

Hematology Segmentation

Task and Approach:

The semantic segmentation task requires the use of two distinct model structure: a convolutional neural network architecture and a transformer-based network, for which I use the UNet and the SAMed_Vit_H models, respectively. Both models are adapted from the TriALS-MICCAI-2024 repository, in which the nn-UNet framework and additional functionalities for training SAMed is included.

Data Preprocessing:

In order for the training and testing data to be used by the nnU-Net framework, all images must be of the same size, shape, format and naming. Upon exploration of the given data, I find that the images were in one of the following size: (360,360), (363, 360), (400, 400), as well as being either in .jpg (3 channels) or .tiff (4 channels) format. As a result, I rename and resize all images into shape (360,360,3) and in .png format for consistency. For testing images, the original image sizes are recorded in a .json file. This is for post-processing of segmentation masks, where the output segmentation masks are resized to match that of the original images.

Segmentation Pipeline:

Once the data is preprocessed, nnU-Net configures the entire segmentation pipeline, including preprocessing, model configuration, training and post-processing. In particular, I use the 2d configuration for UNet and 2d_p512 for SAMed, train for 100 epochs with early stopping, and find the best configuration from the 5-fold-cross-validation training.

Acknowledgement:

The implementation of nnU-Net is adapted from <https://github.com/MIC-DKFZ/nnUNet>. The implementation of embedding SAMed within the nnU-Net framework is adapted from <https://github.com/xmed-lab/TriALS>.

GitHub link: <https://github.com/chloe-nguyenminh/Hematology-Segmentation>