

Making Connections in the Connectome Era

David N. Kennedy

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As Obi-Wan Kenobi of the Star Wars movies fame could have told you, there was a substantial shift in the (data sharing) force recently. With the public release of the “1000 Functional Conectomes” project¹ at the Neuroimaging Informatics Tools and resources Clearinghouse (Biswal et al. 2010; Luo et al. 2009), an order of magnitude more resting state fMRI data is now freely available in the public domain. Collected from over 30 sites, and comprising resting state fMRI data from over 1,200 individual subjects, the “1000 Functional Conectomes” project promotes both data and methodological sharing, and quantitatively demonstrates the power of pooled data analysis. The effort has seen a great public response (Dolgin 2010; Pastrana 2010), including mention in the National Institute of Mental Health director’s blog², and has engendered over 4,000 dataset downloads in it’s first 3 months in the public domain. Biswal et al. (2010) demonstrate a consistent architecture of positive and negative functional correlations as well as a consistent pattern of inter-individual foci of variability. In the normal population, these patterns of functional connectivity are modulated by age and gender. Overall, the report supports the suggestion that resting state fMRI data can (and indeed should) be aggregated and shared.

This work represents a third chapter in an intriguing story of the utility of resting state fMRI. Building upon

evidence of the local stability of the resting state map (Shehzad et al. 2009) and the characterization of the sensitivity of the resting state map to development (Kelly et al. 2009) and various diagnostic conditions (Castellanos et al. 2008; Cullen et al. 2009; Di Martino et al. 2009), this work demonstrates that, despite the variability of multi-site design, remarkably loose control of acquisition details yields resting state data that is remarkably consistent across sites. This holds dramatic promise for enhanced pooling, integration, and emphasizes the need for enhanced neuroinformatics infrastructure to support such international data integration efforts going forward.

The “1000 Functional Conectomes” project site, however, highlights that true ‘data sharing’ is much, much more than ‘data file sharing’. Like with software that can be downloaded, data that can be downloaded is greatly enhanced by a ‘community’ of users and developers (acquirers and compilers in the data instance) working in concert to maximize understanding, quality and utility of the product. Again, analogous to the software development cycle, the “1000 Functional Conectomes” has already demonstrated multiple cycles of user feedback, and data improvement. Factors that have been improved and updated include small-scale instances of slice timing detail correction, laterality correction, addition of community-requested demographic details, etc.

All data providers for such large scale sharing effort take a risk in public release of data; a risk that some ‘issue’ will be raised concerning you data. The investigators that take this risk should be lauded. The community that understands these risks, and works constructively with the data source providers for the greater good of the science and the community are also to be lauded. Public vetting of data makes for better public data, which is in everyone’s best interest. As more examples of this process going well, for both the investigator and community, are accumulated, one

¹ http://www.nitrc.org/projects/fcon_1000/

² <http://www.nimh.nih.gov/about/director/2010/tracing-the-brains-connections.shtml>

D. N. Kennedy (✉)
Division of Neuroinformatics, Department of Psychiatry,
University of Massachusetts Medical School,
Worcester, MA, USA
e-mail: David.Kennedy@umassmed.edu

of the potential barriers (error stigma, or *stigmata erroneus*) begins to be lowered.

In the ‘connectome’ arena, there is also an expected award of a US National Institutes of Health (NIH) grant in response to a solicitation entitled ‘The Human Connectome Project’ (RFA-MH-10-020) is expected shortly³. Highlights of the program announcement include delivery of: non-invasive imaging tools to obtain connectivity data from humans in vivo; a quantitative set of human connectivity data linked to behavioral and genetic data in healthy adult subjects; and a modeling and informatics platform to operate upon the aggregated connectivity data.

These example ‘connectome’ projects, are occurring in conjunction with numerous other ongoing, thriving neuroinformatics efforts that support the understanding of structural, functional, and effective connectivity within the brain. All reflect aspects characterizing the information flow within the nervous system and represent the continued success of neuroinformatics technology (Breakspear 2004; Jirsa 2004). Each of these domains will continue to place demands on neuroinformatics technology in the areas of database development, information processing algorithms, and data modeling to support the new, cutting-edge advances of technology that need to be acutely attuned to furthering the understanding of how the brain works.

As with most ‘eras’, it is the underlying technology that makes the era possible. Neuroinformatics is one of the technological engines driving the connectome era. New advances in acquisition, analysis, databasing, modeling and sharing will continue to be necessary, and we hope you will

continue to read about them first, in the pages of this journal.

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³ <http://grants.nih.gov/grants/guide/rfa-files/rfa-mh-10-020.html>