



**HAL**  
open science

# Diffusion Driven Label Fusion for White Matter Multi-Atlas Segmentation

Guillermo Gallardo, Sylvain Bouix, Demian Wassermann

► **To cite this version:**

Guillermo Gallardo, Sylvain Bouix, Demian Wassermann. Diffusion Driven Label Fusion for White Matter Multi-Atlas Segmentation. OHBM 2018 - Organization for Human Brain Mapping, Jun 2018, Singapore, Singapore. pp.1-2. hal-01737422

**HAL Id: hal-01737422**

**<https://hal.science/hal-01737422v1>**

Submitted on 19 Mar 2018

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

# Diffusion Driven Label Fusion for White Matter Multi-Atlas Segmentation

Gallardo Guillermo \*

Bouix Sylvain †

Wassermann Demian ‡

## Introduction

White matter pathologies such as tumors or traumatic brain injury disrupt the structure of white matter. These disruptions hamper the inference of affected pathways using tractography. A way to overcome this is to use a label fusion technique. Label fusion aims to infer the localization of the brain structure of a subject from its localization in a group of control subjects. The most common technique is known as the voting rule [Xu et al.,1992], where a structure is said to be present in a voxel if it's present in the majority of the voting subjects. Furthermore, this can be improved by weighting each vote by the similarity between the T1 of each voting subject and the subject to be inferred. However, these techniques only rely in the spatial localization of the structures. In this work, we introduce a way to weight the vote of each subject based on how the voted pathway is supported by the test subject's diffusion data. This is, if the diffusion data of the test subject is consistent with the direction of the voted pathway, the vote has a higher weight. We show that adding dMRI to the label fusion process achieves a similar number of true positives than the voting technique, with a 60% less of false positives. However, this incurs in a trade-off of a 40% false negatives.

## Methods

We randomly selected 13 subjects from the HCP500 dataset from the Human Connectome Project. For each subject, we computed whole-brain tractography using each voxel in the white-matter as a seed and simulating 8 particles per seed. We extracted the main tracts from the left hemisphere tractogram (18 tracts in total) using the implementation of the white-matter query language (WMQL), (Wasserman et al. 2016). We randomly selected one of the subjects as test and used the rest as train subjects. We registered the tracts of every train subject into the diffusion space of the test subject. In order to label each the white-matter of the test subject with one of the 18 tracts, we discretize all the registered tracts in voxel coordinates. To decide which label to assign into a given voxel, we propose the model of equation (1). Our model is based on that of Rohlfing et al. (2004). For each voxel in the white-matter of our test subject, we select the label with the highest summation of weighted votes. Given a label, the first term of eq. 1 is 1 if the tract corresponding to that label passes through the voxel in the train subject and 0 if not. In our model, the weights (second term in eq. 1) come from the similarity between the direction of the voted tract, and the dMRI data of the test subject. To compute the weight, we estimate the density of directions for the tract over a sphere. We do so using an angular central gaussian distribution (ACGD). Then, we compute the probability of observing each of the main diffusion directions in the test subject given that the tract passes through that voxel (eq. 2).

## Results

After registering all the tracts to the diffusion space of the test subject we computed parcellations using both the voting rule and our technique. For each technique, we computed its confusion matrix, this is, a matrix of size labels by labels where the entry (i,j) is the number of times the label in the ground truth was i and the technique labeled j. To compute the 'ground truth' parcellation, we discretize the tracts obtained by using WMQL in the whole-brain tractography of the test subject. As the table shows, our proposed achieves a similar number of false negatives while obtaining a 64% less of false positives. This incurs on a trade-off of having 39% more false negatives and 18% less true positives, underlying that our technique a more conservative.

## Conclusions

In this work we presented a labeling fusion technique that relies on dMRI data to infer the localization of white-matter tracts. The results show that our technique is more conservative than the voting rule, which is desired when studying pathologies, at the cost of having more false negatives.

## Acknowledgments

This work was partially financed by the grant R01HD090641, the ANR NeuroRef and the ERC-StG NeuroLang

This work has received funding from the European Research Council (ERC) under the Horizon 2020 research and innovation program (ERC Advanced Grant agreement No 694665 : CoBCoM)

$$\hat{L}(x) = \arg \max_{l \in \text{labels}} \sum_{s \in S} p(L(x) = l | L_s(x)) p(P(x) | D_{sl}(x)) \quad (1)$$

$$p(P(x) | D_{sl}(x)) = \sum_{k \in \text{peaks}(x)} p(k | D_{sl}(x)) \quad (2)$$

---

\*Université Côte d'Azur, Inria

†Psychiatry Neuroimaging Laboratory, Brigham and Womens Hospital, Harvard Medical School

‡Parietal, Inria Saclay - Ile de France

Table 1: Confusion matrix for both techniques and the ratio between them

|            | Diffusion  |       | Voting     |       | Diffusion / Voting |       |
|------------|------------|-------|------------|-------|--------------------|-------|
|            | Background | Tract | Background | Tract | Background         | Tract |
| Background | 3658350    | 11849 | 3568123    | 24619 | 1.00               | 0.48  |
| Tract      | 27932      | 2592  | 17050      | 3163  | 1.64               | 0.82  |

## Table

Figure 1. Outline of our technique. We extract the main white-matter tracts using WMQL, register them to the 'test' subject and then compute a voting rule weighted by diffusion information. For each voxel  $x$  in the 'test' subject, we select the label  $l$  that maximizes equation 1, where  $S$  is the set of 'train' subjects,  $t$  is the 'test' subject;  $L_i(x)$  is the label of voxel  $x$  for the subject  $i$ ;  $P$  are the principal directions of diffusion in the 'test' subject and  $D_{sl}(x)$  are the directions of tract  $l$  in the voxel  $x$  of the 'train' subject  $s$ .

## References

- [Wassermann et al.,2016] Wassermann, D., Makris, N., Rathi, Y., Shenton, M., Kikinis, R., Kubicki, M., Westin, C. . The white matter query language: a novel approach for describing human white matter anatomy. Brain Structure and Function, 2016
- [Rohlfing et al.,2004] Rohlfing, T., Russakoff, D. B., Maurer, C. R. Performance-based classifier combination in atlas-based image segmentation using expectation-maximization parameter estimation. IEEE Transactions on Medical Imaging, 2004.
- [Xu et al.,1992] Xu, L., Krzyzak, A., Suen, C. Y. Methods of Combining Multiple Classifiers and Their Applications to Handwriting Recognition, 22(3), 418435. 1992