A cross-modal, cross-species comparison of connectivity measures in the primate brain

Andrew Reid, Department of Cognitive Artificial Intelligence Donders Institute for Brain, Cognition and Behaviour Radboud University Nijmegen

Abstract:

The estimation of brain connectivity has become a very popular pursuit in human neuroscience, with the establishment of a human “connectome” having many potential theoretical and clinical applications. While invasive methods, in particular histological tract tracing, exist for the purpose of quantifying directed axonal connections in animal models (e.g., Markov et al., Science, 2013), for the human brain such methods are not applicable. In lieu of invasive methods, researchers have turned to neuroimaging approaches as a means of inferring human connectivity. For instance, statistical associations in functional signals, such as the BOLD response or EEG/MEG, can provide us with information about how neuronal activity patterns in different parts of the brain are related to one another. These sorts of observations are called functional connectivity, although because they are associative, and have poor spatial or temporal resolution, they do not (on their own) support inferences about the presence of physical connections.

Another MR-based method called diffusion-weighted imaging (DWI) can be used to approximate the degree of directed diffusion of molecules in the brain, and on this evidence we can infer the presence and microstructure of white matter tissue (containing long-range axonal projections). DWI can be used to perform probabilistic tractography, which estimates the distribution of "streamlines" that start in a specific seed region and terminate in a target region. While this is a promising technique, it suffers from a number of inherent biases, which makes it difficult to infer actual physical connections (including their connection strength and directionality).

In a recent study (Reid et al., Neuroimage, 2015), we characterized the degree of correspondence between these measures of human connectivity — plus a third called structural covariance — with tract tracing evidence obtained from macaque studies. We compared estimates generated from two whole-cortex parcellation schemes, as well as two well-known public datasets. We found the best agreement for local, short-range, and homotopic connections, but also a good deal of divergence. In more recent work, we have been developing a way to perform a similar comparison of seed-based estimates, while avoiding the need to set arbitrary thresholds on the data. These approaches have helped characterize the ways in which connectivity metrics differ in their approximations to an underlying "connectome", and may also be useful for informing future methods seeking to integrate multiple lines of evidence into a more coherent estimate of physical connectivity of the human brain.