

# Supplementary material of “Diffusion MRI Tractography Filtering Techniques Change the Topology of Structural Connectomes”

**Matteo Frigo<sup>1</sup>, Samuel Deslauriers-Gauthier<sup>1</sup>, Drew Parker<sup>2</sup>,  
Abdol Aziz Ould Ismail<sup>2</sup>, Junghoon John Kim<sup>3</sup>, Ragini  
Verma<sup>2</sup>, Rachid Deriche<sup>1</sup>**

<sup>1</sup> Athena Project-Team, Inria Sophia Antipolis-Méditerranée, Université Côte D’Azur, Nice, France

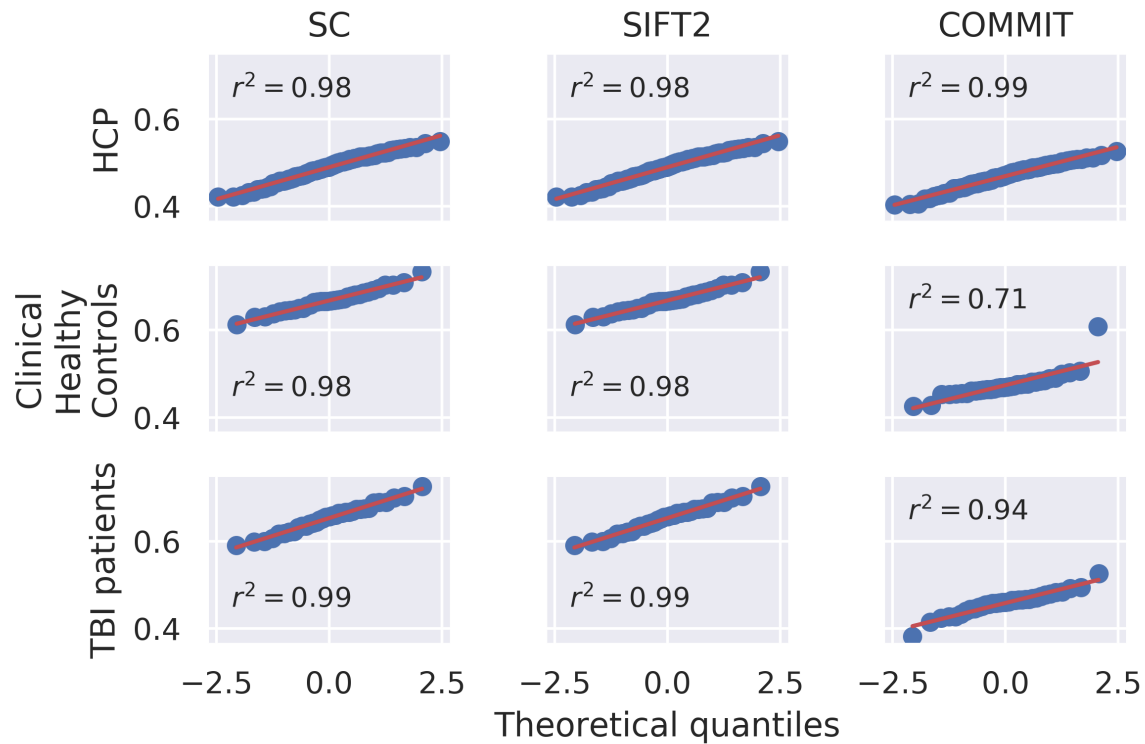
<sup>2</sup> Penn Applied Connectomics and Imaging Group, Department of Radiology, University of Pennsylvania, Philadelphia, PA, USA

<sup>3</sup> Department of Molecular, Cellular, and Biomedical Sciences, CUNY School of Medicine, The City College of New York, NY, USA

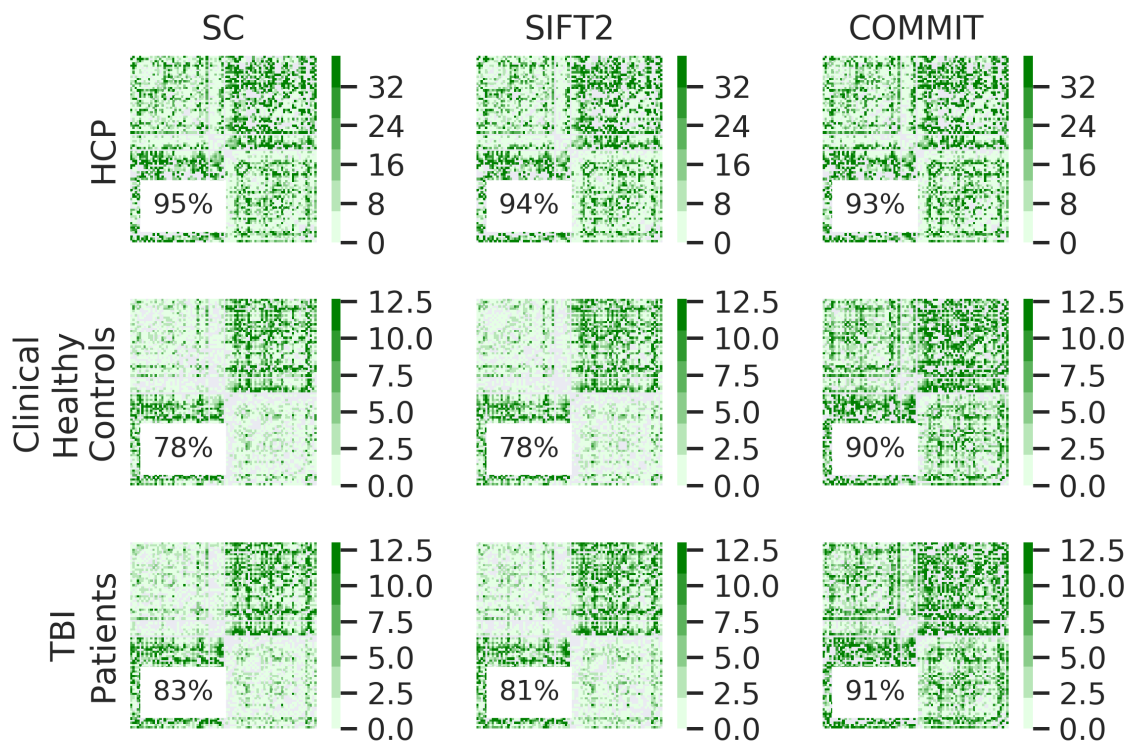
E-mail: [matteo.frigo@inria.fr](mailto:matteo.frigo@inria.fr)

Submitted to: *J. Neural Eng.*

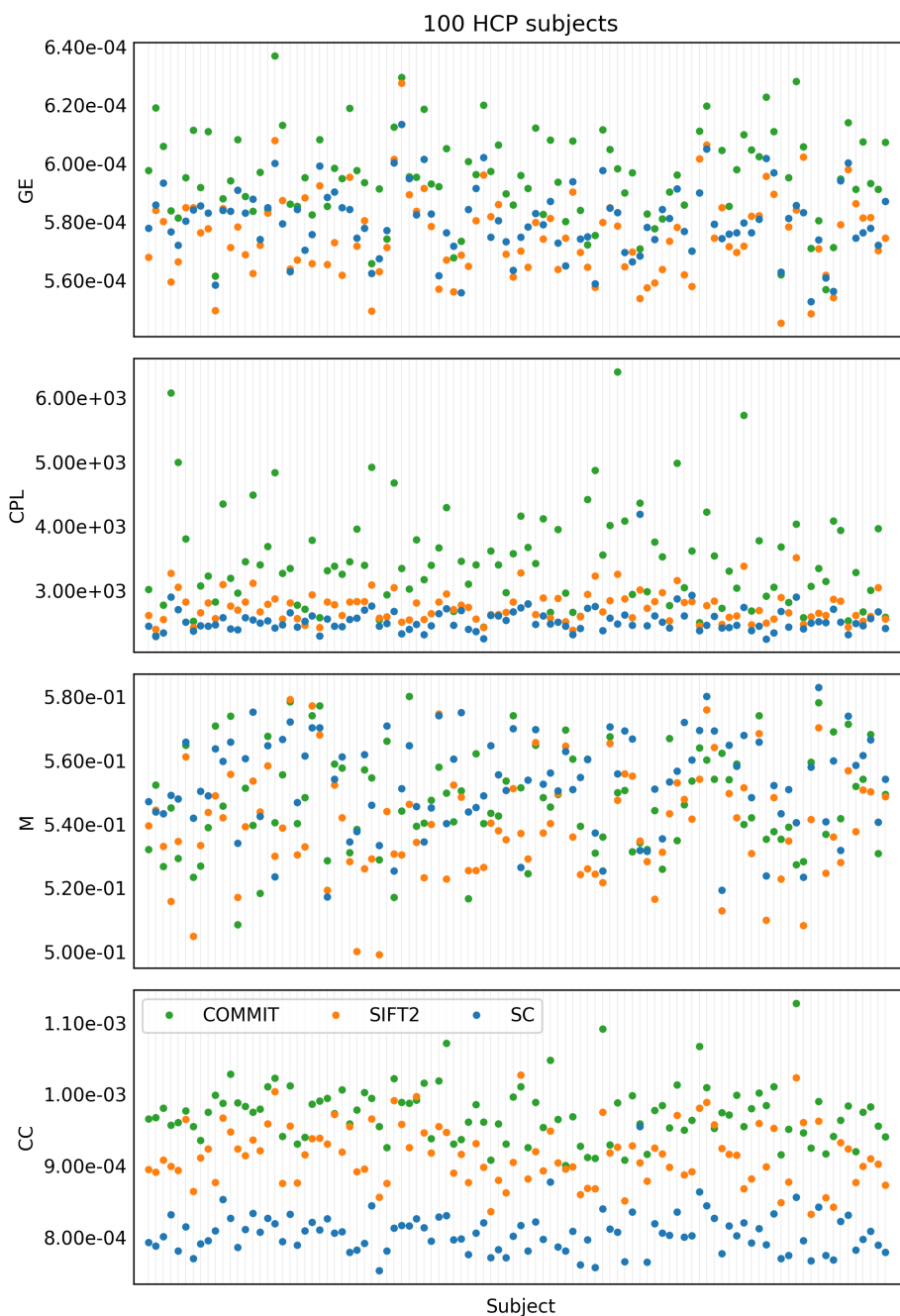
## Appendix A. Supplementary figures



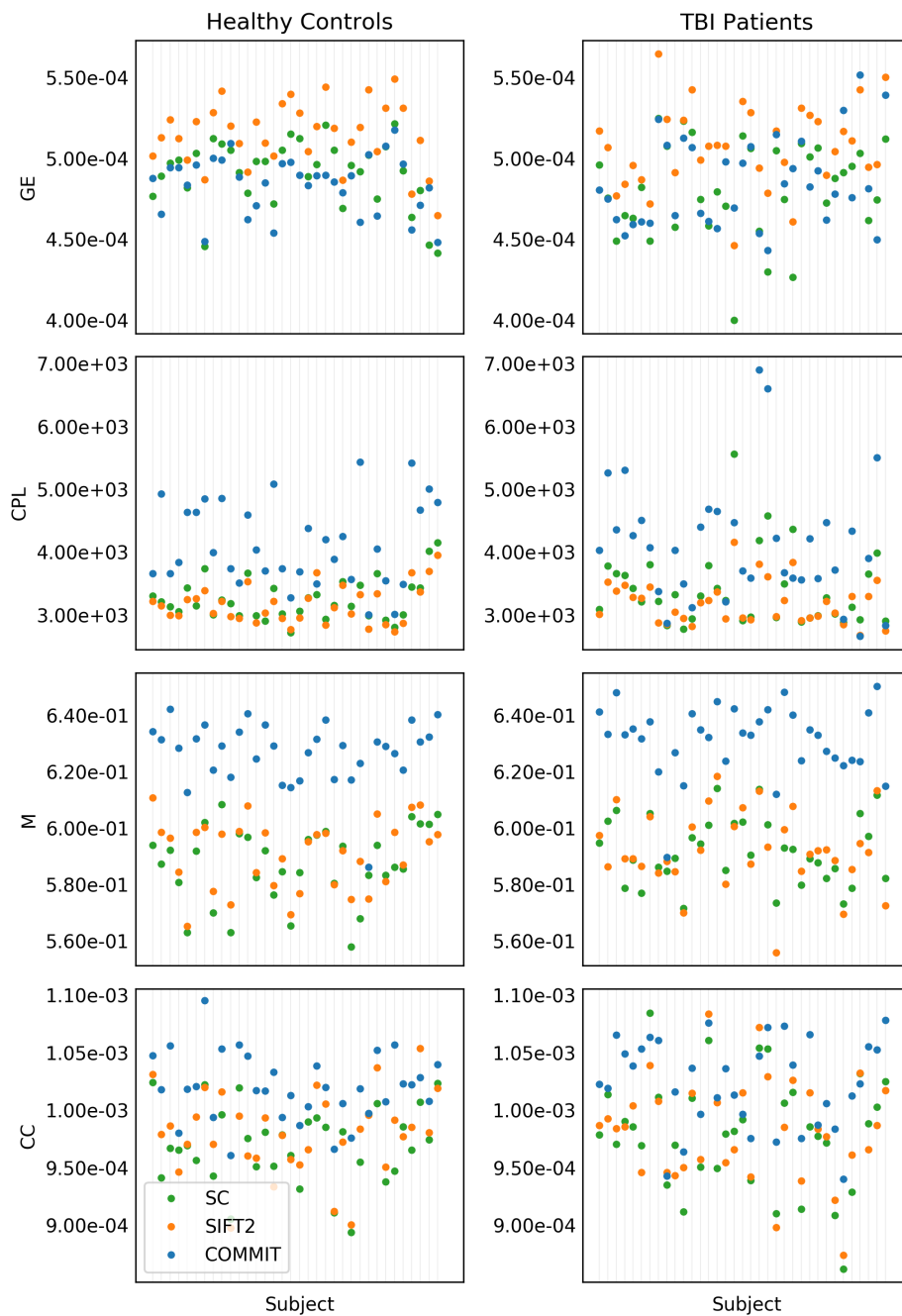
**Figure A1.** Each panel shows the normal probability plot of the raw values of the density of the connectomes obtained from different datasets (rows) and different TFTs (columns). The coefficient of determination  $r^2$  of the line estimated with least-squares fit is reported for each plot. Removing the maximal value from the densities of the COMMIT connectomes of the clinical healthy controls, the corresponding coefficient of determination becomes  $r^2 = 0.96$ .



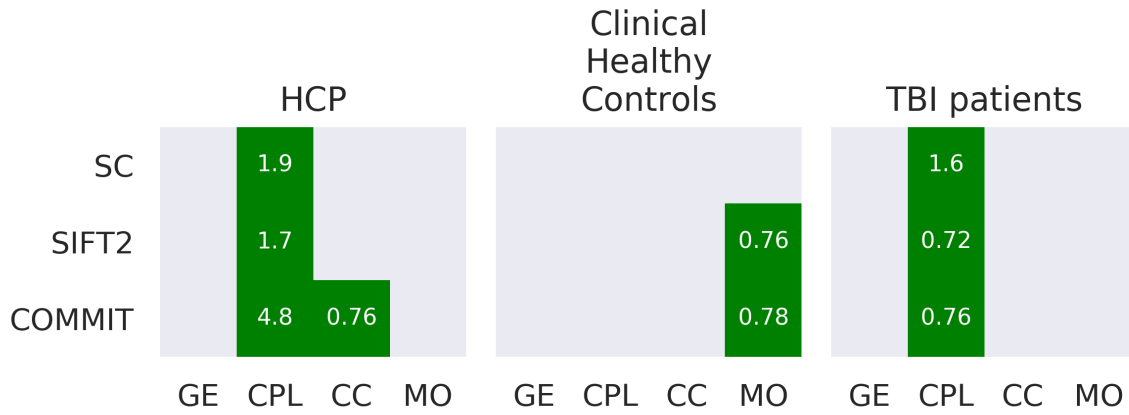
**Figure A2.** Each panel shows the value of the Anderson-Darling test performed on each edge of the connectome for one TFT and one subject cohort. The reported percentage quantifies the portion of edges for which the Anderson-Darling test statistic is lower than the critical value, indicating that the normality assumption should be rejected.



**Figure A3.** For each considered subject from the HCP database the value of the four studied graph-theoretical metrics is displayed. Each panel is devoted to a single topological measure. Values computed for the same subjects are aligned vertically. Blue dots correspond to the value of the metric computed on the SC connectomes, orange dots to the ones computed on the SIFT2 connectomes and green dots on the COMMIT connectomes.



**Figure A4.** For each subject in the clinical dataset the value of the four studied graph-theoretical metrics is displayed. Each panel is devoted to a single topological measure. Values computed for the same subjects are aligned vertically. Blue dots correspond to the value of the metric computed on the SC connectomes, orange dots to the ones computed on the SIFT2 connectomes and green dots on the COMMIT connectomes.



**Figure A5.** Each panel concerns one subject cohort. The result of the Anderson-Darling test performed on the raw values of the GTM computed on connectomes built with a specific TFT are reported. Only the statistically significant values are reported. We can observe that CPL, CC and MO do not consistently exhibit normality of the samples across subject cohorts and TFTs, therefore we can not assume that GTM values are normally distributed in general.