

INTRODUCTION

Comparing different head MRI segmentation techniques for use in EEG source analysis

Abinash Pant ^{1,2,3}, Jae-Hyun Cho¹, Carsten Wolters², Xiaoyi Jiang³, Harald Bornfleth¹

1 BESA GmbH, Gräfelfing, Germany 2 Institute for Biomagnetism and Biosignalanalysis, University of Münster, Germany 3 Faculty of Mathematics and Computer Science, University of Münster, Germany

Accurate segmentation of an individual human head and the resulting volume conductor model has been known to improve EEG and MEG source analysis^{[1][2]}. However, comparison of some state-of-the-art segmentation techniques and their effectiveness in source analysis, namely Multi-Atlas^[11] and Convolutional Neural Networks (CNN)^[13] segmentation, is lacking. We present a comparison between these techniques to segment five tissue types using ground-truth (GT) data from BrainWeb^[9].

MATERIALS & METHODS

Multi-atlas segmentation pipeline

- Simulated atlas based on BrainWeb^[9] dataset. Real dataset obtained from MRBrainS challenge.^[10]
- T1 MRI images used with corresponding ground truth for white matter (WM), grey matter (GM), cerebrospinal fluid (CSF), bone and muscle.
- N4ITK^[12] used for intensity inhomogeneity correction.
- \circ 2 step registration, with a coarse affine transformation^[3] step followed by a non-rigid registration^[4].
- \circ Top N atlases selected on the basis of their similarity with the target image (N=8).
- Simultaneous truth and performance level estimation (STAPLE)^[11] used to decide on atlas consensus.

3D Convolutional Neural Network (3D CNN) segmentation pipeline

- 3D CNN trained to detect WM, GM, CSF, muscle and bone.
- No registration required but all images in the atlas are resampled to the same voxel size.
- Normalization of the intensity to a zero-mean, unary-variance space.
- Theano^[14] framework used as the base and graphical processing unit (GPU) used for faster parallelized computation.
- \circ Pipeline inspired by the popular multi-scale 3D CNN pipeline ^[13] for lesions segmentation.
- An extra pathway for a sub-sampled image is used. It is up-sampled at the classification layer.

• Normalized cross-correlation used for local consensus.

• Morphological operations used to remove noise and isolated voxels from the final segmentation.

Target Image



Fig. 1: Simplified multi-atlas segmentation pipeline

• Final architecture 8 layers deep with a kernel of 3x3x3 voxels at every layer.

 \circ Feature Maps of size 30, 30, 40, 40, 40, 40, 50, 50 at every layer and receptive field of size 25³



Comparing head models of different segmentation methods

- \circ 2000 source locations were randomly chosen inside the grey matter using a 1x1x1 mm grid.
- Each source location has 3 orientations in the 3 cardinal directions.
- Average distance between the sources was 4.13 mm.

- Simulations with 97 EEG electrodes were performed using a FEM head model.
- SimBio[15] was used to generate leadfields for ground truth data and the 2 segmention approaches.
- Magnification factor (MAG) and Relative distance measurement (RDM) values were calculated for the two segmentation techniques against the ground truth.

RESULTS

- Three algorithms, namely STAPLE, local consensus using localized normalized cross correlation (LNCC), and 3D CNN were tested.
- For validation, 5 images were randomly selected as test images.
- Top 8 Atlases were chosen for STAPLE and LNCC using normalized mutual information (NMI).
- LNCC parameters for classifier and kernel size were tuned using 3 training images.
- Dice score was used to







measure the efficacy of the 3 algorithms to detect 5 tissue classes (WM, GM, CSF, muscle and bone).





and MA shows CNN values being closer to the ground truth data.

Fig. 6: Difference of RDM (top) and MAG (bottom) between CNN and MA visualised on the cortical surface (right) and volume (left)

CONCLUSIONS \mathbb{N}

The comparison of the segmentation techniques shows that 3D CNN outperforms multi-atlas based methods, especially in segmenting WM, GM and CSF. This can be attributed to the structural variability of these three tissue classes across subjects which makes it a challenging problem for segmentation algorithms based on atlas consensus, such as the multi-atlas technique. The CNN's lead-field matrix values were closest to those of the ground-truth which is in accordance with the segmentation results. The effect on source analysis will be investigated further.

Yvert, B., et al. "A systematic evaluation of the spherical model accuracy in EEG dipole localization." Electroencephalography and clinical neurophysiology 102.5 (1997): 452-459.
Stenroos, Matti, Alexander Hunold, and Jens Haueisen. "Comparison of three-shell and simplified volume conductor models in magnetoencephalography." Neuroimage 94 (2014): 337-348.
Ourselin, Sébastien, et al. "Reconstructing a 3D structure from serial histological sections." Image and vision computing 19.1 (2001): 25-31.
Modat, Marc, et al. "Fast free-form deformation using graphics processing units." Computer methods and programs in biomedicine 98.3 (2010): 278-284.
Rivest-Hénault, David, et al. "Robust inverse-consistent affine CT-MR registration in MRI-assisted and MRI-alone prostate radiation therapy." Medical image analysis 23.1 (2015): 56-69.
National Institutes of Health. "Retrospective Image Registration Evaluation." Vanderbilt University, Nashville (TN), USA (2003).
SimBio Consortium. "SimBio: A generic environment for bio-numerical simulation." (2000).
Occosco, Chris A., et al. "Brainweb: Online interface to a 3D MRI simulated brain database." NeuroImage. 1997.
Mendrik, Adriënne M., et al. "MRBrains Challenge: Online evaluation framework for brain image segmentation in 3T MRI scans." Computational intelligence and neuroscience (2015).
Mandrik, Adriënne M., et al. "MRBrains Challenge: Online evaluation framework for brain image segmentation in 3T MRI scans." Computational intelligence and neuroscience (2015).
Mandrika, Neuroimage 3.2.7 (2004): 903-921.
Kamnitsas, Konstantinos, et al. "Efficient Multi-Scale 3D CNN with Fully Connected CRF for Accurate Brain Lesion Segmentation." arXiv preprint arXiv:1603.05959 (2016).
Team, The Theano Development, et al. "Theano: A Python framework for fast computation of mathematical expressions." arXiv preprint arXiv:1605.02688

Corresponding author: Abinash Pant (apant@besa.de)