A software application for real-time, clustering-based exploration of tractographies

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Introduction:

Interacting with tractographies is a difficult procedure for various reasons: (a) tractographies are usually represented by hundreds of thousands of intertwined streamlines (tracks) see fig. 1A; (b) data sets are often cluttered with noisy tracks, i.e. tracks which have no relevance in anatomy; (c) the size of the entire tractography is often too large to load in the memory of the graphics card; (d) navigating specific regions of a tractography in 3D space is cumbersome because of the unique shape characteristics of the streamlines.

We present a scientific visualization tool that solves the problem of interacting with tractographies by creating real-time simplifications in terms of the underlying bundle structures. The process that we propose works recursively: starting from a small number of clusters of streamlines the user decides which clusters to explore. Exploring a cluster means that the application re-clusters its content at a finer grained level.
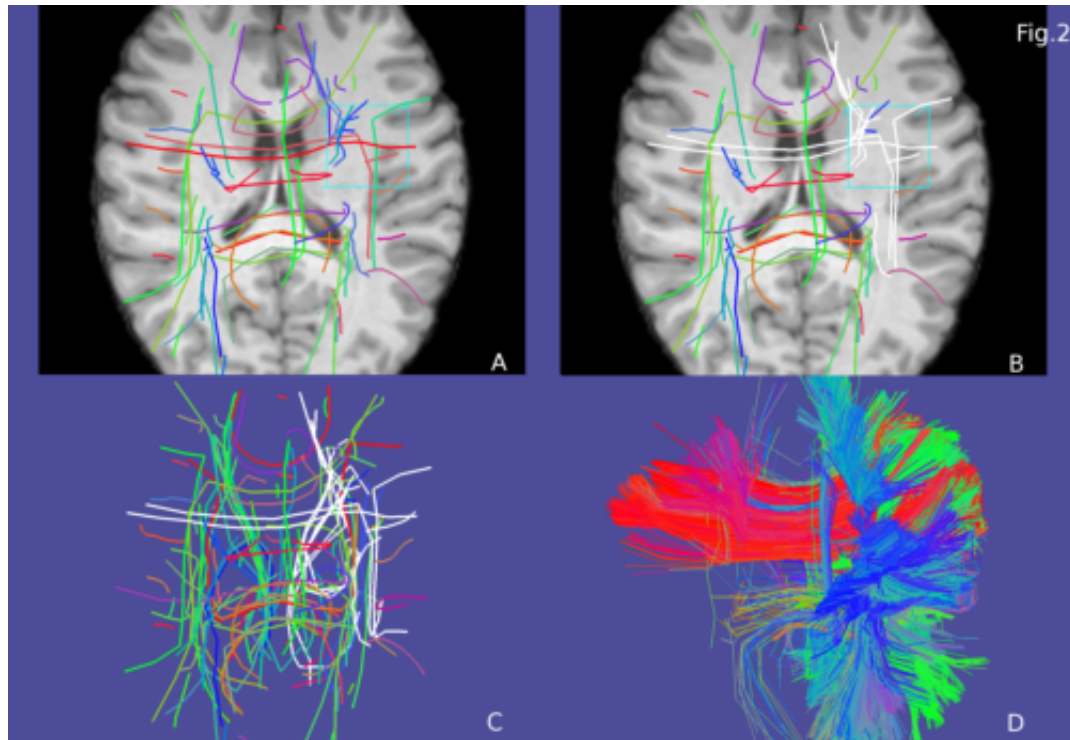
Methods:

The application starts visualizing the brain as a set of a few representative tracks, i.e. the cluster representatives. These representative tracks are provided by a very fast tractography clustering algorithm called QuickBundles [1,9] (see fig.1B) which can cluster thousands of tracks in milliseconds. Each representative track acts as the access point to the streamlines within that cluster and allows the user to address this portion of the tractography as a single unit, which we call "bundle of interest" (BOI). After visually inspecting the simplified tractography (fig.1B) the user interactively selects one or more representative tracks (fig.1C, the selected representative track is in white). When one or more representative tracks are selected the user can see the content of the related clusters (fig.1D). In order to explore the detailed structure of content of the selection the user may ask to re-cluster the selected BOIs into smaller clusters (fig.1E) in order to address and possibly further refine the initial selection. After selecting one or more of the small clusters through their representatives (fig.1F, in white) the user can repeat the visual inspection step (fig.1G), and the re-clustering step (fig.1H) as required in order to unveil the local structures (fig.1I).

Fig. 1
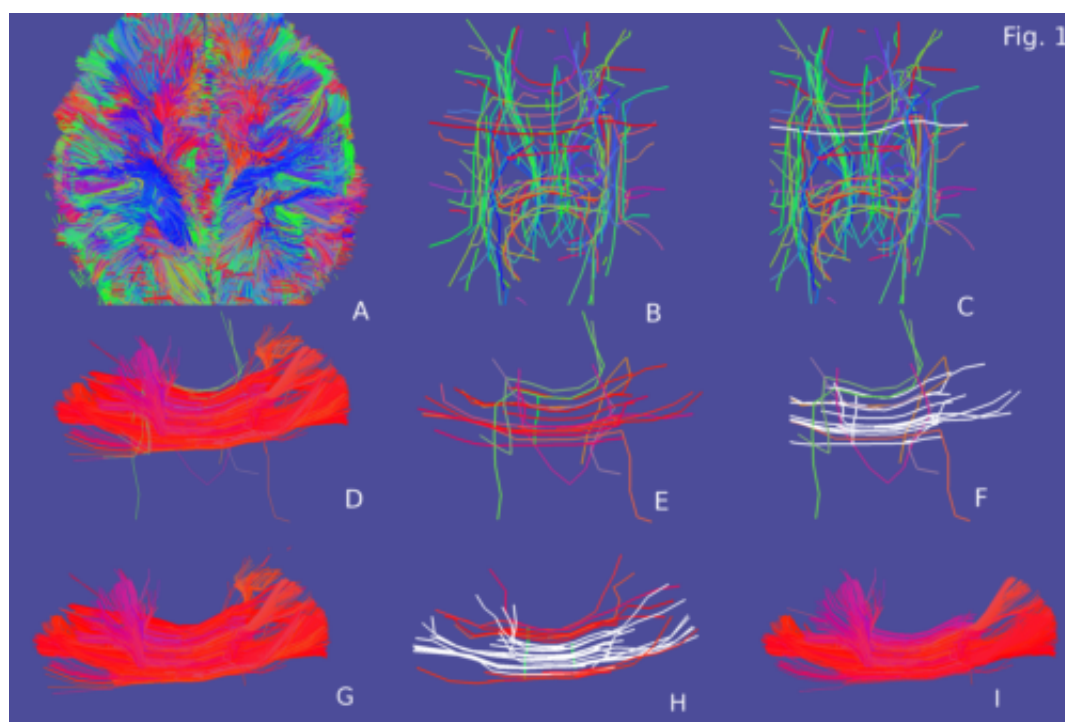
Results:

Additionally the user can visualise slices of structural volumes, e.g. FA or T1 (see fig.2). The volume is aligned in the same space (e.g standard space) of the tractography. Then the user can click a point on a slice to define the center of a cubic ROI and decide its size. After defining one or more ROIs the user can filter out the representative tracks which are not passing through the selected ROIs (fig.2B-C) and see the related subset of tractography (fig.2D).

Thus fig.1 and fig.2 show results of interactive tractography exploration using both BOIs and ROIs with user interactivity directly in the 3D space. This enables medical practitioners and researchers to meaningfully navigate the entire space of the tractography and to better understand diffusion MRI data.

Conclusions:

We presented a novel visualization tool which provides an entirely original way to interact with very large tractogaphies. This goes far beyond the methods used in [4-8] and, as far as we know, beyond any other available medical imaging software thanks to the scalability of the QuickBundles algorithm [1]. We provide a software implementation of this application which is written completely in Python language. We use the modules DIPY [2,10] and FOS [3] as building blocks of the software system. The application is available under an OpenSource license at [3].

Modeling and Analysis Methods:

Diffusion MRI Modeling and Analysis

Abstract Information

References

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