The braingraph.org Database of High Resolution Structural Connectomes and the Brain Graph Tools

Csaba Kerepesi\textsuperscript{a,c,**}, Balázs Szalkai\textsuperscript{a,**}, Bálint Varga\textsuperscript{a,**}, Vince Grolmusz\textsuperscript{a,b,*}

\textsuperscript{a}PIT Bioinformatics Group, Eötvös University, H-1117 Budapest, Hungary
\textsuperscript{b}Uratim Ltd., H-1118 Budapest, Hungary
\textsuperscript{c}Institute for Computer Science and Control, Hungarian Academy of Sciences, H-1111, Budapest, Hungary

Abstract

Based on the data of the NIH-funded Human Connectome Project, we have computed structural connectomes of 426 human subjects in five different resolutions of 83, 129, 234, 463 and 1015 nodes and several edge weights. The graphs are given in anatomically annotated GraphML format that facilitates better further processing and visualization. For 96 subjects, the anatomically classified sub-graphs can also be accessed, formed from the vertices corresponding to distinct lobes or even smaller regions of interests of the brain. For example, one can easily download and study the connectomes, restricted to the frontal lobes or just to the left precuneus of 96 subjects using the data. Partially directed connectomes of 423 subjects are also available for download. We also present a GitHub-deposited set of tools, called the Brain Graph Tools, for several processing tasks of the connectomes on the site \url{http://braingraph.org}.

Introduction

Mapping all the inter-neuronal connections of the human brain with more than 80 billion neurons is not possible today. The discovery of connections between much larger areas of the gray matter of the human brain is feasible by applying diffusion tensor imaging (DTI) data acquisition and a subsequent data processing workflow.

The NIH-funded large Human Connectome Project (HCP) \cite{1} regularly releases its high-quality functional- and diffusion MRI datasets of hundreds of healthy human subjects. One of the most interesting applications of the published data is the mapping of the connections of the human brain on a macroscopic level: State-of-the-art computational methods make possible of discover-
ing neural fiber connections between 1015 anatomically identified gray matter areas (also called Regions of Interests, ROIs) of the brain [2, 3, 4, 5]. If we have DTI data from several human subjects, then these 1015 anatomically labeled cerebral areas can be corresponded between the individual cortices and sub-cortical gray matter areas through the subjects.

We will get braingraphs or connectomes from this workflow if we identify the nodes (or vertices) with the 1015 ROIs, and we connect two such vertices by an edge if the workflow finds neural fibers, connecting the ROIs, corresponded to the two vertices. Therefore, by studying braingraphs we ignore the spatial orbits of the neural fibers in the white matter that connect the gray matter areas and can focus on the presence and the absence of connections between those ROIs. The edges of the graphs can be labeled by physical properties of the neural fibers connecting the corresponding ROIs.

Since the nodes of these graphs are corresponded to the very same set of 1015 anatomical areas, one can make comparisons between the braingraphs of individual subjects or groups of subjects in several ways and foci (e.g., [6, 7, 8, 9, 10, 11, 12, 13, 14, 15]).

Here we present the http://braingraph.org repository of connectomes, computed from the high-quality data of the Human Connectome Project [1], and some related software tools for the analysis and the visualization of braingraphs at the GitHub depository https://github.com/.

Discussion and Results

The human braingraphs can be downloaded from the site http://braingraph.org/download-pit-group-connectomes/.

The following repositories are available:

*Full set*

The set contains the connectomes of 426 subjects from the Human Connectome Project’s public data release [1]. For each subject, we have prepared five graphs, with 83, 129, 234, 463 and 1015 nodes. Each graph is available as a separate GraphML file of name nnnnnn_connectome_scale_xxx.graphml. Here the first 6 digits refer to the subject ID from the Human Connectome Project’s public release; and the last two or 3 digits to the vertex number in the graph. Scale 33 corresponds to 83 vertices, scale 60 to 129 vertices, scale 125 to 234 vertices, scale 251 to 463 vertices and scale 500 to 1015 vertices.

In each file (i.e., in each graph) the following weights are given for each edge:

- **FA_std**: the standard deviation of the fractional anisotropies [16] of the fiber(s);
- **fiber_length_mean**: The mean of the fiber lengths, defining the graph edge, in millimeters.
- **fiber_length_std**: The standard deviation of the fiber lengths, defining the graph edge;
- **FA_mean**: The mean of the fractional anisotropies [16] of the fibers;
- **number_of_fibers**: the count of the fibers, defining the edge in question.


Directed graphs

The set contains 423 braingraphs with the 1015 nodes resolution. The edges of the graphs are directed by the Consensus Connectome Dynamics-based [13, 14, 15] method, detailed in [15]. Every edge description field in GraphML format contains the directed status of the edge: if it is directed, then the source and target nodes are given, if the edge is not directed then it is noted as: `<edge directed="false" source=u target=v>` , where u and v stand for vertex numbers, specified with anatomical information in the vertex-description field of the file. The edge weights are also noted as separate attributes.

Partial set

contains only the graphs of 96 subjects, otherwise the format is the same as the entries of the full set. This smaller set formed the basis for the studies [6] and [7].

Per-lobe connectomes

contain the subgraphs of the braingraphs of 96 subjects that are induced by the different lobes of the brain. That is, for each lobe, only those edges are listed that have both endpoints in the lobe. The edges carry the five weights, specified above.

Per-ROI connectomes

contain the subgraphs of the braingraphs of 96 subjects that are induced by the different ROIs of the brain. That is, for each ROI, only those edges are listed that have both endpoints in the ROI in question. All the edges carry the five weights, specified above. Small ROIs, even with just one vertex (e.g., the left amygdala) and large ROIs, with dozens of vertices (e.g., the right inferior-parietal lobule with 26 nodes) are also present in the set.

The Brain Graph Tools

is a GitHub-based repository of some software programs for the easy processing of the http://braingraph.org-deposited data. The depository can be accessed at https://github.com/kerepesi/Brain-Graph-Tools. There are three main set of tools on the site:

- The Budapest Reference Connectome workflow (with RefBrainGraph.pl), contains the tools of preparing consensus connectomes from a set of braingraphs, as in [10, 6]. Graphs, called \( k \)-consensus connectomes, contain the edges of \( n \) connectomes that are present in \( k \) or more braingraphs (\( k \leq n \)).

- The Brain Diversity workflow contains the tools GenPreFile.pl and BrainDiversity.pl, and is capable of performing a related task: from \( n \) connectomes, the individual variability of the edges of the distinct lobes or ROIs are calculated as in [8]. The output contains interactive Google Charts visualizing the variabilities.
• The Brain Evolution Workflow, containing GenPreFile.pl and BrainEvolution.pl, is capable of comparing the random evolution of graph edges with the phenomenon, described as the “Consensus Connectome Dynamics” in [13, 14]. The generated figures are also given as interactive Google Charts.

Further information is given in a README file at the site https://github.com/kerepesi/Brain-Graph-Tools/blob/master/README.

Methods

The data source used was the Human Connectome Project’s website: http://www.humanconnectome.org/documentation/S500 [1].

The connectomes were computed by using the Connectome Mapper Toolkit [2] http://cmtk.org for segmentation and partitioning. For tractography, we
used the MRtrix processing tool [5] applying randomized seeding and the deter-
ministic streamline method with a maximum of 20 000 fibers.

The braingraphs are deposited in compressed form (by either 7-zip or zip)
and are labeled by the HCP subject IDs. Some misconfigured systems contain 7-
zip decompressing tools that do not decode properly the end-of-line characters;
in this case, we suggest using a Linux system for decompressing the files.

Data availability:

The Human Connectome Project’s MRI data is accessible at: http://www.
humanconnectome.org/documentation/S500 [1].
The graphs (both undirected and directed) that were prepared by us from
the HCP data can be downloaded at the site http://braingraph.org/
download-pit-group-connectomes/. The Brain Graph Tools are available
at https://github.com/kerepesi/Brain-Graph-Tools.

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References

[1] Jennifer A. McNab, Brian L. Edlow, Thomas Witzel, Susie Y. Huang,
Himanshu Bhat, Keith Heberlein, Thorsten Feiweger, Kecheng Liu, Boris
Keil, Julien Cohen-Adad, M Dylan Tisdall, Rebecca D. Folketh, Hannah
C. Kinney, and Lawrence L. Wald. The Human Connectome Project
and beyond: initial applications of 300 mT/m gradients. Neuroimage,
80:234–245, Oct 2013. doi: 10.1016/j.neuroimage.2013.05.074. URL
http://dx.doi.org/10.1016/j.neuroimage.2013.05.074.

[2] Alessandro Daducci, Stephan Gerhard, Alessandra Griffa, Alia Lemkaddem,
Leila Cammoun, Xavier Gigandet, Reto Meuli, Patric Hagmann, and
Jean-Philippe Thiran. The connectome mapper: an open-source processing
pipeline to map connectomes with MRI. PLoS One, 7(12):e48121, 2012.
doi: 10.1371/journal.pone.0048121. URL http://dx.doi.org/10.1371/
journal.pone.0048121.

[3] Bruce Fischl. Freesurfer. Neuroimage, 62(2):774–781, 2012.
[4] Rahul S. Desikan, Florent Ségonne, Bruce Fischl, Brian T. Quinn, Bradford C. Dickerson, Deborah Blacker, Randy L. Buckner, Anders M. Dale, R Paul Maguire, Bradley T. Hyman, Marilyn S. Albert, and Ronald J. Killiany. An automated labeling system for subdividing the human cerebral cortex on mri scans into gyral based regions of interest. *Neuroimage*, 31(3):968–980, Jul 2006. doi: 10.1016/j.neuroimage.2006.01.021. URL http://dx.doi.org/10.1016/j.neuroimage.2006.01.021.

[5] J Tournier, Fernando Calamante, Alan Connelly, et al. Mrtrix: diffusion tractography in crossing fiber regions. *International Journal of Imaging Systems and Technology*, 22(1):53–66, 2012.

[6] Balázs Szalkai, Csaba Kerepesi, Bálint Varga, and Vince Grolmusz. The Budapest Reference Connectome Server v2.0. *Neuroscience Letters*, 595:60–62, 2015.

[7] Balázs Szalkai, Bálint Varga, and Vince Grolmusz. Graph theoretical analysis reveals: Women’s brains are better connected than men’s. *PLOS One*, 10(7):e0130045, July 2015. doi: 10.1371/journal.pone.0130045. URL http://dx.plos.org/10.1371/journal.pone.0130045.

[8] Csaba Kerepesi, Balázs Szalkai, Bálint Varga, and Vince Grolmusz. Comparative connectomics: Mapping the inter-individual variability of connections within the regions of the human brain. *arXiv preprint arXiv:1507.00327*, 2015.

[9] Balázs Szalkai, Bálint Varga, and Vince Grolmusz. The advantage is at the ladies: Brain size bias-compensated graph-theoretical parameters are also better in women’s connectomes. *arXiv preprint arXiv:1512.01156*, 2015.

[10] Balázs Szalkai, Csaba Kerepesi, Bálint Varga, and Vince Grolmusz. Parameterizable consensus connectomes from the human connectome project: The budapest reference connectome server v3.0. *Cognitive Neurodynamics*, Feb 2016. doi: http://dx.doi.org/10.1007/s11571-016-9407-z.

[11] Balázs Szalkai, Bálint Varga, and Vince Grolmusz. The graph of our mind. *arXiv preprint arXiv:1603.00904*, 2016.

[12] Balázs Szalkai, Balint Varga, and Vince Grolmusz. Mapping correlations of psychological and connectomical properties of the dataset of the human connectome project with the maximum spanning tree method. *arXiv:1602.04776*, Feb 2016.

[13] Csaba Kerepesi, Balázs Szalkai, Bálint Varga, and Vince Grolmusz. How to direct the edges of the connectomes: Dynamics of the consensus connectomes and the development of the connections in the human brain. *PLOS One*, 11(6):e0158680, June 2016. URL http://dx.doi.org/10.1371/journal.pone.0158680.
[14] Csaba Kerepesi, Balint Varga, Balazs Szalkai, and Vince Grohmsz. The dorsal striatum and the dynamics of the consensus connectomes in the frontal lobe of the human brain. arXiv, 1605.01441, May 2016.

[15] Balázs Szalkai, Csaba Kerepesi, Bálint Varga, and Vince Grohmsz. High-resolution directed human connectomes and the consensus connectome dynamics. 1609.09036, September 2016.

[16] Peter J. Basser and Carlo Pierpaoli. Microstructural and physiological features of tissues elucidated by quantitative-diffusion-tensor mri. J Magn Reson, 213(2):560–570, Dec 1996. doi: 10.1016/j.jmr.2011.09.022. URL http://dx.doi.org/10.1016/j.jmr.2011.09.022.