

Mapping Population-based Structural Connectome

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Advances in understanding human brain structural connectomes require improved approaches for the construction, comparison and integration of high-dimensional whole-brain tractographic data from a large number of individuals. This article develops a population-based structural connectome (PSC) mapping framework to address these challenges. Simultaneously characterizing huge numbers of white matter bundles within and across different subjects, PSC registers different individuals' brains, relying on a coarse construction, decomposes variation in the bundles, and extracts novel connection weights. PSC can be used to extract binary networks, weighted networks and streamline-based connectivity representations of brain connectomes from many large-scale neuroimaging studies. PSC facilitates analyses relating structural connectomes to demographic and behavioral measures. A test-retest dataset is used to improve and validate the robustness and reproducibility of PSC. We apply PSC to Human Connectome Project (HCP) data, to characterize normal variations in structural connectomes among healthy subjects, such as the heritability analysis. PSC facilitates the understanding of normal brain structure, the structural bases of neuropsychiatric disorders, and the effects of environmental and genetic factors on the structure of connections.

This is a joint work with zhengwu zhang; Maxime Descoteaux; Jingwen Zhang; Gabriel Girard; Maxime Chamberland; David Dunson; Anuj Srivastava.