ROAST: a free, fully-automated, Realistic, vOlumetric-Approach-based Simulator for Transcranial electrical stimulation

Yu Huang[a,b], Abhishek Datta[b], Marom Bikson[a], Lucas C. Parra[a]

[a]Department of Biomedical Engineering, City College of the City University of New York, New York, NY 10031

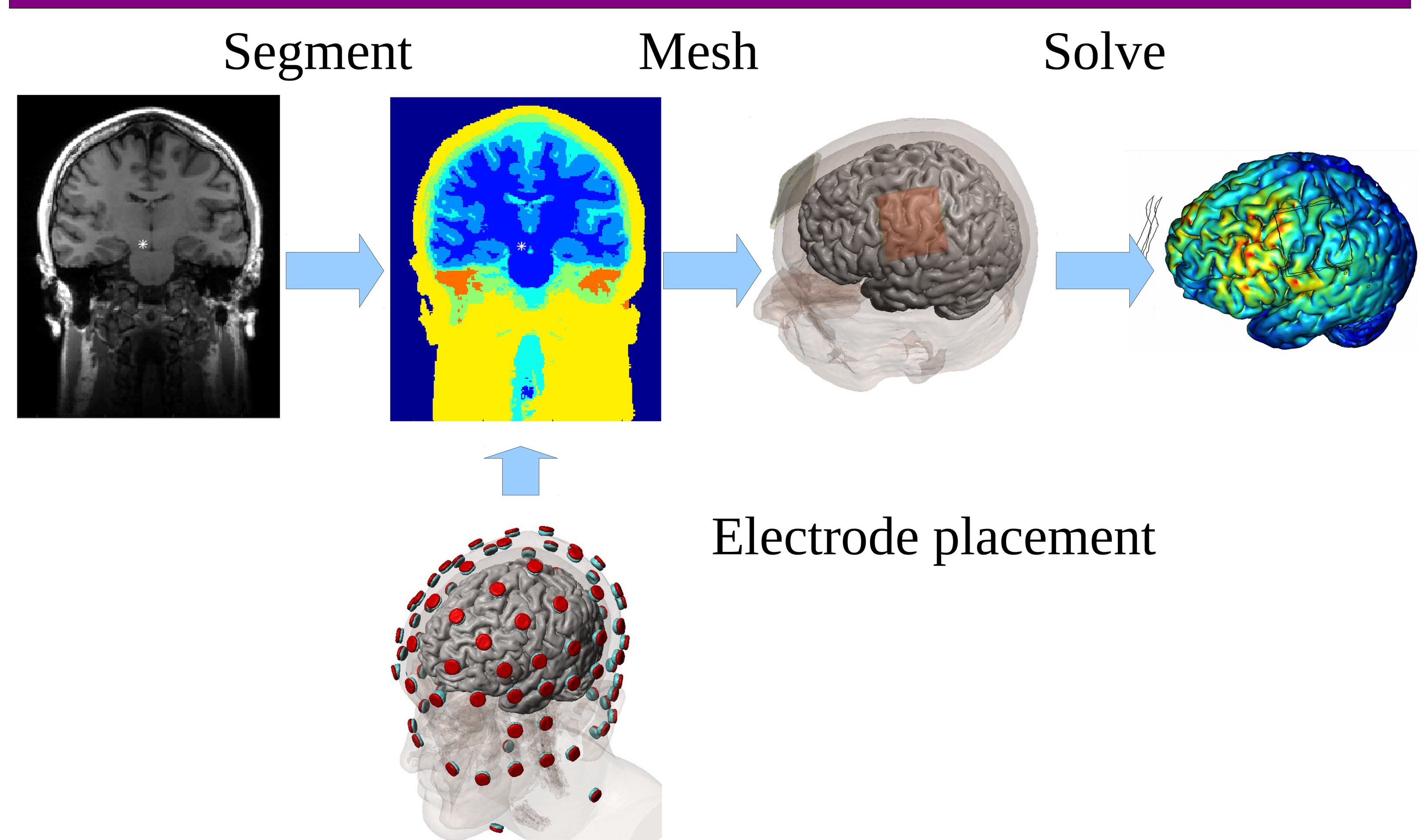
[b]Research & Development, Soterix Medical, Inc., New York, NY 10001

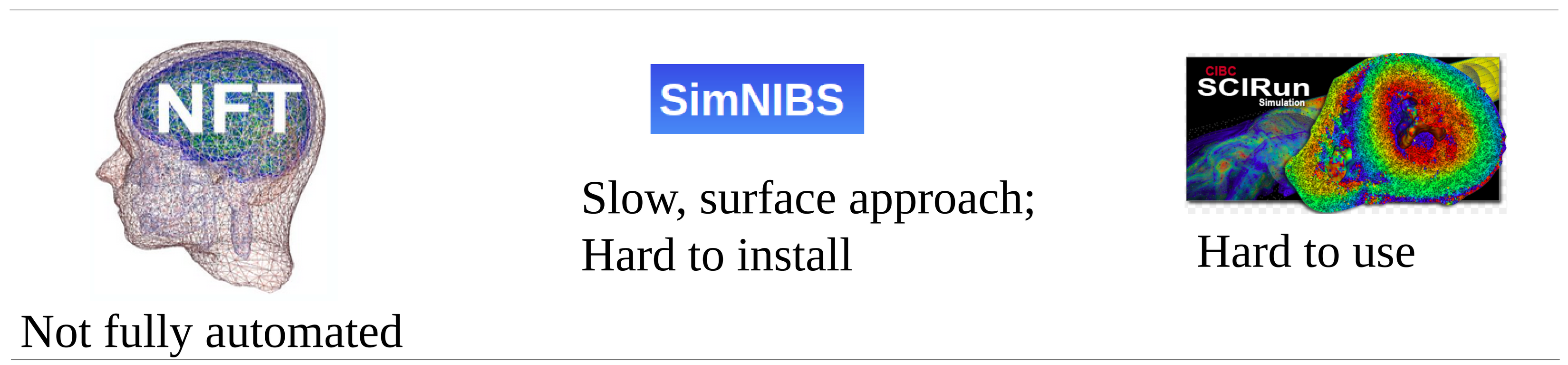
BETTER. SMARTER. Soterixmedical

Abstract

Research in the area of transcranial electrical stimulation (TES) often relies on computational models of current flow in the brain. Models are built on magnetic resonance images (MRI) of the human head to capture detailed individual anatomy. To simulate current flow, MRIs have to be segmented, virtual electrodes have to be placed on these anatomical models, the volume is tessellated into a mesh, and the finite element model is solved numerically to estimate the current flow. Various software tools are available for each step, as well as processing pipelines that connect these tools for automated or semi-automated processing. The goal of the present tool -- ROAST -- is to provide an end-to-end pipeline that can automatically process individual heads with realistic volumetric anatomy leveraging open-source software (SPM8, iso2mesh and getDP) and custom scripts to improve segmentation and execute electrode placement. When we compare the results on a standard head with other major commercial software tools for finite element modeling (ScanIP, Abaqus), ROAST only leads to a small difference of 9% in the estimated electric field in the brain. We obtain a larger difference of 47% when comparing results with SimNIBS, an automated pipeline that is based on surface segmentation of the head. We release ROAST as a fully automated pipeline available online as a open-source tool for TES modeling.

Method





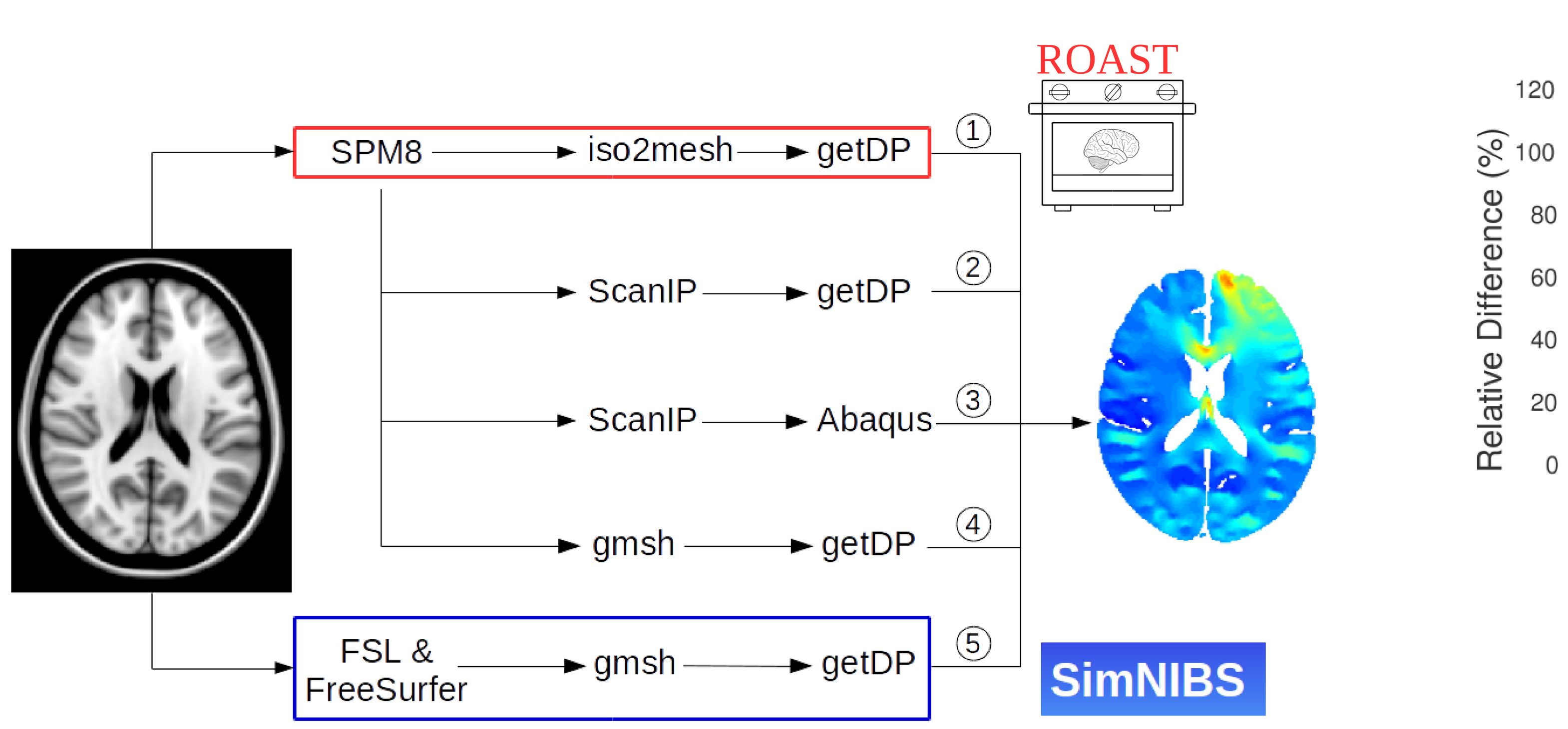


Fig. 1: Candidate pipelines for building a current-flow model of the head. The input and output of each pipeline is the MRI and the electric field distribution, respectively.

Results

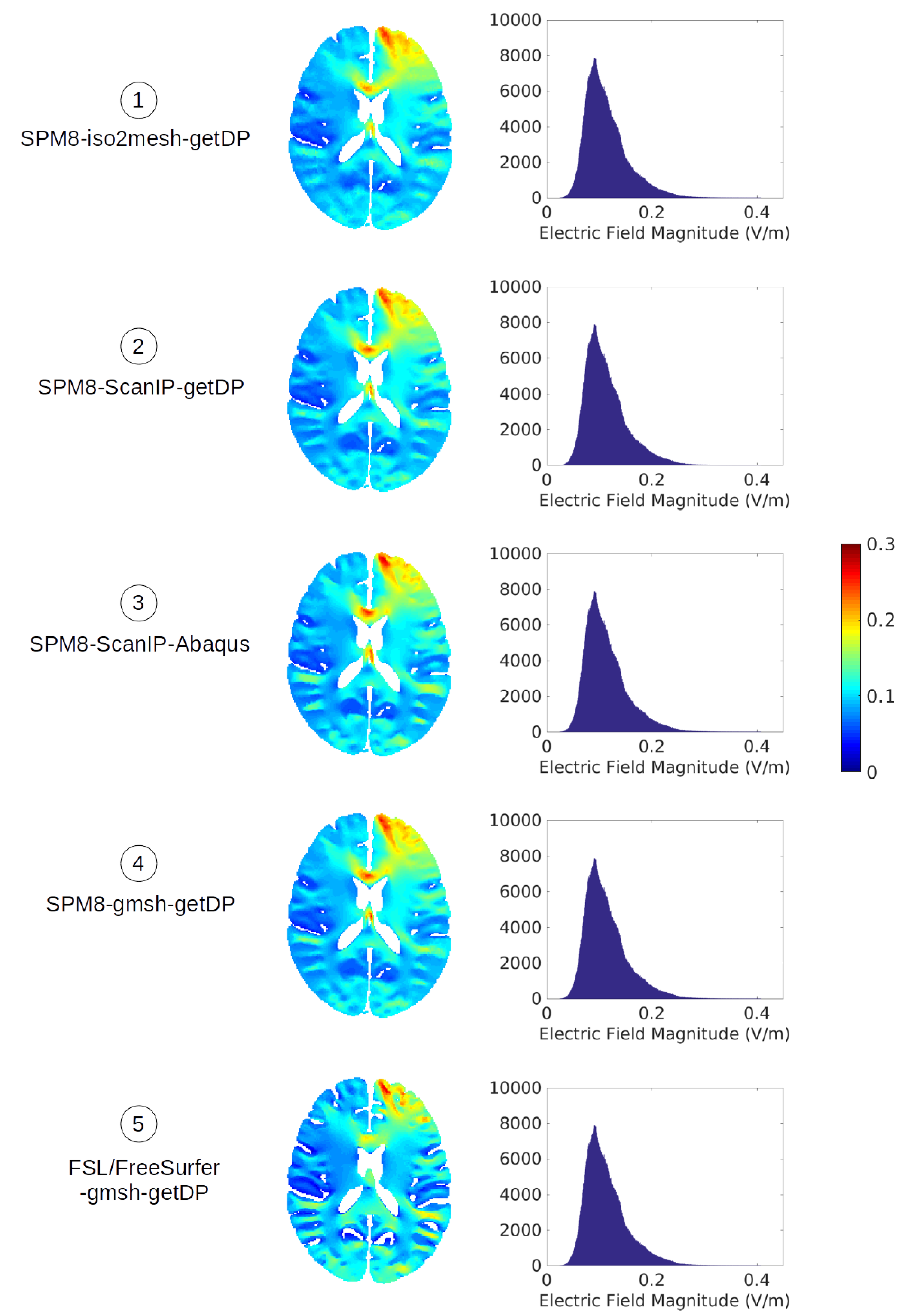


Fig. 2: Example brain slices showing electric field distributions output by the five modeling methods from Fig. 1. Histograms of the electric field magnitude in the brain are also shown.

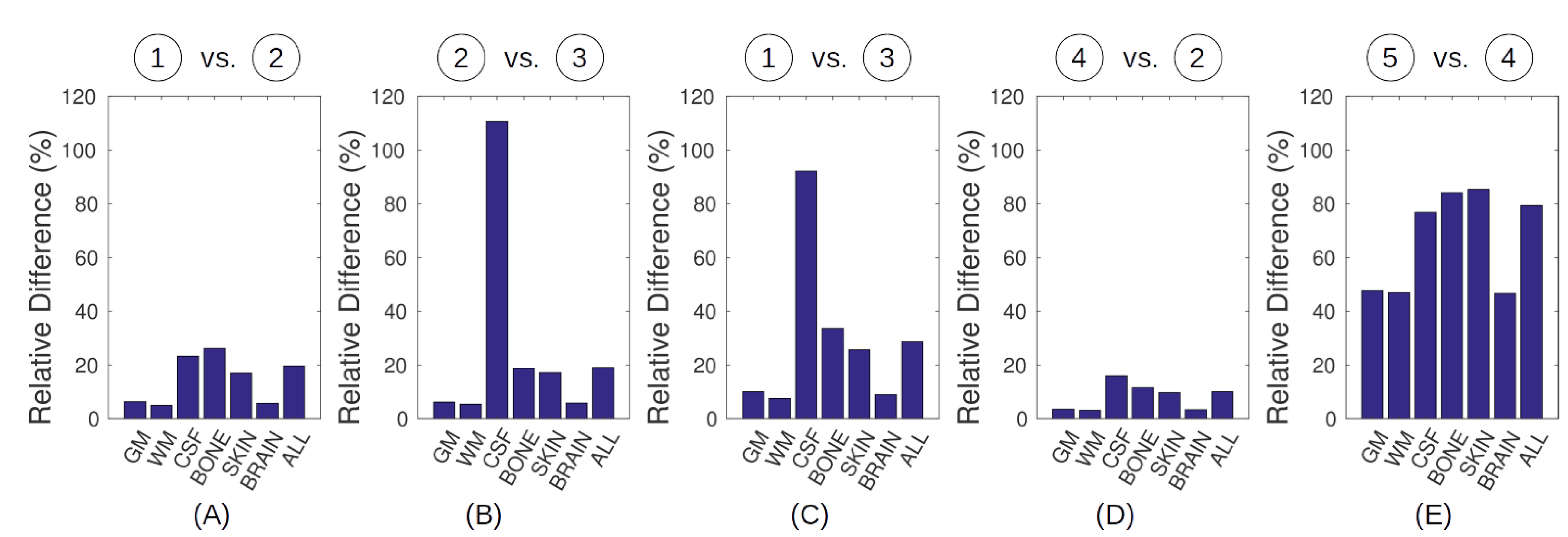


Fig. 3: Comparisons between different pipelines in terms of how they predict the electric field distributions. Each bar represents the relative difference for the corresponding tissue. GM: gray matter; WM: white matter; CSF: cerebrospinal fluid; BRAIN: gray and white matter; ALL: all the tissues combined.

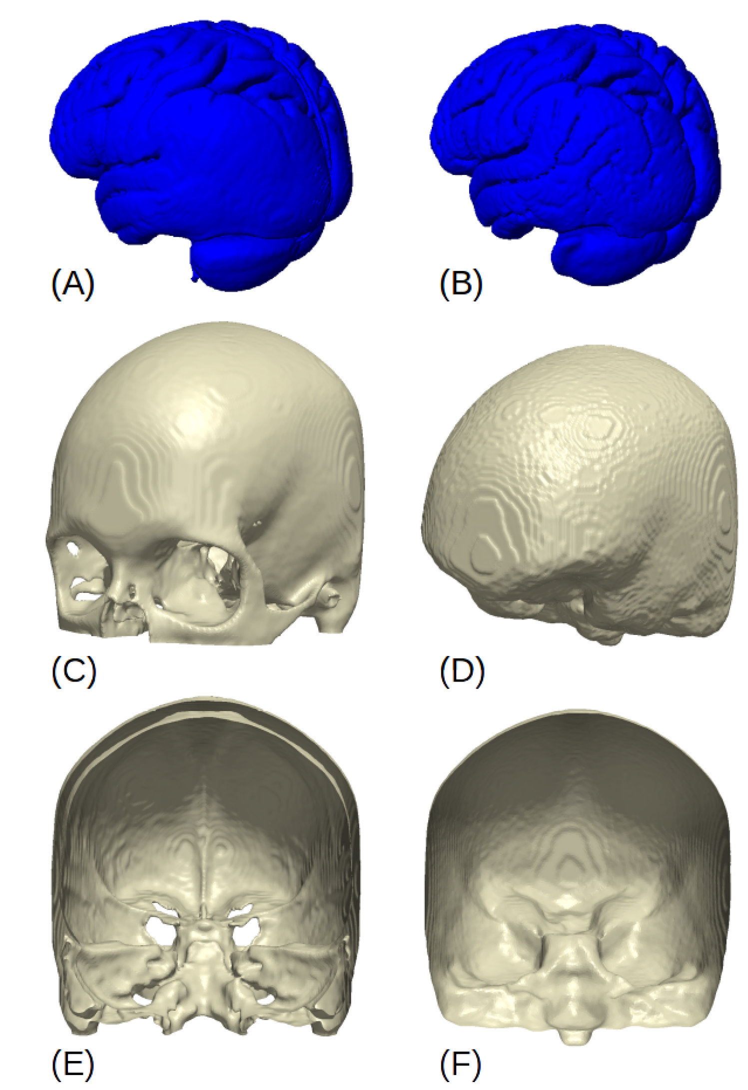


Fig. 4: SPM-generated segmentation (left) and SimNIBS-generated segmentation (right) of brain (A&B) and skull (C--F) for the MNI-152 head. (E) and (F) are cut views of (C) and (D), respectively.

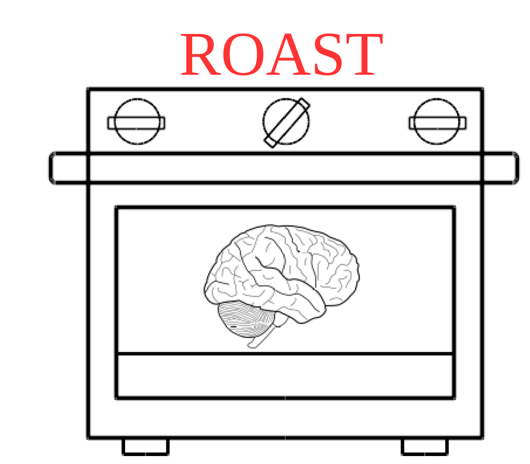
Discussion

Pros: free except Matlab; fully automated; easy to install (just download); easy to use; fast (10~30 min); realistic volumetric approach; batch processing for multiple subjects.

Cons: needs Matlab license; lacks fancy graphic user interface; basic visualization of results; abnormal anatomy requires manual touch-up; no quality assurance.

The high difference between ROAST and SimNIBS indicates the genuine difference in these two categories of modeling methods. Surface approach in SimNIBS is better at capturing the gyri and sulci on the cortex, but not good at modeling the fine details of the skull structure, where the volumetric approach in ROAST is good at. Future work may consider combining the brain segmentation from FreeSurfer with the skull/scalp segmentation from SPM for building improved TES models.

Ongoing work is trying to find out which approach is more accurate by using both the analytical solutions from a spherical model and the actual intracranial *in vivo* recordings from human subjects under TES.



Free to download

https://www.parralab.org/roast/

Reference:

Yu Huang, Abhishek Datta, Marom Bikson, Lucas C. Parra, Realistic vOlumetric-Approach to Simulate Transcranial Electric Stimulation -- ROAST -- a fully automated open-source pipeline, bioRxiv 217331, Nov 10, 2017.

ACKNOWLEDGEMENT:

The authors would like to thank Chris Thomas at Soterix for insightful discussions. We also would like to thank Alexander Opitz for pointing us to the free solver getDP. We also thank Jens Madsen for assistance with Matlab GUI programming. This work was supported by the NIH through grants R01MH111896, R44NS092144, R41NS076123, and by Soterix Medical Inc.