

Biotronics3D 3Dnet - Medical

User's Manual HTML5 Platform - Software Version 2.15

3Dnet™ Medical HTML5 Platform ver. 2.15.250325.85b6bae3 User's Manual ver. 1.35 Updated April 2024
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1 Proprietary Notice and Disclaimer

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



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



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2 Introduction

3Dnet Medical is a DICOM 3.0 compliant, cloud-computing solution for scheduling of medical examinations and for medical image archiving, distribution and advanced visualisation. 3Dnet Medical enables radiologists and clinicians to access images at any time and any place using a zero-footprint client for advanced visualisation and image processing. 3Dnet Medical runs in a web 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 web browser memory during the visualisation session. Upon closing the web 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: pre-defined 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, Android, iOS) and supports all the modern web browsers: Chrome, Firefox, Safari, Edge, etc. Images and patient records coming from systems outside of 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 encapsulated (DICOM SC, RF, ECG, OT, SR is also supported). The presented intended purpose refers to 3Dnet medical device modules which are PACS and Viewer.

2.1 Intended Purpose

3Dnet is intended to be used by physicians for archiving, communication and the display of 2D/3D visualisation of DICOM compliant medical image data, such as CT, MR, PT, Ultrasound, CR, MG, NM, DX, OT, XA, XR, XC, RF, DR, DS, SR, OCT, PX, ECG, ES, IO modalities, and for reporting.

3Dnet Viewer provides several levels of functionality to the user:

- Basic analysis tools such as 2D review, orthogonal multi-planar reconstructions (MPR, oblique MPR, curved MPR, Slab MPR, AvgIP, MIP, MinIP) measurements, annotations, reporting, distribution, etc.
- Tools for in-depth analysis, such as segmentation, endoscopic view, colour volume rendering, greyscale volume rendering, 3D volume review, path definition and boundary detection.
- Specialist tools and workflow enhancements for specific clinical applications which provide targeted workflows, custom UI, measurement and visualisation; including Virtual Colonoscopy, Vessel Analysis, Calcium Scoring, PET/CT, lung CT Analysis, dental CT, and Breast and Prostate DCE-MRI.

3Dnet can be used to display medical imaging data of covered modalities on patient population and the medical conditions covered by each modality.

3Dnet is intended for health-care professionals and medical researchers, with knowledge on medical imaging and experience in digital imaging diagnosis and interpretation. 3Dnet viewer is a diagnostic reading software package, intended to be used by qualified physicians, often being radiologists. 3Dnet PACS contains all the characteristics to allow the clinical staff to be able to manage clinical data, allowing the information to be ready and prepared, allowing the physicians to access in a fast and secure way this information.

The PACS software provides different functionality depending of the needs of the different users of the system (reporting physicians, referral physicians, clinical staff and technical staff, including system administrators).

3Dnet offers optional modules like RIS, Teleradiology, Referrer Portal and Health Portal that are non-medical device modules. In particular, the viewer included in the Health Portal to allow patients to visualise their images, is not part of the medical device and has no medical diagnosis purpose.

2.2 Performance Characteristics

3Dnet is a state-of-the-art cloud-computing solution for medical imaging through which physicians can store, share, visualize and analyse medical images and collaborate with colleagues online. 3Dnet enables healthcare professionals to access their work at anytime and anyplace using a zero-footprint viewer, free of the previous necessity to restrict themselves to isolated workstations. By combining server-side rendering and progressive streaming, 3Dnet delivers unprecedented visualization performance of large data sets even over low Internet bandwidths. The image processing functions are handled on the server, so there is no need to download software or data to the local device.

Client recommended specifications:

- Hardware: Any platform supporting HTML5, display 1280 x 1024 / 32-bit minimum resolution. Diagnostic reading of images requires a medical grade monitor.
- Operating System: Windows 10/11 and Mac OS X (x86 or x64), or any platform (Mac, Windows, Linux, Android) supporting HTML5.
- Web browser: HTML5 supporting web browsers: Chrome 110+, Firefox 109+, Safari 16+, Edge 109+, etc.
- IT networks: +2 Mbps Secure network (Do not use open networks).
- IT security measures: Keep system up to date, keep account information secure, report any suspicious activity on your equipment or account.



The use of 3Dnet on or mobile computers or devices is not intended to replace full radiology workstations and should be used only when there is no access to such a workstation.



Review of images require an optimum display of images. Only use suitable monitors and printers for diagnosis review of images. Follow the maintenance and care instructions given in the manufacturer's documentation.



Any serious incident that has occurred in relation to 3Dnet should be reported to Biotronics3D and the competent authority of the Member State in which the user and/or patient is established;

2.3 Residual Risk

Insufficient training may lead to inappropriate physician actions with risks to the patient:

- A user who makes mistakes and judgement errors using the product due to inexperience or unfamiliarity with the product.
- A user who does not read and/or adheres to the instructions for use for the product and uses it inappropriately or for a non-indicated purpose.
- The software may misrepresent images or parts of images making it difficult for the user to provide a correct diagnosis.
- The user is unable to understand settings, measurements or other information presented by the software which could lead to misdiagnosis.

These risks have been effectively reduced and mitigated considering diagnosis are performed by qualified Radiologists and 3Dnet was designed by safety providing an intuitive workflow avoiding mistakes, avoiding violation or abbreviation of instructions and procedures, providing alternative visualisation modes enabling to check any doubt that may exist in the representation, and providing an intuitive workflow enabling always to understand the presented information.

Software errors may lead to inappropriate physician action with risks to the patient:

- The software produces an incorrect measurement due to a software failure.
- The software fails to calculate or miscalculates data and provides inaccurate information to the user.
- The hardware on which the software is installed is below the recommended system specifications.
- A failure in the network connection (either operating system or hardware) prevents the software from importing or exporting data to or from a file or directory not based on the client hardware.

These risks have been effectively mitigated and reduced to an acceptable level through safety design and development practices. The accuracy of the clinical measurements in our system, depends on how the images were acquired - acquisition protocols, scanners etc. Test are conducted to verify probe performance during verification and validation testing. Review of code by peers is performed to assure that equations are coded correctly. The software is installed by competent IT professionals that verify the system specifications before install. Data is maintained on the local client hardware if a temporary network failure due to external factors occurs ensuring no data is lost.

A data breach may expose or compromise the access to data with risks to patients and users:

- Unauthorised person accesses the software and patient records.
- Users or patients records are breached by external agents.
- Users or patients records are breached by internal agents.
- Patients records are deleted or made unavailable.

These risks have been effectively mitigated and reduced through the implementation of user, role, work-list and organization management; Audit Log; Network Security; Physical security; penetration testing; Password enforcement; Organizational procedures for HR; Data deletion procedures; backups; grid computing.

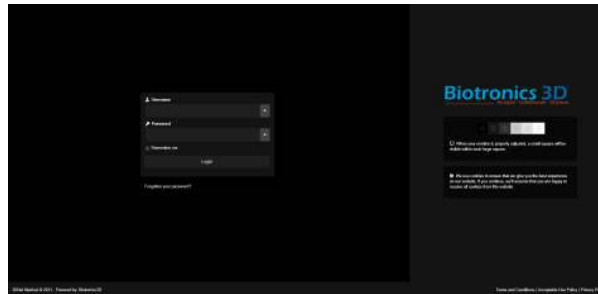
Risks have been reduced to acceptable levels and individual and overall benefits outweighs the risks.

3 User

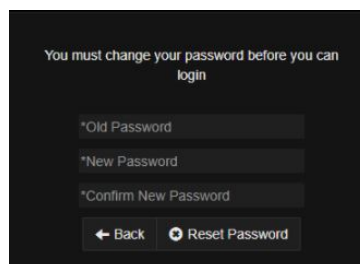
3.1 Login

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

Your password may have been set to auto expire by your organisation. If it has expired, you will be prompted to create a new one. Your new password must be different from the old one.



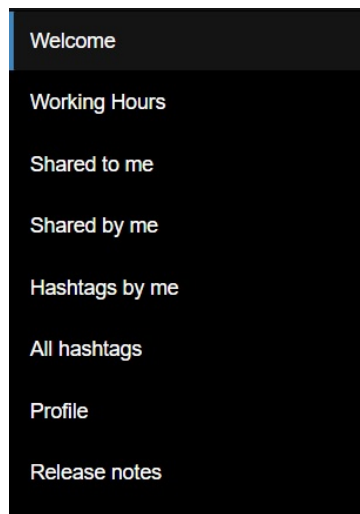
The login page



The reset menu for expired passwords

3.2 Home page



After you've successfully logged in, you will be redirected to the Home page. It is divided into the following sections:

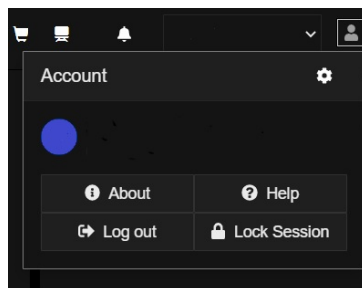


The Home menu

- The 'Welcome' tab contains general information.
- The 'Working Hours' tab lets you check your schedules. Administrators can also check the schedules of staff and associates.
- The 'Shared to me' tab where you will find studies shared to you by other users.
- The 'Shared by me' tab where you will find studies you shared to other users.
- The 'Hashtags by me' tab where you can manage the hashtags you created.
- The 'All hashtags' tab where you will find all the hashtags created by users.
- The 'Profile' tab contains general settings for the viewer, RIS, and your account.
- The 'Release notes' tab contains the changelog for 3dnet.

3.3 Profile

To access your profile settings, open the account menu by clicking on the portrait icon  at the top right corner of your screen then click on the cog .



The Account menu

Alternatively, the profile settings can also be accessed by selecting the 'Profile' tab on the Home page.

The Profile page is divided into the following sub-menus:

General Information. This tab allows you to add and modify your credentials (title, name, email-address, signature) and change your language settings.

Study Browser Settings. This tab contains the following settings for the PACS:

- 'Report Default Template Dark Theme': this option lets you change the default template of the reports to a dark theme. This does not affect the printed version of the report.
- 'Query/Retrieve default to current org node': this option lets you set your organisation's DICOM node as the default node for Query/Retrieve tasks.
- 'Browser Date Filter': this option lets you filter studies by date of creation.
- 'QR Date Filter': this option lets you filter Query/Retrieve tasks by date.
- 'Studies Listed Per Page': this option lets you select the number of studies displayed per page. It is set to 32 by default.
- 'Session Max Inactivity Time (minutes)': this option lets you set the maximum time of inactivity before a session timeout. It is set to 40 minutes by default.

Viewer Settings. This tab allows you to configure the graphical user interface and the Diagnostic Viewer according to your preferences. It contains the following options:

- 'PT/CT Colormap': this option lets you change the colour settings of the PT/CT scan overlay. It is also accessible in the viewer.
- 'SUV': this option lets you select the default Standard Uptake Value displayed in the viewer.
- 'Continuous Annotation Mode': when selected, this option lets you use more than one annotation at a time when using the viewer.
- 'Show Study Prior Order': when this option is selected, studies linked to the same patient that are added in a viewport will display a coloured label in the bottom-left overlay. The current study will be marked in orange as 'Current study', the priors will have a 'Preceding' green label, and the more recent studies will have a 'Succeeding' blue label. In both cases a number will indicate the study chronological order compared to the current study.
- 'Show DICOM Overlay for MG Studies': when this option is selected, DICOM information will be displayed on mammogram studies for presentation states.
- 'Display ext. cross ref. lines by default': when this option is selected, lines from external cross referenced studies will be displayed on the viewer, if applicable.

- 'Open one view port by default': when this option is selected, the viewer will display studies in only one viewport by default.
- 'Reverse mouse interaction in window when window levelling': when selected, this option will invert the mouse bindings for window when window levelling in the viewer.
- 'Reverse mouse interaction in level when window levelling': when selected, this option will invert the mouse bindings for level when window levelling in the viewer.
- 'CAD markers in white': when this option is selected, Computer Assisted Diagnosis markers will be displayed in white instead of their default green.
- 'Ignore frame of reference UID': when selected, this option will prevent studies using the same frame of reference UID from being linked together. This option does not affect series within a single study.
- 'Study Scrolling by Default': when selected, this option will enable continuous scrolling between studies.
- 'Hide scale on mammography viewports by default': when selected, this option will prevent the scale from showing on mammography scans. It can still be manually enabled in the viewer.
- 'Patient Info To Hide': this options lets you filter out patient information.
- 'DICOM Info To Hide': this option lets you to filter out DICOM information.
- 'Measurement Font Scale': this option lets you select the scale of the measurement font.

RIS Settings. This tab contains the following settings for the RIS:

- 'Auto restore previous columns when opening Scheduler': when this option is selected, the scheduler will automatically restore the columns you had open the last time you used it.
- 'Show full resource labels in Scheduler': when this option is selected, the scheduler will display the labels of each resource in full.
- 'Linked Resources': this option lets you set one or more default resource(s) for your organisation.

Working Hours Settings. This tab allows you to add or modify your working hours to support the study allocation process for Teleradiology.

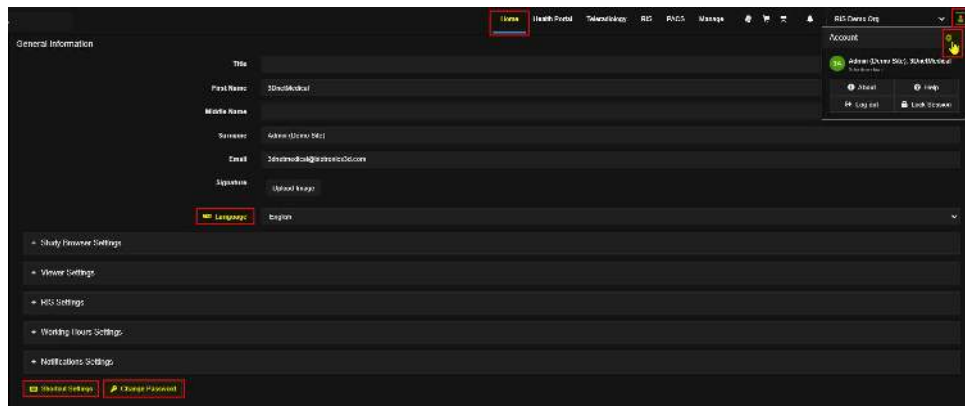
Notification Settings. This tab allows you to configure your notification preferences for email notifications and the frequency of these notifications.

At the bottom of the 'Home' page, you will find two buttons:

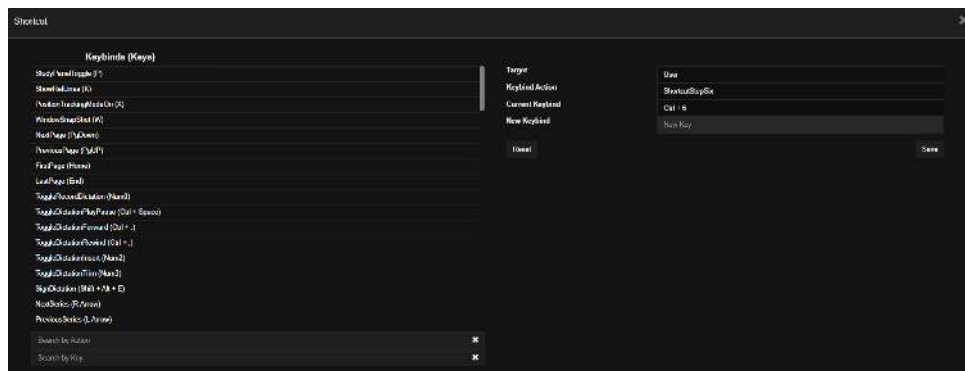
The **Shortcut Settings** button allows you to view and/or edit keybinds for the diagnostic viewer. Select an action from the list and either view or update the keybind to apply a new configuration.

The **Change Password** button allows you to update your password.

If you are in a grid / linked structure, changes will be applied over the grid.



The Profile page



The keybindings menu

3.4 Password Reset

To reset your password, go to your profile via the left hand menu or the account menu at the top right of your screen.

Scroll down to the bottom of your profile and select 'Change Password'. You will be asked to enter your existing password, and to create and confirm a new password of your choice. Answer the security question displayed and click 'Save' to finish resetting your password.

You can now log in using your new password.

If you have forgotten your password, you can reset it by clicking on the 'Forgotten your password?' option in the login screen. Enter the email address associated with your account. An email will then be sent to this address. Follow the instructions within to reset your password.



The password reset menu

4 Study Browser

4.1 Layout

To open the study browser, click on the PACS tab located in the upper part of your screen.

The PACS study browser is divided in three sections:

The filters and search tools:

This section allows you to refine your search by selecting filters for the studies. Use the search box to find patients/studies by typing any relevant information listed in the worklist columns such as study description, name or date of birth of the patient, name of reporting physician(s), etc. Refer to section 'How to Search for a Patient' for further details. The filters and search tools are divided into the following:

- The Worklist:

This drop down list allows you to choose between worklists. A worklist is a save of applied filters (see subsection below). New worklists can also be created via this option. Refer to section 4.3 "How to Create a New Worklist" for further details.

- The Folder filter:

This drop down list allows you to choose between folders. In the context of the PACS study browser, a folder is a grouping of studies with variable retention times.

- The Refresh button:

Use this button to refresh the work list with your applied filters.

- The Clear button:

Use this button to clear all of your applied filters.

- The Date filter:

Use these buttons to search for studies within a specific time frame.

- The Status filters:

Use these buttons to search for studies with a specific status.

- The Modality filters:

Use these buttons to search for studies with specific modalities.

- The Audit Status filter:

Use this button to search for studies with a specific audit status.

- The Priority filter:

Use this button to search for studies with a specific priority status.

- The Institution filter:

Use this button to search for studies linked to a specific institution.

The CSV search option:

This section allows you to filter studies by using a CSV file. To use it, drag and drop the file on the relevant box. To clear this filter, click on Remove.

- The navigation buttons:

Use these buttons to navigate between pages in the worklist.

The toolbar contains the following settings:

- Upload Studies:

This tool opens up a menu from which you can import studies into the PACS. This can either be done by dragging and dropping a dcm/zip file, choosing a DICOM folder, or by importing information from a CD. Tick the "Clear on Complete" checkbox to remove upload information once the upload has finished.

- Query/Retrieve:

This tool allows you to perform a Query/Retrieve to import a study in the system. Refer to section 4.4 "Query and Retrieve" for further details.

- Download Studies:

This tool allows you to export selected studies to your current machine. The download menu will list information relevant to the studies you have selected and offer the following options for the download: "Hide MRI Protocol Details; Dicomize document; Anonymise; Exclude Viewer; Export PNG". Please note that this function requires popups to be enabled on your browser. Download in PACS and select Anonymise DICOM metadata check box to anonymize the default tags. Also, you can do so in Send to Dicom mode. If you have a gateway with org, select the Anonymise DICOM metadata check box to anonymize the default tags.

- Send to DICOM Node:

This tool allows you to send selected studies to a DICOM node. It is also available on the Patient Record window.

Refer to section 4.5 “How to Send a Study to a DICOM Node” for further details.

- Move to Folder:

This tool allows you to move selected studies between folders. Note that each folder has a different retention time.

- Share Studies:

This tool allows you to share selected studies with another user. Refer to section 4.6 “How to Share a Study” for further details.

- Merge:

This tool allows you to merge/unmerge patient(s) starting from a selected study. Refer to section 4.7 “How to Merge a Patient” for further details.

- Patient and Study Reconciliation:

This tool allows you to perform quality control and quality assurance operations, including reconciliation on studies. Refer to section 4.9 “Patient Reconciliation” for further details.

- Delete Study:

This tool allows you to delete selected studies. You must add a reason for deletion before the study can be deleted.

- Notes:

This button will display a note panel below each study in the worklist. The panel includes existing notes and an option to write new ones.

- Export Studies as CSV:

This tool creates a CSV file from all the studies currently displayed in the worklist. The file will automatically be downloaded onto your machine. Up to 4096 studies can be included in the file.

- Table Columns Selected:

This setting allows you to hide or display columns in the worklist. To enable/disable a column, click on its relevant check box.

The PACS Worklist contains the following columns:

- Critical Findings
- Study Claim
- Tickbox
- Patient Name
- Patient ID
- Accession Number
- Study Date
- Date of Birth
- Study UID*
- Study Description
- Gender
- Modality
- Images
- Institution
- Institution (DCM)*
- Reporting Physician(s)
- Referring Physician(s)
- SPSID
- Received Date*
- Update Date*
- Transcriptionists*
- Current Node*
- Original Node*
- Performing Physician*
- In RIS/HIS*
- Report Date*
- TAT*
- TTR*
- Study Types*
- Peer Reviewer*
- Current Patient Location*
- Operator Name*
- Requesting Physician*

- Requesting Service*
- Hashtag*
- Electronic Signature*
- Audit*
- Contract*
- Second Opinion*
- Other Patient ID*
- Patient Age*

The * Denotes a column hidden by default.

The screenshot displays the Biotronics 3D PACS interface. At the top, there is a navigation bar with tabs: Home, Health Portal, Toleradiology, Peer Review, RIS, PACS, Manage, and RIS Demo Org. Below this is a search bar with the text 'Search (Name/ID/DOB/Accession/Ref/Study Descr)'. To the right of the search bar is a 'Drop CSV file to search' button. Below the search bar is a table of patient studies. The table has columns: Patient Name, Patient ID, Accession No., Study Date, Date of Birth, Study UID, Study Description, and Gender. The table contains several rows of data, including studies for BANNER, Bruce; RIBEIRO, Paulo Luis Rodri...; GILLESPIE, Dizzy; CLARKE, Arica; LEEDSCADAVERT; WASHINGTON, Dinah; TATUM, Art; 123, Test; LARGE RABBIT; KENT, Clark; LEE, Ho; TEST, Annie; DOG ELBOW EXAMPLE; JACKSON, Michael; PAULS, Homer (Mr); PATIENT6, Test; TEST, Patient3; TEST PATIENT2; SMITH, George; HOLOGICA; and BILATERAL, My. Below the table is a 'The PACS Worklist' section. The worklist shows details for a specific study: TEST, Test2021 19/04/1952 U-ID10000007. It includes a table with columns: Study Description, Study Date, Accession No., Images, Modalities, and Institution. The table shows one row: CT Head, 17/12/2020 08:37, ACN00001237, 98, MR, 3DNETMEDICAL. Below the table are buttons for 'Download' and 'Clear'.

4.2 How to Search for a Patient

To find a study in the PACS study browser using the search box, type in information related to that study such as patient name, ID, birth date, institution, accession number, referring physician, etc. The search criteria can be any information displayed in the worklist columns. Please remember to enter information in full to get more accurate results (e.g. 30/04/1989 as birth date instead of simply 30/04). To refine your search results, click on the arrow icon next to the search box to select a specific category to search. Alternatively, the search category menu can also be opened by using the '>' key.

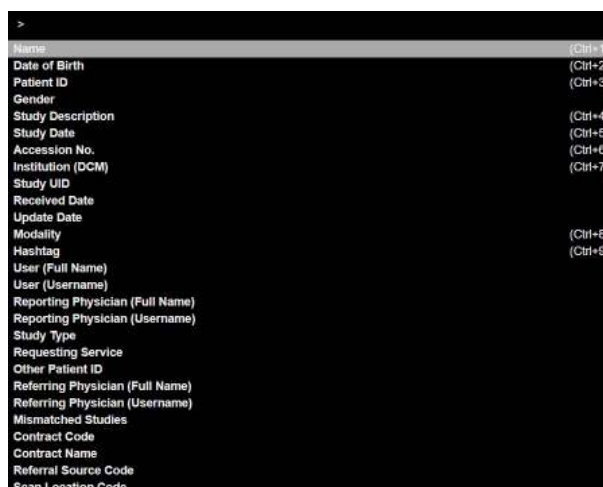
To sort the patient list, for example by study date or patient name, click on the respective column head in the study list.

Mismatched Studies To look for a study that was not matched properly in the RIS, select the 'Mismatched Studies' option in the search box. Using the 'Y' key will list all available mismatched studies. Using the 'N' key will list all available matched studies.


Filters

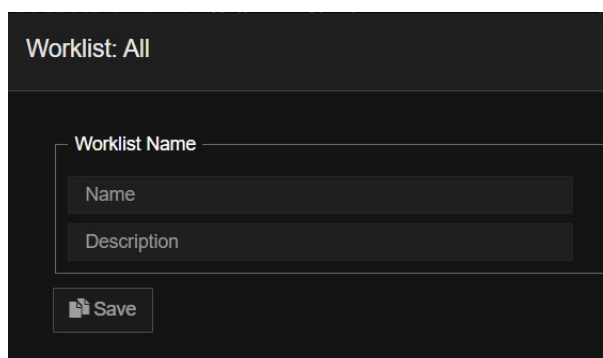
The study browser also offers quick filters that will allow you to display patients/studies according to certain

criteria such as modality type, study status, study date, and more. Please refer to section 4.1 to get an overview of the filters available in the PACS study browser.




4.3 How to Create a New Worklist

To create a new work list in the PACS study browser, start by configuring your current worklist filters and parameters. Then select the "New Worklist" option in the worklist menu or click on the worklist icon  at the top left of your screen. This will open a new menu. Enter a name and a description for your worklist then click enter. Your worklist will then be ready to use.



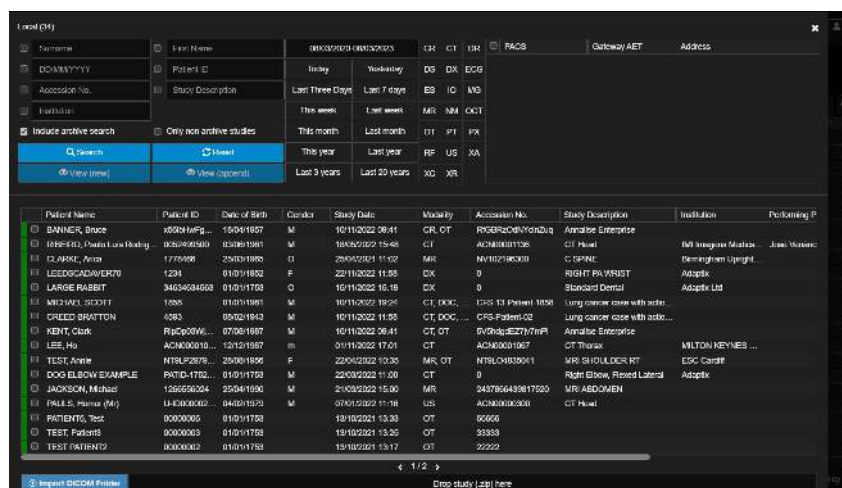
The Worklist creation menu

4.4 Query and Retrieve

If you need to import a study from an external PACS system, you can perform a Query/Retrieve. To do so, click on the Query/Retrieve  button in either the PACS study browser, the Patient Records of a selected study or the diagnostic viewer. This will open a new menu.

The menu is divided in three sections:

- The search parameters at the top left of the screen.
- The PACS systems list at the top right of the screen.
- The study list at the bottom of the screen.



The Query/Retrieve menu


To import a study, start by selecting a PACS system to import from. This will populate the study list with the relevant studies. Their status bar will be listed in white. This indicates that they have not yet been imported into the system. Scroll through the list or use the search parameters to find studies to import. You can also include or exclude local studies by selecting the "Include archive search" "Only non archive studies" tick boxes respectively.

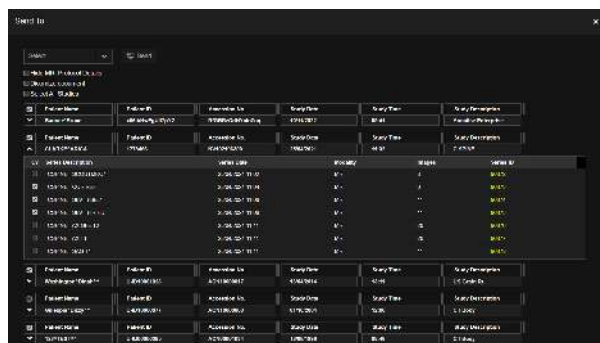
Once you have found the studies you wish to import, select them by clicking on their tick boxes. Their status bar will blink orange to indicate that they are being imported. After the process is completed, their status bar will turn green.

Studies can also be imported from internal DICOM folders and CDs. To do so, drag and drop the folder in the import box at the very bottom of the screen or click on Import and navigate to the DICOM folder.

If you are accessing the Query/Retrieve tool from the Patient Records page or the Diagnostic Viewer, you will have the option to automatically merge the imported study with the currently selected patient. To do so, click on the tick box at the bottom of the Query/Retrieve menu. The check box is automatically selected when importing from an internal folder or CD. Deselect it if you wish to import the study without merging it with the current patient.


4.5 How to Send a Study to a DICOM Node

To send a study to a DICOM node, click on the "Send to DICOM Node"  icon in the toolbar of the PACS study browser. This will open a new menu. Note that at least one study must be selected for this option to be available.




The "Send to DICOM Node" menu

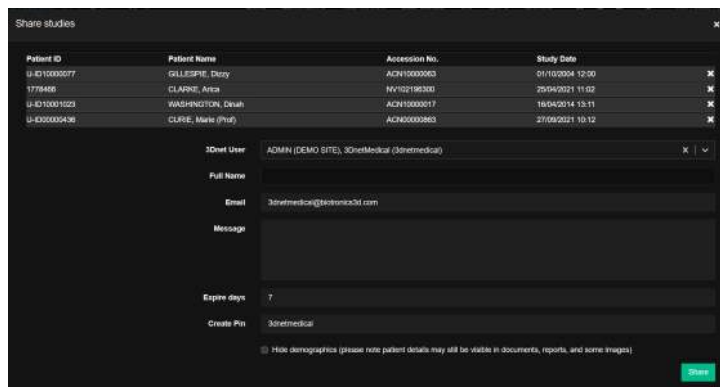
In the menu, start by selecting a DICOM node in the drop down list at the top. The node must have been previously configured to be available. Then select the studies you wish to send by either clicking on the "Select All Studies" tick box or by choosing them manually.

You may wish to only send specific series of a study to the DICOM node. To do so, start by displaying the series of a study by clicking on on the 'Show Series' button  to the left of the patient name column. This will open a new table listing all the series contained in the study. Select the ones you wish to send by ticking their checkbox. Finally, the studies can be DICOMised and/or have their MRI protocol details hidden.

Once you have configured your selection, click on the "Send" button.

4.6 How to Share a Study

To share a study with another user in the PACS, start by selecting the studies you wish to share, then click on the Share study  button. This will open a new menu.



Patient ID	Patient Name	Accession No.	Study Date
U-8310000077	CLLESPIE, Dany	AC210000000	01/10/2024 12:30
1778486	CLARKE, Anna	AC210000000	25/04/2021 11:02
U-8310001023	WASHINGTON, David	AC210000001	16/04/2014 13:11
U-8300000436	CLARE, Marie (Prof)	AC240000000	27/09/2021 10:12

3net User: ADMIN (DEMO SITE), 3netMedical (3netmedical)

Full Name: _____

Email: 3netmedical@biotronics3d.com

Message: _____

Expire days: 7

Create Pin: 3netmedical


☐ Hide demographics (please note patient details may still be visible in documents, reports, and some images)

Share

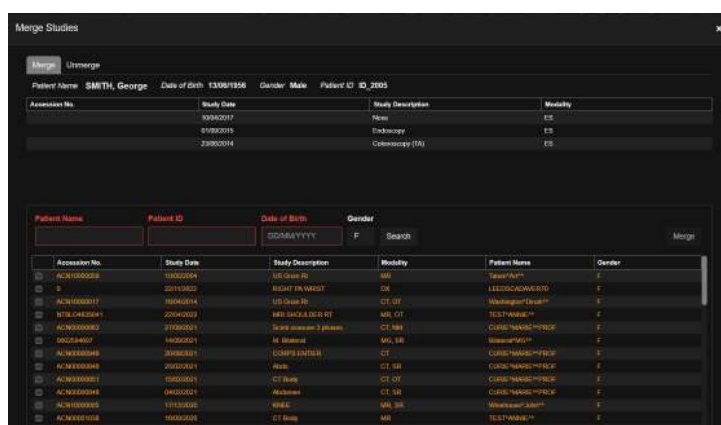
The Share study menu

The studies you have selected for sharing are listed on top of the screen. Choose a user to share them with in the drop down menu below. Once you have chosen a user, the remaining fields will automatically be filled with the information associated with that user. Double-check that it is accurate and choose an expiration time (set to 7 days by default). You may also choose to hide the demographic information by ticking the relevant check box. Once you have verified that the share information is accurate, click on Share to send the studies. Shared studies will be available under the 'Shared to me' and 'Shared by me' tabs in the Home page (see Section 3.2). Organisations can also request for shared studies to use our referrer portal. Please contact our support if you would like to enable that option for your organisation.

4.7 How to Merge Patients

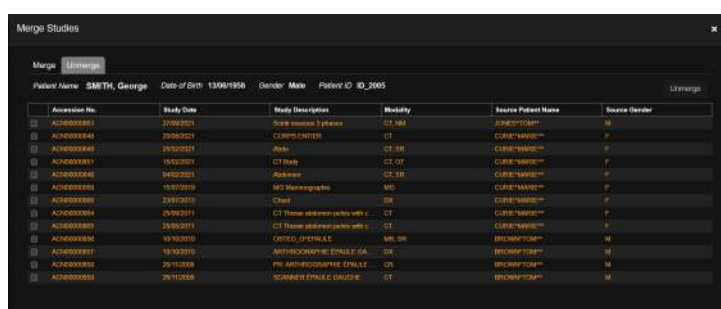
To merge patients from a study in the PACS study browser, start by selecting a single study, then click on the Merge  button. This will open a new menu.

To find patients to merge with the one from the initially selected study, use the Patient Name, Patient ID, Date of Birth, and Gender search boxes. To get more accurate results, use more than one search box at a time. The search results will be displayed in a list below, in orange. Tick their check boxes to select them. Once you have made your selection, click Merge on the right side of the menu. You may be asked to confirm the merge order.



The Merge menu

If you have merged patients that should not have been merged, you can undo the process. Click on the Unmerge tab at the top of the Merge menu.




The Unmerge menu

Select the study to unmerge by ticking its check box, then click Unmerge. You will be asked to confirm the unmerge order.

4.8 How to Assign and/or Update Study Status

- Assign/update Status:

This tool allows you to assign or change institutions, physicians, statuses, and peer reviewers of selected studies. Refer to section 4.2 “How to Assign and/or Update Study Status” for further details.

To assign and/or update the status of a study in the PACS study browser, start by selecting studies you wish to assign and/or update, then click on the Assign/Update Status  button. This will open a new menu.

The menu is divided in two parts: the Assign section and the Status section. Navigate between the two by using the directional buttons.

Both the Assign and Status sections will list four fields of information to help you identify a study. These are: the patient's name, unique ID, accession number, and the study date. That information cannot be changed with the Assign/Status tool.

In addition to this, each section contains their own set of information that can be edited.

The Status section contains the following information:

- Study Status
- Audit Status

The Change Demographics Information section allows you to change the patient's first, middle, and last name, their ID, date of birth, and gender. You can also create a new UID for the selected study if the information belongs to a new individual by ticking the relevant check box.

The Change Study Information section allows you to change the Study Accession Number, the Study Description and Date, and the Patient Location. You may also choose the status of the UID by either keeping it, having a new one assigned, or manually assign a new one by ticking the relevant check box. Please remember to only change the Study UID if you are assigning the images/series to another patient.

When you change the fields from the 'Change Study Information' section of the patient and study reconciliation tab for the whole study without changing the study UID, then the fields will only be updated in the database, rather than deleting and re-inserting the study.

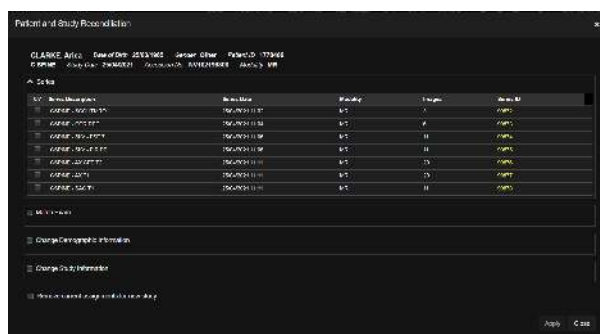
For an example, If you change the Study Description in the following study as below and click Apply, then the description will be updated in the database only without deleting and re-inserting the study.

If RIS is disabled in an org, you can then update the patient demographic information in the PACS using the Study Reconciliation icon. If RIS is enabled for an org, you cannot update patient information using the Study Reconciliation icon and you will have to update it using RIS.

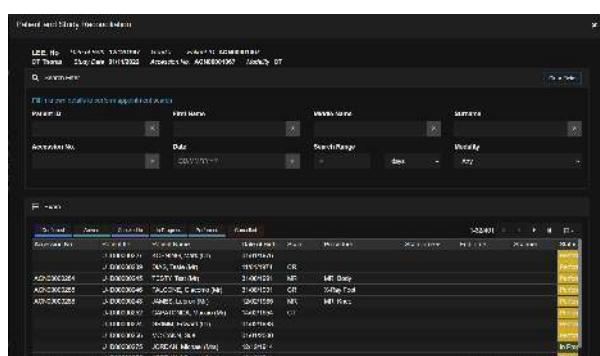
Renaming a series

Rename the series description in PACS for non-grid setups using the following process:

- Click Patient and Study reconciliation.
- Select the check box to Change Study Information.
- Click Edit Series Description drop-down and rename the series.



The Study Reconciliation menu



The Match Exam sub-menu

The demographic and study options

5 Patient Records

Left click on a study in the PACS study browser to access the patient records page of the study. The patient records page is divided into the following sections:

Demographics

This section of the patient records lists information regarding the patient. It includes:

- Their last name in capital letters, followed by their first and middle names.
- Their date of birth.
- Their gender.
- Their patient ID.

The Viewer Options

These buttons allow you to open the viewer and configure how the viewer will be displayed on your device. The selected option has a blue underline. The buttons include:

- The Embed button: If this option is chosen, the viewer will be opened in the current window.
- The numbered buttons: If one of these options is chosen, the viewer will be opened in one or several number of windows or monitors depending on your configuration and the number you selected.
- View: Click on this button to open the viewer.

The Miscellaneous Options

- Back: Click on this button to return to the PACS study browser.
- Docs: This tool allows you to upload documents relevant to the selected patient. Refer to section 5.1 ‘Uploading Documents to the Patient Records’ for further details.
- Query/Retrieve: This tool allows you to check if a study is present in a DICOM node and perform a Retrieve to import it in the system. It is also available in the PACS study browser and the viewer. Refer to section 4.4 ‘Query

and Retrieve” for further details.

- Activate/Deactivate the Timeline: Click on this button to display a time line of the different studies relevant to the patient.
- Send to DICOM Node: This tool allows you to send selected studies to a DICOM node. It is also available in the PACS study browser and the viewer. Refer to section 4.5 ‘How to Send a Study to a DICOM Node’ for further details.

The Navigation Buttons

Use these to navigate from study to study, using the order in the study browser list.

The Patient Priors

This section contains a list of all studies reconciled under the same patient record. The study matching is done automatically by looking at the Patient’s ID, Name and Date of Birth. If any of these do not match, the system will not link the study to a known patient record. The matching criteria will vary depending on your organisation settings.

The currently selected study will be indicated by a grey bar on the left side.

Each study will display its date and time, description, accession number, modality, name of reporting physician, and report status.

Additionally, all studies in the list have their own toolbar. It contains the following tools:

- Chat: This tool allows you to communicate with other users with access to the study. It also lists events related to the study.
- Notes: This tool allows you to leave comments below the selected study. It can also be used to flag the study with hashtags.
- Series: Toggling this button will display a list of the series within the study. From there, you can select the series you wish to access in the viewer by ticking their respective check boxes. If no series is selected, all of them will be accessible in the viewer. Series can also be hidden in the Health Portal. Refer to section 5.3 ‘Hiding a Series’ for further details.
- Patient and Study Reconciliation: This tool allows you to perform quality control and quality assurance operations, including reconciliation on studies. It is also available in the PACS study browser. Refer to section 4.9 “Patient Reconciliation” for further details.
- Snapshots: Toggling this button will display snap shots taken in the viewer below the selected study. Snap shots can be downloaded by clicking on the download icon in the top right part of the snap. Double-clicking on any snap will display them in a new window. This new window contains options to locally save or print the snapshot.
- Docs: Toggling this button will display a list of documents linked to the study. These documents can then be downloaded or opened using any integrated PDF tool.
- Report: This tool allows you to view and manage reports linked to the study, including drafts. Signed reports have access to the Send and PDF tools also found in the Reports Area. Peer reviewed reports are also available under the Peer Review tab. Refer to section 5.4 ‘Report Editor’ for further information.
- Download: This tool allows you to export selected studies to your current machine. The download menu will list information relevant to the studies you have selected and offer the following options for the download: “Hide MRI Protocol Details; Dicomize document; Anonymise; Exclude Viewer; Export PNG”. Please note that this function requires popups to be enabled on your browser. It is also available in the PACS study browser. Please note that this tool serves a different function than the snap download button and cannot be used to download snapshots from the viewer.
- Delete Study: This tool allows you to delete selected studies. You must add a reason for deletion before the study can be deleted. It is also available in the PACS study browser. This tool is only available for users with the relevant permissions.
- Study Assignment Status: This indicator shows you if a study has been assigned to a physician or transcriptionist and if so, to whom it has been assigned. It will also show you who else is currently looking at the study. Refer to section 5.3 ‘Study Assignment Status’ for further information.

The Reports Area

This section allows users with the relevant permissions such as administrators, reporting physicians and transcriptionists assigned to the study, to view, create, and edit reports. Other users will only be able to view the reports. Refer to section 5.4 ‘Report Editor’ for further information.



5.1 Uploading Documents to the Patient Records

To upload a document to the Patient Records, start by clicking on the Docs button. This will open a new menu. To upload a file, drag and drop it in the menu. Supported formats are: PDF, JPEG, BMP, TEXT, WORD, AVI. Please note that DICOM images cannot be uploaded via this menu. To upload DICOM images, use the Upload Studies tool in the PACS study browser. Refer to subsection ‘The Toolbar’ of section 4.1 ‘Layout’ for further information.

If you wish to upload the document as an order form, tick the Order Form check box. Click on Upload to proceed with the upload or Reset to cancel it.

Once documents have been uploaded, they will be listed in the Docs menu along with information such as their name, type, upload date, and the name of the user who uploaded them. They can also be downloaded by clicking on the relevant buttons.

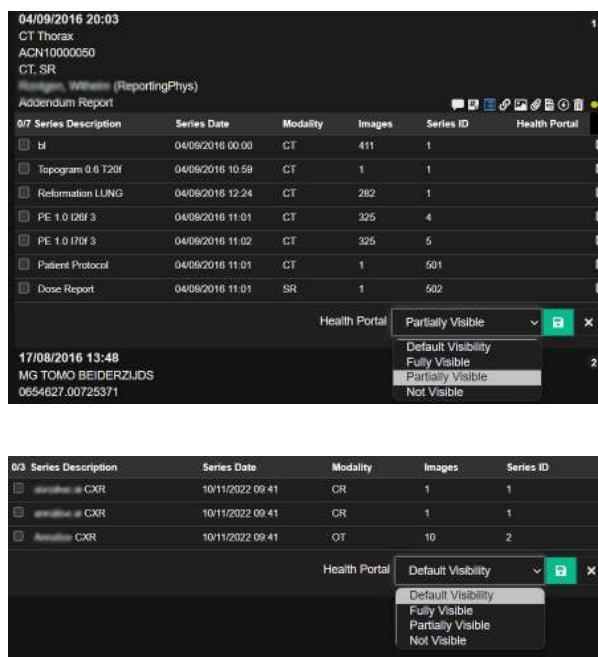


5.2 Hiding a Series in the Health Portal

To hide a series in the Health Portal, open the Series tool of the Patient Records. Then open the Health Portal drop down list. It has four options:

- **Default Visibility**: Choosing this returns the configuration to its default state
- **Fully Visible**: Choosing this will make all series visible.
- **Partially visible**: Choosing this will enable a new column with check boxes on the right side of the table. Toggle the series you wish to show by ticking their check box.
- **Not Visible**: Choosing this hides all the series.

Once you are satisfied with your choices, click on the Save icon. To discard your choices, click on the Cancel icon.



The Health Portal options

5.3 Study Assignment Status

The study assignment status is an indicator found in the PACS study browser and the Patient Records.

In the PACS study browser it is located in the second column of the study list starting from the left.

In the Patient Records, it is located at the end of any study toolbar.

The status icon changes its state in real time to indicate if a study has been assigned or opened. Hovering over the icon with your cursor will display a tooltip showing the assigned user (if applicable) and any other user with the same role currently looking at the study. Studies being viewed by other users are shown by a green rectangle around the icon.

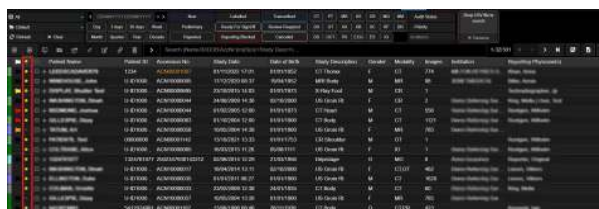
The different statuses are:

- Grey: This indicates that the study is not assigned to any physician or transcriptionist.
- Yellow: This indicates that the study has been assigned to a physician.

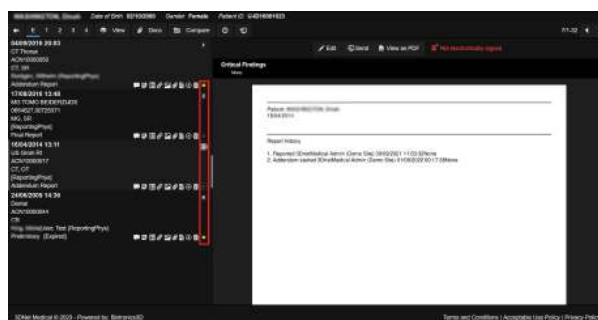
There are two ways to assign a study. If you are a reporting physician or transcriptionist, click on the assignment status icon of any unclaimed study to claim it. Alternatively, use the Assign/Update Status tool in the PACS study browser. Refer to section 4.8 'How to Assign and/or Update Study Status' for further information.

Rejecting a study

Reporting physicians and transcriptionists can reject studies assigned to them. To do so, click on the assignment status icon. You will then be asked to provide a reason for rejection.



The study assignment status location in the PACS study browser.



The study assignment status location in the Patient Records.

5.4 Report Editor

The Reports Area of the Patient Records Page is divided in two modes, the Reading mode and the Edit Report mode.

Edit Report Mode

Beyond standard editing tools such as font type and size, the Edit Report mode offers the following functions:

- Save Draft: Clicking this button will save your current draft. It can be configured so that drafts are saved automatically after any change.
- Report History: Click on this button to return to Reading mode. This option is only available for reports that are already signed.
- Sign: Clicking this button will open a new menu allowing you to sign the report. See below for sign-off options.
- Delete: Clicking this button will delete your current draft. Note, this cannot be used to delete a report. Currently, there are no ways to erase reports.
- Macros: If your organisations has set Macros, they will be available in this drop down list.
- Annotation Colour: This allows you to choose colours for any annotation you wish to make.
- Annotation Shape: This allows you to select a shape for annotation purposes. Clicking on this button will automatically enable annotations.
- Annotate: Clicking on this button turns on annotations.
- Snap: Clicking on this button opens the Snapshot editor. From there you can integrate snapshots taken in the viewer to the report or upload your own.
- Template: This drop down list allows you to choose a template for your report, if available.
- Critical Findings: This drop down list allows you to flag the study to indicate the severity of the findings. This optional feature is not enabled by default. Please contact support to enable it for your organisation.
- Incoming Disease Code: This section will list any suspected condition prior to the study using ICD-10 codes. It cannot be edited. This optional feature is not enabled by default. Please contact support to enable it for your organisation.
- Outgoing Disease Code(s): Use this drop down list to add any confirmed condition to the report using ICD-10 codes. This optional feature is not enabled by default. Please contact support to enable it for your organisation.

Drafts

Until a report has been signed, it is considered a draft by the system. Drafts can only be edited by users with the relevant permissions (e.g. a reporting physician assigned to the study). You can also access a preview of what your draft will look like once signed by clicking on the Report button of the study toolbars in the Patient Priors (see section 5.1 'Patient Records') and selecting the report you are currently working on.

Signing a Report

Once you are done editing a report, click on Sign. This will open a new menu.

Select a signing parameter in the drop down list. Four are available for new reports:

- Preliminary: Choose this to create a preliminary version of the report. You or other authorised users will still be able to make changes the report before finalisation.
- Dictated: Choose this option if you are a reporting physician and used the dictation tool of the viewer. You or other authorised users will still be able to make changes the report before finalisation.
- Transcribed: Choose this option if you are a transcriptionist and the report contains a dictation that has been transcribed. You or other authorised users will still be able to make changes the report before finalisation.
- Final: Choose this to sign the report as complete. The report cannot be edited further once it has been signed

using this option. Use the Addendum option (see below) to add or correct information in a finalised report.

Once you have selected the signing option, click on Sign. Click on Sign And Next to sign the report and automatically move to the next patient. To discard your choice, click on Cancel.

If you wish to make further changes to a report that was signed as final, you will need to use the Addendum signing option. To do so, open the Report Signing Menu of a finalised report. You should find a new option in the drop down list called Addendum. Select it then select a reason for your addendum in the second drop down list below. Click on Sign to complete the changes. There is no limit to the number of addenda that can be made.

Reading Mode In this mode, you can consult the currently active report, send it to a PACS target, or open it as an embedded PDF. Users assigned to the study can also choose to edit the report. Signed reports also include a first page listing the history of the report. Addenda are listed after the initial report in the document.

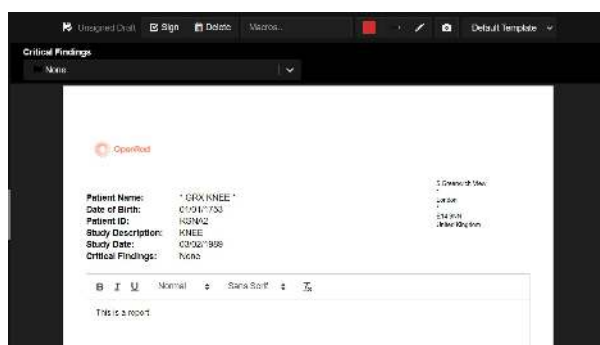
Sending a Report

To send a report, click on Send in the Reading Mode of the Reports area. This will open a new menu. This menu can also be accessed by ticking the Send check box in the Report Signing menu.

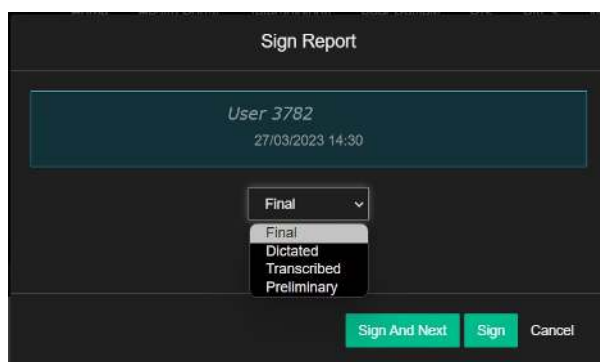
Choose your format (DICOM, HL7, or plain text document) and Gateway (or PACS target when using DICOM format) from the respective drop down list, then click Send.

Voice Recognition

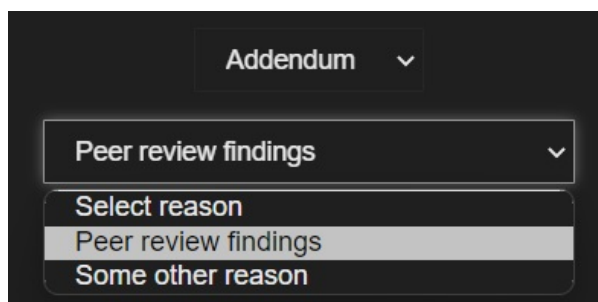
For information on how to use one of the integrated voice recognition tools, refer to the documentation offered by the provider. If you would like to enable a voice recognition tool for your organisation, please contact one of our sales team.



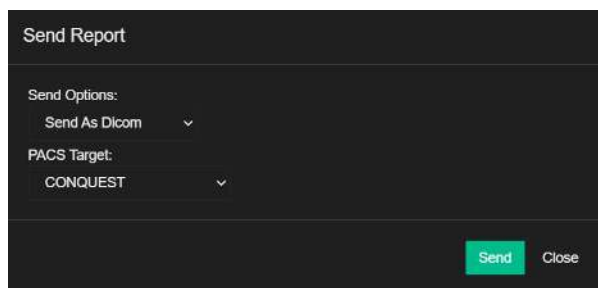
The Report Area in Editor Mode



The Report Signing Menu



An example of Addendum options.



The Send Menu and options

5.5 Anonymization of patient records

You can set the tags to anonymise studies in PACS by using following two options:

- Download Studies

Click Download in PACS and select Anonymize check box, it'll display the tags that you can choose to anonymize. You can add one or multiple tags in the empty field. The tags that are not selected will not be anonymized.

- Send to Dicom mode

If you have a gateway with org, select the Anonymize check box and select the Anonymization tags.

Note: The respective Org setting needs to be applied for the relevant tags to be displayed for anonymization.

6 The Viewer

6.1 Study Panel

The viewer can be accessed via the Patient Records page of any study by clicking on the View button. It can either be opened in an embedded window or in an entirely new window depending on your selection in the Patient Records page. Refer to section 'Patient Records' for further information.

Alternatively, the viewer can also be accessed via the PACS study browser by right-clicking on a study. Note that this will open the viewer in an embedded window.

Viewer Layout

The viewer is split into two main sections: the Side Panel and the Visualisation Area.

The Side Panel: This panel contains a series of general tools and information:

- Close: Click on this to close the viewer and return to the previous page.
- About: Click on this to access general information about 3DNet. You can also access this information via the Account menu.
- Hanging Protocol: This tool allows you to define and manage rule sets for hanging protocols. Refer to [NOT CREATED YET] for further information.
- UI picker: This tool allows you to configure the number of viewports displayed in the viewer, see which hanging protocol is applied if any, and switch between steps.
- Hide Side Panel: Click on this to hide the Side Panel completely. To display the side panel once more, click on

the 'Show Side Panel' icon at the top left of the screen.

- Dictation: This tool allows you to dictate information for the final report. Refer to section 'Report Editor' for further information on dictated reports.
 - Load Cached Study Session: Click on this to load the existing cached state of the study in the database.
 - ViewerState: Click on this to create a recording of your actions in the viewer. Only one recording can be created at any given time, creating a new recording will erase the previous one. Recordings are not saved between sessions.
 - Query/Retrieve: This tool allows you to check if a study is present in a DICOM node and perform a Retrieve to import it in the system. It is also available in the PACS study browser and the Patient Records window. If opened with a right-click, the Query/Retrieve menu will be pre-populated with information related to the current study. Refer to section 'Query and Retrieve' for further details.
 - Live Support: Click on this to access our Live Chat support service.
 - Opened Studies: Click on this to open a menu listing the studies you have consulted.
 - Send to DICOM Node: This tool allows you to send selected studies to a DICOM node. It is also available on the Patient Records window and the viewer. Refer to section 'How to Send a Study to a DICOM Node' for further details.
 - Basic Information: This small section contains information about the patient's name, gender, date of birth, and ID.
 - Studies: Click on this button to display a list of all the series available in the study as well as study priors and documents linked to the studies on the lower half of the Side Panel. Refer to section 'The Viewer Studies Panel' for further information.
 - Annotations: Click on this button to display a list of annotations on the lower half of the Side Panel. From there, you can choose to toggle annotations, change their colour, add notes to them, or even delete them. Annotations are automatically deleted after a session.
 - Snapshots: Click on this button to display a list of snapshots on the lower half of the Side Panel. To open a snapshot in the viewport, right-click on it or drag it to a viewport of your choice. Snapshots also can be printed, sent to a PACS, downloaded, or deleted from that list.
- You can hide the fields in the viewer by selecting the respective fields in 'Patient Info To Hide' and 'Dicom Info To Hide' in the 'DICOM Overlay Order' viewer settings.

The Visualisation Area

The Visualisation Area is divided into the following sections:

Window/Level information

This displays information relating to window and level in real time. Click on it to open a new menu to adjust the window level settings. Some of those settings can also be accessed via mouse controls (see 'Mouse controls' below).

Mouse Navigation

In the viewer, several settings can be adjusted by holding and dragging the mouse:

- Zoom: To zoom with the mouse, hold and drag any section at the far left end of the scan. Drag to the right or bottom to zoom in. Drag to the left or top to zoom out.
- Window and level: To adjust the window levels with the mouse, hold and drag any section at the top of the scan. Drag to the right or top to make the image brighter. Drag to the right or up to make the image brighter. Drag to the left or down to make image dimmer.
- Moving the image: To move the scan in the viewer with the mouse, hold and drag any section in the middle of the scan.

Slices

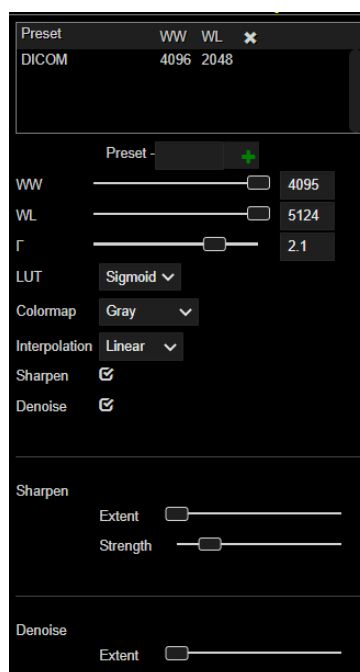
There are three ways to navigate between slices of a scan in the viewer:

- By scrolling with the mouse.
- By clicking on Play in the Play bar. The speed can be adjusted by clicking on the Play Adjustment button.
- By selecting a slice in the Play bar.

Suspend Study

The presentation state of the viewer is automatically saved after every action. This enables you to temporarily switch to another study in the middle of a reporting session. Studies can be opened, put on hold, and restored. This feature allows for easy switching to different reporting sessions and patients without losing progress.

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. If no studies were opened on a specific day, that day tab will be empty. It is possible to collapse and expand each day tab to explore it.



The window and level settings

6.2 Studies

The Studies subsection of the Side Panel in the viewer is divided in three parts from top to bottom:

- The Modality Filters: This allows you to filter the different studies by modality.
- The Study Priors: This list contains all the study priors linked to the current patient. Each study has its own number. The number of the study currently opened is highlighted in blue. Each study also contains general information such as date, modality, and accession number.
- The Contents section: This list contains all the documents and series linked to the study. Click on the Documents

tab to open a submenu listing all reports and other documents linked to the study. Click on a series to open it in the viewport. You can also open it by dragging and dropping it into the viewport. To print it, click on the printer icon at the bottom right of the series.

- Managing series

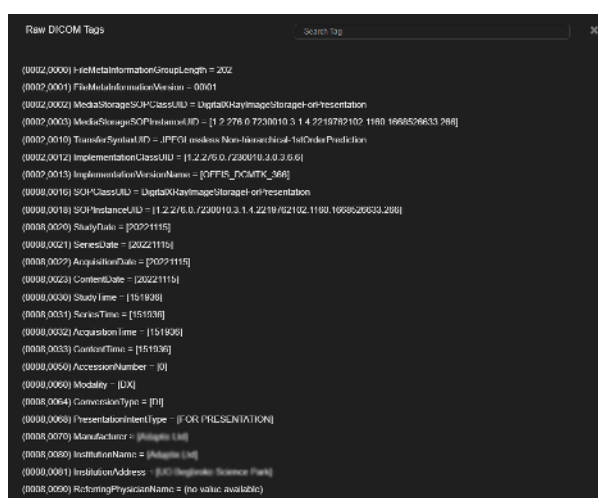
Series can be managed in the Study Priors list by right clicking on them. This opens a new subpanel. From there, you can add notes to the study, check the hanging protocol if one is applied, and choose whether to display a single series or multiple ones.

DICOM tags

You can access a list of the DICOM tags of a study by control clicking on any study in the Contents section. The cardiac MRI multi-frame series can synchronize with each other, based on the time in the DICOM tag. Also, we have added the icon to the 2D context menu to toggle it.

Scan overlay

Scans can be overlaid by selecting one scan then shift clicking on a second scan. Overlay colours can be customised in the Profile menu (see section 3.3 'Profile').



A DICOM tags list

6.3 Hanging Protocols

A hanging protocol (HP) is the series of actions performed to arrange images for optimal 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.).

New Hanging Protocol

To create a new HP, start by configuring the layout of the viewer via the different tools at your disposal such as the UI picker. Once you are satisfied with your configuration, click on the Hanging Protocol icon in the sidebar. This will open a new menu.

Begin by choosing the amount of series you wish to display by ticking the relevant check box at the top of the menu (either 1, 2, or all the series). Next click on the 'Add New Ruleset' button in the toolbar above the protocol list. This will open a new menu.

In that menu, you can configure rules, steps, and auto-population conditions. Once you have chosen your settings, click on the save icon at the top right of the menu. Your new Hanging Protocol will now be available in the protocol list.

Hanging Protocol management

To edit an existing HP, select it in the protocol list by ticking its check box in the protocol list. Then click on the 'Edit' icon. This will open a new menu.

In that menu you can modify settings such as study rules, filters based on description, modality, or institution,

steps, screen layouts, and add steps shortcuts. Once you are satisfied with your changes, click on the save icon.

Study Rules

Once the protocol is saved, you can access more advanced options to further customise the protocol. In the advanced HP options menu, the user can use logic filters such as contains, excludes, match, is not empty, and more. These can be applied to DICOM tags such as study description, series description, or even modality. These options can be set for each individual view port, for every step of the protocol. Study Rules tab allows the user to enable or disable various options. Cross reference lines, synchronized scrolling, synchronized zoom, pan and window level. You can also add rules for DICOM tags modality and study description (exclude, match, contains, etc). Further down, you will find a matrix depicting the layout in each screen and the number of steps that are saved in the protocol. It is also possible to modify the number and positioning of enabled view ports per screen from the editor itself, clicking with the right mouse button on the blue and green tiles on the displayed matrix. Selected tiles are displayed in green. Related filters tags can be found at the bottom.

Series Rules

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

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 view port depending on the option you selected among Single, First, Next.

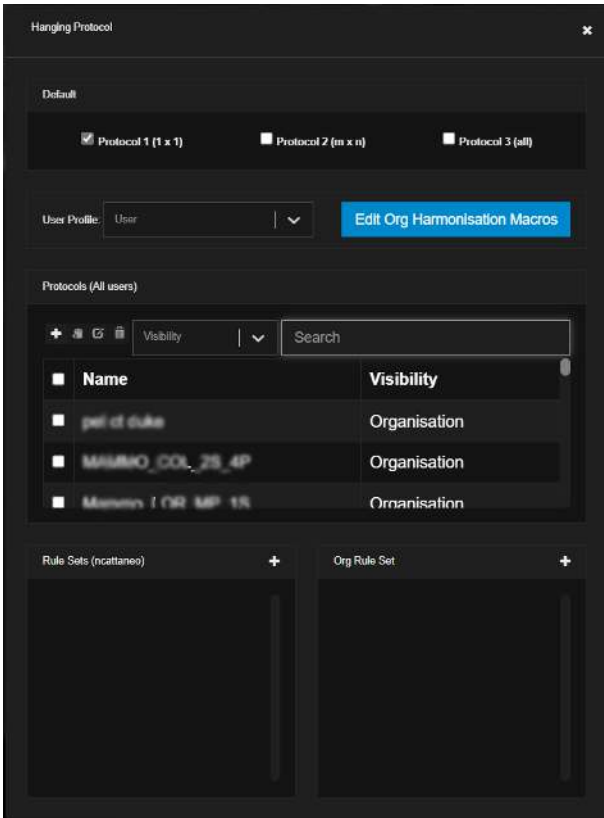
- Single: the HP will trigger if and only if the selected series rules apply to one and only one series. Two or more positive matches will result in the protocol not triggering.
- First: the first series that matches with the series rules will be displayed.
- Next: if there is more than one series matching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

- Navigating through a series:

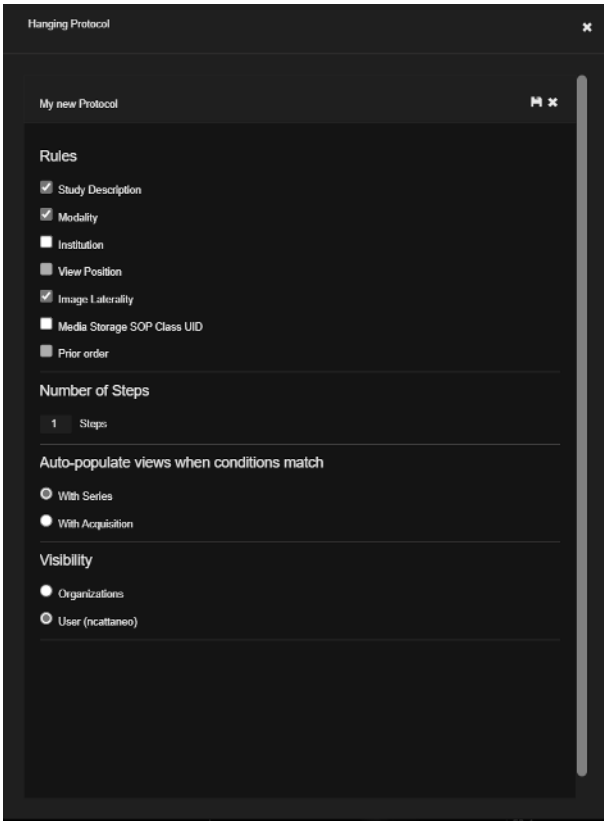
Press the left and right arrows from the keyboard to scroll through the slices in the series and use page up/down to navigate through the series of a study in the active viewport.

VR Orientation:

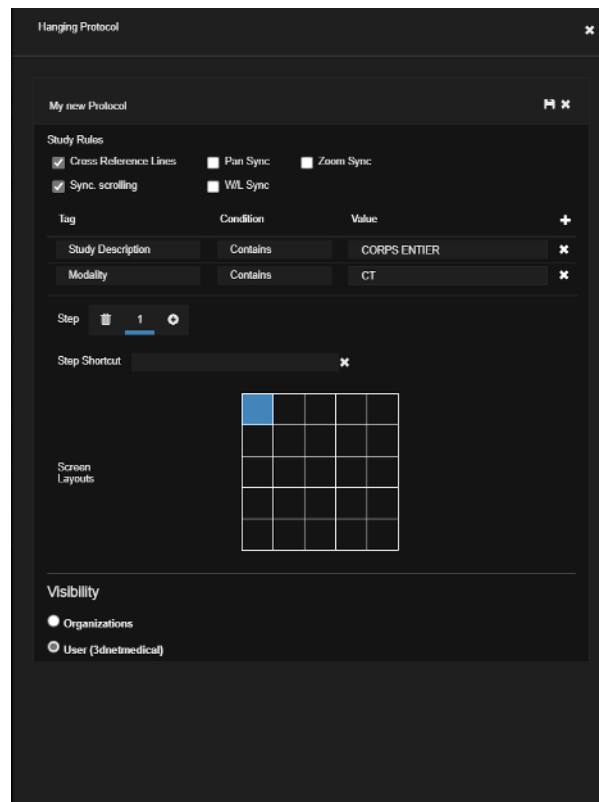
Select VR Orientation from the Series Config tab. You can select various orientations from the drop-down list. You can select hanging protocol orientation for VR Viewport from axes orientations such as Default (default orientation for the study), Custom (the custom orientation when creating hanging protocol), etc. The system applies the selected orientation to the VR Viewport when applying Hanging Protocols.



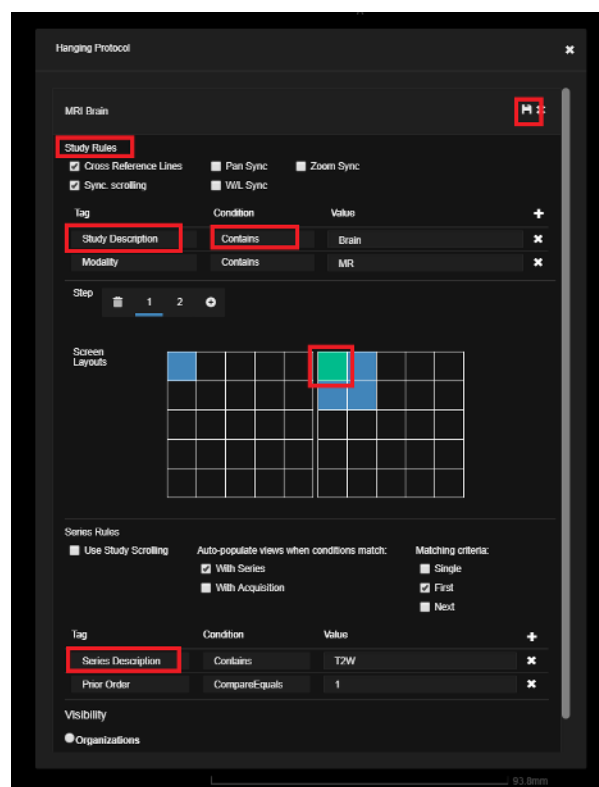
The Hanging Protocol menu

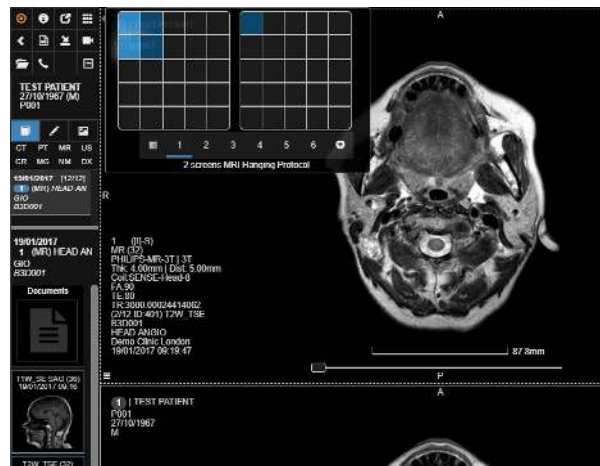


The New Ruleset menu



The HP management menu





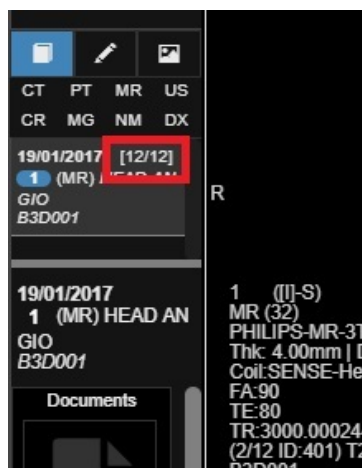
The Series Rules menu

6.4 Series Filter

From the Side Panel, you can filter the series in the study and display all of them with one click. Depending on the modality of the study, you can access different filters, such as:

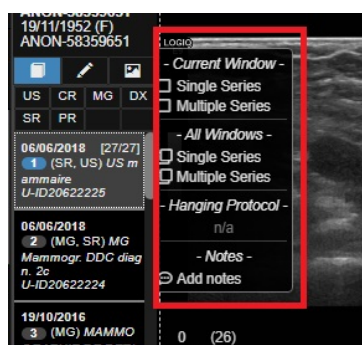
- CT: thin slices, thick slices or reconstructions, all.
- MR: diagnostic, localisers, all.

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.



6.5 Switch Protocols

Right click on the study description of one of the studies in the Study Panel to access the Hanging Protocols quick switch menu. In this menu the user will be able to quickly switch between Single Series or Multiple Series layout. Users have the ability to trigger the protocols in one screen or multiple screens. Each choice of protocol is presented for a 1 screen configuration and multiple screens configuration. Further Hanging Protocol option can be displayed and triggered, if a custom HP exists and satisfies the criteria needed to apply it.



6.6 Viewer Control Centre

Viewer Control Centre lets you view the Hanging Protocols steps, switch between the steps, and add steps to it. The Viewer Control Centre is in synchronization with the Viewer. The layout you select in the Viewer Control Centre, the same layout is displayed in the Viewer too.

You can resize the layout as per your convenience for better visibility. You can view following two types of Viewer Control Centres:

- External Control Centre
- Embedded Control Centre

To open the Viewer Control Centre,

- Select a study from PACs.

- Select the icon for Control Centre. Note: The Control Centre is unavailable when Embedded Viewer is selected.
- Select External Control Centre or Embedded Control Centre from the drop down.
- Click View.

External Control Centre:

In the left side of the Viewer Control Centre, you can view the steps. Also, you can delete a step or scroll down to add a new step.

The grid that you select in the Control centre is reflected in the Viewer as well as shown below: For an example, if you select four grids in the control centre displayed on the left side of the image, the viewer displays four grids as displayed on the right side of the image.

You can arrange the series in the viewports of control centre. Drag and drop an image from the series to the viewport. It is also reflected in the Viewer. Load multiple studies in the control centre by expanding the studies.

You can drag studies from the different series in the viewports for better visuals of the priors.

When you select multiple monitors, select the double arrow icon in the top right corner of each study to view following options:

- Window 1- displays all studies from the selected series to window 1
- Window 2- displays all studies from the selected series to window 2
- All Windows- spreads the studies evenly in both windows

Click the Snapshots icon in the bottom left corner of the control centre to switch to snapshots. You can toggle between series and snapshots. If you drag and drop window snapshots, it replaces the entire window.

Search a Study description / Accession No. / Body Part / Series description using the search bar displayed above the series section. The control centre filters and displays the requirements.

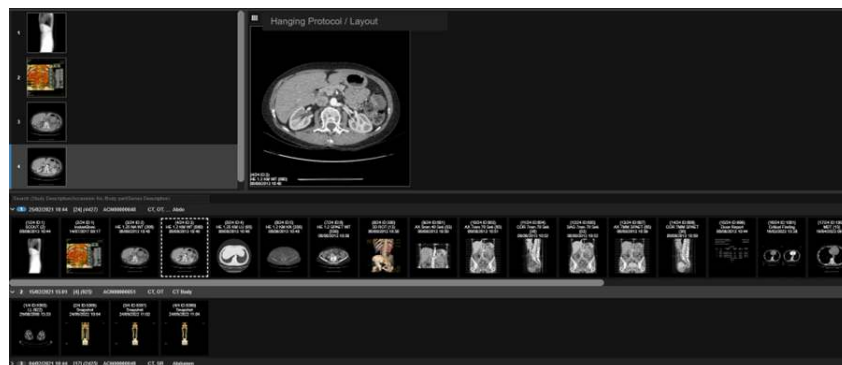
Zoom in / Zoom out the studies in a series using the Zoom bar provided at the bottom right corner of the series section.

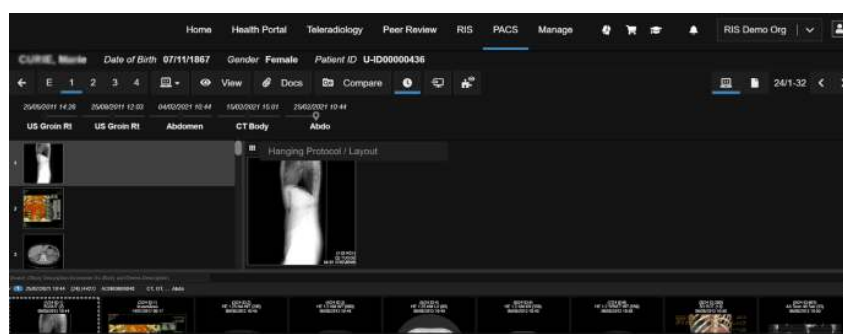
Click Wrap Series in the bottom right corner to see the studies without having to scroll them.

In the main viewer window and in the Control Centre, you can view the additional information of steps by selecting between the matching hanging protocols.

Embedded Control Centre-

Select Embedded Control Centre in the Study Browser page. You can view the control centre in the Study Browser itself. You can switch to Study Browser by clicking the icon on the top right corner of the page.





7 General Diagnostic

7.1 Operation with Series

The 3Dnet Medical offers advanced functionalities for series and image manipulation in the viewing area. The series thumbnails information (amongst the other standard information) displays the series and the image count. You can perform following operations to diagnose a case quickly:

7.1.1 Adding a Series

Follow either of the processes to add a series into the viewing area:

- Activate a viewport by clicking on it.
- Left click the series in the Study Panel that you want to view on the current viewport.
- Right click the series in the study panel to add that series to the Visualization area keeping the newest series to the right.
- Drag and drop the series to the desired viewport. Note: You can replace the series or insert the new series to the right, left, above or below of any viewport.



7.1.2 Functionalities involving Series and Viewports

Multi-phase series:

In case of multi-phase series, left click the 'Play' icon at lower right corner of thumbnail to open the multi-phase thumbnails.

- Dicom header tags:

Press CTRL + left click on the thumbnail to see the Dicom header of the series. In the Dicom header panel, you can search and filter the specific tags.

- Swapping a series:

Press the 'Alt' key and drag and drop the active series into the desired viewport. The series in the destination is replaced. You can swap, copy, move, or insert the series below, above, left, and right. To change the series in a viewport, click the viewport and left click on the series in the series panel.

- Activate a viewport by clicking on it.

- Maximizing a viewport:

Double click on a viewport to maximize it.

Note: In the user profile, the 'Maximise viewport on double-click' option must be enabled.

- Scrolling through a series:

You can scroll a series using one of the following options: - Use the mouse wheel to scroll through a series.

- Move the mouse to the right side of the viewport (Hotzone) and drag it on the screen while holding left mouse button.

- Scroll by using the slide bar positioned in the lower part of each viewport.

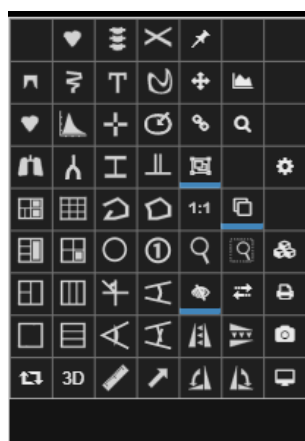
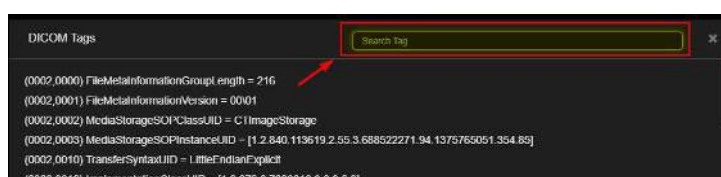
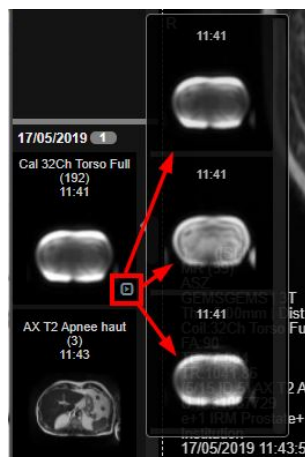
- Press the 'Y' key on the keyboard to delete a viewport.

- Press the 'Home' or 'End' key in the keyboard to jump to first or last step of a Hanging Protocol.

The application automatically plays the movie of a supported series within the viewer.

- Context Menu:

Click the 'Hamburger menu' icon (three horizontal lines) in the lower left corner of an active viewport to view the context menu which opens a set of tools for image visualization, processing and measurements. If you hover the mouse over a tool, a tooltip appears describing the function of that tool. Alternatively, you can open the same menu by right clicking anywhere inside a viewport.



7.2 Create Reformatted Series

Using the Export tool the user can create and save a reformat to a PACS target from a native acquisition. This tool is accessible through context menu. This enables the user to create and save a reformat in a new plane, like a coronal or sagittal view from native axial. It also allows to save a whole 3D MPR reconstruction starting from the native series.

- Once you select the tool, a reformat menu appears.
- Use the slider to select the from and to slices, set thickness, distance and mode render mode, including MiP, minIP, AvIP).
- Select a PACS target to send the reformat to.

Once the reformation is sent to PACS, the recently opened studies icon in the top left of the viewer flash intermittently. This means the series has successfully been sent to PACS. - Right clicking the mouse on the recently opened studies icon refreshes the viewer and the new series is available in the study panel on the left side of the window.



7.3 Select and Add Series in a New Viewer Page

You can select two or more series that are already displayed on the screen and compare them in a separate page of the viewer.

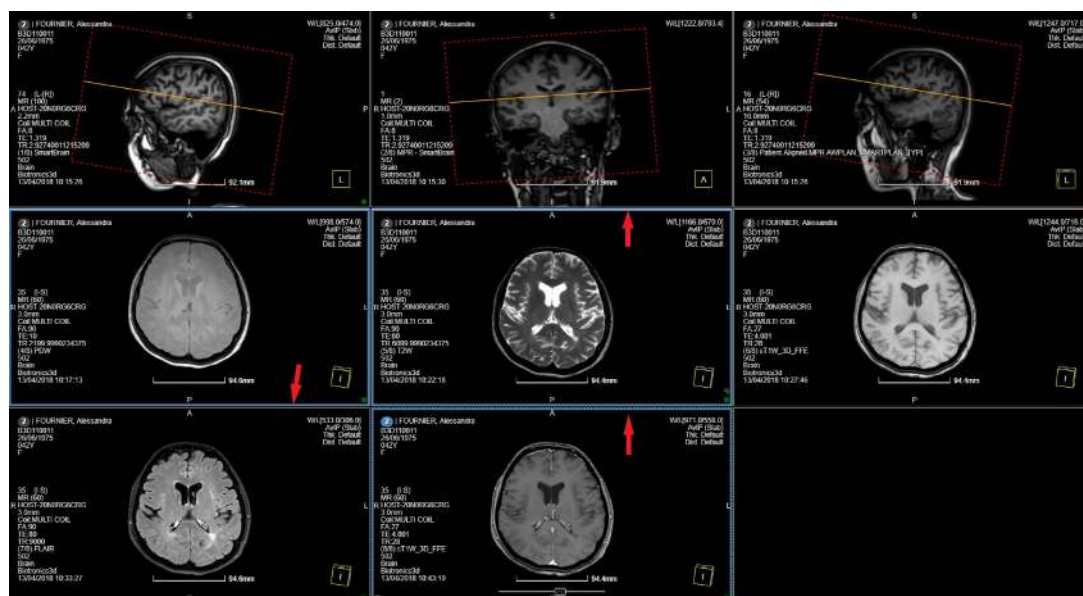
To do this:

- Hold (Ctrl+Shift) and left click on the series to compare. When you select a viewport, the edges are highlighted in blue.
- Release (Ctrl+Shift).

The selection stays. - Now, if you press (S) on the keyboard, a new page is created, showing only the series contained in the selected viewports.

With this new layout, you can analyse the images in a comparative view.

- Press (E) key to go back to the previous page.



7.4 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 left mouse button takes a certain function.

In our software, the viewport is divided in nine hot areas as a 3x3 matrix, 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+left mouse button)(cell 3x2).

Click one of the nine regions and drag the mouse over in order to perform the operation desired.

- Resetting an image:

Click the bottom left corner to reset the image to the initial grayscale and size.

- Scrolling images:

You can scroll through a stack of images using one of the following options:

- The mouse scroll.
- Up and Down arrows on the keyboard
- Left and Right arrows will navigate through the series of that study.
- Use the Slider, with play option to view images in cine at the bottom of the viewport. You can modify the frame rate (speed), direction or to jump directly to the first or last image in that series.

- Rotating an image:

- Drag across the image in 3D with the help of mouse to rotate the image in a viewport.
- Rotate and flip an image rotation by clicking the orientation icons in the Context menu.

- Zooming an image:

You can zoom an image using one of the following options:

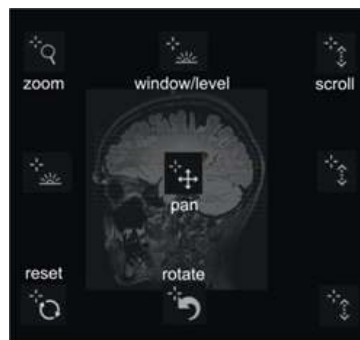
- Click and drag the top left corner of a viewport to zoom the image in the viewport.
- Click the 'Show Magnifying Glass' icon Link to the table in the Context menu to display a magnifying glass over the image. You can resize the magnifying area with the mouse by dragging the edges of the rectangle. You can do an invert grey inside the zoom rectangle.
- Click 'Rectangle Zoom' icon in the Context menu to zoom with a dotted rectangle.

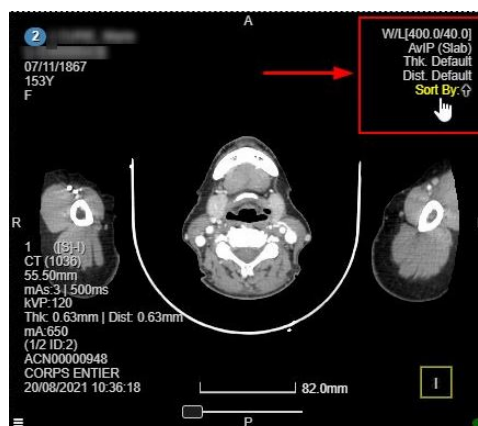
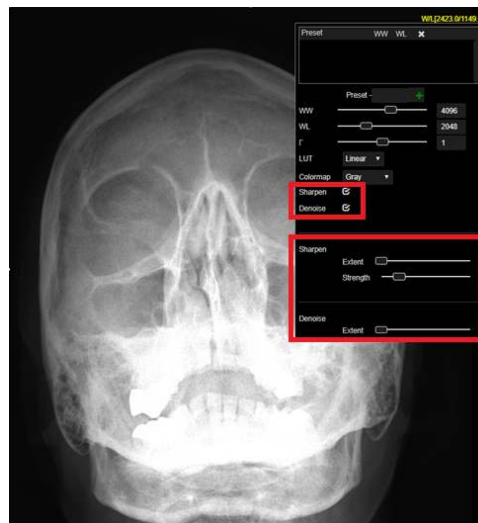
- Inverting the Grayscale:

- Click the 'W/L' in the top right corner. A dialog box appears.
- Select Inv. Gray option from the drop-down list in the Colormap field. This displays the image in negative mode.

- Windows Level (W/L) functions:

- By clicking on the WL text, you can select a Window Level pre-set for different organs or tissues in case of CT images.
 - You can add your own preferred pre-sets by entering the Window Width (WW) and Window Level (WL) values, enter a name in the Preset text box field, and then click the '+' icon.
 - Also, you can use the keyboard shortcuts keys (keys: 1,2,3,4...) for Window Level pre-sets.
 - Additionally, you can apply denoise and sharpen to 2D images, such as an x-ray using the WL menu in the top right corner of each viewport.
 - The different texted hot zones in the top right corner of the viewport allow Window/Level adaptations, slab and projection adjustments, changes in thickness, distance, and sorting.
 - Invert the window level by holding right mouse button and moving around the image in a viewport.
- You can access this option in the Viewer settings in the Profile page.
- Select the last two checkboxes in the list below to individually enable the window or the level.





7.5 Synchronized Navigation

This section explains synchronization and navigation within studies and between studies:

- The view ports will be synced by default for the same study; same orthogonal plane.

To check that viewport are synced, go to context menu and double check that blue line is present on icon 'Linking Off'.

Note: The Linking On icon is selected by default. You can click the same icon to unlink the viewports.

- Reference Lines-

Click the 'Show or Hide reference lines' tool in the Context Menu to view the cross-reference lines between axial, sagittal and coronal views.

Note: The 'Show Reference Lines' is selected by default. You can view the blue underline beneath the icon, which highlights the tools that re currently active.

- 3D Localization of the cursor-

Left click in the image in a viewport to see other viewports being synced. You can see an orange cross in the rest of the viewports.

- Live 3D Localizer-

- Select the viewports that you want to link together.

- Left click on the image in the viewport and press 'X' to view the 3D live localizer. The localizer will be visible in all synced viewports.

Toggling this feature, you can easily track a structure in multiple views at the same time (useful when comparing the same structure in different type of acquisitions).

- Linking Two Series from two separated studies (e.g. current study and a prior):

-Open the two series from two different studies of the same patient in the Viewer.

- Click sequentially on the first and second viewport and then press the 'J' key or click the 'Link Series/For' icon in the Context menu.

- Syncing views manually-

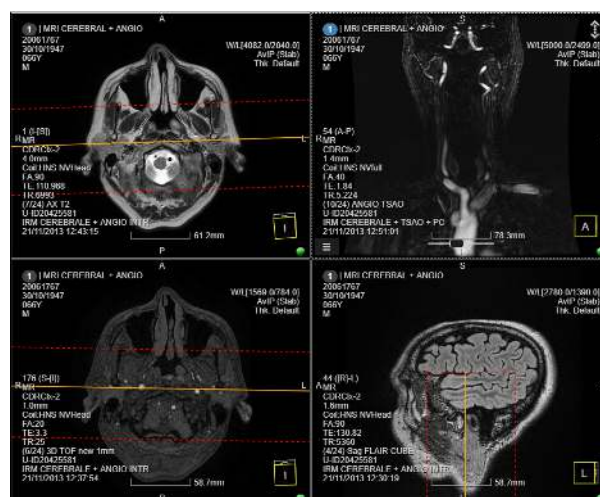
Follow the process below to link two or more viewports:

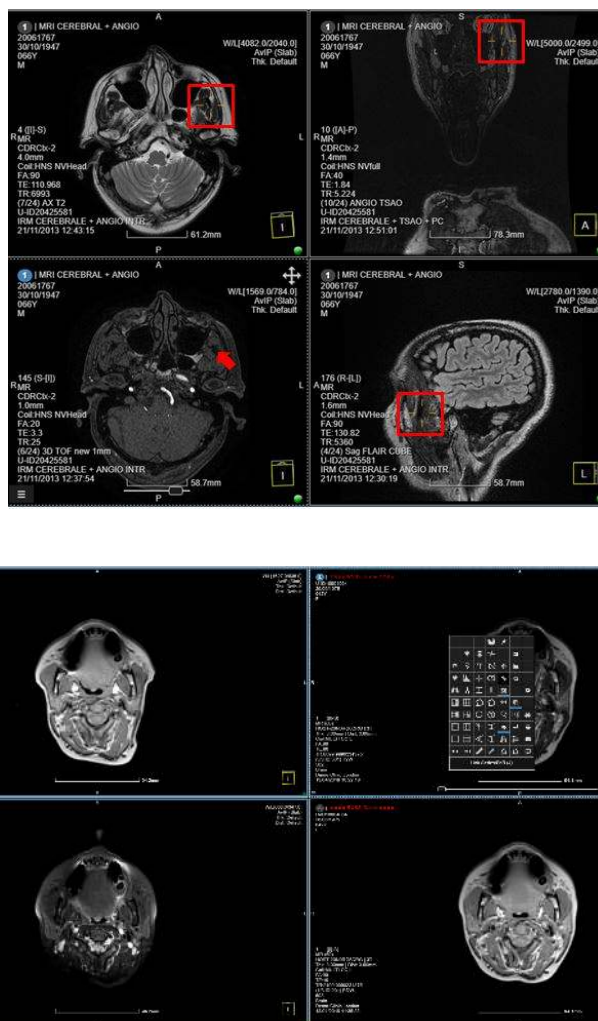
- Click on the viewports you want to select. Selected viewports are highlighted in blue.

- Right click the mouse button to open the Context menu while holding Ctrl + Shift on the keyboard.

- Select the Link Series tool in the Context menu.

The viewports are synced.





7.6 Synchronized Studies in the Viewer

3Dnet Cloud viewer synchronizes scrolling and reference lines in the different viewports on separate viewports. You can also 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. Also, there's an icon on the top left of the viewer as well to do viewer settings, in addition to the profile settings option.

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. This can also be enabled or disabled by clicking on the 'Plane Link' icon on the context menu. The 'Plane Link' enabled is the default option when the viewer is launched.

You 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 the two series while the 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 on the context menu to apply the new manual sync.

This feature is useful when, within the same examination, users want to apply a slight offset between two series. For example, in series without contrast compared to series with contrast agent, the user wants to apply offset to balance patient movement occurred at the time of contrast medium injection.

There is no automatic linking between series sharing the same plane but belonging to different studies, but the series can be synced manually. This is the case, for example, when comparing a current study against the prior.

To do the manual linking between 2 different studies on the same plane:

- First disable Plane Link if on/ enabled.
- Scroll through and set the slice of synchronisation for each series.

7.7 Synchronized Image Manipulation

3Dnet Cloud Viewer features syncing tool for image manipulation. Other than scrolling, the user can sync Pan, Zoom, WL. In order to toggle these tools on, the user can click on the corresponding icon in the context menu. Synchronizing series will make the action propagate to other viewports, if in those viewports are displayed images taken in the same study, or same DICOM plane, or if the study description DICOM tag matches.

7.8 Annotations

Accuracy of measurements depends on the image quality (image resolution, signal-to-noise ratio (SNR) and image artefacts), round-off errors, the window level, the zoom level, and other viewing factors such as the viewing device.

In the best ideal viewing conditions, the accuracy of the measurement is bound to the acquired resolution, SNR and the artifacts of the image.

The accuracy cannot be better than the size of the smallest element given by the image resolution.

The image resolution depends on the required image and the type of the scanning device.

The parameters are Field-of-view, Acquisition matrix, and Slice distance. For an example, In the acquisition plane, for a field-of-view of about 50cm, the smallest detail in an image acquired with a 512x512 matrix is about 1x1mm.

Note: In a direction perpendicular to the acquisition plane, the smallest detail cannot be better than the distance between slices. The measurements and annotations tools are in the viewport tool set.

Annotations tool are:

- Ruler
- Angle
- Cobb angle
- Open angle
- Circle
- Polygon
- Polyline
- Arrow
- Pixel HU or intensity
- Hip displacement
- Vertebra labelling,
- TT-TG distance (tibial tuberosity trochlear groove distance), Wiberg angle.

Follow the process to view annotations:

- Click Multiple Actions (Link to icons table) in the Context Menu to perform repetitive measurements.

Note: All the measurements and annotations performed on images are listed in the Annotations panel on the left side of the screen and if applicable the annotations are marked on the scrollbar at the bottom of the viewport in the associated colour. Refer to the image.

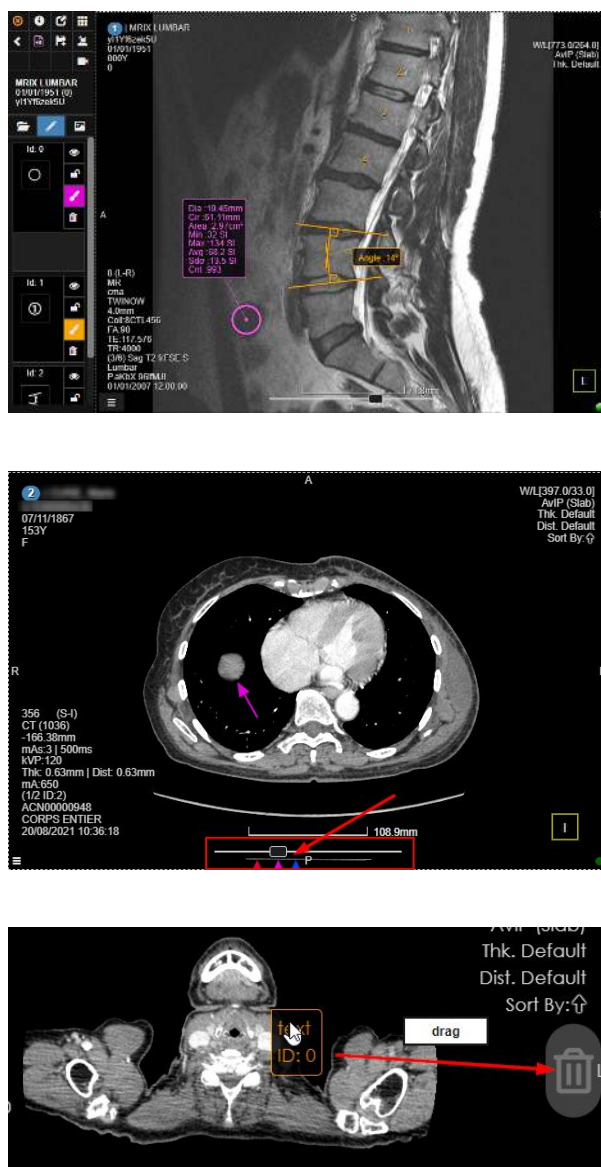
- Click the marker to view the image in the series where you have made the annotations.
- Click Visibility (Eye symbol) (Reference to table) in the Annotations panel on the left side of the screen to show or hide the annotations in the active viewport.
- Select the colour of each annotation by clicking the coloured brush in the Annotations panel.

You can delete an annotation using one of the three methods:

- Delete a measurement by clicking the Trash can icon in the Annotations panel or
- Press Delete in the keyboard by selecting the measurement in the viewport or
- Drag and drop the measurement to the Trash can icon on the right side of the active viewport.

Note- - The Trash can icon is visible when you select the annotation.

- The Trash can icon turns red, the annotation is deleted.



7.9 Snapshots

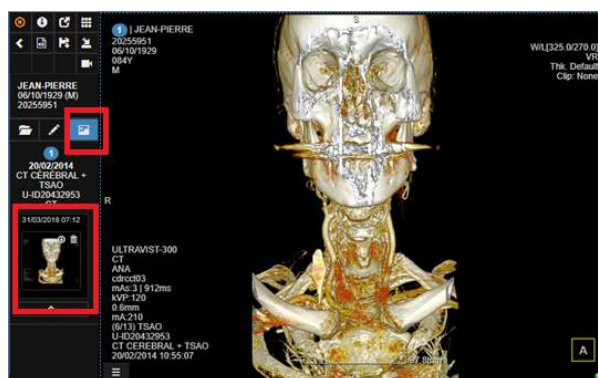
The Snapshot function in 3Dnet Medical is like the DICOM Key Image concept. It is available in the toolbar located in the context menu of each viewport. You can save a snapshot of an image that can then be stored in the PACS archives for future references. The snapshot can be attached to a report, sent to a printer, or saved as JPEG, BMP, PNG, etc. on your local computer.

To capture a snapshot:

- Make the changes to the image (measurements, arrows, text, reconstructions).
- Click the snapshot of viewport on the Context menu and the window to capture an image.
- See the snapshots by clicking the Snapshot tab in the left side of the screen.
- Click the Download icon to save a snapshot to the local drive as PNG, BMP or JPG.

These images can be saved and stored in PACS as key images.

The snapshots are saved with annotations, measurements, and specialized reconstructions. Snapshots are not just a screen capture, but a complete cached, saved state for the study in the moment when the snapshot was taken. You can load a snapshot and resume scrolling, add annotations, measure structures, and use advanced picture analysis tools.

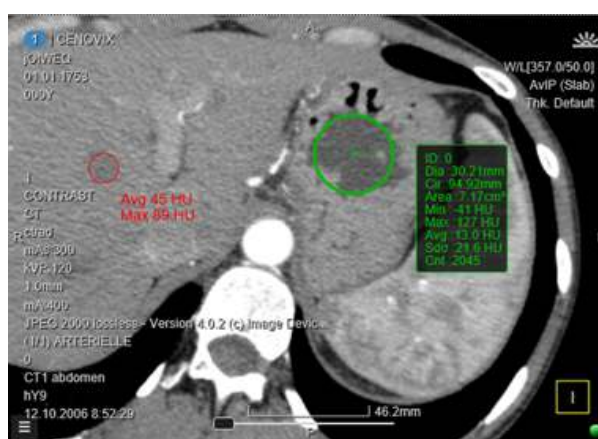


7.10 Hounsfield Units and ROI Densities

- Press the (U) key on your keyboard to see the Hounsfield unit for each pixel on mouse movement over an image.
- Press the (O) key to probe densities inside a circle. The HU value is displayed with red next to the mouse cursor.
- Press 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 like min, max, average, and standard deviation

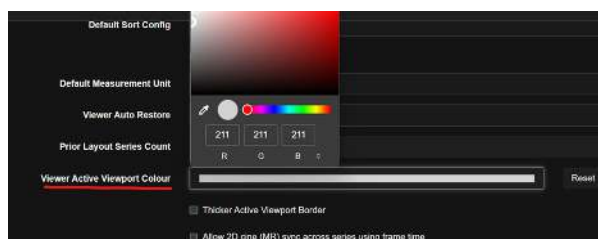


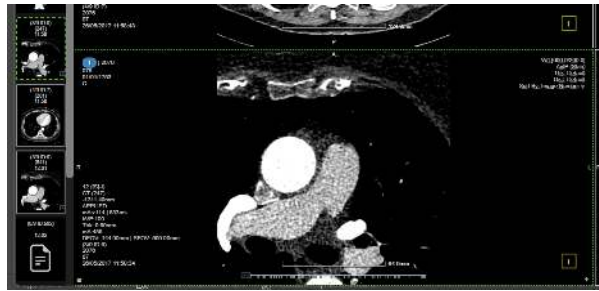
7.11 Active Viewport Border

An org admin can set the colour of the active viewport in the viewer setting from the viewer as well as in the user setting from the Manage page.

Also, an org admin can choose to thicken the active viewport border by selecting the Thicker Active Viewport Border check box.

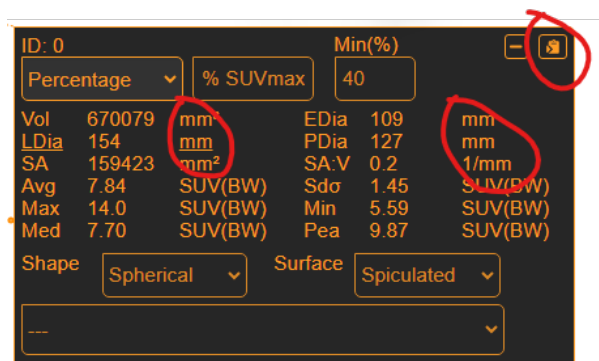
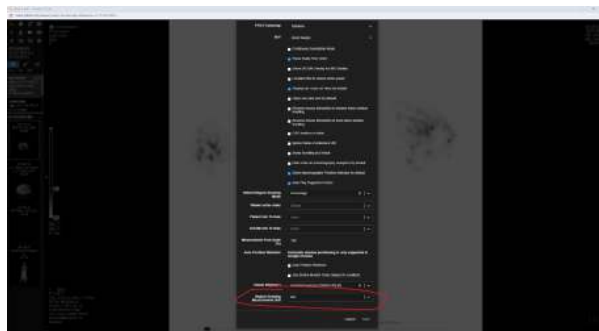
See the active viewport border is coloured in the following example:





7.12 Region Growing Measurement

Change the region growing measurement from cm (default) to mm in Viewer.
Also, you can copy the text in the region growing label to clipboard.



7.13 DICOM Print

In the Viewer, you can access the DICOM Print tool in multiple ways:

- Through the context menu by selecting the DICOM Print tool icon.
- The same icon in the study panel on the left side of the screen. Using the icon in the study panel shows the DICOM print volume selection tool. You can set the volume to append for printing using the slider to select the slices to print.

Note: The window level and some display options can change in this menu.

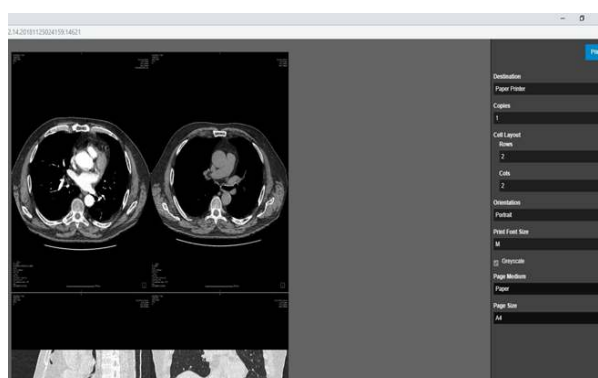
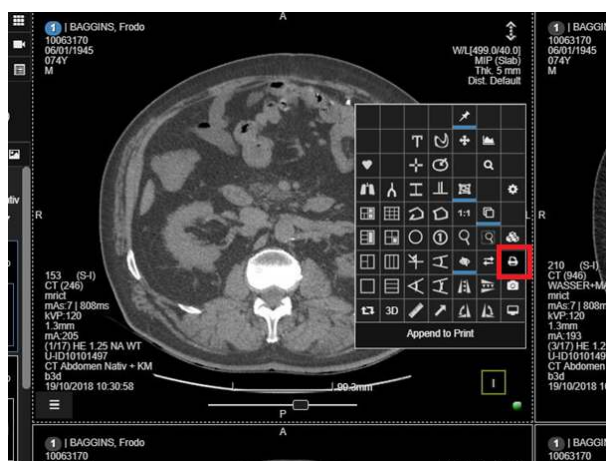
Printing an image:

- Click 'Append to Print' to see the DICOM Printer layout manager.

Also, you can add single slice to the printing queue or an image selecting it from the current layout. To do so, you can use the context menu to access the 'Append to DICOM Print' icon. This adds the selected single screenshot of the viewport to the queue.

Alternatively, you can add the slice to the queue by pressing (Ctrl+P) on the keyboard.

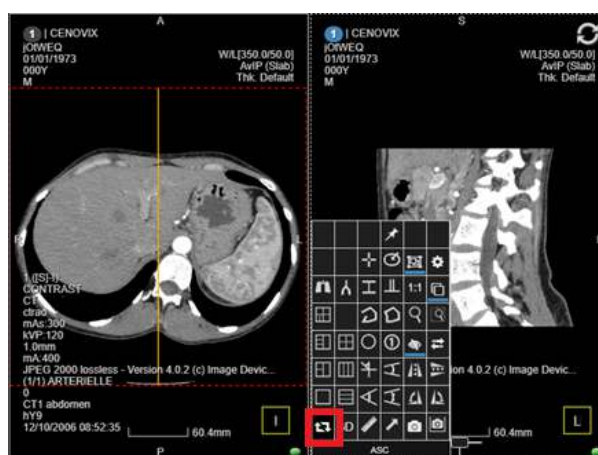
- Set the printer, the number of rows and columns, print medium (paper, film, blue film, etc), medium size (A4, A3, 14in x17in, etc), and the number of copies in the printer menu.
 - To delete an image, move the mouse on the image and click the 'X' icon in the top left of each image.
 - Scrolling down to see all images that have been selected for printing.
 - Click the blue coloured print icon in the top right to print the file.
- You can set up the Printer in the Gateways tab of the Manage page.



7.14 Multiplanar Reformatting (MPR)

Coronal and sagittal MPR views can be quickly generated and displayed next to the axial view.

- Click the 'Axi/Sag/Cor' icon in the context menu to iterate through the viewpoints.
 - Analyse the images using double-oblique multiplanar reconstructions using the 'MPR' icon in the Context menu.
- Also, a quick way to go to MPR layout is by pressing the (Q) key.
- Reposition the crosshair by clicking the intersection of the two perpendicular lines and dragging 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 crosshair on all three views is achieved by clicking the left mouse button on the image.
- To maximise a viewport press (T).
- See the fused data using the Fusion tool in the context menu of the viewports in MPR.



7.15 Volume Rendering (VR)

Like all the other image processing techniques in 3Dnet Cloud Viewer, Volume Rendering is also performed directly on the server and the result is streamed to the client computer. Volume rendering is accessible on any computer connected to a 3Dnet server, without the need of specialized hardware resources.

To generate a Volume Rendering image:

- Click the '3D' icon in the context menu.
- Press the (Q) key in your keyboard to switch between base mode in the axial view, to MPR, and then to volume rendering views.

You can rotate, zoom, or pan an image with the regular tools, using the mouse.

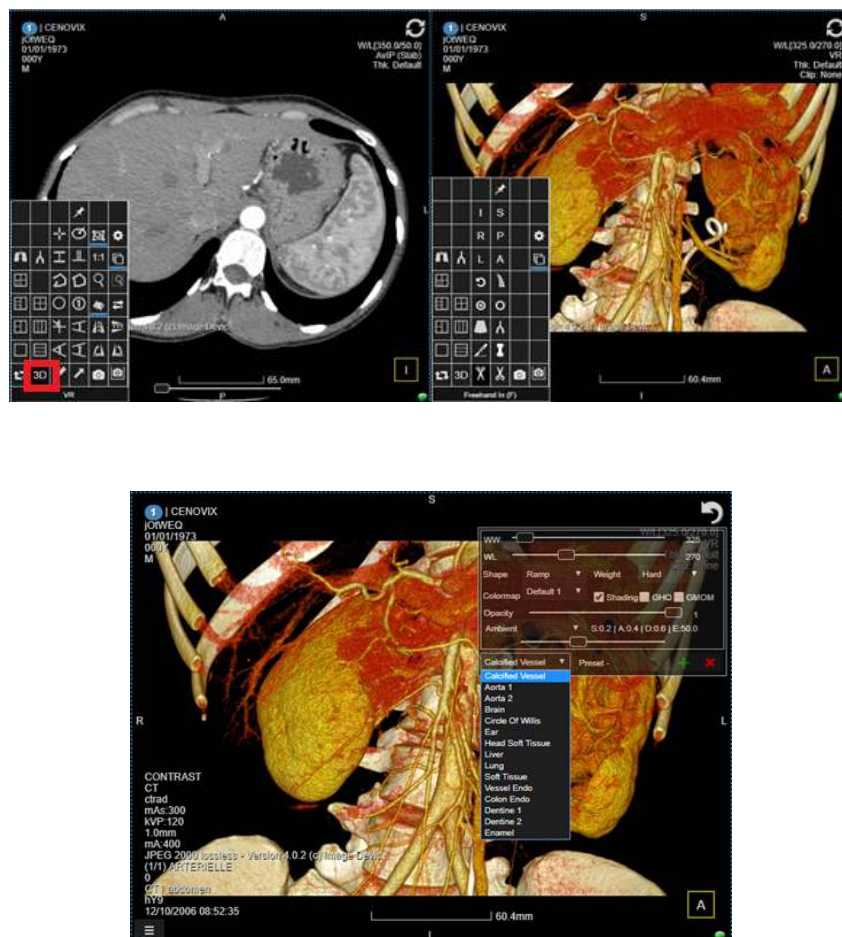
In the volume rendering mode, there are several specific tools like knife sculpting, inner freehand sculpting, outer freehand sculpting, dilate, erode, etc.

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

Click the WL text in the top right corner, to view the presets and filters for the volume rendering transfer function. Use these presets and filters to hide or show different part of tissues or organs.

You can change the parameters of a volume rendering images by modifying the WW or WL, opacity, ambient light, add or remove Shading, colourmap or by selecting presets for various tissues or organs.

The modifications of these parameters show or hide certain anatomical structures.



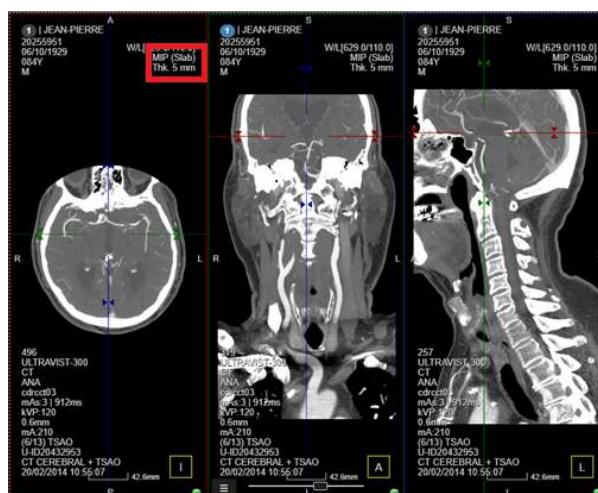
7.16 Maximum Intensity Projection (MIP)

- To quickly go to a MIP view, press the (Z) key.

The viewer displays a thick MIP view with a 5 millimeters thickness of the slab by default.

- Alternatively, select the MIP mode from the top right side of the viewport. Here, you 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.



7.17 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 Cloud Viewer offers easy methods to perform PET-CT fusion, both manually and automatically.

To manually perform the fusion:

- Open a CT acquisition in the viewer.
- Move the mouse on top of that series thumbnail.
- Click using Shift +Left Mouse Button.

The fusion is performed in the viewer between the two series selected. The process works in the same way if you first populate the Viewer with the PET acquisition, then click Shift +Left Mouse Button on the CT thumbnail in the study panel.

Also, you can set Hanging Protocols to automatically perform the fusion whenever PET and CT images are available for the same study.

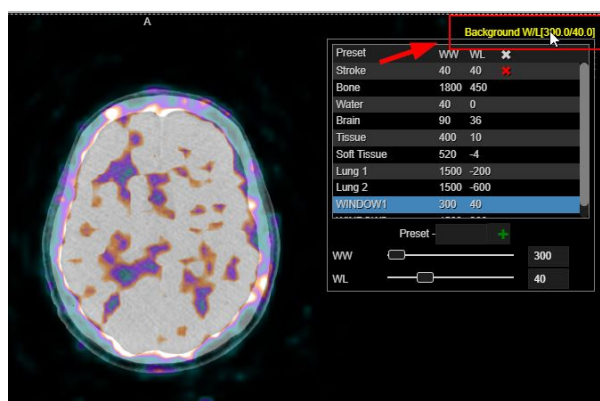
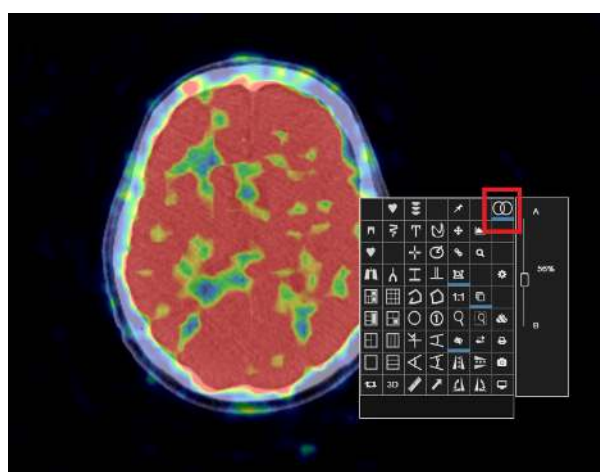
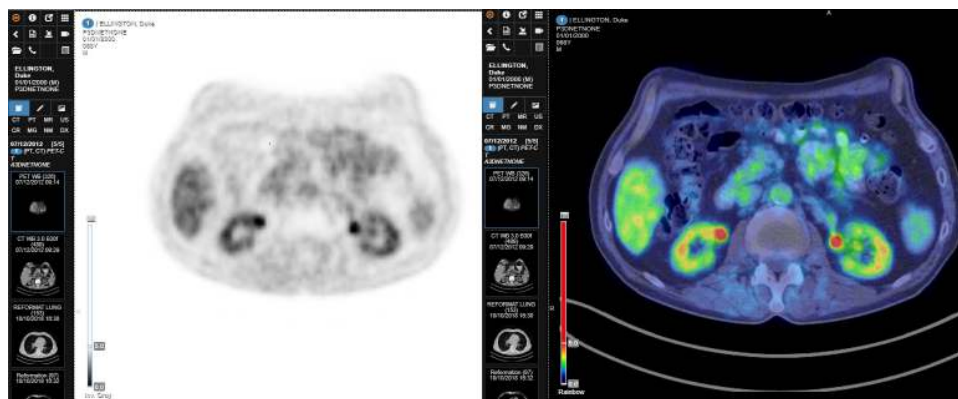
To set this up manually:

- Perform the fusion in the Viewer.
- Locate and select the Hanging Protocol tool clicking on the corresponding button in the viewer's top left.
- Once the protocol is saved, the saved layout is replicated with fused images for future studies if they are available.

Once the fusion is performed, you can adjust the slider on the left of the viewport to change the fusion threshold. At the top of the slider there is an icon that displays the SUV parameters tab. In this tab, you can find the information for: total dose (MBq), half-life, acquisition time, patient's gender, patient's weight (kg), SUV Type.

At the bottom of the slider, you can select the colourmap to use (Greyscale, Rainbow, etc). You can change the Window/Level of the CT background by clicking the upper right Window/Level hot zone in the viewport.

- Use the Circle Annotation tool (Link to table) to draw a static ROI and get information about the SUV in that area of interest. Use the shortcut key (O) to display the SUV values in a ROI. This ROI can be resized by holding (shift Mouse Scroll Wheel).
- Use the 'U' key to see the SUV values in a pixel. The keys 'U' and 'Q' displays the SUV values where you point the cursor.
- To adjust the fusion overlay, use the button on the top right of the context menu (Link to table) and slide the vertical slider.



7.18 Sculpting Tools

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

- Clipping:

There are three types of clips that you can apply to an image:

- Elliptical
- Plane
- Box

Add clipping to an image using the following process:

- Click '3D' in the context menu.

You can see the 'Clip' text in the top right corner of the viewport.

- Select the 'Clip' option.

A drop-down list appears.

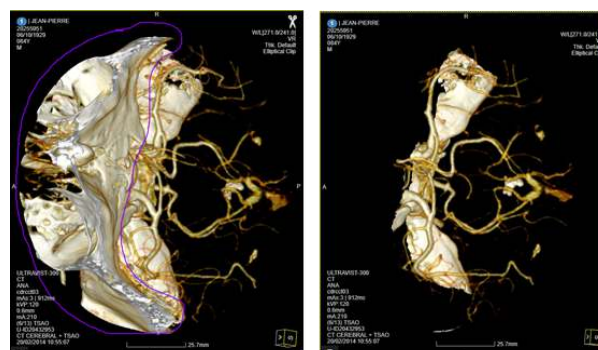
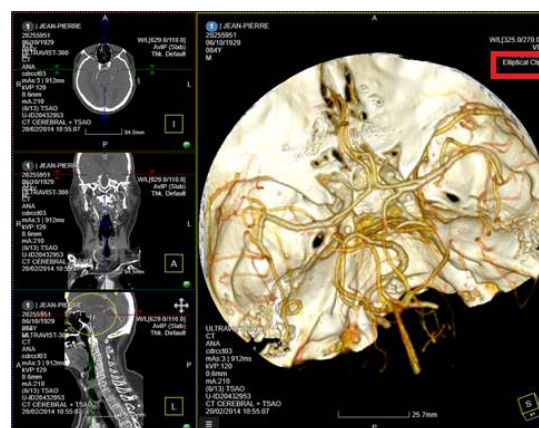
- Select the type of clip you want to apply.

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

Also, you can use the following options from the context menu (Link to table)

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

To undo a cut, remove the Sculpting operation from the Annotations panel. The diagnostic viewer displays the initial image.



7.19 Spine Labelling Tool

Click the 'Spine Labelling Tool' icon on the upper part of the context menu (Link to table) to access the Spine Labelling tool.

To start labelling:

- Click once on the first vertebra.

The default starting position for labelling is C1.

- Left mouse click on the first vertebra to start labelling.
- Move the cursor down (or up, if starting from the last vertebra).
- Click on the subsequent vertebrae to be labelled one by one, the labels appear in order (C1, C2, C3... T1, T2, T3...) and in blue (i.e., edit mode).
- To stop labelling, double click anywhere in the screen.

Editing the label:

- Edit the labelling already done by double clicking on the labels.
- Place the cursor on the label (whilst on edit mode) and move the mouse wheel (up or down) until the desired label appears.
- Left click on the next vertebra to resume the labelling (the order follows from the previously changed label).
- This enables the editing mode of the curve.

When the curve is on edit mode, the labels are shown in blue colour instead of orange. In the edit mode, you can delete a label pointing at the label and pressing the (Delete) key or drag the point of the label to change its position.

- Use edit mode to change the starting point if starting the labelling from the last vertebra - change the starting point to Co5 (scroll once upwards), subsequent labels will appear in the reverse order (i.e. Co4, Co3...S5, S4, S3... L5, L4, L3...).

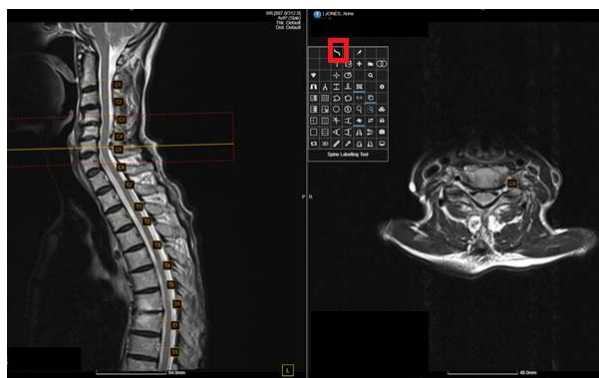
- In edit mode, hover over the label and use left mouse to move the label around; to delete press the 'Delete' key. Hovering over the label will also show the line connecting the label to corresponding vertebra.

The label of a point can be changed by positioning the cursor on the label and using the mouse wheel to change the label. On a sagittal view, moving the cursor towards the bottom part of the screen causes the numbering in the label to increment. The opposite happens when moving the mouse towards the top of the screen. In this case the number in the label decrements.

If you start labelling from the top, the labelling tool starts counting from C1.

If the labelling is starting from the bottom of the picture:

- Apply the first label (C1), position the cursor on the label.
- Scroll once upwards and the labelling will switch to Co5.
- Following clicks going towards the top of the screen progresses as follows: Co5, Co4, Co3, ..., S5, S4, S3, ..., L5, L4, L3... etc.
- Hover with the mouse on the labels to highlight the curve of the line that goes through each individual point.





7.20 Bronchoscopy

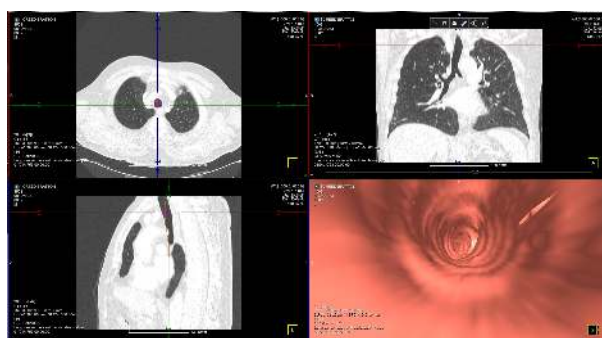
Click the 'Bronchoscopy' icon in the context menu to fly through the curve. You can see three MPR and a VR Pipeline Viewport.

With this feature, you can fly through the curve with perspective rendering.

To fly through the curve,

- Create a curve like manual CPR. The VR Pipeline Viewport displays the 3D rendering.
- Click on any part of the curve. It displays that part in the VR Pipeline Viewport.
- Click Play to walk through the curve.

Also, you can select Toggle Layout to maximize the VR Pipeline Viewport.



7.21 KiM Graph

Drag the graph in the viewport by selecting the KiM graph icon in the Viewer Context menu.

The tool tracks where the mouse pointer is and displays the floating measurement labels. Also, you can toggle in between the layout and turn off the KiM tracking.

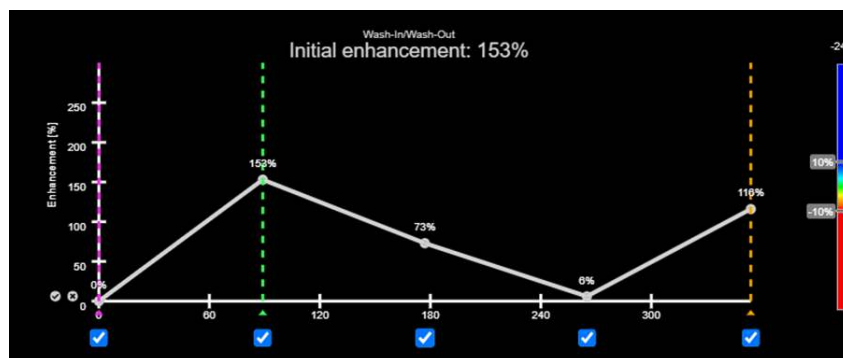
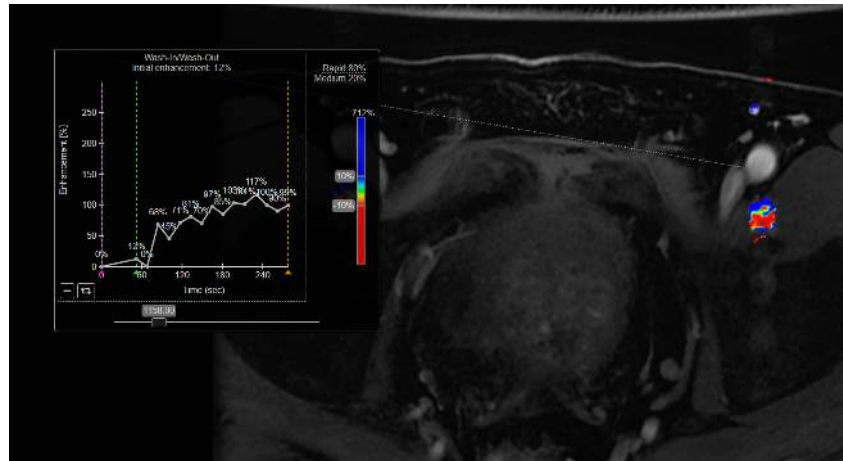
Edit the KiM time points.

Click the pen icon in the KiM graph to edit the time points.

Deselect the time point that you want to exclude and it will be excluded from the graph.

Select it again to add the time point.

KiM graph also displays the enhancement curves for the segmentations in the standard KiM view and the KiM floating graph view, instead of only showing in the new MPMRI module.



7.22 Prostate Module

To work with the Prostate module, select a study from PACS and click MP MRI icon from the context menu. You can see the following dialog box.

This dialog box appears blank and you can select the appropriate options from the respective drop downs.

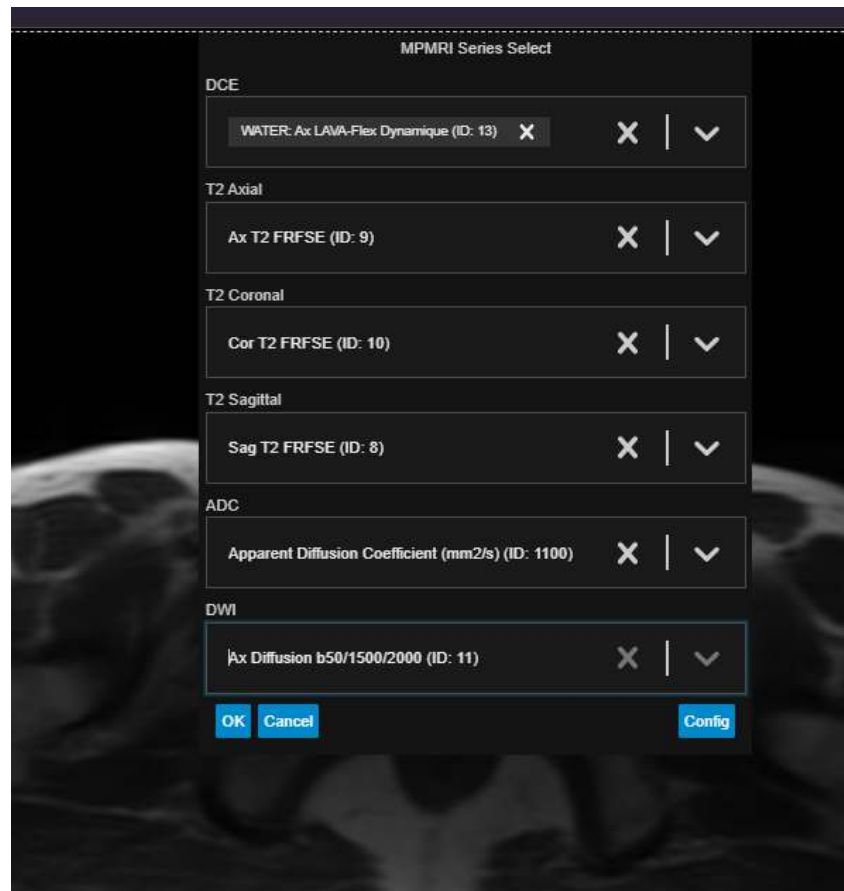
Also, you can click the Config to configure the Presets. You can add multiple rules using the plus button a bit like hanging protocol rules. 'Match all' means that a series that matches all the rules in the box will go there. 'Match any' means that a series that matches any of the rules will go there.

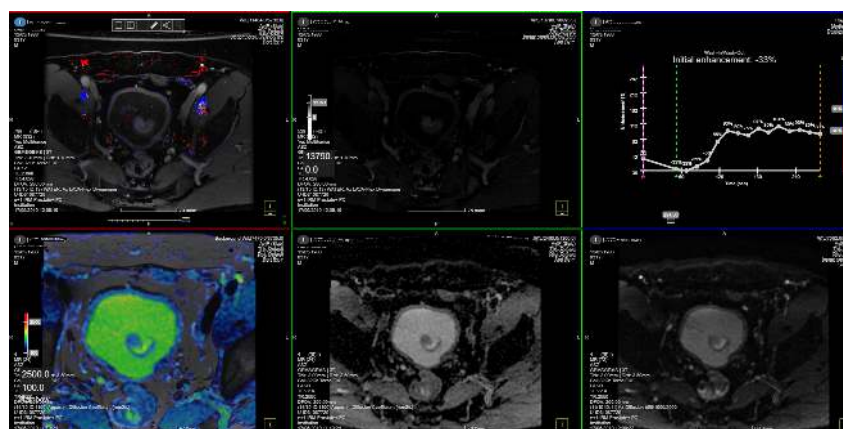
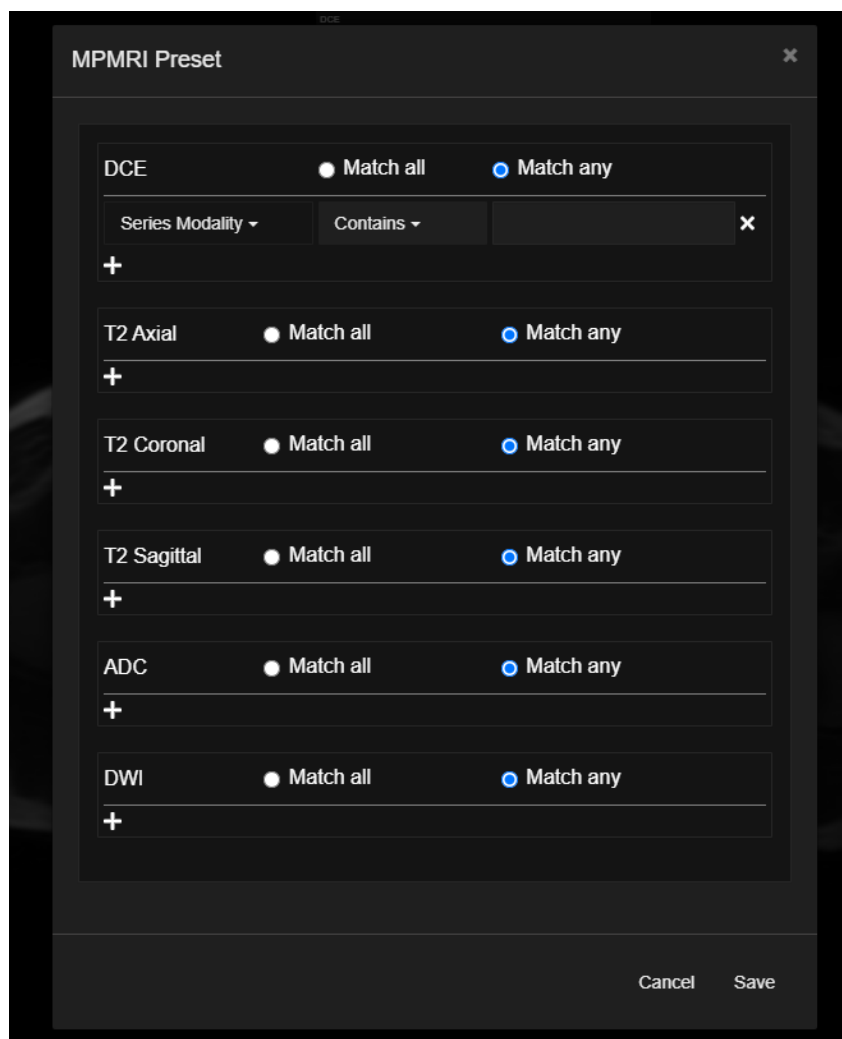
When you click ok, you can see various viewports appearing in the viewer.

The Fusion viewport displays the fusion of ADC with T2W. You can draw KiM region in the top first viewport and see the statistics of that region in the top third viewport.

Turn off KiM tracking by selecting KiM Tracking icon in the context menu. Also, you can select Toggle mp-MRI Layout from the Context menu to toggle between different viewports. You can see the type of scans in different axes. The 3 scans you can see are the T2 Axial, Coronal, Sagittal. If you scroll in one of the axes, it'll display the location relative to other raxes using the indicators. Use the same sliders in the Fusion viewports to vary colors. Also, you can select the fusion opacity using the Fusion icon from the context menu.

KiM Polygon Segmentation- Using this icon, you can draw the segmentation in the KiM Viewport and itll display the volume. Also, the Statistics of the region - the same statistics as the KiM region will be displayed. Switch back to the graph to see the measurements.





7.23 CT Dental

You can do the following functions using CT Dental option from the context menu:

- Rotate All Axes

Rotate the dental images in all axes by selecting the Rotate All Axes check box in Viewer. To do so,

- Select the CT Dental icon in the context menu.
- Select Rotate All Axes check box.

You will be able to rotate the image in all axes.

- Cross Section Distance:

Set the cross-section difference to view the distance between two points in a dental curve.

To do so:

- Select CT dental icon in the context menu to view the dental viewports.
- Draw a dental curve.

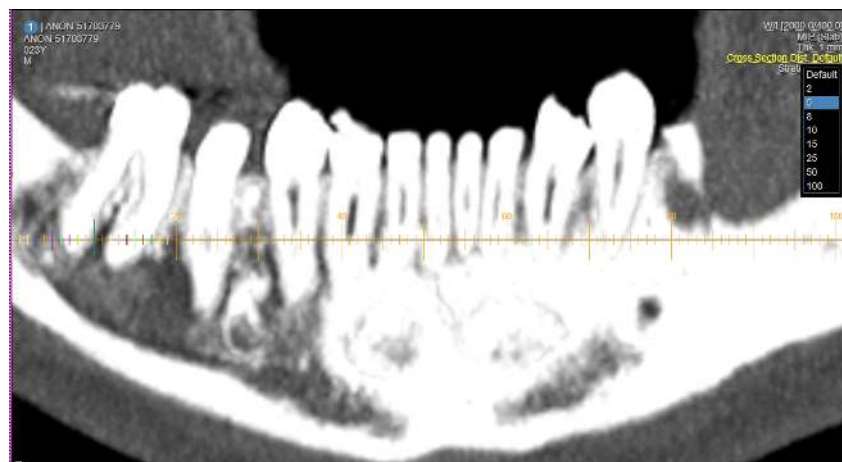
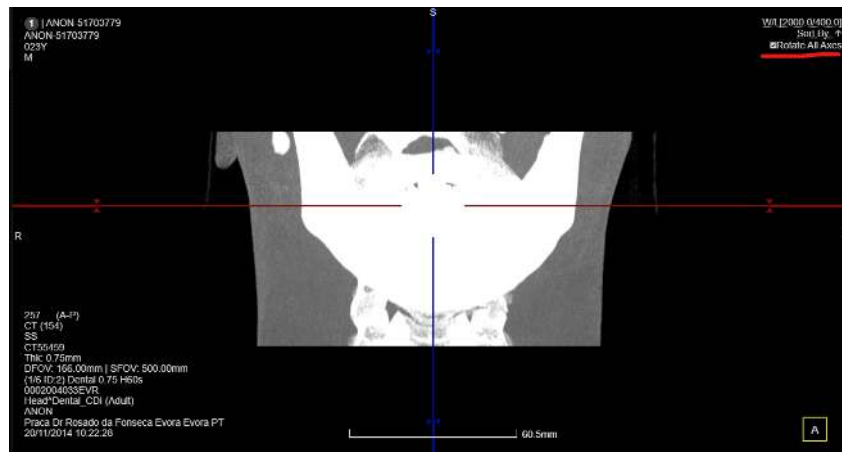
When you finish the curve, you can see multiple viewports.

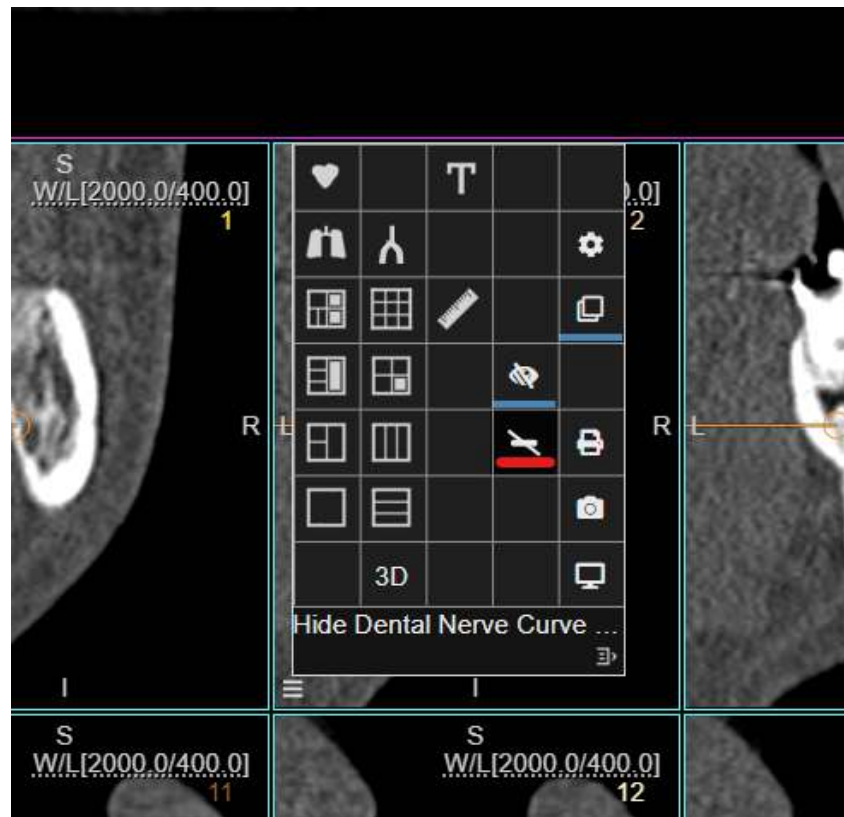
- In the viewport, select the Cross Section Dist to set the required distance.

- Hide Dental Nerve Curve

Hide the dental curve by right-clicking the cross section viewport and selecting Hide Dental Nerve Curve icon.

Double click the curve line to edit it.



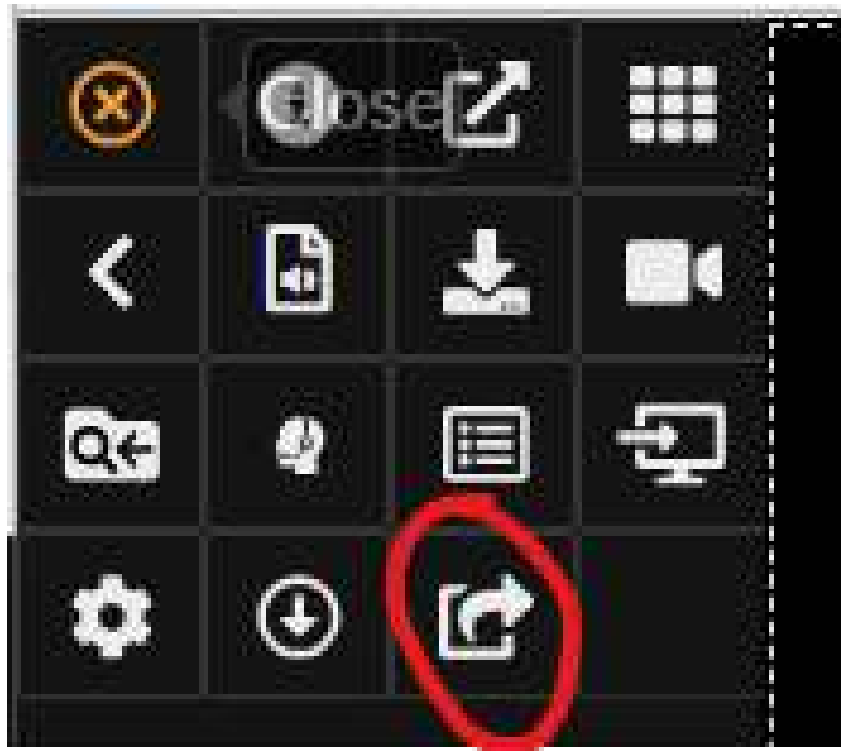


7.24 Share Study

Share a study by clicking the Share Study icon in the Viewer.

After clicking the Share study icon, following dialog box pops up:

Fill in the details to share the study and click Share. View the studies previously shared by the user in the Shared by me tab.



Share Study Shared by me

Patient ID	Patient Name	Accession No.	Study Date
U-ID10001024	DISPLAY, Shutter Test	ACN00000695	23/10/2015 14:03

Full Name

Email

Message

Expire days 7

Create Pin

☐ Hide demographics (please note patient details may still be visible in documents, reports, and some images)

Share

Share Study Shared by me

TEST, Test2021 - Sent to: [test@biotronics3d.com](#) @11/12/2024 (a month ago)

17/12/2020 08:37

CT Head

ACN00001237

MR

[ReportingPhys]

[Status]

REDMOND, Joshua - Sent to: [test@biotronics3d.com](#) @03/12/2024 (2 months ago)

01/02/2005 12:00

CT Head

ACN10000044

CT

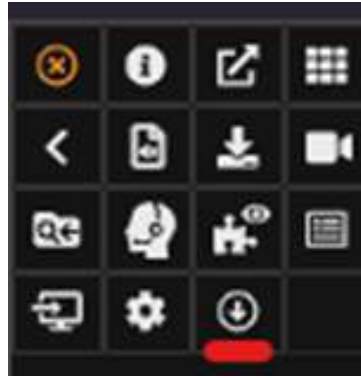
[ReportingPhys]

[Status]

COLMAN, Ornette - Sent to: [test@biotronics3d.com](#) @29/11/2024 (2 months ago)

7.25 Download Study

Download a study in the viewer by clicking the Download Study icon.



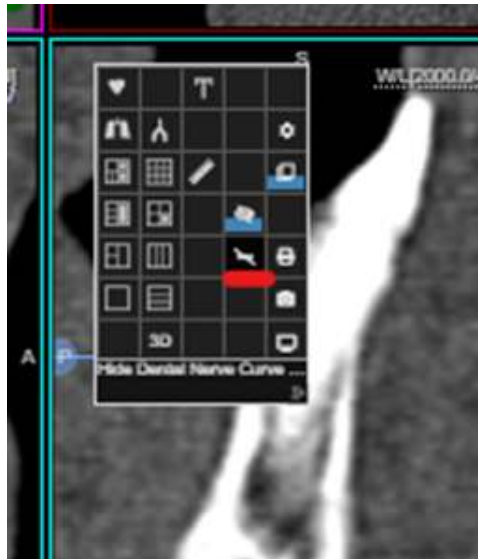
7.26 Pin Measurement

Pin measurements in the Viewer by clicking the pin icon:



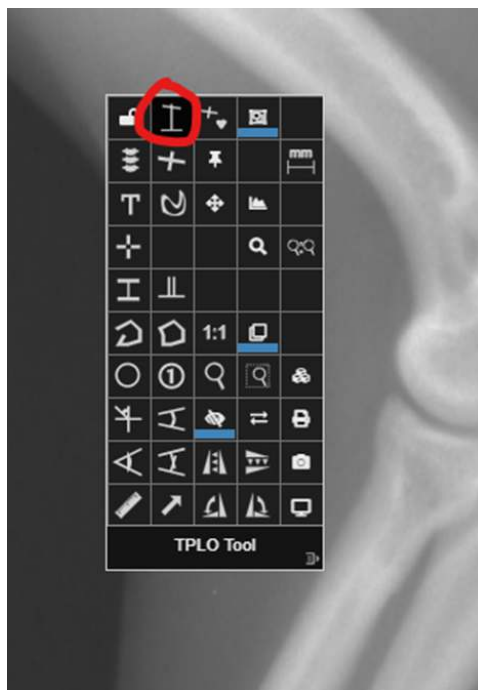
7.27 CT Dental Nerve Curve

Click the Show / Hide the Dental Nerve Curve button in the viewer context menu in CT dental cross section viewports to hide or show the dental nerve curve lines. If hiding is enabled, the dental nerve curve won't show in edit and unedited mode. Only the intersection ellipse will be displayed in unedited mode. The curve points on the slice will be displayed in edit mode.



7.28 TPLO Planning Tool

Click the TPLO Planning tool in the context menu of the viewer to view the tibial plateau angle for the animal in the Vet Org.



8 Vascular CT

Vascular CT is an advanced clinical application module and it can be used to evaluate stenosis and visualise obstructions in vessels. To launch this module, click on the bloodvessel button in the context menu. This launches a viewport layout specially for this module showing MPR, VR, CPR, and cross section views.

The context menu contains a different set of tools specially designed for this module, among which we have:

- Bone segmentation and removal tool.
- Blood vessel segmentation tool.
- Table segmentation and removal tool.

- Blood vessel tracker tool: extract the center line of a blood vessel for stenosis analysis.

Table and Bone Removal

You can remove the table and the bones from the images by selecting the appropriate tool in the context menu. Click on the table and on the bone over the image, respectively. This deletes all the structure from the image. If the structure is not completely deleted, repeat the process until these structures are removed completely and click on the table and on the bone over the image, respectively. This will delete all the structure from the image. If the structures are not completely deleted, repeat the process until they are removed completely, by clicking on the table and bone areas in the image, respectively. Also, you can select the pin icon in the context menu to pin the tools.

Blood vessel tracker

Use the Blood vessel tracker tool to segment the blood vessel and extract the centreline. - Click on the start of the blood vessel. - Drag the mouse over to the end of the blood vessel. - Release the left mouse button. After computing the centreline, the tool displays a stretched CPR image. You can edit the tracking of the blood vessel by selecting the 'Tracker Editing' tool. Click on the desired location along the computed centreline to adjust any of the points. This respectively updates the CPR view.

Stenosis Analysis

To perform the stenosis analysis:

- Click the stenosis icon in the context menu. - Keep the left mouse button pressed. - Draw a line on the blood vessel segment under analysis. - Release the mouse.

The software automatically identifies the thinnest part of the blood vessel (depicted with red line on the CPR) with reference to the blue line level (the reference). The stenosis ratio is computed and displayed, together with the blood vessel cross-sectional diameters and surface area.

From this view, you can select between Stretched or Straightened CPR.

Contour Correction

Using the Contour Correction tool, users can manually correct the automatic contouring performed by the application. Select the tool from the context menu by clicking on the Contour Correction icon. It is possible to operate the manual correction from the viewports with the cross section of the blood vessel (around the CPR viewport). Maximize the viewport by double clicking one cross section viewport.

To correct the automatic contour, select the tool then draw on the orange circle (or outside). To modify the automatic contour, double click on the side you wish to keep. To expand the contour, follow the following steps:

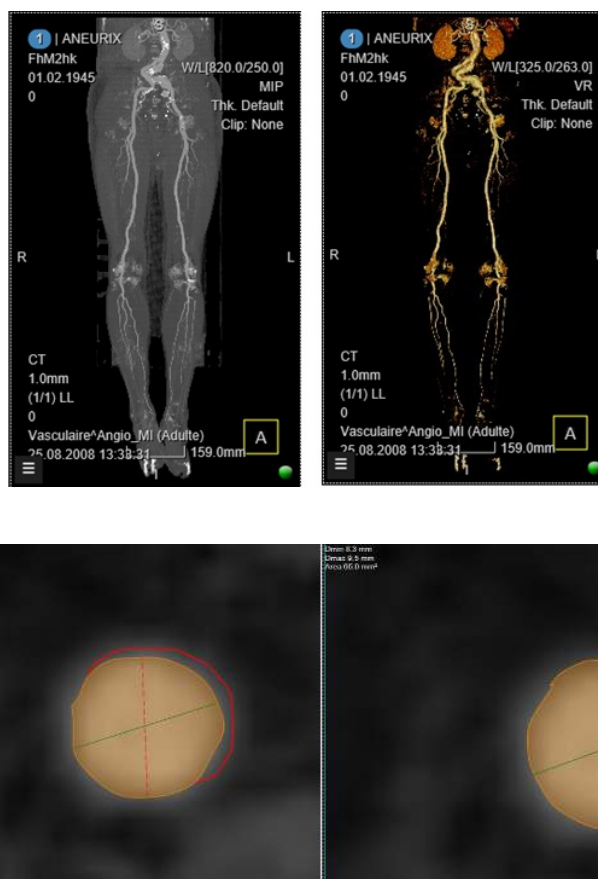
- Draw a curve line around the default automatic contour to highlight a portion of the blood vessel to add to the countered area.

- 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.





9 Lung CT

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

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.

After using the Region Growing tool, an information table will appear in a corresponding label. This table displays valuable information regarding the lesion contoured like volume, diameter, surface area, doubling time, and more. The labels can be collapsed/expanded by the user using the collapse button (+/- sign) and these labels can be independently moved around as required.



10 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. Clicking on the KiM icon triggers a 2x2 layout with:

- Top left: 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.

On the graph in the bottom right viewport, user 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). 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 at the top right in the bottom right viewport.

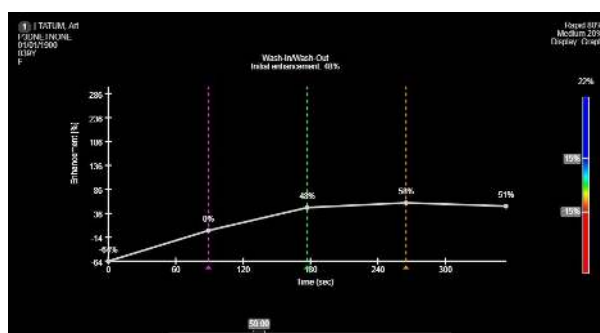
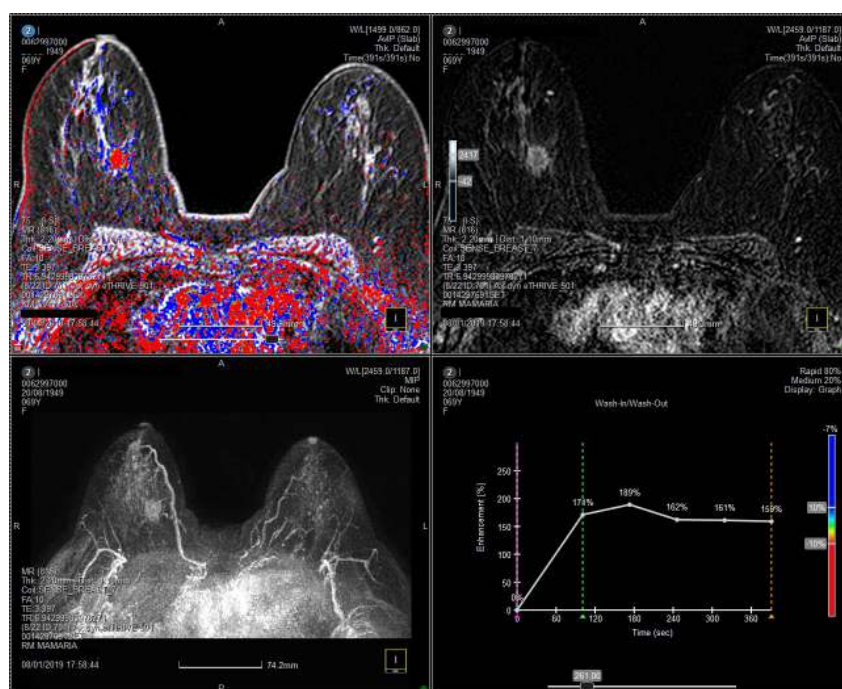
If Medium is set to 20 percent and rapid to 80 percent, increases between 20-80 percent will be considered Medium rate of change. Values over 80 percent will be considered Rapid. Changes in the threshold will be reflected on the table chart and visually in the coloured overlay in the top left viewport. The quicker the change in

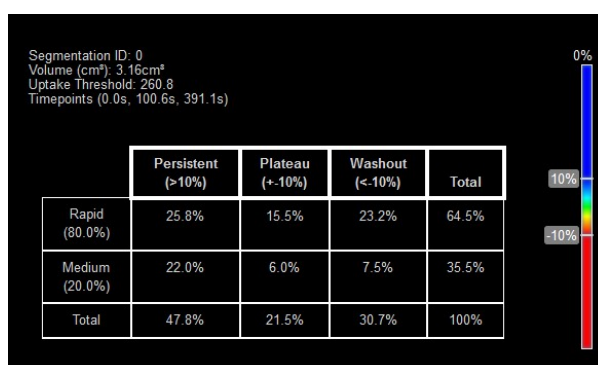
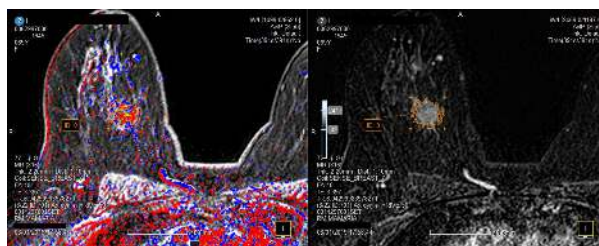
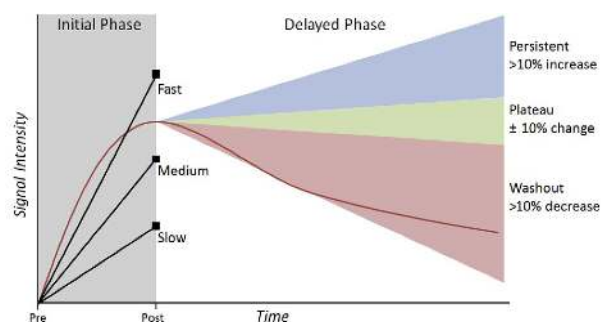
SI, the more intense the blue or red will be. The curve annotated with Slow represents a pixel that did not increase to a level of significant enhancement on immediate contrast-enhanced series. This pixel would not be coloured in the parametric map and will not be included in the analysis, regardless of the pixel value on delayed contrast-enhanced series. As it is set up in our example, Medium and Fast curves are those which increase faster than 20 percent or 80 percent respectively, 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 percent 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 percent on delayed contrast-enhanced series will be coloured red to represent significant and washout enhancement.

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

- 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
- A chart showing the percentage of pixel for each uptake classification.

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. For example, a pixel shown with transparent blue depicts a medium enhancement, while a fully opaque one exhibits fast initial phase.



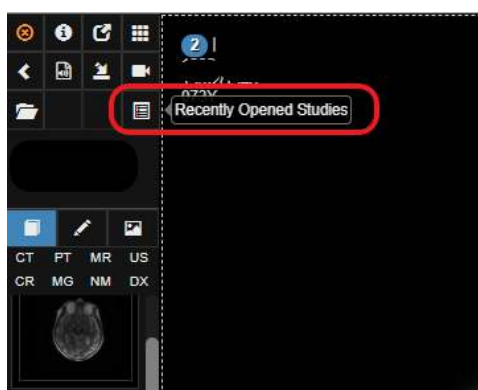


11 ADC Map

ADC maps can be created with 3Dnet from diffusion images. This is done in the viewer, by loading on the screen a diffusion image and using the Export Tool in the context menu. Once the tool is selected, a export menu will be displayed. From this menu the user can create the ADC Map by setting the B value range and the name for the new series.

The user can customise the new series that is going to be created indicating: the series description; selecting which DICOM target this series will be sent to; the range of B Values; a threshold to optimize the noise in the picture; option to include an exponential ADC map in the reformation. Including the exponential ADC Map will effectively generate two separate series.

Once the new sequence is completely set up and ready to be exported, click on the blue send icon. This will start the processing of the map. Once the processing is completed and the new series reaches 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.



12 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. The label is 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, the score table, and the risk graph.

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

If an entire coronary branch does not present any lesion, the check icon can be used 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 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.

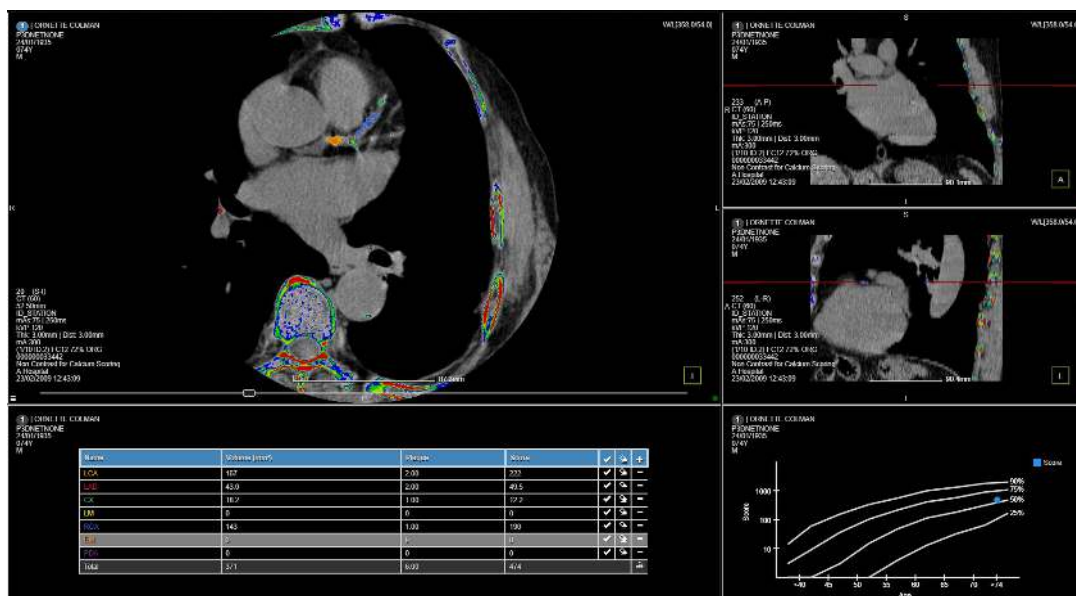
To calculate the risk factor using the values in the table, click on the Update Graph icon in the bottom right corner of the table. This will display, as a result, the risk factor in the risk graph with a blue dot. Once the graph is drawn, it automatically updates when a contour is performed on a new 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

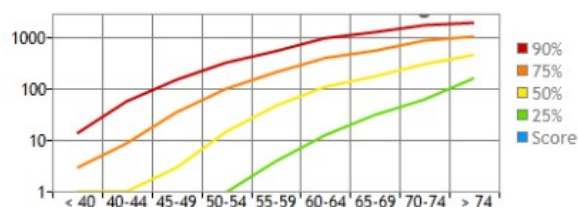
artery and the total CAC score is equal to the sum of the score of each artery. This score is then adjusted according to patient's age and gender. Based on this, a percentile of risk is assigned.

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.

13 Colon CT

3Dnet Medical offers a complete colonoscopy CT 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 colonoscopy CT 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. This is useful to display a supine and prone acquisition side by side for a direct 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). The points of interest, represents

markers indicating 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.

The centreline and segmentation is automatically performed and presented to the user. Press (Spacebar) on your keyboard or click with the right click 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. By default, the crosshair is not visible in the MPR views during the fly-through. 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 fly-through.

The fly-through can also be controlled with the playback control bar. Users can follow the fly-through end to end, jump to the start or the end, reverse the direction and adjust the speed using this control bar. This bar also displays a number that represents the distance in milliliters from the starting point. If a suspicious formation or a lesion is spotted, users can:

- Mark it using the Colon Point tool using the corresponding 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.

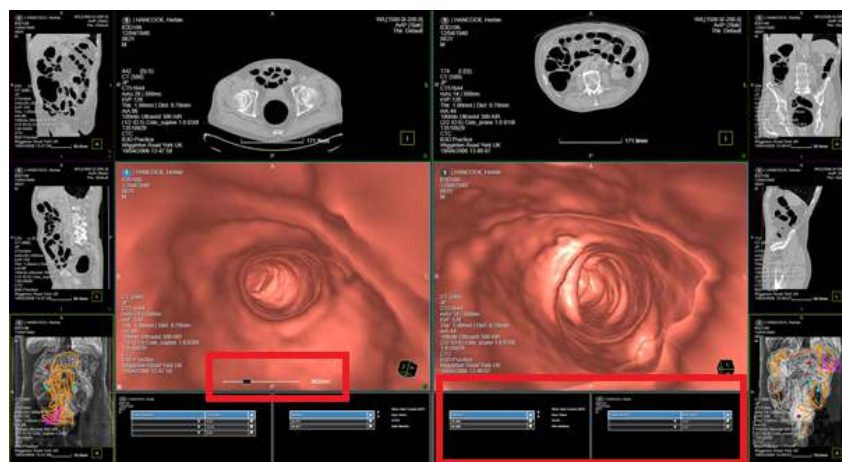
Once the measurements and markers are set, users can check them one by one selecting each entry in the measurements table and in the markers table. Selecting an entry from these two tables will display that marker or measurement in all viewports for quick and effective analysis.

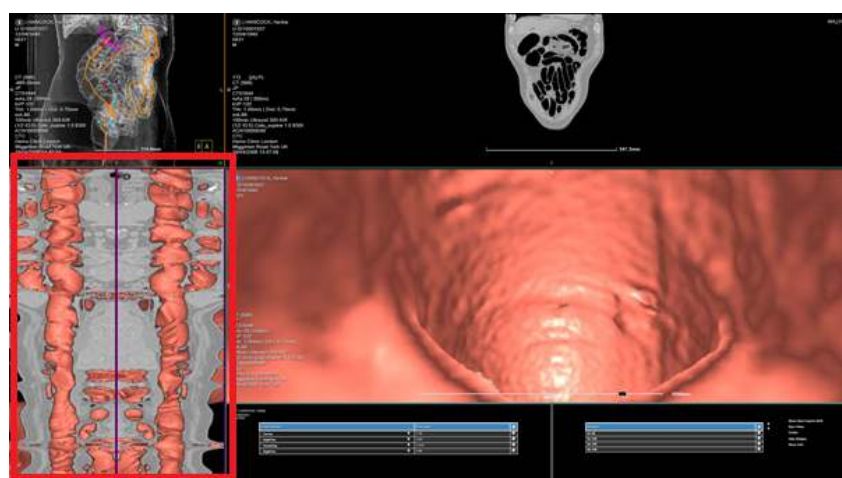
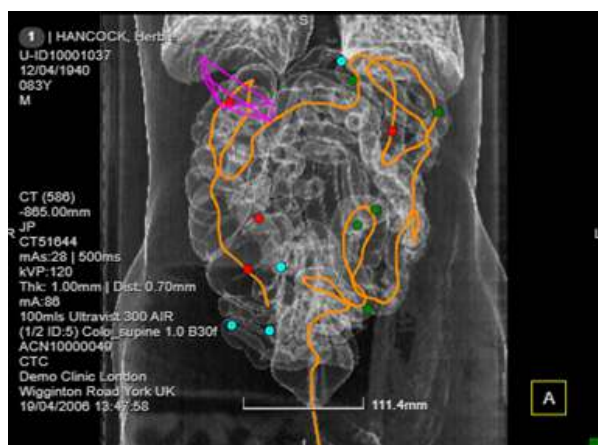
In the markers viewport users can access a list of options:

- 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. This will be displayed in more detail later.
- Hide Markers: hides markers from the centreline and segmentation view.
- Hide CAD: hides CAD from the centreline and segmentation view. This is only available if CAD pre-processing is enabled.

In this VR viewport users can see the extracted centreline and segmentations, which is indicated with an 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.

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.



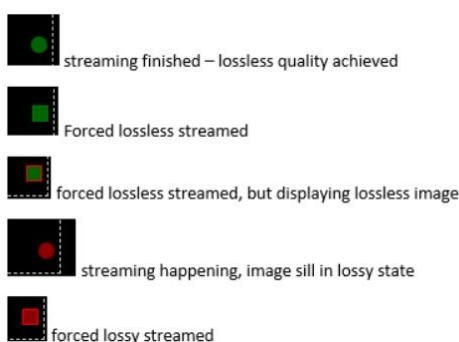
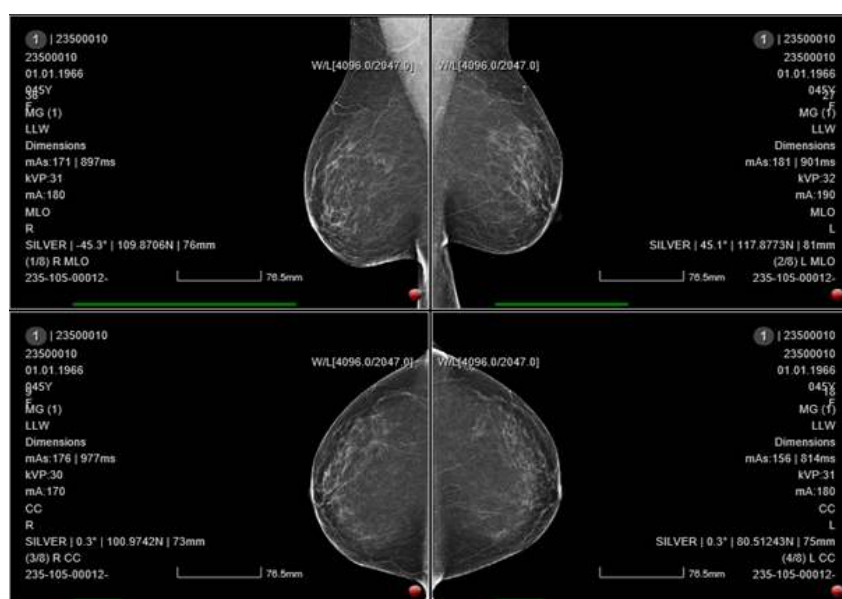


14 Image streaming and compression

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. This is represented with a 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 cog icon from the viewport context menu. 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.

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 bottom of the viewport to show the progress of the streaming.



15 Reporting

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.

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. For example, only showing

MRI macros for MRI studies, and only showing CT macros for CT studies.

It is also possible to copy/paste texts over from 3th party sources as e.g. internet. If there are unsupported tags or links in the copied text, they will be presented as flat text.

Click the floppy disk button to save the result, or the camera icon button 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. After the text and images are inserted, click the Sign button to sign the report preliminary or final. If desired, the reporter can also select 'Sign Next' to jump immediately to the next patient without the need to go back to the worklist. For preview, click the View as PDF button.

If the user has been given the right (Manage - User - Organization Settings - Permission Settings - tickbox at 'Manually Send Report'), the report can be manually sent to a Hospital Information System, Radiology Information System or to a DICOM system by clicking on the Send button. Here the user has the following sending options:

- HL7: send the report with a HL7 ORU message.
- Send as DICOM: encapsulate the report as a DICOM file.
- Send as document.

The user is also able to select one of the configured PACS Targets.

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.

Navigate the multiple documents in the Docs table of a report using the navigation arrows. When no docs are attached to a study the navigation buttons are disabled.

Select all series associated with a study at once by clicking the series icon. Also you can press Shift + click on your keyboard to select series within a range.

RADIOGRAFIE ANONIM Date of Birth 08/26/1997 Gender Female Patient ID 0000145199

← Back E 1 2 3 4 View Docs Compare 9/1-35

03/29/2014 10:56 AM
[Description]
0001117017STR
CR

Unsigned Draft Sign Delete Macros... Default Template

uyesia

4, Erythrou Stavrou Str. &
Kifissias Av
151 23 Marousi
Athens
State
11111
United Kingdom

Patient Name: RADIOGRAFIE ANONIM
Date of Birth: 26/08/1997
Patient ID: 0000145199
Study Description:
Study Date: 29/03/2014

Sans Serif Normal A B I U

New report

3DNet Medical © 2018 - Powered by: Biotronics3D Terms and Conditions | Acceptable Use Policy | Privacy Policy

Sign Report

3DnetMedical Admin (Demo Site)
30/09/2021 15:47

Final

☐ Electronic Signature

☒ Send

Send Options:

Send As Dicom

PACS Target:
DVD BURNER

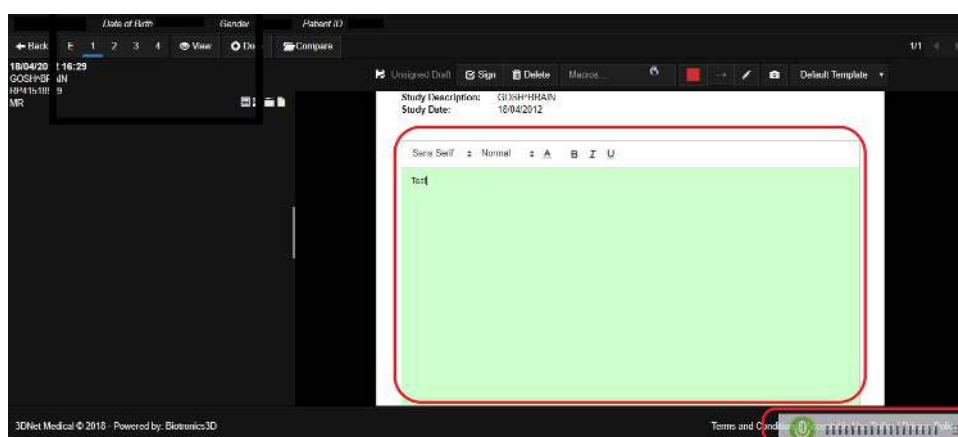
Sign & Next Sign Cancel

15.1 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. This enables users to take advantage of powerful features such as adding a pre-defined block text, linking actions to specific words (like full stop, or next line), sign report as finalized with a button press on the speech mic, open next patient with a button press on the speech mic, etc.

An overlay in the bottom right corner of the report indicates that the voice recognition 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 enable per user, so users can carry their profile options from one workstation to another.

Org admin can also choose to select Voisis integration from the Nuance, Voisis, or Augnito integrations. In the Manage page, select the Voisis check box in the Integration Info tab for a user to enable Voisis speech to text feature. Record the speech and it will be reflected as a text in the PACS report.



15.2 Critical Findings

If your system is configured to show critical findings functionality, the system will bring right above the report pane on the study information and reporting page a small box where the reporter can select a critical findings flag.

When no critical findings flag is selected by the reporter, the system will set the critical findings flag by default to 'none'.

When a critical findings flag is selected by the reporter, the selected flag will be reflected in the box itself and in the report template making sure that the critical findings flag will always be mentioned in the report, even when printed or e.g. exported as pdf.

Note: when you are using 'older' templates which are not yet configured to show this critical findings flag, please get in touch with support@biotronics3d.com to update your report template.

The reporter can change the critical findings flag as long as the report is not yet signed. As soon as the report is signed, the critical flag can only be changed by writing an addendum.

When the report is sent out through HL7, the critical findings flag is part of the outbound HL7 (ORU) message.

A critical findings flag is by default visible in the appropriate worklists across the 3DNet solution e.g. PACS, Teleradiology, Advanced Peer Review,.... The column is visible on the most left side of the worklists.

By each next left mouse click (LMC) on the 'white' flag column header, one can filter and sort on the various critical findings flags.

Critical Findings

Urgent

Biotronics 3D
Analyze - Collaborate - Discover

Patient Name: TEST, Patient5
 Date of Birth: 01/01/1753
 Patient ID: 00000005
 Study Description:
 Study Date: 13/10/2021
 Critical Findings: Urgent

B I U Normal Sans Serif T_x

New report

Default Refresh Clear Day 3 days Week Month Preliminary Ready for Sign Off Reported Canceled

Quarter Year Lustrum Decade

Search (Name/ID/DOB/Accession No.)

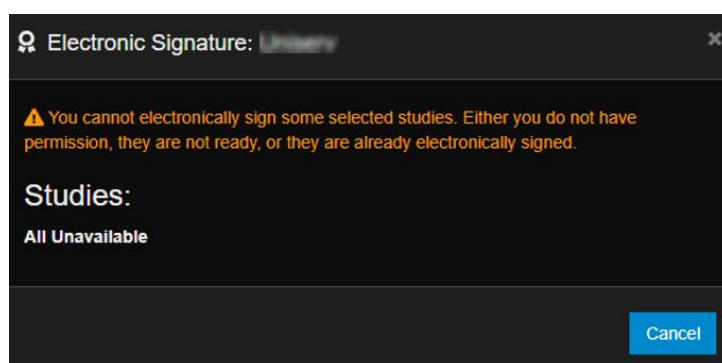
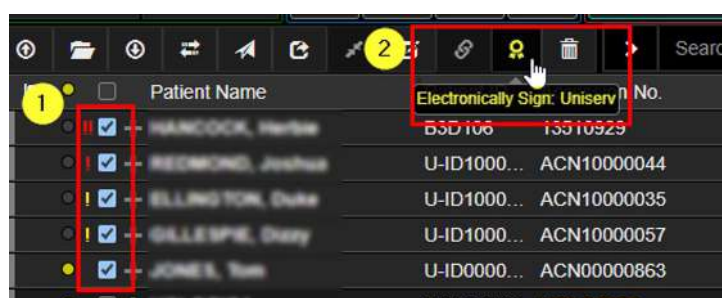
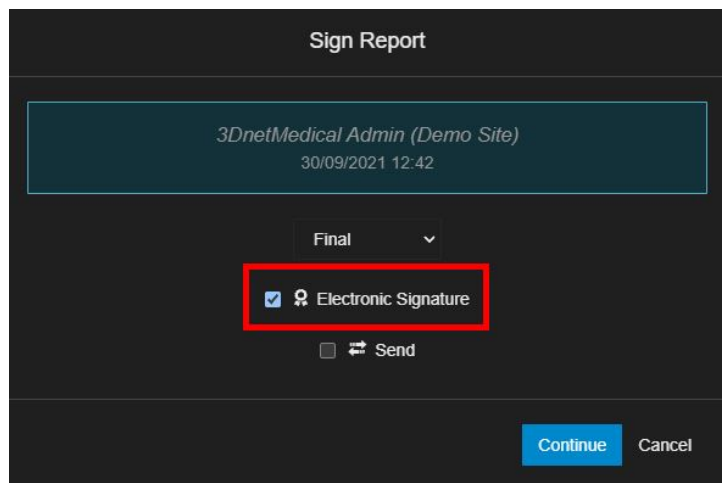
Patient Name	Patient ID	Accession No.
FALCON, George	123456789	ACN10000044
FALCON, Andrew	137	ACN10000017
FALCON, George	ACN10000057	55555
FALCON, George	ACN00000863	HOLOGIC4
FALCON, George	0002594697	ACN00000848
FALCON, George	ACN00000849	ACN10000005
FALCON, George	U-ID1000...	

15.3 Digital Signature

If your system is configured to work with electronic signatures and the user has been given the permission by the administrator to sign electronically (Manage - User - Integration Info), then the reporter has the option to activate the electronic signing by checking the tickbox next to 'Electronic Signature'. When the button 'Continue' is hit, the configured electronic signing portal will be loaded and the reporter has the ability to sign according to the protocol on the configured portal (example below from Uniserv-portal).

Users can electronically sign whilst reporting, but he/she can also decide to sign 'in bulk' directly from PACS worklist. To do this, the user needs to select the studies to be signed and hit the 'Electronically sign' icon just above the worklist. If there is an issue, the system will warn the user by pop up on the screen.

To the comfort of the user, a new column 'Electronic Signature' is made available in the PACS worklist. The user can sort on this worklist by left mouse click on the column header.





16 Mobile Device

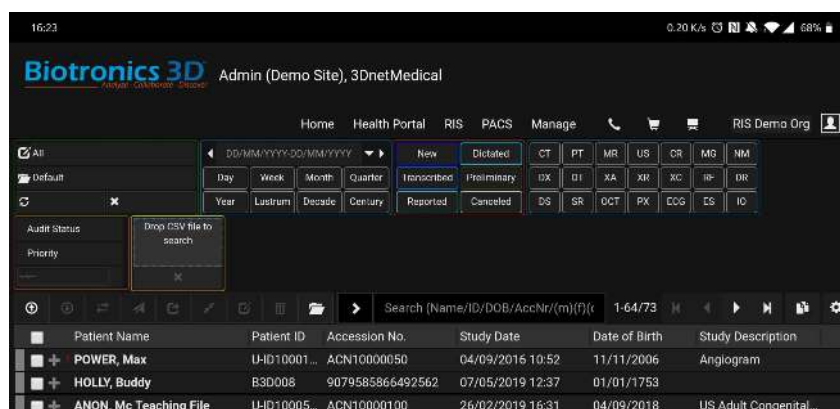
3Dnet users can easily access their work from a mobile device such as a tablet or mobile phone. Users will be able to get the same settings, customisations and worklists or folders through the Mobile App, as in the desktop version of our Portal.

16.1 Navigation Mobile 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).

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.

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 (E) to open the Diagnostic Viewer into an embedded view. Click on the Eye icon to view images



16.2 Mobile 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 or out.
- Slide one finger Up or Down or Left or Right to scroll through the pictures (or use the slider at the bottom of the screen).
- Touch the screen with two fingers and slide them across the screen to adjust the WL (or use the WL 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.

- Access the Context menu using the three horizontal lines icon in the sidebar.

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

- WL Presets and WL scroll bars to adjust WL.
- MiP, minIP, AvIP selection button.
- Slice thickness menu.
- Gap distance menu.

The tools displayed in the context 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. To delete a measurement or an annotation, select it with your finger, then drag it on the Bin icon in the right hand side of the viewport.

There are two possible layouts in the Mobile Viewer App: one viewport, or two viewports (to compare two series against each other). In order to switch between the two layouts, select the Layout icon in the sidebar. Tapping on this icon will split the viewer in two, side by side or one on top of the other (depending on the screen orientation and resolution)

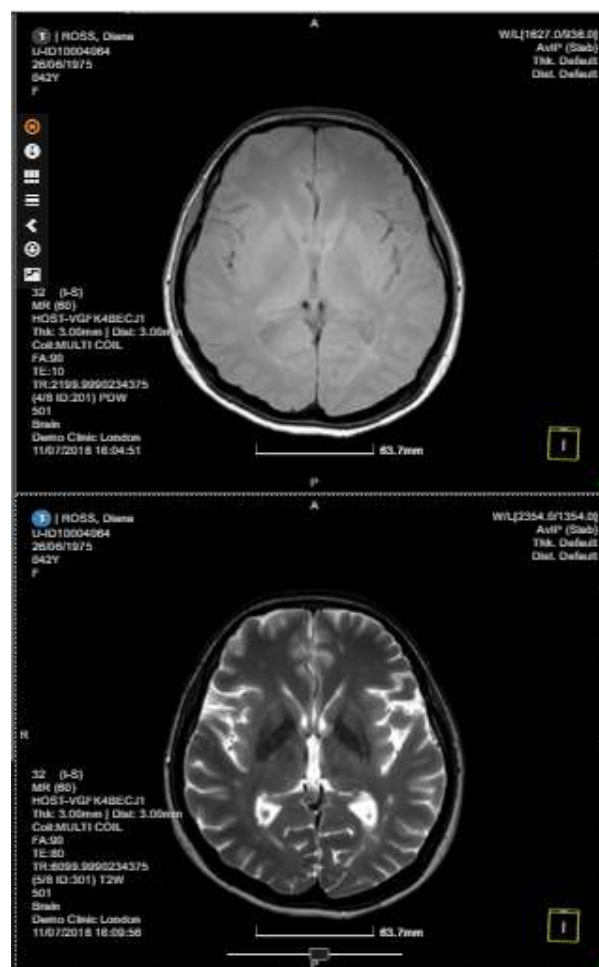
If the two series share the same Frame of Reference, synchronised scrolling will be enabled by default. Use the study panel on the left hand side of the screen to select the series to compare. Users can compare a series from the same study or from a prior. To open a prior, select the required study from the top part of the study panel, then

select the series you need to open. Tap on the study description to open the study, then select a series to compare to put it on the screen. Users can display or hide the Study Panel by clicking on the Panel icon. To show or hide all overlays, select the Show or Hide Overlays icon in the context menu.





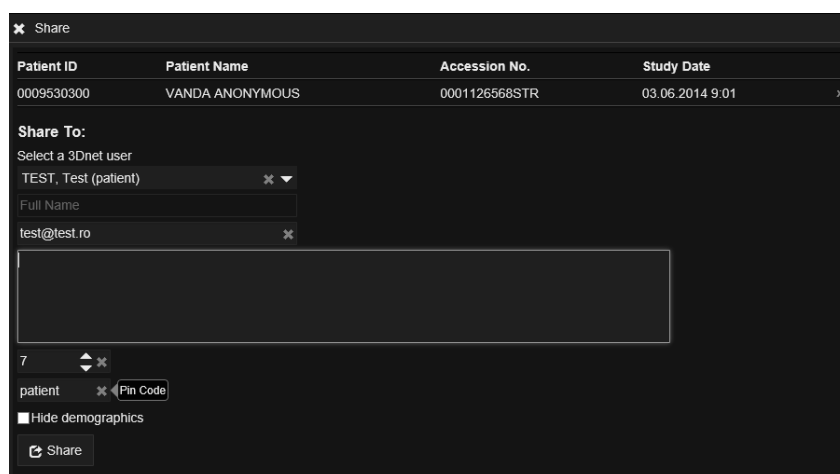
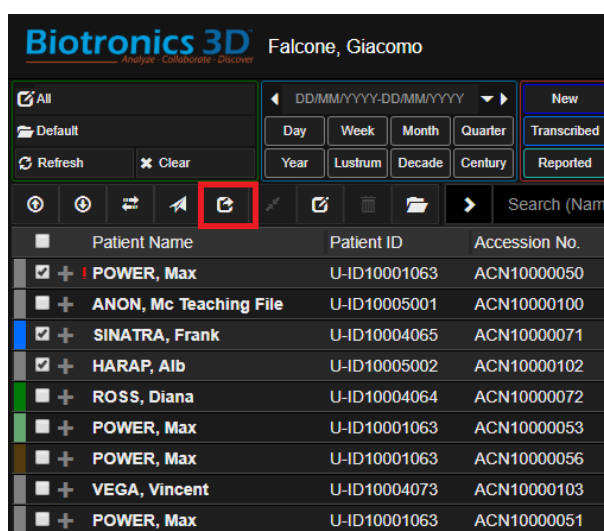




17 Collaborative tools

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 be checked first). 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 the box to hide patient demographics box. After all the information is entered, press the share button. The recipient will receive an email with a URL link. Clicking on the study will launch a 3Dnet window requesting for the PIN Code. If the recipient already has an account with 3Dnet system will check saying that he is already a user. If not, then he must tick the box indicating that he will create a new account. As an existing user, the recipient will be requested to introduce the use name and password, in addition to the PIN code. As new user, the recipient will be requested to create an account by introducing his user name, first name, last name, and password. Once the account is created, the recipient can access 3Dnet by typing his user name and password on the login page. The system will display a page with a list of studies shared with him. To open a study, the user clicks on the eye symbol located on the right. To see the report of a study, the user clicks on the document symbol on the right.





[Study Shared]

Dear Dr. Thomas Johnson,

System 3DnetMedical has shared studies with you. Please follow the link(s) to view them:

[1461026100026 \(PET/CT:17 septembre 2012\)](#)

Message from System 3DnetMedical: I'd like to share radiological studies with you. I will send the study pin separately.

Should you have any problems or require any assistance, please contact your organisation administration:

Biotronics3D

3dnetmedical@biotronics3d.com

Kind regards,

3dnetMedical.com

<http://www.3dnetmedical.com/>

17.2 Worklists

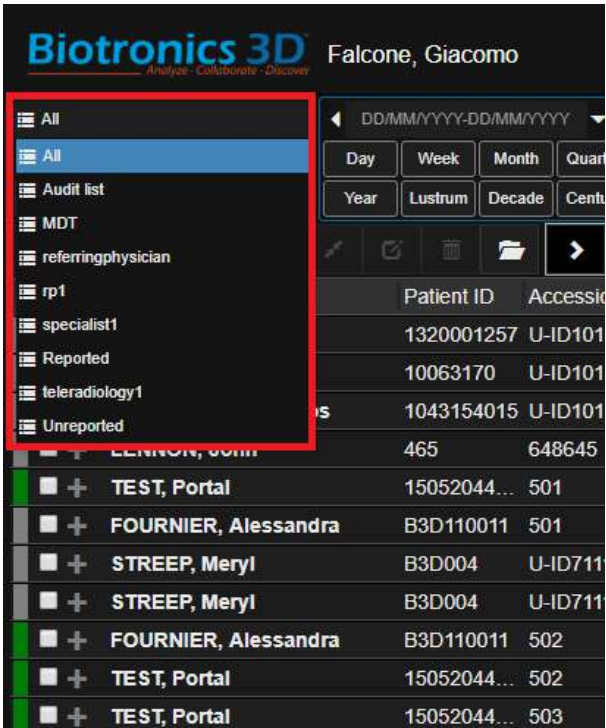
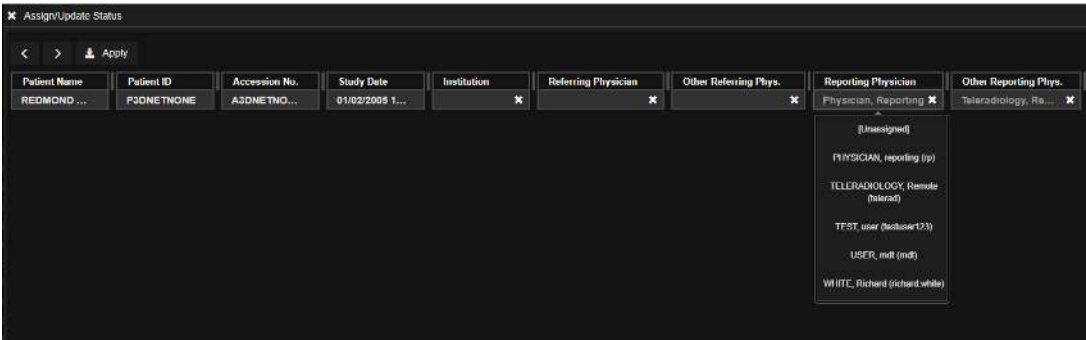
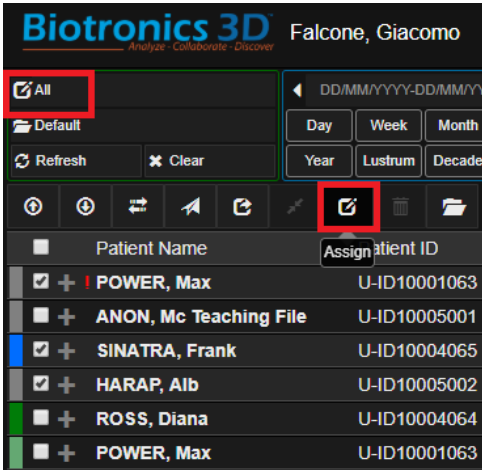
The worklists are accessible from the upper left corner of the Study Browser. This feature is useful for creating worklists for Reporting Physicians and Referring Physicians. The study assignment to a certain user can be done in two ways:

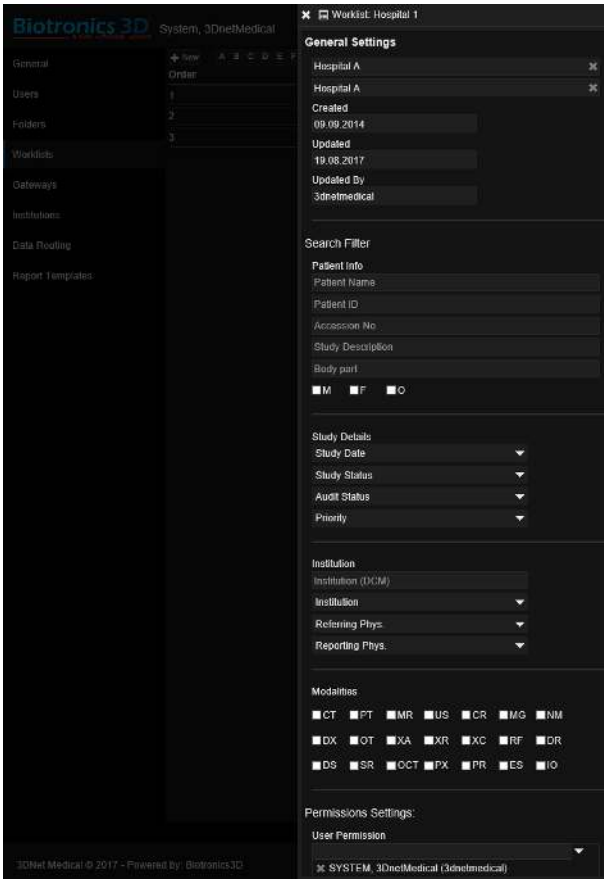
- Manual (as described below).
- Automatically, by reading physician information in the DICOM tags of the study or by reading HL7 ORM, ORU messages.

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

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. The worklist concept can also be used to configure the PACS system in the grid mode for multi-site 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.

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 corresponding manage tab. It can be configured 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 or User Permission.

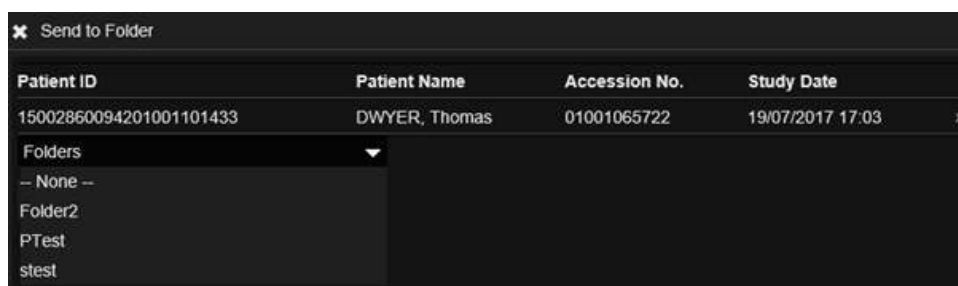
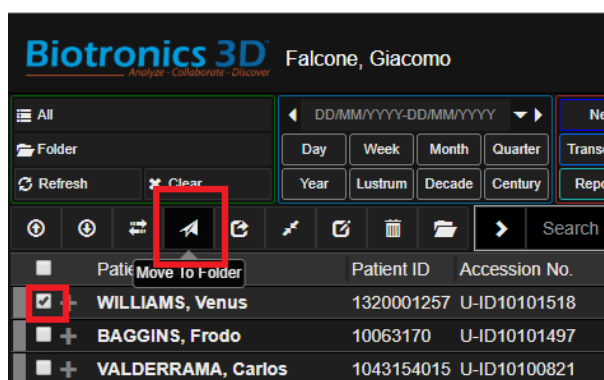
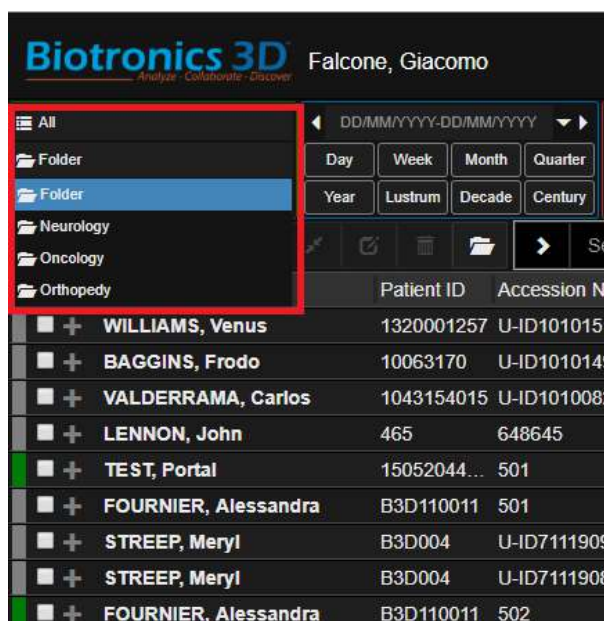




17.3 Folders

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 Orthopaedic patients, a folder for Neurology patients and so on so forth. The folders can be accessed from the Study Browser directly. Users can see only folders which are granted access to by the system administrator.

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 on the upper left side of the screen. This will display an interface with a list of available folder to choose.

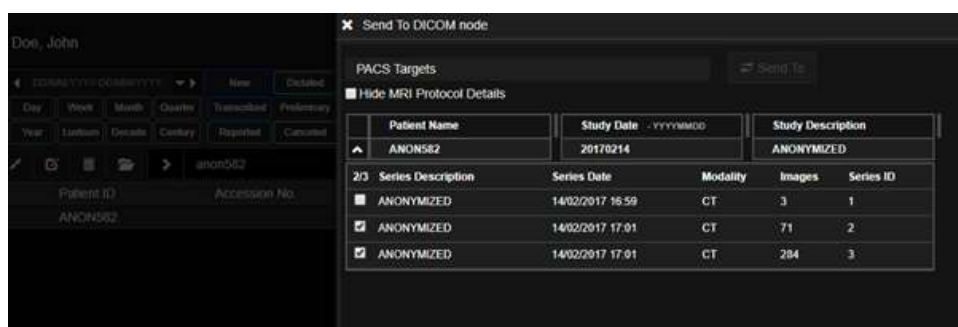


17.4 Patient CDs

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 button on the download interface.

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

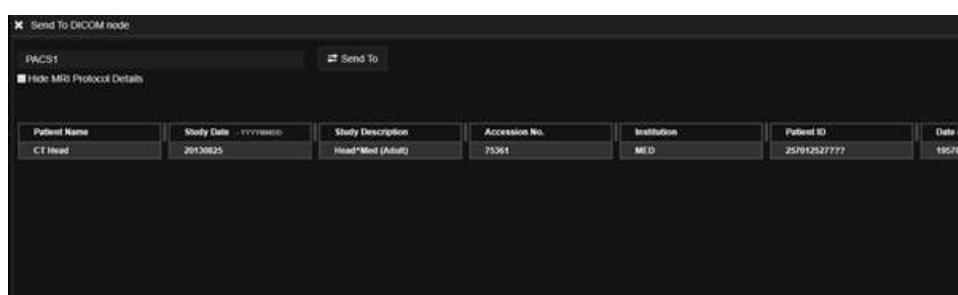


17.5 Send a Study to Another PACS Target

Using the tool to send studies, 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 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.

The list of DICOM tags that are anonymized can be found on the Gateway management page, after selecting the correct Gateway and PACS target, in the section for updating the export tags. Users can add and remove DICOM tags from the list presented in the interface.

While sending the study, the users can select which series to send to the target CD/DVD Burner (or PACS target). Simply use the tick box next to each series to select or deselect a series.



✖ Send To DICOM node

Residence	Scheduled Procedure Step ID	Advanced Editor	Anonymize
	56001-00		<input type="checkbox"/>

Biotronics 3D Falcone, Giacomo

Gateway: DESKTOP-OBASME2

DESKTOP-OBASME2

LAN

PACS Targets Printer Targets Scanner Targets

+ New A B C D E F G H I J K L M N O P Q R S T

Name	AET
PACS1	3DNETCLOUD
PACS2 ECR	3DNETCLOUD_Lo

PACS Target: [3DNETCLOUD_Local]

PACS2 ECR

3DNETCLOUD_Local

192.168.0.182

100

Study Retrieval Limit

0

Set As Default

Prior Auto Retrieve

Query/Retrieve

Update Export Tags

StudyTime (00080030)

StudyDate (00080020)

AccessionNumber (00080050)

InstitutionName (00080001)

InstitutionAddress (00080001)

ReferringPhysiciansName (00080090)

StationName (00081010)

PatientName (00100010)

StudyDescription (00081030)

PatientID (00100020)

PatientBirthDate (00100030)

PatientAddress (00101040)

PatientSex (00100040)

AdditionalPatientHistory (001021b0)

MedicalRecordLocator (00101090)

StudyId (00200010)

RequestingPhysician (00321032)

RequestingService (00321033)

ServiceEpisodeId (00380060)

CurrentPatientLocation (00380300)

PatientInstitutionResidence (00380400)

ScheduledProcedureStepId (00400009)

AdvancedEditor (FFFFFFFD)

Anonymize (FFFFFFFE)

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Doni, John

3DNETCLOUD-OBASME2

New Deleted

Day View Month Overview Transcribed Preliminary

Year Location Details Country Reported Cancelled

anon562

Patient ID Accession No.

ANON562

✖ Send To DICOM node

PACS Targets

Hide MRI Protocol Details

Patient Name	Study Date	Study Description
ANON562	20170214	ANONYMIZED

Series Description	Series Date	Modality	Images	Series ID
ANONYMIZED	14/02/2017 16:59	CT	3	1
ANONYMIZED	14/02/2017 17:01	CT	71	2
ANONYMIZED	14/02/2017 17:01	CT	284	3

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

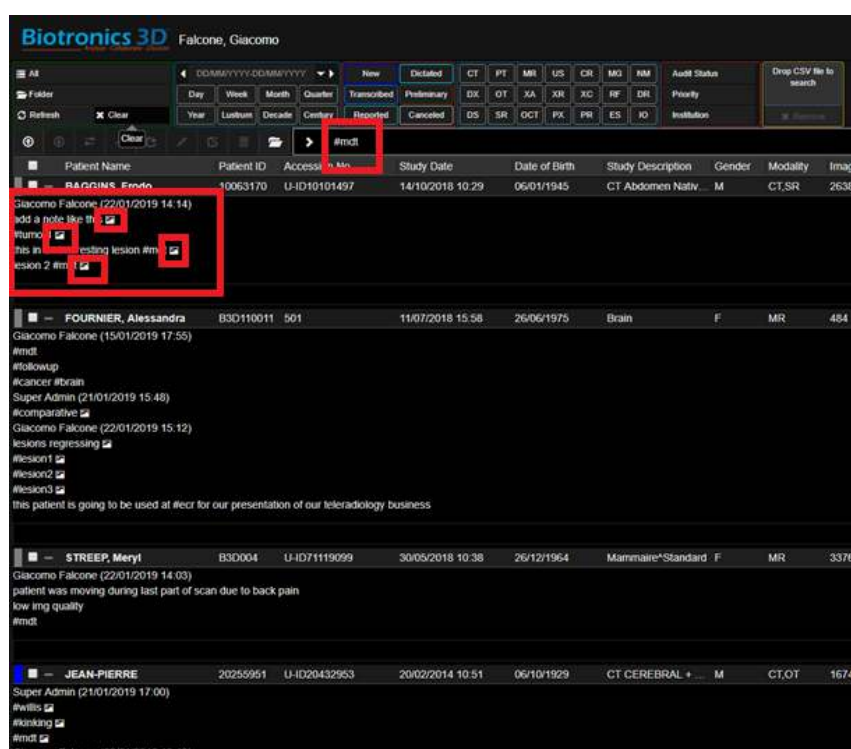
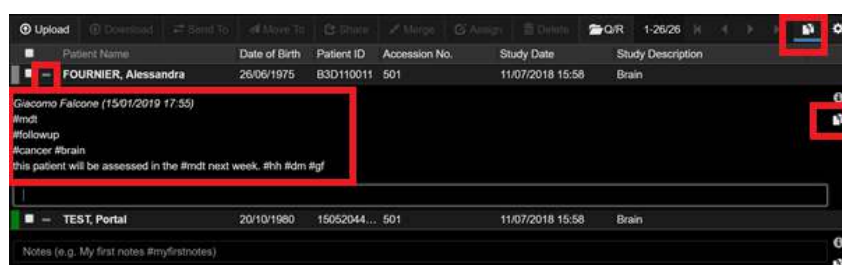
In 3Dnet Medical, users can add notes and tag studies for clinical meetings or to create ad hoc worklists for selected studies, on the fly. Notes and tags can be added using the Note Tool in multiple ways. These notes and tags can also be used to tag lesions or key images.

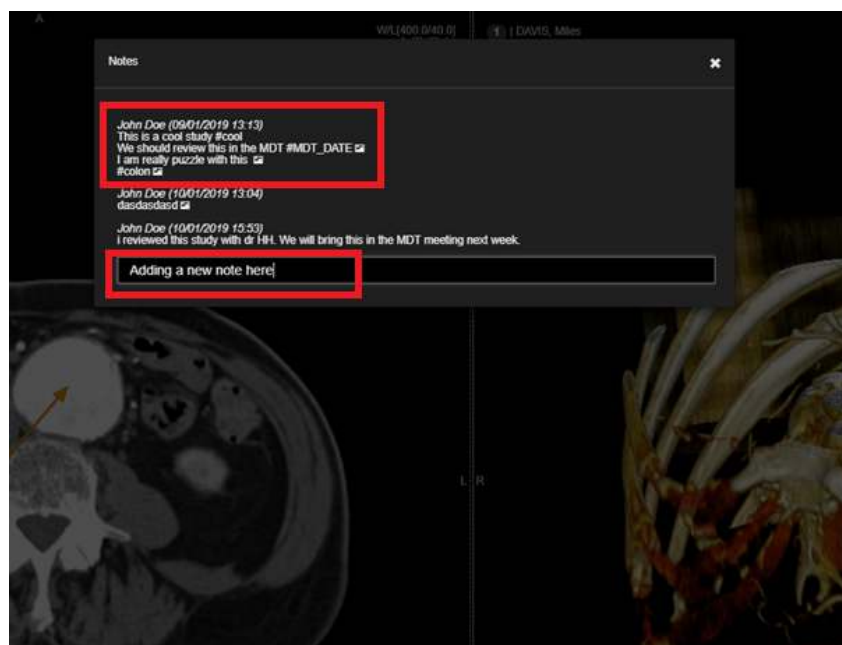
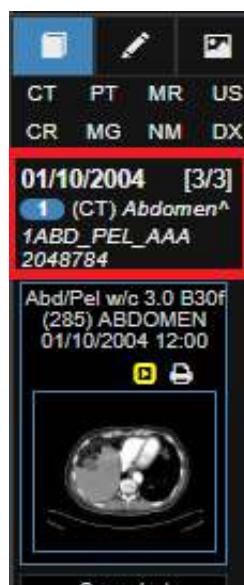
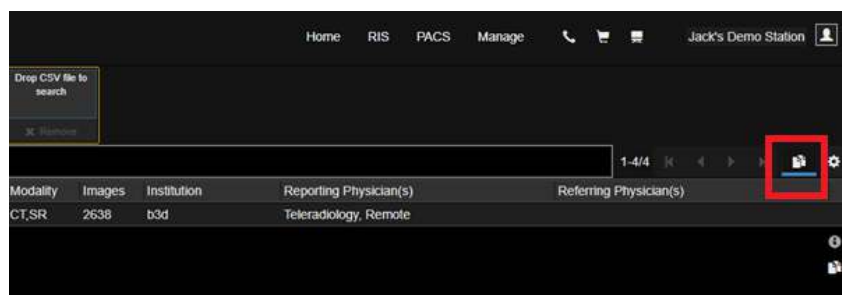
Notes and tags can be viewed by clicking on the notes icon in the top right of the worklist. This will expand every study, exposing notes that might have already been added to that patient. To add a new note or tag, use the text box at the bottom of every expanded patient record line.

For example, 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. 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.

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. Notes can also be accessed from the Patient Information Page (left click on a study in the worklist to access this page). For example, users can tag lesions (lesion1, lesion2, etc.) and key images adding a note with the correlated presentation state. 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 there.





17.7 Presentation States

Presentation states can be saved in different ways. This section brings it all together and describes how to export the presentation states. Please read also 6.4 (Snapshots) + 18.6 (Study Tagging (MDT and Collaboration Tool), Notes and Lesion Tagging) to understand different ways on how to create presentation states.

This section elaborates as well on how to export presentation states.

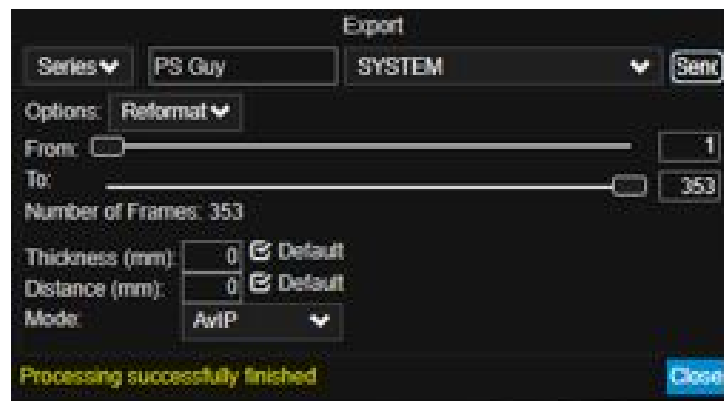
When a user has made an annotation, the image can be saved as a presentation state, which makes it possible that the annotation can also be viewed on another viewer, different from 3DNet. To be able to do this, create an annotation on an image and save it as a presentation state by RMC (Right Mouse Click) on the image by selecting Export. In the Export pop up, please select 'Presentation State only' first, then provide a name. Select the target and hit 'Send'. The system will then start processing and tell the user when the processing has finished.

When the new series (with the PS) has arrived, the Recently Opened Studies icon will flash. RMC on the icon will refresh the study and add the new created PS to the original series. In other words, when the original series is opened, you will find on the top right of the original series the possibility to show/not show the different saved presentation states.

Exporting a presentation state: In the Study Information Page, you will find a new series called PR which stands for 'Presentation State'. You can find and download the series. Please make sure to download not only the PR, but also the original series that you used to create the PR. Exporting only the PR overlay will not work, you always need to have also the original series. Once downloaded, you can upload and open the series and the presentation state in any other viewer that supports presentation states. Please refer to the manual of the 3th party Dicom Viewer to learn how presentation states can be shown in the specific viewer.

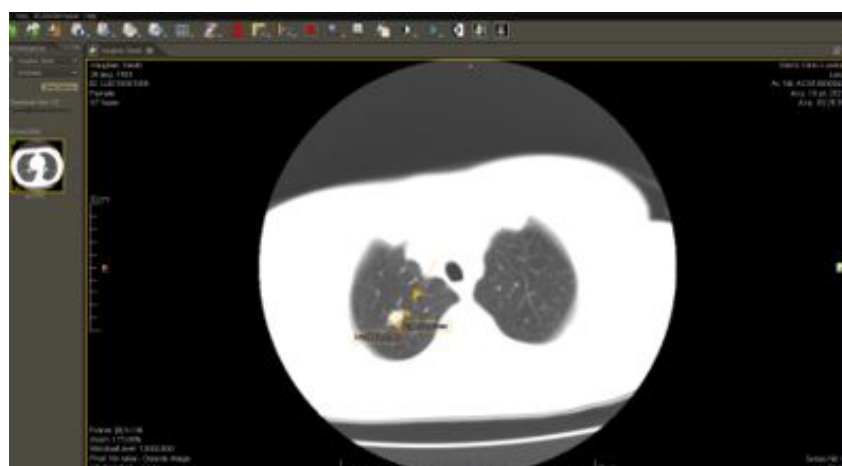
(Please do take into account that we only export annotations and no other components (like e.g. W/L). The way the annotations are presented in other viewers is also dependent on how the other viewers present those. E.g. dashed lines can show up as full lines. The option to save a Presentation state is not available if the image/study type is not supported for (Presentation State) export. Please note as well that the PR series will not populate a new series thumbnail in the viewer.)





Final Report

2/6 Series Description	Series Date	Modality	Images	Ser	Download
<input type="checkbox"/>	25/05/2004 08:32	CT	353	4	2
<input type="checkbox"/> Reformation	03/06/2021 16:30	CT	354	5	
<input type="checkbox"/> Reformation1	03/06/2021 16:36	CT	16	6	
<input type="checkbox"/> Reformation	03/06/2021 16:40	OT	361	7	
<input checked="" type="checkbox"/> guy DMC	16/07/2021 09:26	CT	36	8	
<input checked="" type="checkbox"/> PS TEST 2	07/09/2021 13:49	PR	1	11	



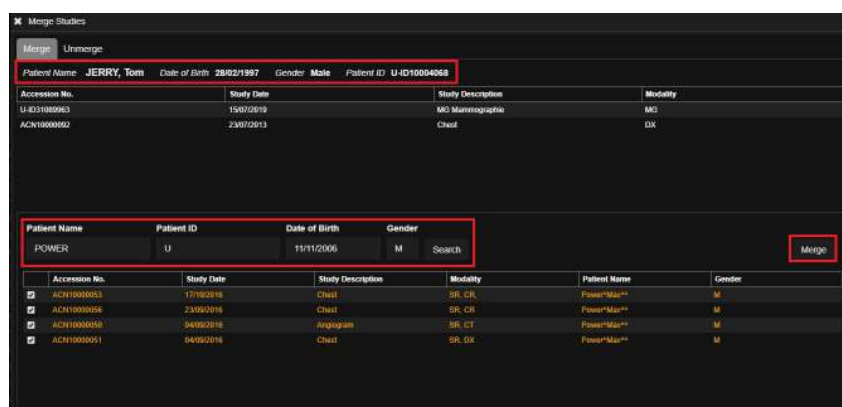
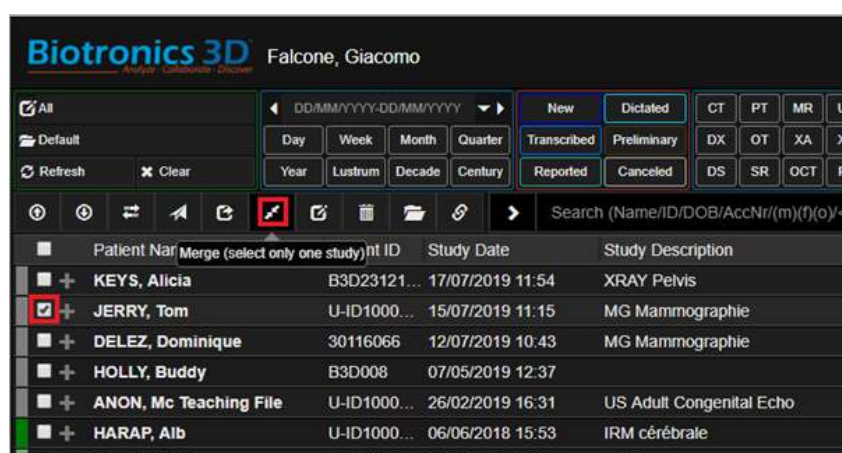
18 Data Integrity

18.1 PACS Study Merge

Users can merge two separate studies in PACS, manually creating a link between them and matching the patient information. Tick the box correlated to the study that carries the correct information. This study will represent the source of truth for this process. Then select the merge button at the top of the study browser.

Clicking on Merge will display the merge interface. At the top of this interface is the study selected from the study list. The details of this study will be propagated to the target study. Below, use the search fields to find the target study that will be merged into the source study.

Select the search results, then click on the merge button to merge the studies together. The information related to the study at the top will be propagated to the studies selected at the bottom. A link is now created. To revert this process, simply select a study from the study list, select the merge tool, and then click on the Unmerge tab at the top of the interface. If a link is present, click on Unmerge to break the link and unmerge the studies.



18.2 Link a PACS Study with a RIS Appointment

3Dnet Medical provides ways to ensure data integrity through the RIS and 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 (orange). This will alert the user on which studies must be merged or amended. Using the study merge tool, the user can search the database and match studies that are not linked. It also allows to match a patient with a record that carries the correct patient details, which effectively amends mistakes.

Match Appointment

Patient Name	Patient ID	Accession No.	Study Date	Date of Birth	Study Description	Gender	Modality	Images	Institution	Report
BEIDERBECKE, Bix	B3D201	109	10/07/2018 10:48	06/11/2003	mr chest	M	MR	163	SP202 U.Szp.Kl. Nr.	

☒ Appointments Clear selection

Accession No.	Patient ID	Patient Name	Date of Birth	Scan	Procedure	Start Time	End Time	Scanner	Status
ACN00000263	B3D201	BEIDERBECKE, Bix	06/11/2003	MR	another procedure				Performed
ACN00000242	B3D201	BEIDERBECKE, Bix	06/11/2003	MR	MR Chest	10/07/2018 11:00	10/07/2018 11:15	MR 2	Confirmed

Details

Check fields match latest correct information before saving

Accession number: ACN00000242

Patient

ID: B3D201
 Name: BEIDERBECKE, Bix
 DOB: 06/11/2003
 Gender: M

Address:
 129 N Main St
 Davenport

Exam

Modality: MR
 Procedure: MR Chest
 Resource: MR 2
 Scheduled: 10/07/2018 11:00 - 10/07/2018 11:15
 Status: Performed

Scan started 10/07/2018 11:48 **Scan finished** 10/07/2018 12:03

Save Cancel

18.3 Series Unlink Tool

With the function 'Series Unlink' users can change demographic and/or study information. A user can also select one or more series to separate from the original study. In that case, a new StudyUID needs to be created. One will have the possibility to verify the newly inserted Study UID when the button 'Verify study UID' appears on the screen. If the newly inserted StudyUID is unique, the system will let you know with the message 'No study exists in the system with this UID'. If the number is not unique, the system will bring up the data from the already existing Study UID and will ask you if it is ok to use this study and patient info. Click on 'Use this study and patient info' to continue. If all required changes are inserted and checked, click on 'yes' to continue. System will ask to confirm the changes once more and if 'OK' is selected, the changes will happen. If the study date is changed, please do take into account that this will trigger simultaneously the changing of the series, acquisition and content date fields in the dicom information.

01/01/2011 08:27
 Abdomen
 ACN10000035
 CT
 [ReportingPhys]
 [Status]

2/4	Series Description	Series Date	Modality	Images	Series Unlink
<input type="checkbox"/>	FC12 Vol. 3D-Q06	01/01/2011 08:34	CT	76	4
<input type="checkbox"/>	FC52 Vol. ORG	01/01/2011 08:34	CT	76	5
<input checked="" type="checkbox"/>	FC12 Vol. 3D-Q06 CE	01/01/2011 08:39	CT	1067	9
<input checked="" type="checkbox"/>	FC51 Vol. ORG CE	01/01/2011 08:41	CT	401	10

Health Portal Default Visibility ▼ 🔒 ✕

Series Unlink

Are you sure you want to unlink the following series?

Patient Name:	Series Description	Series Date
FC12 Vol. 3D-G06 CE	FC12 Vol. 3D-G06 CE	01/01/2011 08:39
FC01 Vol. 0RG CE	FC01 Vol. 0RG CE	01/01/2011 08:41

☒ Change Demographic Information

First Name	Middle Name	Last Name	Patient ID	Date of Birth	Gender
				01/01/1900	M

☒ Change Study Information

Accession No.	Study Description	Study Date
ACN10000035	Abdomen	01/01/2011

☐ Auto generate study UID ☒ Assign new study UID

Study UID

Verify study UID

☐ Remove current assignments for new study

No Yes

Accession No.: 123456789
 Study Date: 07/10/2019
 Study Description: Mammographie de depistage
 Patient ID: U-ID00000246
 First Name:
 Middle Name:
 Last Name:
 Date of Birth: 31/08/1991
 Gender: F

Use this study and patient info

Are you sure you want to continue with these changes? ☒ OK ☐ Cancel

Series Unlink Successful

DICOM Tags

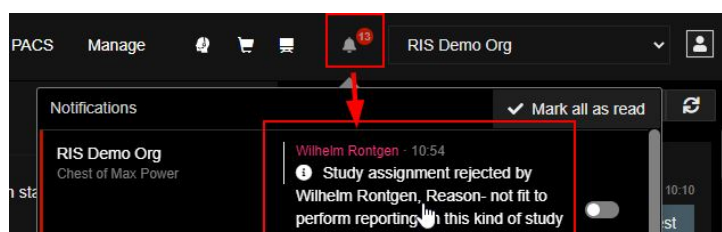
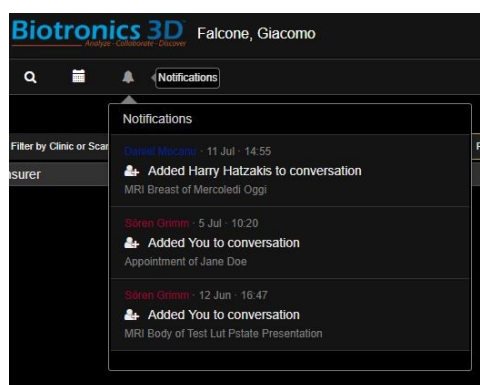
(0008,0020) StudyDate = [20110101]
 (0008,0021) SeriesDate = [20110101]
 (0008,0022) AcquisitionDate = [20110101]
 (0008,0023) ContentDate = [20110101]
 (0010,0030) PatientBirthDate = [19000101]
 (0040,0002) ScheduledProcedureStepStartDate = [20090310]
 (0040,0004) ScheduledProcedureStepEndDate = [20090310]
 (0040,0244) PerformedProcedureStepStartDate = [20090310]

19 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. When new notifications arrive, a red dot is displayed on the notification bell. On the notification panel, a list of the notifications is displayed. Here, the username of the person that performed the action that is notified is displayed in colour, and a brief description of the action is below the username.

As an example: when an assigned reporter unclaims or rejects a study, a notification will be sent out that reporter X has unclaimed study Z while mentioning as well the reason for rejection.



20 Keyboard Shortcuts

The system defines the following 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 or 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: maximise 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 viewports in a new page.
 E: after opening the selected viewports in a new page, it will go back to the previous view.

21 Troubleshooting

This section provides some basic troubleshooting guides for some issues that the user may encounter when using the system. Please contact your local technical support of the system if you encounter any other issues.

Login issues

- Check your internet connection (contact your local IT administrator or your internet service provider). If your internet is slow or unstable, you may have problems loading the page or submitting your username/password.
- Double-check that you are entering your username and password correctly and without typos or extra spaces. Check the caps-lock on your keyboard.
- Make sure that cookies are enabled. Check your browser if it has any extensions or security settings that block cookies, pop-ups, or scripts, they could interfere with the login process. Try disabling them temporarily or using an incognito or private window to see if that helps.
- Clear your browser cache. Your browser may have outdated or corrupted data in its cache and cookies. To remove the cached data, open your browser and go to the settings or options menu. Select the option to clear browsing data, history, or cache.
- Contact your local technical support of the system.

'Load Error' issues

- Check your internet connection (contact your local IT administrator or your internet service provider). If your internet is slow or unstable, you may have problems loading the page or submitting your requests.
- Contact your local technical support of the system.

'Data cannot be loaded' issues

- Check your internet connection (contact your local IT administrator or your internet service provider). If your internet is slow or unstable, you may have problems loading the page or submitting your requests.
- Try to load the data again.
- Contact your local technical support of the system.

'Failed to process' issues

- Check your internet connection (contact your local IT administrator or your internet service provider). If your internet is slow or unstable, you may have problems loading the page or submitting your requests.
- Contact your local technical support of the system.

22 Revision History

Table 1: Manual Revision History Table.

Author	Version	Date	Description	Approved by
H. Hatzakis	1.0	19/05/2006	Initial Version	S. Grimm
S. Grimm	1.1	15/12/2006	Updated File Browser Functionality 3dnet Ver 2.0	S. Grimm
E. Coto	1.2	08/06/2007	Updated Layouts Functionality 3dnet Ver 2.1	S. Grimm
E. Coto	1.3	17/12/2007	Updated Navigation Functionality 3dnet Ver 2.2	S. Grimm
S. Grimm	1.4	13/06/2008	Updated Appearance Functionality 3dnet Ver 2.4	S. Grimm
S. Grimm	1.5	19/12/2008	Added Bone and Table Removal Functionality 3dnet Ver 2.5	S. Grimm
W. Hernandez	1.6	01/06/2009	Added Reformation Functionality 3dnet Ver 2.6	S. Grimm
W. Hernandez	1.7	14/12/2009	Full revision with minor syntax changes 3dnet Ver 2.7	S. Grimm
S. Grimm	1.8	01/12/2010	Minor syntax changes 3dnet Ver 2.8	S. Grimm
S. Grimm	1.9	04/07/2011	Minor syntax changes 3dnet Ver 2.9	S. Grimm
S. Grimm	1.10	15/08/2012	Minor syntax changes 3dnet Ver 2.10	S. Grimm
L. Carter	1.11	12/09/2013	Minor syntax changes 3dnet Ver 2.11	S. Grimm
S. Grimm	1.12	10/11/2014	Minor syntax changes and added dicom print 3dnet Ver 2.12	S. Grimm
S. Grimm	1.13	21/04/2015	Added manufacture, warning and CE symbol 3dnet Ver 2.12	S. Grimm
S. Grimm	1.14	05/01/2016	Added recommended hardware 3dnet Ver 2.13	S. Grimm
W. Hernandez	1.15	02/08/2016	Updated manufacturing address	S. Grimm
S. Grimm	1.16	04/02/2018	Update UI pictures changed to Ver 2.14	S. Grimm
G. Falcone	1.17	04/04/2019	Update Symbols, adding more detailed Information	S. Grimm
G. Falcone	1.18	07/05/2019	Updated Manual with Advanced modules	S. Grimm
G. Falcone	1.19	08/01/2020	Updated Manual with Revision History, added more detailed information of various features.	S. Grimm
G. Falcone	1.20	24/02/2020	Added more detailed information of various features	S. Grimm
G. Falcone	1.21	17/03/2020	Update according with requirements of Regulation (EU) 2017/745 (MDR)	S. Grimm
G. Falcone	1.22	08/04/2020	Updated section 5.7 and 5.8.	S. Grimm
S. Grimm	1.23	01/06/2020	Updated manual building process using Latex	S. Grimm
G. Heyns	1.24	08/10/2021	Updates on existing features and added new information on new features	S. Grimm
G. Heyns	1.25	21/10/2021	Updates on existing features and added new information on new features	S. Grimm
G. Heyns	1.26	31/01/2022	Updates on existing features and added new information on new features	S. Grimm
N. Cattaneo	1.27	10/03/2023	Added more detailed information on existing features	S. Grimm
K. Leung	1.28	29/06/2023	Removed support for Internet Explorer	S. Grimm
K. Leung	1.29	25/07/2023	Updated intended use of Health portal	S. Grimm

R. Chinchane	1.30	05/10/2023	Updated RIS section	S. Grimm
R. Chinchane	1.31	14/11/2023	Updated Patient Records section	S. Grimm
R. Chinchane	1.32	12/12/2023	Updated Viewer Control Centre section	S. Grimm
R. Chinchane	1.33	10/01/2024	Updated General Diagnostic section	S. Grimm
K. Leung	1.34	18/01/2024	Updated Troubleshooting section	S. Grimm
J. Correia	1.35	10/04/2024	Updated manufacturer's address and recommended OS	S. Grimm