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JIVE integration of imaging and behavioral data

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Abstract

A major goal in neuroscience is to understand the neural pathways underlying human behavior. We introduce the recently developed Joint and Individual Variation Explained (JIVE) method to the neuroscience community to simultaneously analyze imaging and behavioral data from the Human Connectome Project. Motivated by recent computational and theoretical improvements in the JIVE approach, we simultaneously explore the joint and individual variation between and within imaging and behavioral data. In particular, we demonstrate that JIVE is an effective and efficient approach for integrating task fMRI and behavioral variables using three examples: one example where task variation is strong, one where task variation is weak and a reference case where the behavior is not directly related to the image. These examples are provided to visualize the different levels of signal found in the joint variation including working memory regions in the image data and accuracy and response time from the in-task behavioral variables. Joint analysis provides insights not available from conventional single block decomposition methods such as Singular Value Decomposition. Additionally, the joint variation estimated by JIVE appears to more clearly identify the working memory regions than Partial Least Squares (PLS), while Canonical Correlation Analysis (CCA) gives grossly overfit results. The individual variation in JIVE captures the behavior unrelated signals such as a background activation that is spatially homogeneous and activation in the default mode network. The information revealed by this individual variation is not examined in traditional methods such as CCA and PLS. We suggest that JIVE

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