Brain Tumor Segmentation with Random Forests and Neural Networks

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Abstract

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1 The Dataset

1.1 General Information

Image segmentation is primarily done in two ways: Either designing an algorithm from first principles or using available data to train an algorithm. As for this challenge, designing an algorithm without data is very difficult, the method of choice is training an algorithm from data. For the Multimodal Brain Tumor Image Segmentation Benchmark (Menze et al., 2015) in 2015, 3D MR tumor scans where collected from the BRATS 2012 and BRATS 2013 challenge and from the NIH Cancer Imaging Archive (TCIA). In total, data for 55 low-grade glioma patients and 220 high-grade glioma patients is provided. The data is a 16-bit 3D scan of shape (depth=155, height=240, width=240), where all datasets have been aligned to the same anatomical template and interpolated to $1\,\mathrm{mm}^3$ voxel resolution. For each patient, four scan types are available: T1, T1c, T2 and Flair. In the case of the BRATS data, the labels are from expert annotations of one to four raters. The TCIA data labels were obtained by fusing the results of multiple segmentation algorithms from the BRATS 2012 and BRATS 2013 challenge and reviewed by expert raters.
Four classes are predefined:

0) background
1) necrosis
2) edema
3) non-enhancing tumor
4) enhancing tumor

Each 3D image for each scan type is saved in a seperate `.mha` file. The average size per file is about $2.2\,\mathrm{MB}$, leading to approximately $2.2\,\mathrm{MB} \cdot 275 \cdot 4 = 2420\,\mathrm{MB}$ of compressed data. Uncompressed, the data size increases to about $60\,\mathrm{GB}$. In fig. 1, examples for LGG and HGG and the different scan types are shown.

1.2 Utilizing the Dataset

The given images are sliced 3D scans. As we want to do segmentation in two dimensions, we just take each slice as a separate input image. In total, this are $155 \cdot 275 \cdot 4 = 170500$ input images. This full dataset proved too be to large to use it for training. After trying out multiple subsets, it was decided to use only the LGG part of the dataset and to sort out images where the tumor to background ratio is less than 0.1%. This dataset only takes $110\,\mathrm{MB}$ compressed on disk. We split this dataset of 3315 images further up into a training set of 2652 images (80%) and a test set of 663 images. This dataset is used for both the random forest and the U-Net. The classes are reduced from five to two: background and tumor.

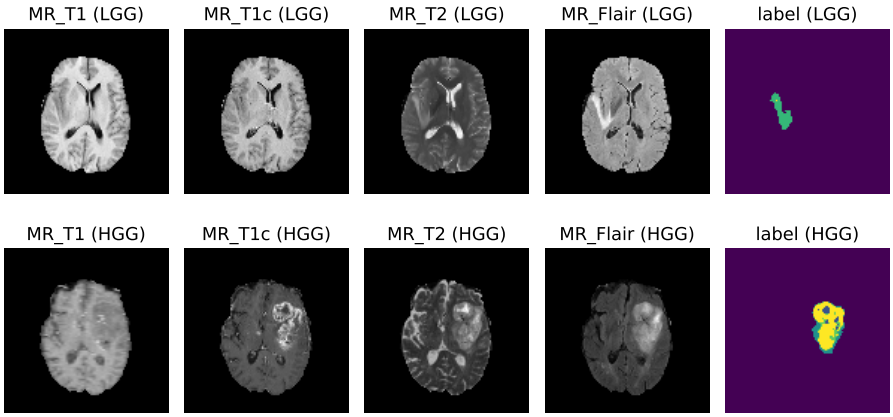

Figure 1: Dataset examples.

2 Random Forest

The random forest is a set of decision trees, where each tree is fitted to a random subset of the data and predictions are made by taking averages over the predictions of individual trees. It

2.1 Features

A random forest classifies each pixel separately. Therefore, using only the pixel intensities would only give a good classification if the tumor can be identified on a single-pixel level. To include information about the local structure, multiple features are defined, such that each input pixel is an N-dimensional vector.
The features we chose for this task are:

1. Gaussian filter
   - Convolution with a Gaussian kernel
   - Smoothes the image
2. Laplacian of Gaussian (LoG) filter
   - Convolution with the Laplacian of a Gaussian kernel
   - highlights edges (edges are 0)
3. Gaussian gradient magnitude filter
   - Convolution with the gradient of a Gaussian kernel
   - highlights edges (edges are extrema)
4. Eigenvalues of the Hessian matrix
   - determines the surface concavity
5. Eigenvalues of the structure tensor
   - Summarizes gradient direction
6. Equalized histogram
   - Enhances contrast

Except the equalized histogram, they all share the tuneable kernel width σ, which is set to $\{0.3, 0.7, 1., 3.5\}$. In total, $N = 29$ filters are used. In fig. 2, the features are shown for one example image of the dataset for $\sigma = 0.3$. The tumor region in the bottom left can be clearly identified for the Gaussian (bright), Laplacian of Gaussian (dark) and the equalized histogram (bright). However, for other examples the tumor is more pronounced in the other features.

In principle one could also utilize the different scan types as features. However, the dataset is already very big and therefore it was decided to not take the other scan types as features. This also allows for

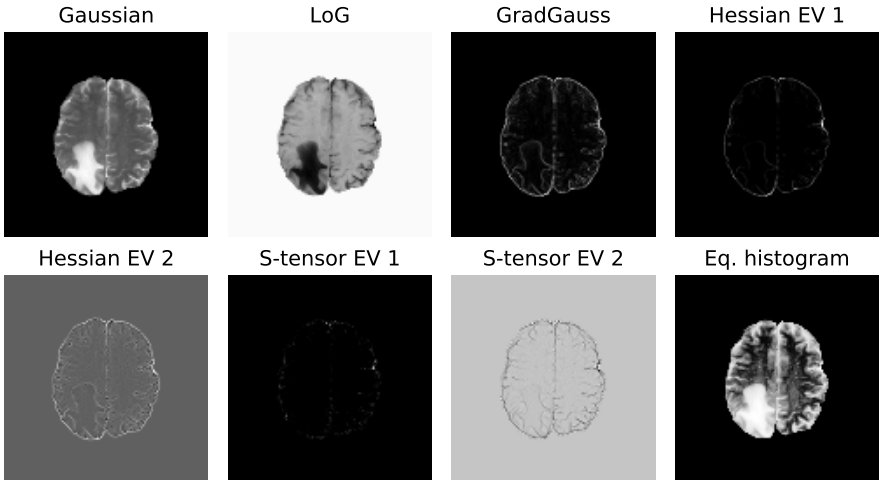

Figure 2: Features for the random forest.

a fair comparison between the random forest and the U-Net, as they are then trained with the same dataset.

References

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