**Automatic Segmentation for Biomedical Images: A Deep Learning-Based, Generalizable Semantic Segmenting Tool for MRI and CT**

**Student**: April Yan

**Mentors**: Dr. Jayashree Kalpathy-Cramer & Jay Patel

**Introduction**:

Semantic segmentation is considered the most explored medical imaging task to recognize structures of interest for making medical decisions. By labeling each pixel/voxel with a corresponding class, it can achieve accurate, early-stage diagnosis. It also refers to “the process of transforming raw images into clinically relevant, spatially structured information”, such as outlining organ boundaries, acquiring tumor dimensions, and identifying different functional regions [1]. With the revolution of machine learning in biomedical image processing, thousands of automatic, deep learning-based algorithms for semantic segmentation have been published annually. However, these tools tend to fit specific tasks, in terms of varying clinical goals, image modality (e.g., Magnetic Resonance Imaging (MRI), Computed Tomography (CT)), image size, voxel spacing, and so on [2]. For example, a well-developed algorithm for brain tumor segmentation may not generalize to a task of segmenting vessels in the liver. As a result, the generalizability of segmentation, which represents fully automated tools that can perform any semantic segmentation tasks given any data without human intervention, becomes an emerging research field nowadays, regarding the fact that 70% of international competitions have been thriving for the automation and generalizability of semantic segmentation of medical images (e.g., Medical Segmentation Decathlon) [1].

As the increasing desire for a general-purpose “segmenter” for medical imaging, we aim to design an automatic semantic segmentation pipeline for biomedical/clinical images, mainly MRI and CT, including image preprocessing, network architecture, training, and testing. The key design choices consist of preprocessing parameters, which are mostly to be fixed except for different intensity normalization for MRI and CT, and U-Net model hyperparameters, which will be tuned and selected automatically.

**Methodology:**

As it is mentioned above, semantic segmentation is crucial to the quantitative characterization of medical images by labeling corresponding regions. However, most current algorithms target only one or a few segmentation tasks, so an automated pipeline is desired for image data processing and deep learning-based segmentation. The whole pipeline involves preprocessing, deep-learning network architecture, training, and testing for the performance of segmentation, which will be discussed in sequence. The final tuned network will then be evaluated with ten public datasets of MRI and CT for different organs and tissues, consisting of training and test sets. Each of the ten has one to three regions of interest (ROI), whose ROI masks (i.e., ground truth) are manually labeled by radiologists, collected by Medical Segmentation Decathlon.

Several preprocessing steps need to be implemented by incorporating and modifying previous codes, including resampling, registration, bias correction, skull stripping, and intensity normalization. Raw images with different field of view and size will be first resampled, such as rescaling or cropping, to primarily select regions of interest and shrink the size of data [3]. They will be then registered or aligned, in terms of variable fields of view, organ locations, and orientation so that target regions overlap, and differences can be compared readily [4]. Next, registered images will be corrected for bias (i.e., inhomogeneity), which is a “low-frequency smooth undesirable signal” resulting in an intensity gradient in the area that represents the same type of tissue [5]. Brain MR images usually require skull stripping to remove non-brain tissues, such as skin, eyes, and neck [6]. Last but least, image intensities need to be normalized across samples based on image modality and intensity distribution. It is mentioning that CT has different normalization methods than MRI. For example, CT image brightness is usually adjusted through windowing, which has different window levels and width for different organs and tissues [7].

After the preprocessing is done, processed image patches are fed into a U-Net model to predict corresponding segmented classes of pixels with manually labeled ROI as reference. Data augmentation techniques need to be applied, such as rotation, scaling, flipping, Gaussian noise, etc. U-Net, a u-shaped convolutional neural network, is comprised of an encoder to extract high-resolution image features and a decoder to generate a segmentation map with about the same size as the input image [8]. While optimizing the cross-entropy loss, Dice Similarity Coefficient (DSC), Hausdorff Distance (HD), we will be tuning hyperparameters, including but not limited to input patch size, optimizer, learning rate, batch size and so on, depending on image modality and type of organs in input images. DSC is defined below:

where D is the dice coefficient, g is the ground truth, p is the predicted probability from the network, and is a constant [9]. HD is particularly useful in evaluating segmentation of small organs and is demonstrated below in Figure 1:

Text

Description automatically generated Text

Description automatically generated

Chart

Description automatically generated with low confidence

Figure 1. A schematic showing the Hausdorff Distance between points sets X and Y [9]

where X and Y represent predicted and ground-truth boundaries, respectively and one-sided HD, hd(X,Y) and hd(Y,X), measure how far two sets of boundary points are [10]. Finally, the network will be evaluated using test data set using DSC and HD.

**Timeline**:

Below is a table to demonstrate a rough timeline of progress of my capstone project.

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| **Estimated Time** | **Aims/Achievements** |
| March | * Get familiar with concepts of MRI preprocessing steps and deep-learning models of semantic segmentation by reading papers/codes |
| April | * Study common algorithms/theories used in different preprocessing steps by reviewing literature and code provided by mentors * Get a basic understanding of datasets (MR and CT images) |
| May – August | * Modify code of preprocessing pipeline * Fine tune the training model using selected datasets * Summarize preliminary results |
| September – October | * Continue modifying preprocessing pipeline and tuning models * Evaluate and compare our pipeline with other state-of-art methods |
| November - December | * Finalize results, including figures, tables, code * Finish writing report * Prepare for final presentation |

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