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Abstract

A core goal of human connectomics is to characterize the neural pathways that underlie brain function. This can be largely achieved noninvasively by inferring white matter connectivity using diffusion MRI data. However, there are challenges. First, diffusion tractography is blind to directed connections, or whether a connection is expressed functionally. Second, we need to be able to go beyond the characterization of anatomical pathways, to understand distributed brain function that results *from* them. In particular, we need to characterise effective connectivity using functional imaging modalities, such as FMRI and M/EEG, to understand its context-sensitivity (e.g., modulation by task), and how it changes with synaptic plasticity. Here, we consider the critical role that biophysical network models have to play in meeting these challenges, by providing a principled way to conciliate information from anatomical and functional data. They also provide biophysically meaningful parameters, through which we can better understand brain function. In a translational setting, well-validated models may shed light on the mechanisms of individual disease processes.

Keywords: biophysical model, networks, connectivity, connectome, Bayes, DCM, generative embedding, bottom-up model, MEG, EEG, FMRI, diffusion, multi-modal