

# Multi-Sequence MRI Segmentation using Boosting

Bilal Javed, Toluwalope Gbakinro  
Technische Universität München

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## Abstract

In this short paper we would discuss our approach in segmenting brain tissue for multi-sequence brain MRI's using boosting. The approach is multi sequence since in contrast to many segmentation techniques that use only the T1 scan; we use T1, T1IR, and T2FLAIR MRI's for the segmentation. The project was done for the MRBrains13 competition and the training and testing data was also provided by them. The overall goal was to segment the brain into three tissue types. These include white matter, gray matter, and cerebrospinal fluid. Boosting was used as the machine learning tool for the segmentation process. Various features were included at different stages to improve the overall accuracy of the segmentation process.

## 1 Algorithm

We have used boosting as our segmentation algorithm. Since we have to segment the brain into more than two tissue types therefore, we have selected AdaBoostM2 as our segmentation algorithm. The details of this algorithm can be found in [1]. We have used a total of one hundred weak learners to train the algorithm. 5000 training samples were randomly drawn from each of the five training images to get a total of 25000 training samples

## 2 Implementation

### 2.1 Pre-Processing

In the pre-processing step we normalized all the 20 images, 5 training and 15 testing images for their intensity values. Apart from normalization, the training labels were also fused during the pre-processing steps as mentioned in the website. Hence the training algorithm was trained to segment the brain scan into four labels.

### 2.2 Feature extraction

A total of seven features were extracted from each image. These include three intensity values for T1, T1IR, and T2FLAIR. The five training images with

labels for testing were registered to each of the T1 scan for all the 15 testing images to give five atlases that were later used to calculate the probabilities for each of the four labels for each tissue types.

### **3 Results of our implementation**

The training algorithm was first used to predict the labels for the five training images for which the ground truth was available. In the first run only intensity values were used to segment the tissues. Intensity based features alone were not improving the results that much therefore, atlas based segmentation techniques were used in the end to improve the dice coefficient for the five training images. The same approach was used to classify the 15 testing images. All scans were classified on an Intel core i3 processor and the average running time for the classification of a single image was from 5 to 6 minutes.

We would also like to mention that this is only a preliminary report and after receiving the results we would further enhance our approach and this document.

### **4 Acknowledgments**

We would like to thank our supervisor Dr Tingying Ping for her guidance and supervision in completing this project.

### **5 References**

1. J Zhu, S Rosset, H Zou, T Hastie “Multi-class adaboost” Ann Arbor, 2006 - [vista.eng.tau.ac.il](http://vista.eng.tau.ac.il).