Machine Learning Project Proposal

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Introduction

I chose to focus on brain tumor segmentation as it is an important task for a patient's disease management. Automating this task can streamline and support the work of medical experts and directly affects treatment planning and monitoring. This process will also reduce the chance of human error. The reliance on AI in medical imaging will improve patient care in the future.

Dataset

The BraTS dataset [5] [1] [2] is an image dataset containing brain MRI images with annotated areas containing tumor locations, shapes and sizes. The BraTS challenge is an annual competition part of the MICCAI conference aiming to segment the MRI images and it is evaluated on a blind test set by the organizers. The dataset contains mutli-modal scans obtained from various institutions. All the segmentation was done manually that are then approved by expert neuro-radiologists.

As part of the dataset exploration, I plan to plot histograms to approximately estimate the bins that the images will be separated into. The dataset contains 4 masks per image of the MRI. These are the 4 modes of the network that will be built. Each mask corresponds to a different property of the tumor. Histograms of each type of mask will also help integrate them together based on their semantic meaning.

As part of the preprocessing, normalization is important as the images come from different institutions. First z-score normalization will be done and then clipped to exclude any outliers following the process done by [4].

The BraTS dataset is a well structured dataset but if there are any missing values, I will take the average of the nearby grid of pixels surrounding the missing value pixel. This semantically is more reasonable than use the average of the entire image. However the value of a few pixels may not have a great impact on the output or performance.

For noise reduction, Gaussian filtering will be used. The amount of smoothing needs to be controlled carefully to prevent oversmoothing across the smaller tumor segments.

Proposed Methods

The primary objective of this project will be to reproduce and evaluate segmentation models. Once reliable results are obtained, I will design a preprocessing decision tree based on a rudimentary metric to identify which samples are more likely to have tumors or which have a higher size or shape. Following this I will apply simpler U-net architectures to enhance performance, similar to an ensemble method. This is a combination of two-stage pipeline models and a coarse to fine segmentation. In traditional two stage pipeline model, the first stage is a classification into positive and negative samples. Here in the proposed method, the first stage will be a multi-class classification problem with the outputs containing variable amounts and grouping of image pixels classified as a tumor. Convolution as well as other statistical methods will be used first for a quick form of classification as the first stage aims to take lesser time.

Another approach I plan to explore is to consider the dataset not as images but instead as a volume and apply sparse tensor methods for segmentation. MRI images with tumor segments have sparse masks and tensor decomposition is an important technique that can be used to effectively identify and classify these segments.

Evaluation metrics

The evaluation metric for this segmenation task will be the dice similarity coefficient (f1 score). The Hausdorff distance is complementary metric to the Dice metric. Another metric that can be used is the Jaccard similarity coefficient or the Jaccard index. Both the Dice index and the Jaccard index score based on the overlap between the predicted area and the ground truth area.

Dice metric or F1 score =
$$\frac{2 * \text{True positive}}{2 * \text{True positive} + \text{False Positive} + \text{False Negative}}$$
(1)

$$Jaccard index = \frac{True positive}{True positive + False Positive + False Negative}$$
(2)

The Jaccard index penalizes under and over segmentation than the Dice index. These metrics are better metrics than accuracy or precision as in segmentation tasks, the masks are often sparse. Predicting the majority class as the entire mask will lead to a high accuracy but such results are meaningless.

Expected Outcomes

The expectation for the decision tree before the U-Nets is to identify the MRI images with a high chance the tumor being present. The tree will classify the images into different categories based on shape and size of detected anomalies. By evaluating the U-Nets for each group separately, I aim to create networks specialized in a specific type of tumor segmentation instead of a model that works with every image. This approach should make interpreting results from the U-Nets more straight-forward and the provide a more reliable confidence estimate for each group.

References

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