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Segmentation of White Matter Tractograms Using Fuzzy Spatial Relations

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Introduction

Clinicians or researchers often want to isolate precise white matter tracts in order to test hypotheses related to a pathology. Segmenting white matter into reproducible tracts is difficult due to the huge amount of fibers and their vague anatomical definitions. The most common method, selecting fibers passing through manually delineated ROIs, is time-consuming and poorly reproducible for tracts with convoluted trajectories [4]. Differently, manually segmented ROIs can be transferred from training images to test subjects via non-linear deformations [4]. The resulting segmentation might not be accurate when training and test images do not share the same topology (e.g. due to a tumor). Other methods rely on unsupervised clustering and use a labeled atlas [5]. With a different perspective, a near-to-English query language (WMQL) allows the user to interactively define divisional terms, relative clauses and logical operations to segment anatomical tracts [1]. However, the shape of the resulting tracts can vary among subjects since WMQL is based on simple binary relations and bounding boxes. We propose to include qualitative anatomical definitions, modeled as fuzzy sets [6], into a semi-automatic segmentation algorithm, and to automatically compute an "anatomical coherence score" for every fiber of the tractogram.

Methods

Whole brain tracts were computed for 10 subjects from the HCP Project [7] using the SDSTREAM deterministic tracking algorithm of MRTrix3 [3], and the fractional anisotropy (FA) was extracted from the diffusion tensor. An initial segmentation, based on an exhaustive list of spatial relations (Fig.1) is performed with WMQL [1]. All anatomical labels are computed using FreeSurfer. To reduce the computational load and ease the visualization, a clustering step is implemented. Every cluster is then approximated with a prototype, computed as the fiber closest to the cluster centroid. We propose a new metric, called weighted functional varifolds, which takes into consideration the geometry, connectivity [4] and FA [8] of a fiber. The parameters were manually tuned based on experiments and anatomical considerations. Two fibers, with possibly different numbers of points, are similar only when they follow adjacent paths, their endpoints are close to each other and their FAs, mapped point-wise, are similar. An "anatomical coherence score" is then assigned to every prototype, based on the satisfaction of spatial relations, with respect to anatomical structures, defined as fuzzy sets in the image domain, thus coping with their intrinsic imprecision [6]. First, for every fuzzy set, we compute the mean value along the points of the prototypes. Then, we assign to the prototype the minimum score value, which is propagated to the fibers of the cluster. By thresholding it, clinicians can segment a tract in a fast and easy way and, notably, adapt the segmentation to a specific task.

Results

The evaluation focused on the Uncinate Fasciculus (Fig.1). The whole-brain tractogram (b) is initially segmented using WMQL (e) based on an exhaustive list of spatial relations (d). Then, we use the DBSCAN algorithm to separate fibers into clusters. Two other techniques (hierarchical and spectral) gave comparable results (not shown here). In (g) the prototypes are displayed. The fuzzy sets (f) are computed from the previous list and mapped onto the fibers (h). The coherence score is normalized between 0 and 1 (h). The final segmentation output is obtained setting a threshold of 0.5 (i). Fig. 2 shows the effects of the thresholding for a single subject (a), and the results for three subjects (b) where the threshold of 0.5 has been identified as the most anatomically accurate and reproducible by a neurosurgeon.

Conclusions

We presented a new semi-automatic tool for segmentation of white matter tractograms combining shape, connectivity, FA and anatomical information. The segmentation can be adapted in an intuitive way tuning a single parameter.

Biliography

[1]

D. Wassermann et al (2013), 'On Describing Human White Matter Anatomy: The White Matter Query Language, Med Image Comput Comput Assist Interv, vol. 16, pp. 647–654.4.

[2]

P. Gori et al. (2016), 'Parsimonious Approximation of Streamline Trajectories in White Matter Fiber Bundles', IEEE Transactions on Medical Imaging, vol. 35.12, pp. 2609–2619.

[3]

J.-D. Tournier, F. Calamante, A. Connelly (2012), 'MRtrix: Diffusion tractography in crossing fiber regions', International Journal of Imaging Systems and Technology, vol. 22.1, pp. 53–66.

[4]

Y. Zhang et al. (2010), 'Atlas-guided tract reconstruction for automated and comprehensive examination of the white matter anatomy', NeuroImage, vol. 52.4, pp. 1289–1301.

[5]

P. Guevara et al. (2012), 'Automatic fiber bundle segmentation in massive tractography datasets using a multi-subject bundle atlas', NeuroImage, vol. 61.4, pp. 1083–1099.

[6]

I. Bloch (2005), 'Fuzzy spatial relationships for image processing and interpretation: a review', Image and Vision Computing, vol. 23.2, pp. 89–110.

[7]

Van Essen, D. C., Smith, S. M., Barch, D. M., Behrens, T. E. J., Yacoub, E., Ugurbil, K., et al. (2013). 'The WU-Minn human connectome project: an overview', Neuroimage, vol. 80, pp. 62–79.

[8]

K. Kumar, P. Gori, B. Charlier, S. Durrleman, O. Colliot, C. Desrosiers (2017), 'White matter fiber segmentation using functional varifolds', MICCAI Workshop, Springer (LNCS).

Additional information

Figure 1 – Workflow

a.

b.

d.

IMAGING	*DISSECTION*
Catani (ScienceDirect, 2008)	***Ebeling*** (Acta Neochirurgica, 1992)
• Endpoints in temporal_anterior_section	• Inferior of Putamen
• Crossing orbito_frontal_gyrus	• Inferior of Claustrum
Wakana (NeuroImage, 2007)	***Peltier*** (Journal of neurosurgery, 2010)
• Crossing temporal lobe	• Anterior of Amygdala
• Crossing frontal lobe	
Leng (Neuroradiology, 2016)	
• Crossing superior_temporal	

e.

WMQL

f.

c.

g.

h.

1
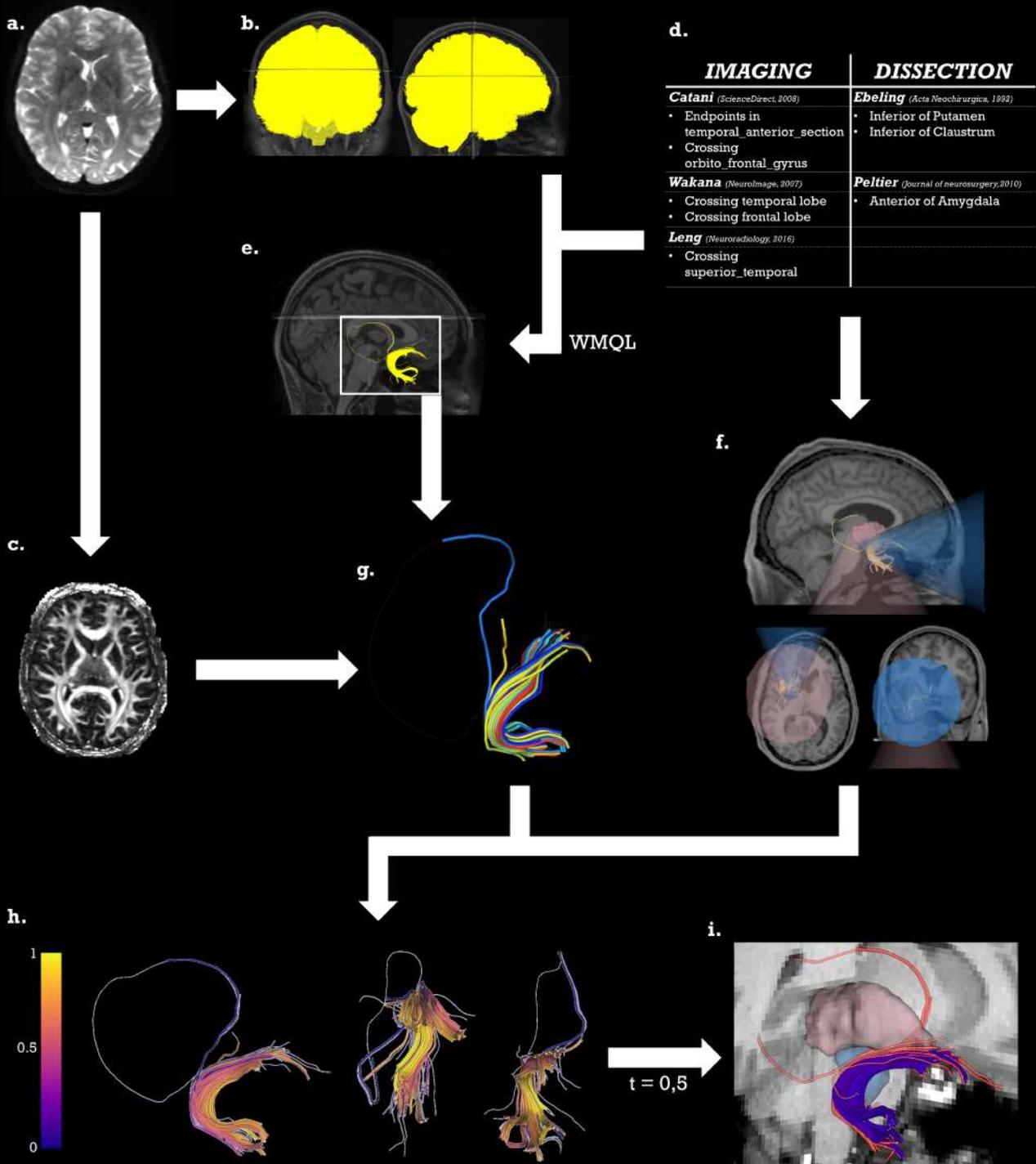
0.5

0

i.

t = 0,5

Fig. 1

From the DWI (a) both a whole brain tractogram (b) and an FA map (c) are computed. Through the use of spatial relations (d) an initial segmentation (e) is performed with WMQL. The same relations are applied to produce the spatial fuzzy sets (f), in the figure just the amygdala and putamen are showed. Combining diffusion, connectivy and geometric information a set of clusters is generated. The fuzzy values are then mapped onto the prototyes (g) of each cluster and propagated to the other fibers (h). Using a threshold the user is able to modify the final segmentation (i)

Figure 2 – Thresholding Effects Comparison and Reproducibility

HCP Dataset
Subject: 100307
Field Strength: 3T
Voxel Size: 1,25x1,25x1,25 mm

VIEW

THRESHOLD

CORONAL SAGITTAL AXIAL ISO

a.

0

0,25

0,5

0,75

b.

t = 0
t = 0,5

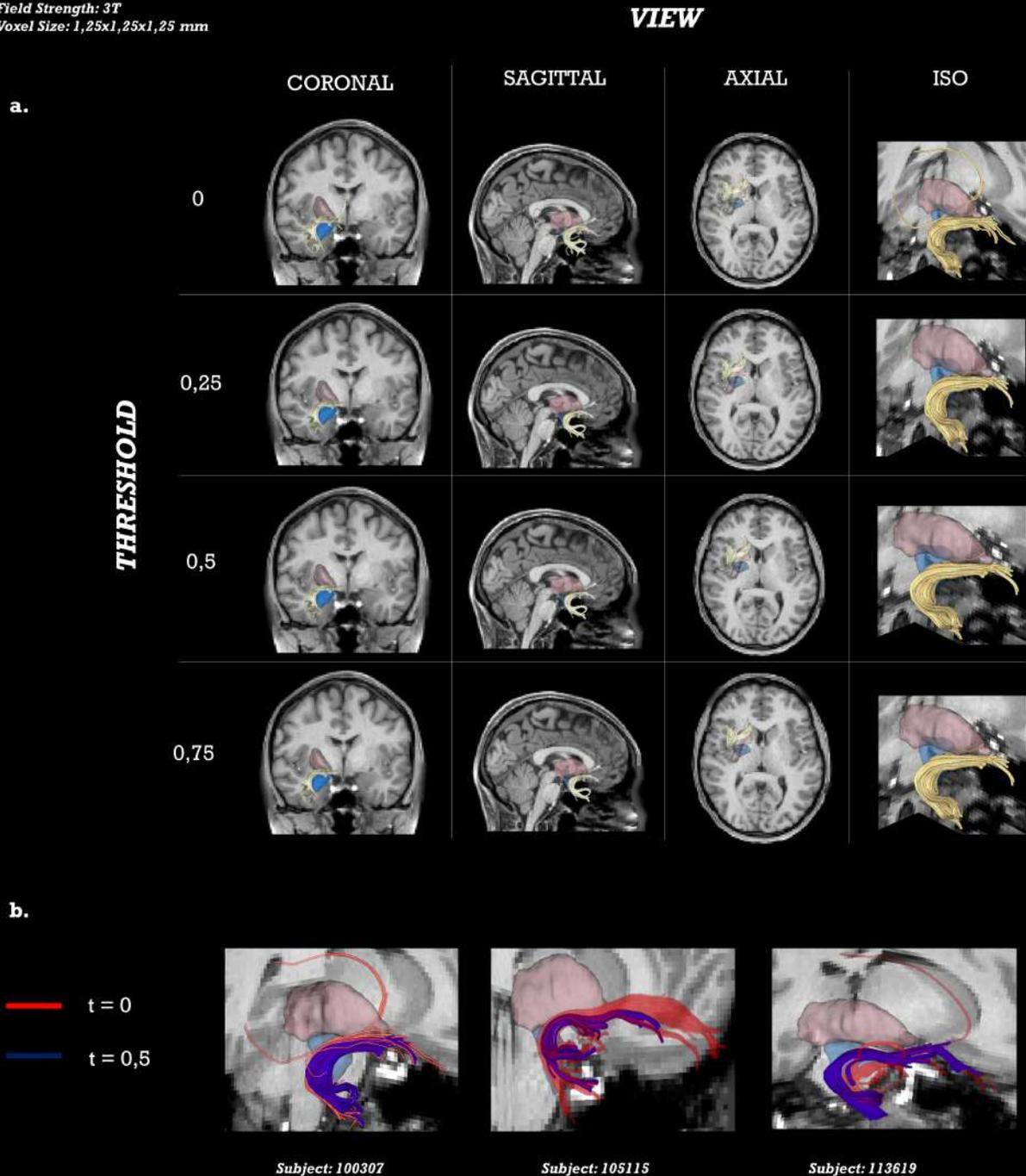Subject: 100307   Subject: 105115   Subject: 113619

Fig. 2

a. Effects of different level of thresholding on a single subject (t=0 keeps all fibers, t=1 removes all fibers).
b. Inter subjects reproducibility. The threshold value 0,5 has been identified by a neurosurgeon as the most anatomically coherent and reproducible. The results have been validated and evaluated as anatomically coherents.