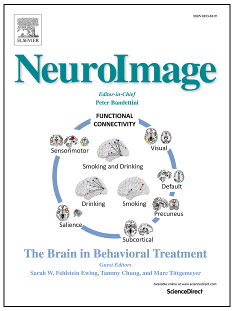

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Structural covariance of brain region volumes is associated with both structural connectivity and transcriptomic similarity

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Abstract

An organizational pattern seen in the brain, termed *structural covariance*, is the statistical association of pairs of brain regions in their anatomical properties. These associations, measured across a population as covariances or correlations usually in cortical thickness or volume, are thought to reflect genetic and environmental underpinnings.

Here, we examine the biological basis of structural volume covariance in the mouse brain. We first examined large scale associations between brain region volumes using an atlas-based approach that parcellated the entire mouse brain into 318 regions over which correlations in volume were assessed, for volumes obtained from 153 mouse brain images via high-resolution MRI. We then used a seed-based approach and determined, for 108 different seed regions across the brain and using mouse gene expression and connectivity data from the Allen Institute for Brain Science, the variation in structural covariance data that could be explained by distance to seed, transcriptomic similarity to seed, and connectivity to seed.

We found that overall, correlations in structure volumes hierarchically clustered into distinct anatomical systems, similar to findings from other studies and similar to other types of networks in the brain, including structural connectivity and transcriptomic similarity networks. Across seeds, this structural covariance was significantly explained by distance

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