OnkoDICOM 2025

User Manual

An Open Source Program
to support Radiation Oncology
Radiomics & Imaging Research

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Home page: https://onkodicom.com.au/
Project page: https://github.com/didymo/OnkoDICOM

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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 on radiological images. The investigation of patient outcomes uses radiological images.

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

While radiological images are 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.

OnkoDICOM provide one view of this future.

1.1 Radiation Oncology Research

Data has undergone a revolution with the introduction of the internet. Everything is now recorded and so new tools and techniques have been developed for data storage (new databases using different approaches from the well-known relational database), retrieval (the use of the Application Programming Interface or API that allows an outsider to access your available data), and data structure (the development of ontologies describing knowledge structure).

Basically the infantry of χ^2, Student t-test, Kaplan-Meier and log-rank are being challenged by the the new squires of statistics who are called Linear Regression, Logistic Regression, Decision Tree, Support Vector Machine, Naive Bayes Algorithm, k-Nearest Neighbours, k-Means and Neural Networks known as and who serve the Lords of Machine Learning known as Multi-Layer Perceptron, Convolutional Neural Networks living in or close to the hallowed country of Deep Learning.

Fortunately the old algorithm of radiation oncology and medical research has not changed dramatically, just the data curation method and statistical tools.

1.1.1 Data Management in the 20th Century

Until now Medical Research has started with a clinical question, following which there is the collection of pertinent data that is then analysed and finally interpreted in light of the original clinical question.

While this process still works, it is poorly matched to our modern Oncology Information Systems which will store our medical data. Our medical data comes in two categories - there is the set of data points that are present and defined for the most or all patients. Take the cancer site for instance. The pre-OIS method was to write or dictate "Prostate Cancer" into a letter/note. The researcher would open the documentation, read the site and enter it into their bespoke spreadsheet in a column called 'Cancer Site' or 'Site'. They might enter *prostate* or *C61*; or if they were tired and a little careless, enter ***prostrate*** ... and so their data would suffer a diminution in quality and an error in analysis. Following data analysis and manuscript completion, the spreadsheet would be stored ... somewhere ... and rarely reused again, even when the same study were undertaken 5 years later.

WHAT A BLESSED WASTE OF RESEARCH TIME! Always dredging the same data out of the same notes!

1.1.2 Data Management in the IT-enabled 21st Century

There is an alternative. During your routine clinical work, you meet data items that occur repetitively (in fact, 20% of our items occur 80% of the time, and 80% of our items occur 20% of the time!). The following modern business rules are consistent with oncological knowledge structure, ubiquitous and therefore NOT optional:

- All cancer patients has a site specified according to the ICD10-Topography list.
- All cancer diagnoses are described by a histopathology specified according to the ICD10-Morphology list.
- All cancer diagnoses are staged according to the AJCC/UICC TNM Classification.
- All cancer patients after diagnosis and staging are seen in consultation to define a course of treatment that consists of therapies in a defined order.
- Following completion of treatment decided at consultation, cancer patients are assessed during follow up for local, regional and distant recurrence.

If the organisation of a department requires that these data points (e.g., site, histopathology, stage, treatment components, therapy prescription, etc) are recorded in the OIS using drop-down choices (or more accurately NOT in free text), this **Routine Clinical Data** becomes almost instantaneously and repetitively retrievable. If entered, it can be retrieved by database report, and that same report can be used to measure consistency and completeness leaving the research effort to quality assurance correctness and collect new non-routine data.

In this way, each researcher adds and enhances the collected data. By this method, larger data repositories can result. But this means that oncologists must know how to use their OIS to store data (if you don't store it, you can't retrieve it!). So if you want to do Radiomics research, you need to get your head around data collection and how to make it easy.

There is another change in the Routine Clinical Data era. Since the data is already collected, you can start asking clinical questions of the data you have, rather than using the clinical question as an impetus to collect data.

1.1.3 Data Management and Artificial Intelligence

Artificial Intelligence is the rage word for the current "green cordial" to be imbibed by the masses in an orgy of optimism. Much of the optimism is pushed by individuals who either have little understanding of medicine and its ethos with respect to data, or by medical practitioners acutely unaware of the status of medical data as it exists. What is never mentioned is the role of curation of medical data by medical practitioners.

AI usually starts with a process of "data cleaning" but this is NOT the same process as going back to notes and reports to establish that the data is correct. The process is much more akin to examining a field called *Laterality* and reconciling entries such as "Left", "left", "L", "Left", "Loft", "left side" all to the same entry like "L". Generating data without these variations is best achieved by not having free text entries when choices are obvious and limited.

AI is able to generate synthetic data when variable values are absent. When generating models, rows of data with missing values will generally be excluded. Data from my department has shown that only 18.84% of patients have complete data, and that the distribution of data is skewed to diagnoses that have undergone quality assurance by medical staff.

With its ability to collate clinical and imaging data, OnkoDICOM is uniquely positioned to permit the production of Machine Learning models AND to apply them to future patients. Be warned though, a model can only be applied accurately if you present it with exactly the same data as was used to build the model.

1.2 Clinical Data

OnkoDICOM has the ability to hold Clinical Data in a DICOM Structured Report format. It will automatically upload those data from a correctly specified CSV file held in a correctly specified site (see Add-On Options for the details).

Patient ID	Date of Birth	Gender	Marital Status
Date of Diagnosis	ICD10 Site	ICD10 Morphology	Grade
Laterality	Size (mm)		
max. T stage	max. N stage	max M stage	max Overall Stage
Intent (first course)	Surgery	Radiotherapy	Chemotherapy
	Immunotherapy	Hormone therapy	Brachytherapy
Local Control Status	Regional Control Status	Distant Control Status	
Local Control Date	Regional Control Date	Distant Control Date	
Alive Status	Cancer Death Status	Last Contact Date	Date of Death

Table 1.1: List of personally Mandatory, Basic Data Elements

Please be cognisant of the need for patient confidentiality if you are using data sets identified with the patient's name. Personally I use a standard database report with a fixed MD5SUM algorithm to generate a new ID number, and then anonymise the patient's image files with that number.

When opening a patient in OnkoDICOM, the CSV file will be checked and if there is a line matching the patient ID, the DICOM-SR file will be automatically generated.

The Batch Processing allows you to extract all the DICOM-SR data for all patients in the selected directory so that you can check for anonymisation. If an identoifying column remains, it can be deleted from that extracted CSV, and then can be reapplied from within Batch Processing.

1.2.1 Required Data

The amount of required data is determined by your clinical question, the known number of prognostic variables, and any variable which is being modelled. If you wish to model local recurrence after radiotherapy then you will need some fields with the instances of Radiotherapy = Y/N and Local Recurrence = Y/N.

My basic set of required data includes 31 fields and is listed in Table 1.1.

These elements are sufficient to answer many of the major oncological questions, e.g., what is the cure rate of one group of therapies rather than a different group of therapies for a particular disease and disease stage?

Obviously there are many other variables for particular cancers which are also needed, e.g., Gleason score, ER/PR/HER2 status, but these are additional to the above data rather than substitutionary.

1.3 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*".

Unsurprisingly, you can have any number of patterns. Other features can include a reading frame's *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-skills here, not email sending!) or a lot of money to buy one of the commercial offerings that will make the process easy (got $80K+ to 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. Either take courses to get proficient in Python[1]/MatLab[2], or trry to convince your department to spend a lot of money on something that they probably don't understand or think is worthwhile.

1.3.1 Features

The terms "features" in Radiomics refers to the particular statistical methods used to analyse an area of the image defined by an overlying ROI. There are many features that can be calculated. For example, the average of the CT# of the enclosed pixels could be calculated, that would be a 'feature', or its median value. There are many ways to characterise the selected image area using features such as energy, entropy, distribution, kurtosis, volume, sphericity, length of consecutive pixels of similar grey scan,etc, etc, etc.

1.3.2 PyRadiomics

In OnkoDICOM, the extraction of features from image area defined by the ROI *is undertaken by the **PyRadiomics** library. This is an open source Python library and has been widely used and is validated, and produces 100 feature variables. There are of course many more features that can be extracted, but these will wait until there are widely available libraries to use. Other commercially available products like Radiomics Toolbox will produce more (3900) features.

1.4 DICOM Standard

The DICOM standard is the current agreed structure for image configuration to permit interoperability, that is, allow images from one place to be viewed any other place in a viewer configured to this predictable standard.

These files consist of many parts - a lot of metadata and a lot of image data. The image data is all numerical and is converted to grey scale display by the viewing software. The metadata is defined in 'tags' which can be perused in the OnkoDICOM interface. Some of this metadata is easily understood (patient name, patient ID, referrer's name, time of scan, type of scanner), while others are not. Needless to say it all has some purpose.

1.4.1 Viewing DICOM files

OnkoDICOM is based around imaging file sets of all types:

- plain imaging files

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[1] Arguably the most popular computer programming language at present, it is Open Source and has a multitude of libraries of computer functions.

[2] An extremely popular closed-source prototyping software tool freely distributed in academia but costly in the real world.

  - CT
  - MR
  - PT
- paired imaging file sets
  - PT/CT
  - PT/MR
- radiotherapy file sets, a.k.a. **DICOM-RT**, a subset of the DICOM standard. The well formed data set consists of 4-6 file types which are all referenced to each other, and these are:
  - the CT image files
  - one RTSTRUCT file
    These files are either prefixed with '*RT-*' or called '*rtss*'. If it exists, there is **only ONE** such file for each image set. If you find an image set with 2 RTSTRUCT files, either discard the RTSTRUCT files, or copy the image set and separate the RTSTRUCT files. Within this file, the ROI names should be unique.
  - one RTPLAN file
    This file contains the beam parameters for the machine which was to deliver the radiotherapy.
  - one RTDOSE file
    RTDOSE files can represent beams or whole plan dosimetry, make sure that you retrieve RTDOSE files for the whole plan, not individual beams. The RTDOSE file can also hold a calculated DVH.
  - SR files
    Structured Report files are DICOM-compatible files which contain text. In OnkoDICOM, SR files are used to hold PyRadiomics (PyRadiomics-SR) and Clinical Data (ClinicalData-SR).

1.4.2 Business Rules of DICOM-RT function

OnkoDICOM will work with radiotherapy files in multiple ways. Complete or partial DICOM-RT file sets will be opened, although:

1. IF no imaging file set is selected for viewing, other DICOM-RT files cannot be opened
2. IF a RTDOSE file is not included, isodose display and DVH functions will not work
3. IF a RTSTRUCT file is not included, ROI display and PyRadiomics will not work, however an RTSTRUCT can be produced by Create ROI, ISO2ROI or SUV2ROI.
4. The RTPLAN file is not used for anything at present.

1.4.3 Storing Derived Data in DICOM

OnkoDICOM will store additional data in various DICOM compatible sites:

- **DVH parameters** will be calculated and stored in RTDOSE.
  The opportunity to produce this will occur the first time a RTDOSE file is opened in OnkoDICOM. After changes to the ROIs present in the RTSTRUCT file, the DVH can be recalculated using the button in the DVH Tab screen.
- **PyRadiomics output** will be calculated and stored in a DICOM-SR file. This file will be linked to the image set used for the calculation.
- **Clinical Data** will be pulled from a provided spreadsheet (in CSV format) where the patient's ID numbers will be matched to identify the correct row, and stored in a DICOM-SR linked to

the image set open during the import. This process will be described and illustrated later.

1.4.4 Exporting Derived Data from DICOM files

OnkoDICOM can export individual PyRadiomics and DVH data into CSV spreadsheets after calculation. OnkoDICOM can also export aggregated PyRadiomics, DVH and Clinical data from multiple image sets.

2. OnkoDICOM

2.1 Why OnkoDICOM?

In order to undertake Radiomics/Image Analysis research as a radiation oncologist, you need either very high levels of IT ability (you have to be able to 'speak' Python fluently) or have access to a lot of money to buy one of the costly commercial offerings that will make the process easy.

The first ability is rare in a radiation oncologist, and even if you were able, a decade of medical training will severely blunt those abilities. The second circumstance is difficult as funding sources will often not understand image analysis or why you want to do this.

And mixed in with difficulties is the problem of data curation. Here are some of the data realities:

Rubbish Data

It has been said often, *rubbish in, rubbish out*. It's corollary however is rarely stated, *good data in, good analysis out*.

Unfortunately most data mining activities in medicine at present belong in the rubbish category for several reasons.

The extent and quality of routine oncology data is very poor.[1] Even data collected by registry staff and dedicated nurses is consistently 20% in error. This stems from the fact that it takes 10 years to train a willing brain to understand the oncological paradigm in detail so that nuances of oncology knowledge structure (and thus the data) can be understood and fit into an oncologically relevant

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[1] A 2017 report on routine data quality in the local Oncology Information System using an instantaneous data pull revealed that for 12000+ patients with an entered cancer diagnosis, only 18.84% had all 19 basic 'should know' clinical data points were completed. The author was heard to say that this data set is probably 18.8% better than any other data source in his state.
https://pubmed.ncbi.nlm.nih.gov/29968624

storage scheme.

Generally this is achieved by using the out-of-date paradigms that have us filling in spreadsheets, rather than reporting data directly from Information Systems.

Quality Assurance

As for all clinical reports in the literature, oncology imaging and clinical data has to be quality assured. For imaging data that means access to a system with capabilities like the treatment planning system.

Standard Naming

The Regions of Interest (ROI) defining anatomical contours and tumour volumes in imaging files have to be standardised if data is to be supplied collaboratively for research. [2] OnkoDICOM implements a Standardised Naming list which consists of Local Name, and Foundational Model of Anatomy ID number with which is associated definitions and Preferred Name. OnkoDICOM also possesses the ability to change all local names into FMA ID numbers. It also possesses the ability to change FMA ID numbers into local names. This permits data harmonisation across international borders.

Data Quantity

It is now believed that medical data is “Big Data”. This is not true. The majority of medical data storage consists of unstructured, untagged medical imaging. As an illustration, a recent PET/CT scan pair (218 PET & 546 CT images) occupied 293MB of disk storage, while the attached report occupied 16.7kB.

Likewise, a recent Chest CT was found to contain 1003 images and occupy 507MB. So clearly it’s more accurate to say “Big Medical Imaging Data”, not “Big Clinical Data”.

Very few sites will have enough data individually to answer clinical questions with any real degree of certainty. A recent study at our institution into early stage lung cancer comprised 89 patients. It is frequently quoted that to validate each radiomic feature in a study requires 10 patients/feature. The PyRadiomics library produces about 100 features.

It therefore follows that it will not be possible to achieve the required numbers of image sets until individuals and departments start to collect routine clinical data which is highly structured and quality assured, and share it.

Data Burden

Radiotherapy data includes many ROIs which have been created for the purposes of fooling the planning algorithms into doing what the planners want. These ROIs are rarely removed but waste computer time in calculations, and run the risk of generating significant correlations.

OnkoDICOM assists with easy ROI Deletion, either in individual or batch mode.

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[2] The local radiotherapy department undertook an analysis before Standardised Naming was introduced that showed that 75 lung cancer plans possessed 760 discrete ROI names.

Cost

While file curation costs time, it requires software.

You could use the department's TPS but this can be problematic in getting access, getting files in and out, and having restive physicists who don't like TPS being man-handled for other purposes by people they don't trust!

Clinical Questions

The hope of Radiomics, indeed of all efforts based on Machine Learning, is that data in the image might help with decision making in clinical medicine. In order to achieve this reality, clinical questions must be set by oncologists and answered from curated data trusted by the oncologist. The process of data mining and analysis is driven by the clinical question, not vice versa.

At present the enthusiasm for techniques such as Deep Learning hide several difficulties:

- What is actually going on with these statistical techniques? There is disquiet with published data sets being inaccurate. There are instances of systemic inaccuracy being driven by non-representative training samples.
- Media publicity and academic publication do not establish usefulness.
- Machine Learning research is unstable with new and altered algorithms being used.
- 'Clinical' endpoints used available are generally limited and blunt, e.g., death, cancer type.
- You can see nothing, it's all numbers. Doctors are inherently visual people, Radiomics researchers have not discovered how to provide pictures for us.
- the conclusions of the machine learning algorithms are rarely presented in a manner which means anything to a clinician.

And Now?

So now there is OnkoDICOM . . . borne of these frustrations, and tailored to streamline curation and generation of quality image stores. The creation of the software has been overseen by a radiation oncologist with the intention of curating, collating and manipulating ROIs across imaging modalities (from CT/MRI/PT > CT/MRI/PT) and instances (Diagnostic, planning and follow up scans) along with clinical data.

2.2 Overview

OnkoDICOM is a software product that straddles the divide between the radiation oncologist and radiomics data production and use. It has just undergone it's fourth development cycle.

The original basis in 2019 for this software was a well-known, well respected, stable, GitHub-based, open source project called **dicompyler**[3] written in Python that allowed a radiotherapy plan (DICOM-RT) to be opened, inspected and anonymised. The CT could be viewed, resized and re-windowed and could overlay any Regions of Interest (ROI) from the RTSTRUCT file. It could also calculate and then 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 conventional graphing function called the Dose Volume Histogram (DVH). But it did not do enough for modern radiotherapy where data acquisition and image analysis is now an active research area.

OnkoDICOM has matched and exceeded dicompyler's functions by adding functions to support image-based research into routine clinical cases. The viewing of the CT scan has been improved by adding pre-set windowing options for Brain, Head & Neck, Bones and Lung; and also allowing the user to make up new settings locally.

The assessment of the ROIs and isodoses has been greatly enhanced. When loading a set of files that include a RTDOSE and RTSTRUCT file, dose-volume parameters can be calculated and stored back into the RTDOSE file. This can be exported for analysis individually or collectively.

A tool for profiling the CT# (CT numbers) across an image called 'Transect' has been 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) which is more accurate than manual drawing.

OnkoDICOM will also pull data from a spreadsheet file based on common identifiers, so that clinical information regarding diagnosis, staging, treatment and outcomes (your mandatory minimum data set) can be saved with imaging data in DICOM-SR format (ClinicalData-SR). This data can be extracted collectively into spreadsheet files also.

Feature extraction from the imaging data underlying the ROIs is achieved using the PyRadiomics pipeline which produces NRRD & mask files and a large amount of Radiomics data (100 individual items) which are saved in DICOM-SR format (PyRadiomics-SR). The Radiomics, DVH and Clinical Data held with the imaging data forms an independent data repository that can be selected in Batch Processing mode for aggregated data extraction and Machine Learning to address clinical questions and 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, 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

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[3] **Panchal A, R Keyes R** *SU-GG-T-260: dicompyler: An Open Source Radiation Therapy Research Platform with a Plugin Architecture* Med. Phys. 37, 3245, 2010

directory structures to aid later research.

Within OnkoDICOM there are plugins for mapping Standard Names. The included names are all mapped to a Foundational Model of Anatomy (FMA) ID, and the process of updating names can be batched for a single directory containing many patients. Volumes have predefined prefixes (GTV, CTV, PTV, OTV) and permit any suffix decided. This standardisation allows the harmonisation of collected DVH and PyRadiomics data across multiple datasets without further modification. The latest version of ONkoDICOM also permits Standard Names to be translated into FMA ID numbers, and back again. This is useful since the individual user can decide on their own Standard Naming pattern, but allow conversion into a different standard via the FMA ID correlation.

Other functionality includes the transfer of preset isodose levels to ROIs (ISO2ROI; requires only a RTDOSE file), and the transfer of preset SUV values to ROIs (SUV2ROI; only requires patient weight and a PET scan) with automated naming.

The appearance of ROIs and isodoses in the DICOM View window can be configured for variable line & fill appearances.

Other functions permit the manipulations of ROIs by deletion, renaming, & creation, PET/CT overlay, and image fusion.

The completion of the 2022 work cycle in OnkoDICOM has seen the Draw ROI function completely re-written, a Force Linking function, a new start window, patient subgroup selection for batch processing and a function for Machine Learning.

OnkoDICOM has be compiled into executables for Windows and Linux. It can be run as python code using the original GitHub repository also. There are instructions on the website.

2.3 Installing OnkoDICOM

OnkoDICOM is available in two formats from the GitHub website (https://github.com/didymo/OnkoDICOM).

2.3.1 Python Install

This is likely to be the less used option. The install instructions are on the website.

2.3.2 Windows Install

The Windows executable can be sourced from the GitHub release page (https://github.com/didymo/OnkoDICOM/releases). If you are replacing the version, you must manually uninstall the old version before installing the new version.

This is the method that will be used by most users and it works well.

During the installation a new directory (’**OnkoDICOM**’) will be written in your user directory. In this directory will be all of the files referenced by the icons and Add-On Options. These files include:

- **batch_isodoseRoi.csv**
  a spreadsheet file listing the isodose values to be converted to ROIs in the batch processing function ‘ISO2ROI’.
- **imageWindowing.csv**
  a spreadsheet file listing the CT# values used in producing specific window views like ‘Lung’ window, or ’Bone’ window. These values can also be added in Add-On Options.
- **isodoseRoi.csv**
  a spreadsheet file listing the isodose values to be converted to ROIs in the individual curation function ‘ISO2ROI’ accessed from the Isodose panel in the Main DICOM window.
- **organName.csv**
  a spreadsheet file of 4 columns listing the Standardised Names used to name anatomical structures. The columns include the Preferred Name, the FMA_ID, the expanded anatomical name, and the URL for the entry in the Foundational Model of Anatomy Ontology [4]. This spreadsheet is used for checking names, and for the Name2FMAID option in Batch Processing. These values can also be added in Add-On Options.[5]
- **patientHash.csv**
  a spreadsheet of two columns listing the patients anonymised by OnkoDICOM. The first column contains the original patient ID (e.g., Last Name, First Name), and the second contains the new de-identified Patient ID.
  The contents of this file identify patients and it is your responsibility to protect access to this file.
- **volumeName.csv**
  a spreadsheet file of 2 columns listing the Standard Prefixes used to name volume structures. The columns include the Standard Name (e.g., Gross Tumour Volume), and the Standard Prefix to be used. The initial list includes GTV, CTV, ITV, PTV_, OTV, SUV, ISO and LN_, as

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[4] The FMA Portal

[5] When adding new names and using copy/paste functions, it is possible that OnkoDICOM will fail to run with the next start. If this is the case, open the organName.csv file in a text processor and check to see whether one of the new entries has “” characters.

these are my default prefixes. Characters following the prefixes are ignored in checking for compliance. Other values can also be added in Add-On Options.

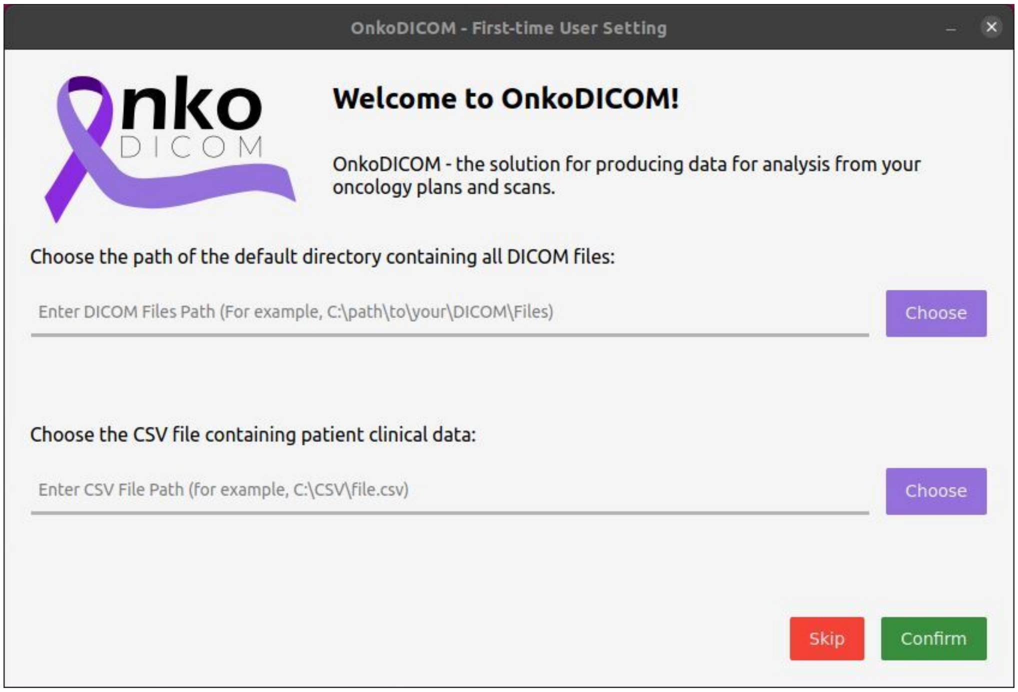
- **imageFusion.json**
  a JSON file that should be manipulated in the Add-On Options screen called Image Fusion – Autoregistration.
- **ICD10_Morphology.csv**
  a spreadsheet listing the ICD10 Morphology (histopathology; adenocarcinoma, squamous cell carcinoma, etc) codes for different tissue types. There is no mechanism to change these values in OnkoDICOM.
- **ICD10_Topography.csv**
  a spreadsheet listing the ICD10 Non-Cancer Topography codes for diseases (infective, degenerative, etc). There is no mechanism to change these values in OnkoDICOM.
- **ICD10_Topography_C.csv**
  a spreadsheet listing the ICD10 Cancer Topography codes for anatomical sites. There is no mechanism to change these values in OnkoDICOM.
- **line&fill_configuration**
  a text file listing the setting for drawing ROI and isodose curves and fills in the main DICOM window. These values should be changed in Add-On Options.

With each update install this directory will not be overwritten. The original files will be updated and are available on the OnkoDICOM GitHub site.

2.4 Splash screen

When you open OnkoDICOM you will be greeted with a splash screen. The first install has a specific screen only seen once. Later openings will display a different screen.

2.5 Open OnkoDICOM the first time



OnkoDICOM - First-time User Setting

Welcome to OnkoDICOM!

OnkoDICOM - the solution for producing data for analysis from your oncology plans and scans.

Choose the path of the default directory containing all DICOM files:

Enter DICOM Files Path (For example, C:\path\to\your\DICOM\Files)

Choose the CSV file containing patient clinical data:

Enter CSV File Path (for example, C:\CSV\file.csv)

This window will only appear on the first launch of OnkoDICOM, and will ask the user to nominate the directory folder containing the image sets.

The CSV file chosen will be used to automatically load and update clinical data for any opened image set whose identifiers match the Patient ID.

If the user wishes to change the default directory later, it can be changed in the **Add-On Options** window.

2.6 Open OnkoDICOM the second time

This is the welcome window that will be presented when you subsequently open OnkoDICOM, which presents you with two options.

From OnkoDICOM2022 onward, you are now able to move from one option to the other without re-starting the program.

Welcome to OnkoDICOM!

OnkoDICOM - the solution for producing data for analysis from your oncology plans and scans.

2.6.1 Individual Patient Curation

This button will allow the opening of a single image set for the purposes of visualisation, curation and manipulation of a single patient's image set.

This is where you can use and learn to understand the functionality. Repetitive manipulation is supported in the second option.

2.6.2 Batch Processing

Batch Processing of a whole directory will ease data cleaning and harmonisation, and data export of ROIs, Naming, and derived data.

This functionality will be described later.

3. Suggestions for Use of OnkoDICOM

3.1 Initial Curation of DICOM-RT files

At the start there is a learning curve discovering what is actually in your DICOM-RT files, and discovering whether you are actually able to access other DICOM-RT, diagnostic and follow up scans necessary.

OnkoDICOM use revolves around a directory structure rather than a PACS system and files are manually downloaded and organised by the user.

3.2 Curation and Quality Assurance of DICOM-RT files

My DICOM-RT files are over-populated with RT/planner/dosimetrist generated volumes that have not been removed. Naming is non-standardised, highly variable and often erroneous. In the same way that retrospective data has to be ‘cleaned’, so these variations have to be harmonised. Until you have explored many individual DICOM-RTs to understand the consistent patterns, you shouldn’t do Batch Processing on ROI Names.

Start by obtaining some DICOM-RT files that consist of CT, RTSTRUCT, RTPLAN and RTDOSE from your physicist. If there are multiple plans available decide which is most applicable, probably the last plan before the date of treatment start.

Learn how to harmonise the names. OnkoDICOM uses a paradigm where the name that you use consistently must match a FMA_ID number. It doesn’t matter that we may call it a ‘left eye’, but others may call it ‘eye left’, ‘Eye_L’, L_Eye’, ’globe’, ‘GLOBE’ or even ’eyeball’, so long as you are consistent with your name and it is linked to **FMA_ID 12515**[1]. OnkoDICOM has a function to

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[1] Search FMA anatomical names here - https://bioportal.bioontology.org/ontologies/FMA/?p=classes&conceptid=root

interchange your names into FMA_ID when you want to collaborate, and to change FMA_ID back into your names in a shared file. Hence my names can be turned into your names throught the link of FMA_ID numbers. In this way the data is interoperable.

3.3 Anonymity of Patient Files

Plan how you will deal with your image repository. The hospital servers are an excellent place as the directory will become very large very quickly. One DICOM-RT can be 120-150MB. Many commercial CTs and MRIs will be substantially larger as they will provide many coronal and sagittal reconstruction image sets, personally I just keep the axial scans of narrow thickness only. While your scans stay on the hospital servers, you are protected by hospital security. Patient confidentiality is greatly at risk if you do not anonymise your patients' files when uploading them to repositories outside of your servers, even on portable laptops.

> **It is your professional and ethical responsibility to maintain patient confidentiality when using OnkoDICOM, OnkoDICOM will not do it for you.**

3.4 How much Data is Enough?

The image sets you will need will be determined by your research questions. If you wish to correlate something from pre-diagnostic imaging to treatment (e.g., when did the site of the GTVp start to change its PyRadiomic signal?), or something post-treatment with treatment (see pneumonitis question below), then you are going to need more image sets. The Patient IDs in all the image sets must be identical if you are to undertake the research. With the advent of the subgroup selection function in Batch Processing, it now makes sense to arrange the repositories according to the clinical phase of discovery, rather than by patient.

Give thought based on whether you will want to include multiple image sets whether before or after radiotherapy. Up to 2002, OnkoDICOM can anonymise any image set it can open, but at present each file will end up with a very different Patient ID. To harmonise multiple image sets, I use Dicompyler for DICOM-RT & CT, and Aliza for other image sets. I use a Hash ID derived from patient data in the Oncology Information System (MOSAIQ).

3.5 Research Questions

The field of Radiomics can only achieve significance in Oncology if important clinical questions are answered. Clinical questions are asked by oncologists, not data miners. Oncologists already know that clinical data for investigation must be pristine, and so quality assurance of the data substrate which is engineered for the clinical investigation is required. OnkoDICOM can support your image based research questions by allowing you to produce new ROIs and output data for analysis.

For example if you wish to investigate the imaging differences between the radiotherapy and immunotherapy causes of pneumonitis, you are likely to have a DICOM-RT with the radiation plan, and at least one follow up CT scans with changes of pneumonitis. OnkoDICOM can produce the following:

1. Using the DICOM-RT, produce DVH data for the plan
2. Using the DICOM-RT, employ **ISO2ROI** to render a number of isodose lines in ROIs (e.g., ISO2000) on the DICOM-RT
3. Using the Follow Up scan, employ **CreateROI** to define all of the pneumonitis in any arrangement you desire (all in Lung_R, all in Lung_L). This can be done by contouring all of the pneumonitis changes and then employing **ManipulateROI** to select out the pneumonitis overlapping either lung.
4. Using Image Fusion, employ **TransferROI** to copy ISO2000 from the DICOM-RT to the Follow Up scan.
5. Using the follow Up scan with the transferred ISO2000, employ **ManipulateROI** to further subdivide the pneumonitis into those inside ISO2000 and those outside.
6. Use **PyRadiomics** to calculate the features of these newly defined ROIs.

If you have a large number of pneumonitis image files in one directory, the batch processing allows you:

- to calculate all the DVH graphs for all DICOM-RT in the directory and export them all to one spreadsheet file.
- to perform ISO2ROI on the whole directory
- perform PyRadiomics on all image sets with CT and RTSTRUCT files produce a PyRadiomics-SR file, and export all PyRadiomics data from the SR file to a spreadsheet file.

3.6 Here's what my data looks like!

This section will reveal to you why OnkoDICOM exists. Clinical data requires curation. This short pictorial essay to show what I start with. The pictures relate to just 6 H&N plans.

3.6.1 ROI Names

Here are the five (yes, FIVE) screens worth of ROI names from the 6 patients. Those that match the Standardised Names are not displayed, those requiring only a case change are auto-selected for checking. All others have to be deleted, modified or ignored.

Select directory to perform batch processing on:

/mnt/hgfs/MILLER-53714352/Desktop/ImmuNA.OnkoDICOM

6 patients found.

ROI Name	Option	New Name	Dataset Location
LASER	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
MARKS ON CAST	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
MQ	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
PTV5600	Ignore	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
PTV7000	Ignore	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
SPINALCORD	Modify	SpinalCord	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
BRAINSTEM	Modify	Brainstem	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
EYE_L	Modify	Eye_L	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
LENS_L	Modify	Lens_L	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
EYE_R	Modify	Eye_R	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
LENS_R	Modify	Lens_R	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
OPTICN_R	Modify	OpticNerve_R	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
CHIASM	Modify	Chiasm	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
MANDIBLE	Modify	Mandible	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
PAROTID_L	Modify	Parotid_L	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
PAROTID_R	Modify	Parotid_R	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
COCHLEA_L	Modify	Cochlea_L	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
COCHLEA_R	Modify	Cochlea_R	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
GLOTTIS	Modify	Glottis	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
CONSTRICTORS	Modify	Constrictors	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
OPTICN_L	Modify	OpticNerve_L	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
OESOPHAGUS	Modify	Oesophagus	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
BRAIN	Modify	Brain	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
tissue artefact	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
external	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
external-5mm	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
sptv7000	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm

Batch Processing will be performed on datasets in the selected directory.

Select directory to perform batch processing on:

/mnt/hgfs/MILLER-53714352/Desktop/ImmuNA.OnkoDICOM

6 patients found.

ROI Name	Option	New Name	Dataset Location
sptv5600	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
ring7000	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
ring5600	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
shoulder avoid	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
ml avoid	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
post avoid	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
avoid	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
cold	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
hot	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
external exp 1	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
external - 1	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
6650 (Trial_2)	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
5320 (Trial_2)	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
4500 (Trial_2)	Delete	FMA_website	/3B59A662EBE93D5E9032983392F5299E/rtss.dcm
External	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
bridge	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
External-5mm	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
AirTissue	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
Maxilla	Ignore	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
LN_HN_2a2b34_R	Ignore	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
LN_HN_1b2a2b345_rp_p_L	Ignore	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
LN_HN	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
PTV_6000	Ignore	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
PTV_7000	Ignore	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
SPTV_7000	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
SPTV_6000	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
shoulder_avoid	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm

Batch Processing will be performed on datasets in the selected directory.

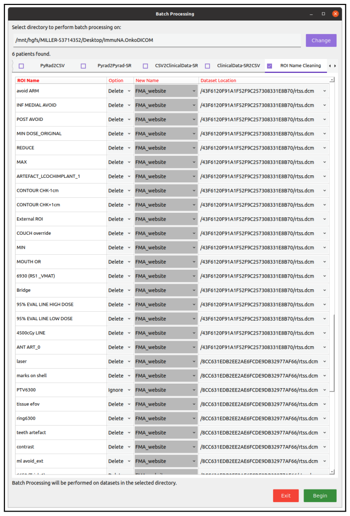
Select directory to perform batch processing on:

/mnt/hgfs/MILLER-53714352/Desktop/ImmuNA.OnkoDICOM

6 patients found.

ROI Name	Option	New Name	Dataset Location
ml	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
ParotidPRV	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
max dose	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
external+1	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
external-1	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
4500 (Trial_1)	Delete	FMA_website	/3B5F25F294EAADFAE66EF94FDD05F67A/rtss.dcm
STRAIGHTENING TATTOO	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
CouchCentre	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
VESSELS	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
PTV_56	Modify	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
Lowest node level	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
neck node excision bed	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
PTV_66	Ignore	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
MUCOSA	Modify	Mucosa	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
MID-LINE STRUCTURES	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
SUBMANDIBULAR_R	Modify	Submand_R	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
COCHLEAR_L	Modify	Cochlea_L	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
lungs	Modify	Lungs	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
SPINAL CANAL	Modify	SpinalCanal	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
BS	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
body	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
skin-0.5CM	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
SPTV6600	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
SPTV5600	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
RING6600	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
RING5600	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
MIDLINE_AVOID	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm

Batch Processing will be performed on datasets in the selected directory.



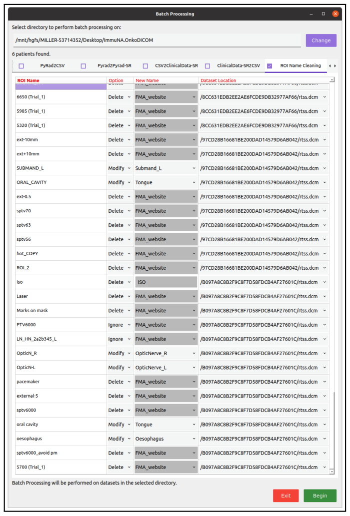
Select directory to perform batch processing on:

/mnt/hgfs/MILLER-53714352/Desktop/ImmuNA.OnkoDICOM

6 patients found.

ROI Name	Option	New Name	Dataset Location
avoid ARM	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
INF MEDIAL AVOID	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
POST AVOID	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
MIN DOSE_ORIGINAL	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
REDUCE	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
MAX	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
ARTEFACT_LCOCHIMPLANT_1	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
CONTOUR CHK-1cm	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
CONTOUR CHK+1cm	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
External ROI	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
COUCH override	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
MIN	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
MOUTH OR	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
6930 (RS1 _VMAT)	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
Bridge	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
95% EVAL LINE HIGH DOSE	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
95% EVAL LINE LOW DOSE	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
4500cGy LINE	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
ANT ART_0	Delete	FMA_website	/43F6120F91A1F52F9C257308331E8B70/rtss.dcm
laser	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
marks on shell	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
PTV6300	Ignore	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
tissue efov	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
ring6300	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
teeth artefact	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
contrast	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
ml avoid_ext	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm

Batch Processing will be performed on datasets in the selected directory.



Select directory to perform batch processing on:

/mnt/hgfs/MILLER-53714352/Desktop/ImmuNA.OnkoDICOM

6 patients found.

ROI Name	Option	New Name	Dataset Location
6650 (Trial_1)	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
5985 (Trial_1)	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
5320 (Trial_1)	Delete	FMA_website	/8CC631EDB2EE2AE6FCDE9DB32977AF66/rtss.dcm
ext-10mm	Delete	FMA_website	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
ext+10mm	Delete	FMA_website	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
SUBMAND_L	Modify	Submand_L	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
ORAL_CAVITY	Modify	Tongue	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
ext-0.5	Delete	FMA_website	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
sptv70	Delete	FMA_website	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
sptv63	Delete	FMA_website	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
sptv56	Delete	FMA_website	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
hot_COPY	Delete	FMA_website	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
ROI_2	Delete	FMA_website	/97CD28B16681BE200DAD14579D6AB042/rtss.dcm
Iso	Delete	ISO	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
Laser	Delete	FMA_website	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
Marks on mask	Delete	FMA_website	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
PTV6000	Ignore	FMA_website	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
LN_HN_2a2b345_L	Ignore	FMA_website	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
OpticN_R	Modify	OpticNerve_R	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
OpticN-L	Modify	OpticNerve_L	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
pacemaker	Delete	FMA_website	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
external-5	Delete	FMA_website	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
sptv6000	Delete	FMA_website	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
oral cavity	Modify	Tongue	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
oesophagus	Modify	Oesophagus	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
sptv6000_avoid pm	Delete	FMA_website	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm
5700 (Trial_1)	Delete	FMA_website	/B097A8C8B2F9C8F7D58FDCB4AF27601C/rtss.dcm

Batch Processing will be performed on datasets in the selected directory.

3.7 Manage Frustration

OnkoDICOM will not do everything that you desire, it is software that undergoes development once a year according to the number of University of Wollongong Computer Science students who elect to be involved in the project. The current state of the software is the result of 8 excellent motivated teams working over four years. To date, all Computer Science students in the teams have gained High Distinctions for their work, and when seeking employment all have used the project as evidence of their proficiency in software development.

The project is developed in Python, and collaboration is invited. The project owners invite feedback, though users should understand that OnkoDICOM2023 will be released around October 2023, and so any real dysfunction and perceived lack of functionality will remain at least until then.

4. “Individual” OnkoDICOM

4.1 Why?

In the initial learning phase, it is important to start curating DICOM-RT image sets using the individual functions. There are patterns of use peculiar to individual departments which must be perceived before they can be altered as a batch. Individual use of the components will also give insight into how ROIs and other data might be used and combined to answer clinical questions.

4.2 Splash screen

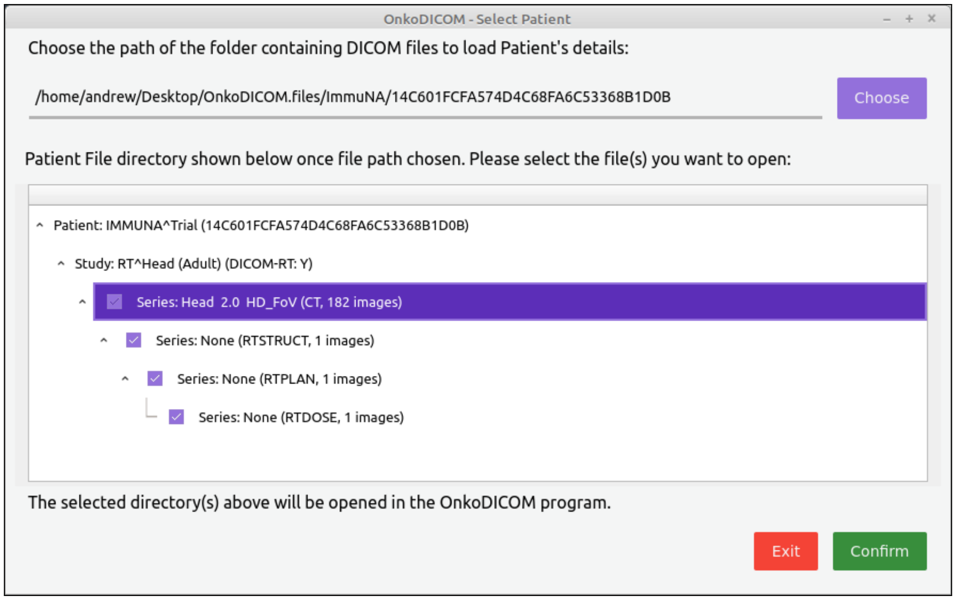
When you open OnkoDICOM you will be greeted with a splash screen.

Welcome to OnkoDICOM!

OnkoDICOM - the solution for producing data for analysis from your oncology plans and scans.

4.3 Select Patient Window

After selecting the individual patient option, the patient selection screen will appear displaying the contents of the default directory listed according to their DICOM tag/UID links, rather than according to the directory groupings.



Choose the path of the folder containing DICOM files to load Patient's details:

/home/andrew/Desktop/OnkoDICOM.files/ImmuNA/14C601FCFA574D4C68FA6C53368B1D0B

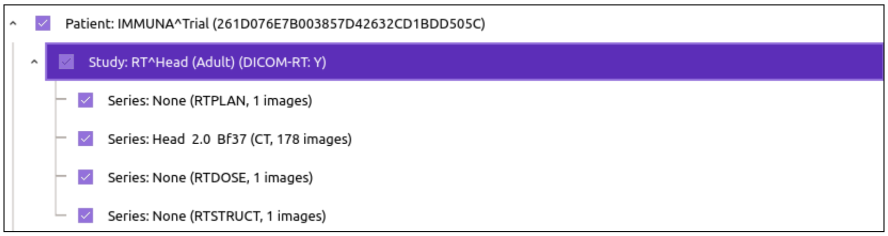
Patient File directory shown below once file path chosen. Please select the file(s) you want to open:

- Patient: IMMUNA^Trial (14C601FCFA574D4C68FA6C53368B1D0B)
  - Study: RT^Head (Adult) (DICOM-RT: Y)
    - ☑ Series: Head 2.0 HD_FoV (CT, 182 images)
      - ☑ Series: None (RTSTRUCT, 1 images)
        - ☑ Series: None (RTPLAN, 1 images)
          - ☑ Series: None (RTDOSE, 1 images)

The selected directory(s) above will be opened in the OnkoDICOM program.

This process will take more time with larger directories. Once the files structure has been loaded, you will find that if you return the data will display unchanged. However if you remove or add files into the directory, the file data will be out of date.

To select a patient or set of files, the specific boxes must be ticked. You cannot open files from different patients at the same time. The selected line has a purple background.



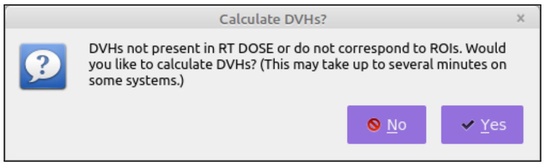
- ☑ Patient: IMMUNA^Trial (261D076E7B003857D42632CD1BDD505C)
  - ☑ Study: RT^Head (Adult) (DICOM-RT: Y)
    - ☑ Series: None (RTPLAN, 1 images)
    - ☑ Series: Head 2.0 Bf37 (CT, 178 images)
    - ☑ Series: None (RTDOSE, 1 images)
    - ☑ Series: None (RTSTRUCT, 1 images)

Here the top DICOM study for the patient has been selected. If a collection of DICOM studies are available and wish to be considered together (e.g., fused, or ROIs interchanged), care must be taken to use the same identifiers on all image sets.

OnkoDICOM has a pseudo-anonymising function (“Anon“) but this will not produce the same identifiers for multiple studies. At the moment, CT & MRI can be anonymised by dicompyler[1] or Aliza[2], and PET can be anonymised by Aliza.

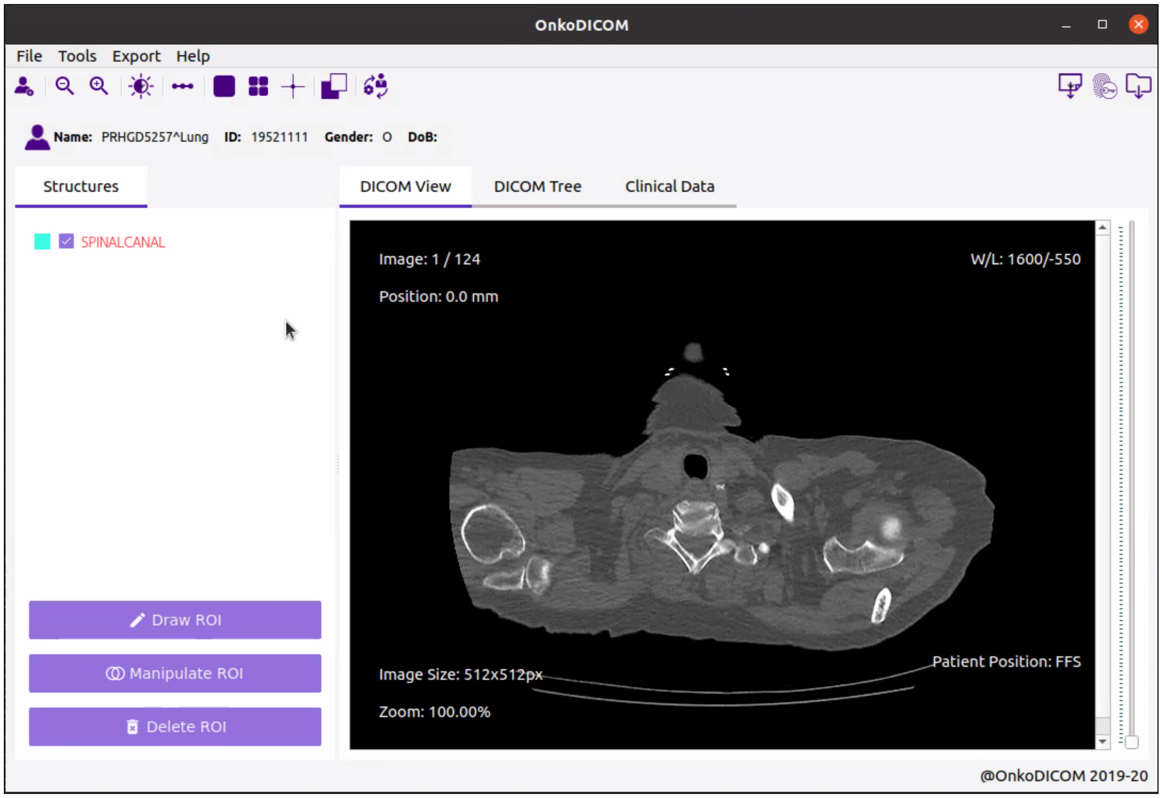
4.4 Main Screen

If the selected image set includes an RTDOSE and RTSTRUCT, you will have the opportunity to calculate DVHs. If the file is being opened for the first time, it is advisable to NOT calculate the DVH as there may be many non-clinical ROIs present in the RTSTRUCT file. It is better to clean the ROI list and then calculate the DVHs.



DVHs not present in RT DOSE or do not correspond to ROIs. Would you like to calculate DVHs? (This may take up to several minutes on some systems.)

After answering the DVH question, the OnkoDICOM Main Screen will appear. All individual functions are accessed from this screen.



Name: PRHGD5257^Lung ID: 19521111 Gender: O DoB:

Image: 1 / 124
Position: 0.0 mm
W/L: 1600/-550
Image Size: 512x512px
Zoom: 100.00%
Patient Position: FFS

The layout consists of several rows across the top with a drop down menu strip, a strip of purple icons, a strip containing the patient’s identifiers, and then two vertical tabbed areas.

---

[1] https://www.dicompyler.com/

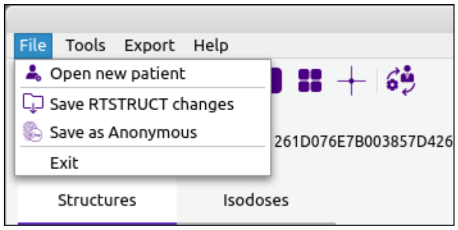
[2] A capable and cheap DICOM viewer - https://www.aliza-dicom-viewer.com/

The left hand vertical area contains information and functions relating to Structures or Regions of Interest (ROIs) pulled from RTSTRUCT, and Isodoses pulled from RTDOSE.

The right hand vertical area contains 6 tabs for the DICOM View of individual image set (either CT, MR or PT), the Dose-Volume Histogram (DVH) view, the DICOM Tree, Clinical Data, Image Fusion and PET-CT viewer. These will be explained in detail below.

4.5 Main Screen - Drop-down Menu Strip

File



The File item has 4 choices:

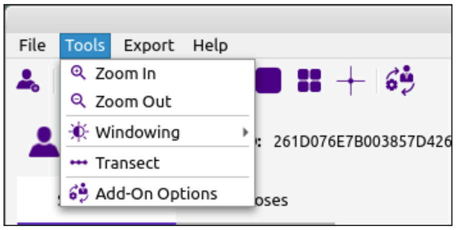
Open New Patient
When the curation of the current image set is complete, and you wish to open another image set.
This menu choice has an identical function with the first icon on the next Icon line.

Save RTSTRUCT changes
After you have made manual changes to ROIs, either by renaming, deleting or creating ROIs, you will be asked to confirm these actions and finally need to save the updates.
If you try to open a New Patient and have unsaved RTSTRUCT changes, you will be asked to confirm saving or losing of the RTSTRUCT changes.

Save as Anonymous
If you wish to de-identify the image set, the ANON process will change the patient identifiers in all of the files , and ask if you wish to undertake PyRadiomics after the identity change. If you have run PyRadiomics before de-identification, you so not need to run it again.
The ANON process will also write the old and new identifiers into a CSV file which is displayed in Add On Options under the **Patient ID - Hash ID** tab

Exit
This choice will close OnkoDICOM.

Tools



The Tools item has 5 choices:

Zoom Out
This menu choice will decrease the size of the image.
This menu choice has an identical function with the second icon on the next Icon line (magnifying glass -).

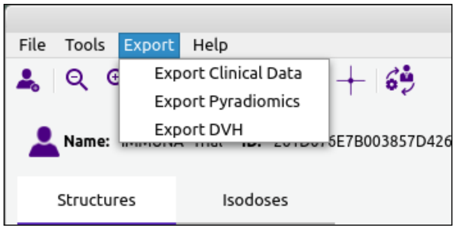
Zoom In
This menu choice will increase the size of the image.
This menu choice has an identical function with the third icon on the next Icon line (magnifying glass +).

Windowing
This menu choice will change the image setting - Lung, Soft Tissue, Bone, or Brain settings.
This menu choice has an identical function with the fourth icon on the next Icon line. New Windowing settings can be added using the **Image Windowing** tab in Add On Options

Transect
This menu choice allows a line to be drawn across the image display, and produces a graph showing the CT# traversed by the line.
This menu choice has an identical function with the fifth icon on the next Icon line.

Add On Options
This menu choice will open a screen with multiple tabs which will allow you to set multiple preferences for OnkoDICOM.
This menu choice has an identical function with the last icon on the next Icon line.

Export



The Export item has 2 choices:

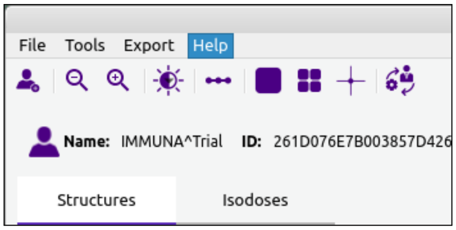
Export PyRadiomics

This menu item engages the PyRadiomics pipeline that produces the 132 features of all of the ROIs present inside the RTSTRUCT file. Once started the process cannot be aborted without closing the program. The results will be saved into a DICOM-compatible Structured Report in the directory holding the image set.

Export DVH

This menu item produces DVH data from the RTDOSE and RTSTRUCT files in the image set. Computed DVH data is saved inside the RTDOSE file.
When an image set containing a RTDOSE/RTSTRUCT pair is opened and there is no stored DVH data, the DVH will be calculated and stored.

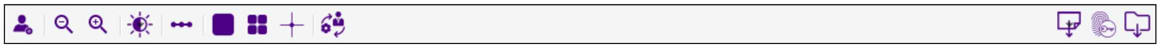
Help



Help

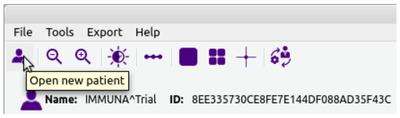
This menu item will open a web browser and load the OnkoDICOM website where you will find this document.

4.6 Main Screen - Purple Icon Strip



The Icon strip contains 11 icons on the left and 3 on the right. The icons from the left are:

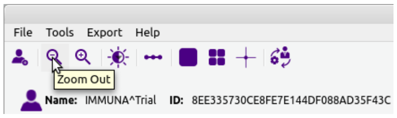
4.6.1 Open New Patient



Name: IMMUNA^Trial ID: 8EE335730CE8FE7E144DF088AD35F43C

When the curation of the current image set is complete, and you wish to open another image set.

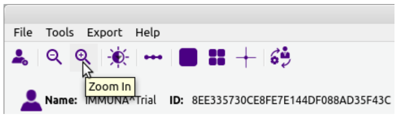
4.6.2 Zoom Out



Name: IMMUNA^Trial ID: 8EE335730CE8FE7E144DF088AD35F43C

This menu choice will decrease the size of the image.

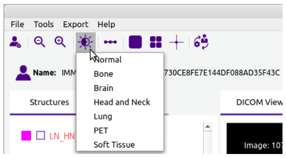
4.6.3 Zoom In



Name: IMMUNA^Trial ID: 8EE335730CE8FE7E144DF088AD35F43C

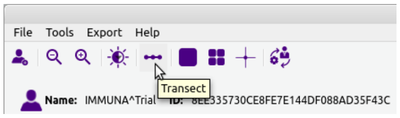
This menu choice will increase the size of the image.

4.6.4 Windowing



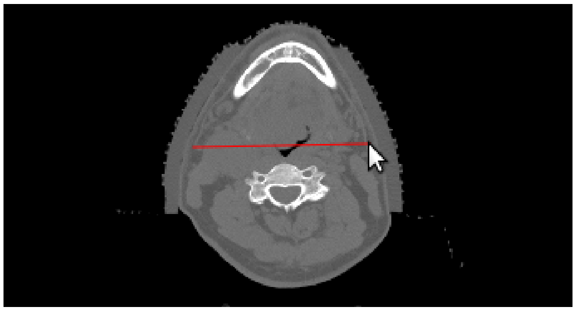
This menu choice will change the image setting - Lung, Soft Tissue, Bone, or Brain settings.

4.6.5 Transect

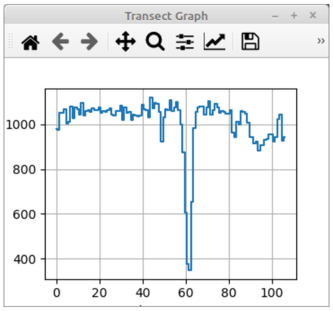


Name: IMMUNA^Trial **ID:** 8EE335730CE8FE7E144DF088AD35F43C

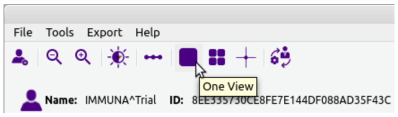
This menu choice allows a line to be drawn across the image display, and produces a graph showing the CT# traversed by the line.



>>>



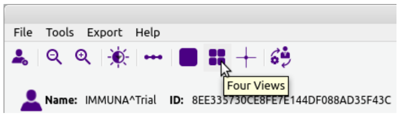
4.6.6 Single Window DICOM View



Name: IMMUNA^Trial **ID:** 8EE335730CE8FE7E144DF088AD35F43C

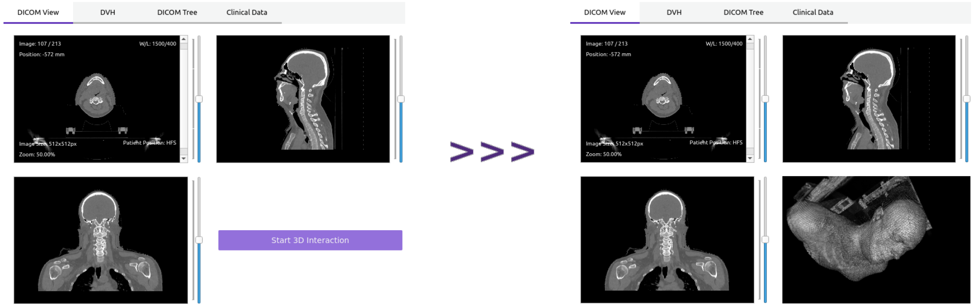
This is the default view of any DICOM images opened in OnkoDICOM, whether CT, MR or PT.

4.6.7 Four window DICOM View

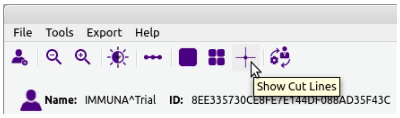


Name: IMMUNA^Trial **ID:** 8EE335730CE8FE7E144DF088AD35F43C

This is an optional view of any DICOM images opened in OnkoDICOM, whether CT, MR or PT. A 3D view can be activated in the fourth window if desired.

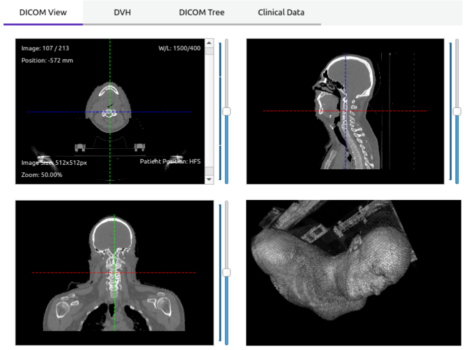


4.6.8 Show Cut Lines (Cross hairs in Four Window DICOM View)

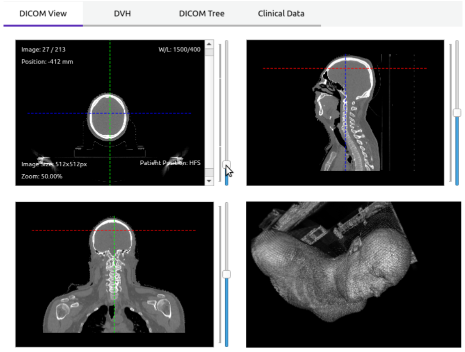


Name: IMMUNA^Trial **ID:** 8EE335730CE8FE7E144DF088AD35F43C

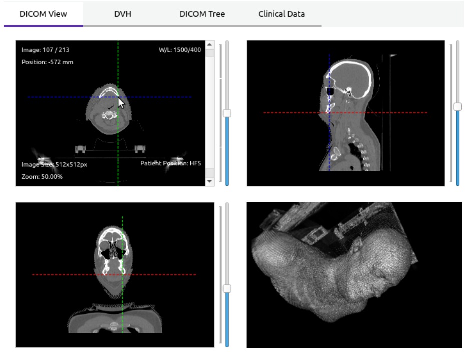
The cross hairs in the 3 windows show the position of the displayed image



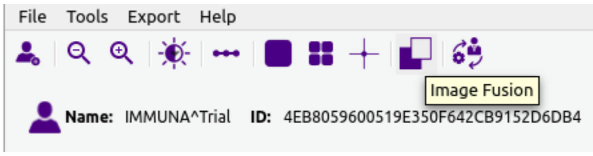
The sliders to the right will move the image and the cross hairs on the other views.



Clicking the mouse inside the image will move the three views to that position.



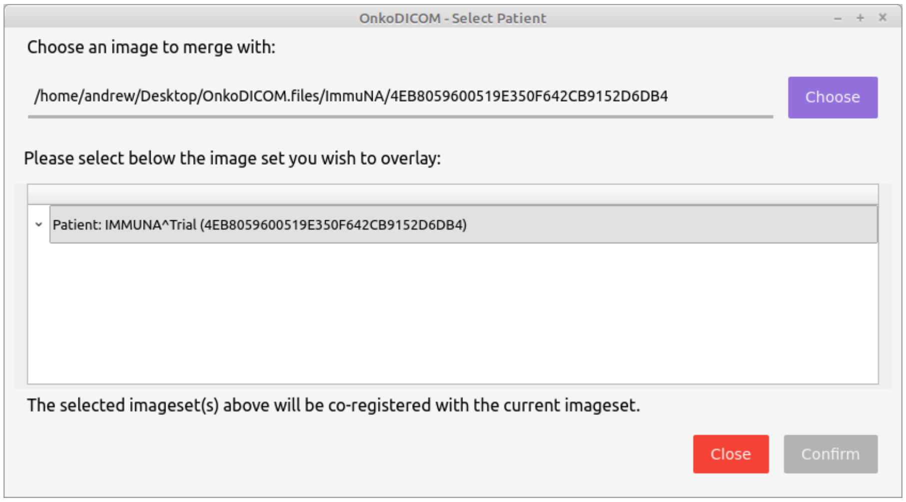
4.6.9 Image Fusion



Name: IMMUNA^Trial **ID:** 4EB8059600519E350F642CB9152D6DB4

Image Fusion can be undertaken as either a manual or an automated process.

Pressing the image fusion button activates a process which uses the loaded image set as the base for the fusion. A second patient selection window will open. Only non-identical image sets with the same identifiers can be loaded for fusion.



Choose an image to merge with:

/home/andrew/Desktop/OnkoDICOM.files/ImmuNA/4EB8059600519E350F642CB9152D6DB4

Please select below the image set you wish to overlay:

Patient: IMMUNA^Trial (4EB8059600519E350F642CB9152D6DB4)

The selected imageset(s) above will be co-registered with the current imageset.

AutoFusion

The auto-fusion process will run and then switch to a 3-window view and display the results. One scan will project in green, the second in purple. Areas of matching contrast, i.e., bone over bone, lung over lung will appear as grey scale.

In the fourth window is a button allowing transfer of ROIs between the two scans. All or selected ROIs can be transferred. If an identically named ROI is present on both scans, a suffix will be added to the imported ROI.

The ROIs are selected for transfer by double click on individual ROIs or by using the arrow button for all ROIs.

Manual Fusion

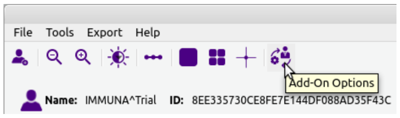
Once the *Base* and *Overlay* image sets have been loaded, they are displayed in a 3-axis view like AutoFusion, in a new tab along with the additional manual controls.

- There is an option called **Overlay Colours** to change the Base/Overlay fusion colour pairing from Purple/Green, to Blue/Yellow, or Red/Cyan as desired.
- The three buttons under the colour selection are for ***fine control***.
    - The first **crossroads button** parallels the adjustment for Translate and is achieved by clicking on the part of the screen towards which the *overlay* image should move.
    - The second **rotary button** parallels the adjustment for Rotate, but is a little more difficult to use.
    - The **window button** provide an area in the fusion which only shows the base image to check parts of the image for confluence.
- The slider controls under **Translate** provide L/R, P/A and I/S adjustment.
- The slider controls under **Rotate** provide Pitch, Yaw and Roll adjustment.
- **Opacity** can also be adjusted by moving the slide to make the *base* or the *overlay* more transparent as needed.
- The remaining four buttons allow for:
    - resetting a fusion back to the starting overlay,
    - saving the DICOM Transform object back into the directory of the *overlay* image set,
    - loading of the DICOM Transform object from the *overlay* image's directory to re-enact a previous fusion, and
    - visualisation of the Transform object current parameters.

In the fourth window is a button allowing transfer of ROIs between the two scans. All or selected ROIs can be transferred. If an identically named ROI is present on both scans, a suffix will be added to the imported ROI.

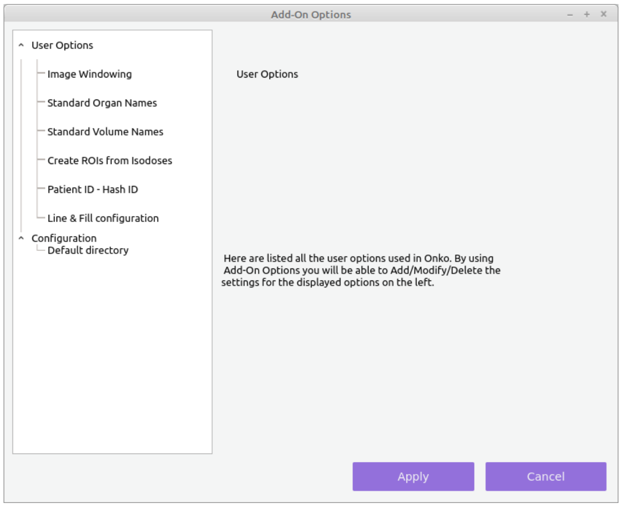
The ROIs are selected for transfer by double click on individual ROIs or by using the arrow button for all ROIs.

4.6.10 Add-On Options



Name: IMMUNA^Trial **ID:** 8EE335730CE8FE7E144DF088AD35F43C

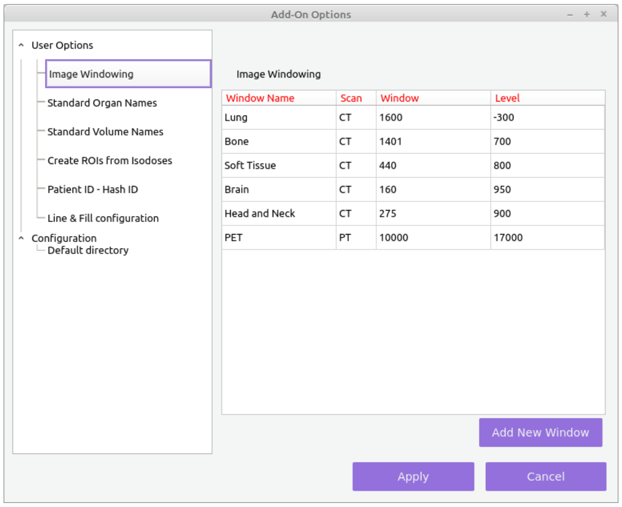
This menu choice will open a screen with multiple tabs which will allow you to set multiple preferences for OnkoDICOM.



Here are listed all the user options used in Onko. By using Add-On Options you will be able to Add/Modify/Delete the settings for the displayed options on the left.

Image Windowing

The Image Windowing tab allows the user to add additional settings to view different image types and tissues.



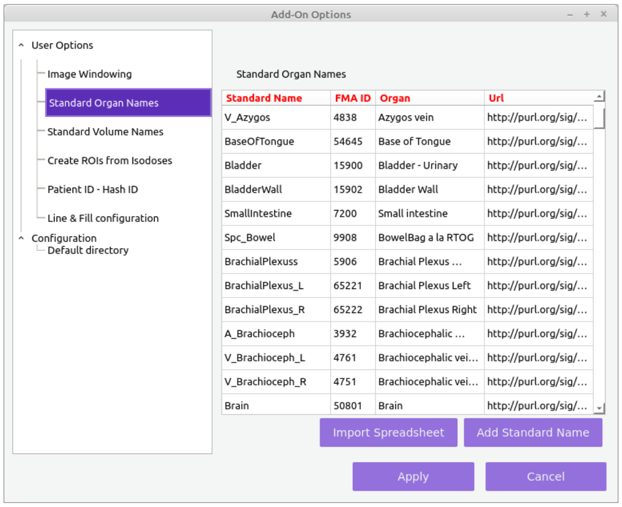
Window Name	Scan	Window	Level
Lung	CT	1600	-300
Bone	CT	1401	700
Soft Tissue	CT	440	800
Brain	CT	160	950
Head and Neck	CT	275	900
PET	PT	10000	17000

Standard Organ Names

The use of Standardised Naming is a fundamental requirement to allow collaboration between different individuals and groups in research. This is particularly important in Radiomics research where the definitions of various names should be explicit and correct and inter-operable. The current most appropriate method is to use the Foundational Model of Anatomy which assigns an ID to each anatomical entity. This module contains a listing of applicable codes correlated with FMA IDs and the web page that defines the entity.

It is incumbent on the user to ensure that changes to the Standard Names are anatomically consistent with reality.

In future editions, OnkoDICOM will possess a function to interchange Standard Name with FMA ID.

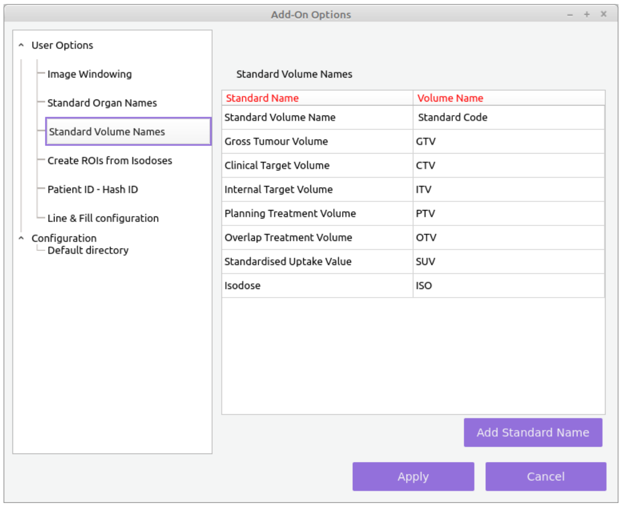


Standard Name	FMA ID	Organ	Url
V_Azygos	4838	Azygos vein	http://purl.org/sig/...
BaseOfTongue	54645	Base of Tongue	http://purl.org/sig/...
Bladder	15900	Bladder - Urinary	http://purl.org/sig/...
BladderWall	15902	Bladder Wall	http://purl.org/sig/...
SmallIntestine	7200	Small intestine	http://purl.org/sig/...
Spc_Bowel	9908	BowelBag a la RTOG	http://purl.org/sig/...
BrachialPlexuss	5906	Brachial Plexus ...	http://purl.org/sig/...
BrachialPlexus_L	65221	Brachial Plexus Left	http://purl.org/sig/...
BrachialPlexus_R	65222	Brachial Plexus Right	http://purl.org/sig/...
A_Brachioceph	3932	Brachiocephalic ...	http://purl.org/sig/...
V_Brachioceph_L	4761	Brachiocephalic vei...	http://purl.org/sig/...
V_Brachioceph_R	4751	Brachiocephalic vei...	http://purl.org/sig/...
Brain	50801	Brain	http://purl.org/sig/...

Standard Volume Names

The use of Standard Prefixes is peculiar to Radiation Oncology. This list covers the accepted prefixes in use in the definitions of volumes - GTV, CTV, ITV and PTV.
The standard prefixes for ROIs autogenerated from isodoses (ISO) and PT scans (SUV) are also included.

The prefix OTR covers “Overlap Target Volume” defining overlaps between PTV and OAR/PRV where dose may be ameliorated.



Standard Volume Names

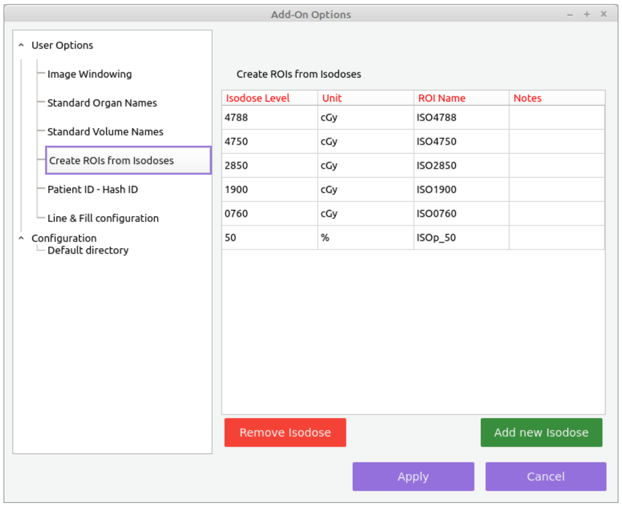
Standard Name	Volume Name
Standard Volume Name	Standard Code
Gross Tumour Volume	GTV
Clinical Target Volume	CTV
Internal Target Volume	ITV
Planning Treatment Volume	PTV
Overlap Treatment Volume	OTV
Standardised Uptake Value	SUV
Isodose	ISO

Create ROIs from Isodoses

The Create ROIs from Isodoses is new functionality activated by a button in the lower part of the Isodoses window. When used it will produce ROIs from the isodoses present in the configured list.

The isodose levels can be set as absolute isodoses (6000cGy »ISO6000) or as a percentage of the prescribed dose (50% isodose »ISOp_0).

The list can be increased or reduced as desired.



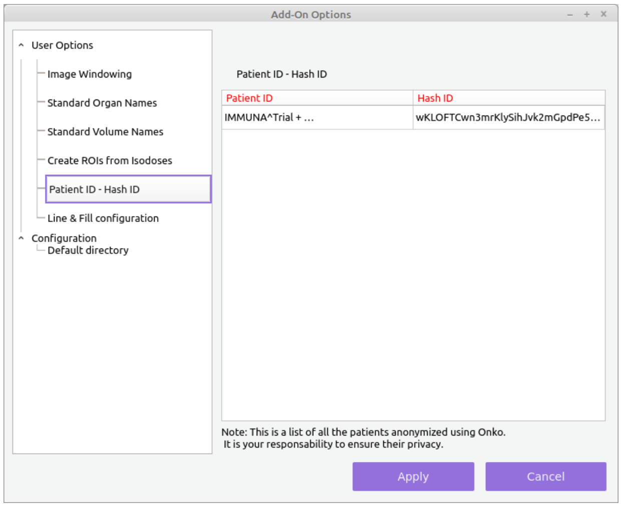
Create ROIs from Isodoses

Isodose Level	Unit	ROI Name	Notes
4788	cGy	ISO4788	
4750	cGy	ISO4750	
2850	cGy	ISO2850	
1900	cGy	ISO1900	
0760	cGy	ISO0760	
50	%	ISOp_50	

Patient ID - Hash ID

The Patient ID - Hash ID was described previously. When the ANON function is used a new directory is produced with a Hash ID that relates to the image set but has no identifiers of the original patient left in the DICOM tags. The old and new identifiers are written into a spreadsheet that can be saved elsewhere.

The contents of this file identifies patients, if it is use, you have the responsibility to ensure the security of this file.

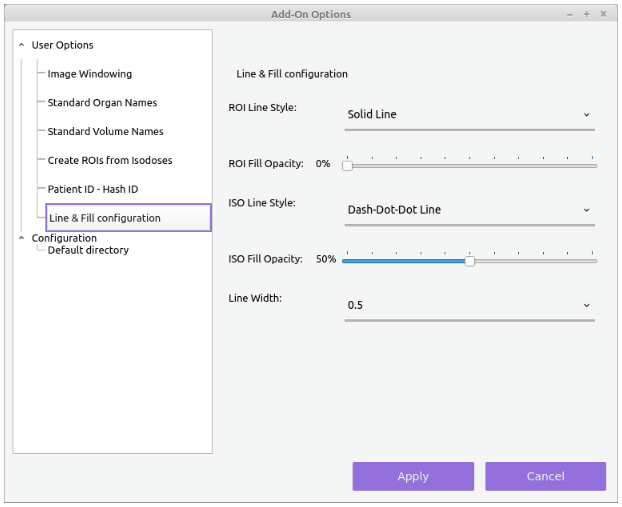


Patient ID	Hash ID
IMMUNA^Trial + ...	wKLOFTCwn3mrKlySihJvk2mGpdPe5...

Note: This is a list of all the patients anonymized using Onko.
It is your responsability to ensure their privacy.

Line & Fill Configuration

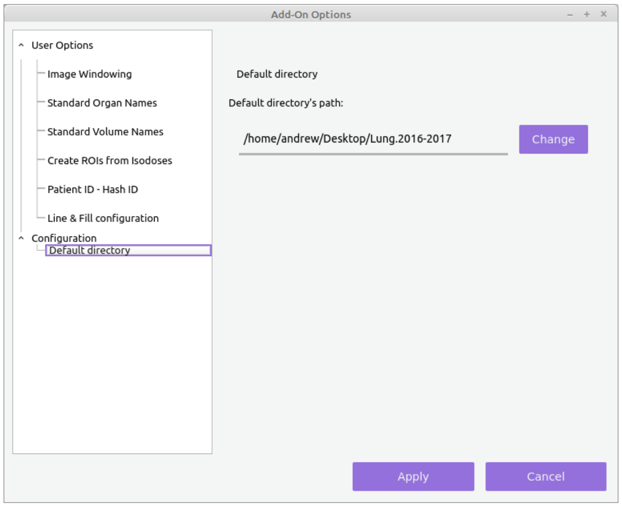
The Line & Fill Configuration allows the user to alter the appearance of the ROI and isodose overlays in the main DICOM View windows.



ROI Line Style: Solid Line
ROI Fill Opacity: 0%
ISO Line Style: Dash-Dot-Dot Line
ISO Fill Opacity: 50%
Line Width: 0.5

Default Directory

The Default Directory will always have an entry as it is set with the first start of OnkoDICOM. A different default directory can be set here.



Default directory

Default directory's path:

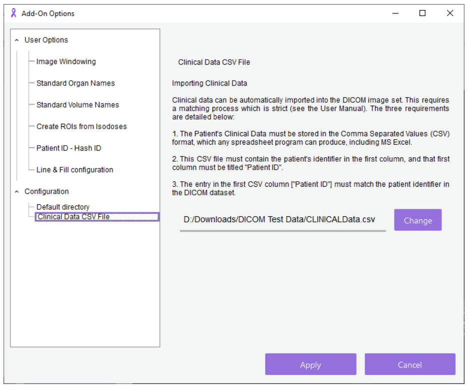
/home/andrew/Desktop/Lung.2016-2017

Clinical Data Directory

This Option identifies the location a clinical data CSV file. Apart from 2 columns, any text data can be added, so long as three conditions are met:

1. It is a CSV (Comma Separated Variable) format file.
2. The first spreadsheet column is the Patient ID.
3. Clinical Data Patient ID in CSV matches the Image set Patient ID (Clinical Data). No match, no imported.
4. The second spreadsheet column is the Patient Diagnosis (use ICD10).

Ensure that the CSV contents have no patient identifiers. Record durations rather than dates as entries are recorded in plain text.



Clinical Data CSV File

Importing Clinical Data

Clinical data can be automatically imported into the DICOM image set. This requires a matching process which is strict (see the User Manual). The three requirements are detailed below:

1. The Patient's Clinical Data must be stored in the Comma Separated Values (CSV) format, which any spreadsheet program can produce, including MS Excel.

2. This CSV file must contain the patient's identifier in the first column, and that first column must be titled "Patient ID".

3. The entry in the first CSV column ["Patient ID"] must match the patient identifier in the DICOM dataset.

D:/Downloads/DICOM Test Data/CLINICALData.csv

Export Data

This icon provides the choice to export PyRadiomics data or DVH data. In both cases the data will be exported to DICOM-SR files stored with the imaging files.

ANON

This icon will launch the Pseudo-anonymisation process to de-identify the DICOM files associated with the selected image set. At the end of the process, the old Patient ID and the new Patient ID will be recorded in the **Add-On Options | Patient ID - Hash ID** section

Save RTSTRUCT

After using the Create ROI, Delete ROI or Manipulate ROI buttons, the RTSTRUCT changes need to be saved into the RTSTRUCT file. This file activates the save.

If you forget to save the changes, you will be reminded if you try to change to a new patient.

4.7 Main Screen - Patient Identity Strip

The third line down provides the information present in the DICOM tags that identify the patient.

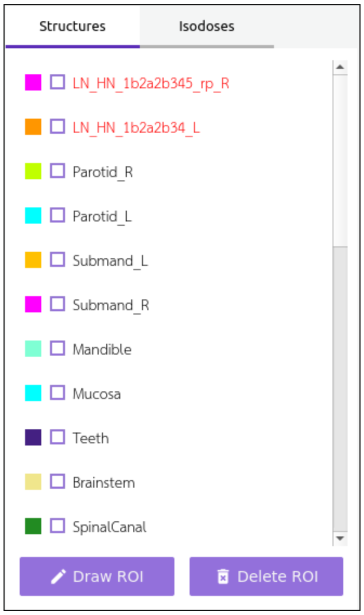
The **ID:** entry is important if you wish to pull Clinical Data in with the image files as a DICOM-SR (Structured Report) file. The patient’s image file ID and the entry into the first column of the Clinical Data CSV file (‘Patient_ID’) must match.

Name: IMMUNA^Trial **ID:** 8EE335730CE8FE7E144DF088AD35F43C **Gender:** O **DoB:**

4.8 Main Screen - Left Hand Vertical Window

4.8.1 Structures Tab

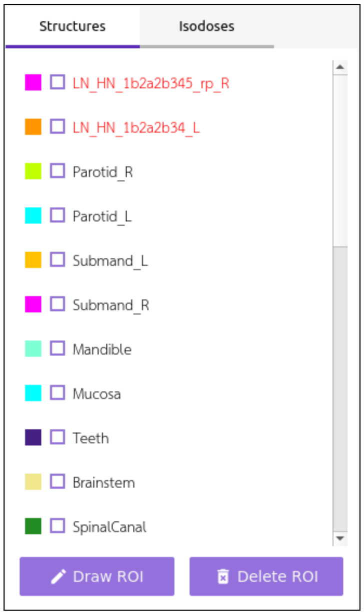
The left vertical window contains three buttons at the bottom that allow the user to alter ROIs. After manipulating ROIs, the new ROIs need to be saved into the RTSTRUCT file using the last icon on the right.

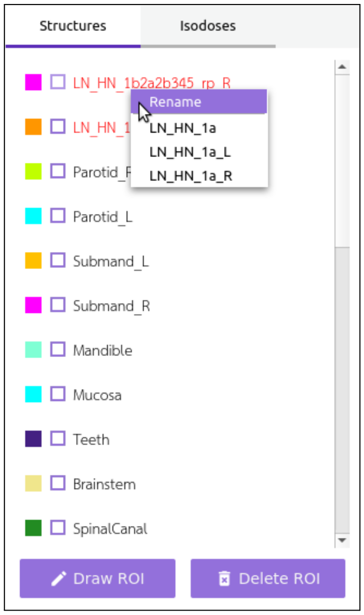


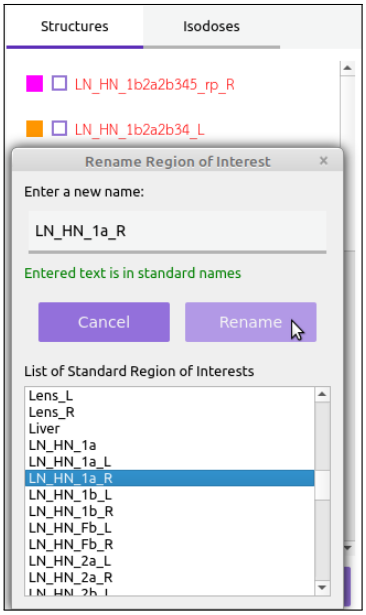
The left hand vertical window lists the ROIs found in the RTSTRUCT file. Any non-standard name will be coloured red.

If the user desires to use a standard name beginning with ‘LN_’ for all contours of lymph node regions, the prefix can be added to **Add-On Options | Standard Volume Names**.

Within this window, the ROI name can be altered to a Standard Name with a right click. A [Central image], after which one of the options can be selected or the Rename option can be selected to choose another name by typing or from the list provided.







Enter a new name: LN_HN_1a_R

Entered text is in standard names

At the bottom of the window are three buttons, to Manipulate, Delete or Create ROIs. These functions are described later.

4.8.2 Manipulate ROI

This function uses existing ROIs to create new ROIs by manipulating 2 ROIs:

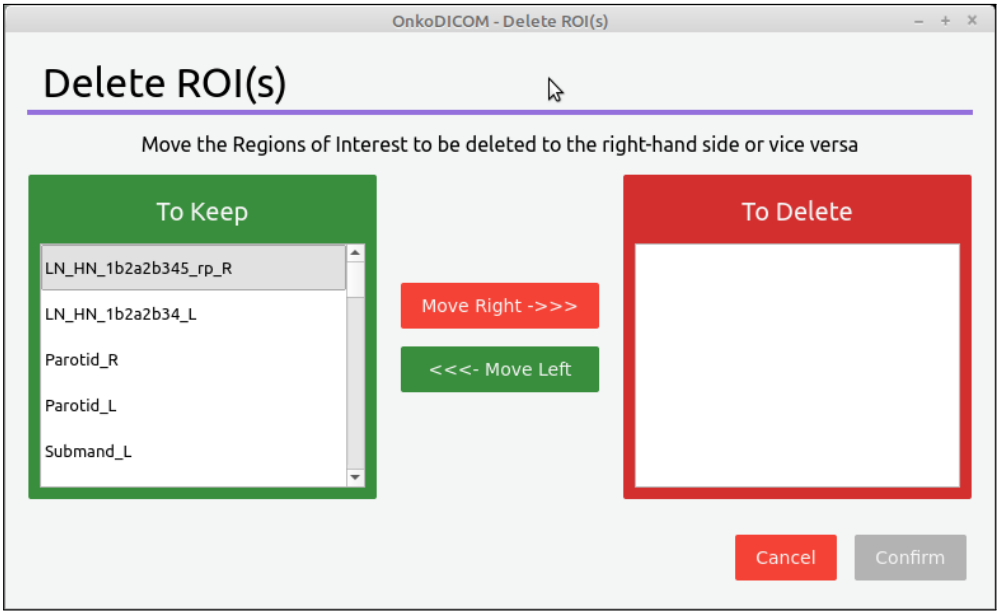
- union (e.g., Lung R + Lung L = Lungs)
- intersection (e.g., region of PTV overlapping with OAR = OTV)
- exclusion. . .

or by using a single ROI:

- expansion
- contraction
- inner rind (based on the ROI line)
- outer rind (based on the ROI line)

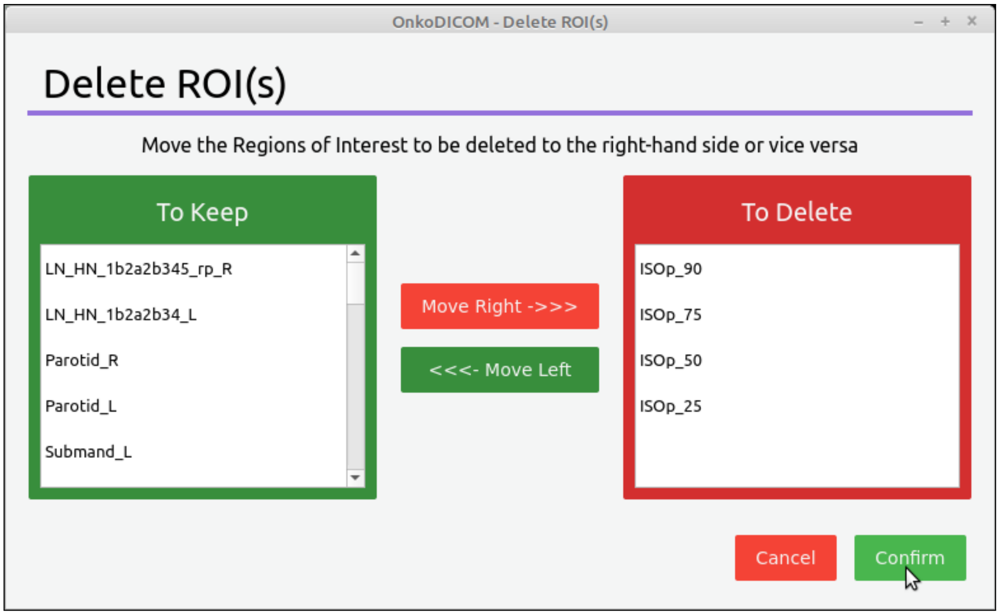
4.8.3 Delete ROI

The Delete ROI button opens a new screen with all of the existing ROIs on the left in a green column. Any selected ROI can be moved to the red column on the right and then deleted, after an additional confirmation.



Move the Regions of Interest to be deleted to the right-hand side or vice versa

LN_HN_1b2a2b345_rp_R
LN_HN_1b2a2b34_L
Parotid_R
Parotid_L
Submand_L



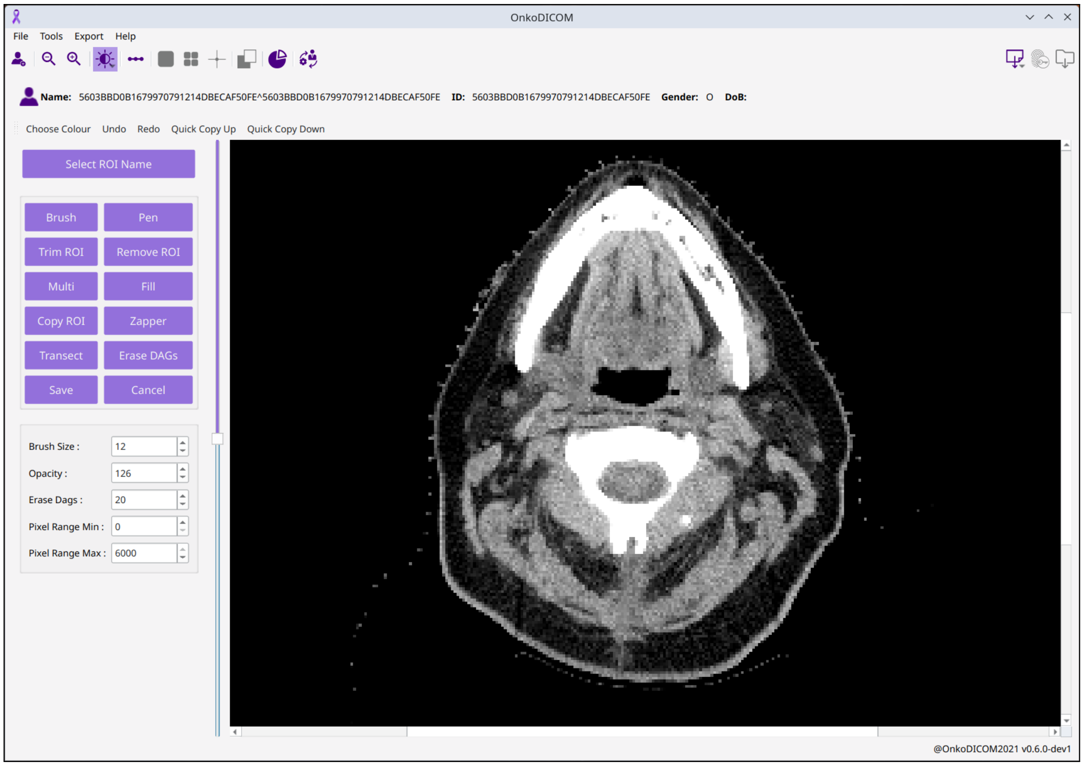
Move the Regions of Interest to be deleted to the right-hand side or vice versa

To Keep	To Delete
LN_HN_1b2a2b345_rp_R	ISOp_90
LN_HN_1b2a2b34_L	ISOp_75
Parotid_R	ISOp_50
Parotid_L	ISOp_25
Submand_L	

4.8.4 Draw ROI

[Renewed in 2025]

To create ROIs, first set the main DICOM View to the desired window level display. Press the **Draw ROI** button and a new window will appear.



Name: 5603BBD0B1679970791214DBECAF50FE^5603BBD0B1679970791214DBECAF50FE **ID:** 5603BBD0B1679970791214DBECAF50FE **Gender:** O **DoB:**

Brush Size : 12
Opacity : 126
Erase Dags : 20
Pixel Range Min : 0
Pixel Range Max : 6000

The top row provides five functions that permit you to **Set the Colour** of the ROI, **Undo** or **Redo** the last action, take the current ROI and **Quick Copy Up** one Slice, or **Quick Copy Down** one Slice.

Below this are thirteen buttons and five value selections which allow for manipulation of the Draw functions. Moving down and left to right, the functions are:

- **Select ROI Name** which provides a Standardised List of Anatomical Names based on the FMA[3]. You must choose one name. [If you wish to have a novel, non-standard name, choose any name, do the contour, save it and then change the name in the DICOM View window.]
- **Brush** provides a circular brush of the size listed in the first value setting box under the purple buttons. The perimeter of the brush will be the selected colour. When drawn across the image the colour will be superimposed, and on mouse button release only the pixels matching the **Pixel Range** will be retained. To contour:
  - LUNGS, set the Pixel Range to 0 – 850.

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[3] Foundational Model of Anatomy

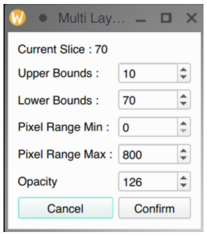
  - BONES, set the Pixel Range to 1125 – 6000
  - FAT, set the Pixel Range to 900 – 960
  - PAROTID GLANDS, set the Pixel Range to 980 – 1040
  - MUSCLE, set the Pixel Range to 1000 – 1120
  - ... it pays to experiment to find the correct numbers!

- **Pen** provides a tool to draw a loop. All of the pixels inside the loop matching the Pixel range will be selected.

- **Trim ROI** provides a function to *reduce the ROI borders*, it will not expand the borders.

- **Remove ROI** will remove the drawn ROI on the current slice, but leave other slices intact.

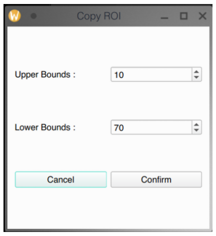
- **Multi** creates an ROI for the pixel range described within the nominated slices.



Current Slice : 70
Upper Bounds : 10
Lower Bounds : 70
Pixel Range Min : 0
Pixel Range Max : 800
Opacity 126

- **Fill** functions to 'lasso' an area matching the pixel value boundary set on click of the mouse.

- **Copy ROI** permits the drawn ROI to be copied to the nominated slices.



Upper Bounds : 10
Lower Bounds : 70

- **Zapper** is a delete function. a Click of the mouse on an unwanted area will remove the individual contour.

- **Transect** is a function which allows a line to be drawn across the screen to interrogate the CT numbers of pixels. This can inform your choice of min and max on the Pixel Range.

- **Erase DAGs** will remove small islands that have been selected when using the Pixel Range function [4].

- **Save** will save the ROI and exit the window back to the DICOM View screen. The RTSTRUCT

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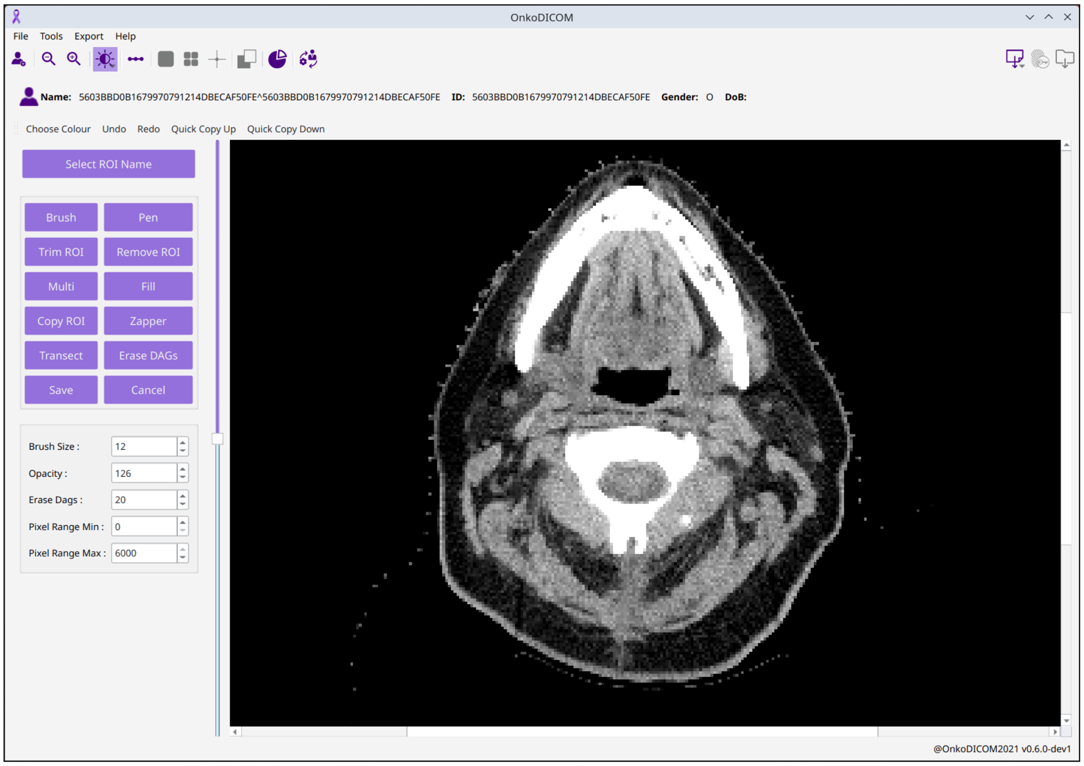
[4] Originally a word meaning the dried faeces left dangling from the wool on a sheep's rear end; used colloquially for small hanging bits of refuse like pilling on a jersey.

must be saved for this to become permanent.

- **Cancel** will exit the Draw ROI function and return you to the DICOM View window, discarding all changes.



Name: 5603BBD0B1679970791214DBECAF50FE^5603BBD0B1679970791214DBECAF50FE ID: 5603BBD0B1679970791214DBECAF50FE Gender: O DoB:

Brush Size : 12
Opacity : 126
Erase Dags : 20
Pixel Range Min : 0
Pixel Range Max : 6000

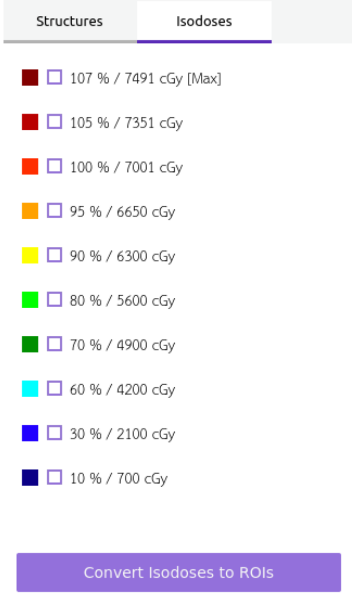
The five value selection boxes include the following:

- **Brush Size**, I’m not going to explain this!
- **Opacity**, where a value of 0 is complete transparency. This is unusable as the selected pixels cannot be appreciated. Values below 50 are not recommended. A value of 255 will render the selection completely opaque, which is also of limited usefulness if you wish to use **Trim ROI** as the new boundary cannot be appreciated.
- **Erase Dags** sets the number of connected pixels which will be erased by the **Erase DAGs** function. Setting this number too high risks losing required contours.
- **Pixel Range Min:** sets the value for exclusion of pixels, namely that all pixels **LESS** than the selected value will be ignored.
- **Pixel Range Max:** similarly sets the value for exclusion of pixels, namely that all pixels **MORE** than the selected value will be ignored.

4.8.5 Isodoses Tab

The second left hand vertical window lists a range of isodose levels that can be displayed over the image in the DICOM View window. The isodoses for display cannot be configured, only turned on or off.

At the bottom of the window is one button, this functionality will take specified isodoses and using the ISO2ROI function will produce new ROIs and save them in the RTSTRUCT file. The isodose levels that can be specified in the **Add-On Options** screen as either isodose (cGy) or percentage levels [see above].



■ ☐ 107 % / 7491 cGy [Max]
■ ☐ 105 % / 7351 cGy
■ ☐ 100 % / 7001 cGy
■ ☐ 95 % / 6650 cGy
■ ☐ 90 % / 6300 cGy
■ ☐ 80 % / 5600 cGy
■ ☐ 70 % / 4900 cGy
■ ☐ 60 % / 4200 cGy
■ ☐ 30 % / 2100 cGy
■ ☐ 10 % / 700 cGy

The button titled **Convert isodoses to ROIs** triggers the conversion of specified isodoses derived from the dose data in the RTDOSE file into ROIs stored in the RTSTRUCT file. The process is also called *ISO2ROI*.

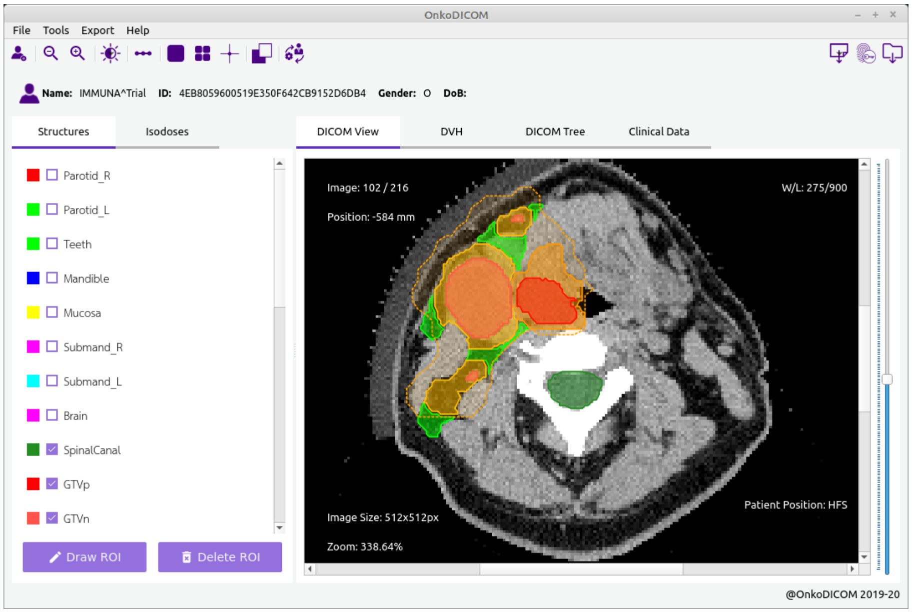
The specification of isodoses to be converted is entered into the **Add-On Options | Create ROIs from Isodoses** screen.

4.8.6 Right hand Vertical Window

DICOM View Tab

The first tab allows the user to view the DICOM image files whether CT, MRI or PET. This window is where the zoom, transect, windowing functions alter the image, and includes the 3-window and cross hair functions.

This view shows a CT scan with Structures (ROIs) and isodose turned on.



Name: IMMUNA^Trial **ID:** 4EB8059600519E350F642CB9152D6DB4 **Gender:** O **DoB:**

Image: 102 / 216
Position: -584 mm
W/L: 275/900
Image Size: 512x512px
Zoom: 338.64%
Patient Position: HFS

DVH Tab

This tab displays the graphical Dose Volume Histogram (DVH) which requires both RTDOSE and RTSTRUCT file to be present. The results are stored within the RTDOSE file.

If an image set with RTDOSE and RTSTRUCT is opened and the DVH is not stored in the RTDOSE file, the user will be asked if this should be undertaken. This can take some time if there are many and/or large ROIs present.[5]

The DVH window includes two buttons at the bottom. The first allows the user to export the DVH for the single patient to a single spreadsheet file (in CSV format).[6] The second button allows the user to recalculate the DVH after the ROIs have been altered. This new data will be stored in the RTDOSE file.

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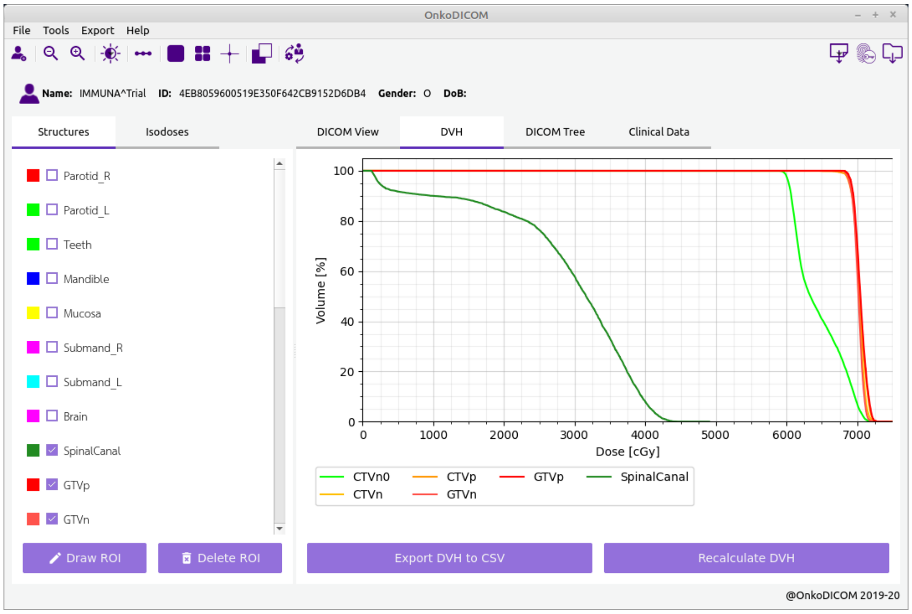
[5] The user is advised to calculate the DVH after the RTSTRUCT file has been cleaned and corrected.

[6] OnkoDICOM has a batch function to collated the DVH data of multiple data sets within a directory.

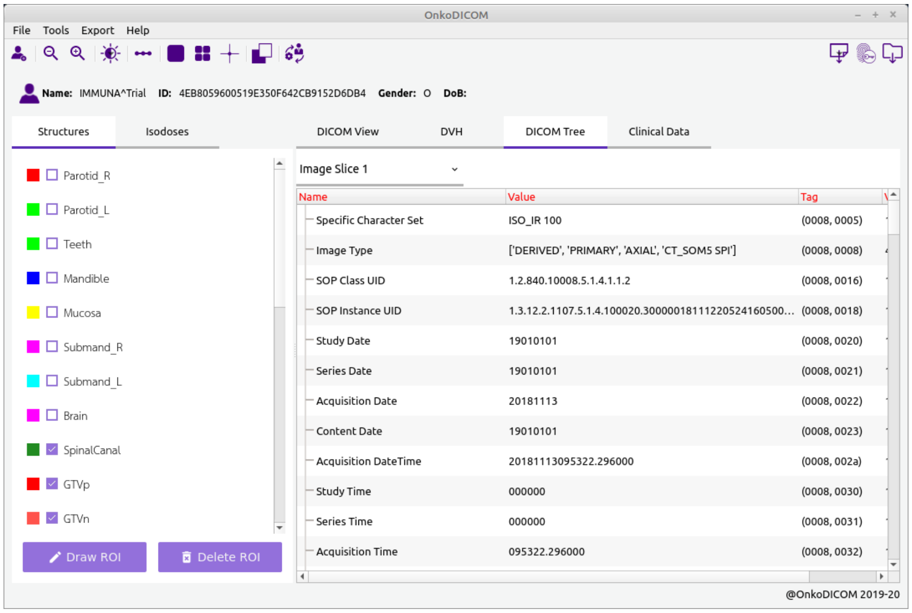


Name: IMMUNA^Trial **ID:** 4EB8059600519E350F642CB9152D6DB4 **Gender:** O **DoB:**

🟥 ☐ Parotid_R
🟩 ☐ Parotid_L
🟩 ☐ Teeth
🟦 ☐ Mandible
🟨 ☐ Mucosa
🟪 ☐ Submand_R
🟦 ☐ Submand_L
🟪 ☐ Brain
🟩 ☑ SpinalCanal
🟥 ☑ GTVp
🟥 ☑ GTVn

DICOM Tree Tab

The third tab allows the user to view the DICOM tags that are components of all DICOM files. These tags identify patients, clinicians, machines, etc. This tab provides a Quality Assurance function to allow the user to determine if the level of de-identification is sufficient.



Name: IMMUNA^Trial **ID:** 4EB8059600519E350F642CB9152D6DB4 **Gender:** O **DoB:**

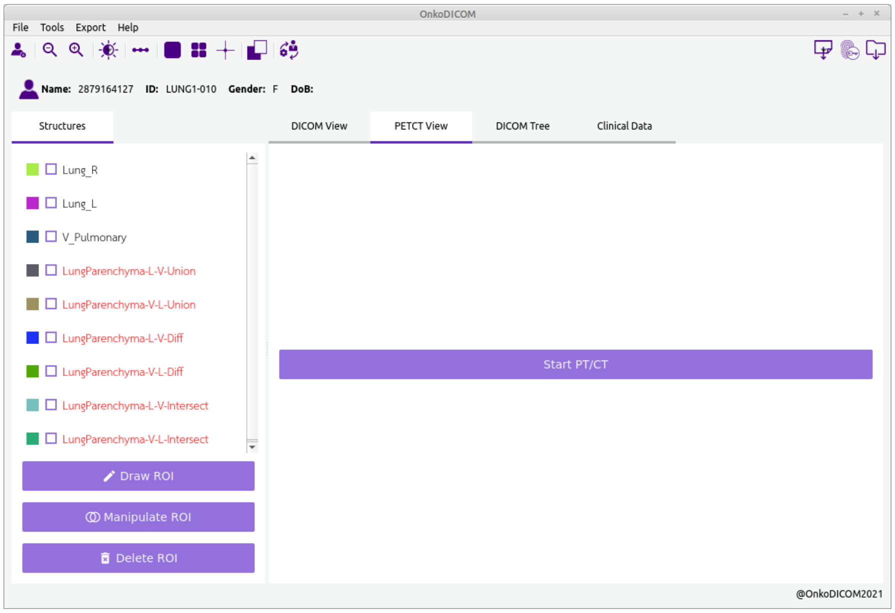
🟥 ☐ Parotid_R
🟩 ☐ Parotid_L
🟩 ☐ Teeth
🟦 ☐ Mandible
🟨 ☐ Mucosa
🟪 ☐ Submand_R
🟦 ☐ Submand_L
🟪 ☐ Brain
🟩 ☑ SpinalCanal
🟥 ☑ GTVp
🟥 ☑ GTVn

Name	Value	Tag
Specific Character Set	ISO_IR 100	(0008, 0005)
Image Type	['DERIVED', 'PRIMARY', 'AXIAL', 'CT_SOM5 SPI']	(0008, 0008)
SOP Class UID	1.2.840.10008.5.1.4.1.1.2	(0008, 0016)
SOP Instance UID	1.3.12.2.1107.5.1.4.100020.30000018111220524160500...	(0008, 0018)
Study Date	19010101	(0008, 0020)
Series Date	19010101	(0008, 0021)
Acquisition Date	20181113	(0008, 0022)
Content Date	19010101	(0008, 0023)
Acquisition DateTime	20181113095322.296000	(0008, 002a)
Study Time	000000	(0008, 0030)
Series Time	000000	(0008, 0031)
Acquisition Time	095322.296000	(0008, 0032)

PET-CT Viewer Tab

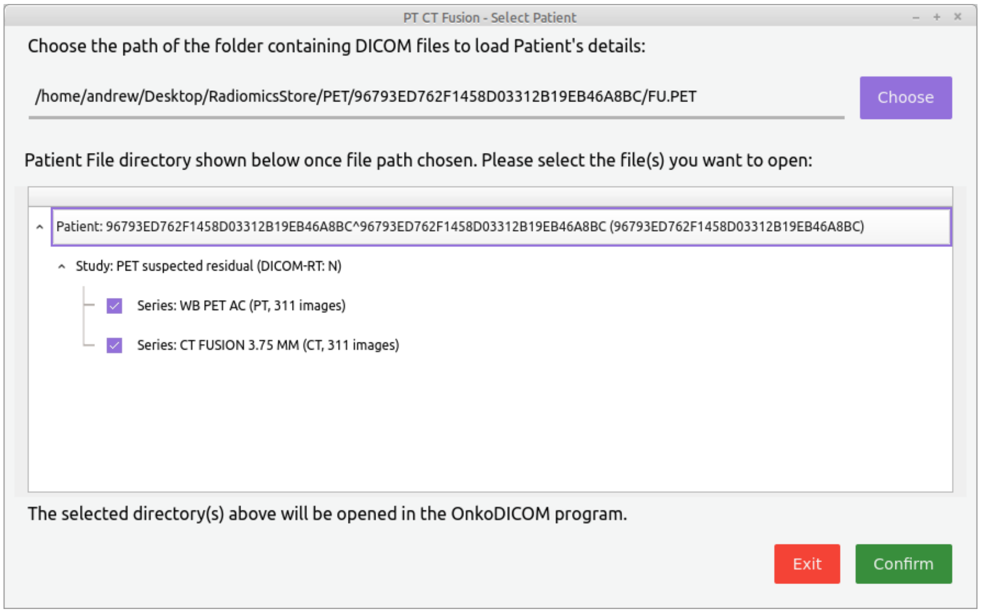
The fifth tab allows viewing a PET-CT pair with overlay, alpha adjustment and 3 slice view.

Activate the viewer by clicking the PET/CT Tab and selecting CT and PET with the same Patient ID. The overlay is automatic. ROI view and SUV2ROI has not been implemented.



Name: 2879164127 ID: LUNG1-010 Gender: F DoB:

Click the Start PET/CT button and select matching CT and PET image sets.



Choose the path of the folder containing DICOM files to load Patient's details:

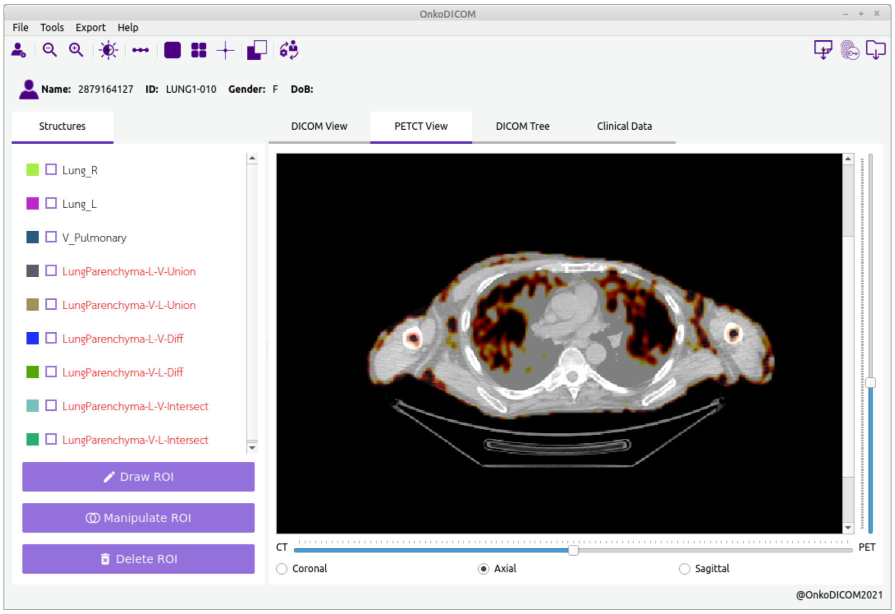
/home/andrew/Desktop/RadiomicsStore/PET/96793ED762F1458D03312B19EB46A8BC/FU.PET

Patient File directory shown below once file path chosen. Please select the file(s) you want to open:

- Patient: 96793ED762F1458D03312B19EB46A8BC^96793ED762F1458D03312B19EB46A8BC (96793ED762F1458D03312B19EB46A8BC)
  - Study: PET suspected residual (DICOM-RT: N)
    - ☑ Series: WB PET AC (PT, 311 images)
    - ☑ Series: CT FUSION 3.75 MM (CT, 311 images)

The selected directory(s) above will be opened in the OnkoDICOM program.

The fused PET/CT will be displayed. The slider on the right moves between slices. The slider on the bottom changes the view from 100% CT on the left to 100% PET on the right. The three radio buttons allow the plane of viewing to be changed.



Name: 2879164127 **ID:** LUNG1-010 **Gender:** F **DoB:**

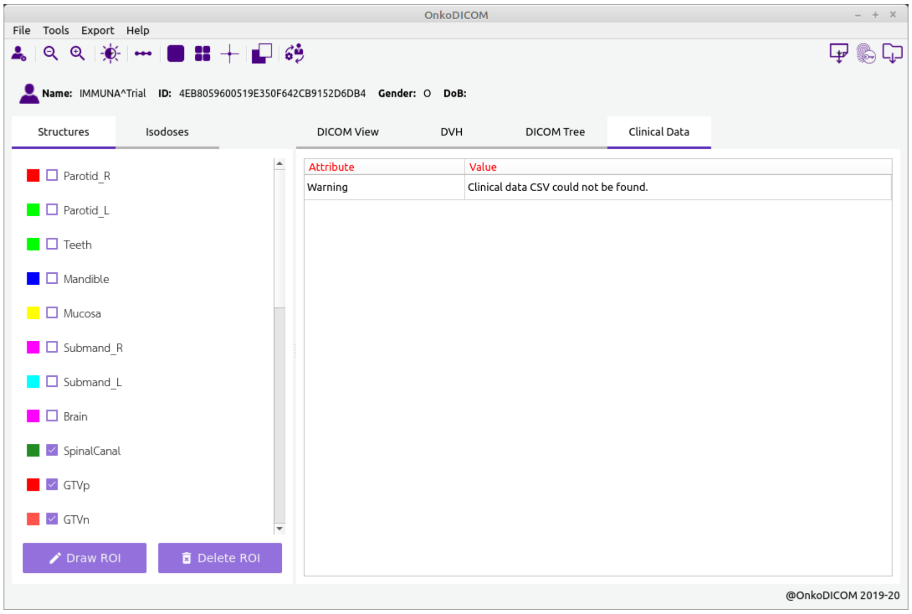
○ Coronal ● Axial ○ Sagittal

The images can be windowed as with other views, however you will need to define the image to which the windowing has to be applied.

Clinical Data Tab

The sixth tab displays the imported Clinical Data present in the ClinicalData-SR file.

The import of Clinical Data into OnkoDICOM is automatic if the required CSV file is present and structured properly. The first column of the CSV view is called “**Patient_ID**” and must contain the same identifier as the DICOM files, and the second column is called “**ICD10**” and contains the diagnosis identifier (for cases with multiple diagnoses). The site of the ClinicalData.CSV file is entered into the configuration screen in Add-On Options.



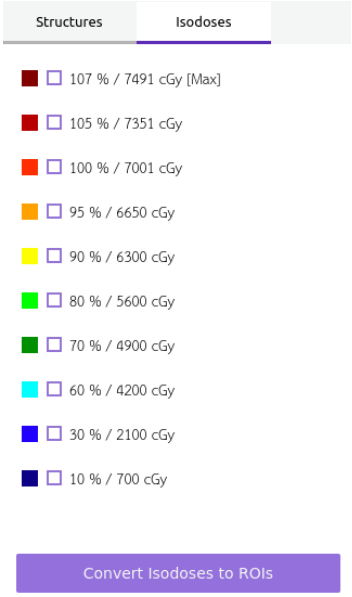
Name: IMMUNA^Trial **ID:** 4EB8059600519E350F642CB9152D6DB4 **Gender:** O **DoB:**

Attribute	Value
Warning	Clinical data CSV could not be found.

Isodoses Tab

The second left hand vertical window lists a range of isodose levels that can be displayed over the image in the DICOM View window. The isodoses for display cannot be configured, only turned on or off.

At the bottom of the window is one button, this functionality will take specified isodoses and using the ISO2ROI function will produce new ROIs and save them in the RTSTRUCT file. The isodose levels that can be specified in the **Add-On Options** screen as either isodose (cGy) or percentage levels [see above].



🟥 ☐ 107 % / 7491 cGy [Max]
🟥 ☐ 105 % / 7351 cGy
🟥 ☐ 100 % / 7001 cGy
🟧 ☐ 95 % / 6650 cGy
🟨 ☐ 90 % / 6300 cGy
🟩 ☐ 80 % / 5600 cGy
🟩 ☐ 70 % / 4900 cGy
🟦 ☐ 60 % / 4200 cGy
🟦 ☐ 30 % / 2100 cGy
🟦 ☐ 10 % / 700 cGy

The button titled **Convert isodoses to ROIs** triggers the conversion of specified isodoses derived from the dose data in the RTDOSE file into ROIs stored in the RTSTRUCT file. The process is also called *ISO2ROI*.

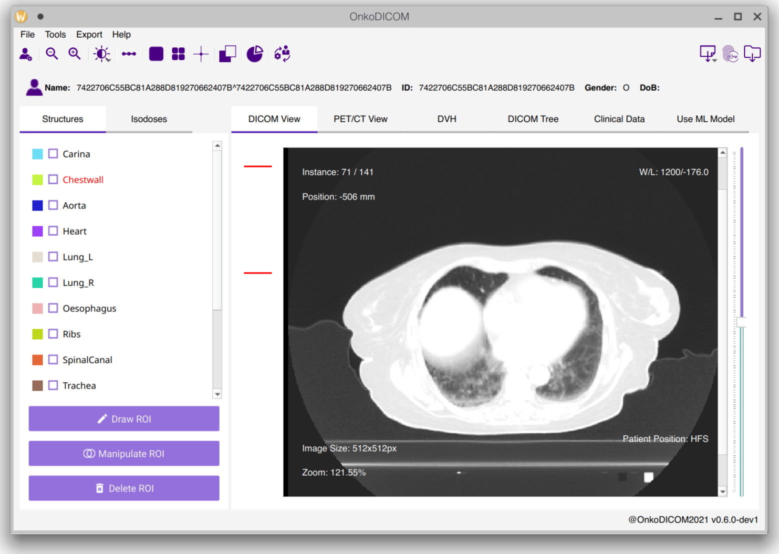
The specification of isodoses to be converted is entered into the **Add-On Options | Create ROIs from Isodoses** screen.

Image Fusion Tab

The fourth tab addresses Image Fusion with ROI Transfer.

In order to undertake an image fusion, you will require a second DICOM image set for overlay which has the same ID as the base image set. OnkoDICOM detects this automatically.

Start with a base image.



Name: 7422706C55BC81A288D819270662407B^7422706C55BC81A288D819270662407B **ID:** 7422706C55BC81A288D819270662407B **Gender:** O **DoB:**

Instance: 71 / 141

Position: -506 mm

W/L: 1200/-176.0

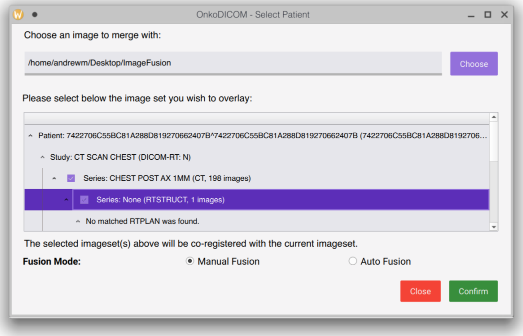
Image Size: 512x512px

Zoom: 121.55%

Patient Position: HFS

The **Image Fusion** icon is ninth icon in the icon strip.

Click this icon, and select the overlay image set with the same Patient ID from the directory [it makes sense to have the image sets needed for fusion all under the same directory].



Choose an image to merge with:

/home/andrewm/Desktop/ImageFusion

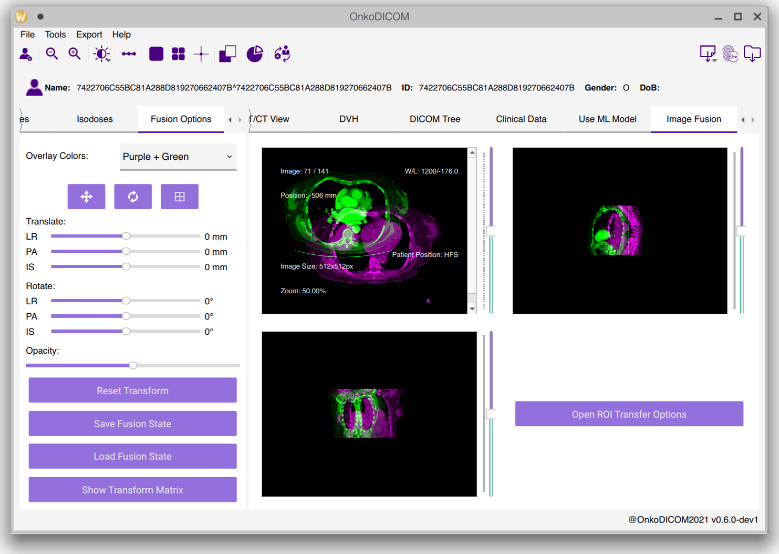
Please select below the image set you wish to overlay:

- Patient: 7422706C55BC81A288D819270662407B^7422706C55BC81A288D819270662407B (7422706C55BC81A288D8192706…
  - Study: CT SCAN CHEST (DICOM-RT: N)
    - ☑ Series: CHEST POST AX 1MM (CT, 198 images)
      - ☑ Series: None (RTSTRUCT, 1 images)
        - No matched RTPLAN was found.

The selected imageset(s) above will be co-registered with the current imageset.

Fusion Mode: ● Manual Fusion ○ Auto Fusion

After selection, a new tab (*Image Fusion*) appears & fuses the second image set. The fourth window button (**Open ROI Transfer Options**) also appears and enables bilateral transfer of ROIs between the two fused image sets.



Name: 7422706C55BC81A288D819270662407B^7422706C55BC81A288D819270662407B ID: 7422706C55BC81A288D819270662407B Gender: O DoB:

Overlay Colors: Purple + Green

Translate:
LR 0 mm
PA 0 mm
IS 0 mm

Rotate:
LR 0°
PA 0°
IS 0°

Opacity:

The option is provided to use different pairings of colours (purple/green, red/cyan, blue/yellow). When anatomically areas overlap, the overlap area will appear white.

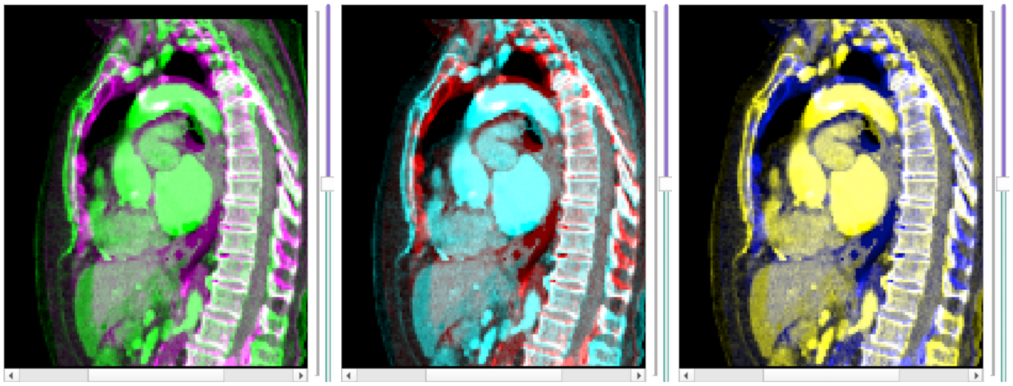


Image Fusion can be achieved using gross movements with the Translate sliders which operate in the XYZ planes, or the Rotate sliders that operate in the PYR (Pitch-Yaw-Roll) axes.

Fine movements can be achieved by clicking on the box with the 4 direction arrows (same movements as Translate) or the two rotation arrows (same movements as Rotate). Clicking on the edge of the window will move the overlay image to towards the cursor in single steps.

Fusions are rarely perfect, so it is prudent to focus on the area needing to be matched. This can be isolated with the cross hairs. When the cross hairs are activated, fine shifts are disabled as clicking just re-sites the cross hairs.

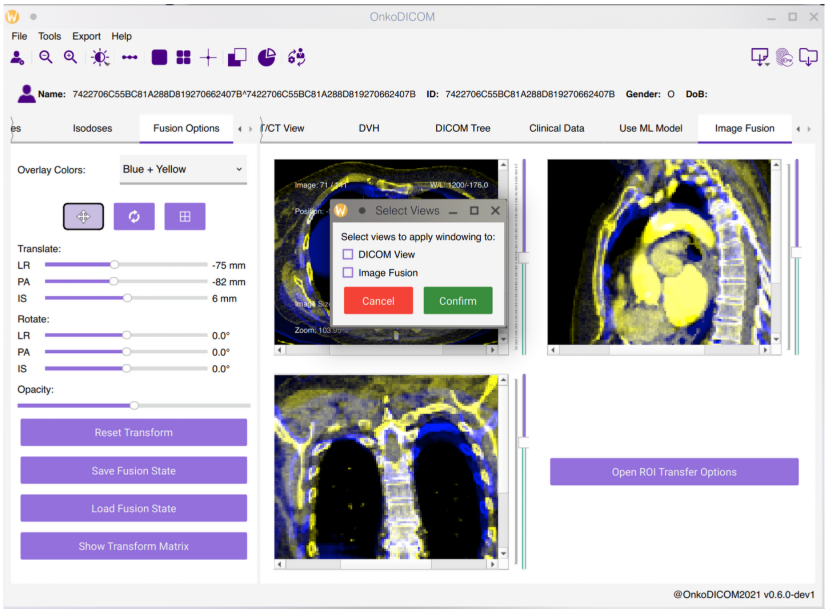
The two image sets are displayed at 50% transparency, but the proportionality can be altered with the **Opacity** slider. IN addition the last window icon activates a transparency window in the overlay image to that the accuracy of the fusion can be better examined.

When you are satisfied with your fusion, you can save the spatial translation parameters by clicking **Save Fusion State**. This will save a DICOM file called Transform.dcm into the directory of the overlay image set.

If you are opening a previously saved fusion, clicking the **Load Fusion State** button will open a file list from which you can select the Transform.dcm file[7]

Reset Transform will remove any applied transformation parameters and return the overlap of the two images to the start point again. **Show Transform Matrix** displays the actual transform parameters, if that happens to be of interest to you.

Should you wish to alter the windowing on the image sets, press the Windowing icon and select the scan to be altered.



Name: 7422706C55BC81A288D819270662407B^7422706C55BC81A288D819270662407B **ID:** 7422706C55BC81A288D819270662407B **Gender:** O **DoB:**

Overlay Colors: Blue + Yellow

Translate:
LR -75 mm
PA -82 mm
IS 6 mm

Rotate:
LR 0.0°
PA 0.0°
IS 0.0°

Opacity:

Select views to apply windowing to:
☐ DICOM View
☐ Image Fusion

Transfer ROI between Image Sets

Once the fusion is satisfactory, ROIs from either data set can be moved to the other.

Select the **Open ROI Transfer Options** button, and 4 pane screen appears. The left panes list the ROIs of the base image set, and the right panes list the ROIs of the overlay image set. The upper panes deal with the ROIs found on the Base image set which can be transferred *in toto*, or by double clicking each required individual ROI required for transfer from base to overlay. The lower panes provide the same process of transfer from overlay to base image sets.

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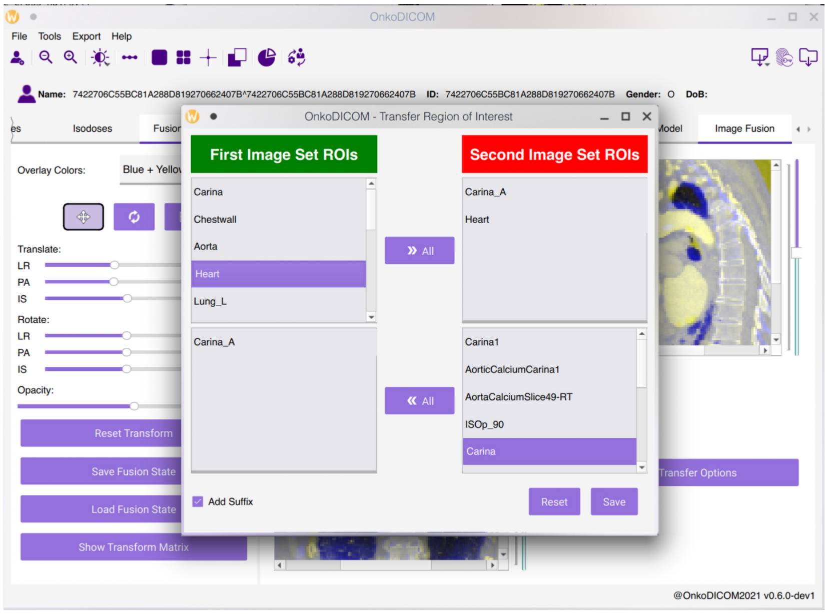
[7] You can save multiple Transformations with different names,; it would be prudent to use a naming schema so that you can load the right files.



Name: 7422706C55BC81A288D819270662407B^7422706C55BC81A288D819270662407B ID: 7422706C55BC81A288D819270662407B Gender: O DoB:

Overlay Colors: Blue + Yellov

☑ Add Suffix

When the selections are completed, **Save** will initiate the transfer. If the requested ROI name is already in the ROI list of the receiving image set, the name will have a suffix (identical names are not permitted in a RTSTRUCT file, and cause mayhem when they occur; in OnkoDICOM, rename all identical files before trying to delete or manipulate ROIs).

Autosegmentation of Anatomical Structures

This function was first added to OnkoDICOM.2025.

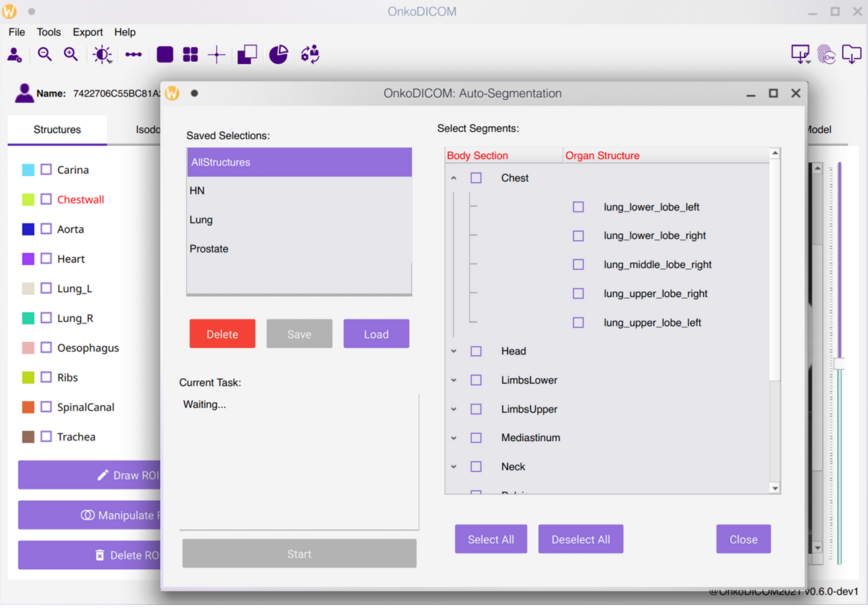
This function was replicated from **Slicer3D** and requires the explicit attribution each time – **If you use this tool please cite: https://pubs.rsna.org/doi/10.1148/ryai.230024** – please provide this with any publication achieved using the AutoSeg function.

This function is activated with the tenth icon.

Selecting the icon opens a new window with three panes. The right-hand full length pane allows for grouped or individual anatomical selections. The upper left-hand pane allows for the grouping of anatomical structures to ease the selection of all ROIs in overlapping regions, e.g., Chest & Mediastinum. These groupings can be saved and named as you prefer. The lower left-hand pane provides messages during the segmentation process so that you can see its progress.

If your computer has , and you can access, an nVidia GPU (Graphics Processing Unit), the segmentation process will be swift. Segmentations using CPU only (if you have an on-chip GPU or a Radeon GPU) will take longer. If you have a nVidia GPU, the calculations will automatically default to using the GPU.

The achieved contours will be automatically saved to the RTSTRUCT file opened when the image set was loaded, or create a new RTSTRUCT file [8]. All of the ROIs added by AutoSeg will be have the suffix “_TS”, so as to prevent name clashes.



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[8] NB: The DICOM standard for DICOM-RT also only allows ONE RTSTRUCT file for all of the ROIs. When OnkoDICOM opens a CT/MRI only image set, it will automatically add a RTSTRUCT file in case you wish to **Draw ROI**. If you forget to open a RTSTRUCT file that is already present then you will have caused a dilemma for yourself.

5. OnkoDICOM Batch Processing

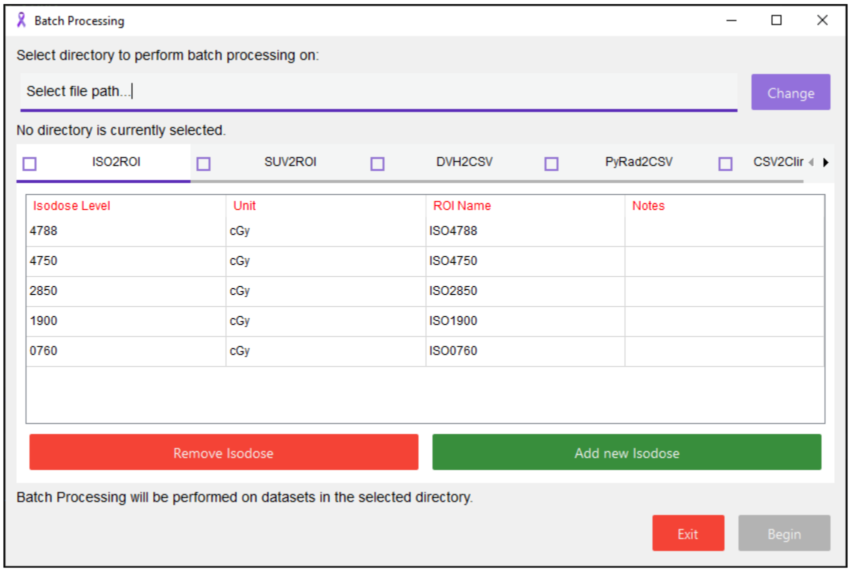
The Batch Processing option can be selected from the start screen. The user is presented with a number of options represented in the tabs on a new screen; under each tab are configuration options pertinent to the function.

After selecting an INPUT directory, the DICOM files in the directory will be accessed and read. For large directories this can take some time (75 patients house 12,000 files).

Welcome to OnkoDICOM!

OnkoDICOM - the solution for producing data for analysis from your oncology plans and scans.

Remember to tick the box in the Tab required.



Select directory to perform batch processing on:

Select file path...

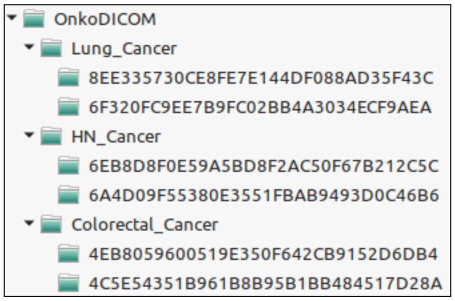
No directory is currently selected.

Isodose Level	Unit	ROI Name	Notes
4788	cGy	ISO4788	
4750	cGy	ISO4750	
2850	cGy	ISO2850	
1900	cGy	ISO1900	
0760	cGy	ISO0760	

Batch Processing will be performed on datasets in the selected directory.

The batch processing presumes that you are working in a directory that contains individual patient image sets in sub-directories. The batch processing will be applied to all files in the sub-directories. If you use the example below, if you point to the **OnkoDICOM** directory, the 6 directories containing the patient's image sets will be processed sequentially. If the chosen directory is **Colorectal_Cancer**, the 2 directories containing the 2 (presumably) Colorectal Cancer patient's image sets will be processed.

Once the process has begun, it may run for a long time. Each PyRadiomics run can take around 5 minutes per image set.

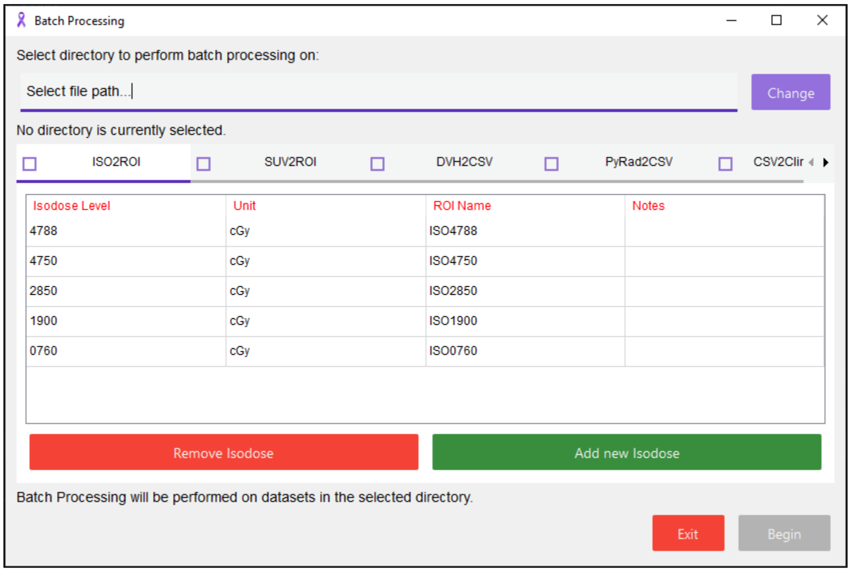


- OnkoDICOM
  - Lung_Cancer
    - 8EE335730CE8FE7E144DF088AD35F43C
    - 6F320FC9EE7B9FC02BB4A3034ECF9AEA
  - HN_Cancer
    - 6EB8D8F0E59A5BD8F2AC50F67B212C5C
    - 6A4D09F55380E3551FBAB9493D0C46B6
  - Colorectal_Cancer
    - 4EB8059600519E350F642CB9152D6DB4
    - 4C5E54351B961B8B95B1BB484517D28A

5.1 ISO2ROI

This function will find any RTDOSE file in the sub-directories and convert lines of isodose into ROIs and save into an associated RTSTRUCT files.

The same individual function exists in the Isodose screen. The range of levels to convert isodoses into ROIs can be changed, with values in centiGray (cGy) or percent of prescription dose.



Select directory to perform batch processing on:

Select file path...

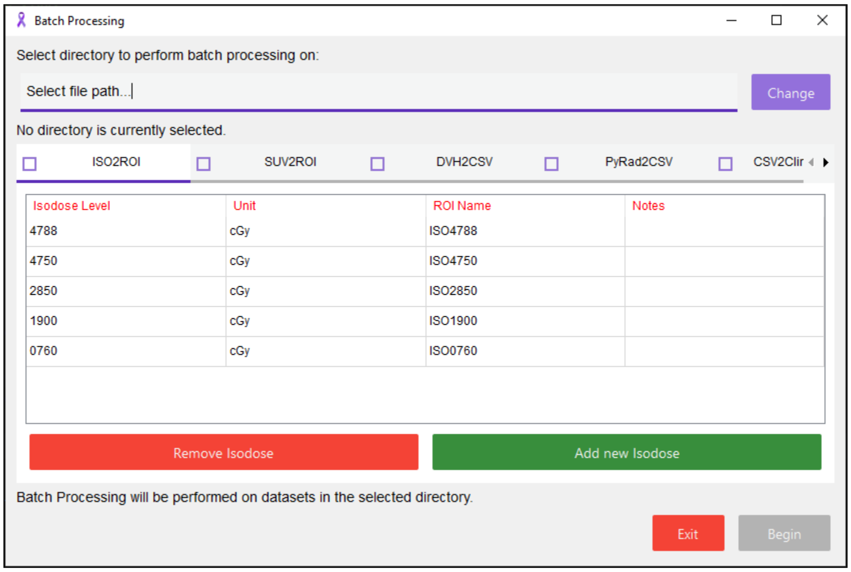
No directory is currently selected.

Isodose Level	Unit	ROI Name	Notes
4788	cGy	ISO4788	
4750	cGy	ISO4750	
2850	cGy	ISO2850	
1900	cGy	ISO1900	
0760	cGy	ISO0760	

Batch Processing will be performed on datasets in the selected directory.

5.2 SUV2ROI

This function will find any PT scan in the sub-directories and convert lines of iso-SUV into ROIs which will be save into attached/created RTSTRUCT files.



Select directory to perform batch processing on:

Select file path...

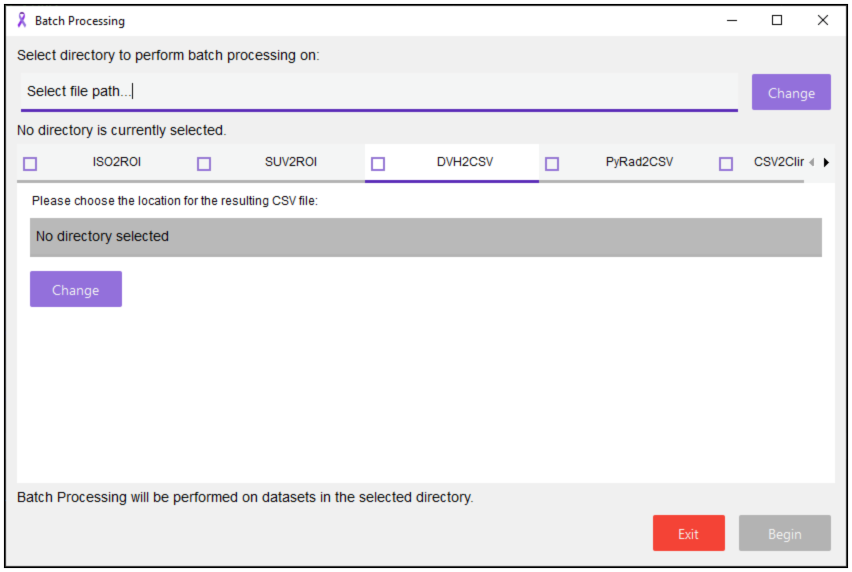
No directory is currently selected.

Isodose Level	Unit	ROI Name	Notes
4788	cGy	ISO4788	
4750	cGy	ISO4750	
2850	cGy	ISO2850	
1900	cGy	ISO1900	
0760	cGy	ISO0760	

Batch Processing will be performed on datasets in the selected directory.

5.3 DVH2CSV

This function will search for and export all of the DVH data stored in the RTDOSE files and output them to a single CSV file. The user needs to define the INPUT directory and the OUTPUT directory for the CSV file.



Select directory to perform batch processing on:

Select file path...|

No directory is currently selected.

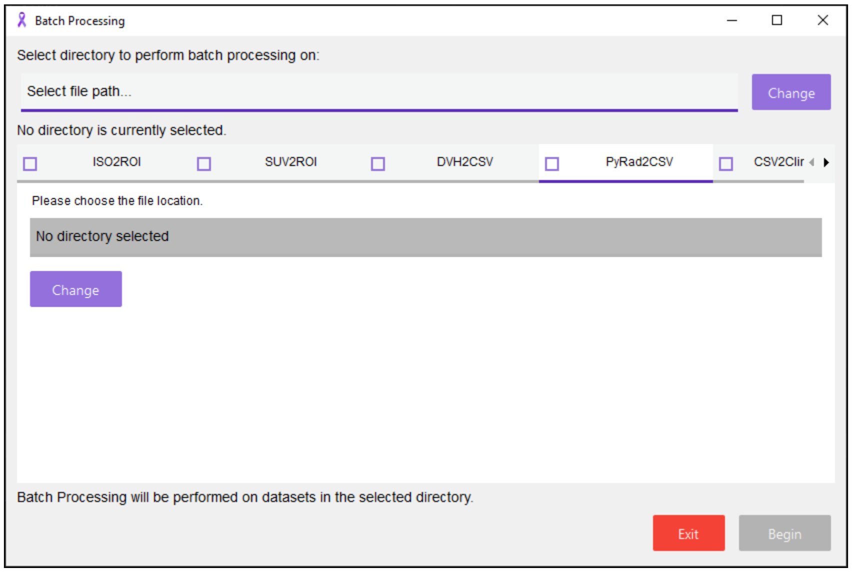
Please choose the location for the resulting CSV file:

No directory selected

Batch Processing will be performed on datasets in the selected directory.

5.4 PyRad2CSV

This function searches for and will export all PyRadiomics data stored in the ClinicalData-SR files and output them to a single CSV file. The user needs to define the INPUT directory and the OUTPUT directory for the CSV file.



Select directory to perform batch processing on:

Select file path...

No directory is currently selected.

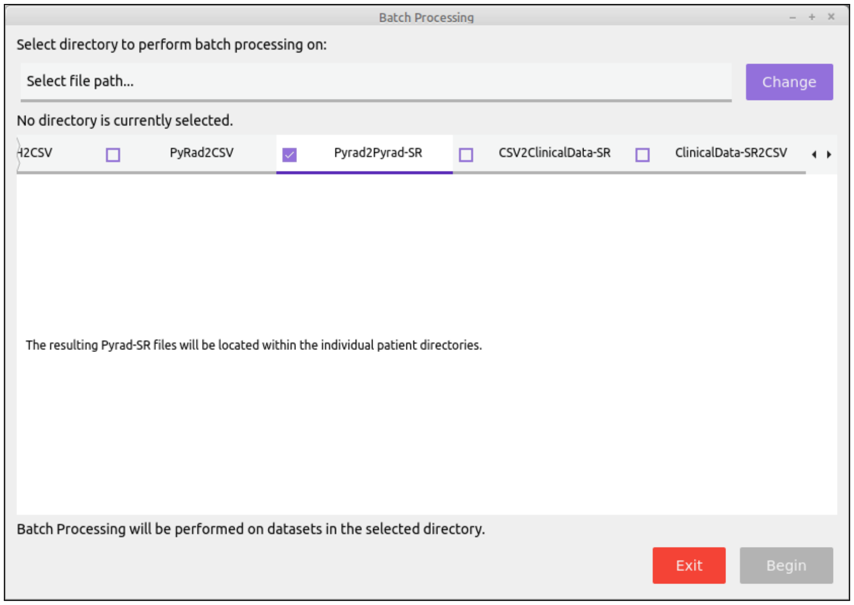
Please choose the file location.

No directory selected

Batch Processing will be performed on datasets in the selected directory.

5.5 PyRad2PyRad-SR

This function searches for and will export all PyRadiomics data stored in the PyRadiomics CSV files and output them to a PyRad-SR file. PyRadiomics CSV files were the OnkoDICOM2019/2020 method for storing PyRadiomics data. The user needs only define the INPUT directory as the output are DICOM files.



Select directory to perform batch processing on:

Select file path...

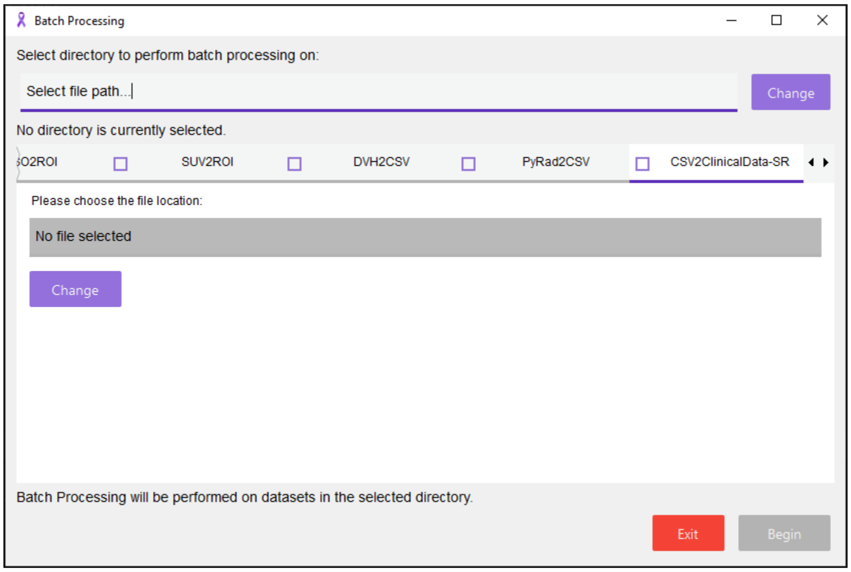
No directory is currently selected.

The resulting Pyrad-SR files will be located within the individual patient directories.

Batch Processing will be performed on datasets in the selected directory.

5.6 CSV2ClinicalDataSR

This function will import properly configured Clinical Data from a selected CSV file. The first column [“**Patient_ID**”] and second column [“**ICD10**”] are mandatory within the CSV file structure. This function provides for data updating. The user needs to define the CSV directory and the INPUT directory for the image sets.



Select directory to perform batch processing on:

Select file path...

No directory is currently selected.

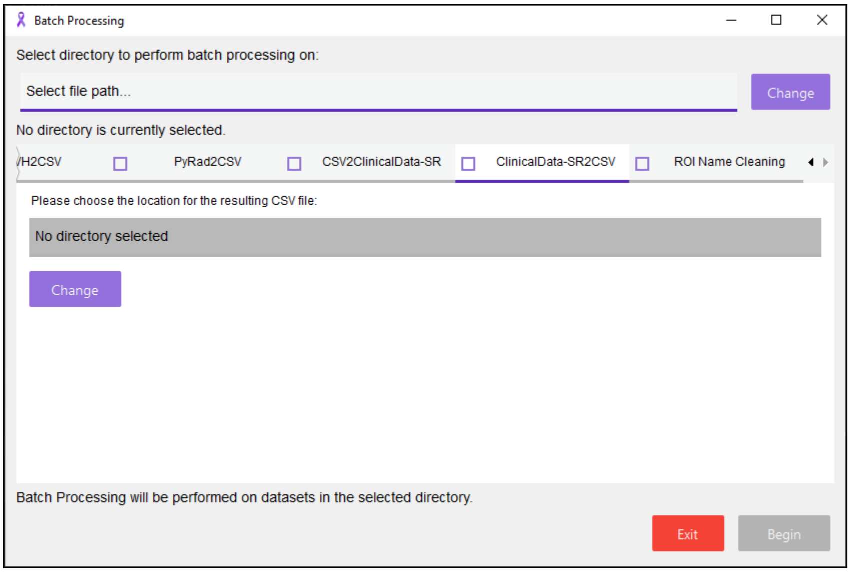
Please choose the file location:

No file selected

Batch Processing will be performed on datasets in the selected directory.

5.7 ClinicalDataSR2CSV

This function searches & collects Clinical Data stored in the ClinicalData-SR files and writes them to a single CSV file. An INPUT directory and the OUTPUT directory for the CSV file are required.



Select directory to perform batch processing on:

Select file path...

No directory is currently selected.

Please choose the location for the resulting CSV file:

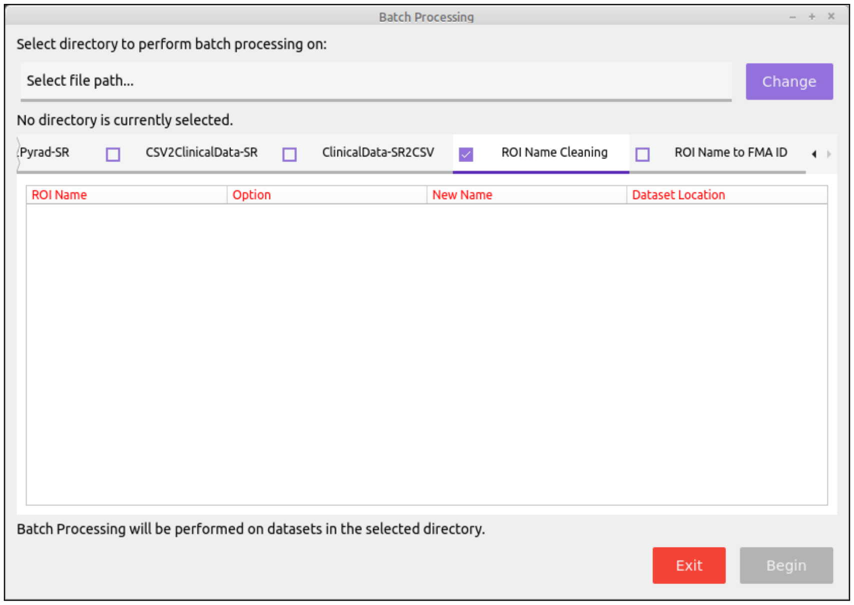
No directory selected

Batch Processing will be performed on datasets in the selected directory.

5.8 ROI Name Cleaning

This function searches all the RTSTRUCT files looking for discrete instances of ROI names and providing the ability to change, delete or ignore suggested alternatives.

At the end of the process, a log file is produced and can be saved.



Select directory to perform batch processing on:

Select file path...

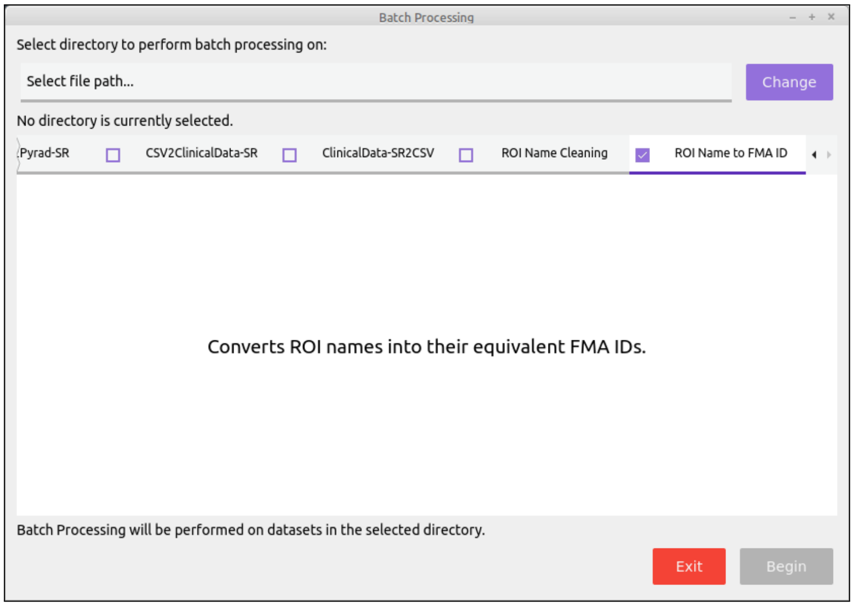
No directory is currently selected.

ROI Name	Option	New Name	Dataset Location

Batch Processing will be performed on datasets in the selected directory.

5.9 ROIName2FMA_ID

This function will replace all of the Standard Names inside RTSTRUCT files with the FMA_ID provided in the Add-On Options file.



No directory is currently selected.

Converts ROI names into their equivalent FMA IDs.

Batch Processing will be performed on datasets in the selected directory.

5.10 Notes