Reduction of False Positive Valued Area by Combining Probability Maps

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INTRODUCTION

Mapping the probability of connectivity is a powerful tool to determine the fiber structure of white matter in the brain. These probability maps are related to the degree of connectivity of the specified seed area. Nevertheless, in many applications it is necessary to isolate a fiber bundle connecting two areas. Multiplying two probability maps with different seed areas, results a new map. Here, the value of one voxel is related to the probability, that this point is connected to both seed areas. A voxel inside the fiber **B**undle **o**f **I**nterest (BOI) will have higher probability. But also voxel outside of the BOI might have high probabilities. For example the two propagated fibers could merge together facing a third area. This false-positive detection makes the interpretation of the multiplied maps very difficult. In this paper we introduce a method capable to separate connected and merged fiber bundles. This is used to suppress false-positive detected fibers. To show the performance of this approach the probability maps of the optical radiation is determined by using seed areas in the **l**ateral **g**eniculate **n**ucleus (LGN) and the primary visual cortex (V1).

METHODS

The *in vivo* DTI-measurements were done on a Siemens 3T TIM Trio using a DW SE EPI sequence. The whole brain was covered with contiguous 2mm slices with an in-plane resolution of 2x2 mm^2. The diffusion-encoding was done in 61 different directions with an effective b-value of 1000 s/mm^2. Distortion correction was applied according [1]. Additionally a 3D T1 MPRAGE dataset with a resolution of 1 mm^3 cubic was acquired.

The T1 weighted dataset was normalized to the MNI template SPM5 [2]. The left LGN and the left V1 were extracted as ROIs from the anatomical atlas using WFU PickAtlas Tool [3] and resliced to the coordinate system of the DTI-dataset.

To calculate the probability map of a specified seed area, a Monte-Carlo based algorithm similar to the PICo method [4] was used. In each iteration the FACT algorithm [5] was propagated through the tensor field. But instead of using the main axes of the DT, the traversed direction was determined by a random experiment. Therefore, the current DT was sharpened by applying an exponent of 4 to the eigenvalues. This modified DT was used as density function for the random experiments.

Fig 1 shows fibers propagated from region A and B. The BOI is part of the Connected Area, where the fibers from A and B are running mainly in the opposite direction. In the Merged Area, which is not part of the BOI, the fibers are running mainly in the same direction. To decide if fibers of the two seed region are merged or connected, the eigenvector with the highest eigenvalue ($\mathbf{e}_1$) was used as reference direction. The sign of $\mathbf{e}_1$ is meaningless but fix and won't change during calculation in our implementation. Dependent of this sign the number of visits was counted by two separate counters for each voxel. Propagated fibers having the same sign of the scalar product between the trajectory and $\mathbf{e}_1$ are facing in the same direction, fibers having the opposite sign are facing against each other. By applying the following equation, the Ratio of Connected Configuration between fibers starting from seed region LGN and V1 was calculated (see Fig 2):

$$f^{con} = (p^{+}_{LGN} * p^{-}_{V1} + p^{-}_{LGN} * p^{+}_{V1}) / p_{LGN\otimes V1} \quad \text{with } p_{LGN\otimes V1} = (p^{+}_{LGN} + p^{-}_{LGN}) * (p^{+}_{V1} + p^{-}_{V1})$$

Thereby, p^{+}_{X} and p^{-}_{X} are the normalized counters of visits for the positive and negative sign and the subscript letter describes the seed region. The map $p_{LGN\otimes V1}$ is equivalent to the Simple Multiplication of the probability map starting from seed region LGN and V1 (see left map of Fig 3). The probability of a connected configuration was calculated by the equation:

$$p^{con} = 1 - \frac{1}{\exp\left((f^{con} - 0.5)/c\right) + 1}$$

The constant c was empirical chosen and set to 0.05. The Connected Weighted Multiplication was realized by applying $p_{LGN\otimes V1} * p^{con}$ and the Merged Weighted Multiplication by applying $p_{LGN\otimes V1} * (1 - p^{con})$ (see right and middle map of Fig 3).

RESULTS

When using the simple multiplication, areas of the optical radiation as well as areas of the splenium have high probabilities (see left map of Fig 3). When the connected weighted multiplication was applied, the area of the optical radiation is nearly identical to the simple multiplication. However, areas containing merging fibers from LGN and V1 like the splenium are strongly suppressed (see right map of Fig 3).

DICUSSION

The introduced approach was capable to extract the optical radiation and showed a much higher specificity with a nearly identical sensitivity compared to a simple multiplication. Using $\mathbf{e}_1$ as reference direction is valid in the most cases, since most trajectories will have small angles to $\mathbf{e}_1$. The performance of this approach might be less in areas of very isotropic diffusivity or crossing fibers. More investigation has to be done in order to quantify this error. Additionally, the determined probability maps depend still on the distance of the seed points. However, using the distance independent map of the Ratio of Connected Configuration (see Fig 2) might be a method to overcome this problem. This needs more discussion and is beyond the scope of this paper. Nevertheless, the here introduced Connected Weighted Multiplication showed a good reproducibility and seems to be a robust method to detect the fiber bundle, connecting two specified areas.

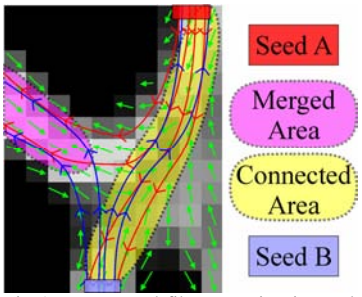

Fig 1: Propagated fibers starting in seed A (red) and seed B (blue). The green arrows indicate the eigenvector $\mathbf{e}_1$, which is used as reference direction.

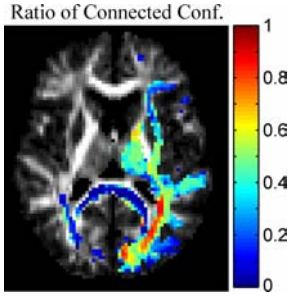

Fig 2: Map f^{con}. In areas of the BOI the ratio is close to one. In areas of merging fiber the ratio is close to zero.

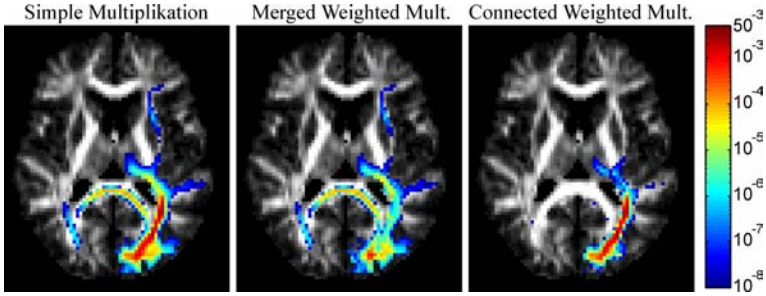

Fig 3: Resulting maps by combining the probability map starting from V1 and LGN to extract the optical radiation. The probabilities are visualized in colors on the underlying FA-map of the subject. All probabilities are visualized with the same logarithmic color encoding in order to make the maps comparable.

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