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Computational Approaches to the Examination of the Functional Architecture of the Human Brain

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In this talk I will discuss how we can establish functional correspondence in neuroimaging data across individuals. We will briefly review the challenges in inferring multivariate fine-grained functional structure shared across individuals from neuroimaging data despite anatomical variability. Specifically, we will discuss the relevance of discrepancies between anatomical and functional correspondence in light of evolution, brain development and disease. I will outline how to use manifold learning techniques to capture the functional connectivity architecture in individuals. These methods capture a multitude of relationships, such as functional connectivity and map them into a space that represents the entire relationship structure. This enables learning of a joint functional atlas in an embedding space representing the structure shared in a population. The resulting functional correspondence has several uses. First, it allows to remove possible anatomical confounds when comparing cohorts, secondly it allows to study the relationship between function and the location of its anatomical anchors. The talk will conclude with a discussion of results in pre-surgery language mapping, resting state networks, and treatment effect prediction.