OnkoDICOM User Manual

@OnkoDICOM2019

Table of Contents

Chapter 1:

Introduction

The world of Radiation Oncology is a small one, but it is dominated by images. The diagnosis of cancer is made from a histopathological image. The stage of the cancer is mainly derived from radiological images. The definition of the areas to be treated with and avoided by radiation is based on overlays of radiological images. The investigation of patient outcomes uses radiological images.

It's an imaging world and the radiation oncologist can't avoid it!

While the radiological imaging is typically viewed as a grey scale image, it is in fact a 3D matrix of numbers which are manipulated into a display image.

For both CT and MRI, the range of numbers far exceeds the ability of the eye to perceive grey. As a result there is a need to manipulate the image for viewing to perceive changes which may be of minor numerical variation. The radiation oncologist has many pieces of software already available in their work environment to achieve this.

The images obtained and stored are however also available for use in Radiomics research. It is hoped that in the future Radiomics will become a normal part of the radiation oncologist's decision making process, but at present the area is in its infancy, and it is not known how this will occur.

RADIOMICS

Radiomics is concerned with extracting features from the area of the image which has been defined as cancer by the oncologist. A feature is a pattern in the image, for example, "a 15 pixel row where all have identical CT numbers", or "a 5x5x5 3D group of pixels, where all pixel values are separated by more than 10 CT numbers". Really, you can have any number of patterns. Other features can include a reading frames energy (average of all pixel values) or entropy (clumping of high or low values on one side) or kurtosis (pixel distribution not following a normal curve). In fact the possible number of features is very high (thousands!).

At present, in order to undertake this kind of data collection you need either very high levels of IT ability (we are talking coding here, not email sending!) or a lot of money to buy one of the commercial offerings that will make the process easy (got $80K spare).

If you are an individual radiation oncologist who wants to get involved by collecting and curating the base data, these are the two challenges. Do courses to get proficient in Python/MatLab, or convince your department to spend a lot of money on something that they probably don't understand or think is worthwhile (many senior doctors think this decision support stuff is a waste of time).

OnkoDICOM

OnkoDICOM is a software product that straddles this divide. The basis for the software was a well-known, well respected, stable, GitHub-based, open source project called 'dicompyler' written in Python2 that allowed a radiotherapy plan to be opened and inspected. It allowed the CT to be viewed, resized and re-windowed. It could overlay any Regions of Interest (ROI) drawn in the RTSTRUCT file. It could overlay the radiation dose deposition pattern (drawn as isodoses) from the RTDOSE file. It allowed for a detailed assessment of radiation coverage of ROI using a graph called a Dose Volume Histogram (DVH). It could anonymise the patient identifiers.

But it did not do enough for modern radiotherapy where data and image analysis is an active area. OnkoDICOM has retained all of dicompyler's functions and added more to support research into routine clinical data.

The viewing of the CT scan has been improved by adding pre-set windowing options for Brain, Head & Neck, Bones and Lung.

The assessment of the ROIs and isodoses has been enhanced by the production of a spreadsheet file so that dose-volume parameters can be analysed separately.

A profiling tool ('Transect') is added to allow the user to inspect the CT numbers at the boundaries of objects to assist with isopixel contouring (defining an area in the CT with the same pixel value boundary).

A data collection window for a combination of clinical information regarding diagnosis, staging, treatment and outcomes to acquire a basic, mandatory minimum data set. This module includes standard codes for countries, disease classification of site and morphology (ICD10), and calculates durations automatically. It can be saved to a spreadsheet file also.

Feature extraction from the CT data underlying the ROIs is achieved using the PyRadiomics pipeline which produces an NRRD/mask file and a large Radiomics spreadsheet. The presence of the NRRD/mask file along with the DICOM files allows for plugin development of other radiomics pipelines. The Radiomics spreadsheet in combination with the DVH and Clinical Data spreadsheets can be used by Machine Learning tools to discover new knowledge.

Finally a plugin ('Anon') undertakes an automated batch process of hash anonymisation, saving anonymised files to a new anonymised directory, with production of the DVH, Radiomics and Clinical Data CSVs, all with the same anonymised identifier. A paired list of patient identifiers and anonymised ID is also produced. This automated process allows for the generation of predictable directory structures to aid later research.

OnkoDICOM will be compiled into executables for Windows, Mac and Linux.

In the short term future, other planned plugins include one for the mapping of Standard Names to Foundational Model of Anatomy (FMA) ID is envisioned and will be added into future releases will allow for the substitution of names not compliant with the Standard Name list. This will allow the collation of DVH and Pyradiomics data across your dataset without further modification. Also OnkoDICOM will be compiled into executables for Windows, Mac.

Another plugin is planned to allow the transfer of isodoses to ROIs from various isodose levels with automated naming. A plugin is planned for the specification of the appearance of isodose and ROI in the DICOM View window (line & fill appearance).

In the medium term future, plans for additional OnkoDICOM functionality include ROI manipulation (deletion, renaming, creation), PET/CT overlay, and image fusion.

What do you need to use OnkoDICOM?

OnkoDICOM will only open a directory that contains a proper DICOM-RT file group, i.e., a complete radiation plan. The files required are:

- CT slices
- RTSTRUCT file
- RTDOSE file
- RTPLAN file (this must be for the whole plan, not individual beams).

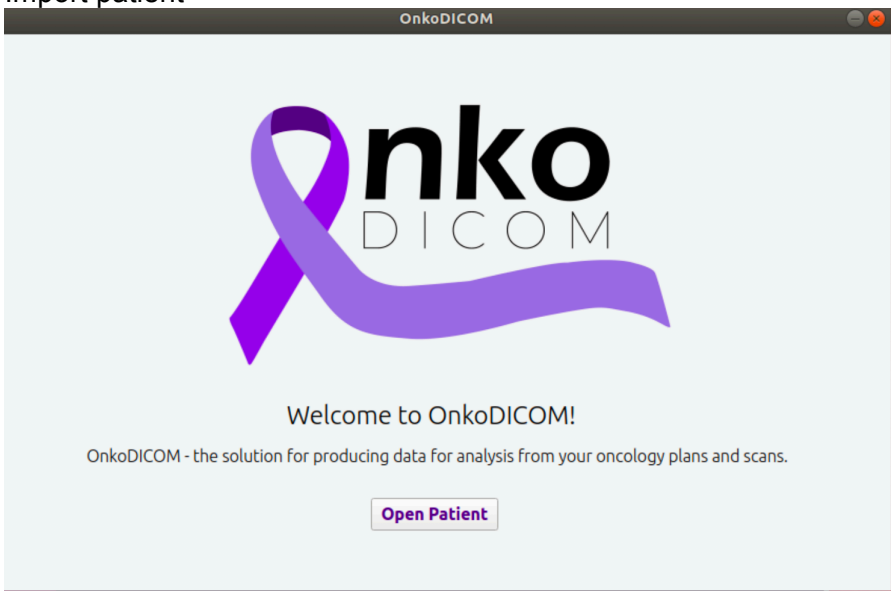
To produce a complete set of spreadsheet files for the patient, you require the above files, and data relating to the patient's diagnosis (ICD10 topography & morphology, TNM and Overall Stage), the details of the initial treatment course (initial intent of treatment and status of all possible therapies) and disease outcome (dates of last review, local/regional/distant failure, status with respect to death and cause). The three spreadsheets produced by OnkoDICOM are:

- DVH.csv
- ClinicalDate.csv
- Pyradiomics.csv

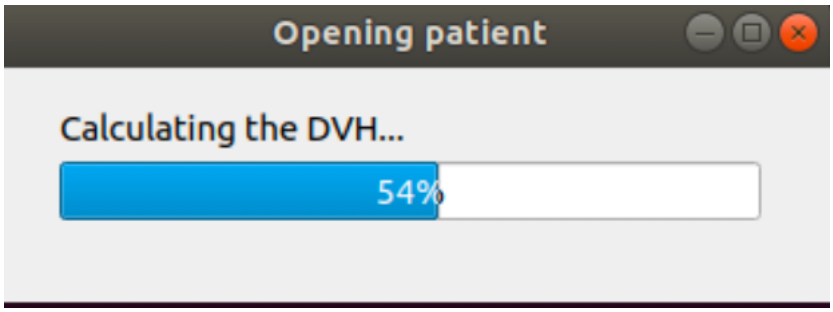
Chapter 2:

Getting started

Import patient



Select the directory or open from inside a directory

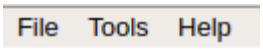


The main window will open

Chapter 3:

The Main screen and its Elements

The Menu bar



File **Open** a new patient file.
Save changes back into the current DICOM file.
Exit the program.

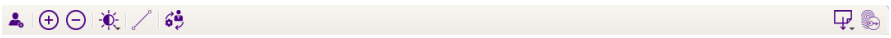
Tools **Zoom In** for a closer view at the scan image.
Zoom Out for a wider-angle view of the scan image
Windowing > choose from the list of predefined window settings.
Transect draw a line across the image and view the pixel density as a graph. Click the button to activate. Closing the graph deactivates.
ROI Creation > ROI by Brush & **ROI by Isodose** are present for future functionality.
Plugin Manager > a window will open which allows the manual configuration for Tools.
Export > clicking on the icon gives you the option to export individually one or more of these three spreadsheet, note that this output will have the same identifiers visible in the Patient Information bar.

- **DVH** produces a CSV file with the data used to graph the cumulative Dose-Volume Histogram
- **Clinical data**.produces a CSV using the data entered into the Clinical Data window. If a CSV is already present, the values will be filled in and an edit is possible.
- **Pyradiomics** produces a large CSV and a NRRD directory using the Pyradiomics pipeline.

[All of these CSV files are located in the same directory as the DICOM Files]
Anonymize and Save launches an automated batch process when you have finished curating the patient's DICOM file. The process will anonymise all files with a hashed ID into a directory with that hashed ID, and then run all three functions above sequentially to produce three CSV files – DVH, Clinical Data and Pyradiomics.

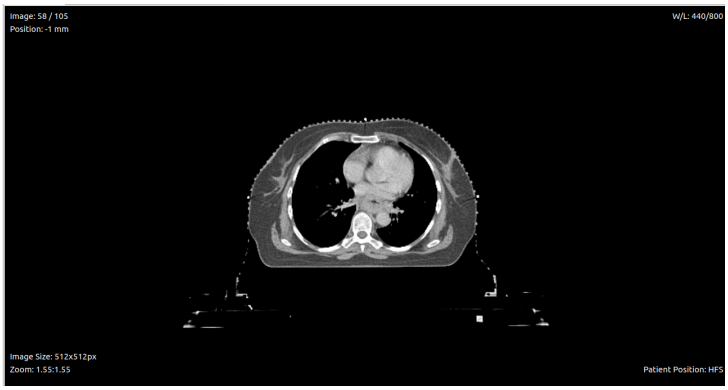
Help This option will take you this user manual.

The Toolbar

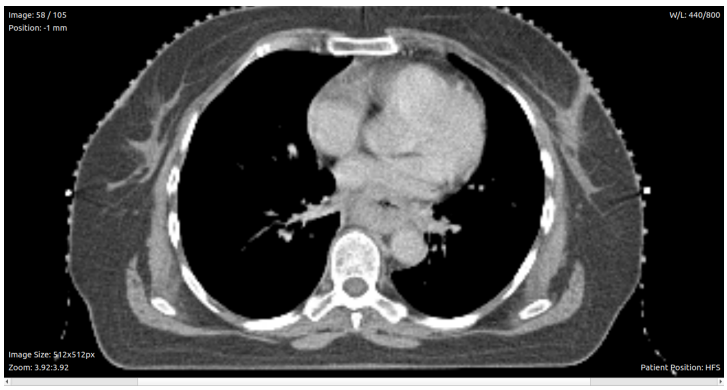


Open Patient and choose from directory.

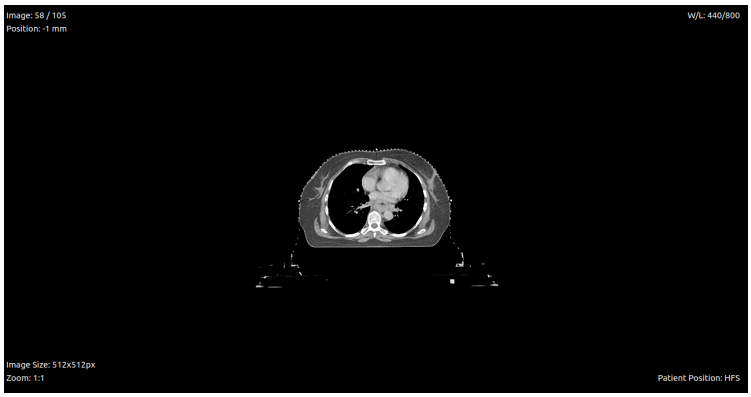
Functions in the **DICOM View** tab.
Zoom In (+) to obtain a closer view of the scan image.
Zoom Out (-) to obtain a wider-angle view of the DICOM image.



A normal view



The view after **Zoom In (+)**

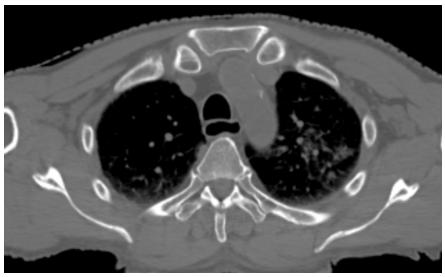


The view after **Zoom Out (-)**

Image Windowing:

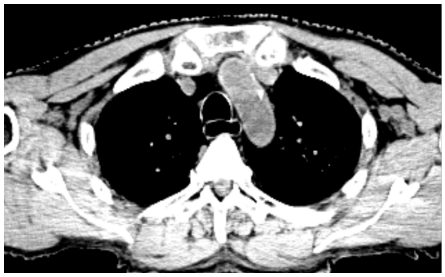
Press the Image Windowing icon to see a drop down list of predefined windows settings; **Normal**, **Lung**, **Bone**, **Brain**, **Soft Tissue**, and **Head and Neck,** each with different contrast and brightness.

[You can add alter or more Image Windowing settings from within the Plugin Manager (see below)]

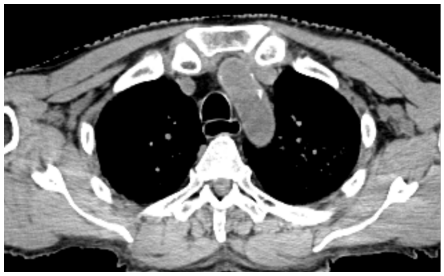


Bone

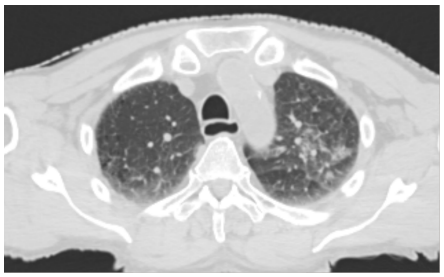
Normal



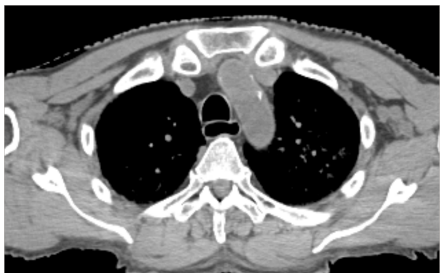
Brain



Head and Neck



Lung

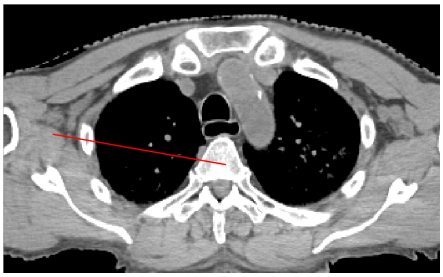


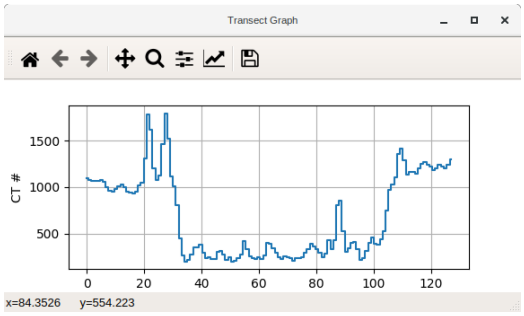
Soft Tissue

Transect
By drawing a line across the image, the CT number values of pixels in the line are graphed. This assists with obtaining pixel numbers for isopixel ROI creation (not implemented yet).

Select **Transect** icon
Left click & hold on the image at your start point, and drag the red line across the image. When you are positioned on your end point release the left button.
When you close the graph the Transect is deactivated.


Normal Image


Draw the Transect line across the image



The Transect graph appears plotting the CT number across the distance of the Transect.
On this graph the soft tissue (~1000) can be differentiated from lung (~200) and Bone (~1200+). Even the vessels in the lung can be seen.
The icons in this view allow you to **Save** this graph as a figure into a chosen directory, **Configure** the subplots by change the figure size, using a **Zoom** rectangle, **Forward** to next view, go **Back** to previous view, and **Reset** the original view.

Add ROI by Brush
this functionality is not available yet

Add ROI by Isodose
this functionality is not available yet

Plugin Manager

The Plugin Manager allows for the addition of extra functions, and for the specification of user-defined settings.

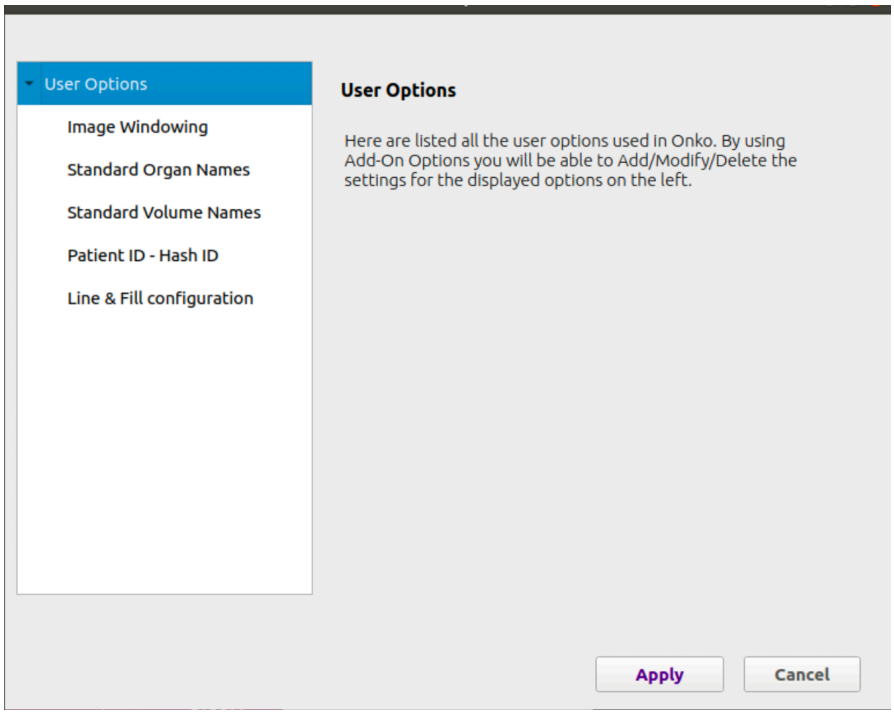
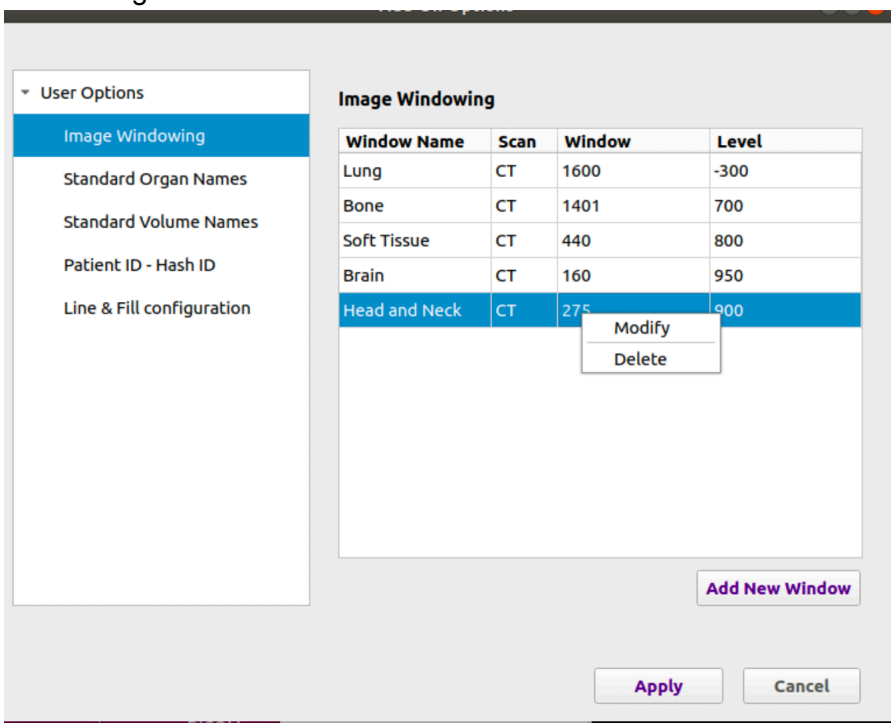
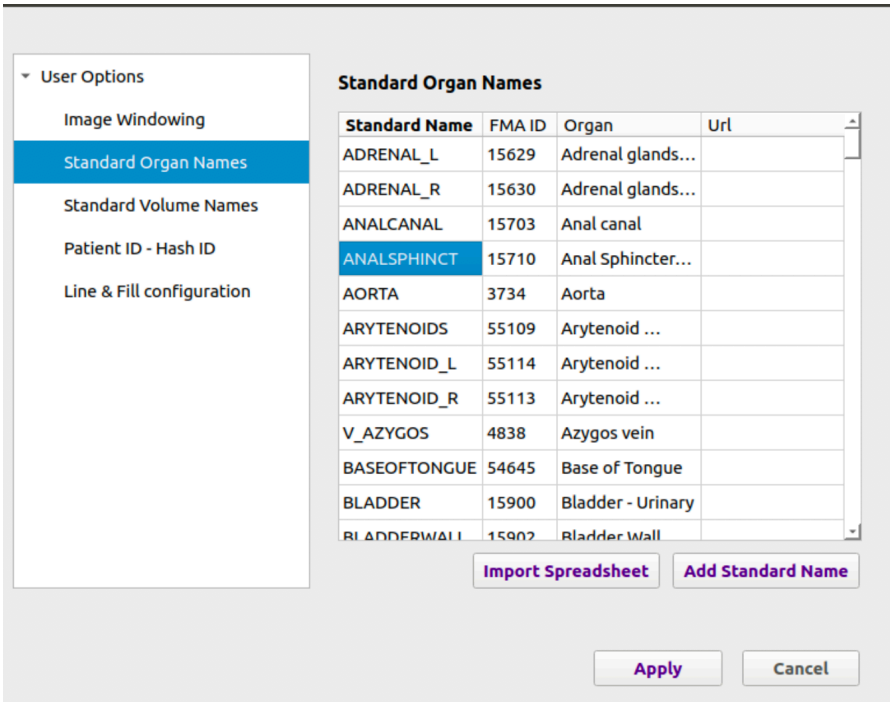


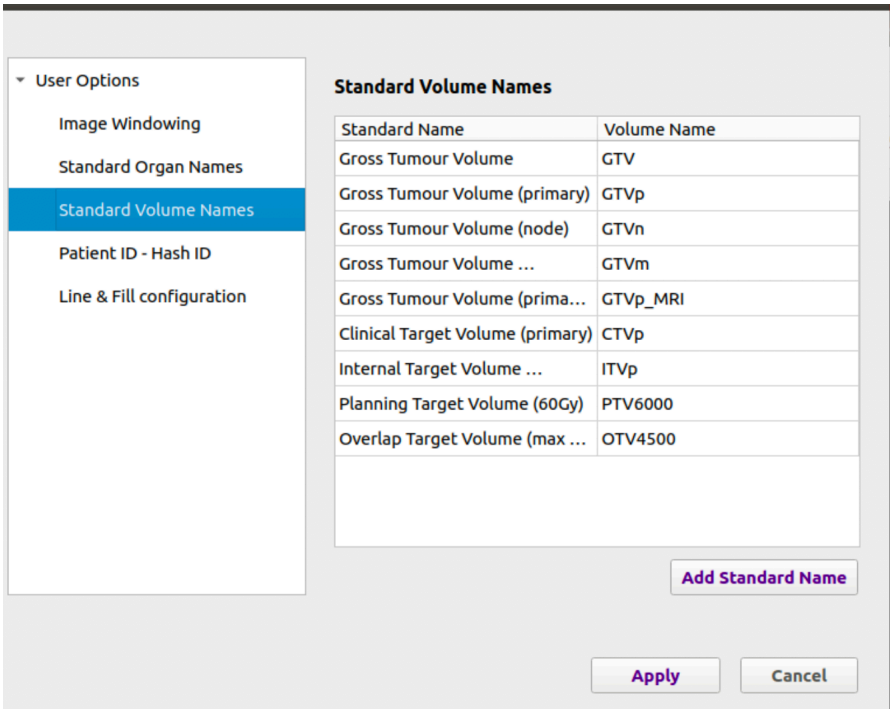
Image Windowing provides the values used for the Image Windowing button. The numbers used are CT numbers.



Standard Organ Names provides a list of Standardised Names with the FMA ID number and a URL for reference to describe which anatomical organ is being named.

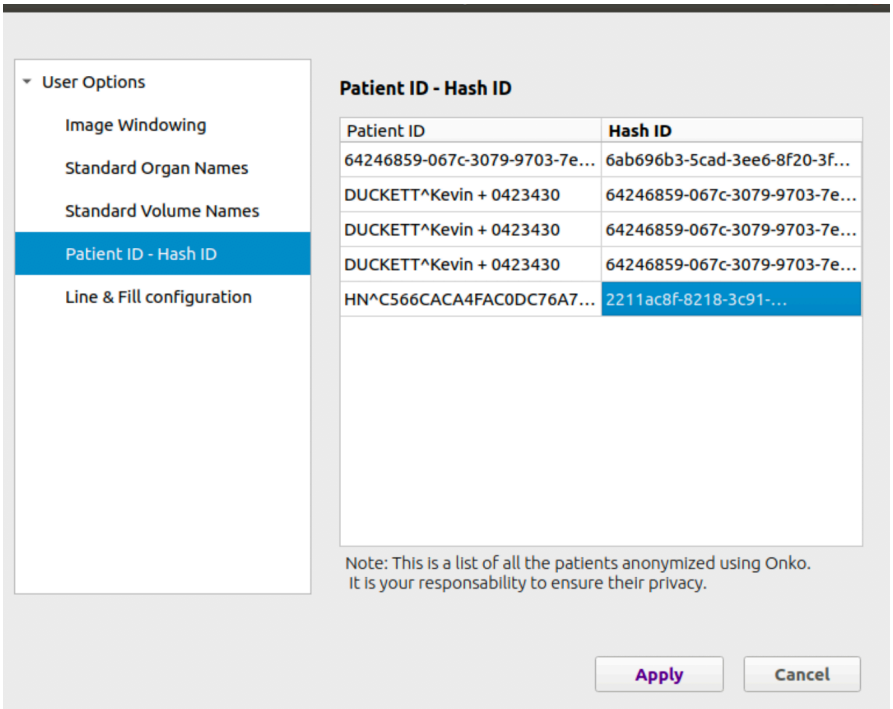


Standard Volume Names provides a list of standard root names for the commonly used GTV/CTV/PTV, as well as OTV (Overlap Target Volume), to demonstrate a semantically consistent nomenclature.

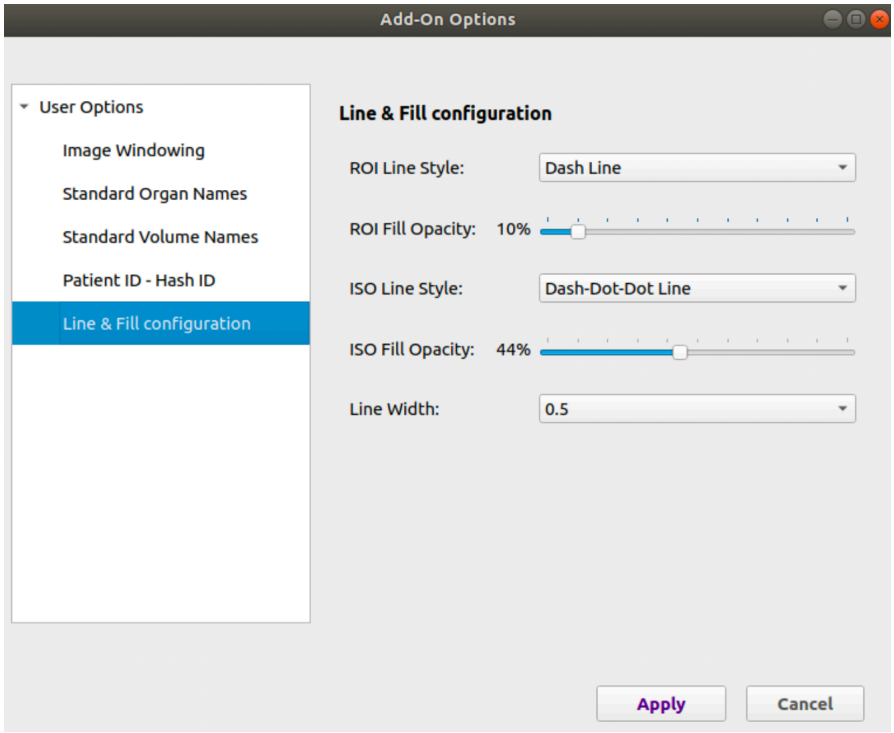


Patient ID – Hash ID provides a list of patients anonymised using the **Anon** function on the icon bar. This list allows for queries about anonymised patients to be answered from the original data. Also repeated anonymisation of identified files will overwrite previously anonymised files, not save new duplicate directories.

IMPORTANT – this is a privacy risk. You are required to keep the patient's identifying data secure within robust firewalls. We recommend that you backup this file regularly, and only have it in your Onko installation when anonymising patients, or editing anonymised files.



Line & Fill conficuration to change the layer sittings of RIOs.



Export
You use this button when you wish to export a single or multiple spreadsheets for an **identifiable patient**.
When you press this button, you will see three options, when you select one, the spreadsheet file will be exported into the patient directory.

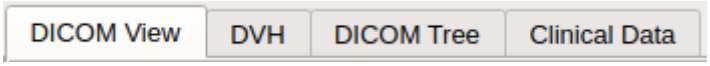
Anonymise and save
You use this button when you wish to export all spreadsheets for an **anonymised patient**.

When you press this button, the three options that you saw in Export will be executed as a batch, starting with the patient identifiers being anonymised to a new 'hashed ID'.
A new directory will be created with the hashed ID name, into which will be saved all of the de-identified DICOM files and the three spreadsheet files all with the new hashed ID.
In addition, the matching pair of original patient identifiers and the new anonymised ID will be written into the Plugin Manager.
Please note that this pair of identifiers is in plain sight, and it is your responsibility to keep this secure and private.

Patient Information bar

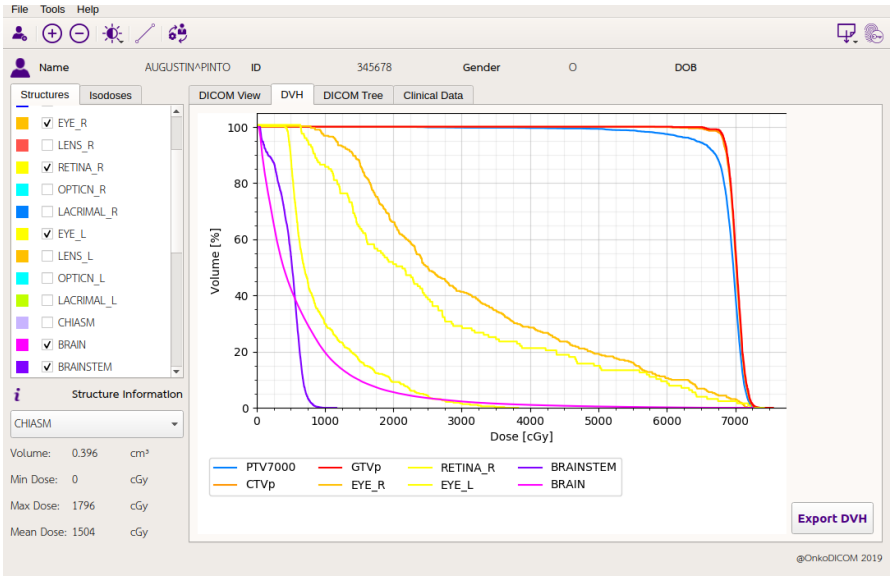
Shows the patient identifiers (Patient first and last name, Patient ID, Gender and, Date of Birth).

View tabs

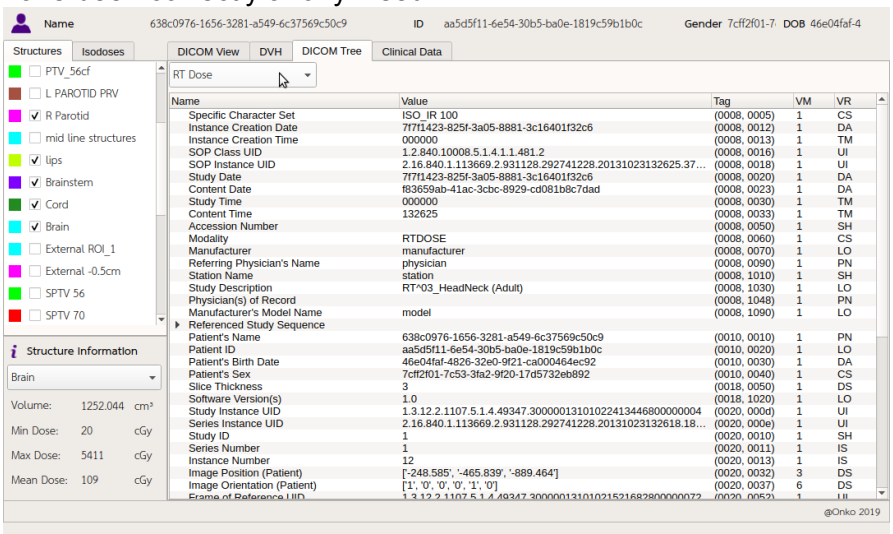


DICOM View provides the display of DICOM image. The functions that work in this window as **Window Level** and **Transect** (described previously).
The slider bar on the right is used to move up and down the slices.

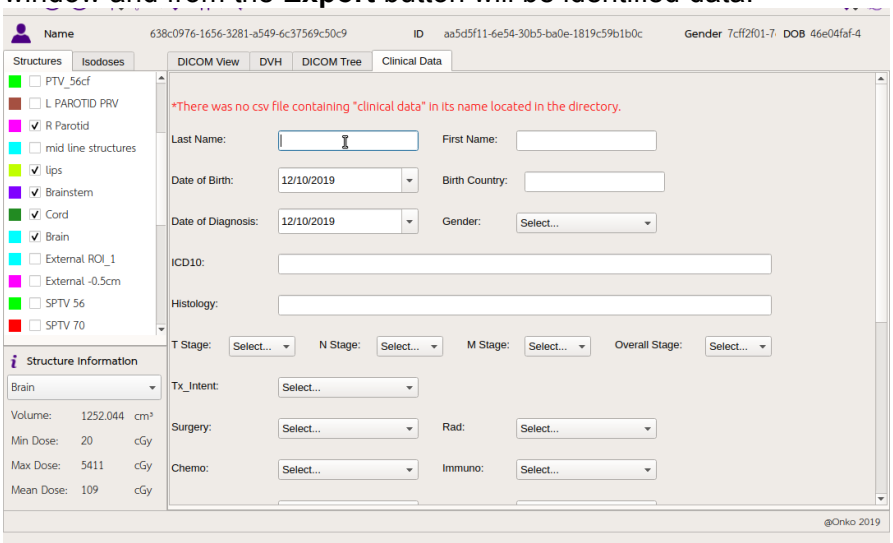
DVH or Dose-Volume Histogram provides a graphic to assess dose deposition in ROIs selected from the Structure List. The DVH values can be exported from this window or the **Export** button for *identified* patients.



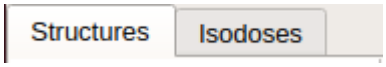
DICOM Tree provides a view of the DICOM header tags which define many aspects of the file being interrogated. The dropdown list on the top left of the window provides the entire list of image files, RTSTRUCT, RTDOSE and RTPLAN files from which one can be selected. This information is crucial to determine that the files have been correctly anonymised.



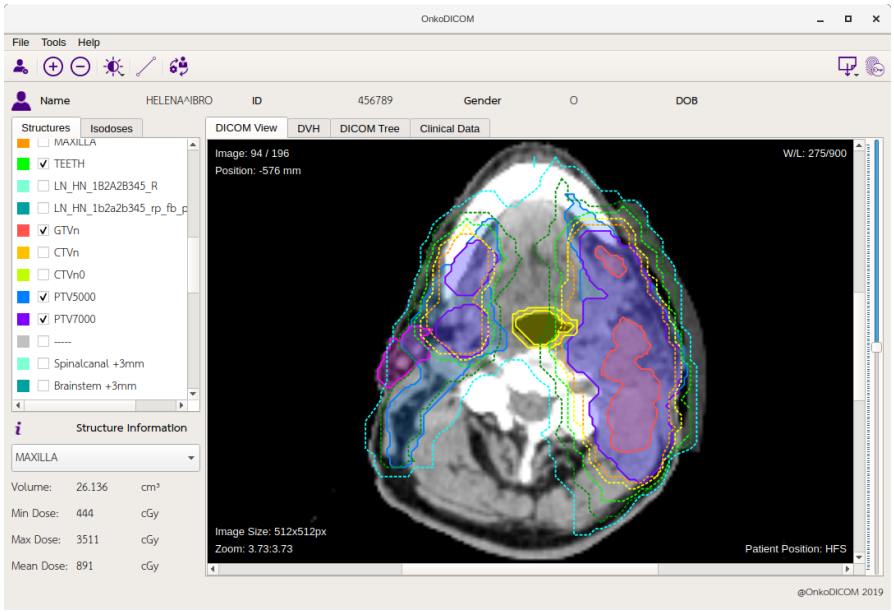
Clinical Data can be added using this screen. Many values will be automatically calculated. If a Clinical Data spreadsheet has been saved previously for the patient, the data will populate and allow you to update it by editing the data. The Clinical Data is saved from this window and from the **Export** button will be identified data.



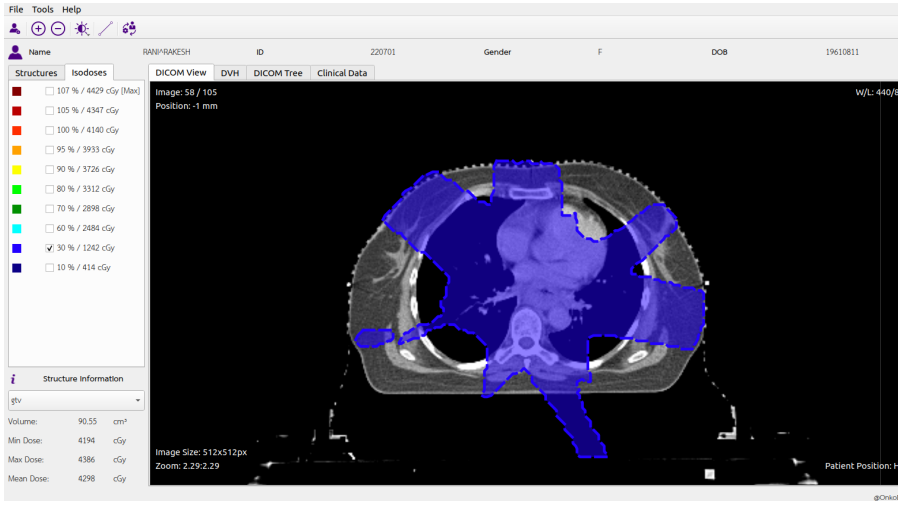
ROIs and Isodoses List



Structures: contains all ROIs and view the selected ones in the DICOM View. The various ROIs selected can be seen overlaid on the planning image. The overlaid ROIs are shown in order of selection (first is lowest). The selected ROIs will also appear in the DVH window.



Isodoses: displays the radiation dose deposition pattern and can be viewed with the ROIs displayed in the DICOM View. The displayed isodoses are calculated from the prescription dose of the plan (RTPLAN file).



Structure information table

Structure Information provides summary data about the selected ROI providing volume of the ROI, it's maximum and minimum dose, and the dose received by 50% of the ROI (mean).