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Authors

Xu, Yinan
Prat, Chantel
Sense, Florian
et al.

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Distributed Brain Connectivity Predicts Individual Differences in Forgetting: A Neurocomputational Analysis of resting-state fMRI

Yinan Xu

University of Washington, Seattle, Washington, United States

Chantel Prat

University of Washington, SEATTLE, Washington, United States

Florian Sense

University of Groningen, Groningen, Netherlands

Hedderik van Rijn

University of Groningen, Groningen, Netherlands

Andrea Stocco

University of Washington, Seattle, Washington, United States

Abstract

A complete and holistic understanding of human cognitive function using a cognitive model should be able to incorporate both the idiographic biological parameters from behavioral data and interactions between connected brain networks identified by neuroanatomical techniques. Here, we argue that first, computational modeling can be used to extract biological parameters, and second, the biological parameter should be identifiable through the corresponding brain functional networks. We tested this empirically with the long-term memory's decay rate (rate of forgetting α) measured from a Swahili-English vocabulary learning task, and resting-state fMRI (rs-fMRI) data, both collected from 33 participants. α was estimated based on a rational model of episodic memory. rs-fMRI data from each brain was processed into a 264 x 264 connectivity matrix, and further selected and grouped into memory-related network matrices using group lasso and cross-validation techniques. We were able to (1) predict the observed α using these connectivity matrices, and (2) show that forgetting can be related to specific brain networks.