York University
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Department of Electrical Engineering and Computer Science

EECS4640/5640: Medical Imaging Techniques

EA-3: Medical Image Analysis Using 3D Slicer

Objectives

The goal of this experiential assignment (EA) is to become familiar with 3D Slicer, an open-source software package for medical image analysis and utilize it in a number of medical image analysis applications.

Your work will be evaluated based on your EA report. When preparing your report, keep in mind these points:

- Prepare the report with complete details of your work for each part.
- Include the screenshots of **the whole screen** (including the date/time) for each section in your report.
- Submit your report (PDF file) in eClass **(Experiential Assignment 3 Report)** by the deadline.

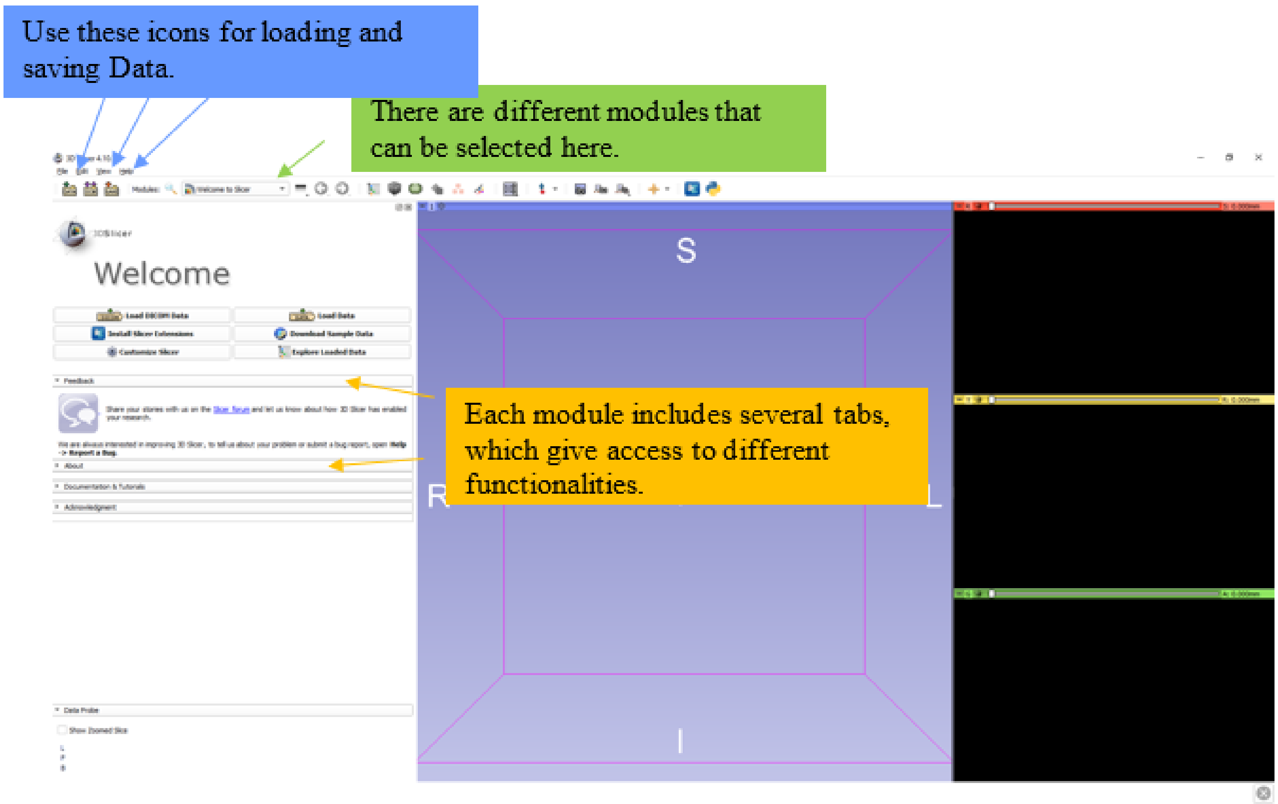
Note: you can download 3D Slicer from link below:

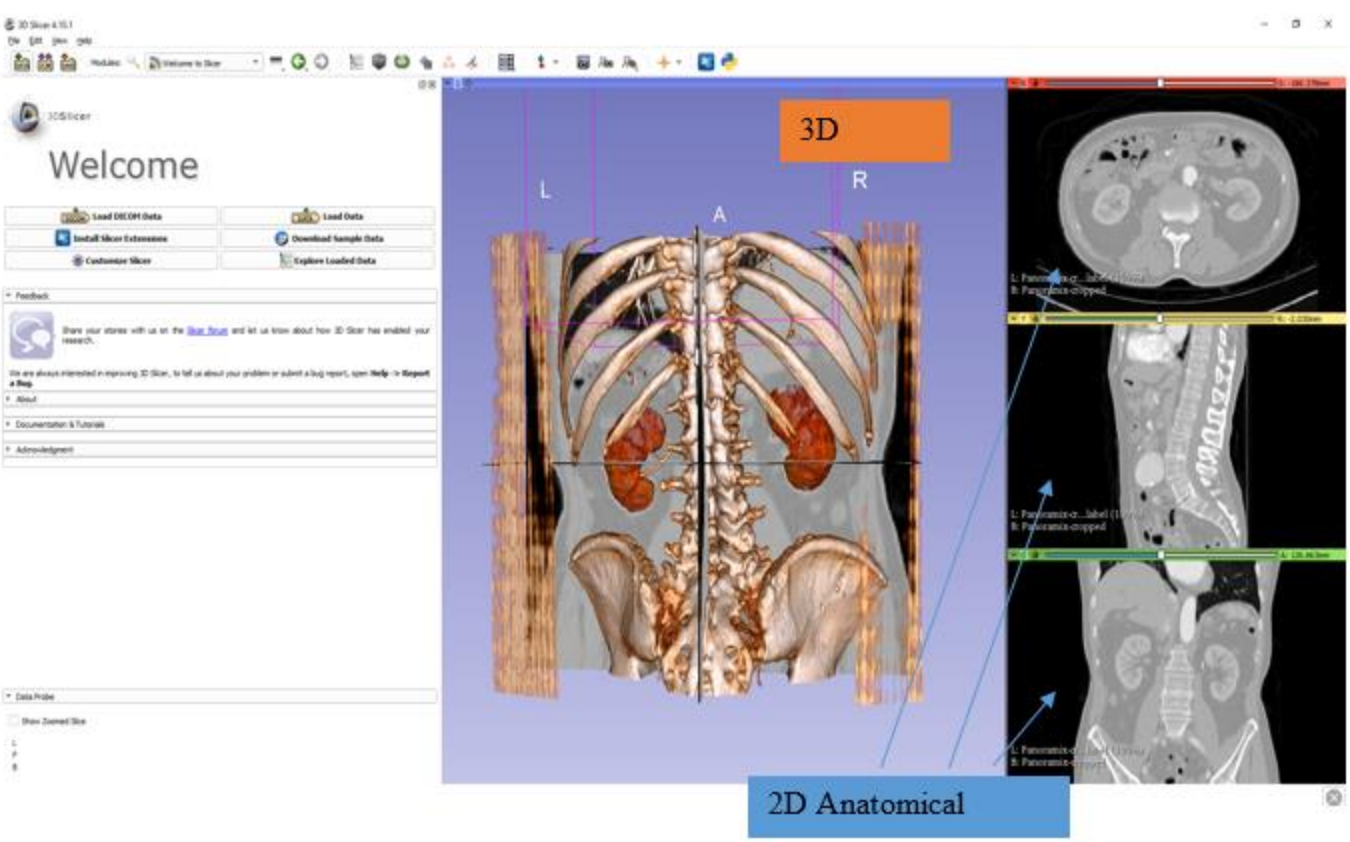
https://download.slicer.org/

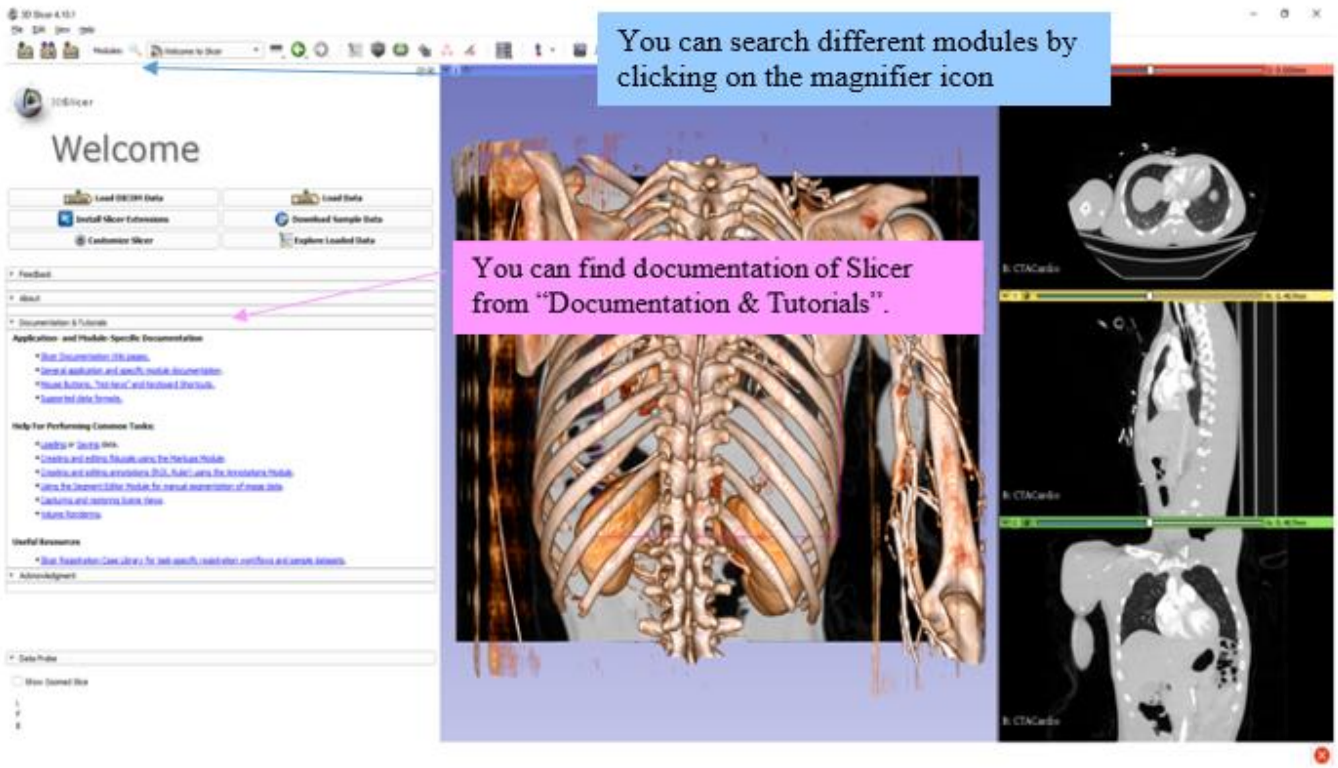
Install the stable release **version 4.8.1** (using the *older releases* link) based on your platform.
Note: all extensions (including those described in the parts 4, 6) can be downloaded from the "extensions" folder associated with this version of 3D slicer.

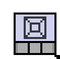
1. Loading data and getting familiar with the interface:

   Once you run the application, you can see the default interface of Slicer:







a) The **Welcome** module panel contains shortcuts for loading different types of data. A series of **sample data** are also available.
   - Click on **Download Sample Data** to access the Sample Data Module.
   - Click on **CTA Abdomen** to download the dataset in Slicer. Note: if the download failed, you can use the downloaded file “Panoramix-cropped.nrrd” that is provided in eClass (in “Imaging Data” folder) and load it in 3D slicer using **Add Data** in the **File** menu.
   - From the toolbar menu you can change the view mode. Look for this  icon, and select **Conventional** from the viewing mode menu.
   - Position the mouse on the little pin icon on the top left corner of the red viewer to display the viewer menu.
   - Click on the link icon to link all three 2D viewers, then click on the eye icon next to it to display the slices in the 3D viewer.
   - Repeat the previous step for the two other 2D viewer.
   - Include a screenshot in your report.

b) You may see that in the 3D viewer the image is not located at the center of coordinates. To handle this issue, position the mouse on the little pin icon in the top corner of 3D viewer and click on the icon which centers the 3D view. Include a screenshot in your report.

c) 3D Slicer can render 3D volumes using tomographic images. Select the **Volume Rendering** module, then select the **Panoramix-cropped** volume and click on the eye icon to see the volume. Include a screenshot in your report.

d) You can select from several presets that applies a pre-defined set of functions for the opacity, color and gradient transfer functions for proper visualization of different anatomies in a specific imaging modality.

From **Display** section, change the **preset** to **CT-coronary-Arteries-2**. How 3D viewer change? Include a screenshot in your report.

e) From the **Advanced** tab select a small ROI (Region of Interest) that includes both kidneys. In order to change the ROI, you should change the **L-R, P-A, and I-S Range**.
Note: You may not see the ROI that you define before you click on the eye icon to **display the ROI**. Include a screenshot in your report.

2. 3D slicer can generate 3D models using the binary label maps obtained from image segmentation. In this part you will generate a label map and a 3D model for the skull. Load the **MR-head.nrrd** file using the **Add Data** icon, and display all linked 2D slices in 3D viewer.

a) Now you should see three orthogonal slices in the 3D viewer. Select the **Editor** Module. First, you should **Add Structure** in the per-structure volumes tab (for example bone). In the **Edit Selected Label Map tab**, there are several tools for editing a label map. Click on the **Threshold Effect**, and change the threshold parameters to segment the skull as accurate as possible. Include a screenshot in your report.
Note: You should set the **Master Volume** and the **Merge Volume** before you make any changes with the editor module.

b) In the **Editor** module, there are a number of tools that can be used to enhance the label maps. To improve the result of the previous part, use the **DilateEffect** and **ErodeEffect**. Include a screenshot for each applied effect in your report. What is the effect of each tool? Explain different parameters that are used in dilation and erosion, and the effect of these parameters on output image.

c) After you finish the labeling process, click on the **Merge and Build** to make a 3D model of skull. Include a screenshot in your report.

3. In this part, you will detect and segment a brain tumor in an MR image and create a 3D tumor model. You will segment the brain tumor using two different approaches as described below.

a) In this part you will segment the tumor manually.
   - Load **BrainTumor.nrrd**.
   - Select the **Segmentations** Module.
   - In the **Active segmentation** create new segmentation and click on **Add segment**.
   - Now you should **Edit selected** segmentation. From **Master volume** section, select the volume that you want to use (BrainTumor).
   - Select the **Paint** tool and set the diameter to 1%.
   - Select one of the 2D viewers that shows the tumor slices clearly.
   - Go through the tumor slices and use the paint tool to segment the tumor region in each slide. <u>You can skip some slices</u>.
   - Select the **None** tool, and then click on **Show 3D**. Turn the visibility of the 2D viewers off. The tumor should be segmented accurately with no excluded region inside (within a slice). Include a screenshot in your report.
   - Save your model.

b) Now you may see some gap between the segmented tumor sections, as you skip some slices. Use **Fill between slices** tool to fill the gap. Include a screenshot in your report.

c) Once your segmentation is completed, you can export the model.
   - Select **Segmentations** Module.
   - Export the model.

   Now in **models** you should see your segmentation. Include a screenshot in your report.

d) In this part you will segment the tumor using a region growing technique.
   - Load the **BrainTumor.nrrd** again.
   - To create a list of fiducials (seeds) for this algorithm, click on the tool bar icon to specify the position of a new fiducial. You can use the **Markups** module to see the seeds that you specified and edit them, if required.
   - Select the **Simple Region Growing Segmentation** Module.
   - Adjust the segmentation parameters to segment the tumor volume and click on **Apply**. The tumor should be segmented accurately with no excluded region inside. Include a screenshot in your report.
   - Once you complete the segmentation process, select the **Model Maker** module, and make a 3D model from your segmentation. Include a screenshot in your report.

4. In this section, you will calculate the Dice similarity coefficient for your segmentation. You need to install an extension for calculating this criterion. An extension is a software package of one or more Slicer modules. After installing an extension, the associated modules will be available to the user like the built-in ones.

   - Click on **Extension Manager** from **view** tab.
   - Find **DiceComputation** and install it. Note: the extension has been provided for different platforms (win, linux, macos) in the "Extensions" folder in eClass. You can install it by clicking on the wrench icon (top right corner of the Extensions Manager) and then **Install Extension from File**.
   - Restart the 3D Slicer application.
   - Now you can find the installed extension in the **modules** tab.
   - Load **sample1.nrrd** and **sample1_gt.nrrd** in a single slicer scene.
   - Segment the tumor in the **sample1** image.
     Note: you can use **simple region growing** method or **paint** tool to segment the tumor.
   - Include a screenshot in your report.
   - Export your segmentation as a **labelmap** using the **segment editor** module.
   - Select the **DiceComputation** module.
   - In the **Parameter** tab click on **Dice** and compute Dice similarity coefficient between your labelmap and the ground truth (to create a labelmap for the ground truth (GT), you can segment the binary image using the **Threshold** tool in the **Segment Editor** module using a threshold range of 1 to 1, and then export the tumor segment to a labelmap in **Segmentations** module).
   - Include a screenshot in your report.

5. In this section, you have a pre-treatment (baseline) and a post-treatment MRI acquired from a breast cancer patient. To assess the treatment effects, you should register the post-treatment scan to the baseline. Some pre-processing is also necessary to obtain a good registration.

a) Compare the unregistered images: first, you should show two images in a single viewer.
   - Load **PostRx.nrrd** and **PreRx.nrrd** in a single slicer scene.
   - Click on the link icon to link all three 2D viewers, then select **PostRx** as the foreground image, and **PreRx** as the background image.
   - Change the percentage of the foreground image to 60%, so you can see both image at the same time.
   - Include a screenshot in your report.

b) Cropping: you should register only the left breast containing tumor, so you should crop the images.
   - Select the **Crop Volume** module, then select the **Input Volume** and **Input ROI**, check **Isotropic Spacing**.
   - Define the ROI around the left breast and click on **Apply**.
   - Select the **Data** module, you should see the cropped image in the **scene** tab.
   - Repeat the previous steps for the **PostRx** image.
   - Include screenshots for both images before and after cropping in your report.

c) MR bias field correction: the effect of undesirable variation in the magnetic field (bias field) on the image intensity should be corrected for a better image registration.
   - Go to the **N4ITKBiasFieldCorrection** module.
   - Select the **input image** and **output volume**, and click on **apply**.
   - Apply the bias field correction for both cropped images.
   - Explain the difference between the corrected images and original images.
   - Include screenshots for both images before and after correction in your report.

d) Mask generation: to ensure that the nonrigid portion of the image registration will not compensate for the tumor changes after the treatment, you should generate masks that include the entire breast but not the tumor.
   - Select the **foreground masking** module.
   - Select the **input image volume** and **output mask**, and select the **output image pixel type** as **uchar**, then click on **apply**.
   - Generate the mask for both corrected images.
   - Include screenshots for both images in your report.

   - Select the result of the previous part (corrected image) as a **foreground image**, and the corresponding mask as a **label map**.
   - Go to the **editor** module and create a merge label map. Click on  icon, to show the label map as a region outline. You may see that the tumor in some slices are not segmented correctly.
   - Select the **paint** tool and correct the mask, if required.
   - Include screenshots for both images in your report.

e) Registration:
   - Select the **General Registration** module.
   - Select the background image as **fixed image volume**, and foreground image as **moving image volume**.
     Note: the background image and foreground image are the corrected PreRx and PostRx images that you generated in part c.
   - Define a new **Slicer Linear Transform**.
   - Check **Rigid, Rigid + Scale, Rigid + scale + skew** in **Registration Phases** tab, and click on apply.
   - Include a screenshot in your report.

   - Select the **Data** module, you can see the registration transformation map by displaying the **Slicer Linear Transform** that you generated.
   - Include a screenshot in your report.

   - In the previous steps you applied an affine image registration. Now you should improve your registration using a nonrigid registration. Define a new **Slicer BSpline Transform**:
   - Select the previous output as an **Initialization Transform**.
   - Check **BSpline** in the **Registration Phases** tab.
   - In the **Mask Option** tab, check **ROI**, and select **Masking Input Fixed**, and **Masking Input Moving**. Note: you should select the masks that you generated in part d.
   - Click on **apply**.
   - Include a screenshot in your report.
   - Repeat the nonrigid registration. This time in **Main Parameters** tab, change **Bspline Grid Size** to 7, 7, 5.
   - Include a screenshot in your report.

   - Select the **Data** module, you can see the registration transformation map (deformation field) by displaying the **Slicer BSpline Transform** that you generated.
   - Include a screenshot in your report.

6. In this part, you will evaluate how a brain tumor change in response to radiation therapy using registration method.

a) First, segment the tumor in the baseline (pre-treatment) and follow-up (post-treatment) images separately:
   - Load **MR_tumor_baseline.nrrd** and **MR_tumor_followup.nrrd** in a single slicer scene.
   - Segment tumor in each image, using the paint tool, and save your segmentations.
   - Include screenshots for both segmented images in your report.

b) Now register the images:
   - Download the **Segment Registration** extension. Note: the extension has been provided for different platforms (win, linux, macos) in the “Extensions” folder in eClass. You can install it by

clicking on the wrench icon (top right corner of the Extensions Manager) and then **Install Extension from File**.

- In the **Segment Registration** module, select the baseline image as **Fixed Image** and its corresponding segmentation as **Fixed Segmentation**. Also select the follow-up image and its segmentation as **Moving Image** and **Moving Segmentation**, respectively.
- Click on **Perform registration**.
- Include a screenshot of the registered images showing the segmented tumor in your report.

c) In this part, you will see the effect of registration on your segmented mask.

- Load **MR_tumor_baseline.nrrd** and **MR_tumor_followup.nrrd** again.
- Select the **General Registration** module.
- Click on the link icon to link all three 2D viewers, then select **MR_tumor_followup.nrrd** as the foreground image, and **MR_tumor_baseline.nrrd** as the background image.
- Select the background image as **fixed image volume**, and the foreground image as **moving image volume**.
- Define new **Slicer Linear Transform**.
- Check **Rigid** in **Registration Phases** tab.
- You can adjust the **Advanced Optimization Settings**, if required.
- Click on **Apply**.
- Include screenshots of the overlaid images before and after registration, and also a screenshot of your optimization settings in your report.

- Segment the registered follow up image again, using the paint tool.
- Compute the Dice similarity coefficient for the segmented tumors on registered and non-registered follow up images.
- Include a screenshot in your report.