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Prediction of Longitudinal White Matter Change in Healthy Elderly Individuals

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PREDICTION OF LONGITUDINAL WHITE MATTER CHANGE IN HEALTHY ELDERLY INDIVIDUALS Melissa Lancaster[1], Sally Durgerian[2], Michael Seidenberg[1], John Woodard[3], Kristy Nielson[2,4], J. Carson Smith[5], Monica Matthews[1], Alissa Butts[4], Nathan Hantke[4], Stephen Rao[6]; [1]Rosalind Franklin University of Medicine and Science, [2]Medical College of Wisconsin, [3]Wayne State University, [4]Marquette University, [5]University of Maryland, [6]Cleveland Clinic — Diffusion Tensor Imaging (DTI) studies have shown that significant alteration in white matter (WM) integrity differentiates healthy older adults from persons with Mild Cognitive Impairment (MCI) and Alzheimer's disease (AD). Most studies, however, have been cross-sectional and have not related longitudinal DTI changes to cognitive change. Here we report changes in WM integrity and cognition in healthy older adults over an 18-month interval. Sixty-seven cognitively intact elders underwent neuropsychological testing and DTI at baseline and after 18 months. Groups were formed based on change from baseline to follow-up on the Rey Auditory Verbal Learning Test (recall sum across trials 1-5, delayed recall) and Mattis Dementia Rating Scale-2. Declining participants (N=21) showed a minimum of 1 SD reduction on at least one cognitive measure, while Stable participants (N=46) showed comparable scores at each time point. WM regions-of-interest were derived from Freesurfer. Hierarchical linear regression was used to predict fractional anisotropy (FA) change in regions frequently identified in DTI studies of MCI and AD including transentorhinal cortex, temporal lobe, and posterior cingulate. Groups did not differ at baseline in age, cognition, FA, or WM volume. After controlling for age and baseline FA, cognitive status (Declining, Stable) predicted the baseline to 18-month reduction in FA in the right hippocampal gyrus (p=.004) and left fusiform gyrus (p=.01) with a trend in the left middle temporal gyrus (p=.06). Future research should examine WM changes in other brain regions and determine whether DTI diffusivity measures are related to cognitive decline.

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ASSESSING THE TRAIT-LIKE CHARACTERISTICS OF INTRINSIC CONNECTIVITY Craig Moodie[1], Krista Wisner[1], Angus MacDonald, III[1]; [1]University of Minnesota, Twin Cities — The assumption that sharing an entire genome might bestow twins with analogous neurobiological substrates and congruent cognitive abilities has not yet been examined in the context of intrinsic connectivity. Even though recent studies have revealed endogenous functional networks present at rest and during active states, it remains to be seen to what extent these brain networks might cohere or vary across individuals according to heritable factors. This study quantifies morphometric similarities between twins in the context of task-related activation in order assess whether or not familial psychometric phenotypes vary in a trait-like fashion. fMRI data from monozygotic twins participating in the Minnesota Trust Game, hand imitation and verb generation tasks were collected on a Siemens 3T scanner and processed via the FSL imaging analysis software. Statistical analyses of task-related activation and independent component networks were then used to generate voxel-wise and intraclass correlations within and across twin pairs. It was found that functional connectivity was higher within twin pairs than across all individuals, and that twin group assignment improved models predicting the relative strength of network connectivity. Additionally, the observed components in each paradigm were both task-relevant and analogous to previously established networks. Trait-like networks that lead to morphometric similarities, and that are associated with task-related brain activation, were discovered across paradigms and, consequently, it is evident that brain structures and processes are heritable. Moreover, these results suggest that variations in heritable network dynamics can engender individual differences, and can even be explanatory variables for neuropsychiatric illnesses.

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NEUROMETRICS OF INTRINSIC CONNECTIVITY NETWORKS: RETEST RELIABILITY AND CROSS-VALIDATION USING A META-LEVEL METHOD Krista Wisner[1], Kelvin Lim[2], Angus MacDonald III[1,2]; [1]Department of Psychology, University of Minnesota, [2]Department of Psychiatry, University of Minnesota — Connectivity of the resting brain can be parsed into distinct networks that closely resemble brain circuits evoked by cognitive tasks such as visual-spatial processing. Although such empirically-derived intrinsic connectivity networks (ICNs) have become a popular method for investigating brain functioning, the relationships between ICNs and a repertoire of cognitive processes have yet to be examined when also considering the neurometrics of the ICNs. Using a meta-level independent component analysis (ICA) to generate the most consistent networks, we produced ICNs from three separate datasets collected from two samples of healthy adults in order to examine the 9 month retest reliability of ICNs and to test the cross-validation of the findings. Functional implications of ICNs were investigated by correlating ICNs with a BrainMap meta-analysis of task-based activity networks (Laird, et al., JCN, 2011). In each dataset, 17 of the 18 BrainMap networks were represented in ICNs derived from resting-state fMRI. Networks associated with vision, interoception, language, and the default mode showed the strongest 3D spatial correlations (3DSC, r ? 0.60) between BrainMap networks and ICNs in all three datasets. Additionally, the retest reliability was greatest for the interoception, language, inhibition, and default mode ICNs (3DSC r ? 0.80; Dice Similarity Index ? 0.70). Furthermore, ICNs associated with the said functions showed the strongest 3DSC (r ? 0.70) between the reliability sample and cross-validation sample. These findings illustrate the robustness of a large set of ICNs from resting-state data and demonstrate the neurometric properties that make this approach practical for studying individual differences.

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EXTENSIONS TO THE NEUROSYNTH FRAMEWORK FOR LARGE-SCALE AUTOMATED SYNTHESIS OF FUNCTIONAL NEUROIMAGING DATA Tal Yarkoni[1], Russell A. Poldrack[2], David C. Van Essen[3], Tor D. Wager[1]; [1]University of Colorado Boulder, [2]University of Texas at Austin, [3]Washington University School of Medicine — The explosive growth of the human neuroimaging literature has led to major advances in understanding of human brain function, but has also made aggregation and synthesis of neuroimaging findings increasingly difficult. To address this problem, we recently introduced a highly automated brain mapping framework called NeuroSynth that uses text mining, meta-analysis and machine learning techniques to generate a large database of mappings between neural and cognitive states (Yarkoni et al, 2011). The NeuroSynth framework can be used to automatically conduct large-scale, high-quality neuroimaging meta-analyses, address long-standing inferential problems in the neuroimaging literature (e.g., how to infer cognitive states from distributed activity patterns), and support accurate 'decoding' of broad cognitive states from brain activity in both entire studies and individual human subjects. Here we describe new extensions and improvements to this framework, including (i) a more flexible search and analysis interface that lets users dynamically define sets of activation coordinates for real-time analysis; (ii) new algorithms for automatically detecting experimental contrasts, sample size, and stereotaxic space information; (iii) topic modeling-based meta-analysis images to supplement existing term-based images; (iv) preliminary integration with a new stand-alone visualization service that supports user-uploaded images; (v) preliminary integration with a "Neuroimaging Coordinate Repository" designed to support manual validation of automatically extracted data; and (vi) a pilot crowdsourcing interface that lets other researchers annotate and code existing information in the database. These additional features extend the functionality of the existing platform by improving usability, broadening the range of potential applications, and promoting interoperability with other neuroinformatics platforms.