

Accepted Manuscript

Machine learning based brain tumour segmentation on limited data using local texture and abnormality

Stijn Bonte, Ingeborg Goethals, Roel Van Holen



PII: S0010-4825(18)30112-4

DOI: [10.1016/j.combiomed.2018.05.005](https://doi.org/10.1016/j.combiomed.2018.05.005)

Reference: CBM 2956

To appear in: *Computers in Biology and Medicine*

Received Date: 6 March 2018

Revised Date: 2 May 2018

Accepted Date: 2 May 2018

Please cite this article as: S. Bonte, I. Goethals, R. Van Holen, Machine learning based brain tumour segmentation on limited data using local texture and abnormality, *Computers in Biology and Medicine* (2018), doi: 10.1016/j.combiomed.2018.05.005.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

Machine learning based brain tumour segmentation on limited data using local texture and abnormality

Stijn Bonte^{a,b,1,*}, Ingeborg Goethals^a, Roel Van Holen^b

^a*Department of Nuclear Medicine, Ghent University Hospital, Ghent, Belgium*

^b*Medical Imaging and Signal Processing (MEDISIP), Department of Electronics and Information Systems, Ghent University, Ghent, Belgium*

Abstract

Brain tumour segmentation in medical images is a very challenging task due to the large variety in tumour shape, position, appearance, scanning modalities and scanning parameters. Most existing segmentation algorithms use information from four different MRI-sequences, but since this is often not available, there is need for a method able to delineate the different tumour tissues based on a minimal amount of data. We present a novel approach using a Random Forests model combining voxelwise texture and abnormality features on a contrast-enhanced T1 and FLAIR MRI. We transform the two scans into 275 feature maps. A random forest model next calculates the probability to belong to 4 tumour classes or 5 normal classes. Afterwards, a dedicated voxel clustering algorithm provides the final tumour segmentation. We trained our method on the BraTS 2013 database and validated it on the larger BraTS 2017 dataset. We achieve median Dice scores of 40.9% (low-grade glioma) and 75.0% (high-grade glioma) to delineate the active tumour, and 68.4%/80.1% for the total abnormal region including edema. Our fully automated brain tumour segmentation algorithm is able to delineate contrast enhancing tissue and oedema with high accuracy based only on post-contrast T1-weighted and FLAIR MRI, whereas for non-enhancing tumour tissue and necrosis only moderate results are obtained.

*Corresponding author

Email address: StijnD.Bonte@UGent.be (Stijn Bonte)

¹Campus UZ, IBiTech, entrance 36; Corneel Heymanslaan 10, B-9000 Gent, Belgium

Download English Version:

<https://daneshyari.com/en/article/6920488>

Download Persian Version:

<https://daneshyari.com/article/6920488>

[Daneshyari.com](https://daneshyari.com)