## **Depressive Rumination, the Default-Mode Network, and the Dark Matter of Clinical Neuroscience**

## **Supplemental Information**

## **Introduction**

#### *A Brief History of the Brain's Intrinsic Functional Connectivity*

An early discovery from fMRI studies was that functionally similar neural regions showed correlated activity even when they were not actively prompted. Biswal and colleagues [\(1\)](#page-4-0) first demonstrated this in an fMRI study of motor regions. Using the activation maps derived from a bilateral finger-tapping task, Biswal *et al.* specified a region-of-interest 'seed' in left motor cortex and queried the time courses of all other voxels during rest to identify other regions in which activity was correlated with activity in this seed region. This analysis showed that, in addition to nearby voxels, contralateral motor cortex and midline cortical regions showed timecourse correlations with the seeded left motor cortex. Thus, in this resting-state analysis, it was the *correlation* of the time courses, rather than the *magnitude* of a response, that determined network connectivity. Moreover, the functional connectivity map that resulted from this analysis was spatially similar to the map of regions that were activated by the *bilateral* fingertapping task.

Subsequent research expanded on Biswal *et al*.'s [\(1\)](#page-4-0) conceptualization of an implicit functional organization in the brain. In a meta-analysis of PET studies of visual processing in humans, Shulman *et al.* [\(2\)](#page-4-1) identified regions in which metabolic activity decreased during an active task, that included the posterior cingulate cortex (PCC), bilateral parietal cortex, ventral medial prefrontal cortex (vmPFC), and medial temporal

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lobe (MTL) regions. These decreases in activity, which showed remarkably little spatial variation despite a wide range of extrinsic tasks, prompted investigators to begin to study a consistent, spatially organized baseline state of metabolic functioning. Perhaps most notably, Raichle and his colleagues [\(3\)](#page-4-2) examined metabolic demands during eyesclosed rest and described a 'default-mode' pattern of metabolic activity in the brain that included PCC, bilateral parietal cortex, and vmPFC. By using PET to examine blood flow and oxygen consumption, Raichle *et al.* were able to determine an absolute level of metabolic activity during rest, rather than a relative level of activity during the transition from rest to activity. Thus, the default mode network (DMN) identified by Raichle *et al.*  reflects an ongoing metabolic demand of these regions, a physiological baseline rather than the relative baseline of blood oxygenation level-dependent (BOLD) fMRI signals  $(4).$  $(4).$ 

Investigators have begun to examine factors that may explain the functional connectivity of the brain regions that comprise the DMN. One likely candidate is monosynaptic white-matter connectivity among these regions; another potential factor is common connectivity with a third structure. In testing these possibilities, Greicius and colleagues [\(5\)](#page-4-4) conducted a study examining both functional and structural connectivity by using BOLD signal and diffusion tensor imaging (DTI), respectively, to visualize connectivity. To obtain seed regions for DTI, Greicius *et al*. used probabilistic independent component analysis (ICA) to analyze fMRI data. ICA decomposes the whole-brain data into independent spatiotemporal components, including the DMN [\(6\)](#page-4-5). Using DMN regions, including the PCC, vmPFC, and MTL, as seed regions, Greicius *et al.* identified white-matter tracts that directly connected PCC to vmPFC and PCC to

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MTL, but not to structures outside the DMN. Thus, the temporal correlation of activity in these regions at rest is likely due, at least in part, to tracts that link DMN regions directly.

In an important extension of formulations of macro-architectural organization of the brain, Fox and colleagues [\(7\)](#page-4-6) posited that components of the brain's intrinsic functional organization — the DMN, described above, and the task positive network (TPN; a network of structures that increase in activation during performance of attention-demanding tasks) — have a competitive, anti-correlated relation with each other. Fox *et al.* noted that, during performance of cognitive tasks, structures comprising the TPN (dorsolateral prefrontal, lateral parietal, and anterior insular cortices) were characterized robustly by increases in activation, whereas structures comprising the DMN showed reliable decreases in activity. Importantly, Fox *et al.* documented this same negative relation between DMN and TPN during resting-state fMRI scans: fluctuations in activation in one network were associated with inverse activation fluctuations in the other network.

# **The DMN in MDD**



**Table S1.** Studies Measuring Brain Resting-State Activity in Patients with MDD, Relative to Healthy Controls [\(8-25\)](#page-4-7)

MDD, major depressive disorder; PET, positron emission tomography; SPECT, single photon emission computed tomography.

# **Supplemental References**

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