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פרויקט גמר – קורס דימות תהודה מגנטית

דו"ח מכין

Brain tumor segmentation

סגמנטציה של גידולים מוחיים

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Abstract:

In this project, we will implement an algorithm for segmentation of brain tumors in multi-modal MR images based on classic segmentation algorithms.

Data:

For training and testing our algorithm we will use the BRATS data set which consists of 27 MR images, each include 4 modalities (T1, T1gad, T2, Flair) and ground truth.

Method:

We will examine three segmentation algorithms:

- 1) GMM- this algorithm assumes that the data's histograms are distributed as a mixture of Gaussians. In the first step the algorithm find the Gaussians characteristics (in an iterative EM process) and in the second step it decides which voxel belongs to each Gaussian.
- 2) SVM- the algorithm finds the hyperplane that splits the training data into groups of interest with the highest distance from the support vectors or minimize the hinge loss function if linear separation of the groups is not possible.
- 3) Level set- the algorithm is optimizing the segmentation mask and smoothen the segmentation contour.

We will examine the different algorithm and learn their capabilities. We will examine the different algorithms over the different modalities, multimodal input data and over different feature vectors. We will also examine the use of brain atlas as a spatial prior. We will implement a segmentation algorithm from a combination of those methods. Our algorithm will be trained and tested over the BRATS brain dataset. We will evaluate over algorithm using the known dice metric (this will allow us to compare our results).

Our algorithm will be consisting from two components:

1. Initial segmentation state: using GMM and/or SVM.
2. Segmentation mask optimization: using level-set method.

Assumptions:

- 1) The brain tumor intensities can be divided into separate Gaussians for healthy tissues and for tumor different tissues. In case this assumption fails, we assume that if healthy tissues were assigned to the same Gaussian as the tumor they can be easily removed from the segmentation results in a robust way.
- 2) We assume there is a robust function that can take the algorithms results and use it for better segmentation. For this assumption, we also need to assume that when one algorithm fails the other algorithm's prediction is correct.
- 3) We assume there are common characteristics of tumor tissues between different MR images.

References:

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