in the workflow: reporting physician, referring physician, OrgAdministrator, uploader, technologist, clerical, transcriptionist or patient. Different privileges can be assigned to different users, such as ability to report, permission to delete a study, send a study to a DICOM node, download study, upload study, add/edit/delete text notes,

assign a study with a user, transfer studies between folders. These permissions are granted with the checkboxes in the last two rows in the figure above. In the same panel, the system admin can assign permission to a user to see certain folders or worklists in the system.



Assign a role to a user and user permissions for each folder.

Userclasses Technologist, Patient, Clerical, Referring Physician, share the same default permissions (in the image below).



Default userclass permissions: Technologist, Patient, Clerical, Referring Physician have the ability to see patient info (see studies in the worklist).

Reporting Physician and Transcriptionist userclasses, in addition to this, have the permission to save a report.



Reporting Physician userclass can see studies in the worklist and report those studies.

Uploaders userclass can by default Upload studies to the system, in addition to being able to see studies in the worklist.

Organization Admin (OrgAdministrators) have by default all the permissions, expect for the study merge.



Org Admins permissions.

These default permissions and roles can be very easily modified by an OrgAdmin.

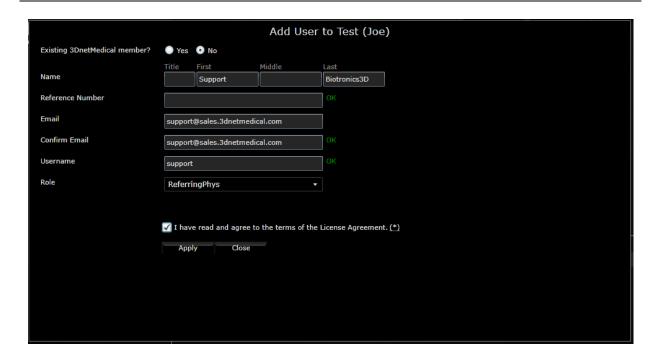
It is also worth mentioning that Users can have customized permissions that are different depending on the worklist/folder that they are accessing. A user belonging to userclass Technologist (radiographer) can, for instance, have all the permissions in a worklist, and the default permissions in another worklist.

Dedicated worklists per userclass or per user can be created through the manage page by an Org Admin. This would enable a referring physician to only see patients assigned to him through RIS/PACS, or a Reporting Physician to bypass a general worklist with all the studies and only see studies assigned to him. In the same way, receptionists or Technologists can receive the permission to move patient to another folder or to upload/download studies.

3Dnet also supports Active Directory integration. Go to Manage Users, Add AD User. This will open a new window with AD Groups and Users. Select a user and click on Add User. Another window pops up with the user information already filled in. There is no need to add a password in this sign up step as AD users authentication is done live from AD. At system login the user must type his/her AD username and password.



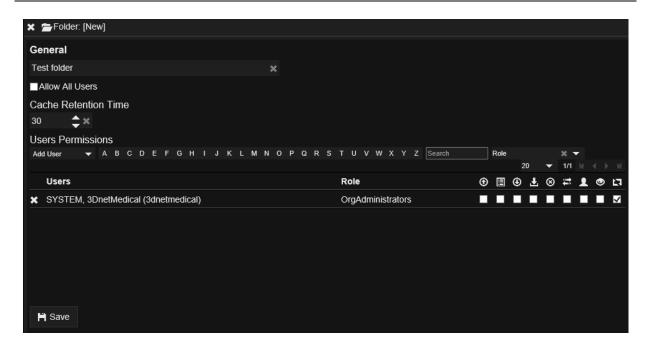
Active Directory users.



18.2 Manage folders

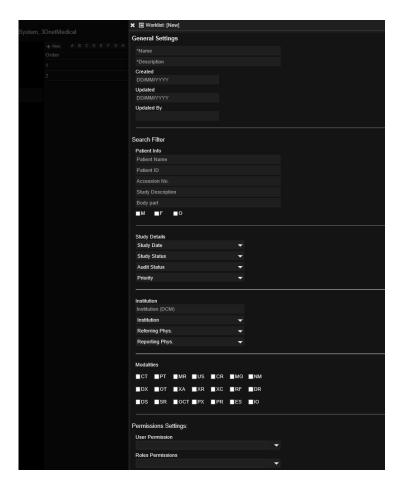
3Dnet Medical allows to distribute the incoming studies to various folders in the system based on information in the DICOM header, for example Instituion Name or Referring Physician. Figure below shows how to create a folder in 3Dnet. Go to the **Folders** tab and click the **New** button. You can configure a folder with the following options:

- Allow all users to see that folder
- Cache retention time: how long a study will be kept in that folder
- Add user which users will be granted access to this folder
- Configure user permissions for each of the users with access to this folder



Adding a folder.

18.3 Manage worklists



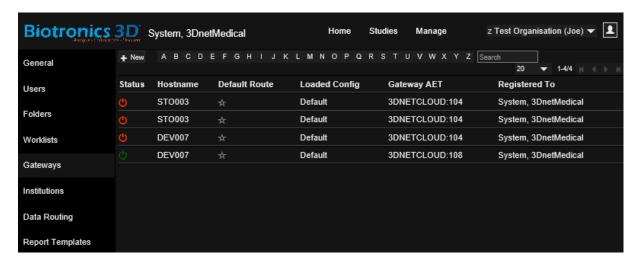
Worklists configuration.

The admin user can also create, edit or remove worklists from the **Manage** panel. In the **Worklists** tab, click on the **New** button to create a new worklist.

In the form above, enter the Worklist name and description. In the **Search Filter** section, select the filtering criteria for that worklist. There are many options here, which are shown in the figure above. For example if one desires to create a worklist showing only studies of one patient, then enter the Patient Name and Patient ID. If one desires to create a worklist with studies assigned to a certain Reporting Physician then select the user from the Reporting Physician dropbox menu. In the **Permissions Settings**, the admin user is able to assign access permissions to this worklist to certain users.

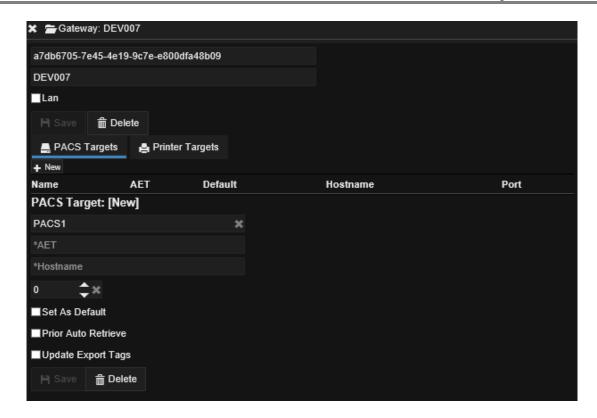
18.4 Manage gateways

From the **Gateways** tab one can configure DICOM nodes and DICOM printers for communication with 3Dnet DICOM server (DICOM Send, Query/Retrieve, DICOM Print).



List of gateways configured in the system for a test organization. Only the green is online, the red are offline.

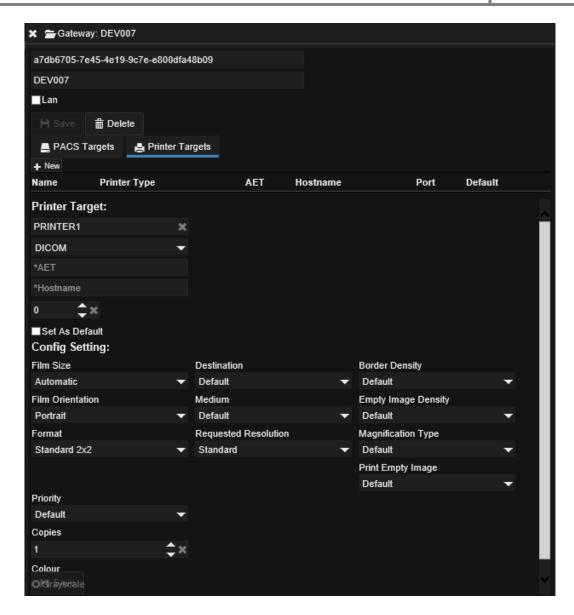
To add a DICOM node, click on a gateway, then click on PACS Targets and then click on New. Here the user is requested to enter the AET, Port and IP of that node.



Adding a DICOM node in the system.

The generic name PACS can denote any DICOM node in the network: modalities, modality diagnostic workstation, 3rd party viewers, 3rd party PACS systems. All can be configured to query/retrieve study from the 3Dnet archive.

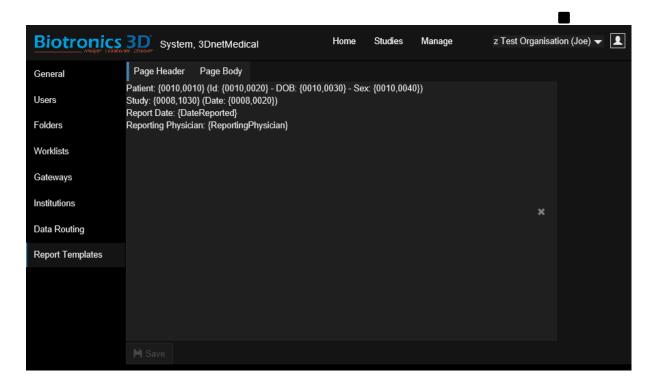
To configure a DICOM film printer, click on the **Printer Targets** and then click on **New.**



Adding a DICOM film printer to the system.

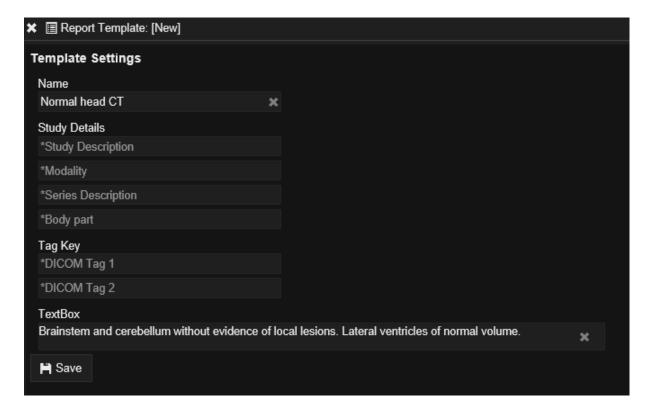
18.5 Report templates

In the **Report Templates** the user can create pre-defined reports for radiologists to use in their daily work. Use the **Page Header** to define the report header by extracting information from the DICOM header of the study, such as: Patient Name, Patient ID, DOB or exposure parameters in case of CT or digital X-ray.



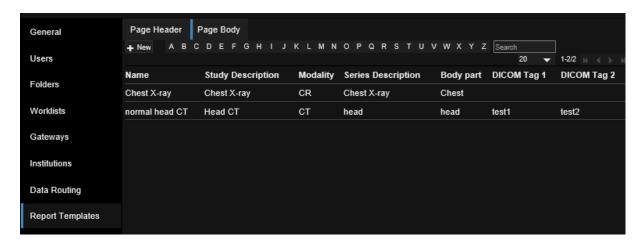
Setting up templates for report - report header.

Use the **Page Body** to construct the preset templates for certain studies like in the figure below for a head CT study. Click Save to save the template in the PACS database. Next time the user opens a head CT study for reporting, this template will be selected automatically (based on the information entered in the Body Part and Modality tabs in the figure below).



Setting up templates for report - report body

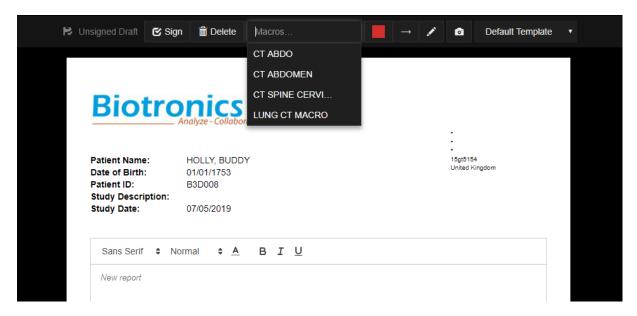
All the pre-defined report templates will be listed in the Report Templates form.



List with report templates

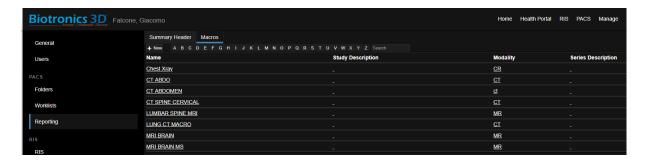
18.6 Report macros

Macros are blocks of text that can be used to populate the report in one click. Users can find a list of the available macros using the Macro button on top of the reporting textbox.



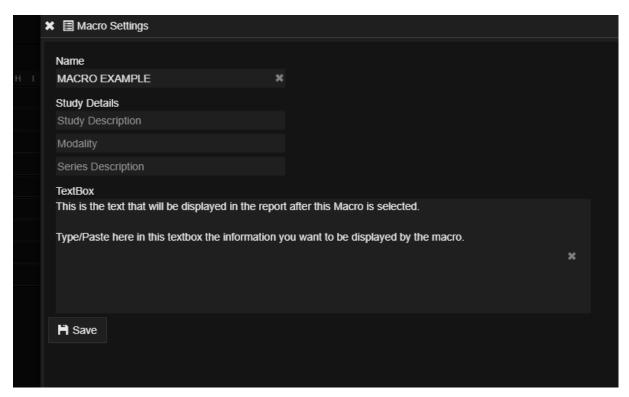
Click on the Macro button and select the appropriate macro. In the example, only CT macros are showing (Macros that have been assigned to Modality: CT).

Only macros assigned to the relevant modality will be displayed. To set up macros, open the Manage page, find Reporting on the left, then Macros (highlighted in blue in the picture below).



Macro manage page.

A list of the available macros is displayed, along with information regarding the matching of the macro itself with Modality, Series Description and Study Description. To create a new macro, click on New in the top left of this list.

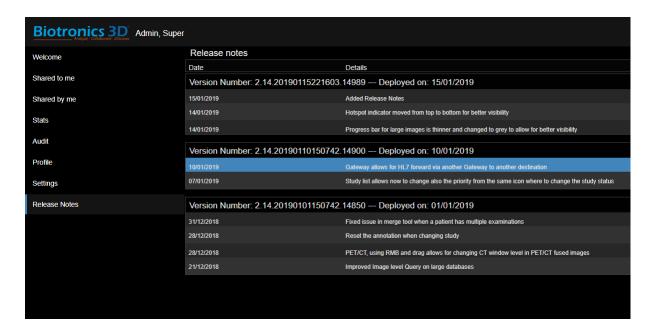


New Macro wizard. Select a Macro name and fill out the Study Details to match the Macro with specific DICOM tags.

Use the Study Details fields Study Description, Modality, Series Description. The software will inspect the DICOM tags of each study in order to successfully match the correct Macro with the study the user is reporting.

18.7 Release notes

Users can check the latest release notes to see what's changed on every new software update. Click on the user's name/last name at the top left of the page, then find Release notes tab in the left index. A chart similar to the one in the following picture will appear, with date, time, software version release and details for every change.



Release note panel. Check what changed since the last update.

This tool is very useful to have a brief history of the changes and fixes that occurred since last version.

19 Teleradiology

Biotronics3D provides a suite of tools created specifically to promote Teleradiology in an easy but complete way. Often Teleradiology businesses present a workflow in which studies are sent to PACS (3Dnet Cloud) from a number of separate institutions. Each separate institution can be organized in clusters and cover a very large geographic area. Biotronics3D can put a network in place, so that studies that are received through DICOM interface are automatically routed to dedicated reporting worklists/folders or assigned to specific reporting physicians. Studies can be sorted and assigned based on multiple different parameters (Institution of origin, Study Description, Priority Status, Modality, etc) based on the information carried in the DICOM tags. In this way 3Dnet provides the infrastructure and the tools to automatically process the studies to redistribute them (upon arrival in our Cloud) to the correct target (study routed to folder/worklist, assigned to reporters, assigned a pre-defined Time To Report, etc).

To enable a high quality Teleradiology workflow 3Dnet uses, among others, the following features:

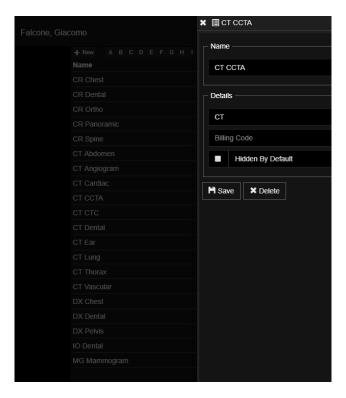
- Study Type
- Study Notes
- Worklist Post Processing
- Worklist Triaging

Through the implementation of these features, users can then apply rules to automatically route studies with a certain Study Type, Study Note, Priority, Origin, etc., to ad hoc worklists. Each worklist can then be made visible for pre-determined users or a whole userclass. This makes it possible to create workflows in which studies coming from certain Institutions (eg. Cardiac only

clinic) are automatically routed to pre-determined users (Cardiac specialized Reporting Physicians); all the Urgent studies uploaded to the Cloud will be assigned to the on call radiologists; etc.

19.1 Study Type

Upon arrival in the Cloud or order association from RIS, a study can be automatically assigned to a Study Type or marked with a #hashtag (Study Note). A Study Type defines a unique name and characteristics for certain type of study, using Modality and Billing Code.



Add a Study Type by selecting the corresponding Modality and Billing Code. Create multiple Study Types to give your triaging more flexibility.

Add a Study Type by finding the Study Type tab in the manage tab. Click on New to display the menu demonstrated in the picture. Add a name and details (Modality, Billing Code). Hit Save or Delete to remove it from the list.

19.2 Worklist Post Processing

Teleradiology businesses often receive studies from multiple separate locations and organisations, which might use very different study descriptions (eg: CT Lung in Clinic 1; CT Chest in Clinic 2; CT Thorax in Clinic 3). Upon study insertion in the Cloud or Order Association, use a set of custom search criteria to define a list of studies. Automatically apply an action to the

search result. Actions can be: a) assign a Study Type to the search results; b) assign a Study Note (#hashtag) to the search results.

Using Study Types and Study Notes, create automatic rules to assign the search results to a specific ad hoc Worklist, assign the studies to pre-defined Users, etc.



Set a list of Rules (search criteria) to apply to the study list every time a study is inserted in the Cloud. Apply actions to search results.

In the example, a protocol has been created. This protocol is applied every time a new study is uploaded to the 3Dnet Cloud (Trigger Event: Study Arrival). When the trigger event happens, a search is performed (as described in the Rules field). This search will get as a result all the studies that match the following rules (as in the example): Modality matches "CT"; Study Description contains (~) "Colon"; Institution of origin is "Clinic 1 London". An automatic Action is taken against the search result: the "CT CTC" Study Types is applied, Study Note "#CAD" is applied. This enables the following workflow (example):

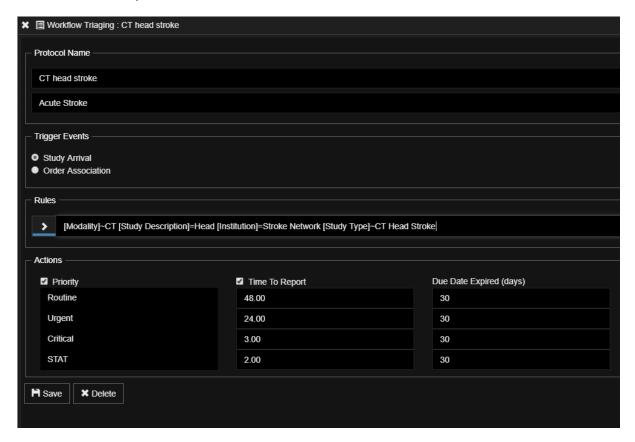
- Study is inserted in B3D cloud
- Study matches search result for the protocol created
- Action taken against the study: assign Study Type, assign Study Note
- Study is automatically routed for CAD processing of lesion
- Study receives CAD elaboration; Study is available in study list when searching for "#CAD"

This workflow can be applied to multiple use cases and adapted to the local customisation.

19.3 Worklist Triaging: TTR, TAT, Due Date

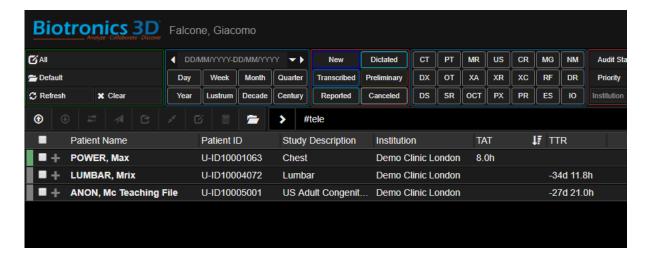
Worklist Triaging enables Users to mark studies with a pre-determined TTR (Time To Report) and Due Date (number of days before study expires), based on the Study Priority (Routine, Urgent, Critical, STAT). This tool, coupled with the tracking of the TAT (Turn Around Time) is very important in a Teleradiology environment, because it makes it very easy and quick to track the performance and quality of the business. Alerts can be sent out to relevant Reporting Physicians upon breaching of the TTR or when the TAT surpasses a certain threshold.

In the example below, a protocol for CT Acute Stroke is being created. Critical Priority is assigned to every study uploaded from the Stroke Network (every study that follows the Rules: Modality = "CT", Study Description = "Head", Institution of origin = "Stroke Network", Study Type = "CT Head Stroke").



Set automatic TTR and Due Date for studies that satisfy the search criteria (Rules).

Users can define the default TTR and Due Date for each Priority Level.

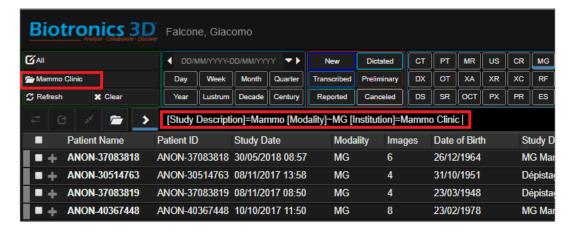


TTR and TAT can be tracked in the study list. In the picture, Reported study displays a TAT of 8 hours, which is in line with the allocated TTR for a routine Priority study. Two studies in the list are unreported and have respectively 34 days and 27 days to be reported. Upon breaching of the TTR, studies will be deleted (Due Date Expired).

In the example above, TAT and TTR are listed for the studies in the study list. TAT and TTR tracking are available for Organisations that require the 3Dnet Teleradiology features.

19.4 Study assign (to worklist or to user) and anonymization

Using Study Notes, Worklist Post Processing and Study Types, it is possible to automatically assign studies (that obey to the rules set in the backend) to custom made Worklists. It is then possible to grant access to said Worklist to individual users or to a whole userclass (all the Reporting Physicians, all the Referring Physicians, etc). Users that have the permission to see and interact with the content of the Worklist will be able to access the studies automatically routed to that Worklist.



Studies that obey to the rules highlighted in the Omnisearch bar are automatically redirected to the "Mammo Clinic" worklist. An admin can grant access to this worklist to certain users.

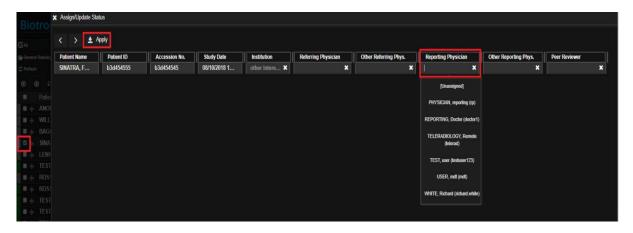
In the example above, the user that is currently logged has access to the "Mammo clinic" worklist. Said Worklist is automatically populated by studies that follow the rules set in the

Manage page of the 3Dnet platform (upon insertion in the 3Dnet Cloud of an MG study coming from the institution "Mammo Clinic", that study is automatically displayed in the "Mammo Clinic" worklist. This worklist has been made accessible to users that are allowed to report Mammograms). In the example above the user currently logged in can access the worklist and report images but has not the right to see patient demographic. This results in an anonymised worklist, where the user can only access part of the Patient Info (Date of Birth, Study Date), but can't see the Patient Name and ID for data protection reasons.

An OrgAdmin type of user can also manually assign studies to a specific user with the "Assign" feature, clicking on the correlated button at the top of the study list.



Select the "Assign" button to manually assign a study.



Locate and select the "Assign" tool button at the top of the study list. Use the dialog that will open to select a Reporting Physician (or a user in another userclass) and manually assign one or more study to that user.

In the example above, a study has been selected from the study list (tick box highlighted in the left side of the image). The user clicked on the "Assign" button. Now it is possible to locate the correct field, in this case Reporting Physician, and choose from the drop down menu the designated person.

20 RIS/PACS desktop integration

This document summarizes the workstation desktop integration of 3Dnet with a RIS client (Radiology Information System). The goal of the integration is to allow users to perform single login and initiate 3Dnet synchronised to the same user, patient, and examination(s).

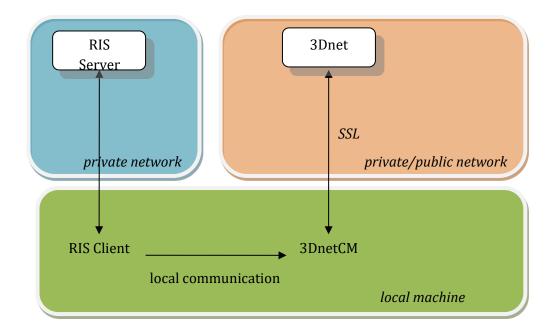
20.1 Pre-requisites

- Client workstation has network access via https to a 3Dnet public/private installation.
- Net 4.5
- Latest version of Google Chrome
- Requires administrative rights to install

20.2 3Dnet Connection Manager

3Dnet Connection Manager (3DnetCM) is a small application that must be installed on every client machine in order to access 3Dnet. Its primary purpose is to facilitate communication with the RIS client and enable:

- Synchronized, secure, authenticated login to 3Dnet from the RIS client.
- Study display based on current RIS selection.
- Session locking.
- View and setup connection configuration.



3DnetCM receives instructions from the RIS Client. Messages are sent as of the form:

B3Dnet.ConnectionManager.App.exe

b3dnet:///?command=<command>&userid=<userid>&authtoken=<authentication>&datai ds...

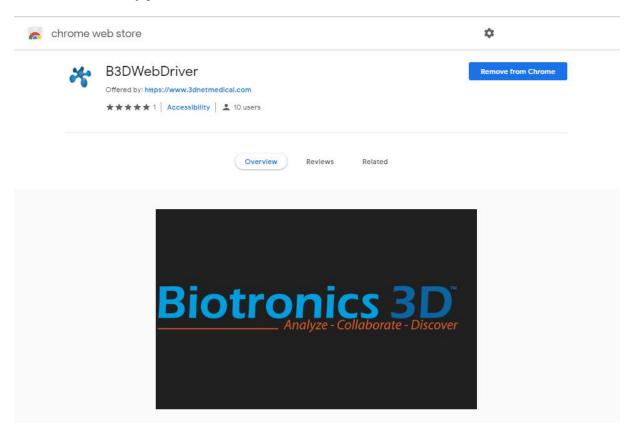
There is one single command line argument that is a URL safe string.

In all cases success/failure is indicated through integer return value.

More information about the Connection Manager can be found in the dedicated documents that have been shared with your organization.

20.3 Google Chrome extension

The user can apply a Google Chrome extension to the browser, to enhance the functionalities of the viewer. This extension will, once the diagnostic viewer is launched, maximize the pop-up windows in the medical diagnostic displays (high resolution). Depending on the number of diagnostic monitors that the user has, he or she can select the number of pop-up windows. These windows will automatically maximize in each of the diagnostic monitors without the need for the user to manually position the viewer windows in the monitors.



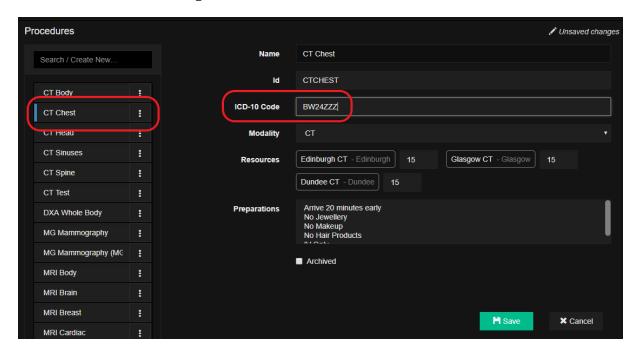
Screenshot of the Chrome extension on the Chrome Web Store.

The chrome extension will self-update, so the user can always use the latest version possible.

21 ICD-10

The ICD-10 Procedure Coding System (ICD-10-PCS) is an international system of medical classification used for procedural coding. Each code consists of seven alphanumeric characters.

The user can set a list of procedures from the manage page and apply the corresponding ICD-10 code as described in the image below.



Manage page, Procedures list. Add the ICD-10 code for every procedure.

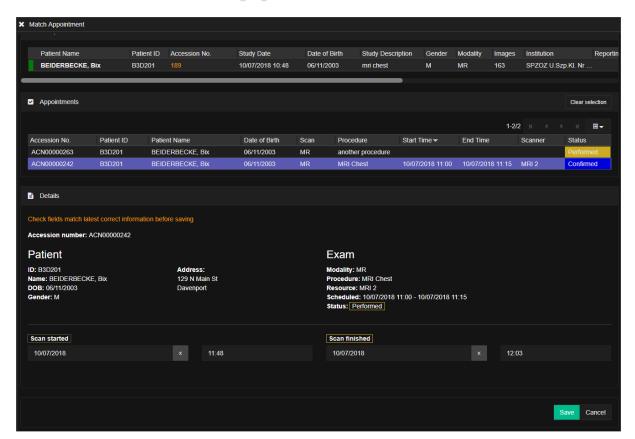
22 Data integrity - Mismatched study merge

3Dnet Medical provides ways to ensure data integrity through the RIS/PACS architecture. In the event of an interruption of the communication between RIS and PACS or data entry mistakes, users can take advantage of the Mismatched Study Merge tool.

When mismatch occurs between data in RIS and PACS, the record in the worklist will appear in a highlighted colour, see picture below. This will alert the user on which studies must be merged or amended.



Highlighted mismatched studies.

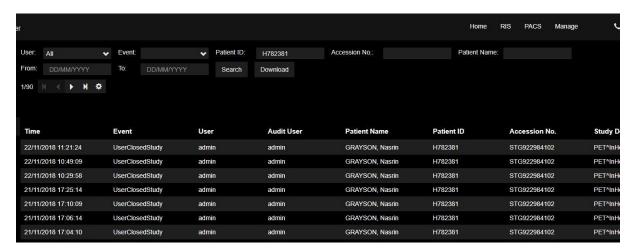


This is the Mismatched study merge tool. Here the user can find 2 studies and match them for data integrity.

Using the Mismatched study merge tool, the user can search the database and match studies that are not linked or match a patient with a record that carries the correct patient details (to amend mistakes).

23 Audit trail Tool

Admins can access an audit tool that logs every relevant action taken by each user.

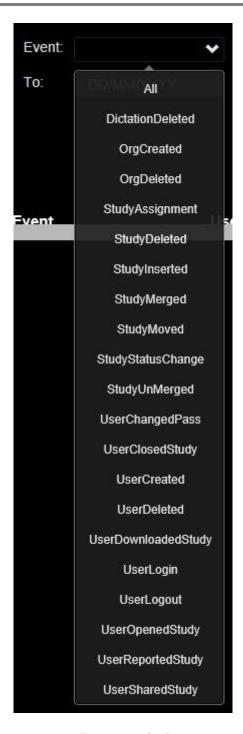


Audit tool interface

The user can apply multiple search criteria: search by user, by event, patient ID, etc. As shown in the picture.

Search results can be downloaded in excel format and printed.

This is an example of the events tracked in one of our organization. The list can be expanded or reduced depending on configuration settings.



Events tracked

24 3Dnet Gateway

3Dnet Gateway is a stand-alone application which manages the DICOM communication between modalities or any DICOM node and the 3Dnet core system, set up as public cloud in a datacentre or as private cloud in the customer's premises. The application runs as a service and can be installed on any computer in the network. 3Dnet Gateway supports the following DICOM commands but not limited to: C-Store, C-Get, C-Find, C-Move, C-Echo, Storage Commitment, client/server Query/Retrieve. As you can see in the picture above, in the **Configuration** tab the user can configure the insertion model (Study Level or Series Level) as well as ticking the Compression on Disk option and enabling SSL encrypted communication between server and clients.



Gateway configuration.

In the **Remote Studies** tab there is a client Query/Retrieve feature, which allows the user to interrogate other DICOM nodes in the network and to move studies from that node to the 3Dnet archive via C-Find and C-Move commands.



Gateway DICOM Query/Retrieve.

More advanced configurations, such as HL7 communication or compression of studies for archiving for example, can be done directly in the config files (e.g. web.config) and database.

24.1 Gateway anonymization

Using the gateway it is possible to organize workflows so that anonymization is operated automatically when a study is uploaded to the cloud. A modality or another PACS node can send a study to the 3Dnet Gateway, which will operate an anonymization of a set of DICOM tags before uploading the images to the cloud.

The anonymizer uses a scripting language, where each DICOM element can have its own replacement script containing instructions for what to do with the element when it is processed. This script can:

- Replace: If you want to replace the contents of an element with new static text, enter the text in the Replacement text field for the element.
- Remove: If you want the element to be removed from the DICOM object, blank the Replacement text field for the element
- Insert empty: If you want to insert an empty element or replace the contents of an element with an empty (zero-length) string
- Hash: if you want to replace the current string in a DICOM element, encrypting it to a new string

As a reference, here is a link with a detailed explanation of how the anonymizer tool we use works. https://mircwiki.rsna.org/index.php?title=The MIRC DICOM Anonymizer

Below an extract from a script currently in use for one of our deployments. This is a screenshot from the list of DICOM tags and the action connected to it to automatically modify it or leave it as it is.

```
dicom-anonymizer - Notepad
File Edit Format View Help
<script>
 -137
 DICOM-PS3.15E-Basic
 Project
 Project
 99
 SiteName
 Trial
 9999
 <e en="T" t="00080005" n="SpecificCharacterSet">@keep()</e>
<e en="F" t="00080008" n="ImageType"></e>
<e en="T" t="00080012" n="InstanceCreationDate">@remove()</e>
<e en="F" t="00080013" n="InstanceCreationTime"></e>
 <e en="T" t="00080014" n="InstanceCreatorUID">@hashuid(@UIDROOT,this)</e>
 <e en="T" t="00080016" n="SOPClassUID">@keep()
 <e en="T" t="00080018" n="SOPInstanceUID">@hashuid(@UIDROOT,this)</e>
 <e en="T" t="00080020" n="StudyDate">@hashdate(this,PatientID)</e>
 <e en="T" t="00080021" n="SeriesDate">@remove()</e>
<e en="T" t="00080022" n="AcquisitionDate">@remove()</e>
 <e en="T" t="00080023" n="ContentDate">@hashdate(this,PatientID)
 <e en="T" t="00080024" n="OverlayDate">@remove()</e>
 <e en="T" t="00080025" n="CurveDate">@remove()</e>
 <e en="T" t="0008002a" n="AcquisitionDatetime">@remove()</e>
<e en="T" t="00080030" n="StudyTime">@empty()</e>
<e en="T" t="00080031" n="SeriesTime">@remove()</e>
<e en="T" t="00080032" n="AcquisitionTime">@remove()</e>
 <e en="T" t="00080033" n="ContentTime">@empty()</e>
 <e en="T" t="00080034" n="OverlayTime">@remove()</e>
 <e en="T" t="00080035" n="CurveTime">@remove()</e>
<e en="T" t="00080050" n="AccessionNumber">@hash(this,16)</e>
<e en="F" t="00080052" n="QueryRetrieveLevel"></e>
<e en="F" t="00080054" n="RetrieveAET"></e>
 <e en="F" t="00080056" n="InstanceAvailability"></e>
 <e en="T" t="00080058" n="FailedSOPInstanceUIDList">@hashuid(@UIDROOT,this)
 <e en="T" t="00080060" n="Modality">@require()</e>
<e en="F" t="00080061" n="ModalitiesInStudy"></e>
<e en="F" t="00080064" n="ConversionType"></e>
<e en="F" t="00080064" n="PresentationIntentType"></e>
 <e en="T" t="00080070" n="Manufacturer">@empty()</e>
 <e en="T" t="00080080" n="InstitutionName">@remove()</e>
 <e en="T" t="00080081" n="InstitutionAddress">@remove()</e>
 <e en="T" t="00080082" n="InstitutionCodeSeq">@remove()
<e en="T" t="00080090" n="ReferringPhysicianName">@empty()</e>
<e en="T" t="00080092" n="ReferringPhysicianAddress">@remove()</e>
<e en="T" t="00080094" n="ReferringPhysicianPhoneNumbers">@remove()</e>
 <e en="T" t="00080096" n="ReferringPhysiciansIDSeq">@remove()</e>
 <e en="F" t="00080100" n="CodeValue"></e>
 <e en="F" t="00080102" n="CodingSchemeDesignator"></e>
<e en="F" t="00080103" n="CodingSchemeVersion"></e>
<e en="F" t="00080104" n="CodeMeaning"></e>
<e en="F" t="00080105" n="MappingResource"></e>
```

Anonymize script in use in one of our deployments.

<e en="T" t="0008010c" n="PrivateCodingSchemeCreatorUID">@hashuid(@UIDROOT,this)</e>
<e en="T" t="0008010d" n="CodeSetExtensionCreatorUID">@hashuid(@UIDROOT,this)</e>
<e en="F" t="0008010f" n="ContextIdentifier"></e>

<e en="F" t="00080106" n="ContextGroupVersion"></e>
<e en="F" t="00080107" n="ContextGroupLocalVersion"></e>
<e en="F" t="0008010b" n="CodeSetExtensionFlag"></e>

25 3Dnet Medical Radiology Information System

25.1 Log in

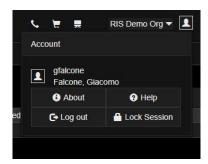
On the main page enter your username and password then click Log In.



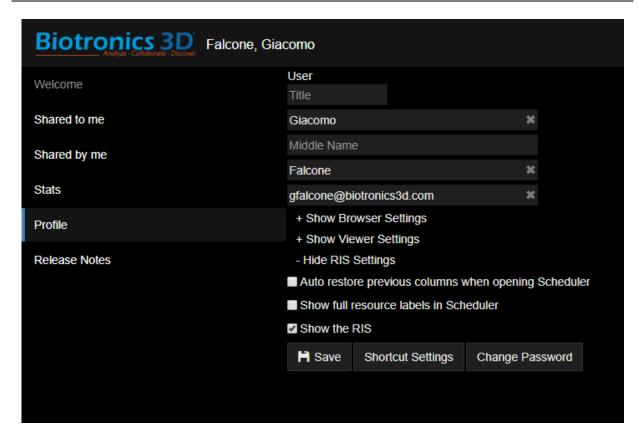
Login page. Note the contents of this box regarding your monitor setup.

25.2 User profile

New users can access the personal panel by clicking in the portrait icon in the top right corner of the screen, where the links to personal settings (by clicking on the user name), help and logout/lock session are located.



Profile control panel.

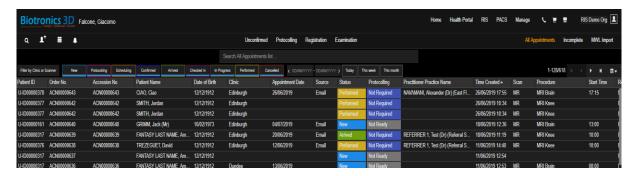


Edit profile information, including passwords and viewer settings. Show RIS settings to display RIS settings.

Click on the **Show Browser Settings** tab to choose the preferred languange for the user interface and the number of studies that will be listed in the worklist at the same time. Click on the **Show Viewer Settings** tab to configure the graphical user interface and the Diagnostic Viewer viewer according to your preferences. Click on the **Show RIS Settings** tag to configure the preferences for the RIS.

26 Appointments list

Click on the **RIS** tab located in the upper part of the welcome page to display the appointment list. This worklist displays appointments currently registered in the RIS system, showing the patient Last Name, First Name, Patient ID, Accession Number, Modality, Study Description, Referring Physician, etc.



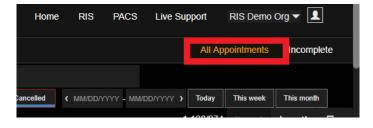
Appointment list interface and searchbar.

To order the patient list, for example by study date or patient name, click on the respective column head in the appointment list. The patient browser also offers quick filters to display patients sorting by time (today, this week, this month, etc), workflow status (patient arrived, scan in progress, appointment cancelled, etc), or filter by Clinic/Scanner. Filtering by Clinic or Scanner will display only appointments that have been assigned to a specific Clinic (hospital) or Scanner (modality).

Workflow status is color coded:



Users can display all appointments in the database by clicking on All Appointments, above the study list, on the right hand side. Click on Incomplete to display patient records that have not been fully completed.



Close-up on the "All Appointments" button.

Above the appointment list, users can pick one of the pre-defined dedicated worklists: Unconfirmed, Protocolling, Registration, Examination. Each tab serves a specific purpose and is designed to facilitate the daily workflow of users with different duties.



Select the appropriate filter to get different worklists.

- Unconfirmed: this list pertains to the receptionist/clerk. Shows appointments that are yet to be confirmed (unscheduled).
- Protocolling: displays all the appointments created, filled and saved as ready to be protocolled. This is the dedicated tab for the technicians or clinicians in charge of protocolling the appointment.
- Registration: this is the dedicated list for the receptionist/clerk, show patients that are expected to arrive on the day. By default it displays a list of appointments that are in the following workflow status: Confirmed, Arrived, Checked In. It also filters by date: Today.
- Examination: displays patient information for technicians and clinicians: it is by default filtered in such a way to display patients marked as (workflow status) Arrived. Time filter is: Today.

Filters pre applied to these worklists can be changed at any time by any user. Upon leaving the worklist, the filtering will be reset to the default values.

27 Appointment scheduling

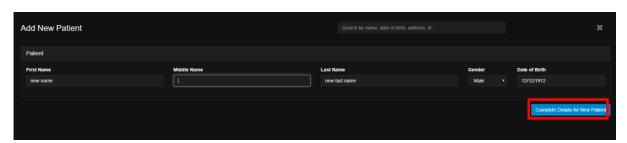
27.1 Create a new patient record and add an appointment

Appointments can be created for existing patients and newly added patients. Click on the search icon in the top left to perform a search using the patient's name, date of birth or address information pressing Enter once completed. If a record for this patient is available, the user can navigate to the patient by clicking the patient details within the search results. Otherwise, the user will be prompted to create a new patient record, and the option to add a new appointment will become available once the patient details are completed.



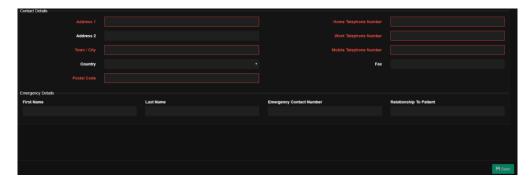
In this example the user types patient demographic in the search bar to check if a patient is already in our DB. No results found. Click on New Patient.

To create a new patient record, click on the blue button (new patient) in the top right corner. Type in the basic information that are required to create a new record (first name, last name, gender, DOB) and click on the blue button "Complete details for new patient".



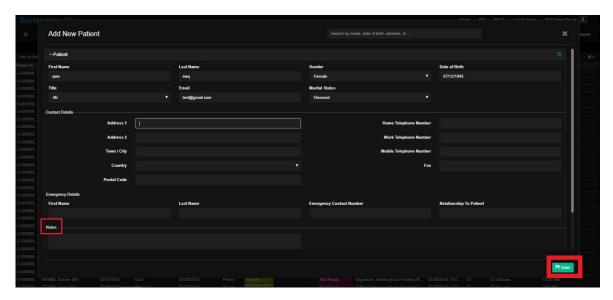
Click on the highlighted button to complete details.

After clicking, a more comprehensive personal details page will display right below. In this new tab, fill in the contact (address, telephone, etc.) and emergency details. Fields in red in the next picture are mandatory. (Only one telephone number is required for the mandatory patient details fields).



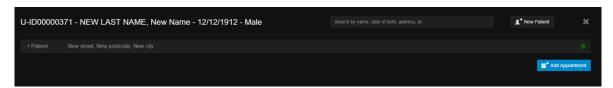
Add Contact details and Emergency details.

Click on the green Save button in the bottom right corner of this window to save the patient record. Users can add notes regarding the patient, for a more efficient workflow. (eg. patient is in a wheelchair, patient needs oxygen, senile patient, first appointment, follow up, rebooking etc.).



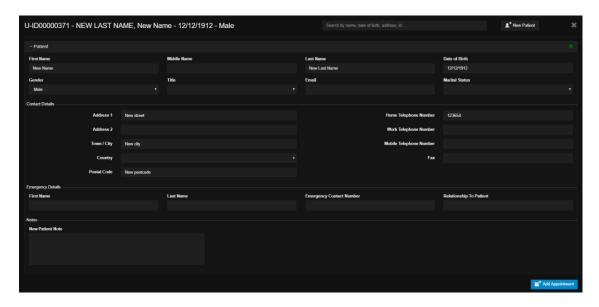
The patient registration panel.

Users can now add an appointment for this patient by clicking on Add Appointment.



Summary of the new record created.

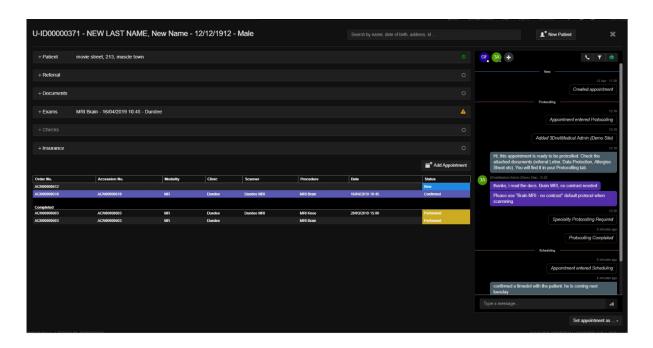
Click on the +Patient tab to expose all the demographic details for this patient.



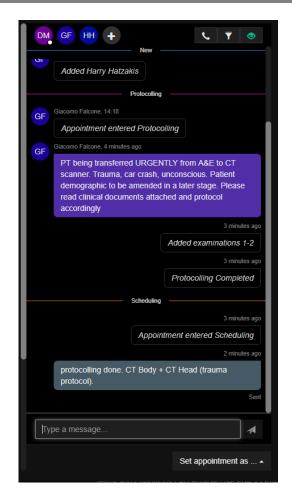
Patient tab exposed.

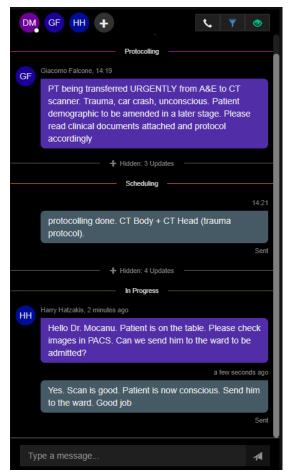
27.2 Interactive Notes and VOIP

As soon as the appointment is added, a new dialog window (following picture) will be displayed. On the right hand side of the screen is a space in which users can add Interactive Notes; this is a unique feature of our software that lets every actor in the radiology workflow (receptionist, radiographer, radiologist, referrer, etc.) exchange information, ask questions, provide feedback about each individual appointment. This feature also records and logs information so that they can be accessed and checked at any stage of the radiology workflow and also after the appointment is completed and the report is delivered to the referrer. Interactive Notes also log the workflow status of the appointment (when the appointment created/protocolled/scheduled/started/completed).



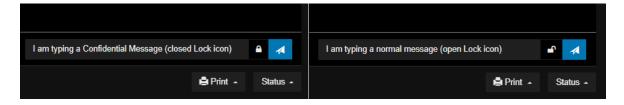
Fill each separate tab (Patient, Referral, Documents, Checks, Exam, Insurance) to create a patient appointment. Click on the button in the bottom right to go to the next stage of the workflow (Set appointment as) by choosing an action from the drop down menu. Use the built in chat log and interactive notes to add users to the conversation, ask for more information or highlight quick notes to other users.





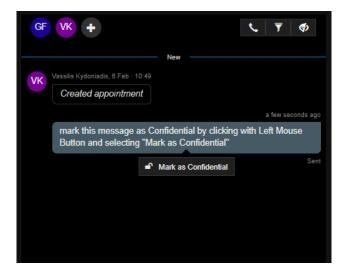
On the left: Interactive Notes window, displaying all the events (Messages, Status Updates); on the right: Interactive Notes window filtering out Status Updates (only text messages displayed).

Users can flag a text message as Confidential. Confidential messages will only be displayed to users that have been granted the correlated permission (granted by an Admin through the Manage panel). To start typing a Confidential message, lick on the Lock icon in the type field, next to the Send button.



Picture on the left: the closed Lock icon indicates that the message will be Confidential; Picture on the right: the open Lock icon indicates that the message will be sent as a normal message.

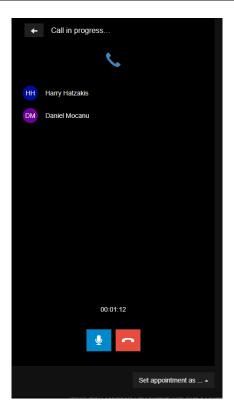
Messages can be marked as Confidential after being sent to the chat: click on the sent message witl the Left Mouse Button, then select Mark as Confidential.



Click on a normal chat message with the Left Mouse Button to transform it into a Confidential message.

At the top of the Interactive Notes view is a list of all the Users involved in the Appointment, displaying the initials of first and last name (in the example: DM, GF, HH). By clicking on the plus sign, it is possible to add more Users by selecting their name from a drop down menu. Click on the icon in the top row to access filtering options: a) search for text through the messages sent; b) show/hide text based on the message type (show/hide Status Updates such as "Appointment entered Protocolling"/ "Appointment entered Scheduling", etc; show/hide User written text messages; show Any (display both Status Updates and User written Messages). Users can Unsubscribe from an appointment to stop receiving notifications by clicking on the correlated eye icon

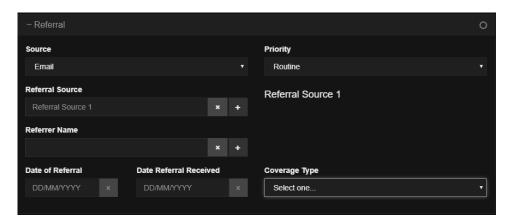
Users can start a one-to-one or a group call using the built-in VoIP (Voice over IP) Call tool. Click on the phone icon to access this feature. Notifications for incoming calls are displayed to the users involved.



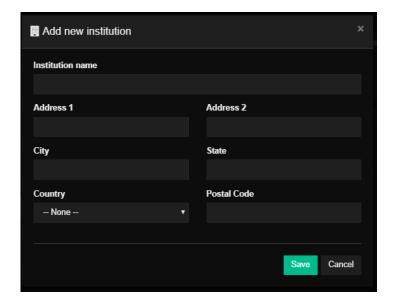
VoIP Call in progress. Other Users involved are listed at the top. Options to mute the microphone and close the conversation at the bottom.

27.3 Referral tab

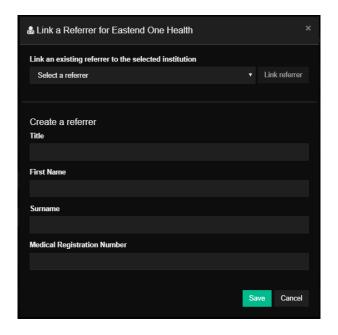
In this tab users can capture the source (phone, email, online, post), the appointment priority (routine, urgent, critical), the Referral Source and Referrer Name (pick one of the referral sources set for this organisation), and the date of Referral/date in which the communication was received. If the Referral Source does not exist based on the received referral then the plus icons provide the ability to add a new Referring Institution and Referrer. Use the coverage Type drop down menu to specify if the appointment is Public Healthcare, Private Insurance, Selft Pay.



Referral tab. Click on the + sign next to Referral source and Referrer Name to add a new Referral Source or a new Referrer Name.



Add a new Institution. This dialog window is presented after clicking on the + sign next to Referral Source. A similar one is presented to add a new Referrer Name.



Link an existing Referrer to the Referral Source or Create (add) a new Referrer.

27.4 Documents tab

In this tab, users can scan and upload a softcopy of the documents related to this an appointment. Documents are arranged and sorted using document labels. Document types can be customized following the local workflow. To upload a document, click on Upload on the right hand side of the Documents tab. Select from the drop down menu a document type, then browse your local hard drive or drag and drop the document in the upload box. Supported formats include jpg, jpeg, gif, png, bpm and pdf. Connect a paper scanner to your device to have the ability to scan a document right into the Documents tab of RIS by clicking on the "Scan" button.

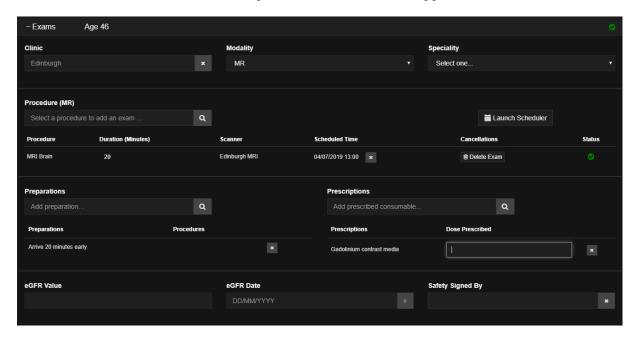


Click on each document label to open the corresponding document.

Documents types are divided between Clinical and Administrative. Clinical documents will be shared with the PACS and will be available for clinicians to check when viewing an examination (referral letter, allergies form, modality safety checks, etc.). Administrative documents (insurance forms, billing, etc.), will not be shared on the PACS.

27.5 Exam tab

The exam tab is used to assign the appointment to a clinic, assign a modality, assign a specialty, assign a procedure (examination type), add a preparation for the exam (arrive early, arrive with no jewellery, etc.) schedule the appointment for a timeslot, record the request for contrast medium (or other consumables) that might have been prescribed by a doctor. Each field will present a drop down menu, with choices that will be entirely customizable depending on the local workflow. This is the tab used to protocol and schedule an appointment.

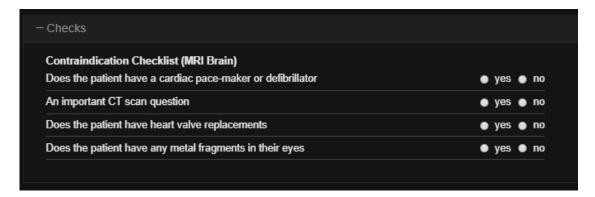


Use this tab to protocol and schedule an appointment.

The information added to this page will be reflected in the appointment list and in the calendar. An appointment added to a specific clinic and specific modality will be displayed in the correlated clinic/modality worklist in the study list and in the correlated calendar column.

27.6 Checks tab

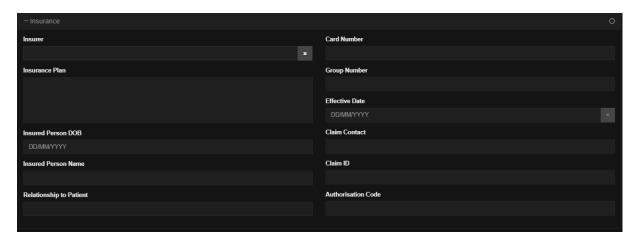
In this tab users will be able to go through a list of user defined checks and questions, which will be tailored depending on the local workflow. The checklist can be modality/procedure/gender dependent, or a general safety checklist. This checklist can be filled by users talking to the patient in person or on the phone/email etc.



Customizable checklist.

27.7 Insurance tab

This tab is used to fill in with Insurance and billing details, as shown in the picture below.

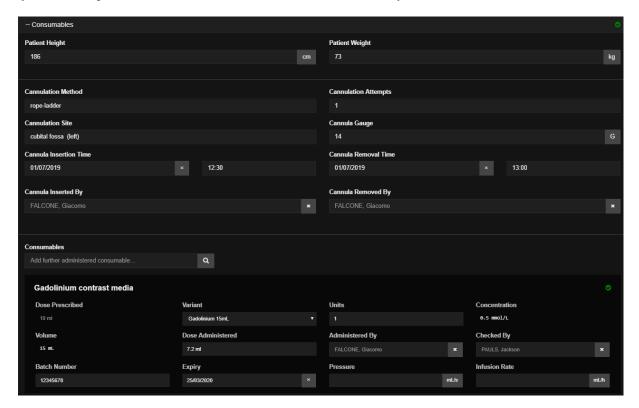


Insurance tab.

27.8 Consumables

The Consumables tab is used to keep track of the items used during an appointment (consumables can be set up using the Consumables Manage interface available for OrgAdmin users). The following screenshot displays the fields available for every RIS user.

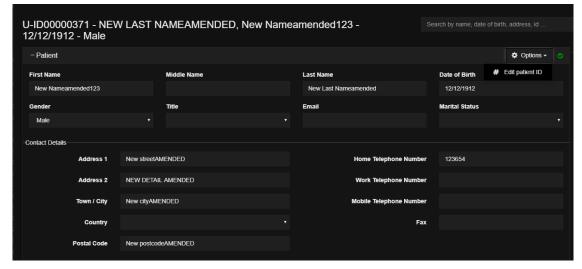
At the top of the tab, users can record a patient's Height and Weight, important to determine the correct dose to administer to the patient. Below this area is a space used to keep track of the cannulation info, if prescribed (method, number of attempts, anatomical site, cannula size, cannula gauge, etc). In the bottom part of this tab is a dedicated space for the consumables used (in the example below is Gadolinium based contrast medium).



Consumables tab within the appointment window.

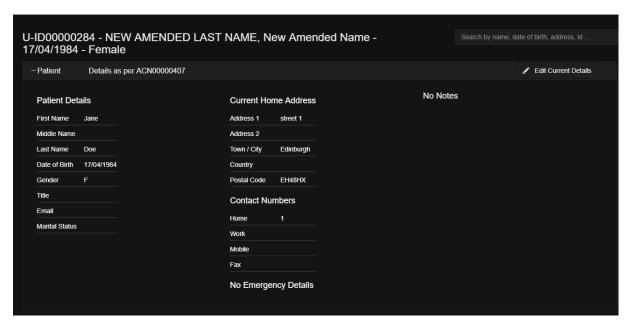
27.9 Edit patient details

To amend or edit patient details for an appointment, find the appointment from the appointment list. Open the record and select the Patient tab. Now simply edit the fields manually.



Amend patient details. Select each field to manually edit the details.

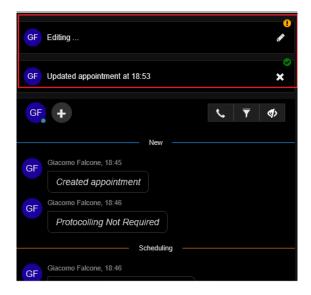
Hit save to propagate the change to all other appointments pending for this patient. Appointments already completed for a patient will display the new amended details in the header of the appointment page, but will display the original patient demographic in the Patient tab in the appointment page. This is to ensure consistency with the details that were displayed during the examination of the images in PACS and that have been used to create a report.



Scan performed: amended details are displayed in the header. Original details displayed in the patient tab.

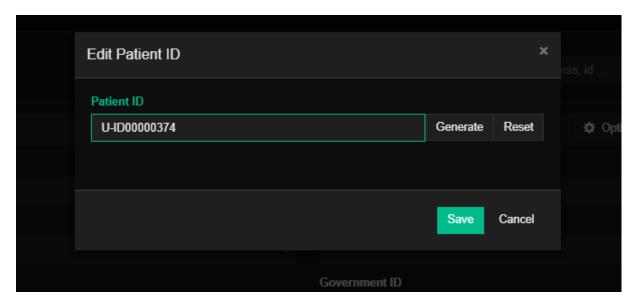
In the image above: the header of the appointment page displays the amended details (New Amended Name, New Amended Last Name, etc.). The Patient tab right below, displays the original patient demographic that were registered at the time of the completion of the appointment. Two or more concurring Users can edit the document at the same time. In the top right of the appointment details form will be displayed who is editing the record/when was the last edit (see par. "Appointment details"). Edited info is automatically updated as soon as the user clicks on the Save button in the bottom right corner of the screen.

If two or more users are viewing the Appointment interface for the same patient at the same time, they will be notified if any information regarding the patient is currently being edited. The notification is displayed at the top of the Interactive Notes display.



Users are notified when patient information is being edited.

To amend a Patient ID, click on the "Options" button in the top right corner of the Patient tab. In the drop down menu, click on "Edit patient ID". The following dialog will appear.

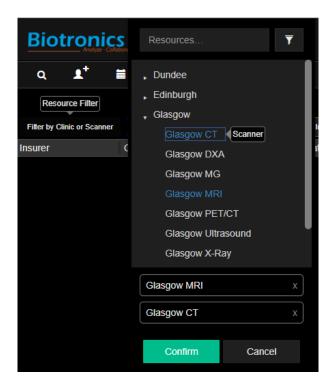


Edit Patient ID dialog. Generate an automatic ID or manually set a value in the field.

Clicking on "Generate" will automatically assign a PID to this patient. Users can also manually edit the field by typing a number with the keyboard. The software will display a green overally around the data entry field if the requested ID is available. If the string entered is already matched to another patient, the overlay will become red and a "Not available" message will be displayed.

28 Worklist filtering and customisation

Click on the "Filter by Clinic or Scanner" button at the top left of the worklist table to open the Resources Selector. Select a clinic and/or a scanner to filter the appointments. Users can search for a resource and, once selected, the resource will display above the Confirm button. The list of appointments is now filtered by the items selected in the Resource Selector. The selected filter is displayed in the filter bar. Remove completely all the resources from the filtering tab will result in a "No resources selected" message. The "All Appointment" list will display the appointments with the filters removed.

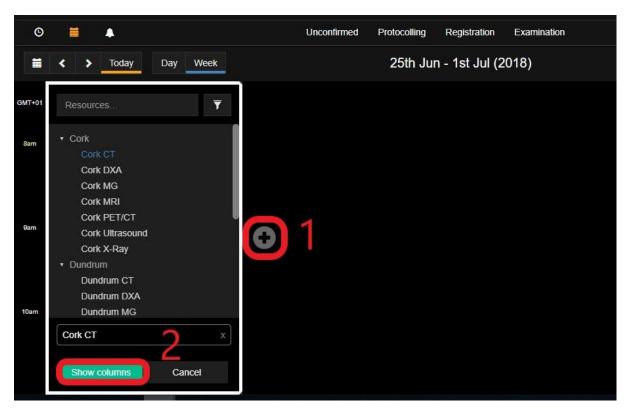


Resources Selector menu. Click on each Resource you want to add to your worklist. Appointments scheduled for those Resources will be displayed in the study list.

To apply Status filters, click on the Status labels at the top of the appointment list. Labels highlighted in blue are active, this means that the study list will display studies currently in that Status. Use the Date Range filters to the right of the status filters to filter appointments by time. Users can either select a range of days to be displayed ("From – To") or click on the Today/This week/This month buttons.

29 Calendar

The calendar is accessible by clicking on the calendar icon in the top left of the screen. A new calendar tab is opened by clicking on the plus sign on the left side of the new window that just opened. Select the correct Resources and click on show columns.



Click on the plus sign first, then select a worklist and click add columns to display the worklist.

Any number of columns can be added repeating the same process. If more than two columns are displayed users can explore their content by maximizing one of them ("use this column" button).

To go back to a collapsed view, click on the restore icon in the top right of the workspace



Collapse a maximized worklist in the calendar.

Next to the minimize icon users can find the options icon (image above, the vertical dots), to click and add a new column, pin and bookmark the column. Bookmarks, which are accessible by clicking on the star icon in the right part of the screen, allow the user to navigate quicker

through multiple tabs, speeding up the workflow. A user can also Pin a worklist to always be on top. Below is a sample of a fully scheduled week with booked patient appointments displayed with a background colour reflecting the appointment status in the workflow (appointment created, ready for protocolling, protocolled, ready for scheduling, confirmed with the patient and scheduled, patient arrived, patient checked in with radiographers, patient being scanned, patient scanned).

The calendar can display one day at a time or a whole week. On clicking the left/right arrows the schedule for the following/previous day/week is displayed.



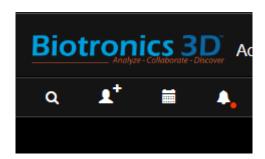
Week display of the "MRI 1" worklist. Appointments appear in different colours depending on the state of the procedure in the workflow. Each coloured block can be deleted, resized, moved to a different timeslot.

A calendar worklist can be displayed for a Daily view or a Weekly view. Users can move in the future or in the past by clicking on the arrow icons in the top left of the screen, next to Today, Day, Week. An indication of the time represented in the table view is visible in the top centre part of the screen, right above the scheduler.

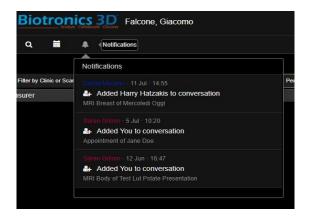
Appointments can be scheduled by opening the calendar and selecting a time slot. Once the time slot is selected, the user can proceed to search for the required patient and create the new appointment. This action will trigger the beginning of the appointment creation routine, which will work as covered earlier in this guide. Every appointment in the scheduler can be moved vertically (sooner or later during one day) by clicking and dragging it around the workspace of the scheduler. Appointments can also be resized, reducing or prolonging the allocated time.

30 Notifications

A very useful feature implemented in our RIS is the notifications system. A notification is a message that the RIS displays in the top left corner of the UI to provide the user with reminders, communication from other people, or other timely information. Users can click the notification to open the event or take an action directly from the notification panel.



The red dot displayed informs the user that a new notification is available for viewing.



Notification panel. The username of the person that performed the action that is notified is displayed in colour. A brief description of the action is below the username.

31 Management page

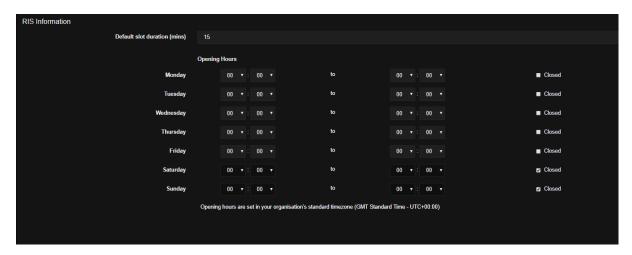
Additional settings can be accessed in the "Manage" section of the site, which is divided into General, Users, RIS, PACS and Advanced. The General panel is used to set the organization name and logo, address and other general info. The Users panel allows the admin to modify general options for each user, as well as grant each individual user different permissions on the portal.

Here is a breakdown of the dedicated RIS settings, that are easily found in the left part of the screen.

31.1 RIS opening hours

In this page admins can set default values for the Opening Hours of the clinic/organizations. Click on the Closed tick box to mark a day in the week for closure of the clinic. Press save to finalize.

At the top of the screen, it's possible to set default duration for each slot. This will be the minimum default slot duration for the timeslots in the calendar/scheduler.



Set the default Opening Hours and default slot duration.

31.2 RIS Resources

Resources can be scanners, clinics and rooms in the RIS Org. Use this page to define a logical diagram of the organization, adding resources and creating logical relationships (set a Parent resource for one or more Resources) among resources.

Use the Search / Create New field to type the name of a resource. If the search does not return any results, create a new Resource. Select the resource type (Hospital, Scanner, Room), name, AE title, parent relationship (if the Resource is a Scanner or Room), modality (if the Resource is a

scanner). Click on Archive to withdraw the Resource from the list. The Resource will be disabled. Resources can be selected from the list and edited.

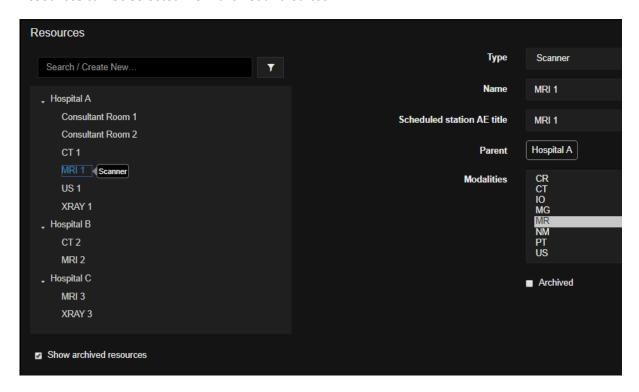


Diagram of the RIS Org, with three hospitals (Hospital A, Hospital B, Hospital C) and the rooms and scanners in each hospital.

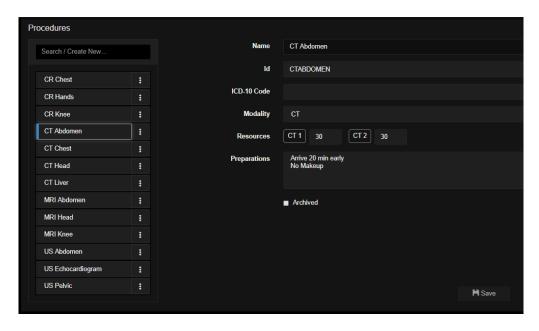
31.3 RIS Procedures

Use this tab to create and edit Procedures (MRI Head, MRI Abdomen, CT Chest, US Thyroid, etc.) for the Organization. Search a Procedure name to find a pre-existing Procedure from the list or create a new one. When the procedure is selected, a menu will be displayed on the right hand side of the screen.

Use this menu to set the Procedure accordingly. Users can add a Name, ID, ICD-10 Code. Define for which Resources (which rooms or clinics) this Procedure will be available and assign this procedure to a specific Modality.

Only relevant Procedures options will be offered to the user when scheduling/protocolling an appointment. Only Procedures assigned to the selected Modality and the selected Resource (Hospital, Scanner), will be displayed. Users can add default appointment duration for appointments marked with this Procedure type.

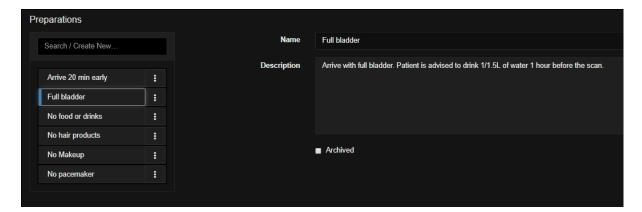
Assign one or more default Preparations (see how to create Preparations in the following paragraph) to this Procedure, so that Patients will be automatically informed about which actions to perform or avoid before the scan.



Procedures tab: use this tab to create a new Procedure or edit a pre-existing one.

31.4 RIS Preparations

Preparations are a set of actions that patients are supposed to perform or to avoid before the scan.



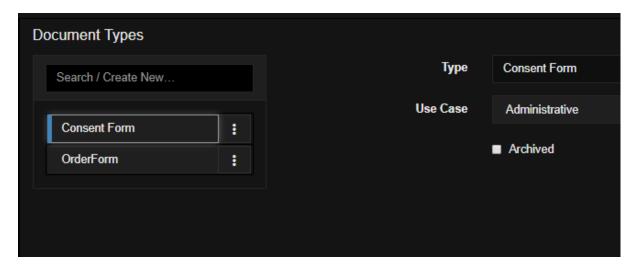
Preparations tab.

Search or create Preparations using the input field on the top left of the screen. Preparations can be manually assigned for an appointment during the scheduling phase or automatically set from the Procedures tab.

31.5 RIS Document types

Set Document types to create labels in the scheduling menu. Use labels accordingly when uploading documents to assign specific Documents to the corresponding document type.

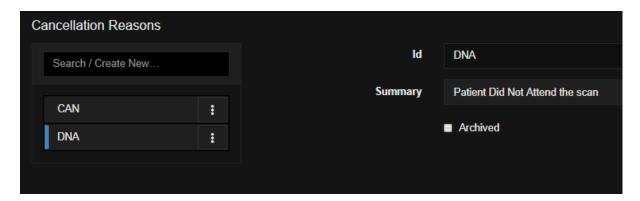
Customize the Document Type name and specify the Use Case (Administrative, Clinical). Clinical Documents will be shared to clinicians in the PACS. Administrative Documents will not be shared and will only be visible in the RIS.



Consent Form Document Type. This type has been flagged as Administrative.

31.6 RIS Cancellation reasons

It is important to record the reasons behind the cancellation of an appointment. In the event of an appointment not attended by the patient, users can add a Cancellation reason to label accordingly a cancelled appointment. Each organization can create and customize its own Cancellation Reasons to best match the local workflow.

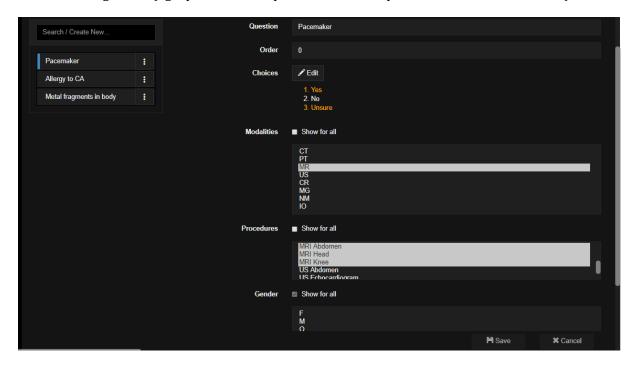


DNA: Patient did not attend.

31.7 RIS Contraindications

Set Contraindications and assign them accordingly to RIS Procedures (scan types). Contraindications will be shown in the scheduling phase. Create a new Contraindication from this menu. Assign a Contraindication to one or more Modalities and one or more Procedures from the list; users can also assign Contraindications based on gender.

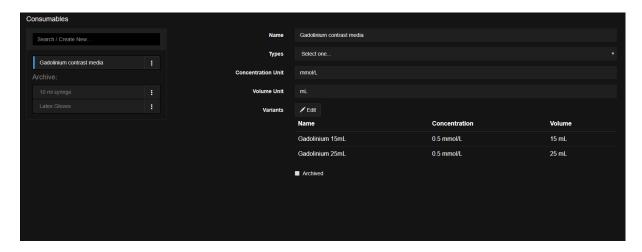
Admins can set the ordering of the Contraindications displayed to the end user by changing the value in the Order field. Use "Choices" to set the options that will be available for the end user in the scheduling menu (eg. option a: Yes; option B: Yes, No; option C: Yes, No, Unsure; etc.).



Contraindications menu.

31.8 RIS Consumables

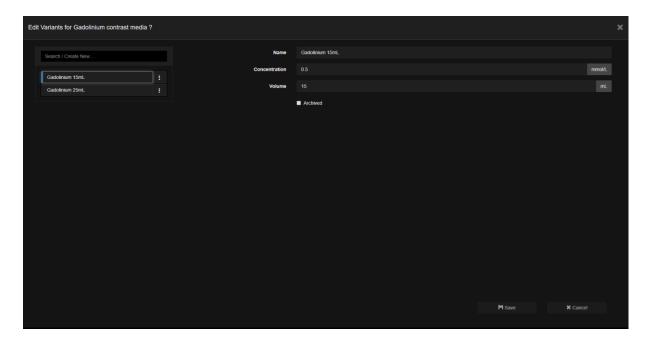
Use the Manage Consumables tab to set up and customise consumables (contrast medium, syringes, etc) within an Organisation.



Add a Consumable then customise the name, type, etc.

Each consumable type can be customised so that one or more variants of it can be displayed. In the example above, a consumable type "Gadolinium Contrast Media" has been created. This type of Consumable has, within this Organisation, two separate variants (Gadolinium 15 mL;

Gadolinium 25 mL). Users can customise each variants clicking on the Edit button next to "Variants" and accessing the following menu (see picture).



Create and edit a variant for the Consumable type selected.

Here users can add a new variant, adding details such as Name, Concentration, Volume; or edit already existing variants (as well as archiving a variant that is not in use anymore).

32 Keyboard shortcuts

- P hides/shows study panel
- K display the reference lines
- W window snapshot
- C viewport snapshot
- U display pixel Hounsfield units
- O display HU ROI (press Shift key to resize)
- I toggles on/off text overlay on images
- S study scroll, all series in one stack
- D switch between axial, coronal and sagittal views

Left arrow/Right arrow – jumps to the first/last image in the series

Left arrow/Right arrow with Study Scrolling Enabled – jumps through the series backwards and forwards

Up/Down arrow - scroll through the volume up and down

Z – switch between AvIP, minIP and MIP modes

Plus (+) and Minus (-) – increase or decrease the slab thickness

Q – switch between axial, VR and MPR views

L – toggle on/off synchronous navigation (link mode)

J - manually link series from different studies for synchronous scrolling

Y – remove viewport

T – maximize a viewport in the MPR mode

X – polyline sculpting

F – freehand sculpting tool (internal)

R – freehand sculpting tool (external)

Period (.) - increase window width

Comma (,) – decrease window width

M – increase window level

N – decrease window level

1,2,3,4,5,6,7,8,9 - window/level presets

<Ctrl+Shift+S> - select multiple viewports

S – after selecting more than one viewport will open the selected vieports in a new page

E – after opening the selected viewports in a new page, it will go back to the previous view

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