Guide to GUI Application ui_for_dicom_ghimire

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1 Launching the application:

To launch the application, run the '.m' file named 'ui_for_dicom_ghimire.m'.

2 Loading DICOM files:

Click 'Locate DICOM folder' above the viewer window, and select a folder that contains your DICOM files.

The application expects that all the DICOM images related to a project are stored in one folder, with some order. The files are loaded in the order they are present in the folder.

3 Anonymizing:

To anonymize the DICOM files, first change the top 3 fields, Patient Name, Patient ID, and Patient Birth Date, under 'Information from DICOM Headers' on the top right of the application window.

Having done this, click on the 'Anonymize and save' button below the text fields. The application will now create a folder called anonymized in the directory where your chosen DICOM directory is present, save the anonymized DICOM files to this folder, and switch the location of the application to this folder.

You will notice that the 3 fields have now changed for all the DICOM files, which are now being read from the 'anonymized' folder.

4 DICOM to jpeg:

To convert the slice of your choice to .jpeg, click the button 'Save as Jpeg' to the right of the viewing window.

The application will ask you to choose a location and a file name that it will use to save the current DICOM slice as a .jpeg image. The application will also save the DICOM header associated with the slice to the same location and under the same name as a '.mat' file. This '.mat' file contains one variable named 'dcmInfo' that contains the DICOM tags associated with the DICOM slice you saved.

5 jpeg to DICOM:

To convert and save a JPEG image as DICOM, click on the 'JPEG to DICOM' button to the right of the viewer window.

The application will first ask you to locate the '.jpeg' file you want to convert. It will then ask you for the corresponding '.mat' file that contains

the associated DICOM headers. The '.mat' file you choose must contain a variable named 'dcmInfo' that contains DICOM tags and associated values.

6 Annotations:

To annotate a slice, click on 'Add annotation' button to the right of the viewing window. The application will now change your cursor to a cross when it is moved into the viewer window. You can press down the left mouse button and drag the mouse to create a closed annotation.

After you release the left mouse button, the application asks you whether you want to **save the annotation**. If you choose 'yes', the application will ask you to assign a name to the annotation. This annotation has now been saved into a '.mat' file called 'annotations.mat' in the directory that contains the DICOM images you are currently working on.

You can also view all the annotations on the current slice with their assigned names in the 'Annotations on Current Page' window to the bottom right of the GUI.

If you later load the same directory, you will be able to view all the annotations you have made previously while working in this directory.

The file 'annotations.mat' contains all the annotations associated with its parent directory as a 'cell'. Each annotation is a structure, 'struct', with 3 fields, 'nslice' which is the index of the slice the annotation corresponds to, 'vertices' which is a 2D array of vertices associated with the annotation, and 'name' which is the user-assigned name of the annotation.

7 Creating 3D, Measuring Area and Volume: Propagate to 3D

To create 3D isosurface and generate area and volume measurements related to your annotations, first locate the slice that contains the annotations you want to use. After this, click the 'Propagate to 3D' button on the bottom right of the GUI, to the left of the annotations window.

The application will now produce a dialog asking for two values with field names 'forward propagation until slice' and 'backward propagation until slice'; your entry to the first field must be a number greater than the index of the current slice and that to the second field must be a number smaller than the index of the current slice.

When you press 'ok', the application will produce two figures, 'Figure 5' and 'Figure 10'. Figure 5 will contain the area and volume information related to all your annotations on the current slice, and Figure 10 will contain a 3D representation created from the annotations on the current slice, using slices in the range specified by the two values 'forward propagation until slice' and 'backward propagation until slice'.