

# From Slicer to IBEX: Texture Analysis in 9 Easy Steps:

## *An Illustrated Beginner's Guide*

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### **Contents**

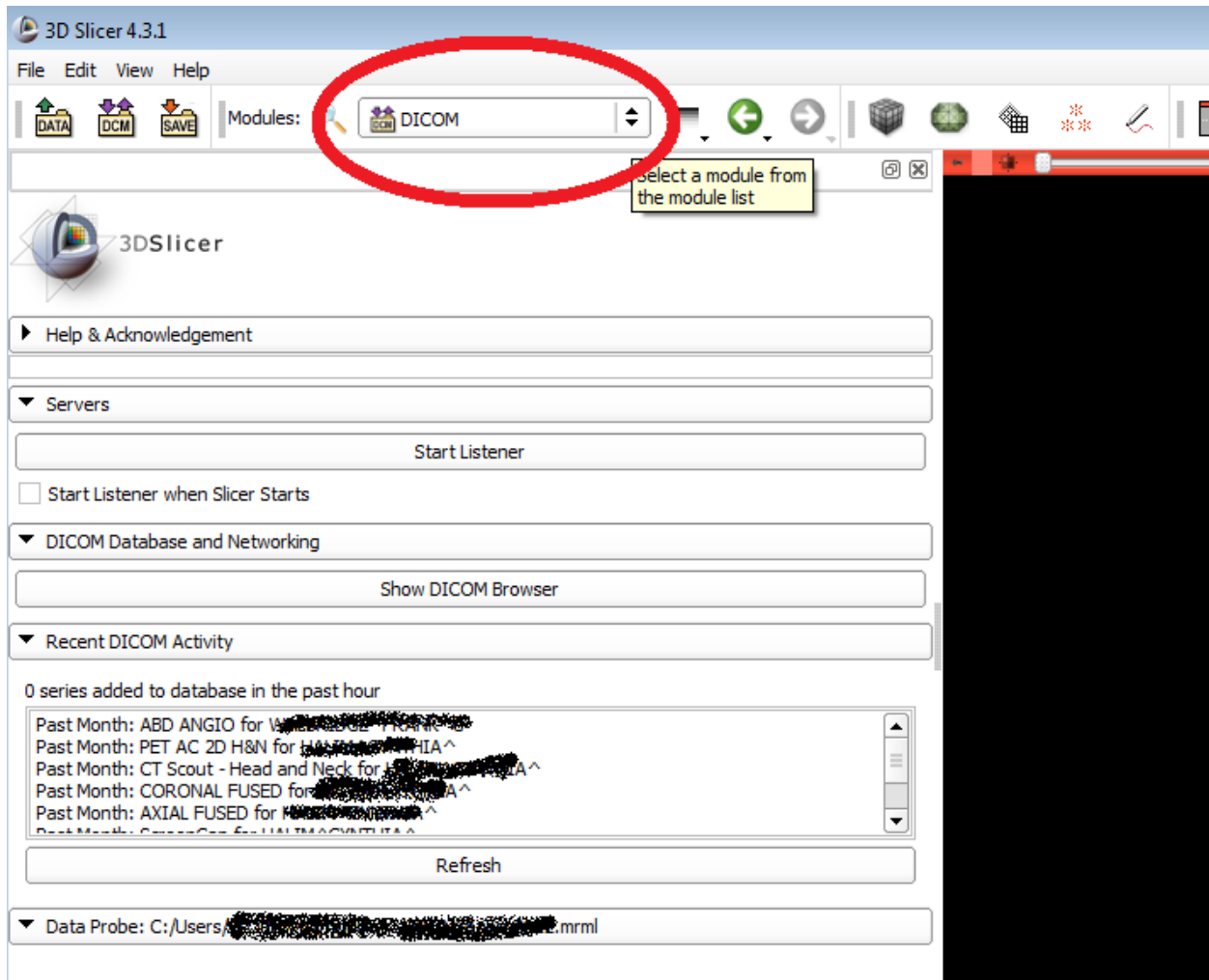
STEP 1) OBTAIN YOUR IMAGES. ....	2
STEP 2) GET YOUR IMAGES INTO SLICER. ....	2
STEP 3) DO YOUR SEGMENTATION.....	4
STEP 4) MAKE A MODEL.....	7
STEP 5) CONVERT INTO RT STRUCTURES. ....	9
STEP 6) IBEX!!!.....	12
STEP 7) SELECT YOUR DATASET .....	15
STEP 8) SELECT YOUR FEATURES AND PRE-PROCESSING METHODS.....	18
STEP 9) PUSH THE BUTTON AND GET YOUR RESULTS .....	19

## STEP 1) OBTAIN YOUR IMAGES.

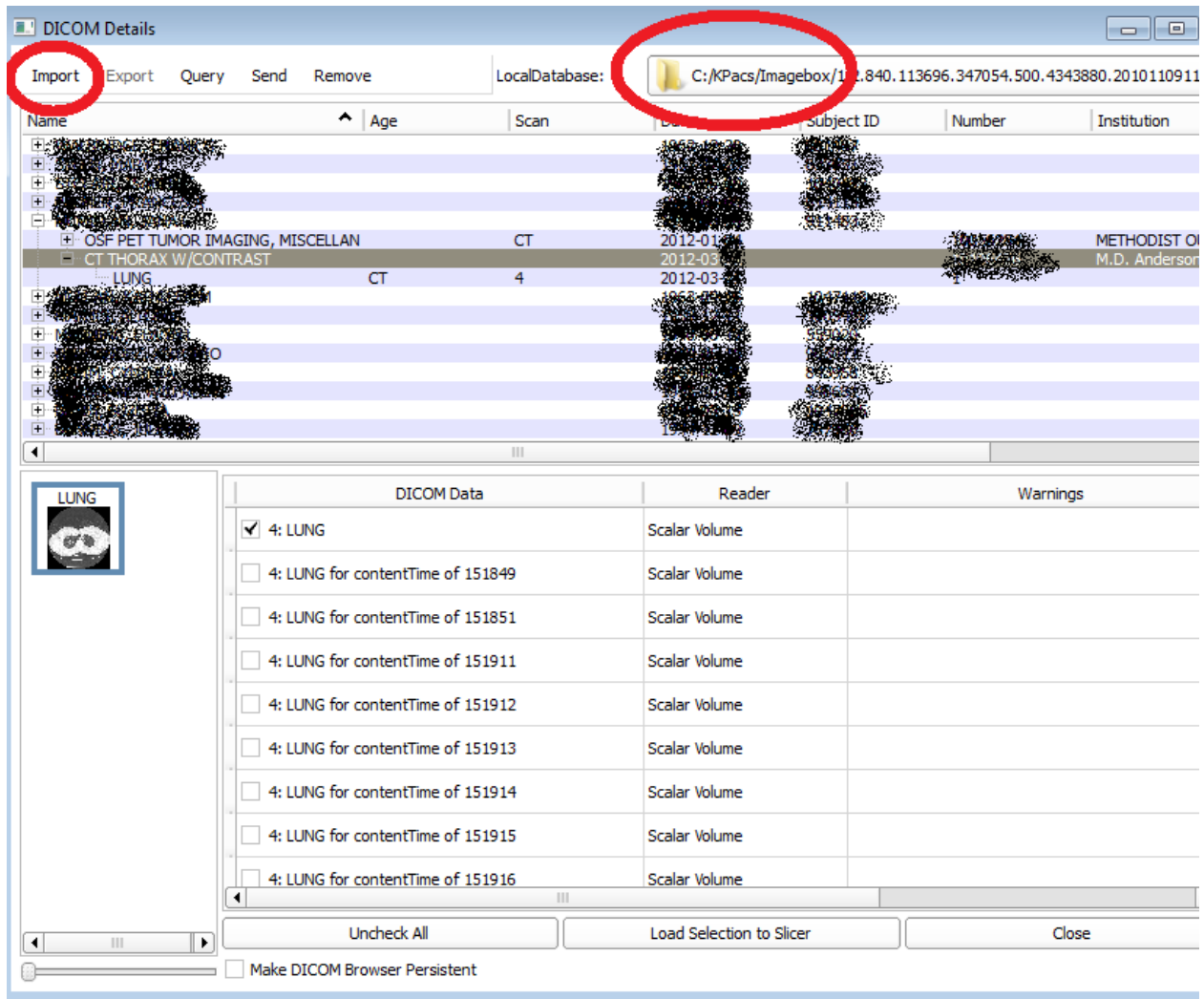
First you'll need to get your DICOM images onto a local drive.

## STEP 2) GET YOUR IMAGES INTO SLICER.

Once you have all of your DICOM images on a local drive, you open 3DSlicer, and then open the DICOM module. This module is how you load cases into Slicer.



From here, you set Slicer's LocalDatabase to the location where your DICOM images are saved. As we mentioned, in our case this was “ C:/kpac/imagebox “ . Then you import the cases into 3DSlicer by clicking “Import”, and selecting the directory where your local database is located. This process of loading cases into Slicer can take quite some time (in the region of around a minute per case).



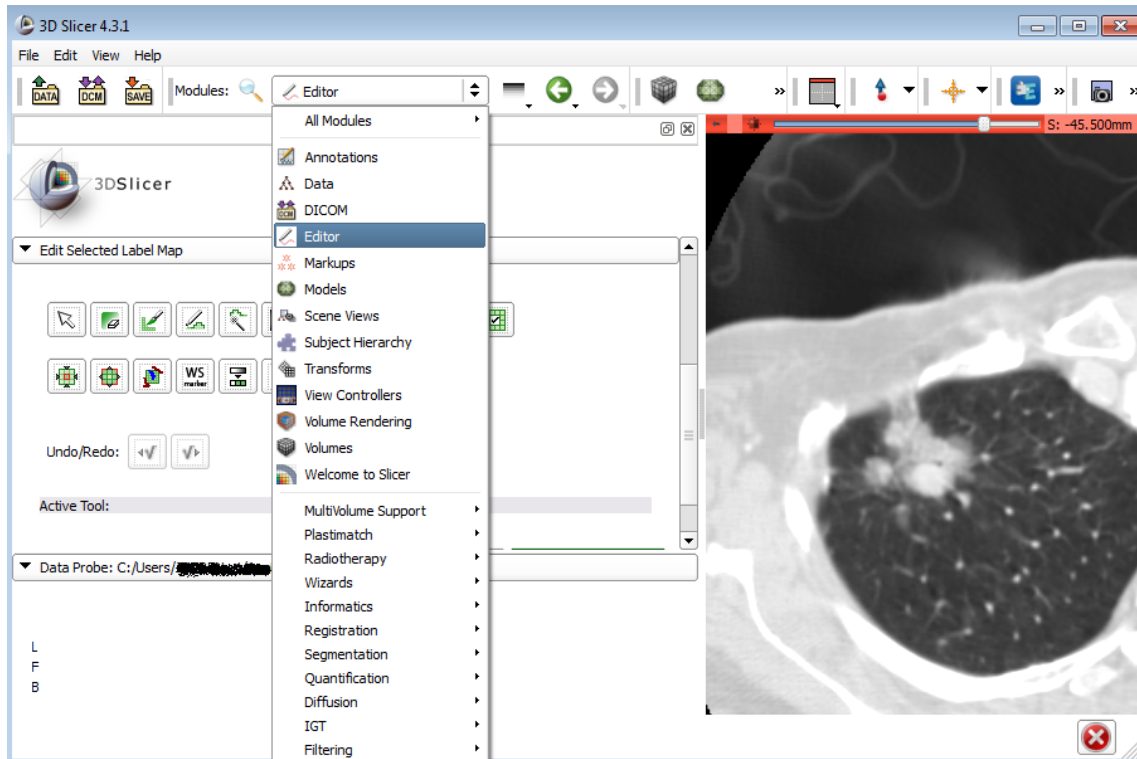
Set the LocalDatabase location, and then “Import” the cases into Slicer.

You only have to import the studies into 3DSlicer once. Slicer will create a file called “ctkDICOM” in the directory where you database is located, and this will point to all of the studies that have already been imported. Once the studies have been imported into your database, and you have an appropriate study selected, click “Load Selection to Slicer”.

**NB - It is important that you have closed any case that is already open in slicer before you load a new one, as failing to do so will simply add the new images on top of those in the already open case.**

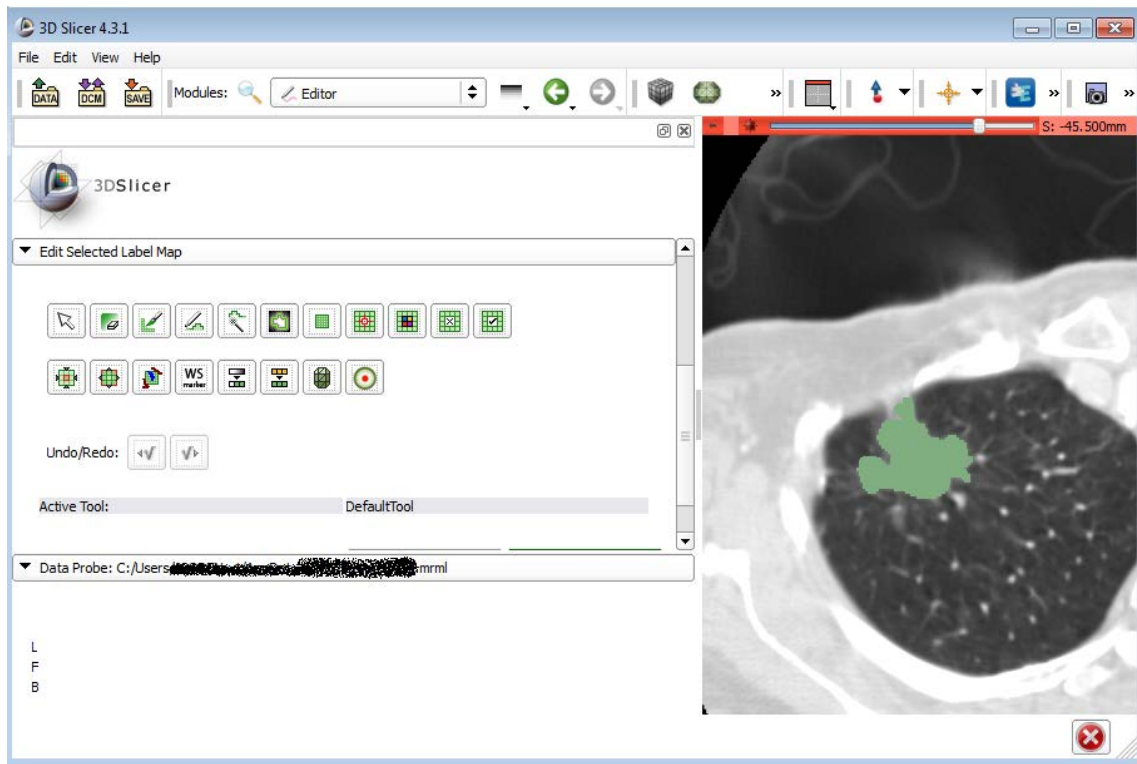
You are now ready to do your contouring using the Editor module.

### STEP 3) DO YOUR SEGMENTATION.



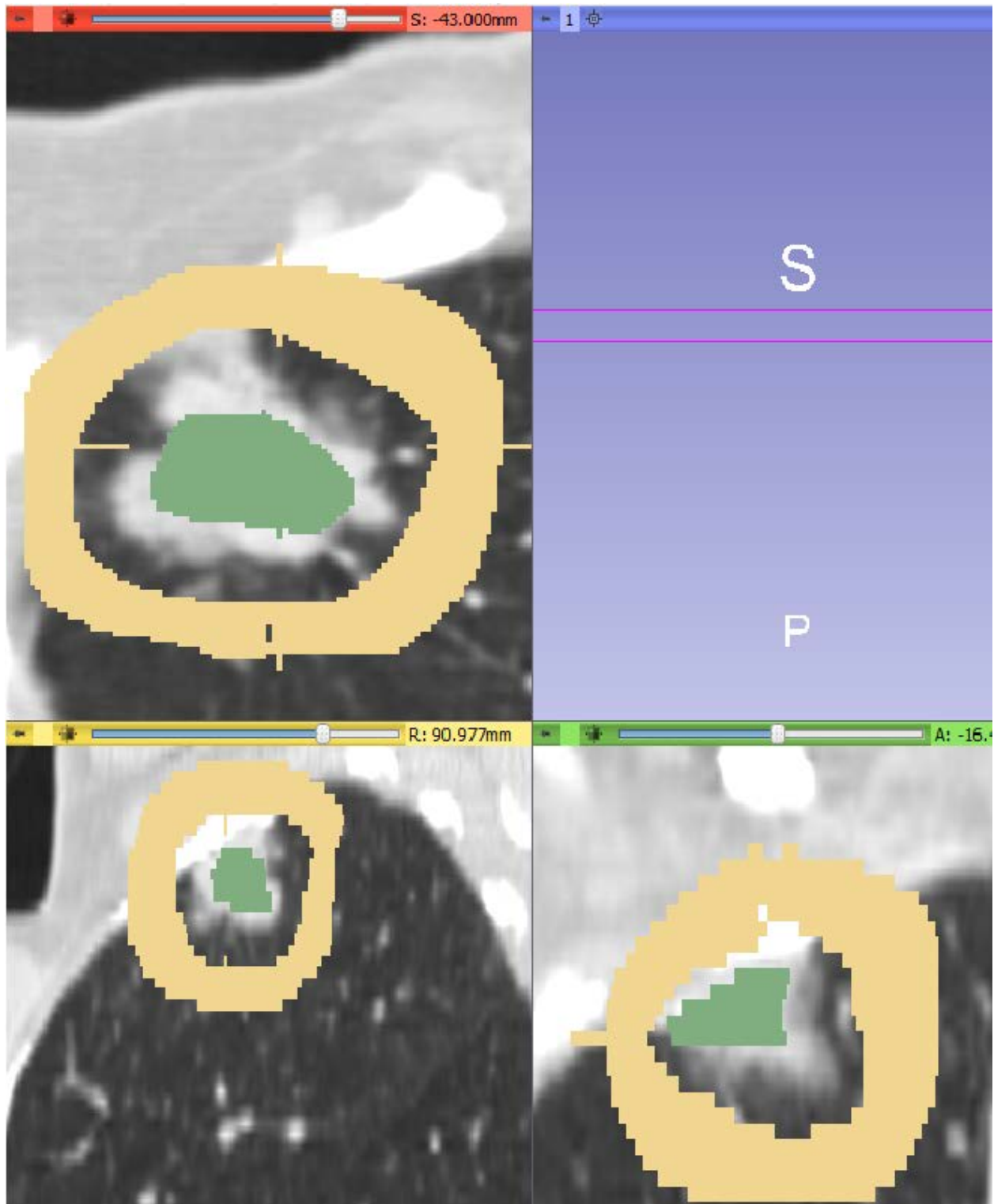
Use the Editor Module to do your segmentation

There are a number of tools that you can use to do contouring, from manual segmentation on a slice-by-slice basis, to whole-volume thresholding, to semi-automatic segmentation using Grow Cut. They all work. The goal here is to create a 'label map', which is a contour drawn on each slice within the Region of Interest. This label map is converted into a 3d model, which will then be sent to IBEX (which does the texture analysis).



The contours/segmentation that you create using the Editor module is a ‘Label Map’.

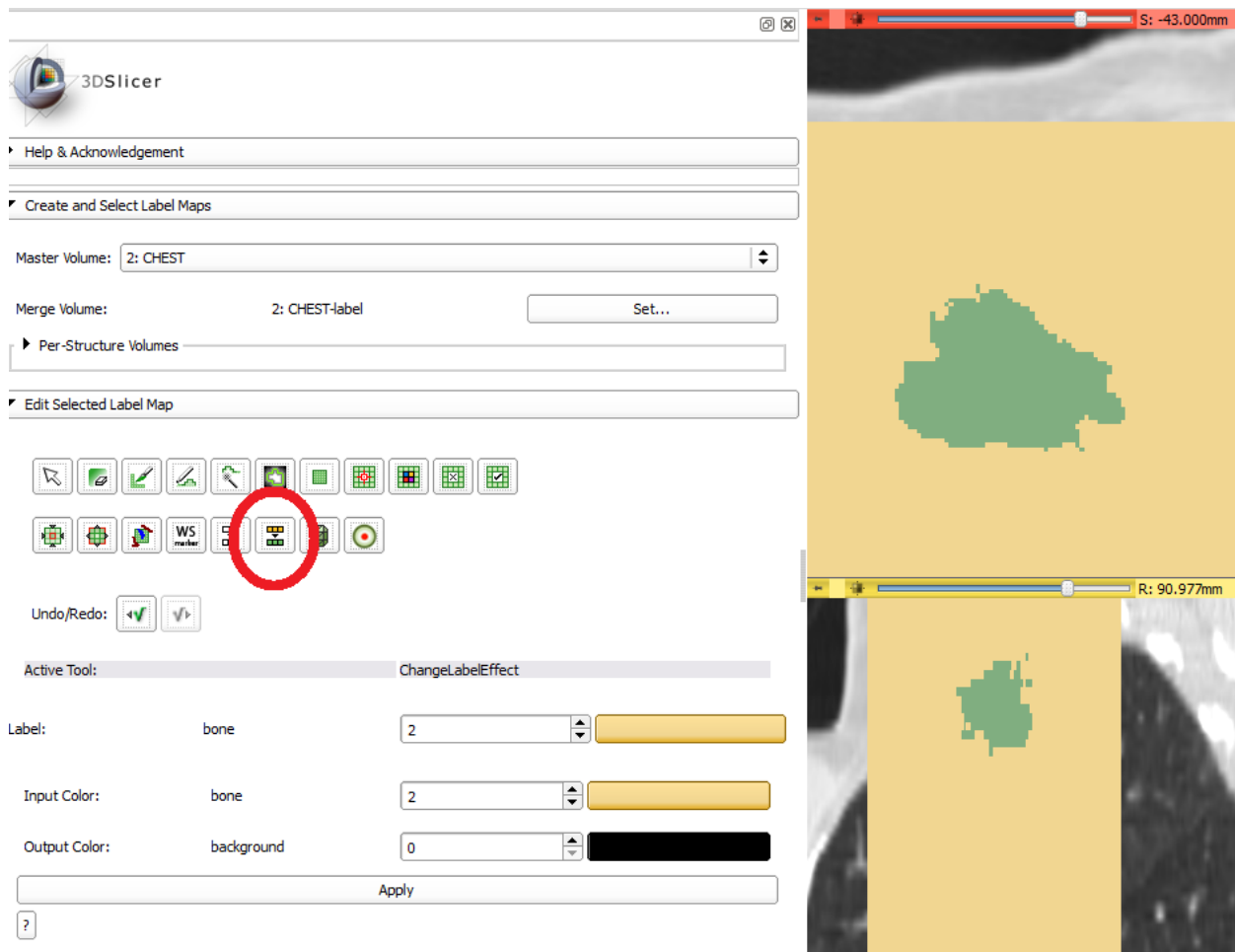
As mentioned, one of the tools that has been validated in scientific literature is the ‘Grow Cut’ tool. Using this method, the drawing tools are used to define two different regions, one “inside” the Region of Interest, and the other “outside”. This can be done using only one slice, or it can be done on multiple slices in multiple planes.



The two competing regions, in this case tumor (in green), and non tumor (in yellow), are loosely defined using the draw functions. Grow Cut will then competitively grow them together to fill in the gaps.

When you have given Slicer 2 different regions to work with, hitting the ‘Apply Grow Cut’ button will run the algorithm (this can take several minutes), and will ‘grow’ the two regions

together. When complete, you will have an ROI (in our case green) that is embedded in a block of non-ROI (which in this case is yellow).



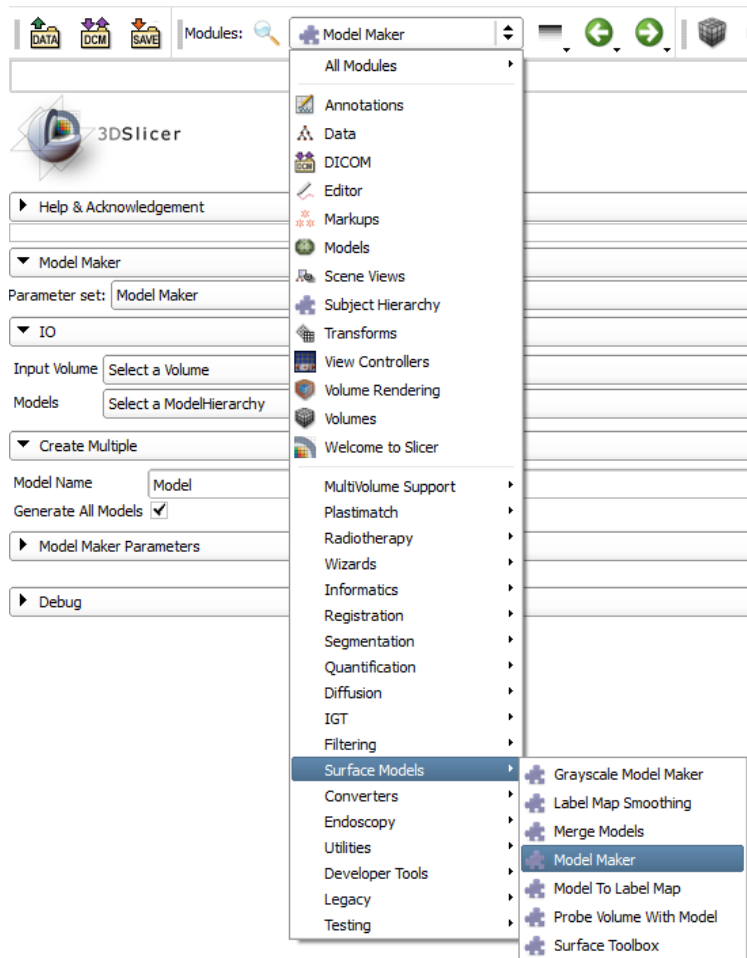
Use the LabelChangeEffect (circled) to change the yellow region outside your ROI into “background”

You can use the LabelChangeEffect to erase the yellow region by converting the yellow region into ‘background’, as seen in the above figure.

This ROI may need to be edited after running Grow Cut, by using the drawing tools (ie Eraser, Paint Brush, etc) in the Editor module. This ROI is called the ‘Label Map’, and is designated in Slicer with default filenames ending in ‘Label’.

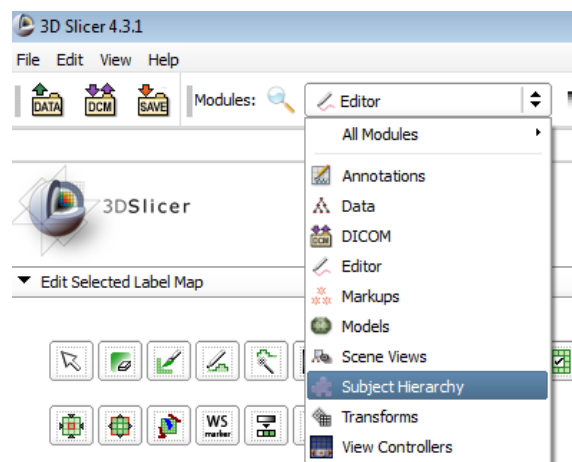
## STEP 4) MAKE A MODEL

Once your label map is complete, you create a surface model using the ‘Model Maker’ module.



Model Maker builds a surface map from the Label Map you constructed with the Editor module.

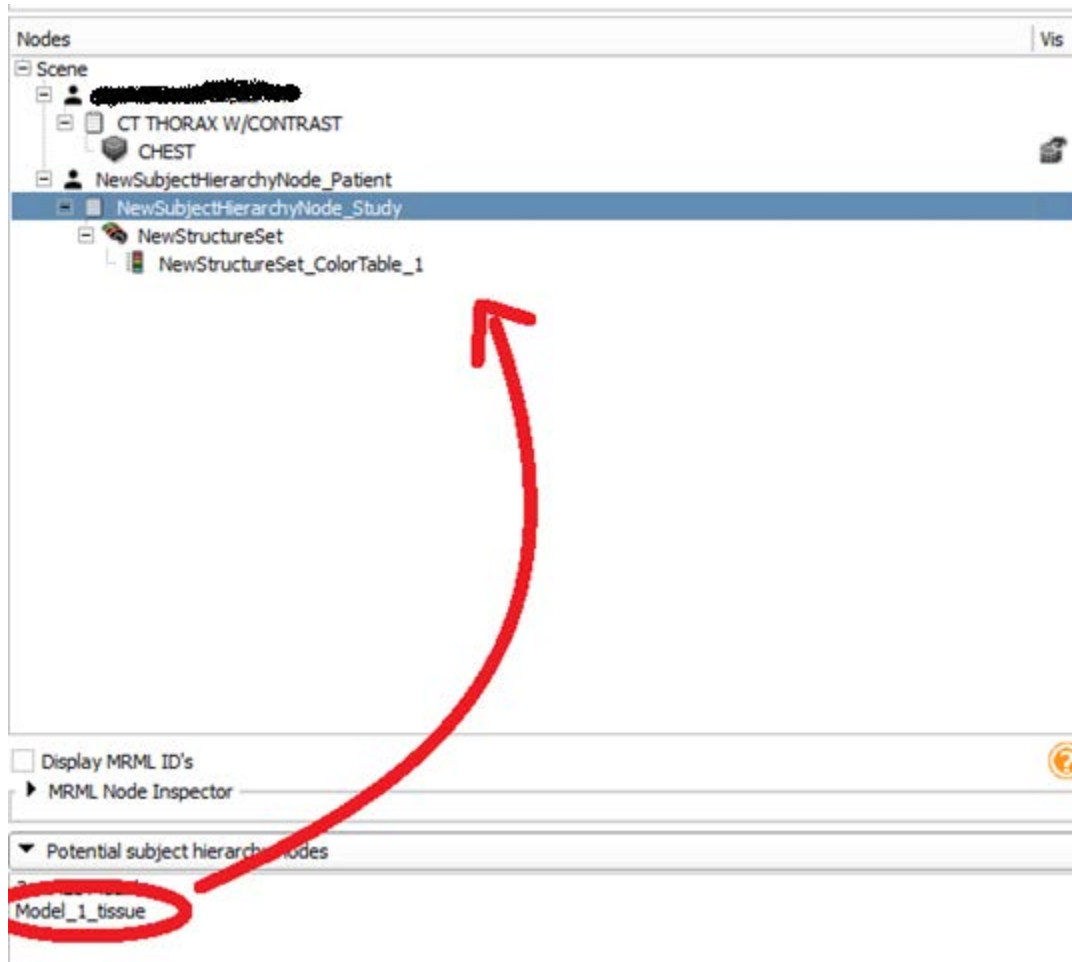
NB – You need to name the model being created, but use an identifiable name (such as a Patient Study Number), not the default name of “model”. The scans will be anonymized later in the process, and this model name is how we will identify patients after the textural analysis.





Then switch to the Subject Hierarchy module and find the surface model on the bottom in the Potential nodes list.

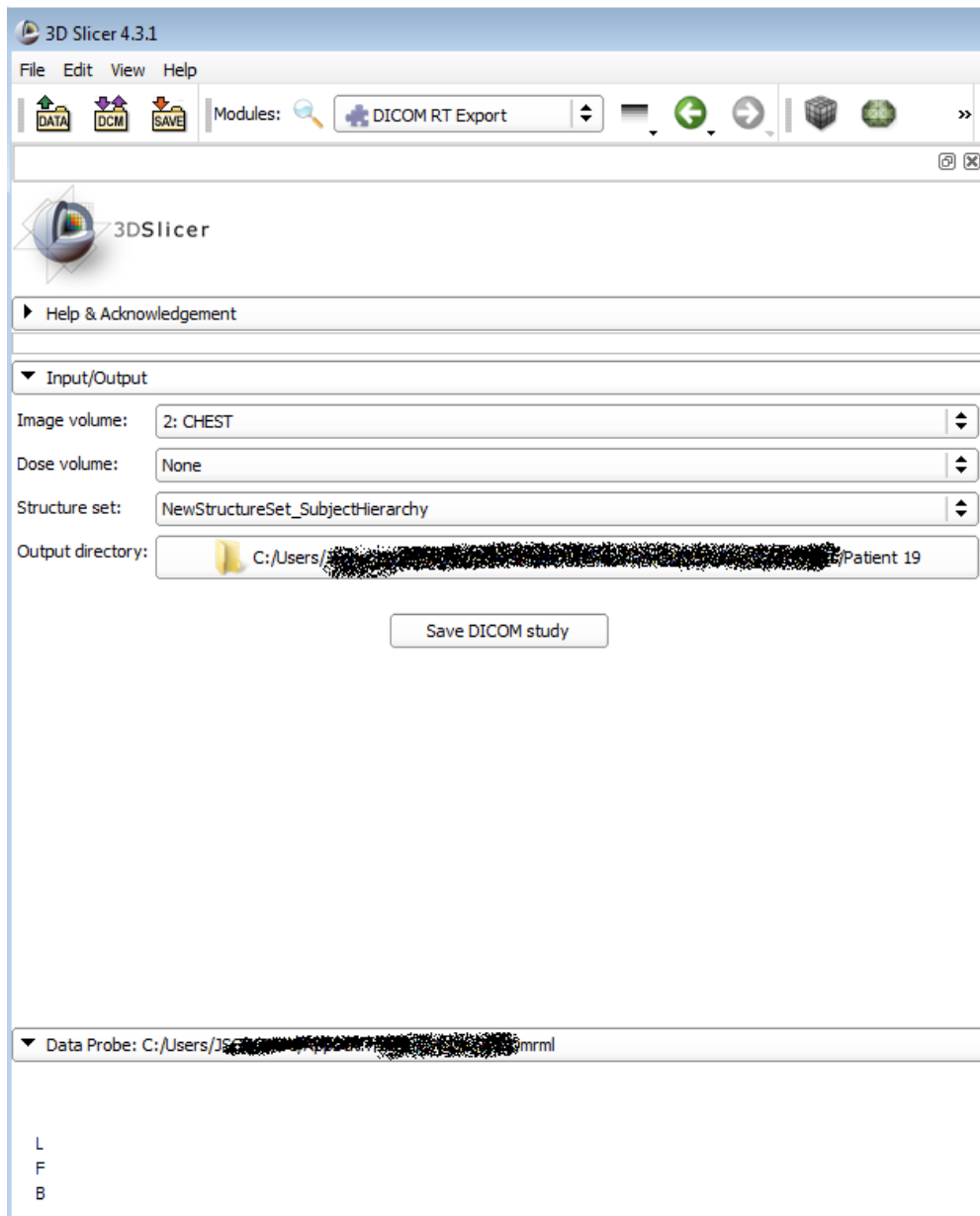
Create a new patient, study and child structure set in the tree (biggest panel on the top) by right-clicking first the scene, then the created objects. Now drag&drop the surface model into the new structure set.



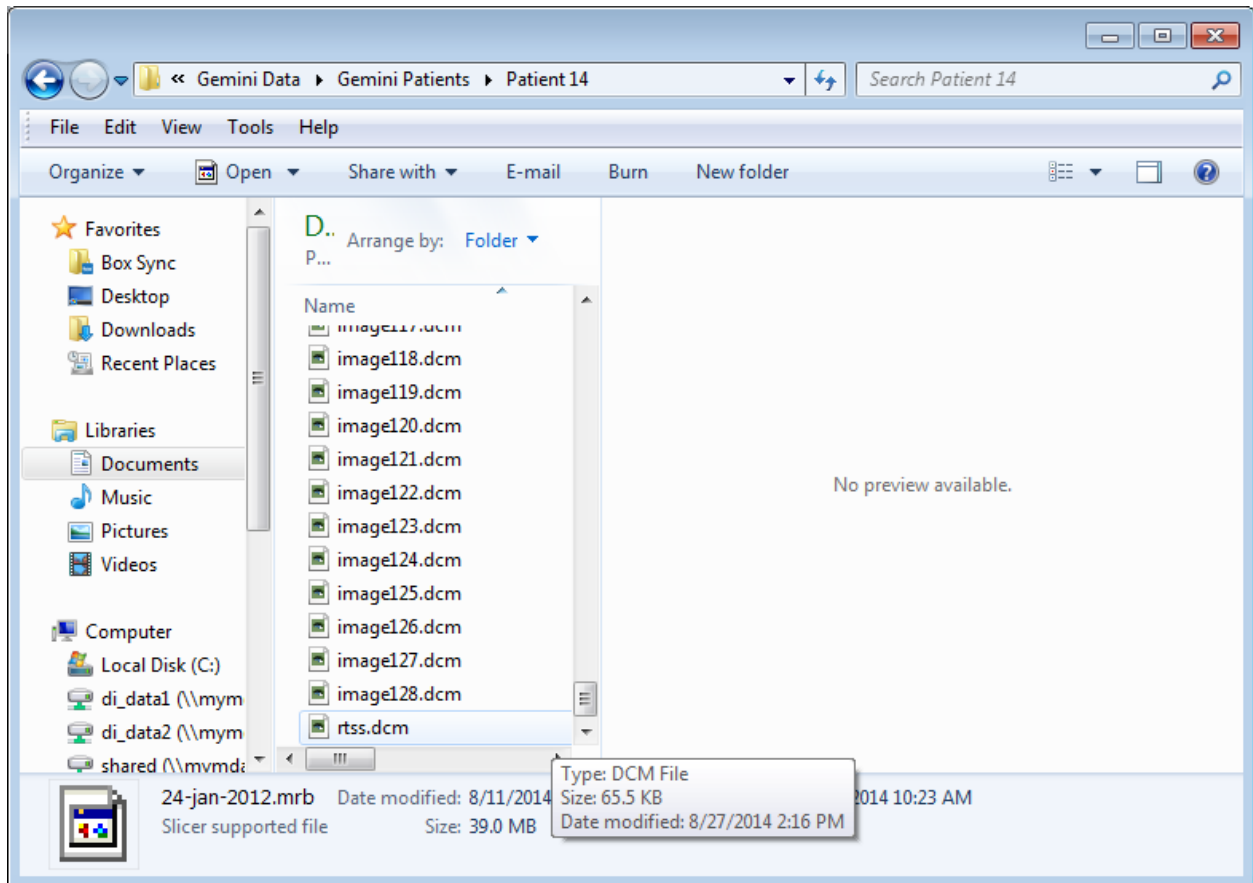
Create a new patient, study, and Structure Set, before dragging and dropping the Surface Model

## STEP 5) CONVERT INTO RT STRUCTURES.

Now go to the DICOM-RT Export module and choose a CT and structure set to export. This DICOM-RT Export module is part of the SlicerRT downloadable add-on, which can be obtained through “View -> Extensions Manager -> SlicerRT “



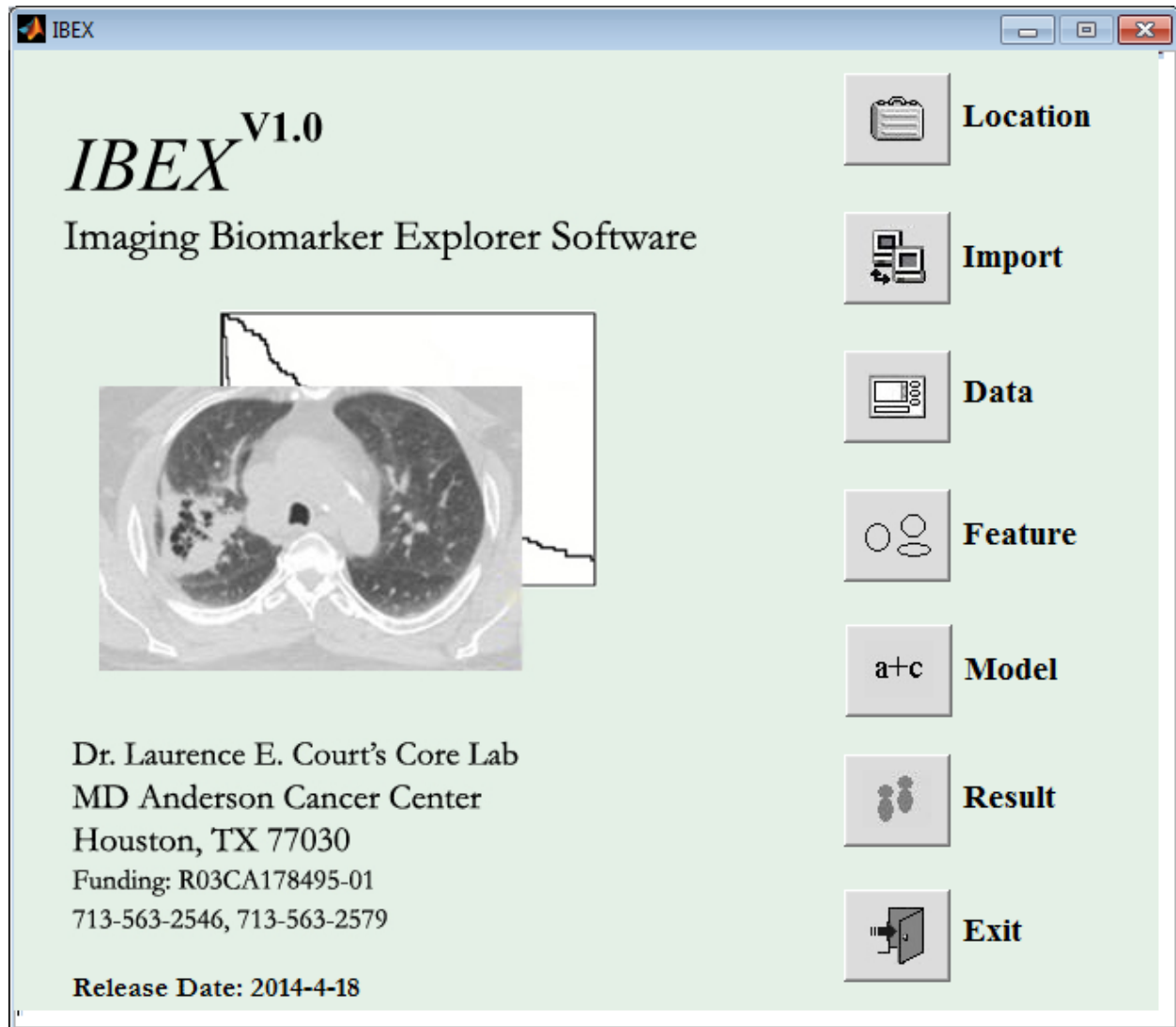
The output is a series of DICOMs and RT structures saved with generic names, ie IMG001.dcm through IMG127.dcm, one for every CT slice, as well as a file named rtss.dcm which contains the contours in an RT structure format. These are best saved to individual folders (ie c:/folder/Patient1Scan1 ) and/or renamed to avoid confusion later.



It is a good idea to move and/or rename these files before they get confusing

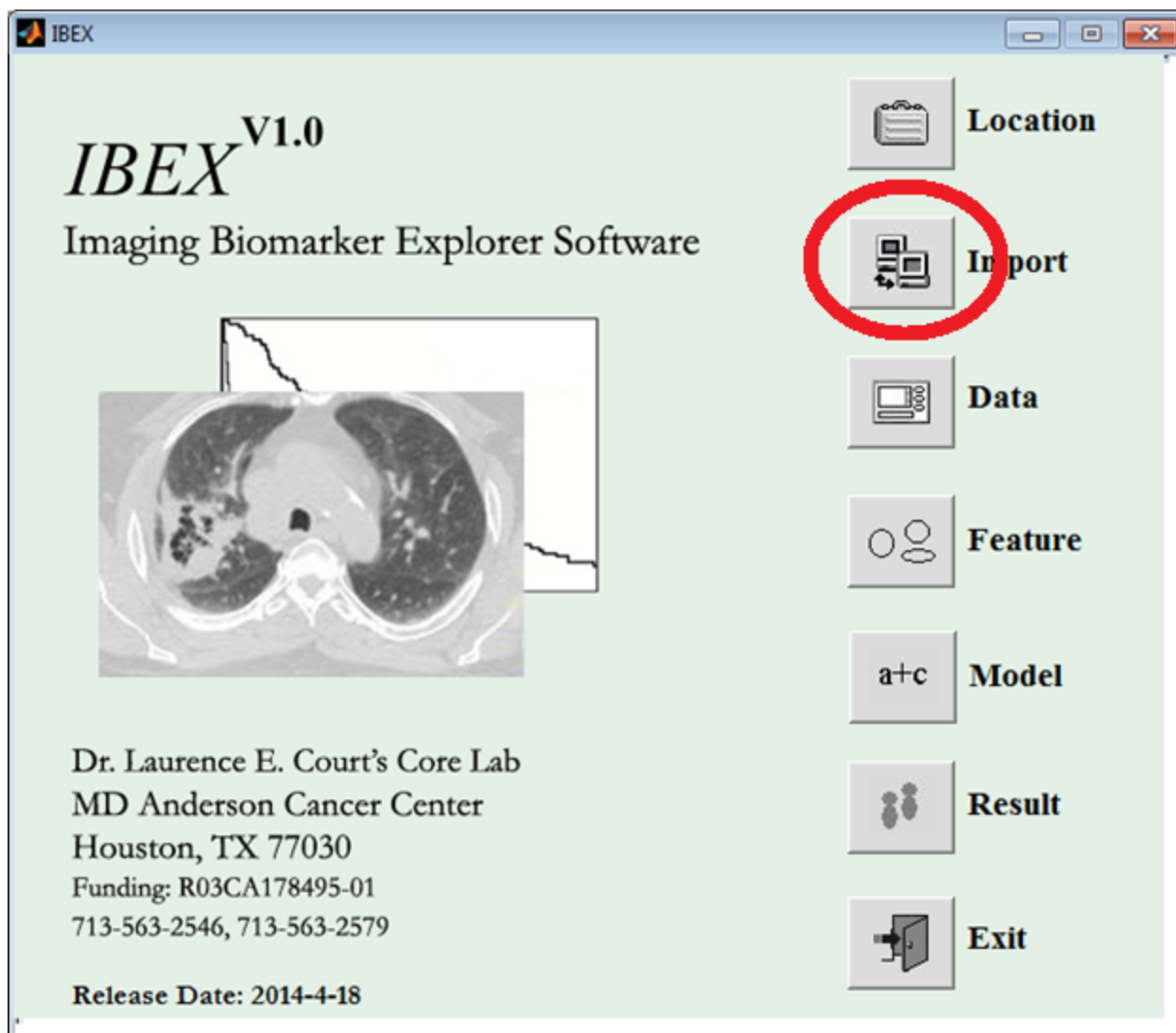
You are now ready to import your images into IBEX.

## STEP 6) IBEX!!!



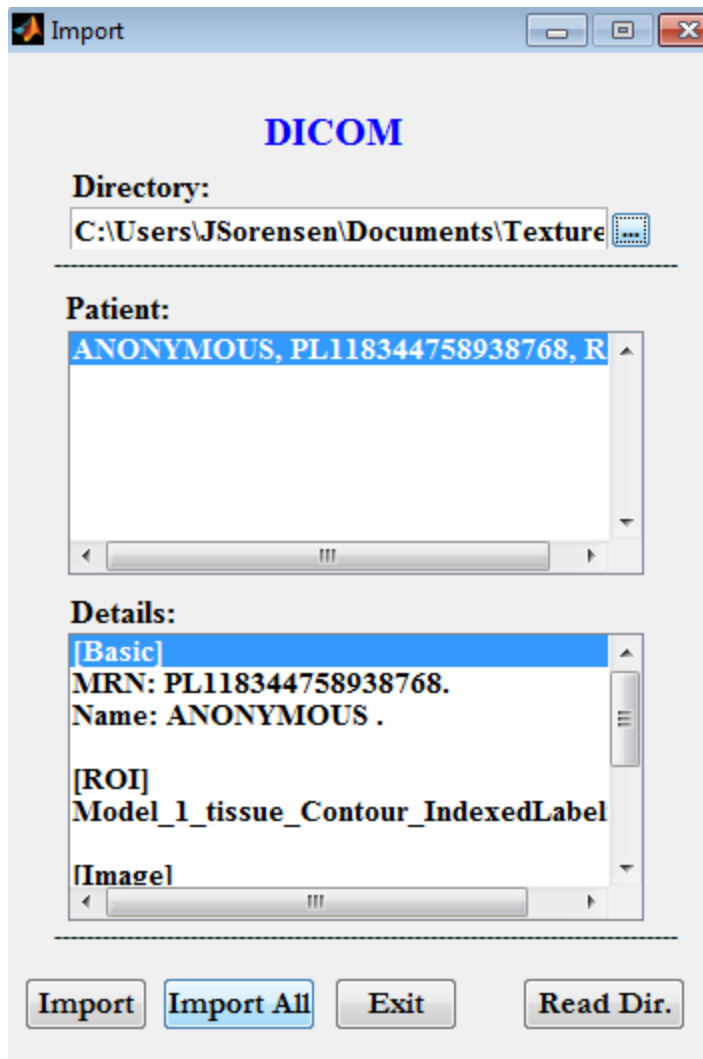
You click on the Import button to load your studies into IBEX

**NB – We have had issues loading more than about 20 scans at a time into IBEX. I haven't explored the exact limit here, but it doesn't like getting too many cases at once. This may be fixed by the time you read this**



From the import menu, you simply choose the directory within which you have saved your DICOMs and RT structures.

IBEX will look for any DICOM images and ROIs, and will show you what it found. This process may take a few minutes if you have a lot of cases.

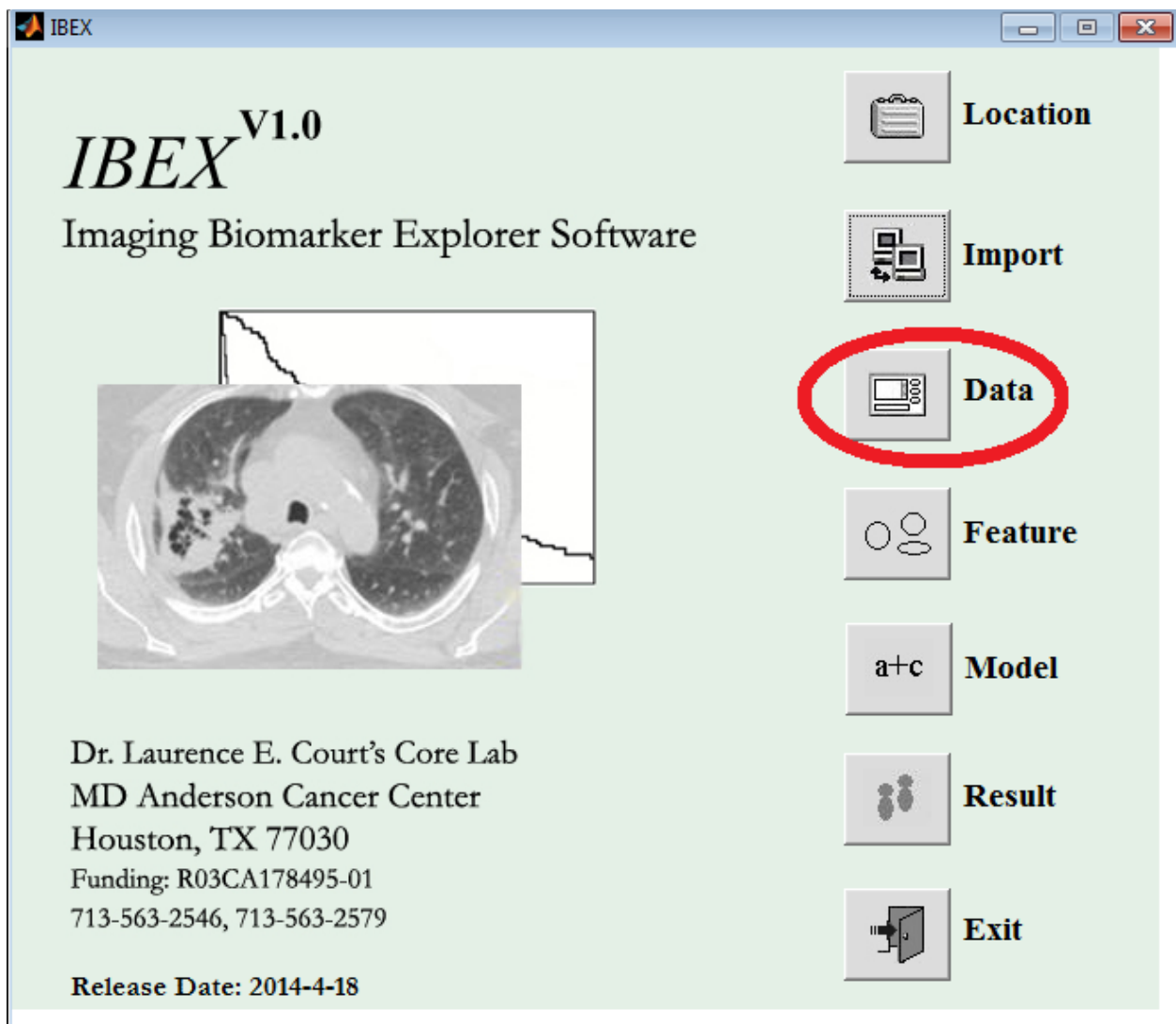


**NB – you can see that the patients have been anonymized during the process of converting the ROIs into RT structures. This is why we gave identifiable names to the models when we created them (ie ‘Model 1’ in this case).**

When IBEX has found all of the DICOMs present, simply click “Import All”. This will also take a while if you have a lot of scans to import.

## STEP 7) SELECT YOUR DATASET

Now we go to the Data menu



Open patient

User: User2; Site: TestingMore

Select a patient:

LastName	FirstName	MiddleName	MRN	Comment	Directory
ANONYMOUS			PL1183447...		ANONYMOUS_PL1183...
ANONYMOUS			PL1658318...		ANONYMOUS_PL1658...
ANONYMOUS			PL1658318...		ANONYMOUS_PL1658...
ANONYMOUS			PL1658318...		ANONYMOUS_PL1658...
ANONYMOUS			PL3172759...		ANONYMOUS_PL3172...
ANONYMOUS			PL412350912		ANONYMOUS_PL412350
ANONYMOUS			PL6931451...		ANONYMOUS_PL6931...

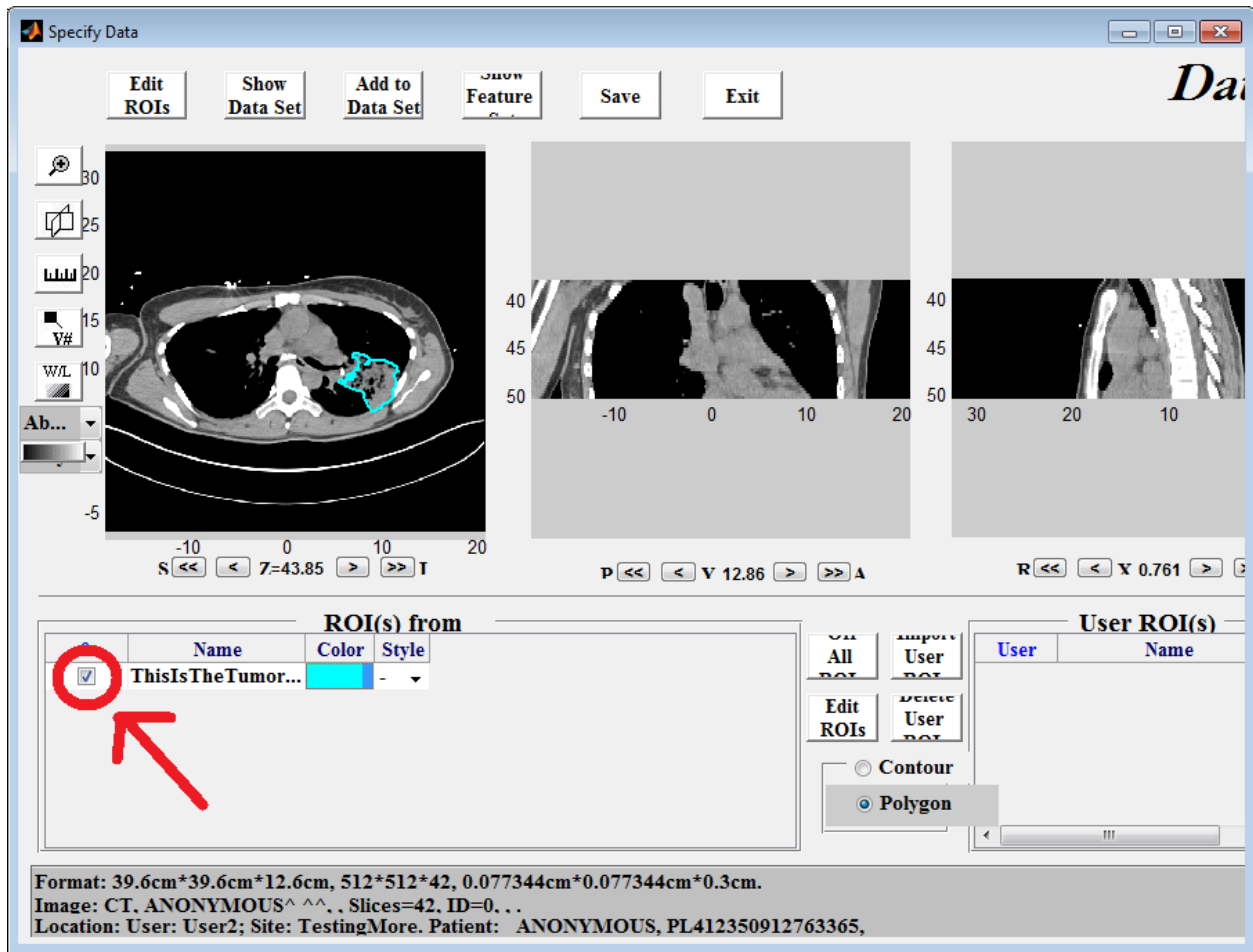
Select image set(s):

Modality	DBName	ScanTime	Slices	Comment	SeriesInfo
CT	ANONYMOUS^ ^^		42		

Open Cancel

You'll need to open each case and select the ROI to add it to your IBEX dataset.

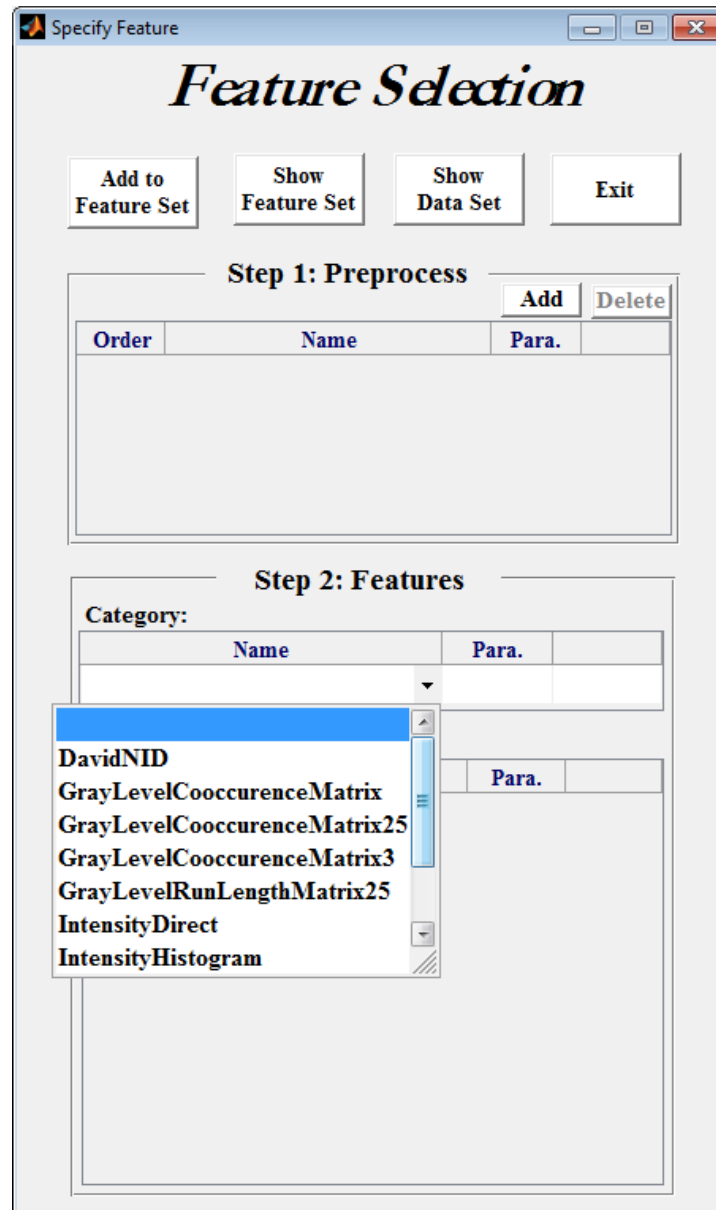




Click the box here to add this case to your IBEX dataset

Once all of your cases have been added to the dataset, you open the Feature Selection menu

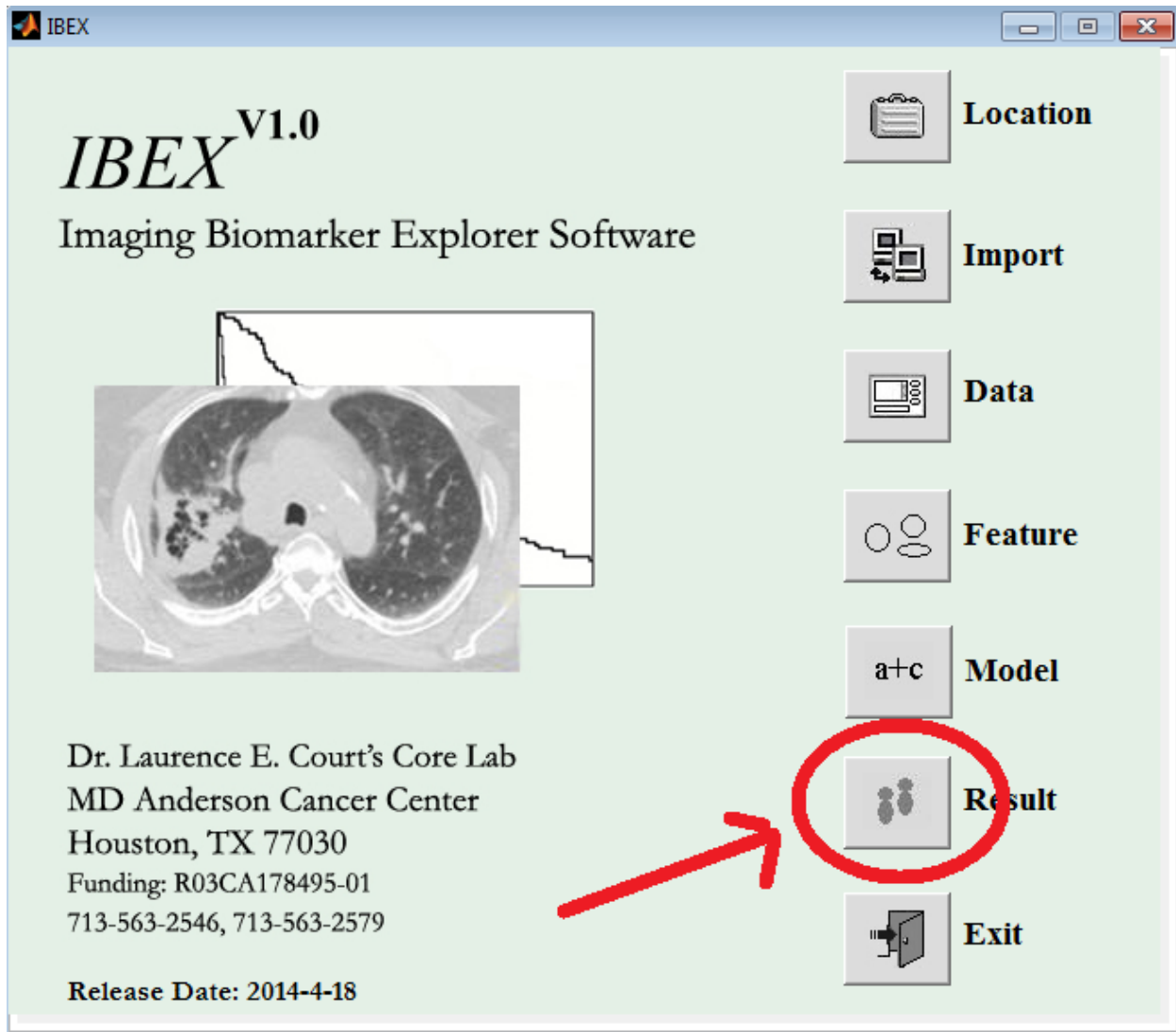
## STEP 8) SELECT YOUR FEATURES AND PRE-PROCESSING METHODS



This is where the magic happens

Pre-processing and feature selection happens here. After selecting a given feature or pre-processing tool, you have to add them to the "Feature Set". There is a lot of material here, and it would require a user-guide of its own to explain. You will need to know ahead of time what kind of pre-processing you want, and what features you are looking for.

## STEP 9) PUSH THE BUTTON AND GET YOUR RESULTS



Once you have created a feature set, you simply click on the “Result” button, select your Dataset and Feature Set, and press the button. This step should only take a few seconds.

	A	B	C	D	E	F	G	H	I	J	K	L
1	DataSet Fi	C:\IBEX\D										
2	FeatureSe	C:\IBEX\D										
3												
4					F1-Intensi	F1-Intensi	F1-Intensi	F1-Intensi	F1-Intensi	F1-Intensi	F1-Intensi	F1-Intensi
5	Index	Image	ROI	MRN	GlobalEnt	GlobalMa	GlobalMe	GlobalMe	GlobalMe	GlobalMir	GlobalStd	GlobalUni
6	D1	ANONYM<ThisIsThe	PL4123505	4.732998	1991	912.23	912.23	988	0	184.0932	0.066692	
7	D2	ANONYM<Model_1	PL1183447	5.768724	1784	854.3689	854.3689	920	131	243.9245	0.023668	
8	D3	ANONYM<Model_1	PL3172755	5.589275	1321	885.253	885.253	957	13	231.9034	0.02704	
9	D4	ANONYM<ThisIsThe	PL4123505	4.732998	1991	912.23	912.23	988	0	184.0932	0.066692	
10												
11												
12												
13												

You will now end up with a large excel spreadsheet describing your results. I advise you to give this to a statistician, and let them worry about it.