

# Hybrid Surface-Volume Segmentation for improved Anatomically-Constrained Tractography

## Poster No:

1280

## Submission Type:

Abstract Submission

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## Introduction:

The "Anatomically-Constrained Tractography (ACT)" framework<sup>1</sup> enhances the biological accuracy of diffusion MRI streamlines tractography reconstruction, by constraining the propagation and termination of streamlines based on tissue segmentation from a high-resolution, high-contrast anatomical image (e.g. T1-weighted).

The tissue segmentation image to be used in this context has historically been derived using a sequence of processing tools provided within the FSL software package<sup>2</sup> - in particular the intensity-based segmentation of the "fast" command<sup>3</sup> - as automated in the *MRtrix3* software<sup>4</sup> command "5ttgen fsl". This can however lead to erroneous segmentations in the presence of image noise and/or poor tissue contrast, with ACT concomitantly applying inappropriate anatomical priors in such locations. The ACT framework itself is however independent of the particular approach used to derive this image, and thus may benefit from the use of more advanced tissue segmentation algorithms.

Here we demonstrate a novel processing pipeline for the derivation of a tissue segmentation image for ACT. It combines information from both surface-based reconstructions of various structures, and volume-based tissue segmentations for structures for which the former is not performed explicitly; we thus name this algorithm "Hybrid Surface-Volume Segmentation (HSVS)". Because these data are mapped back to a common image space, its utilisation does not require modification to the ACT software framework, nor does it incur any substantial computational performance penalty during streamlines propagation.

## Methods:

The operation of the algorithm is demonstrated in Figure 1. The key components incorporated into the algorithm are:

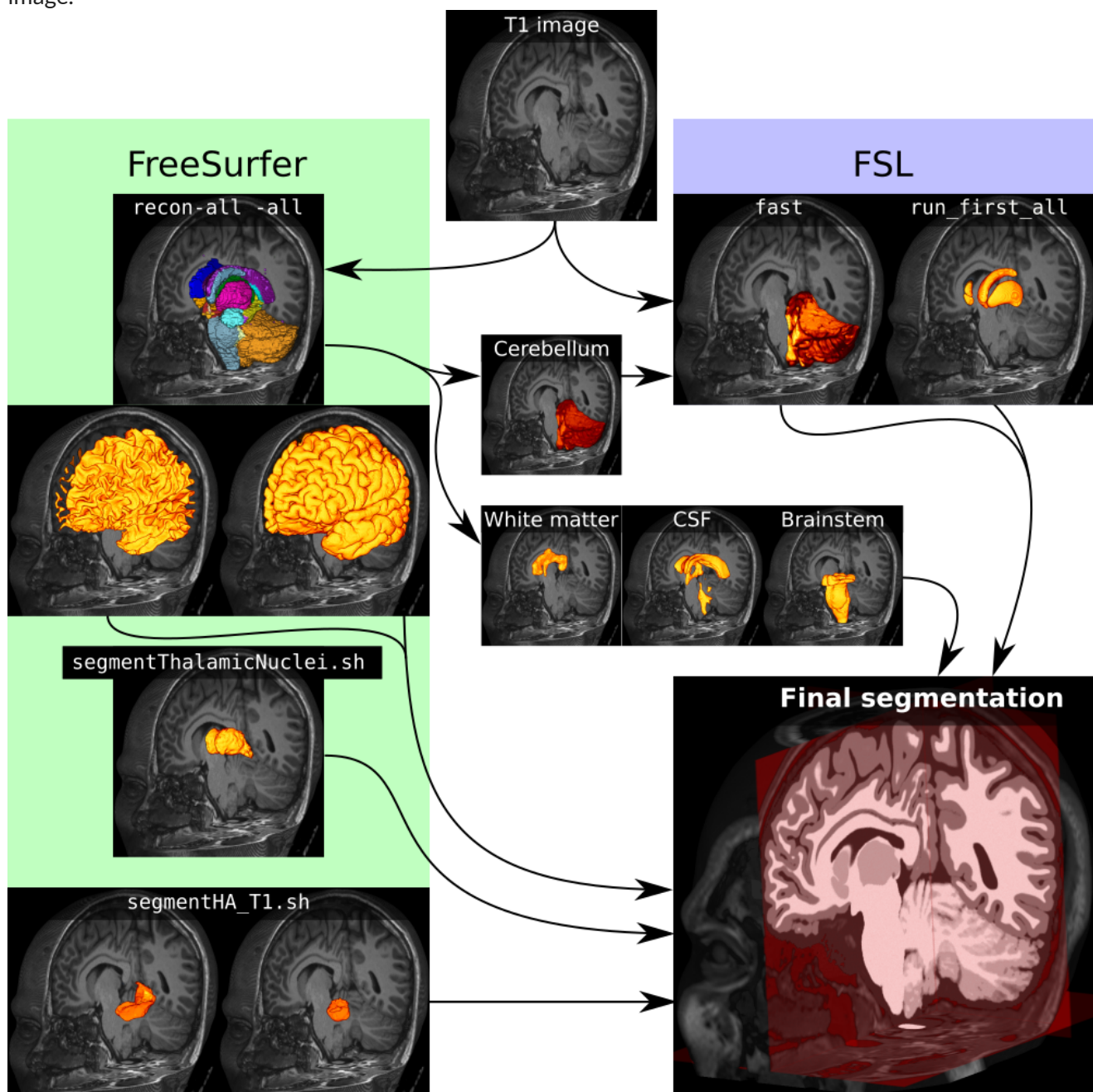
- Native surface-based reconstruction of the cortical ribbon by FreeSurfer<sup>5</sup>, projected to voxel partial volume

fractions<sup>1</sup>;

- High-resolution segmentations of select sub-cortical structures by FreeSurfer modules (if available)<sup>6,7</sup>;
- Surface-based segmentations of sub-cortical grey matter nuclei by FSL FIRST<sup>8</sup>, projected to voxel partial volume fractions;
- Volume-based segmentations of various other non-cortical structures by FreeSurfer (with intermediate projection to surface representations for smoothing);
- Intensity-based tissue segmentation of the cerebellum.

Brain stem structures are projected to the tissue type within ACT that disables application of anatomical constraints to streamlines as they traverse such regions: this permits streamlines to either terminate within the brain stem due to other tractography criteria, or traverse fully through it; this is a simplified version of a recent ACT modification proposal<sup>9</sup>.

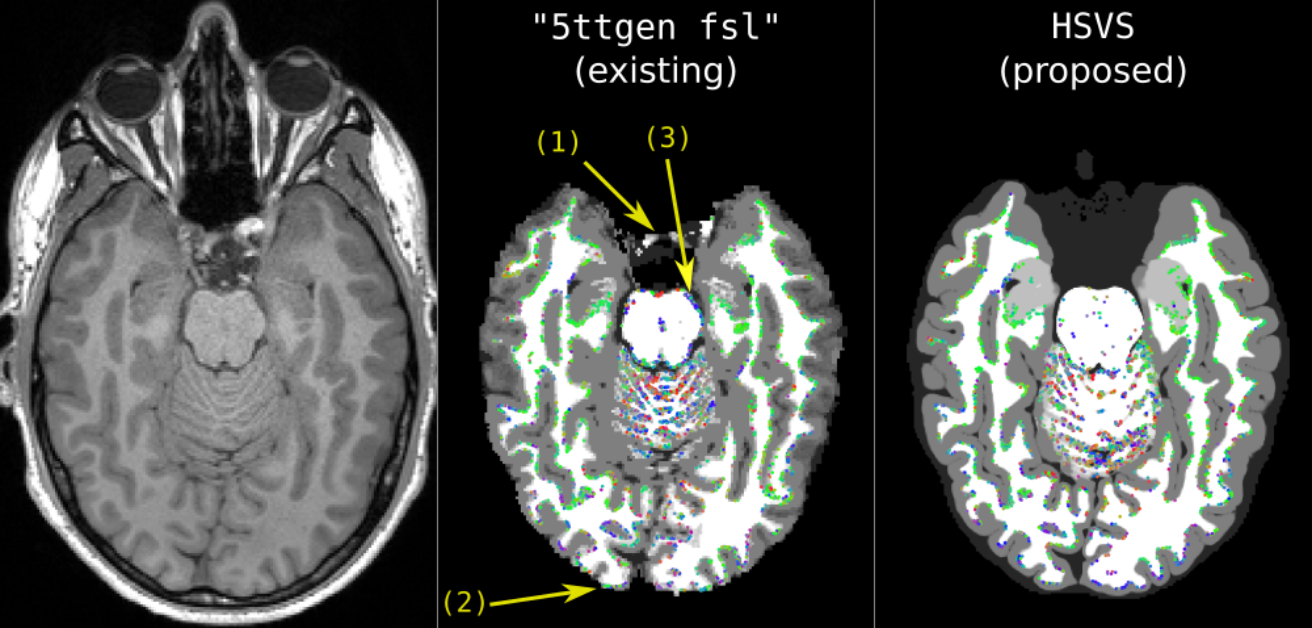
Because almost all segmentation sources involve the use of surface-based information (whether natively or during the course of surface-based smoothing), super-resolution segmentation can be achieved by defining a voxel template for partial volume estimation that is of a higher spatial resolution than the input T1-weighted image.



•Figure 1. Component steps in the derivation of the high-resolution tissue segmentation image (volume projections from front-left of subject).

Results:

Figure 2 shows the differences between the historical and proposed approaches for deriving the tissue segmentation image for ACT, for a challenging axial slice through the midbrain; streamlines terminations from whole-brain fibre-tracking are shown as coloured dots. Arrows highlight areas where the previous approach leads to particularly improper brain masking (1), tissue separation (2), and streamlines terminations (3). The proposed algorithm provides exceptionally clean tissue classifications even in these problematic areas.



·Figure 2. Exemplar axial slice contrasting results of existing and proposed tissue segmentations for ACT. Dots indicate streamline terminations.

Conclusions:

This algorithm enables more accurate reconstruction of white matter connectivity using diffusion MRI streamlines tractography, by utilising state-of-the-art tissue segmentation algorithms to provide more robust tissue interface localisation information to the Anatomically-Constrained Tractography framework.

Modeling and Analysis Methods:

Diffusion MRI Modeling and Analysis <sup>1</sup>  
Segmentation and Parcellation <sup>2</sup>

Keywords:

Brainstem  
Segmentation  
Tractography  
WHITE MATTER IMAGING - DTI, HARDI, DSI, ETC

<sup>1|2</sup>Indicates the priority used for review

My abstract is being submitted as a Software Demonstration.

No

Please indicate below if your study was a "resting state" or "task-activation" study.

Other

**Healthy subjects only or patients (note that patient studies may also involve healthy subjects):**

Healthy subjects

**Was any human subjects research approved by the relevant Institutional Review Board or ethics panel? NOTE: Any human subjects studies without IRB approval will be automatically rejected.**

Yes

**Was any animal research approved by the relevant IACUC or other animal research panel? NOTE: Any animal studies without IACUC approval will be automatically rejected.**

Not applicable

**Please indicate which methods were used in your research:**

Structural MRI

Diffusion MRI

**For human MRI, what field strength scanner do you use?**

3.0T

**Which processing packages did you use for your study?**

FSL

Free Surfer

Other, Please list - MRtrix3

**Provide references using author date format**

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