

Fiberweb : a new web solution for medical visualization and interactions

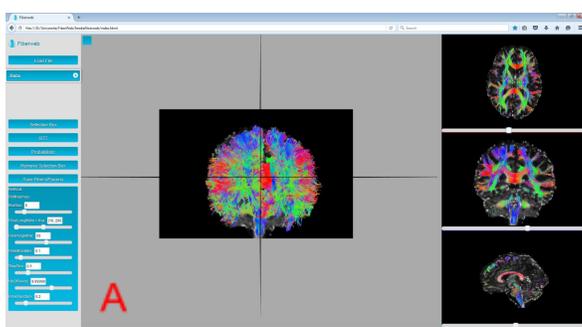
Louis-Philippe Ledoux¹, Jean-Christophe Houde¹, Félix C. Morency², Kevin Whittingstall¹, Jean-René Bélanger², Maxime Descoteaux¹

¹Université de Sherbrooke, Sherbrooke, Quebec, Canada; ²Imeka, Sherbrooke, Quebec, Canada

Target audience – Researchers, physicians and clinicians who need to visualize anatomical datasets and tractography streamlines rapidly and simply in a web browser. It is also of interest to people who want to do quick quality assurance on their data or perform real-time tractography.

Introduction – A novel browser-based solution for medical data visualization and interaction is proposed: **Fiberweb**. WebGL [1] is a recent technology that has not yet been fully explored for medical imaging visualization. Very few software tools allow for medical data visualization in the web browser [2][3][4][5] and none of the existing tool supports efficient data interaction such as streamline segmentation and real-time deterministic [6] and probabilistic tractography. Fiberweb currently supports anatomical dataset, whole brain tractograms, individual bundle and fiber ODF (fODF) peaks orientations [7].

Methods – Fiberweb was made possible due to the release of WebGL and the HTML5 standard. WebGL is a low-level graphics library for 3D rendering in the browser. To simplify development, we use the Three.js [8] high-level library, which wraps WebGL calls and makes it more convenient to use shaders, manage scenes and render primitives. An octree space partitioning data structure is filled at load time to reduce the search area when filtering streamlines. This makes real-time selection of streamlines possible without performance degradation. Fiberweb also supports deterministic [6] and probabilistic real-time tractography. Both algorithms require a



pre-computed dataset of peaks (e.g. extracted from the fODFs), as well as a fractional anisotropy mask. The probabilistic algorithm also requires an uncertainty angle for each peak.

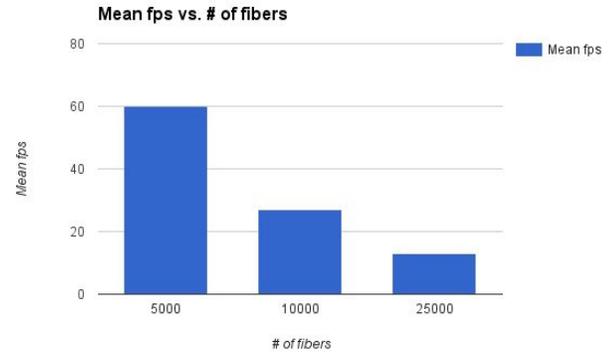
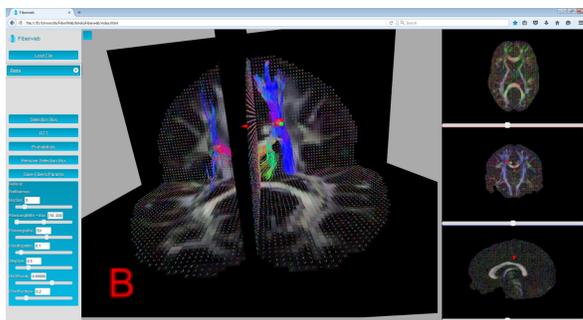


Figure 1 : Mean framerate in regards to # of fibers

While the deterministic algorithm directly uses the peaks, the probabilistic algorithms selects its next tracking direction in a cone of uncertainty formed from the uncertainty angle associated with the peak. In addition to selection and real-time tractography, it is also possible to visualize the streamlines intersecting a slice of the anatomy.

Results – Visualization: Considering displaying an anatomical dataset as the baseline, simultaneously displaying fODFs peaks datasets does not affect the framerate. Image 1a) shows the interface when simultaneously displaying streamlines and an anatomical dataset. The 3D view directly allows for picking, interaction and selection, and the 2D renderers (axial / coronal / sagittal) show how streamlines intersect the anatomical dataset. Displaying streamlines is the main bottleneck of the application. Both the rendering framerate and the maximal streamlines loading capacity are affected by the number of streamlines and the amount of points per streamline. One should note that to avoid bias, the average number of points per streamline is roughly the same across all our datasets. Figure 1 shows that, for very small datasets, doubling the number of streamlines approximately halves the framerate. Going over 25,000 streamlines does not affect the framerate. However, reaching around 80,000 streamlines starts creating memory issues due to browser limitations. This makes it currently impossible to load very large datasets, unless you use a browser with a higher memory limit (like the Firefox Nightly version [9]). Current results are shown on raw streamlines. Using streamline compression [10] and grouping of similar streamlines [11] could help the framerate and fluidity of the application in the future.



Interaction: Streamline interaction works in real-time. Whether we show the intersected fibers or not does not affect the framerate. The real-time tractography framerate starts dropping when we go over 1,000 seeds inside the seeding box. The other parameters do not have a noticeable effect on the framerate, neither does the choice of the algorithm (deterministic versus probabilistic).

Conclusion – We present a new tool that enables both visualization and interaction with diffusion MRI data directly inside the browser. Currently, it is more suitable for quality assurance and control due to the limitations in the sizes of the data the software can handle. For the future, Fiberweb is headed toward two main goals: supporting larger datasets and working on mobile devices like tablets.

Image 1 : a) Full brain and its corresponding anatomy
b) Probabilistic real-time tractography

References – [1] <https://www.khronos.org/webgl/> [2] <https://code.google.com/archive/p/brainimg/> [3] <http://slicedrop.com/> [4] <http://openscience.cbs.mpg.de/brainnetworks/> [5] <http://onpub.cbs.mpg.de/> [6] Chamberland et al., Frontiers 2014 [7] Descoteaux, Wiley EEEE 2015 [8] <https://github.com/mrdoob/three.js/> [9] <https://nightly.mozilla.org/> [10] Presseau et al, ISMRM 2014 [11] Garyfallidis et al, Frontiers 2012