

DICOM RT Viewer

Radiation-Oncology Image, Structure & Dose Viewer

User Manual

Version 1.0

TC Consulting

For educational use only — not FDA cleared

Important Notice

This application is not FDA certified or approved. Its purpose is restricted to educational use only and should not be used in a medical clinic for diagnostic interpretations.

This software is provided “as is” without warranty expressed or implied. The author is not liable for any damages arising from the use of this software. Use at your own risk. Do not distribute without expressed permission from the author.

Throughout this manual, dose, volume and geometric values shown in figures come from anonymized sample data and are for illustration only.

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1. Introduction

DICOM RT Viewer is a desktop application for reviewing radiation-oncology imaging. It loads a CT, MR or PET image set and overlays a DICOM RT Structure Set (contours), RT Dose (dose distribution) and RT Plan (treatment beams). It provides linked multi-planar reconstruction (MPR), a 3D view, plan-evaluation tools (DVH, metrics and clinical goals), image fusion (rigid and deformable), plan comparison and summation, structure editing, reporting, and DICOM network connectivity.

1.1 Key Features

- **Multi-planar views** — linked axial, coronal and sagittal panes with a synchronized crosshair.
- **Structures** — RT Structure Set contours drawn on every plane, individually toggled and color-coded.
- **Dose** — RT Dose colorwash, isodose lines, and prescription / fractionation normalization.
- **Plan evaluation** — cumulative DVH, per-structure metrics (Dx, Vx, homogeneity), conformity indices, and an editable clinical-goals table.
- **3D view** — structure and isodose surfaces, treatment beams with MLC apertures, per-object opacity.
- **Fusion** — load a secondary image (MR, PET or a second CT) and align it by frame of reference, manual nudge, or automatic rigid or deformable registration.
- **Plan comparison & summation** — overlay a second plan's DVH, show a dose-difference or gamma map, and add plans together physically or as EQD2.
- **Structure tools** — create derived ROIs (margins, booleans, rings) and export structures to a DICOM RT Structure Set.
- **Plan report** — export a PDF report (DVH, metrics, goals, screenshots) or CSV.
- **DICOM networking** — query and retrieve studies from a PACS (C-FIND, C-GET / C-MOVE) and send objects to one (C-STORE / C-ECHO), with saved destinations.

1.2 Intended Audience

The manual is written for radiation oncologists, medical dosimetrists, medical physicists, students and researchers who wish to review RT DICOM data. No programming knowledge is required to operate the application.

2. Installation and Requirements

2.1 System Requirements

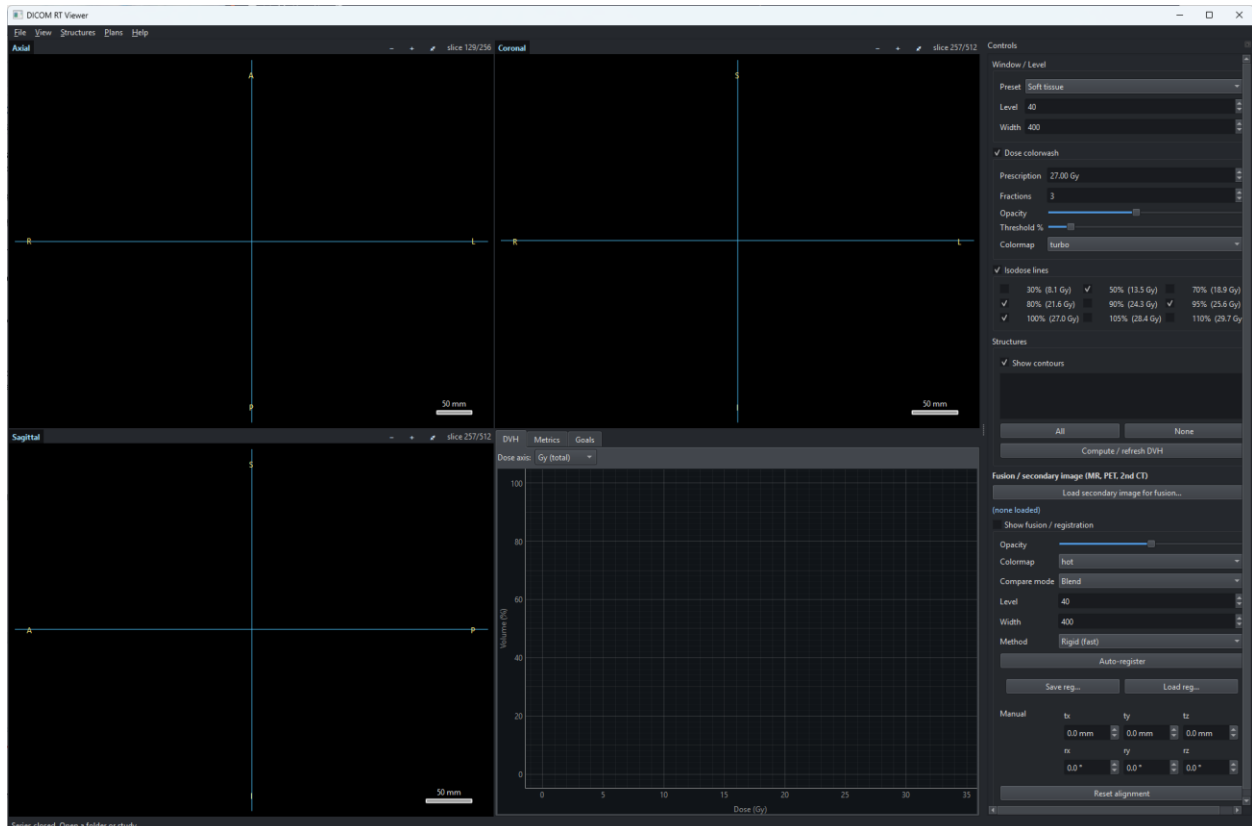
- Quad-core, 2.0 GHz or faster 64-bit CPU with 8-GB system memory minimum.
- Windows, macOS or Linux desktop with a working display (1920 x 1080 or higher resolution).
- A graphics card / driver supporting OpenGL (required for the 3D view).
- An SSD hard drive with 20 GB of free space for program and working files.

2.2 Installing

The DICOM RT Viewer application comes as a pre-compiled portable application. No installation is necessary – just extract and copy the DICOM_RT_Viewer.exe or DICOM_RT_Viewer.app from the distribution package to a folder of your choice.

2.3 Launching the Application

Open Windows Explorer or Mac OS Finder and browse to where you saved the program. Double-click on the DICOM_RT_Viewer.exe or application to launch it:



3. Quick Start

The following steps walk through a typical first session:

1. Launch the application.
2. Choose File → Open Folder... and select the folder containing your DICOM study. The scan is recursive, so sub-folders are included.
3. In the selection dialog, confirm the image series, RT Structure Set, RT Dose and RT Plan. Matching objects are pre-selected automatically.
4. Click OK. The axial, coronal and sagittal panes populate, with contours and the dose colorwash overlaid. The patient's name, medical ID, sex and date of birth (when present) appear in a banner above the Controls panel.

5. Click in any pane to move the crosshair; scroll the mouse wheel to page through slices.
6. Review the plan in the bottom-right panel (DVH, Metrics and Goals tabs).
7. Press Ctrl+3 (or View → Open 3D View) to see structures, isodose surfaces and treatment beams in three dimensions.

4. Loading DICOM Data

4.1 Supported Objects

DICOM object	Role in the viewer
CT / MR / PET image series	Base image volume shown in the MPR panes
RT Structure Set (RTSTRUCT)	Contours / regions of interest
RT Dose (RTDOSE)	3D dose distribution (colorwash, isodose, DVH)
RT Plan (RTPLAN)	Treatment beams, fractions and prescription

4.2 Opening a Study

Use File → Open Folder... to scan a directory, or File → Open DICOM File(s)... to pick individual files. The application groups the files into series and presents a selection dialog. The dialog defaults to the image series that the RT objects reference, and pre-selects the matching RT Structure Set, RT Dose and RT Plan. If the study contains a second image series of a different modality (for example an MR alongside the planning CT), it is offered in the Fusion / secondary image field; choosing it loads that series and sets up the fusion in one step.

4.3 Frame-of-Reference Matching

RT objects are matched to the image series using the DICOM Frame of Reference (and, when available, the referenced series). If a study contains several image series, choose the one your plan was created on. The dialog note reports which RT objects were auto-matched.

4.4 Loading Objects Later

- **Load RT Plan...** — File → Load RT Plan... attaches a plan to the current study and opens the 3D view.
- **Load Fusion / Secondary Image...** — loads a second image series for fusion (see Section 11).

5. The Main Window

The window is divided into four quadrants — the axial, coronal and sagittal image panes and the plan-evaluation panel — with a control panel docked on the right and a status bar along the bottom.

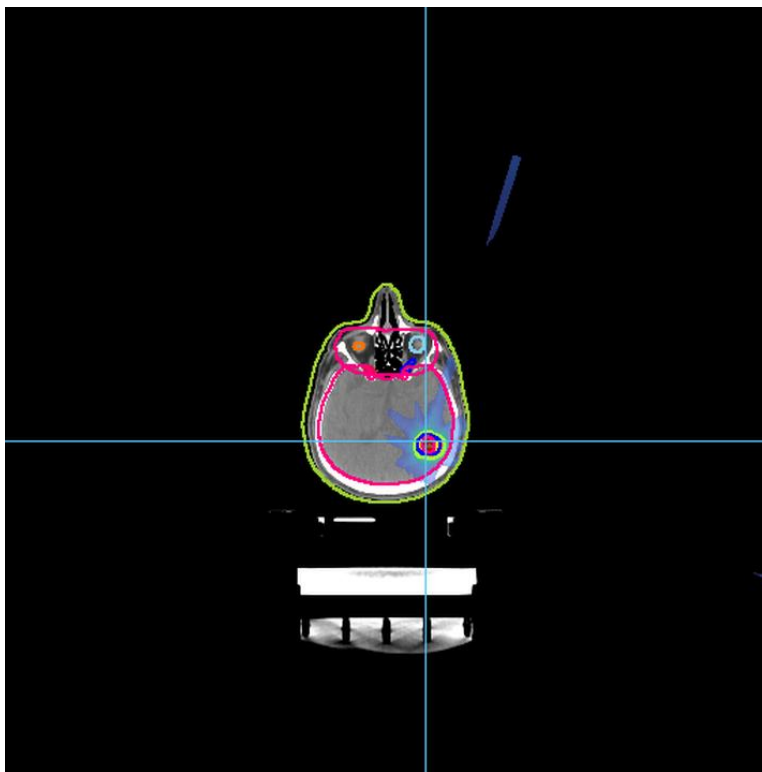


Figure 1. An axial slice showing structure contours (body, brain, eyes, target), the dose colorwash with isodose rings, and the cyan crosshair.

6. Image Navigation and Display

6.1 Multi-Planar Views and the Crosshair

The three image panes are linked through a common point. Clicking in any pane moves the crosshair to that location; the other two panes update to show the same point. The coronal and sagittal panes are reconstructed from the image volume.

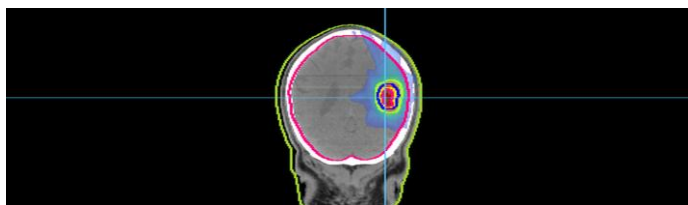


Figure 2. Coronal reformation with structures, dose and isodose lines.

6.2 Scrolling, Zoom and Pan

- **Scroll slices** — roll the mouse wheel over a pane.
- **Zoom** — use the -, + and fit buttons on each pane's title bar, or hold Ctrl and roll the mouse wheel.
- **Pan** — drag with the left mouse button.

Images are anti-aliased when zoomed out and smoothly interpolated when zoomed in for maximum clarity.

6.3 Window / Level

Adjust brightness and contrast with the Window / Level controls in the right-hand panel, or by dragging with the right mouse button inside a pane. CT presets (Soft tissue, Lung, Bone, Brain, Mediastinum) are provided.

6.4 Cursor Read-out

The status bar continuously reports the voxel index, patient coordinates (mm), the image value (e.g. CT number in HU) and the dose (Gy) at the crosshair.

6.5 Orientation, Measurement, Cine and Screenshots

- **Orientation & scale** — each pane shows anatomical orientation labels (L/R, A/P, S/I) and a scale bar in millimetres.
- **Ruler** — View → Measure (ruler), then click two points in a pane to read the in-plane distance in mm.
- **Cine** — View → Play / Pause Cine (Ctrl+Space) scrolls through slices automatically.
- **Screenshot** — File → Save Screenshot (Ctrl+S) saves the current four-pane layout as an image.

7. Structures (RT Structure Set)

7.1 Displaying Structures

Each region of interest is drawn as a color-coded outline on all three planes. In the Structures group of the control panel you can:

- Toggle the display of all contours with the Show contours checkbox.
- Show or hide individual structures using the checklist.
- Select all or none with the All / None buttons.

Structure colors are taken from the RT Structure Set; a color swatch is shown next to each name.

7.2 Creating Derived Structures

Structures → Create Structure opens a dialog to build new ROIs from existing ones. Choose an operation, the source structure(s), a name and a color, then Create structure. The new ROI appears immediately in the contours and the DVH.

- **Margin** — grow or shrink a structure by a true distance in millimetres (positive expands, negative contracts) — e.g. CTV → PTV.
- **Boolean** — combine two structures by union, intersect or subtract.
- **Ring / PRV** — a shell between an inner and outer expansion (e.g. a planning organ-at-risk volume).
- **Crop to** — intersect a structure with another (e.g. crop to body).

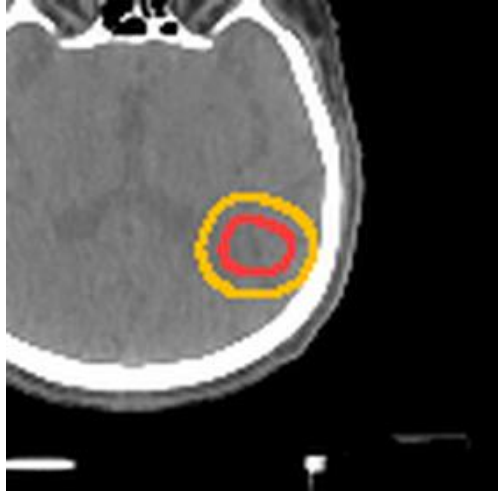


Figure 3. A target (red) and an 8 mm expansion margin (orange) created with the Margin operation.

Margins use a distance transform on the actual voxel spacing, so the millimetre value is honoured even for anisotropic voxels.

7.3 Exporting Structures

Structures → Export RT Structure Set writes the selected structures (original and derived) to a DICOM RTSTRUCT file that references the primary image series. Contours are generated so that a treatment-planning system reproduces the masks exactly (point-in-polygon rasterization).

8. Dose Display (RT Dose)

8.1 Colorwash

When an RT Dose object is loaded it is resampled onto the image grid and shown as a semi-transparent color overlay. In the Dose colorwash group you can set the prescription (reference) dose, opacity, a low-dose threshold (below which dose is hidden) and the colormap.

8.2 Isodose Lines

The Isodose lines group draws contour lines at selected percentages of the prescription (30 %, 50 %, 70 %, 80 %, 90 %, 95 %, 100 %, 105 %, 110 %). Each level is labeled with its absolute dose in Gy.

8.3 Prescription and Fractionation

Set the Prescription dose and the number of Fractions in the Dose controls. When an RT Plan is loaded these values are filled in automatically. The prescription is the reference for isodose percentages and for plan evaluation; the fraction count enables a dose-per-fraction display in the DVH.

9. Plan Evaluation

The bottom-right panel provides three tabs: DVH, Metrics and Goals.

9.1 Dose-Volume Histogram (DVH)

The DVH tab plots the cumulative dose-volume histogram for every visible structure. The dose axis can be displayed in Gy (total), Gy per fraction, or as a percentage of the prescription.

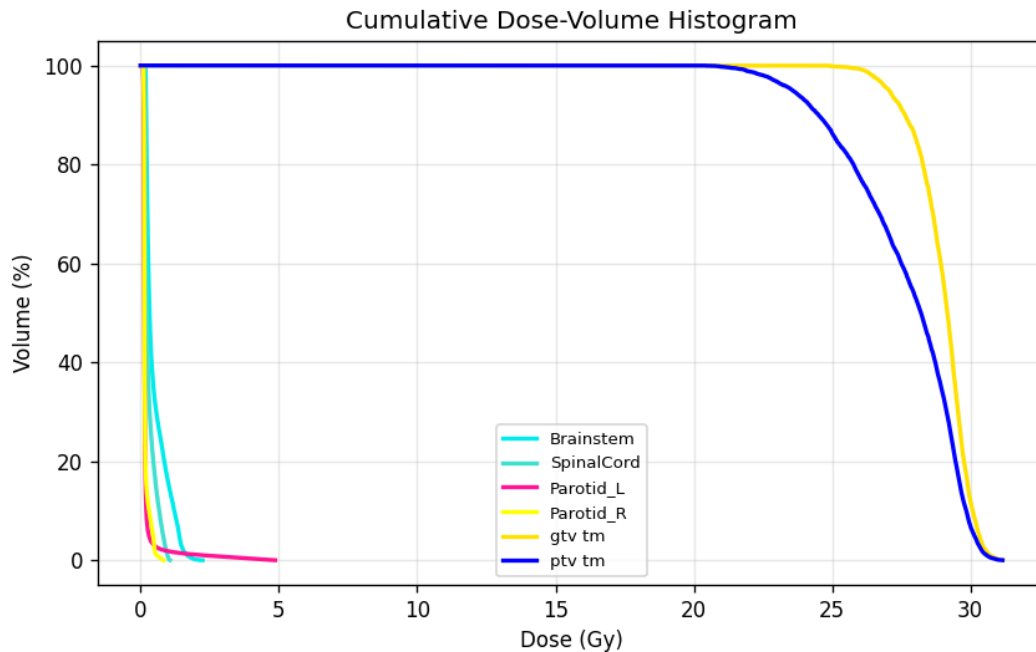


Figure 4. Cumulative DVH for target and organ-at-risk structures.

9.2 Metrics

The Metrics tab lists, for each structure, the volume and the dose statistics below. Homogeneity is reported for every structure and is most meaningful for targets.

Metric	Meaning
Volume (cc)	Structure volume in cubic centimetres
Dmin / Dmean / Dmax	Minimum, mean and maximum dose (Gy)
D98 / D95 / D2	Dose covering 98 % / 95 % / 2 % of the volume (Gy)
HI	Homogeneity index, $(D2 - D98) / D50$ (ICRU 83)

A conformity table reports, for target structures, the target volume, the coverage at the prescription, and the RTOG and Paddick conformity indices.

Tick Show cGy above the table to display the dose columns in cGy with two decimal places instead of Gy; the volume and homogeneity columns are unaffected.

9.3 Clinical Goals

The Goals tab lets you build a checklist of clinical objectives. For each goal choose a structure, a metric, a comparison operator and a target value, then click Add goal. Each goal shows the measured value and a green PASS or red FAIL result that updates as the plan or prescription changes.

- **Dx%** — the parameter is a percent volume (e.g. D95).
- **VxGy / VxGy_cc** — the parameter is a dose in Gy; the result is the volume (% or cc) receiving at least that dose (e.g. V20Gy).
- **Dmax / Dmean / D2cc** — the parameter is ignored.

Goal presets (a dropdown with example organ-at-risk and target goal sets) can populate the table automatically by matching your structure names; the built-in values are examples only, not clinical guidance.

You can also save your own protocol goal sets. Build the goals table for a protocol, then use the Manage row:

- **Save as preset...** — store the current table under a name. Saved presets appear in the Preset dropdown below the built-in ones and persist across sessions.
- **Add preset goals** — apply the selected preset (built-in or saved) to the current table; saved presets are matched to the loaded structures by name so the same protocol can be reused on the next patient.
- **Delete preset** — remove the selected saved preset (built-ins cannot be deleted).
- **Import... / Export...** — share a preset as a .json file, for example to copy an institutional protocol to another machine or a colleague.

Saved presets are stored in goal_presets.json under your .dicom_rt_viewer folder. Preset values (including target-coverage doses) are stored as entered and are not automatically rescaled to a different prescription.

9.4 Beams

When an RT Plan is loaded, the Beams tab lists every beam with the parameters the plan provides. Each row shows the beam number, name and treatment machine, and:

Column	Meaning
Energy (MV)	Nominal beam energy
SAD (mm)	Source-to-axis distance
Gantry / Couch / Coll	Gantry, patient-support and collimator angles
MU	Beam meterset (monitor units)
Dose (cGy)	Beam dose at the reference point, per fraction, in cGy
Type	Beam type (e.g. STATIC / DYNAMIC) or delivery type
CPs	Number of control points (robot nodes, for CyberKnife plans)

A summary line above the table gives the plan label, number of beams, fractions, total MU, total dose per fraction (cGy), the prescription (cGy and Gy) and the treatment unit. Click a column header to sort; columns sort numerically where appropriate.

9.5 Exporting a Plan Report

File → Export Plan Report writes a report of the current plan:

- **PDF** — a multi-page report with a header (patient / plan / prescription), the DVH plot, the per-structure metrics and conformity tables, the clinical goals, and screenshots of the views.
- **CSV** — a metrics table and the DVH curves for use in a spreadsheet.

DICOM RT Viewer — Plan Report

Generated 2026-07-31 14:46

Patient: ANON^TEST ID: RTV001

Study date: 20260101 Plan: tedavi 3 fx

Prescription: 30.0 Gy Fractions: 3 Structures: 4

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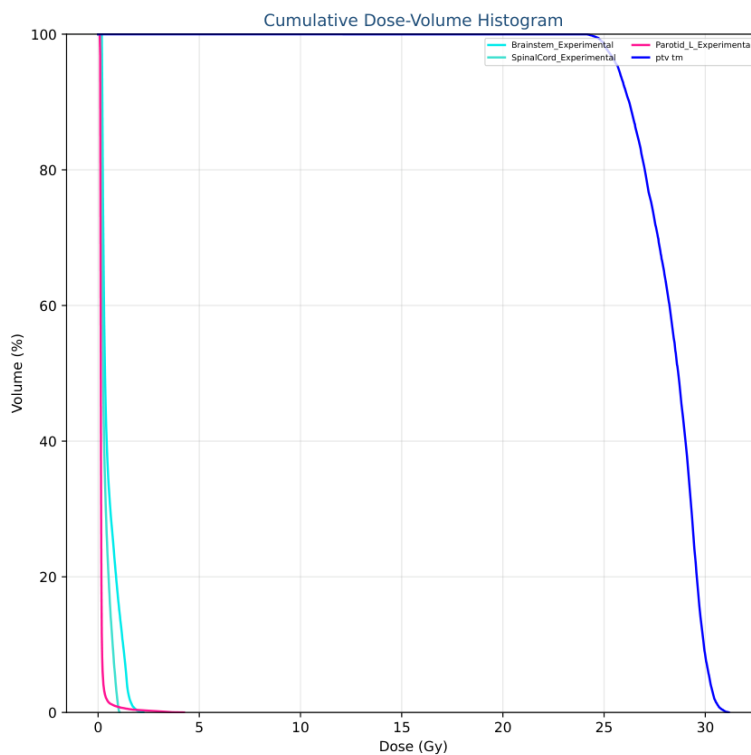


Figure 5. First page of an exported PDF plan report.

10. The 3D View

Open the 3D view with View → Open 3D View or Ctrl+3. Structures and dose are rendered as surfaces in patient coordinates; the camera automatically frames the anatomy.

- **Rotate** — drag with the left mouse button.
- **Zoom** — roll the mouse wheel.
- **Pan** — right-drag or Shift-drag.

10.1 Structures

Each structure has its own row with a visibility checkbox, a color swatch and an opacity slider. Lower the opacity of a large structure (such as the body) to reveal the targets and organs inside it. Use Select all / Deselect all to toggle every structure at once.

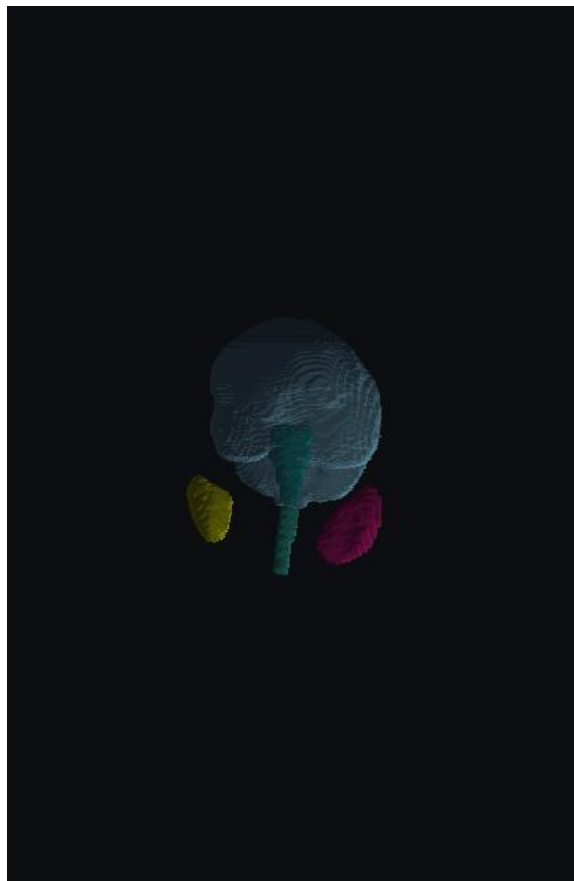


Figure 6. 3D structure surfaces: brain (translucent), brainstem and spinal cord, and the parotid glands.

10.2 Isodose Surfaces

Isodose surfaces are drawn for the selected dose levels, with a shared opacity slider. They appear nested inside one another (higher dose inside lower dose).

10.3 Treatment Beams

When an RT Plan is loaded, each beam appears in the Beams (RT Plan) group. A beam is drawn as a divergent field emanating from the source and converging on the isocenter, with the field aperture outlined at the isocenter plane. The gantry and couch angles are listed beside each beam.

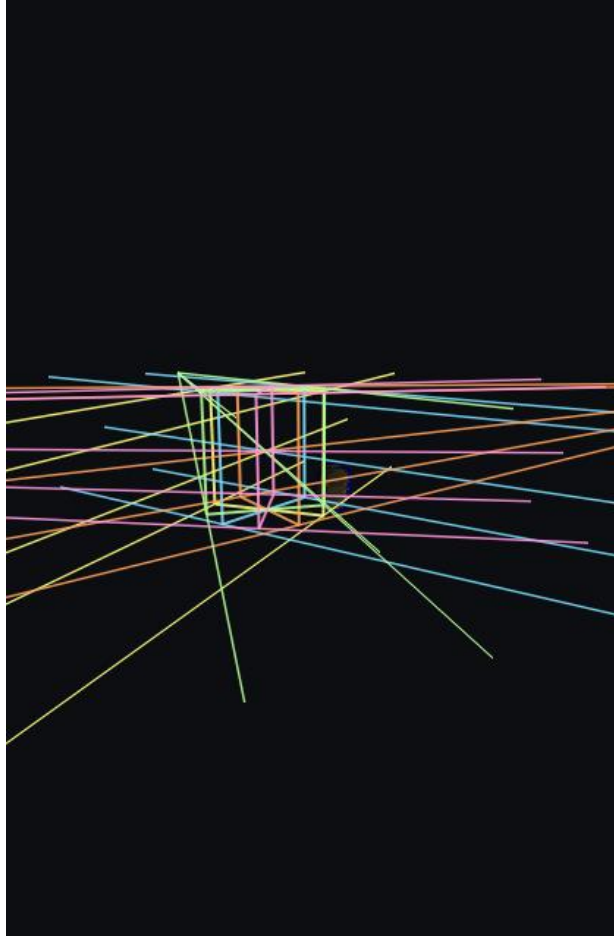


Figure 7. Multiple beams converging on the isocenter from different gantry angles.

10.4 MLC Apertures

If a beam defines multi-leaf collimator (MLC) positions, the field aperture is drawn as the conformal leaf-defined shape (a staircase outline) rather than a plain rectangle. Beams that use only jaws show a rectangular aperture.

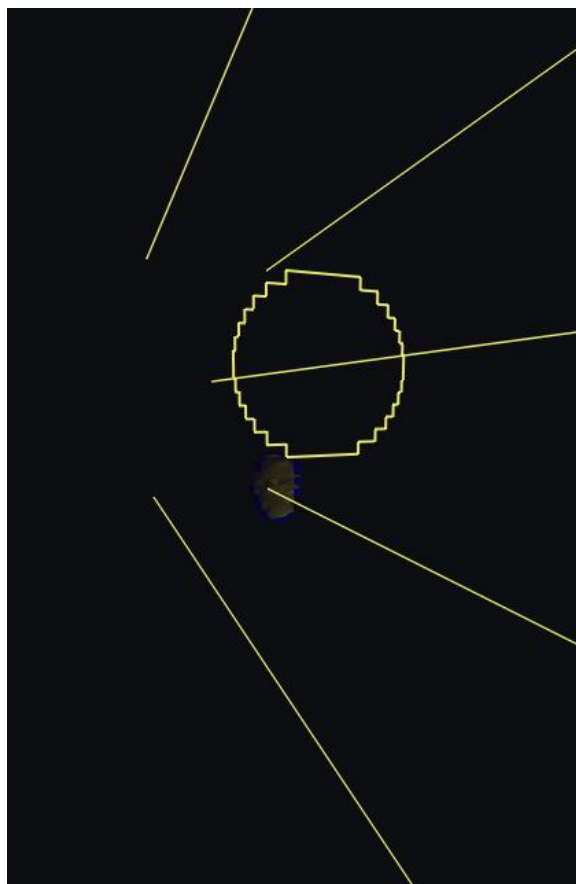


Figure 8. An MLC-shaped (conformal) beam aperture; individual leaf steps are visible along the outline.

10.5 Level of Detail

The Detail control (Coarse / Medium / Fine) trades surface smoothness for rebuild speed. Use Coarse for very large structures and Fine for a polished final view.

10.6 Beam's-Eye-View (BEV)

View → Beam's-Eye-View opens a 2D view looking down a beam's central axis — what the beam “sees”. Choose a beam from the dropdown; the structures are projected (with the beam's divergence) onto the isocenter plane and the field aperture (MLC shape or jaws) is drawn in white over them. Use it to confirm the aperture conforms to the target and to check which organs at risk fall in each beam's path. A graticule shows the central axis and 50 / 100 mm rings; the beam's angles, energy and field size are listed above the image.

11. Image Fusion and Registration

Fusion overlays a secondary image (for example an MR or PET, or a second CT) on the primary study.

11.1 Loading a Secondary Image

There are two ways to load the secondary image. When a study already contains both series (for example after a PACS retrieve of a CT and MR), pick the second series in the Fusion / secondary image field of the load dialog. Otherwise, click Load secondary image for fusion in the control panel, or use File → Load Fusion / Secondary Image, then choose the folder and series. Either way the secondary image is resampled onto the primary grid.

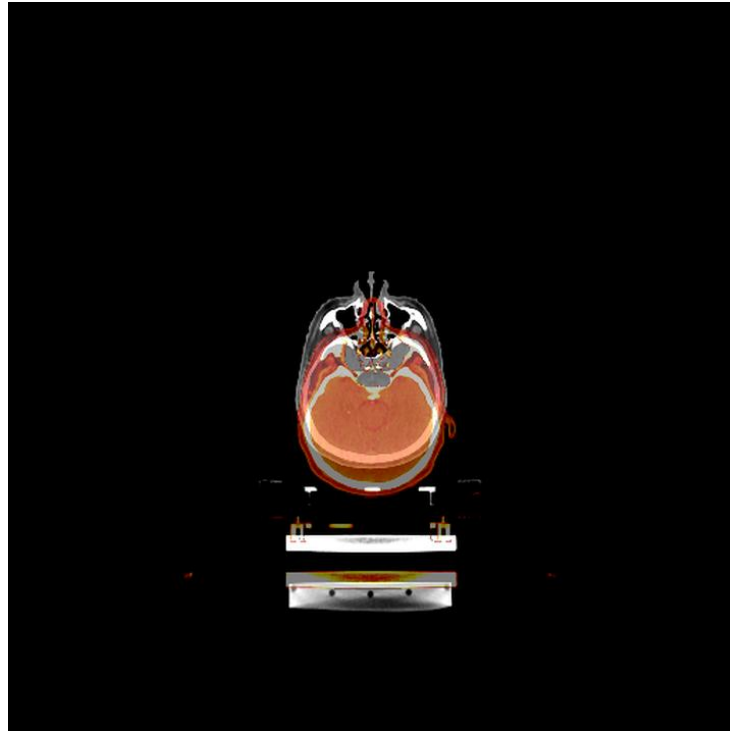


Figure 9. A secondary CT (hot colormap) fused over the primary CT (grayscale).

11.2 Display Controls

Use the fusion controls to set the overlay opacity, colormap, and the window / level of the secondary image. The Compare mode selector offers Blend (a colored overlay) or Checkerboard (alternating tiles of the two images), a quick way to check alignment along edges.

11.3 Alignment

- **Frame of reference** — if both images share a DICOM Frame of Reference they are already aligned; no further action is needed.
- **Automatic registration** — choose a Method (Rigid or Deformable B-spline) and click Auto-register. Rigid is a fast 6-degree-of-freedom alignment by mutual information; deformable additionally warps the secondary image to match local anatomy (slower).
- **Manual adjustment** — fine-tune with the translation (tx, ty, tz in mm) and rotation (rx, ry, rz in degrees) fields; Reset alignment returns to the geometric alignment.
- **Save / Load** — a registration result can be saved to a file and reloaded later (Save reg / Load reg).

12. Plan Comparison and Summation

The Plans menu lets you load one or more additional RT Dose objects and either compare them with the active plan or add them together. Every dose is resampled onto the primary image grid so they share a common geometry.

12.1 Loading Additional Doses

Plans then Load Additional Dose adds an RT Dose file to the dose pool. Plans then Compare / Sum Plans opens the plan dialog, which lists every dose currently loaded and provides the Compare and Sum tabs.

12.2 Comparing Plans

On the Compare tab, choose a dose to compare against the active plan, then use any of:

- **Dual DVH** — overlays the comparison plan's DVH as dashed lines on top of the active plan (solid), so target coverage and organ-at-risk trade-offs are visible at a glance.
- **Difference overlay** — shows the voxel-by-voxel dose difference (comparison minus active) in the image panes as a blue-white-red map: red where the comparison delivers more dose, blue where it delivers less.
- **Gamma analysis** — computes a 3D gamma index between the active plan (reference) and the comparison plan for the chosen dose-difference and distance-to-agreement criteria (for example 3 % / 3 mm), reporting the pass rate and an optional gamma map. It quantifies how closely two dose distributions agree, useful for QA and plan-versus-plan checks.

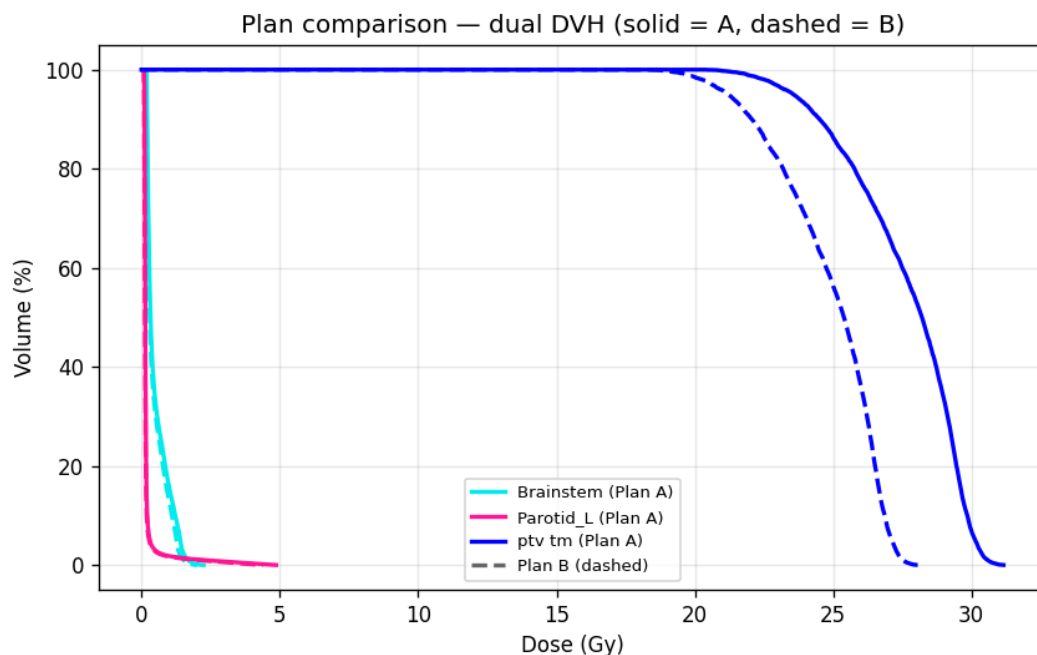


Figure 10. Dual DVH: the active plan (solid) and a comparison plan (dashed) for a target and two organs at risk.

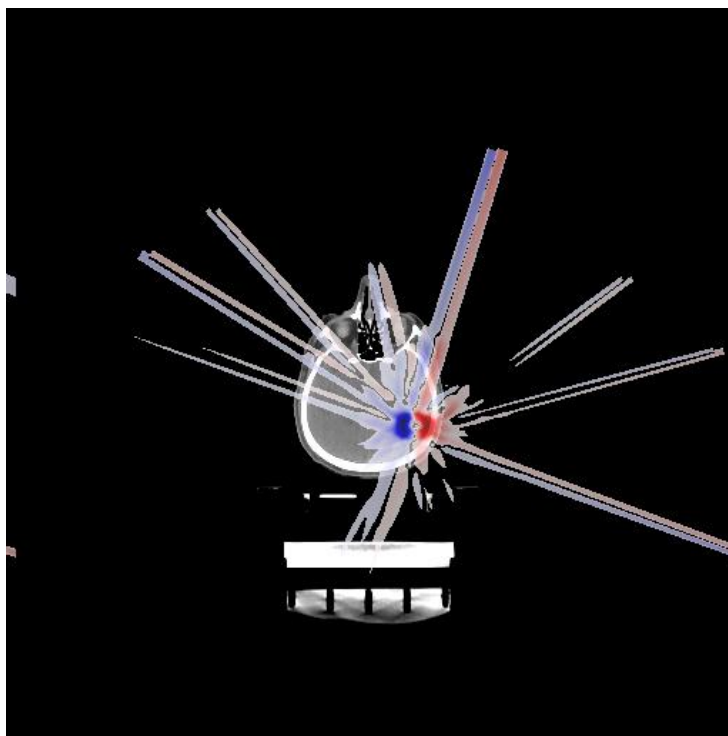


Figure 11. Dose-difference overlay (comparison minus active): red is higher, blue is lower dose.

12.3 Summing Plans

On the Sum tab, tick the doses to add, set each dose's number of fractions, and choose a mode:

- **Physical (Gy)** — a straight voxel-by-voxel dose sum. Appropriate for phases of a single course delivered at the same fraction size (for example an initial plan plus a boost).
- **EQD2 (a/b)** — converts each plan to the equivalent dose in 2 Gy fractions (linear-quadratic model) before summing, using the chosen a/b ratio and each plan's fraction count. Use this when fraction sizes differ (re-irradiation, or brachytherapy combined with external beam), where physical doses cannot simply be added.

Create composite then set as active dose replaces the displayed dose with the sum, so the colorwash, isodose lines, DVH, metrics and 3D surfaces all reflect the total. Revert to original restores the primary dose.

Note: the EQD2 conversion applies a single a/b ratio to the whole grid. Interpret target and normal-tissue doses with the appropriate a/b (commonly about 10 Gy for tumor and 3 Gy for late-responding normal tissue) by re-running the sum with the relevant value.

13. DICOM Networking (PACS)

The application can query and retrieve studies from a DICOM archive and send objects to one. Connection details can be saved and re-used.

13.1 Saved Destinations

Both the Send and Query/Retrieve dialogs let you save connection details. Enter a Name plus the node's Host/IP, Port, its AE title (Called AE) and your AE title (Calling AE), then click Save. Saved destinations appear in the Saved dropdown for reuse; selecting one fills in the fields, and Delete removes the selected one. The list is shared between the two dialogs and stored in your user profile (a destinations.json under .dicom_rt_viewer), so a destination saved in one is available in the other.

13.2 Sending (C-STORE)

File → Send to DICOM / PACS sends the loaded objects to a node. Use Verify (C-ECHO) to confirm the connection first, then tick which objects to send:

- **Images** — the primary and, if loaded, the secondary image series.
- **RT objects** — the RT Structure Set, RT Dose and RT Plan.
- **Fused image** — the registered secondary is generated as a new image series that shares the primary's Study and Frame of Reference, so the archive displays it registered to the primary.

13.3 Query / Retrieve

File → Query / Retrieve from PACS finds studies on a node (C-FIND) and retrieves them:

8. Choose a saved destination (or enter the connection details).
9. Enter query fields (patient name, ID, study date, modality) — leave blank to match all — and click Query (C-FIND).
10. Select one or more studies in the results (Ctrl or Shift-click for several; double-click retrieves immediately).
11. Choose a retrieve method and click Retrieve to download the whole study, or click Series... to pick individual series (see below); the images download and open automatically.

13.3.1 Retrieving Individual Series

To bring back only part of a study rather than everything in it, select a study row and click Series.... The application queries the series in that study (a series-level C-FIND) and lists each one with its modality, description, date and image count. Select one or more series (Select all picks every row; double-click retrieves immediately), then click Retrieve selected → load. Only the chosen series are downloaded — using the same retrieve method (C-GET or C-MOVE) and Local port set in the Query/Retrieve dialog — and then opened. This is useful when a study contains many series and you only need, for example, the planning CT and the RT objects.

Retrieve methods:

- **C-MOVE** — used by most clinical archives. The PACS opens a new connection back to this workstation, so it must be configured with a destination entry matching your Calling AE title, this computer's IP address, and the Local port shown in the dialog (which must be open in the firewall).
- **C-GET** — self-contained (no PACS-side routing needed), but not all archives support it.

If a retrieve returns nothing, the application shows the reason — for example that the PACS does not recognise the move destination, or does not support C-GET. Retrieved images are stored in a temporary folder while you work and are removed automatically when the application closes.

14. Editing, Closing and Anonymizing

14.1 Editing DICOM Tags

File → Edit DICOM Tags opens a viewer/editor for the tags of a loaded series. If more than one series is loaded, choose which one from the Series dropdown at the top — that is how you pick, for example, the CT rather than the RT Dose. The table lists each top-level tag with its group/element, name, VR and value.

- **Editing** — double-click a value to change it. The change is applied to every instance (slice) in the series when you save.
- **“Varies”** — a tag flagged this way does not have the same value on every slice (for example Instance Number or Image Position). Editing it sets the one value on all slices, so change these only deliberately.
- **Read-only** — sequences and binary data (and the pixel data) are shown for reference but cannot be edited here.

Click Save As... and choose a folder. The edited series is written there as a new set of files; the original files are never modified. Export Text... writes the tags shown (with any unsaved edits) to a formatted, aligned plain-text file — handy for reviewing or sharing a tag listing.

14.2 Closing a Series

File → Close Series (Ctrl+W) unloads the current study — images, structures, dose, plan and any fusion — and clears the views, so you can start fresh without leftover data from the previous patient.

14.3 Anonymizing (De-identification)

File → Anonymize prepares a de-identified copy of the loaded data. Each loaded series is listed with a checkbox (images and RT objects, plus the derived fused image when a fusion is active); tick the ones to include — all are selected by default so the set stays complete and linked. Set the replacement Patient Name and Patient ID (default ANONYMOUS / ANON), then choose the options:

- **Remove private tags** — strips manufacturer private data elements (on by default).
- **Blank dates** — clears study / series / acquisition dates and times.
- **Generate new UUIDs** — off by default keeps the original Study / Series / SOP / Frame-of-Reference UUIDs, so the anonymized data still matches the original study and the RT objects stay linked. Turning it on assigns new UUIDs, remapped consistently across all series so cross-references remain valid — the result is treated as a distinct study.

Identifying fields — patient birth date, addresses, physician and institution names, station name, accession number and similar — are always blanked, while clinically useful non-identifying fields such as patient sex are kept. The Manufacturer and Model tags are set to TCC / DICOMRTVIEWER on the output. Then choose an action:

- **Save to Folder...** — writes the anonymized study to a folder you choose, one subfolder per series.
- **Send to PACS...** — opens the Send dialog with the anonymized objects ready to transmit (see Section 13).

De-identification here covers the common identifying elements but is not certified to any formal profile; review the output before releasing it outside your institution.

15. Reference

15.1 Mouse and Keyboard

Action	Result
Left-click in a pane	Move the crosshair (or place a ruler point in Measure mode)
Mouse wheel	Scroll through slices
Right-drag	Window / level (contrast / brightness)
Ctrl + wheel	Zoom (also – / + / fit buttons)
Left-drag	Pan
Ctrl+O	Open folder
Ctrl+S	Save screenshot
Ctrl+3	Open the 3D view
Ctrl+Space	Play / pause cine
Ctrl+R	Reset all views

15.2 Menus

Menu	Commands
File	Open Folder..., Open DICOM File(s)..., Edit DICOM Tags..., Close Series, Save Screenshot..., Export Plan Report..., Load Fusion / Secondary Image..., Load RT Plan..., Query / Retrieve from PACS..., Send to DICOM / PACS..., Anonymize (save / send)..., Exit
View	Reset views, Measure (ruler), Play / Pause Cine, Open 3D View, Beam's-Eye-View (BEV)
Structures	Create Structure..., Export RT Structure Set...
Plans	Load Additional Dose..., Compare / Sum Plans...
Help	About

16. Notes, Assumptions and Limitations

- The viewer is optimized for standard axial, head-first acquisitions. Strongly oblique acquisitions are not reformatted.

- Dose is resampled to the image grid with trilinear interpolation; DVH is voxel-based, so very small structures are approximate.
- Beam geometry is computed for a head-first-supine patient using IEC 61217 conventions.
- Automatic registration offers rigid (6 degrees of freedom) and deformable (B-spline) modes; deformable can take a few minutes on large studies.
- EQD2 summation applies one a/b ratio to the whole grid; choose it to suit the tissue you are evaluating.
- Some anonymized or partially exported RT Plans store a zeroed isocenter and zeroed gantry/couch angles. In that case beams are drawn at the origin and do not align with the anatomy — this reflects the data, not a program error. A fully exported plan displays beams correctly.
- This software is not a certified medical device and must not be used for clinical decision-making.

17. Troubleshooting

Symptom	Cause / Resolution
No images found when opening a folder	The folder contains no CT/MR/PET series; check the path and that files are DICOM.
Structures or dose do not appear	The selected image series does not match the RT objects. Re-open and select the image series the plan was created on.
3D view is empty / “no RT plan loaded”	Open the correct study; the plan appears in the selection dialog. Use File → Load RT Plan... to attach one explicitly.
Beams do not sit on the target	The plan’s isocenter/angles were zeroed on export (see Section 16).
Query works but Retrieve does nothing	For C-MOVE, register this workstation's Calling AE, IP and local port on the PACS (and open the port in the firewall); or the PACS does not support C-GET. The dialog reports the exact reason.
3D view fails to open	OpenGL / graphics driver problem; update the graphics driver.

18. Glossary

Term	Definition
CT / MR / PET	Imaging modalities used as the base image set
RTSTRUCT	RT Structure Set — contoured regions of interest
RTDOSE	RT Dose — the calculated 3D dose distribution
RTPLAN	RT Plan — treatment beams and delivery parameters
MPR	Multi-planar reconstruction (axial / coronal / sagittal)
DVH	Dose-Volume Histogram
Dx / Vx	Dose to x % of a volume / volume receiving x dose
HI	Homogeneity index of dose within a target
CI	Conformity index (RTOG or Paddick)
EQD2	Equivalent dose in 2 Gy fractions (linear-quadratic model)
a/b	Alpha/beta ratio of tissue radiosensitivity (used by EQD2)
Gamma index	Combined dose-difference + distance agreement metric
Isocenter	The point about which the treatment gantry rotates
MLC	Multi-leaf collimator that shapes the beam aperture

PRV	Planning organ-at-risk volume (an OAR plus a safety margin)
C-ECHO	DICOM connectivity verification (“ping”)
C-STORE	Send DICOM objects to a node
C-FIND	Query a DICOM node for matching studies
C-MOVE / C-GET	Retrieve studies from a DICOM node
AE title	Application Entity title identifying a DICOM node
Frame of Reference	DICOM coordinate system shared by related objects

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