Medical Imaging Assignment

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Introduction

In this project, our aim is to explore and implement various tasks related to DICOM image processing. Specifically, we will focus on loading and visualizing DICOM images, creating a rotating Maximum Intensity Projection (MIP) animation, performing 3D rigid coregistration of images, and visualizing a specific region of interest, the Thalamus, in the input image space.

The project consists of two main parts. In the first part, the focus is on loading and visualizing DICOM images using 3D Slicer and the pydicom library. This includes exploring the header information, loading segmentation images and CT (Computed Tomography) images, and rearranging the images based on their headers. The goal is to gain insights into the image content, facilitate targeted analysis, and create an animation to enhance the understanding of the data.

In the second part of the project, 3D rigid coregistration is performed on the medical images. Coregistration involves aligning multiple images spatially to account for patient movement or imaging artifacts. This step improves the accuracy of subsequent analysis, such as segmentation or region of interest localization. The coregistration can be achieved through the use of landmarks or similarity measures, ensuring that the images are accurately aligned in three-dimensional space.

By combining the capabilities of 3D Slicer, pydicom, and 3D rigid coregistration techniques, this project aims to provide a comprehensive solution for loading, visualizing, and analyzing DICOM images.

DICOM Loading and Visualization

Loading the Dataset in 3D Slicer

To begin the project, the DICOM dataset is loaded into 3D Slicer. This step involves selecting the appropriate DICOM files and configuring the loading parameters within the software. By loading the dataset in 3D Slicer, we can take advantage of its advanced visualization capabilities and explore the image data in a user-friendly interface.

Visualizing DICOM Images

Once the dataset is loaded, we can visualize the DICOM images using the tools provided by 3D Slicer. This allows us to interactively explore the images, adjust the windowing settings, and analyze the

anatomical structures present in the dataset. Visualizing the DICOM images provides valuable insights into the image content, so we can correctly visualize the DICOM images in python.
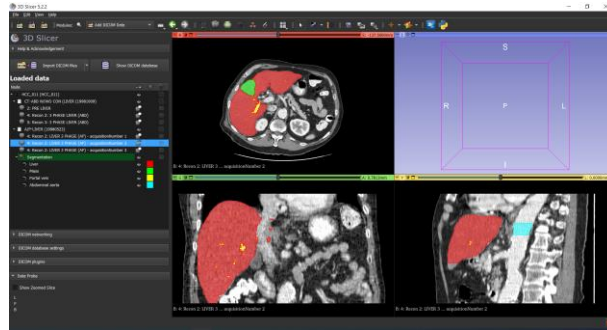
Loading Segmentation Images and CT Images with PyDicom

In addition to 3D Slicer, we utilize the Pydicom library in Python to load specific segmentation images and CT images from the DICOM dataset. The Pydicom library provides functionalities to read DICOM files and extract pixel data, metadata, and header information. By loading the segmentation images and CT images, we can perform further analysis and visualize specific regions of interest within the DICOM dataset.

Rearranging Images Based on Headers

The header information extracted from the DICOM images provides essential details about the acquisition parameters, such as the acquisition number, slice location, and patient information. By leveraging this header information, we can rearrange the loaded images based on specific criteria. For example, we can select a specific acquisition taken before the tumor was removed, for my implementation this was acquisition two.

Creating an Animation with a Rotating Maximum Intensity Projection

To provide a comprehensive view of the DICOM images, an animation is created by rotating the images and generating Maximum Intensity Projections (MIPs). This process involves rotating the images on the sagittal plane at different angles. MIPs are then computed from the rotated images to highlight the maximum intensity values along the sagittal orientation. The animation enables a dynamic visualization of the image data, aiding in the identification of key features and patterns.
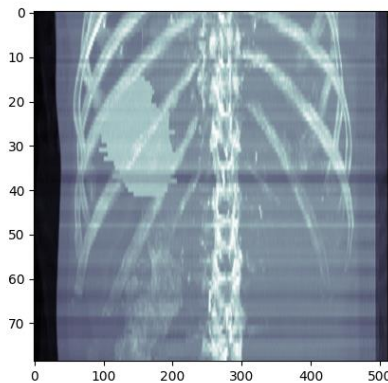
Visualizations

Figure 1: Example of MIP Projection

Coregistration

For the coregistration process, I focused on three DCM files: the reference image (icbm avg152t1talnlin symmetricVI), the segmentation image (AAL31mm), and the input image (RM-Brain3D SPGR). Preprocessing steps were performed to address variations in size and features among the images.

The coregistration was initiated by transforming the reference and input images into 3-dimensional arrays and examining the disparities between them. A coregistration landmarks function was implemented, defining initial parameters and optimizing the transformation using a least squares function. Downsampled arrays were created to reduce computation time, and the resulting coregistration parameters were obtained.

To visualize the effects of coregistration, a comparison of landmark points before and after coregistration was performed. Thalamus region masking was achieved by generating a mask and applying alpha fusion to the input image. The fused image was then transformed back into the input space, and its intensity was matched with the original image. Visualization of the mask in the input space demonstrated the successful masking process.

The performance of the coregistration algorithm was evaluated using metrics such as Mean Absolute Error (MAE), Mean Squared Error (MSE), and mutual information. Lower MAE and MSE values indicated higher similarity between the coregistered input and reference images, while higher mutual information values represented a stronger relationship between the images.

Overall, the coregistration process successfully aligned the input image with the reference image, and the thalamus region was accurately masked and visualized.

Thalamus Region

The implementation of the Thalamus region involved generating a mask by selecting the Thalamus indexes. This was achieved by utilizing the 'get_thalamus_mask()' function. The function identified the specific indexes corresponding to the Thalamus region within the image data. Once the mask was created, it was applied to the input image using the 'visualize_axial_slice()' function, which performed an alpha fusion between the Thalamus region mask and the image. This fusion technique allowed for the visualization and highlighting of the Thalamus region within the image. Additionally, the same fusion process was applied to the reference image for verification purposes. This provided a clear representation of the Thalamus region in both the input and reference images.
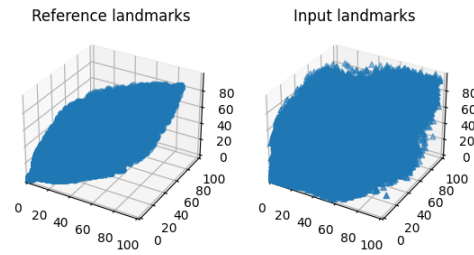
Visualizations
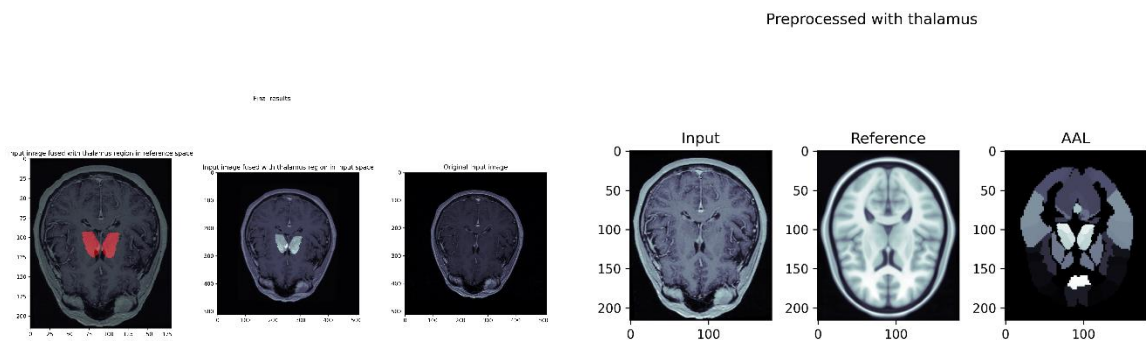
Landmark points comparison before coregistration — Reference landmarks, Input landmarks
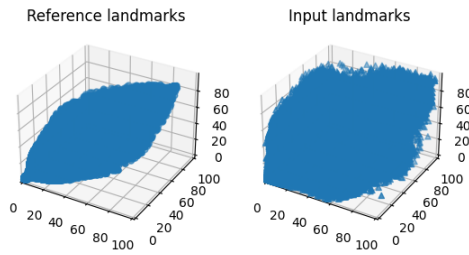
Landmark points comparison after coregistration — Reference landmarks, Input landmarks

Conclusion

Throughout this project, I've had the opportunity to dive into the world of DICOM images and expand my knowledge in the field of medical imaging. It has been very challenging, but I've gained valuable insights and skills along the way.

Initially, downloading the dataset and exploring the DICOM files using 3D Slicer was quite daunting. The format was unfamiliar to me, and I had to invest time in understanding how everything worked. However, with guidance and feedback, I was able to get a better grasp of the project requirements. The programming activities we did before also came in handy, as they provided a good foundation for similar tasks.

The coregistration part was especially challenging. Medical imaging and image processing were new territories for me, so I had to do some serious research to get started. It took time to understand the concepts and find the right approach. Thankfully, the solutions from the programming activities gave me a starting point, and I was able to adapt them to fit the project requirements.

In the end, I feel like I've learned a lot about DICOM images and the fascinating world of medical imaging. Despite the difficulties, it was an incredibly interesting and rewarding experience.