# A graph based approach for evaluation of neuronal fiber tracks connectivity probability

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## INTRODUCTION

To calculate the connectivity probability between two areas in the brain it would necessary to determine the probability of all possible neuronal pathways in the brain. Since there are infinite pathways between two regions it is impossible to calculate the connectivity probability exactly. In our approach, we use the distribution of fiber-ratios outgoing from a specific area to estimate the connectivity probability. Therefore similar fibers in non-crossing regions were clustered together to fiber bundles. By determining the thickness and estimating the fiber-density at the endpoints of the bundles the relative number of fibers can be estimated. A Monte-Carlo simulation was used to estimate the distribution of the relative fiber number inside of crossing-areas. By applying a deep search algorithm outgoing from a specified cluster the fiber distribution respectively the connectivity probability was determined.

## METHODS:

**Simulation:** A phantom with one Y-crossing (a) and three X-crossings (b, c, and d) were generated as shown in FIG 1. It was assumed that pure fiber bundles have a FA-index of 0.86 as in the human splenium and the space between fibers is filled with water with a mean diffusivity of $3.9*10^{-3}mm^2$/s as in CSF [1]. The fiber bundles A, D, B, and C contain 90%, 90%, 35%, and 55% of pure fiber respectively. The diffusion-weighted signal was simulated in 60 diffusion-encoding directions with an effective b-value of $1500s/mm^2$. The multi diffusion tensors model (mDT) [2] as well as the standard single diffusion tensor (sDT) was fitted to the simulated diffusion weighted signals. Crossing areas were defined by applying F-test ($p<0.05$) between the error of the mDT-model (crossing area) and the sDT-model (non-crossing area).
**The FACT** algorithm [3] was applied with a maximum-curvature criteria of 60°, and the trackable area was defined by an FA-index>0.15. In FIG 2 the determined fibers passing through ROI I (see FIG 1) are colored in green and fibers passing through ROI II (see FIG 1) are colored in red.
**Cluster-Graph approach**: The crossing areas (mDT selected voxel) where segmented by a region-growing algorithm. The FACT algorithm was applied in non-crossing areas, since there is no change of the number of fiber there. The fibers were selected if both endpoints touched the border of crossing segment. An EM-cluster algorithm [4] was applied on a six dimensional space containing both endpoints of the selected fibers. The cluster algorithm was configured in a way that the standard deviation of the components were equivalent to the distance of two voxel. A graph was created in which each cluster was represented by two nodes connected by an edge (Streamline Edge) with the probability of one (see FIG 3). For each node, the thickness of the fiber bundle was determined. To estimate the relative number of fibers in the bundle, the fiber density was rated by the FA-index. Different ratios between pure fiber and pure water were simulated with the same configuration as used in the phantom simulation. A polynomial was fitted to the resulting FA-index and the ratio of pure fiber, resulting: $ratio(FA)= 0.81*FA^3-0.47*FA^2+0.96*FA$. Probability maps were determined by a Monte-Carlo simulation. Inside the crossing areas the mDT-model was used. To determine the fiber ratio running from cluster A to X (probEdges A→X) inside a crossing area (see FIG 3), the relative number of fibers contained in node A was distributed to the most probable (determined by the probability maps) voxel of the other nodes touching the same crossing area. The edge probability $p(A→X)$ was set to the ratio of the relative number of fibers that node X got from node A. The edge probabilities were normalized to yield $\Sigma_X p(A→X)=1$. A recursive depth search algorithm was implemented to traverse all possible paths out going from a specified node. The connectivity probability to the start-node was initially set to zero for all nodes except the start-node was set to one. During following the edge A→B, the probability of B was updated by $p^{t+1}(B)=p^t(B)+p(A→B)*p^t(A)$.
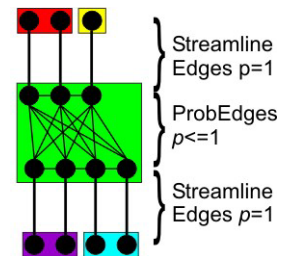


FIG 3: Example of a cluster graph. The different colors represents different crossing regions

## RESULTS:

**FACT algorithm**: FIG 2 shows the FACT tracking results starting from ROI I in green and starting from ROI II in red. Since the fiber ratio of pure fibers is much higher in fiber bundle D than in bundle B and C, the green track runs nearly straight through the crossing area b and c. However the red fibers are either aborted because of the maximum-curvature criteria of the FACT algorithm or directed into the wrong bundle D.
**Cluster-Graph approach**: FIG 4 shows the resulting connectivity probability to the cluster marked by the arrow. The sums of probabilities keep one in all segments of the fiber bundle D and zero for all other. Starting deep search from the cluster marked by the arrow in FIG 5, the probability is zero that any segment of bundle D is connected. The bundle B got a connectivity probability to the start cluster of 0.43 (true value 0.39) and the bundle D of 0.57 (true value 0.61).

## DISCUSSION:

There are two advantages of the introduced cluster-graph approach. First, due to a finite number of pathways from node A to B it is possible to traverse all possible paths to approximate the connectivity probability. Second, by clustering similar fibers together the thickness of fiber bundles can be used to calculate the expected fiber distribution in the crossing areas. Additionally, it is possible by varying standard deviation of the components of the cluster algorithm to realize connectivity estimation at different levels of details. A higher standard deviation results in a simpler graph and a rougher approximation, while using lower standard deviation finer connections can be detected, however with increased calculation time. Even though in the current implementation the estimation of fiber density and the probability calculations in crossing regions were done quite roughly and can be further improved, the high potential of the cluster-graph concept is obvious. Therefore it will be applied to estimate the connectivity probability *in vivo*.
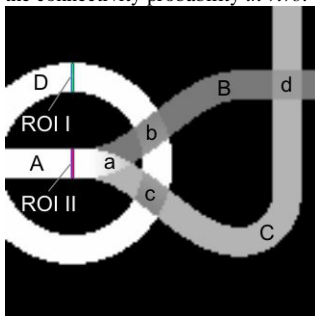


FIG 1: FA-map of the simulated phantom. The different fiber bundles are named by capital letters and crossing areas by low letters.
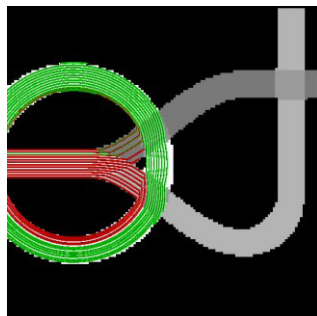
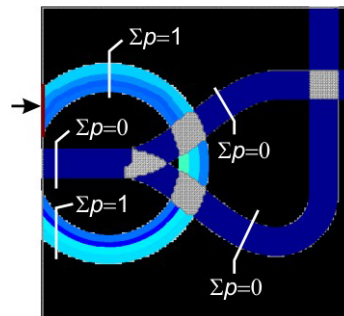FIG 2: Results of the FACT Algorithm. Green fibers are started from ROI I, red fibers are started from ROI II.

FIG 4: Resulting cluster graph starting at the cluster marked by arrow. Colors of the edges indicate the probability of connectivity to the start-cluster.
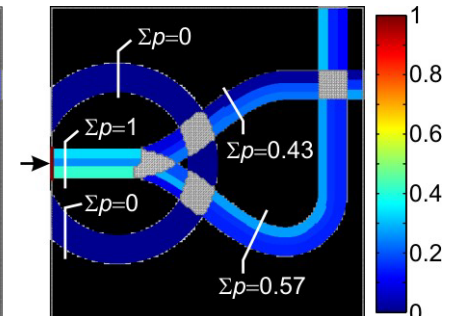
FIG 5: Resulting cluster graph starting at the arrow. The sum of probabilities is lower in bundle B, since there was simulated a lower fiber density as in bundle C.

## REFERENCE

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