A Reproducible Neurobiology of Depressive Rumination

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Short Title: Multimodal Discovery and Replication
Keywords: Multimodal; Microstructure; Resting-State; Triple-Network; Depressive Rumination; Reproducibility

Abstract

Depressive Rumination (DR), which involves a repetitive focus on one's distress, has been linked to alterations in functional connectivity of the 'triple-network', consisting of Default-Mode, Salience, and Executive Control networks. A structural basis for these functional alterations that can dually explain DR's persistence as a stable trait has remained unexplored, however. Using diffusion and functional MRI, we investigated multimodal relationships between DR severity, WM microstructure, and resting-state functional connectivity in depressed adults, and then directly replicated our results in a phenotypically-matched, independent sample (total $N = 78$). Among the fully-replicated findings, DR severity was associated with: (a) global microstructure of the right Superior Longitudinal Fasciculus and local microstructure of distributed primary-fiber and crossing-fiber WM; (b) a functional connectivity imbalance of segregation and integration within the triple-network; and (c) multimodal associations between these microstructural and functional connectivity biomarkers. Taken together, our results provide the first reproducible evidence for a jointly microstructural-functional basis of trait rumination in the depressed brain.

Cognitive models of depression posit that negatively biased self-referential processing plays a critical role in maintaining the disorder[1]. Depressive Rumination (DR) is the perseverative form of this cognitive bias, which involves a repetitive focus on "one's depressive symptoms and on the implications of those symptoms"[2]. DR has been shown to significantly contribute to depressive symptom severity[2], duration[3], and relapse likelihood[4] across multiple forms of depression. Despite its central role in depression maintenance, there are few effective treatments for DR[5,6]. By delineating reproducible neurobiological models of DR, researchers might better understand underlying vulnerabilities, identify more precise treatment targets, and develop more effective neurocognitive interventions for depression[7,8].

A Triple-Network Functional Connectivity Model of Depressive Rumination

At the core of DR is *self-referential processing*[9], which is inwardly directed attention focused on the self. This mechanism is associated with functional activation of modular cortical areas, such as the Precuneus[10] along with the anterior and posterior cingulate cortices (ACC; PCC)[11]; each of these areas has been associated with self-focused cognitive processes that include thought-suppression, mentalization, and prospection[12–15]. Although few studies have explored grey matter structural biomarkers of self-reference, reduced cortical volume of the Precuneus is known to be associated with autobiographical memory disturbances[16,17] and poor metacognition[18,19]. Since self-referential processing is believed to predominantly operate in a task-negative brain state[20], moreover, studies that employ resting-state functional MRI (rsfMRI) uniquely offer some insight into the neurobiology of self-reference[9,21]. Indeed, rsfMRI has enabled researchers to more broadly attribute self-referential processes to the Default-Mode Network (DMN), whose functional connectivity may reflect mind-wandering[20,22] and for which the Precuneus is a core hub[23]. Precise features that differentiate "healthy" mind-wandering from maladaptive ruminative patterns are difficult to distinguish, however, perhaps due to the inherent subjectivity of inner mentation along with fundamental limitations of the resting-state modality in general[24]. Nevertheless, increased DMN activity during internally-focused attention is generally believed to amplify self-referential processing and thereby increase the demand on cognitive resources[25,26]. In particular, recent studies have shown that greater DR severity is associated with lower functional connectivity within a parietal sub-system of the DMN, the Precuneal DMN (pDMN), which is both vulnerable to malfunctioning under conditions of cognitive resource depletion[27], and specifically responsible for regulating the episodic memory retrieval that supports inner mentation[20].

Emotional salience, a second proposed mechanism of DR, may be necessary for assigning a negative bias to self-referential processing. A wealth of literature has shown that emotional salience is associated with both the function and structure of the ACC, Insula, and Amygdala, and can extend to other regions as well[28,29]. Greater sustained activation within the Amygdala has been observed, for example, in response to negative-valence words following non-emotional words in depressed individuals[30]. Whereas the amygdala may act as a source of emotional signaling[31], the ACC assigns salience to emotional signals in the service of goal attainment[32]. In the context of DR, such goals might include relief from depressive symptoms, for instance. Research into the precise role of the ACC in DR have been mixed, however[9,12,33]. On the one hand, discrepancies may reflect the variety of motivational states that are engaged during different task paradigms[34]. On the other hand, they might also allude to its dense interconnectivity with other cortical areas[32] or the multiple specialized functions among sub-regions of the ACC itself[35]. Thus, emotional salience in DR may be more precisely understood within a functional connectivity perspective of the Salience Network (SN)[36]. In fact, a recent study on depressed teenagers found a critical role for the SN in the maintenance of negative cognitive bias and self-criticism in DR[57]. One reason for this finding may be that aberrant functional connectivity of the SN during self-referential processing results in misappropriated "tagging" of self-relevant thoughts with a negative bias[9], perhaps through dysregulated reward circuitry[38]. Along these lines, a recent task-based fMRI study showed that depressed ruminators tend to more actively recruit SN nodes simultaneously during reward anticipation. Hence, emotional salience in the context of DR might also or alternatively be construed as a hypervigilance to self-relevant cues[39].

A third proposed mechanism of DR is impaired *attentional engagement*, which may instantiate repeated failures to disengage from negatively-salient self-referential processing while also preventing attentional shifts toward neutral or positive thoughts[40]. In depressed individuals, this impaired disengagement[40–42] is believed to amplify and sustain the negative bias of self-referential processing by spurring a vicious cycle of self-criticism that drains the cognitive resources needed to counteract the increase[37]. Thus, the mechanism of impaired disengagement may lend explanation to the core perseverative feature of DR, which distinguishes it from more adaptive, reflective forms of rumination[4,43]. Broadly construed, impaired disengagement in DR likely implicates the aberrant structural and functional properties of cognitive control modules, such as the dorsolateral and inferior prefrontal cortices[12,44,45], whose activation patterns are largely titrated by the ACC[32]. The functional connectivity perspective of the Executive Control Network (ECN), which considers these

frontal modules as a collection of network subunits, may therefore more parsimoniously capture the broader role of impaired disengagement in DR.

Perhaps in light of the three proposed mechanisms of DR, the three corresponding resting-state networks (RSNs) previously discussed have become ubiquitous in the study of DR's functional neurobiology—the DMN, SN, and ECN[36,37]. Nevertheless, the three corresponding RSN's have been studied largely in isolation – i.e. with respect to their *within-network* functional connectivity patterns[9,36] – in the context of DR research[9]. Despite their diverse specialized intrinsic functions, however, mounting research has shown that the DMN, SN, and ECN largely interact with one another[46]. Hence, additional insights might be gleaned by studying these particular RSN's as a mesoscale system of networks – the "triple network" – as some have already proposed more broadly in the study of depression[46–49] (*See* **Figure 1**). In fact, only one study to date has explored *between-network* functional connectivity patterns in DR[50]. Specifically, Hamilton et al. (2011) used state-change analysis of rsfMRI to show that higher DR severity is associated with greater DMN dominance over the ECN, with a variable role for the SN across differing levels of depression severity[50]. That study importantly did not include structural brain measures, however, which are still needed to explain DR's persistence as a stable trait[54].

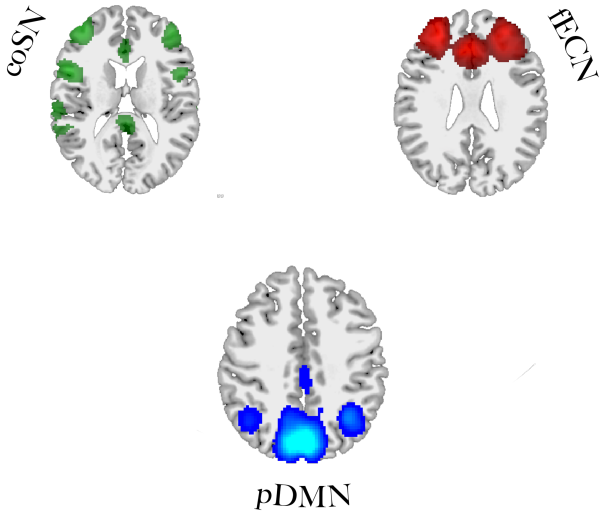


Figure 1: Three resting-state networks (RSNs) are discussed independently in prior studies on DR: the Cingulo-Opercular Salience Network (SN) shown in green, the frontal Executive Control Network (ECN) shown in red, and the Precuneal Default Mode Network (pDMN) shown in blue. These three networks are also described collectively as belonging to the frontoparietal triple network, and their functional properties coincidentally correspond to the three proposed mechanisms of DR, which include self-referential processing, emotional salience, and cognitive control, respectively.

A Microstructural Model of Depressive Rumination

Studies have shown that inter-individual differences in DR severity likely indicate the existence of structural brain correlates of DR[9,12,44,53]. Given that the perseveration implicated in DR has been shown to be a stable trait[54], it would therefore also seem to implicate a complex structural basis that, like in the functional case, cannot be explained modularly through grey matter cortices

alone[44]. It follows that the structural analogue to functional connectivity – microstructural connectivity[55] – may be a useful framework for studying the structural basis of trait DR in particular. Microstructural connectivity is typically studied using methods like diffusion tensor MRI (dMRI), which provides an *in vivo* method for measuring global and local Fractional Anisotropy (FA) based on anisotropic properties of WM in the brain[57]. In fact, BOLD signal clustering of resting-state WM has been shown to generate patterns resembling white-matter tracts[56]. Although recent studies beyond DR literature have shown that WM microstructure of frontoparietal tracts, such as the Cingulum (CCG) and the Uncinate Fasciculus (UF), may support the DMN[58] and ECN[59], only one study to date has explicitly investigated the WM basis for DR[53]. Namely, Zuo et al. (2011) used Tract-Based Spatial Statistics (TBSS) to show that FA of the Superior Longitudinal Fasciculus (SLF) and neighboring motor fibers was negatively associated with DR. Due to its small sample size (n = 16), however, it may also not be possible to generalize its results to other depressed populations[58].

A Microstructural-Functional Model of Depressive Rumination

To review, DR's neurobiology is likely characterized by a variety of neural biomarkers that operate across multiple levels of neural complexity, correspond to at least the three proposed cognitive mechanisms of DR, and seemingly encompass both functional and structural dimensions of the brain. Although studies on modular biomarkers have identified a core set of nodes relevant to each of these mechanisms, the modular perspective cannot account for dynamic interactions across those nodes, among other limitations[62]. Hence, *connectivity* biomarkers, identified across both functional[36,63] and structural[53] modalities[64,65], may be maximally informative for building high-precision models of rumination in depression. Likewise, neuroscientific appeals made to either structural or functional connectivity biomarkers of DR, considered in isolation, might reduce the precision of our etiological understanding[66]. To therefore clarify any systems-level[67] mechanisms responsible for maintaining DR as a stable trait[68–70], multimodal studies of functional *and* microstructural connectivity, considered in tandem, are needed.

In the present study, we propose two hypotheses: 1) a microstructural-functional neurobiology of trait DR exists and implicates both frontoparietal microstructural connectivity and triple-network functional connectivity, corresponding to each of the three proposed cognitive mechanisms of DR—aberrant self-referential processing, negatively-biased salience processing, and impaired disengagement of attention; 2) inter-individual differences in trait DR can be explained multimodally—that is, through joint appeal to triple-network functional connectivity with respect to

128 underlying microstructural connectivity constraints. To test and explore these hypotheses, we utilize
129 data from two neuroimaging modalities, dMRI and rsfMRI. Given the absolute importance of
130 replication in cognitive neuroscience[71] and the growing need for more credible and reproducible
131 neurobiological models of disordered cognition[72], we additionally perform our analyses across two
132 separate datasets, acquired independently and at different locations. This approach, which is rarely
133 used in social or biological sciences[71], enabled us to employ hypothesis testing to determine whether
134 initial discovery findings could be directly replicated in a second independent sample. The findings
135 that did replicate would, in turn, afford a higher degree of confidence in support of our conclusions,
136 and perhaps provide an auxiliary means of inferring generalizability beyond statistical power
137 alone[73].

138 We test our first hypothesis by applying multiple linear regression analyses to dMRI and
139 rsfMRI data independently. The dMRI analyses include both TBSS and global probabilistic
140 tractography methods[57], whereas the rsfMRI analyses encompass both within-network and between-
141 network[74] resting-state functional connectivity based on Independent Components Analysis (ICA)[36].
142 We then test the second hypothesis by jointly examining microstructural-functional connectivity
143 relationships associated with DR. Lastly, we test both of our hypotheses by applying a near-
144 identical analytic pipeline developed for the discovery sample to an independent sample obtained
145 from NKI Rockland[73,75].

146 **METHODS**

147 ***Participants – Discovery sample***

148 Thirty-nine treatment-seeking participants with DSM-IV Major Depressive Disorder (MDD)
149 were recruited for this study from advertisements placed online, in newspapers, and on late night
150 TV. Participants were screened for medical or physical conditions that would preclude participation
151 in an MRI study. They also completed an abbreviated Mini International Neuropsychiatric
152 Interview (MINI)[76] to determine provisional MDD diagnosis, which were then confirmed using in-
153 person Structured Clinical Interviews for the DSM-IV Disorders (SCID)[77] administered by a trained
154 research assistant. Participants were excluded if they met criteria for past year substance abuse or
155 dependence, current or past psychotic disorder, bipolar disorder, and schizophrenia. Participants
156 receiving pharmacological treatment were allowed into the study if there has been no medication
157 change in the 12 weeks prior to study entry. To minimize brain changes associated with aging,
158 individuals were between the age of 18 and 55[78].

159 ***Ethics Statement***

The Institutional Review Board at the University of Texas at Austin approved all study procedures and materials and all participants provided signed informed consent.

Depressive Rumination Measurement

The RSQ (Response Styles Questionnaire)[79] is a 10-item self-report measure of the tendency to ruminate. It consists of a total score and two sub-scales: reflection and brooding. The reflection subscale measures an individual's tendency to turn inward to engage in problem-solving and thereby alleviate negative or depressed mood[4], whereas brooding measures the maladaptive form of rumination believed to be a proxy for DR[4,50]. Brooding specifically reflects the intensity of ruminative responses to expressions of negative emotion[2]. For each item, subjects indicate the frequency of each event on a scale ranging from 0 ("almost never") to 3 ("almost always"), yielding a range of possible scores from 0-30. The brooding subscale has high reliability (α=0.77-0.92)[79], is well-validated within depressed populations[80], decontaminated of any explicitly depressive content[80], and the sub-scale of choice for most neurobiological studies of DR[9,20,36,40,50]. For these reasons, we used the brooding subscale exclusively to measure DR.

Depression Severity Measurement

The Beck Depression Inventory (BDI)[81] is a 21-item self-reporting questionnaire for evaluating the severity of depression in normal and psychiatric populations. It contains 21 items on a 4-point scale from 0 (symptom absent) to 3 (severe symptoms), and instructs the participant to recall depression symptoms occurring over the previous two weeks.

Imaging Acquisition

MRI scans were acquired on a whole body 3T GE MRI with an 8-channel phase array head coil. The scanning protocol involved collection of a localizer followed by a high-resolution T1 structural scan, two resting state scans of 6 minutes each, a second high-resolution structural scan, and finally a 55-direction diffusion tensor (dMRI) scan. For the resting-state scan, instructions were presented utilizing a back-projection screen located in the MR bore and viewed through a mirror mounted on the top of the head coil. Participants were instructed to remain awake and alert and keep their gaze on a fixation cross (+) presented approximately at the center of their field of view for the 6-minute duration of the scan. (*See* **Appendix, Methods: Section A***)*.

dMRI Preprocessing

Preprocessing of Diffusion Magnetic Resonance Imaging (dMRI) data was carried out using a custom preprocessing workflow that included eddy correction, brain extraction, denoising, and tensor/ball-and-stick model fitting tools adapted from the FMRIB Diffusion Toolbox[82]. To achieve

maximal sensitivity and specificity from the dMRI data, preprocessing included rigorous automated and manual quality control steps (*see* **Appendix, Methods: B**).

dMRI: Tract-Based Spatial Statistics (TBSS) / Tractography and DR

A number of approaches to dMRI analysis were implemented. To begin, the whole-brain data was interrogated using Tract-Based Spatial Statistics (TBSS)[83] to identify microstructural characteristics that were associated with brooding severity (*see* **Appendix, Methods: Section C**). We additionally employed the 'crossing-fibers' extension of TBSS[84], which is less often used due to its computational expense, but can uniquely capture group differences in crossing fibers (i.e. "secondary" fibers), unlike TBSS based on the tensor model alone.

For statistical testing, a permutation approach was employed using FSL's "randomise" function with the TFCE Threshold-Free Cluster Enhancement option, generating 10,000 permutations and applying family-wise error (FWE)-correction to obtain cluster inferences. A two-tailed regression model was next generated using FSL's GLM function, whereby RSQ brooding scores were used as the criterion variable with age and gender as nuisance covariates. Age was included due to a well-known confounding influence of age on WM microstructure[85], and gender was included due to some evidence of gender differences in rumination—namely, that females tend to exhibit greater rumination severity than males[86]. The resulting negative contrast mask (i.e. representing those voxels negatively associated with greater DR severity) was thresholded twice—first at p=0.05 and again at p=0.01. The use of two thresholds allowed us to determine those voxels which were most strongly associated with DR (p=0.01), while also yielding a more liberal cluster of voxels (p=0.05) that could be reliably used as a Region-of-Interest (ROI) for multimodal analysis.

Following TBSS, we sought to corroborate our initial group level, voxel-wise dMRI findings using individual-level tractography, which is an alternative dMRI methodology that attempts to reconstruct known WM pathways while retaining each subject's image in native space orientation. Since spatial information is not manipulated in tractography as it is with TBSS[87], tractography could confirm any TBSS findings in native space, while also disconfirm false-positives due to non-physiological factors such as image misalignment, movement, and other factors resulting from the methodological limitations of TBSS[88].

For tractography, we chose to analyze average FA measures from the entire pathways of tracts of interest whose labels included significant voxels from the earlier TBSS stage. These measures were then further analyzed across hemispheres to establish any significant laterality effects[89]. To perform tractography, we specifically used the TRActs Constrained by UnderLying

Anatomy (TRACULA) tool in FreeSurfer (version 5.3.0)[57], which delineates 18 known WM bundles using each participant's joint dMRI and T1-weighted MRI data (*See* **Appendix, Methods: Section D**).

rsfMRI Preprocessing

Preprocessing of baseline rsfMRI data was carried out using a custom workflow based on FSL's FEAT[82], combined with AFNI and FREESURFER tools. Additional denoising steps were taken by controlling for WM and ventricular CSF confounds, and by using FSL's ICA-based Xnoisifier artifact removal tool (FIX) to control for motion and physiological artifact (*See* Appendix, Methods: **Section E**).

rsfMRI: Group Independent-Components Analysis (ICA) / Dual-regression and DR

Group-level Independent Components Analysis (ICA) was performed by employing "temporal concatenation" of the complete, preprocessed rsfMRI time-series from all of the participants and restricted to twenty-five independent component (IC) outputs[90]. Four IC's were manually identified as noise and removed from further examination. Of the remaining twenty-one networks, all were identified using visual inspection by way of reference to the 17 RSN's delineated by the Yeo et al. 2011 atlas[91], thus allowing for identification of the three IC's of the triple-network that were introduced above - the pDMN[20,50], the coSN[47], and the fECN[37,92,93].

A dual-regression approach[94] was next performed on the triple-network RSN's, which were used as regressors for each individual subject's 4D set of fMRI volumes in order to extract time-series that were both specific to each subject and to each of the three IC's[64]. Design matrices and contrasts were then created to test for correlations between brooding severity and total average intrinsic connectivity within each of these RSN's, controlling for age and gender. These regression models were tested separately for each RSN, using two-tailed contrasts in an identical manner to that used in TBSS, with FSL's randomise (10,000 permutations) and TFCE cluster-thresholding with whole-brain FWE-correction[95]. To further correct for analysis-level multiple comparisons among the three triple-network RSN's, we also Bonferroni-corrected our alpha significance level for these models to 0.05/3 or p=0.0167.

Between-Network Functional Connectivity and DR

To investigate interactions between the triple-network RSN's, we utilized FSLNets[96], a MATLAB-based tool that interfaces with FSL. FSLNets utilizes the individual resting-state network IC's generated from the earlier dual-regression stage to perform hierarchical clustering across RSN's and estimate a partial-correlation (Spearman's ρ) matrix for each RSN for each participant.

To perform between-RSN general linear modeling, randomise was again employed with FWE-correction, but this time using the nets_glm function at 10,000 permutations. The design matrices and contrasts used in the earlier FSL GLM analyses, were used in this analysis as well. In summary, whereas the dual-regression approach identified DR-associated clusters (both *belonging to* and *external to* the RSN's) that are more strongly connected to each of the triple-network RSN's considered separately, the FSLnets approach identified DR-associated patterns of between-network correlation among the triple-network RSN's considered collectively.

Replication and Statistical Power

To formally test whether the findings would generalize beyond the discovery sample[73], we directly replicated all stages of analysis using a phenotypically similar, independent sample obtained from the publicly-available, multi-site NKI Rockland dataset[75]. By chance, that dataset contained a sub-sample of participants with equivalent demographics to those participants from our original sample; this included (*N*=39) participants who were between the ages of 18-55, had no history of drug abuse or severe comorbid psychopathology, had both useable dMRI data and rsfMRI data, and reported at least some depressive symptomatology. The participants had also been administered the 21-item Beck Depression Inventory (BDI-II) and the 22-item Rumination Response Scale (RRS)(*See* **METHODS: Depressive Rumination Measurement**), which contained identical brooding sub-scale items to those administered in the 10-item RSQ scale[80]. As part of a larger battery of measures, many but not all participants also completed the Structured Clinical Interview for DSM-IV-TR Axis I Disorders (SCID)[97]. Specifically, 33% of the n=39 participants met full criteria for MDD (18% current/recurrent and 15% in remission), requiring that the remaining participants be included on the basis of broader depressive symptomology. This included 66% with dysphoria as determined by elevated BDI-II scores (≥4)—a cutoff used in prior studies[98,99]. One advantage to including dysphoric participants was that it could possibly allow us to infer whether any replicated biomarkers of DR are specific to DR and not merely conflated with the depressive symptoms specific to an MDD diagnosis.

Furthermore, to minimize the possibility of sample-variant effects due to incongruence of neuroimaging acquisition parameters across samples[100], we spatially and temporally resampled the rsfMRI and dMRI data in the replication sample to match the voxel resolution of the rsfMRI and dMRI data and the sampling frequency (i.e. TR) of the rsfMRI data in the discovery sample (*See* **Appendix, Methods: Sections F & G**). To ensure direct equivalence of neuroimaging data preprocessing in the replication[101], we also applied a nearly equivalent analytic pipeline to that

applied to the discovery sample, but using the pDMN, fECN, and coSN group-ICA RSN definitions from the discovery dataset. Lastly, given the multiple scanner sites used to collect the neuroimaging data in the Rockland sample, we employed mixed-effects regression models (both with FSL's GLM and in R), whereby scanner site was additionally modeled as a random effect.

Since generalizability was a core aim of our study, power analyses were also conducted for detecting a large effect size when using multiple regression with two covariates (age and gender) and a significance level of $\alpha<0.05$ (*See* **Appendix: Methods, Section H**). Given our sub-optimal sample-sizes, we also opted to filter significant findings by a large effect size cutoff of $R^2=0.25$ for non-voxel-wise tests (i.e. tractography, multimodal analysis of beta-coefficients) and $p<0.01$ FWE-corrected threshold for voxel-wise tests (TBSS, Dual-Regression, FSLnets). This step would serve to more stringently identify those findings with the highest putative generalizability as well as those at risk of replication failure. Further, we classified a finding as being a 'full replication' if it replicated with respect to both equivalence in directionality of the effect and the RSN's or anatomical location(s) implicated. Likewise, the fully-replicated findings needed to meet our effect-size cutoff in at least one of the two samples, as well as an FWE-corrected $\alpha<0.05$ level of significance or uncorrected $\alpha<0.001$ level of significance for ROI analyses. Finally, to evaluate analysis-level false-discovery across multimodal replications, we further generated a null-distribution for post-hoc meta-analysis based on replication counts (*See* **Appendix: Methods, Section I**).

RESULTS: INITIAL SAMPLE

Descriptive Statistics and Behavioral Findings

Depressive rumination severity (DR) as measured using the RSQ was normally distributed (M= 9.08, SD= 3.01, range: 17-48, IQR=5; Shapiro-Wilk = 0.976, p = 0.53). Depression severity was also normally distributed (M= 31.94, SD= 8.16, range: 1-15, IQR=10, Shapiro-Wilk = 0.976, p = 0.35) and was modestly associated with DR severity (R^2 = 0.13, $F(1, 37)$ = 5.61, p=0.02). Age was positively skewed (M=27.51, SD = 8.80, range: 18-52) due to an overrepresentation of young adults in our discovery sample. Although age was weakly correlated with RSQ brooding scores (R^2 = 0.09, $F(1, 37)$ = 3.84, $p<0.06$) and interacted with several neuroimaging measures throughout our analyses, no significant interactions with gender were observed in either discovery or replication

318 samples. Nevertheless, we retained both age and gender as nuisance covariates for each regression
319 model to ensure maximal generalizability of our findings and consistency in our analyses.
320
321 **White Matter (WM) Microstructure and Depressive Rumination**

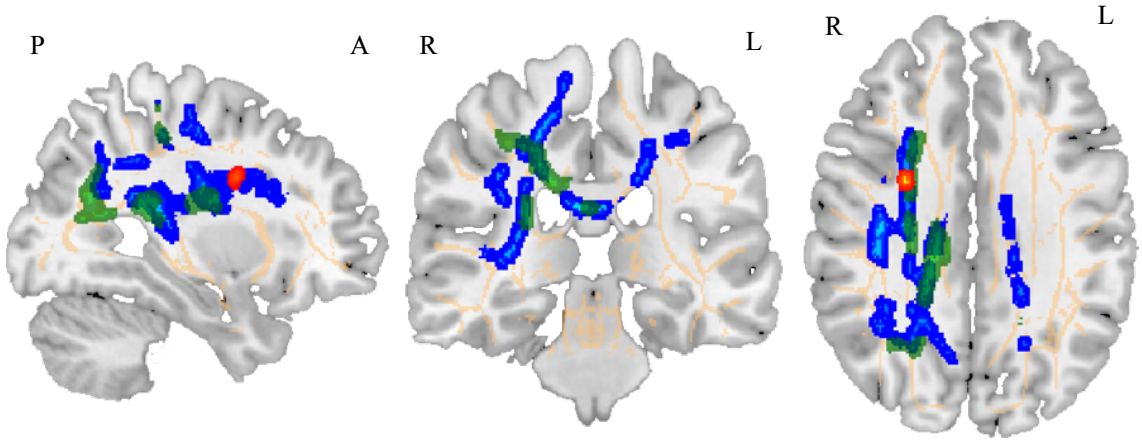


Figure 2: Depressive rumination was associated WM integrity primarily within the temporal and parietal parts of the right SLF including the anterior and posterior Corona Radiata, as well as the right posterior and anterior Cingulum along with the bilateral CST, particularly near its intersection with the posterior Corona Radiata. Here, significant associations with FA (p<0.01) are depicted in blue, significant associations with the F1 partial volume (p<0.01) are depicted in green, and significant associations with the F2 "crossing-fibers" volume in the superior at the Corona Radiata (p<0.01) are depicted in red-yellow. Note too that the FA and F1 clusters are, for the most part, overlapping; this indicates convergence across deterministic and probabilistic diffusion models. Since these measures capture fractional anisotropy of dominant diffusion direction(s) at each voxel, we should also expect them to track each other closely as a confirmation that any detected effects are not the result of corrupted model estimation, or other methodological errors.

322 ***TBSS: Localized White-Matter Biomarkers of DR***
323 Our first set of analyses employed tensor and crossing-fiber variations of TBSS to test for
324 WM microstructural connectivity biomarkers of DR (*see* **METHODS: TBSS; Appendix,**
325 **Methods: Section C**). Results first revealed significantly lower FA in association with higher
326 brooding scores within the right Superior Longitudinal Fasciculus (SLF, both parietal and
327 particularly temporal parts), the Cingulum, and the Corticospinal Tract (CST) (p<0.01 FWE;
328 p<0.05 FWE; *see blue FA and green F1 clusters in* **Figure 2**). Some of these voxels also extended
329 into the Anterior Thalamic Radiation (ATR), Uncinate Fasciculus (UF), and Splenium (p<0.05
330 FWE; p<0.05 FWE; p<0.05 FWE). A subsequent 'crossing-fibers' TBSS analysis closely tracked
331 these findings, but further revealed significant relationships between DR and the microstructure of
332 secondary-fibers (captured by the F2 partial volume) in a small cluster of the right superior Corona
333 Radiata where the SLFT intersects with the Corpus Callosum at the Centrum Semiovale (p<0.01
334 FWE; *see red cluster in* **Figure 2**).

Tractography: Globalized White-Matter Biomarkers of DR

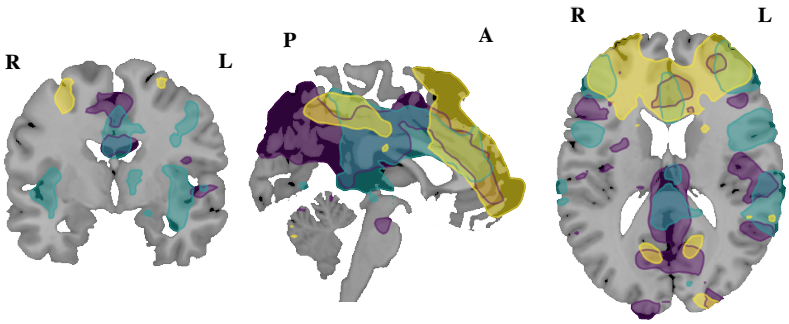
Using global probabilistic tractography, we next sought to both methodologically triangulate our TBSS findings and clarify the "mereology" of DR-associated WM pathways (i.e. their globality vs. locality). Given that TBSS analysis is performed on images where the WM tracks are aligned with an MNI standard, we performed probabilistic tractography on an individual subject basis to provide converging evidence that our findings are not driven by spatial normalization[57]. Using six pathways of interest from the outputs of TRACULA, including the right SLFT (Temporal part), right SLFP (Parietal part), CCG, CST, ATR, and Splenium, and Bonferroni Correction for the six tracts tested ($p_{corrected}$=0.05/6 = 0.0083), we found a robust negative association between weighted average FA of the right SLFT and DR severity (adj. $R^2 = 0.18$, $F(3, 36) = 3.85$, $p<0.005$). This clarified the findings conducted on a voxel-wise (i.e. on spatially normalized) basis with TBSS, by suggesting that the right SLFT may be both globally and locally associated with DR severity, whereas the other DR-associated pathways may be better construed as localized WM clusters.

Tract Hemisphericity

The aforementioned TBSS and tractography analyses indicated that the SLFT WM finding was distinctly right-lateralized. To test this formally, we treated hemisphere as a within-subjects measure and used Analysis of Variance (ANOVA) to compare two GLM's predicting DR for each tractography measure of global average FA. Specifically, the first GLM used left hemisphere as the predictor, whereas the second GLM used right hemisphere as the predictor, controlling for left hemisphere. From this analysis, we found supportive evidence for right lateralization of the SLFT ($F(36,1)=8.71$, $p=0.005$).

<u>'Within-Network' Functional Connectivity and Depressive Rumination</u>

Dual-Regression Findings



<u>Figure 3:</u> The slices in this figure depict the three triple-network RSN's resulting from group Independent Component Analysis (ICA) in the discovery sample. The fECN is shown in yellow, pDMN in purple, and coSN in turquoise. These same RSN definitions were used across both discovery and replication samples.

We next tested whether DR was associated with resting-state functional connectivity of the three triple-network RSN's as identified from the outputs of group-ICA followed by dual-regression (*see* **Figure 3** & **METHODS: rsfMRI Group-ICA** & **Dual-regression**). Results revealed that DR was highly correlated with functional connectivity in multiple clusters, some of which belonged to each respective triple-network RSN (i.e. 'intrinsic' connectivity), but also others that were outside of the respective RSN's (i.e. 'extrinsic' connectivity) (*see* **Figure 4**). With respect to the latter, we found that DR was positively associated with extrinsic connectivity between the frontal Executive Control Network (fECN) and a small cluster (voxels=15) located at a juncture between the left Amygdala and Parahippocampal Gyrus (p<0.05 FWE**;** *see red clusters in* **Figure 4**). Additionally, the Precuneal Default Mode Network (pDMN) exhibited lower extrinsic connectivity with the left somatosensory areas, left Precentral Gyrus and left inferior Frontal Gyrus (p<0.01 FWE; *see blue clusters in* **Figure 3**), but also lower intrinsic functional connectivity between the Precuneus and PCC. Lastly, the Cingulo-Opercular Salience Network (coSN) exhibited lower intrinsic functional connectivity among the dorsal left Precentral Gyrus, left inferior Frontal Gyrus, right superior Postcentral Gyrus, and most prominently in Broca's area bilaterally (p<0.01 FWE ; *see green clusters in* **Figure 4**).

WM Microstructural and 'Within-Network' Functional Connectivity

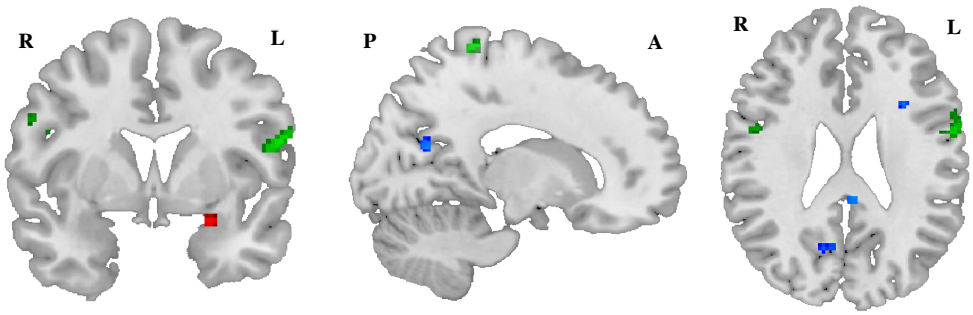


Figure 4: Significant clusters that exhibited lower functional connectivity within the pDMN associated with DR are depicted in blue, and include the PCC, Precuneus, left Precentral Gyrus, left Somatosensory Cortex, and the left inferior Frontal Gyrus. Significant clusters exhibiting lower functional connectivity within the coSN are depicted in green and include the dorsal left Precentral Gyrus, right superior Postcentral gyrus, left inferior Frontal Gyrus, and Broca's area bilaterally. Finally, significant clusters exhibiting greater functional connectivity within the fECN are depicted in red and include the left Amygdala and left Parahippocampal Gyrus.

We next extracted the beta coefficients representing average total connectivity (intrinsic and extrinsic) for each of the DR-associated triple-network clusters discovered through dual-regression. This step would in turn allow us to test for any multimodal relationships between the within-network functional connectivity findings and the microstructural connectivity findings (i.e. informed by tractography and TBSS). To accomplish this, we first created a matched subsample of n=32 subjects, since seven subjects did not have both useable rsfMRI and TRACULA data. As an initial step, we tested for any associations between the dual-regression clusters and average FA extracted from the thresholded (p=0.05) negative contrast mask from TBSS. That analysis revealed that average FA negatively predicted within-network functional connectivity of the pDMN and coSN (adj. $R^2 = 0.14$, $F(3, 29) = 2.75$, $p<0.05$; adj. $R^2 = 0.03$, $F(3, 29) = 1.33$, $p=0.06$), but not the fECN.

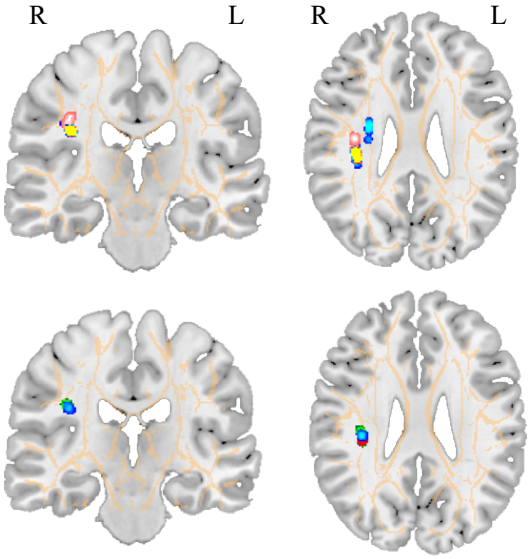


Figure 5: The above images depict correlations between RSN intrinsic/extrinsic functional connectivity and FA of the DR-associated right SLF fibers. The top row of images depicts a negative correlation between right medial SLFT FA and intrinsic connectivity of the coSN (pink) and pDMN (blue), as well as a positive correlation between FA and extrinsic connectivity of the right fECN (yellow) with the left Amygdala. The bottom row of images depicts the positive correlation between FA of secondary-fibers and these same intrinsic/extrinsic functional connectivity relationships.

397 Next, we tested an additional voxel-wise TBSS analysis with average total connectivity beta
398 coefficients as regressors. From that analysis, we found that FA within a small cluster in the medial
399 SLFP was also found to significantly predict total average connectivity of each of the triple-network
400 RSN's (p<0.05, FWE)(*See light blue cluster* **Figure 5**). We also found that FA of a posterior cluster
401 of the right SLFP was positively associated with functional connectivity of the fECN, whereas the
402 medial cluster of the right SLFP was negatively associated with functional connectivity of both the
403 pDMN and coSN (*see* **Figure 5**). We also found that secondary fiber FA in that same right medial
404 SLFT region (i.e. posterior to the DR-associated secondary-fiber cluster described earlier) was
405 positively associated with each of the triple-network RSN's ($R^2 = 0.35$, $F(3, 32) = 6.65$, $p<0.001$**;**
406 adj. $R^2 = 0.24$, $F(3, 32) = 4.28$, $p=0.001$**;** adj. $R^2 = 0.20$, $F(3, 32) = 3.68$, $p<0.01$). That is, localized
407 right SLFP primary and secondary fibers predicted the DR-associated within-network functional
408 connectivity clusters of the triple-network. Since the TRACULA results only provided global
409 measures of FA, averaged across the entire pathway and hence not sensitive to localized clusters,
410 we additionally used the JHU White-Matter atlas to create atlas-labeled ROI's from the significant
411 TBSS clusters (p=0.05 FWE). We could then use these ROI's to perform a supportive analysis on a

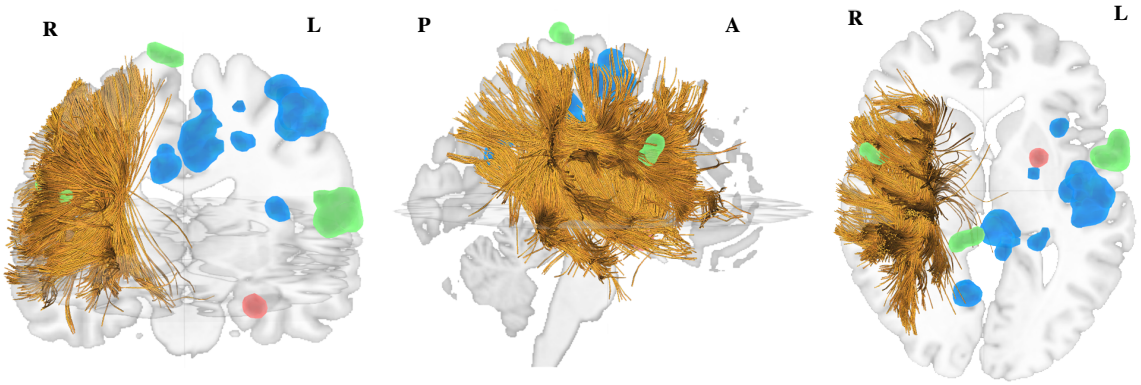


Figure 6*:* For multimodal visualization, right SLFT fibers are depicted above with orange streamlines alongside the significant dual-regression clusters (p<0.05 FWE) of the triple network, which are shown in blue, green, and red. The anterior left amygdala, whose positive extrinsic connectivity with the fECN was positively associated with DR, is displayed in red. The right Precuneus, PCC, inferior Frontal Gyrus, and left somatosensory areas, whose negative intrinsic/extrinsic connectivity patterns were positively associated with DR, is displayed in blue. Lastly, the left Precentral Gyrus, left inferior Frontal Gyrus, and Broca's area, whose negative intrinsic connectivity was positively associated with DR, are displayed in green.

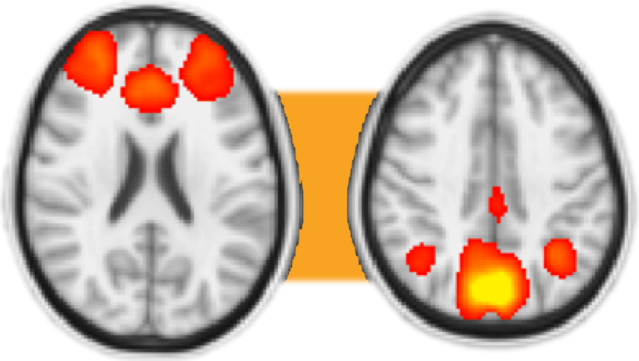
412 non-voxelwise basis. Specifically, this approach would also allow us to explore whether applying
413 atlas definitions to our original TBSS analysis with DR might afford greater specificity into
414 multimodal structural-functional links (*See* **METHODS: TBSS**). That analysis further revealed that
415 the DR-associated WM clusters of the CCG, ATR, UF, and Splenium each predicted functional
416 connectivity of the DR-associated triple-network clusters from dual-regression as well (*See*

Appendix, Results: Section A *for details*). Finally, we tested whether global WM microstructure of the right SLFT, as defined by the tractography measures, might also be driving the multimodal effects (*See* **Figure 6**). The results accordingly showed that average FA of the right SLFT, was positively associated total average intrinsic connectivity of the coSN (adj. $R^2 = 0.13$, $F(3, 29) = 2.62$, $p<0.01$) and pDMN (adj. $R^2 = 0.30$, $F(3, 29) = 5.47$, $p=0.001$**;** adj. $R^2 = 0.19$, $F(3, 29) = 3.48$, $p<0.01$), but negatively predicted the extrinsic connectivity between the fECN and the left Amygdala (adj. $R^2 = 0.09$, $F(3, 29) = 2.07$, $p<0.05$). In sum, both global and local microstructure of right SLFT primary and secondary fibers, along with a variety of other localized WM clusters, predicted within-network functional connectivity patterns of the triple-network associated with DR.

<u>'Between-Network' Functional Connectivity and Depressive Rumination</u>

FSLnets

Based on prior evidence for the role of the pDMN, coSN, and fECN in DR, we next used FSLnets to explore whether between-network functional connectivity of each pair combination of triple-network RSN's was associated with DR (*see* **METHODS: Between-Network Functional Connectivity**). That analysis revealed that DR severity was positively associated with an inverse correlation between the fECN and pDMN ($p<0.05$ FWE) (*See* **Figure 7**), and between the coSN and the pDMN ($p<0.01$ FWE). The third 'between-network' correlation between fECN and coSN was not significantly associated with DR in the discovery sample.



<u>Figure 7</u>: The above image depicts the fECN (*left*) and pDMN (*right*) whose inverse correlation was associated with DR severity ($p <0.05$ FWE).

444 ***WM Microstructure and 'Between-Network' Functional Connectivity***

445 As in the case of the within-
446 network functional connectivity
447 findings, we also sought to test
448 whether the global and local WM
449 biomarkers of DR predicted the
450 between-network inverse correlations
451 from FSLnets. Accordingly,
452 multimodal analysis revealed that
453 average global FA of the right SLFT,
454 predicted the coSN-pDMN inverse
455 correlation (adj. $R^2 = 0.15$, $F(3, 29) = 2.93$, $p<0.01$). Voxel-wise TBSS similarly revealed that the
456 DR-associated coSN-pDMN inverse correlation predicted lower FA of a medial cluster of the right
457 SLFT (adj. $R^2 = 0.17$, $F(3, 32) = 4.17$, $p<0.01$) and another along the right posterior Corona
458 Radiata ($p<0.01$ FWE)(*see red/yellow cluster* **Figure 8**). Correspondingly, FA of the left anterior
459 Corona Radiata negatively predicted the pDMN-fECN inverse correlation associated with DR.
460 ($p<0.05$, FWE) (*see blue and red clusters* **Figure 8**). Finally, we again used the ROI's created from
461 the significant TBSS clusters ($p=0.05$ FWE) to perform a similar non-voxelwise analysis so as to
462 explore whether atlas-defined divisions of WM clusters (i.e. discovered from our original TBSS
463 analysis with DR) might further clarify the nature of their association with between-network
464 functional connectivity. This approach showed that the DR-associated TBSS clusters of the CST,
465 CCG, ATR, UF, and Splenium each predicted the coSN-pDMN inverse correlation, whereas only
466 the left UF predicted the pDMN-fECN inverse correlation (*see* **Appendix, Results: Section B**).

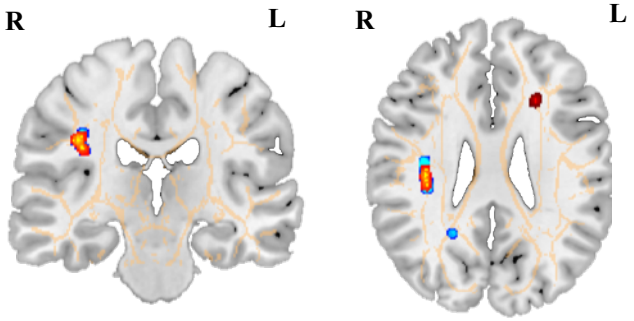


Figure 8: Lower FA of the right medial SLFT and the right posterior Corona Radiata (blue), as well as higher FA of right medial SLFT crossing fibers (red/yellow), was associated with greater pDMN-coSN inverse correlation. Similarly, greater FA of the left anterior Corona Radiata (red) was associated with greater pDMN-fECN inverse correlation.

In summary, the initial discovery sample revealed: 1) associations between DR severity and microstructure of the right-lateralized SLFT, along with localized WM clusters scattered throughout the SLFP, CCG, CST, ATR, Splenium, UF; 2) associations between DR severity and the microstructure of secondary fibers in the right superior Corona Radiata; 3) associations between DR severity and both intrinsic/extrinsic within-network functional connectivity of the triple-network; 4) associations between DR severity and between-network functional connectivity of the pDMN with each of the coSN and fECN of the triple-network; 5) associations between localized right medial SLFP primary and secondary-fiber microstructure and each manifestation of triple-network functional connectivity observed to sub-serve DR; 6) an association between right posterior Corona Radiata microstructure and the pDMN - coSN between-network functional connectivity found in (4) to sub-serve DR; 7) associations between left anterior Corona Radiata microstructure and the pDMN – fECN between-network functional connectivity found to sub-serve DR. 8) a variety of less prominent associations between localized WM clusters of the CST, CCG, ATR, UF, and Splenium, along with multiple manifestations of triple-network functional dysconnectivity found in (3) to sub-serve DR. *See* **Figure 9** for a visual summary.

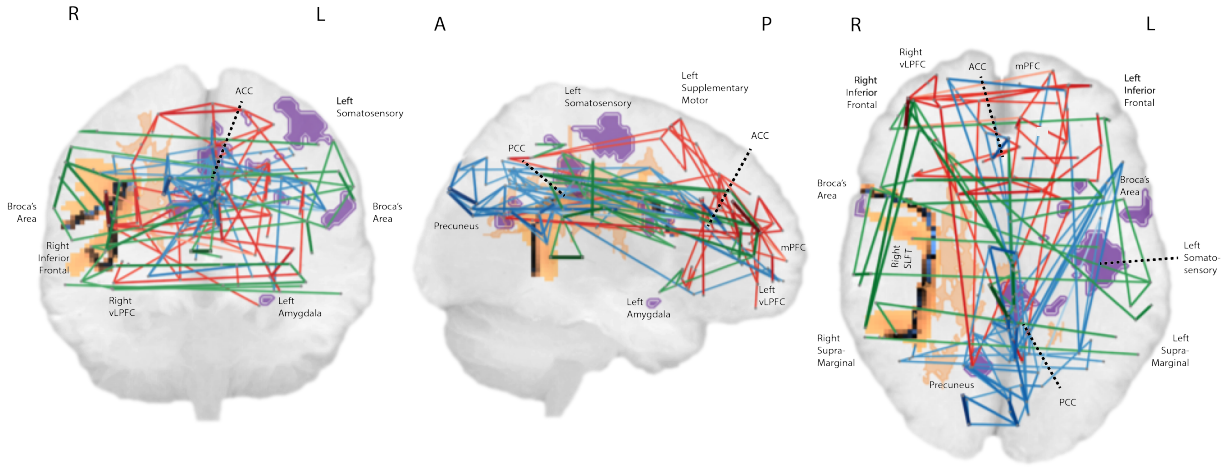


Figure 9: The above multimodal visualization summarizes key microstructural and functional connectivity biomarkers associated with DR in the discovery sample. WM tracts revealed both by TBSS and tractography are represented in copper heatmap. Regions whose within-network functional connectivity patterns are disrupted in DR are overlaid in purple. Finally, each of the pDMN, coSN, and fECN as a whole are here depicted as distinct networks with blue, green, and red edge connections, respectively.

RESULTS: REPLICATION SAMPLE

The replication sample exhibited similar descriptive statistics to those found in the discovery sample, but with some key differences. Perhaps most notably, for instance, depression severity was considerably milder on average in the replication sample (*M*=10.00, *SD*=6.18, range: 4-31, IQR=5.00). Furthermore, DR severity in the replication sample showed a significant positive skew, which we corrected using a log transformation to yield a normal distribution (Shapiro-Wilk = 0.948, $p = 0.07$). On the other hand, average DR severity overall was similar (*M*=11.00, *SD*=2.74, range: 7-20, IQR=2). Also, age exhibited a slight positive skew in the replication sample (*M*=31.36, *SD* = 5.79, Range: 22- 44), as in the discovery sample, along with a similar gender distribution (65% female). *See* **Table 1** for a summary comparing characteristics across initial and replication samples.

Sample Characteristics	Discovery Sample	Replication Sample
Age	*M* =27.51, *SD* = 8.80, Range: 18-55	*M* =31.36, *SD* = 5.79, Range: 22-44
Gender	22 females (56%)	24 females (65%)
DR Severity	*M* = 9.08, *SD* = 3.01	*M* =11.00, *SD* =2.74
Depressive Episodes	Moderate-severe MDD diagnosis only	Mild-severe MDD diagnosis, recurrent depression, dysphoria
Depression Severity	*M* = 31.94, *SD* = 8.16	*M* =10.00, *SD* =6.18
Medication Useage	Permitted if no medication change in the 12 weeks prior to study entry	Permitted if medications were reported as routine. 12-week stability data unavailable.
Other Psychopathology	No severe comorbidity	No severe comorbidity
Scanner Type	Siemens Skyra 3T	Siemens Tim Trio 3T
Multi-site?	No	Yes, 4 separate sites
dMRI parameters	TR/TE=1200/71.1, B=1000, 128 x 128 matrix, 3 mm slice thickness, anistropic voxels, 2 B0 + 53 DWI (55-directions)	TR/TE=2400/85, B=1500, 212 x 212 matrix, 2 mm slice thickness, isotropic voxels, 9 B0 + 128 DWI (137-directions)
rsfMRI parameters	eyes open, TR = 2000 ms, TE = 30 ms, 31 axial slices, voxel size = 3.125 x 3.125 x 3 mm^3 anisotropic	eyes open, TR = 2000 ms, TE = 30 ms, 40 axial slices, voxel size = 3 x 3 x 3 mm^3 isotropic

Table 1: The table above compares key characteristics across samples. In particular, the representation of age, gender, and DR severity was roughly equivalent across samples. On the other hand, the discovery sample included subjects with higher depression severity on average than those included in the replication sample. Although scanner manufacturer and strength was equivalent, the brands differed. Nevertheless, resampling procedures yielded dMRI and rsfMRI data with roughly equivalent core parameters including voxel dimensions, TR, and TE across samples.

Following the application of a nearly identical analytic methdology to that used with our original sample (*See* **METHODS: Replication**), we were able to fully replicate 49% of our cumulative findings across all methodologies, modalities, and levels of analysis. Specifically, twenty findings fully replicated, and two findings perhaps 'partially' replicated, out of forty retested models from the discovery sample.

Regression Findings (Predictor and Outcome)	Initial Sample	Replication Sample
Right SLFT Microstructure and DR Severity	TBSS (p<0.01 FWE, neg) Tractography (R^2=0.25, adj. R^2=0.18, neg)	TBSS (p<0.01 FWE, neg) Tractography (cond. R^2=0.37, neg)
Right SLFP Microstructure and DR Severity	TBSS (p<0.01 FWE, neg) Tractography (R^2=0.17, adj. R^2=0.05, neg)	TBSS (p<0.01 FWE, neg) Tractography (cond. R^2=0.23, neg)
CST Microstructure and DR Severity	TBSS (p<0.01 FWE, neg) Tractography (R^2=0.11, adj. R^2=0.06, neg)	TBSS (p<0.01 FWE, neg) Tractography (cond. R^2=0.17, neg)
CCG Microstructure and DR Severity	TBSS (p<0.05 FWE, neg)	TBSS (p<0.01 FWE, neg)
UF Microstructure and DR Severity	TBSS (p<0.05 FWE, neg)	TBSS (p<0.01 FWE, neg)
Splenium Microstructure and DR Severity	TBSS (p<0.05 FWE, neg)	TBSS (p<0.05 FWE, neg)
ATR Microstructure and DR Severity	TBSS (p<0.05 FWE, neg)	TBSS (p<0.05 FWE, neg)
pDMN Within-Network Connectivity and DR Severity	Dual-regression (p<0.01, FWE, neg)	Dual-regression (p<0.001 unc. ROI-analysis, neg)
fECN Within-Network Connectivity and DR Severity	Dual-regression (p<0.01, FWE, neg)	Dual-regression (p<0.001 unc. ROI-analysis, neg)
pDMN-fECN Between-Network Connectivity and DR Severity	FSLnets (p<0.05, FWE, neg)	FSLnets (p<0.01, FWE, neg)
Right SLFT Microstructure and pDMN Within-Network Connectivity	Tractography (R^2=0.36, adj. R^2=0.30, neg) TBSS (p<0.05 FWE, neg)	TBSS ROI-analysis (cond. R^2=0.36, neg)
Right SLFP Microstructure and pDMN Within-Network Connectivity	Tractography (R^2=0.26, adj. R^2=0.19, neg) TBSS (p<0.05 FWE, neg)	TBSS ROI-analysis (cond. R^2=0.33, neg)
ATR Microstructure and pDMN Within-Network Connectivity	TBSS ROI-analysis (R^2=0.33, adj. R^2=0.26, neg)	Tractography (cond. R^2=0.18, neg) TBSS ROI-analysis (cond. R^2=0.28, neg)
CCG Microstructure and pDMN Within-Network Connectivity	TBSS ROI-analysis (R^2=0.29, adj. R^2=0.22, neg)	Tractography (cond. R^2=0.12, neg) TBSS ROI-analysis (cond. R^2=0.21, neg)
Splenium Microstructure and pDMN Within-Network Connectivity	TBSS ROI-analysis (R^2=0.21, adj. R^2=0.12, neg)	TBSS ROI-analysis (cond. R^2=0.23, neg)
Right SLFT Microstructure and coSN Within-Network Connectivity	Tractography (R^2=0.21, adj. R^2=0.13, neg) TBSS (p<0.05 FWE, neg)	Tractography (adj. R^2=0.50, neg) TBSS (p<0.05 FWE, neg)
CCG Microstructure and coSN Within-Network Connectivity	TBSS ROI-analysis (R^2=0.27, adj. R^2=0.20, neg)	TBSS ROI-analysis (adj. R^2=0.26, neg)
Splenium Microstructure and coSN Within-Network Connectivity	TBSS ROI-analysis (R^2=0.17, adj. R^2=0.08, neg)	Tractography (cond. R^2=0.29, neg) TBSS ROI-analysis (cond. R^2=0.55, neg)
Right SLFT Microstructure and fECN Within-Network Connectivity	Tractography (R^2=0.18, adj. R^2=0.09, neg) TBSS (p<0.05 FWE, pos)	Tractography (cond. R^2=0.31, pos) TBSS ROI-analysis (cond. R^2=0.34, neg)
DR-associated WM microstructure and pDMN-fECN Between-Network Connectivity	FSLnets (p<0.05 FWE, pos)	FSLnets (p<0.05 FWE, pos)

Table 2: The above table depicts key findings (*left column*) that directly replicated across the discovery sample (*middle column*) and replication sample (right column). Each of the middle and right columns states the R^2 value from the respective regression models (adjusted in the discovery sample and conditional on both fixed and random effects in the replication sample), the methodology used to estimate that value (e.g. TBSS ROI-analysis, tractography, dual-regression, FSLnets), and the directionality of the relationship (*neg=negative,pos=positive*). In total, 20 unique findings out of 40 original findings directly replicated across samples.

515 ***dMRI Replications (TBSS and Tractography)***

516 The replication yielded a nearly equivalent set of dMRI findings using both TBSS and
517 tractography methods, with a striking degree of similarity in the voxelwise association between
518 WM microstructure and DR severity across samples. Using TBSS, we again found that FA of the

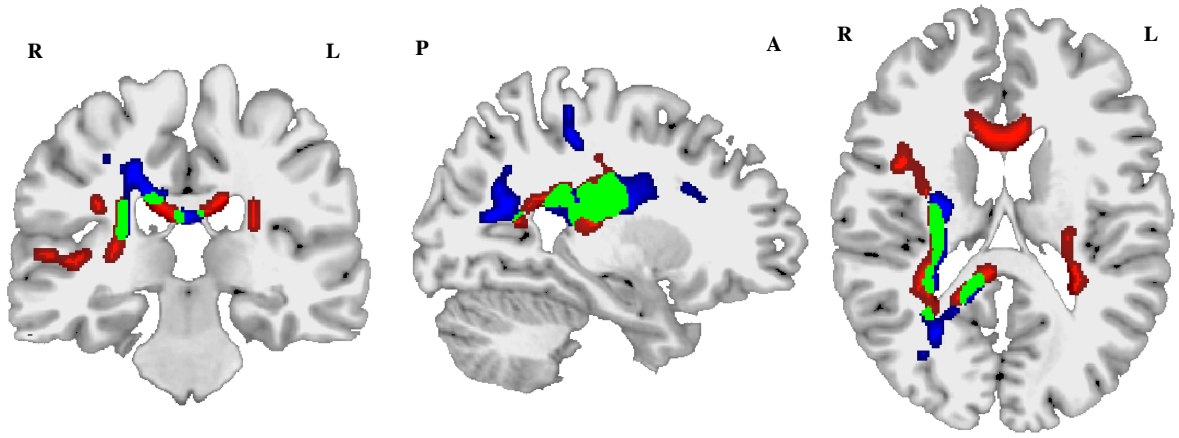


Figure 10: The above mosaic depict TBSS findings from the original sample (blue) and the NKI Rockland replication sample (red). The top row depicts the negative correlations in both samples between DR and FA (p=0.01 FWE in the discovery sample, p=0.05 FWE in the replication sample). These findings overlapped closely (green) along the right SLF and along the splenium. In the replication sample, there was slightly greater coverage, however, of the genu of the Corpus Callosum.

right SLFT, SLFP, CCG, CST, Splenium, UF, and ATR exhibited negative correlations with brooding scores (p<0.05, FWE)(*See* **Figure 10**). At the p=0.05 FWE threshold, 98 voxels, located in the right SLF, CST, and Corpus Callosum (*See top row* **Figure 10**), overlapped in this TBSS analysis across samples. The subsequent 'crossing-fibers' TBSS analysis, however, differed considerably across samples (*see* **Table 2 & Figure 10**). As in the discovery sample, however, the tractography replication demonstrated corresponding negative correlations between DR severity and average FA of localized WM clusters derived from the TBSS ROI-analysis. Additionally, the correlation between DR and global microstructure of the right SLFT was again the only tractography analysis that survived Bonferroni Correction for the six tracts tested (cond. $R^2 = 0.37$, $F(3, 35) = 8.90$, $p_{corrected}<0.05/6 = 0.0083$). As in the discovery sample, the effect of hemisphere was again significant with respect to the SLFT ($F(36,1)=5.43$, $p=0.03$), reiterating the right lateralization of this particular global WM biomarker. Whereas in the discovery sample, DR was also positively associated with microstructure of secondary-fibers in a small cluster of the right superior Corona Radiata, in the replication sample, it was negatively associated with microstructure of secondary-fibers of the Corpus Callosum and bilateral CST ($p < 0.05$ FWE). Although future replications would be needed to confirm, these differences may be largely attributable to the interaction between DR and depression severity across samples (*See* **Appendix, Results: Sections D & E**).

538 ***rsfMRI Replications (Dual-Regression and FSLnets)***

539 Despite very similar
540 microstructural connectivity findings
541 across samples at whole-brain FWE-
542 corrected thresholds (*See green*
543 *overlapping clusters in* **Figure 10**), the
544 initial within-network functional
545 connectivity findings replicated only
546 when using a small-volume ROI
547 correction (i.e. MNI atlas-defined
548 masks of significant regions from the
549 discovery sample). Nevertheless, the
550 results showed similar within-network
551 functional connectivity patterns of the
552 pDMN and fECN with respect to both
553 anatomical location of
554 intrinsic/extrinsic clusters and
555 directionality (p<0.001) (*See*
556 *correspondence of blue and red*
557 *clusters in* **Figure 11**). Within the
558 pDMN, lower intrinsic functional
559 connectivity with the right precuneus replicated (p<0.001). The significant voxels of the pDMN
560 and coSN whose functional connectivity was associated with DR were in close anatomical
561 proximity across samples but not overlapping (*See correspondence of green clusters in* **Figure 11**),
562 whereas 9 voxels of the fECN positive connectivity cluster in the left amygdala/ parahippocampal
563 gyrus cluster were overlapping. The coSN also neuroanatomically tracked the within-network coSN
564 effect observed discovery sample, but in the reverse direction (*See* **Appendix, Results: Section C**
565 *for a discussion of 'partial' replications*).

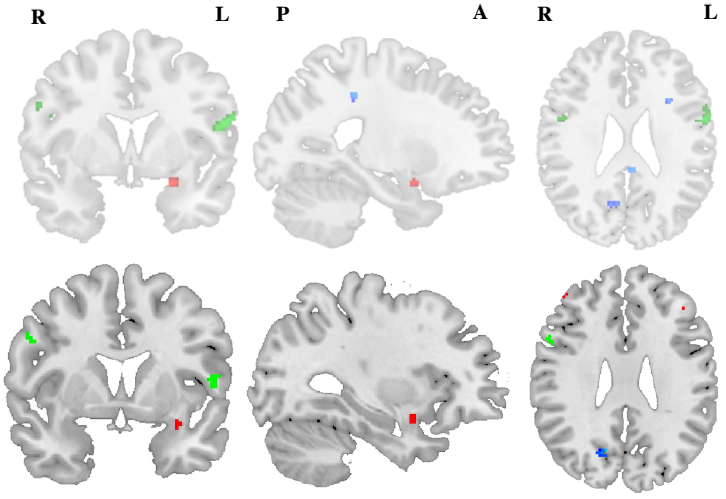


Figure 11: Within-network connectivity findings from the Rockland NKI replication sample (bottom row) compared to those from the initial samplediscovery sample (top row). Significant clusters exhibiting lower functional connectivity within the pDMN associated with DR are depicted in blue. Significant right anterior Insula clusters exhibiting lower functional connectivity within the coSN are depicted in light green, and the right superior Temporal Gyrus cluster exhibiting higher functional connectivity within the coSN is depicted in dark green (right bottom row). Finally, Ssignificant clusters exhibiting greater functional connectivity within the fECN are depicted in red and include the left Amygdala/ parahippocampal Gyrus. Finally, bilateral right anterior Insula clusters located in Broca's area that showed trending lower functional connectivity within the coSN are depicted in light green, and the right superior Temporal Gyrus cluster exhibiting higher functional connectivity within the coSN is depicted in dark green (right bottom row).

566 As with the microstructural findings, on the other hand, the between-network functional
567 connectivity findings from FSLnets also replicated with FWE correction. Specifically, the
568 association between DR and the pDMN-fECN inverse correlation fully replicated (p<0.05,
569 FWE)(*See* **Figure 12**), whereas the coSN between-network associations with DR diverged across

samples (*See* **Appendix, Results: Section C**) in light of the reversed directionality of the coSN's within-network association with DR.

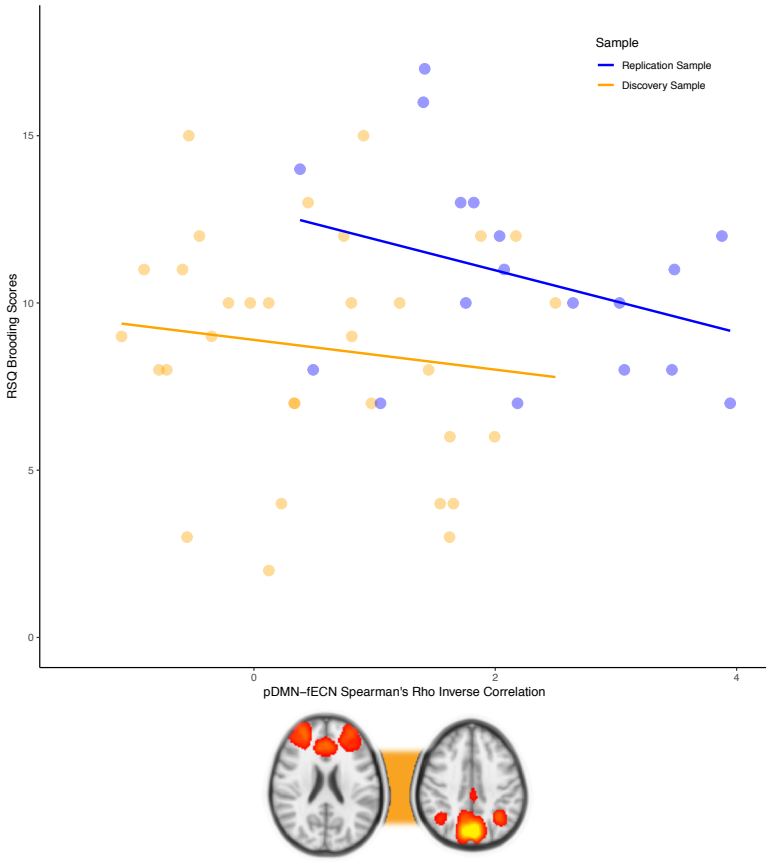


Figure 12: The scatterplot above depicts the association between pDMN-fECN inverse correlation and DR severity that was the one between-network functional connectivity relationship to fully replicate across samples.

Multimodal dMRI-rsfMRI Replications

Finally, when exploring multimodal microstructural-functional relationships in the replication sample, we found that global average FA of the right SLFT, along with localized WM clusters of the SLFP, CCG, ATR, and Splenium again predicted both the within-network and between-network functional connectivity biomarkers of DR (*see* **Table 2**). Importantly, the cumulative average FA measure from TBSS predicted pDMN-coSN between-network connectivity in the replication sample ($R^2 = 0.19$, $p<0.05$), despite there being no replication of the coSN-pDMN inverse correlation in association with DR. Also, global microstructure of the right SLFT and localized microstructure of the SLFP, CCG, ATR, and Splenium were again positively associated with the within-network functional connectivity of the pDMN and with corresponding directionality (cond. $R^2 = 0.36$, $p<0.05$; cond. $R^2 = 0.28$, $p<0.05$; cond. $R^2 = 0.33$, $p<0.05$; cond. $R^2 = 0.22$,

583 $p<0.05$). Additionally, the only fECN-related multimodal effect to replicate was the association
584 between localized right medial SLFT microstructure and fECN within-network connectivity. In
585 contrast, the relationship between WM microstructure and pDMN-fECN functional connectivity
586 across samples was ultimately non-specific to any single tract and implicated the cumulative DR-
587 associated TBSS clusters, as discovered through a final analysis in FSLnets ($p<0.05$).
588 We also found that global microstructure of the right SLFT and localized microstructure of
589 the CCG and Splenium were again positively associated with the within-network functional
590 connectivity of the coSN (cond. $R^2 = 0.50$, $p<0.05$; cond. $R^2 = 0.26$, $p<0.05$; cond. $R^2 = 0.55$,
591 $p<0.05$). Despite reversed directionality in DR's association with coSN within-network functional
592 connectivity, moreover, the directionality of multimodal relationships between WM microstructure
593 and coSN functional connectivity was nevertheless consistent across samples. Notably, secondary-
594 fiber microstructure also appeared to explain the between-network functional connectivity
595 differences across samples. Given that depression severity accordingly differed slightly across
596 samples (*See* **Table 1**), we conducted exploratory analysis to determine whether BDI scores might
597 explain the observed differences in secondary fiber microstructure and coSN functional connectivity
598 across samples (*See* **Appendix, Results: Sections D & E**).
599 In sum, our results ultimately showed that WM microstructure predicted 24-26% of the
600 variance in DR in both the discovery and replication samples, with the majority of the contribution
601 from global microstructure of the right SLFT. Between-network functional connectivity of the
602 triple-network alone also collectively predicted twice as much variance in DR (50-52%) in both the
603 discovery and replication samples, however, when controlling for WM microstructure. Furthermore,
604 our multimodal results indicated that microstructural connectivity of the SLFP, CCG, ATR, and
605 Splenium in particular largely accounted for the triple-network functional connectivity disturbances
606 associated with DR. Lastly, post-hoc analysis of replication-level False Discovery revealed a 0.1%
607 chance of all cross-modal replications being false-positives, and $\pi=0.795$ posterior-probability of
608 the replicated large effects, including the ten multimodal findings, being true positives (*See*
609 **Appendix, Results: Section F**).
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DISCUSSION

Overview

The neurobiology of trait Depressive Rumination (DR) is a heterogeneous network phenomenon. Replicated across two independent samples, findings from the present study conceptually converged across multiple dimensions of analysis. On the one hand, we found that compromised resting-state functional connectivity of the brain's 'triple-network' corresponding to self-referential, emotional salience, and attentional engagement processing, forms a functional neural basis for DR. On the other hand, we found that defective global and local frontoparietal White-Matter (WM) pathways confer microstructural risk factors for DR. Aligned without our initial hypotheses, we then observed strong evidence that these microstructural risk factors multimodally perpetuate the trait functional triple-network disorganization that characterizes DR.

Apart from differences in depression severity, discovery and replication samples were importantly matched on key behavioral characteristics: both comprised thirty-nine adults with equivalent measures of DR, similar demographic and inclusion criteria, and corresponding MRI data parameters following resampling procedures (*See* **Appendix, Methods: Sections F & G**). By directly replicating in this way, we created a unique analytic scenario whereby traditional hypothesis testing could be employed to test the generalizability of broader theories beyond individual findings. Principally among the fully-replicated functional connectivity findings, DR severity was negatively associated with within-network intrinsic connectivity of the Precuneal DMN (pDMN) and extrinsic connectivity of the frontal ECN (fECN) with the left Amygdala. DR severity was also negatively associated with a between-network inverse correlation of the pDMN and fECN. On the other hand, DR severity was associated with functional connectivity within the cingulo-opercular SN (coSN) as well as between the coSN and each of the pDMN and fECN; the precise configuration of those relationships differed across samples, however (*See* **Appendix, Results: Sections C & D**).

Microstructurally, DR severity was negatively associated with FA of a temporal section of the right SLFT, a robust finding that replicated across samples. Among the localized WM findings that replicated, we discovered that DR was strongly associated with localized WM clusters of the parietal SLF (SLFP), superior Corona Radiata (SCR), CCG, Corticospinal Tract (CST), Splenium, UF, and Anterior Thalamic Radiation (ATR). DR severity was also positively and negative associated with the microstructure of secondary "crossing" fibers in clusters that were largely localized to key junctures where the aforementioned primary-fiber pathways intersect.

Multimodally, microstructural biomarkers of DR that included global FA of the right SLFT, along with the localized CCG, ATR, and Splenium clusters, predicted the functional connectivity biomarkers of DR, both within and between the pDMN, coSN, and fECN. In contrast, the sample-specific secondary-fiber biomarkers of DR appeared to account for some of the observed variability in coSN functional connectivity across samples, but future studies will be need to confirm this. To our knowledge, this is the first study to show that WM biomarkers of a behavioral measure predict within-network or between-network functional connectivity biomarkers of the same measure.

WM Microstructure and Depressive Rumination

A growing body of literature on the SLF – the WM biomarker found to most robustly track DR severity– suggests that its microstructure is associated with longer and more severe depressive episodes[102]. Deeper insights might be gleaned, however, from the more fine-grained analysis of the SLF conducted using multiple methodologies in the present study. Using both tractography and TBSS, we learned that DR was associated primarily, but not exclusively, with a specific subdivision of the SLF—an inferior portion connecting the middle/superior Temporal Gyrus with ipsilateral prefrontal/cingulo-opercular areas referred to as the SLFT, which most closely corresponds to SLF III – also known as the Arcuate Fasciculus. Neuroanatomically, the SLFT supplies fiber connections between Wernicke's area for speech production and Broca's area for language comprehension. The SLFT is most likely responsible for language communication between the parietal and frontal lobes, and specifically for maintaining phonological awarenes[103,104]. Accordingly, research on the microstructural basis of conduction aphasia has shown that SLFT deficits may be related to poor awareness of speech repetition[105]. In fact, mammals without vocal repetition ability do not have an SLFT[106]. As confirmed through tests of "hemisphericity" in both samples, moreover, microstructural deficits of the SLFT associated with DR were also distinctly right-lateralized. Although further research is needed, studies have begun to indicate that the right SLFT in particular may provide compensatory support for increased demands on language and higher cognitive thought[107,108]. Hence, the DR-associated language deficits of the right SLFT might reflect a lateralization of the WM pathways supporting internal versus external speech. Indeed, cortical areas connected by the right SLFT, such as the right Temporoparietal Junction and right superior Temporal Gyrus, have been implicated in internal speech faculties[9,109,110]. Hence, the SLFT deficits observed in the present study may allude to repetition defects of internal speech, and more broadly, the perseveration of self-referential language of thought[111], as a key maintaining factor for DR[112–114].

TBSS also revealed a strong association between DR and the microstructure of a variety of localized WM clusters throughout the cortex, which highlights the distributed nature of DR as a microstructural connectivity phenomenon. Additionally, the primary-fiber WM biomarkers were largely consistent across samples, which suggests that these microstructural deficits in particular are robust risk-factors for DR. In contrast, the secondary-fiber biomarkers revealed by TBSS were largely variable across samples—a discrepancy that may be related to the interaction between depression severity and DR (*See* **Appendix, Results: Sections D & E**), but will require future studies with larger sample sizes to understand fully.

As our study indicates, these disturbances in WM microstructure manifest both locally (i.e., restricted to distinct clusters of WM) and globally (i.e., across the entirety of neuroanatomically distinct fiber bundles such as the SLF) in DR. Still, it remains unclear whether both primary and secondary WM biomarkers of DR reflect a trait-like vulnerability or develop over the course of extended periods of persistent rumination. In support of the latter possibility, the "perseverative cognition hypothesis"[54] posits that perseverative cognitive processes like rumination lead to a prolonged stress response, which may further impact myelination patterns in both developing and mature brains[115,116]. To the extent that the perseverative cognition of DR involves repetitive cognitive processing, irregular myelination trajectories might accumulate over time in order to sustain the excess cognitive load inflicted by DR.

Within-Network Functional Connectivity and Depressive Rumination

The results from our functional connectivity analyses broadly implied that disrupted integration and segregation of self-referential and cognitive control systems are associated with DR. These patterns were firstly observed in the form of disrupted intrinsic and extrinsic functional connectivity within each of the triple-network RSN's.

pDMN

The association between DR and functional connectivity within the pDMN was characterized by two core features: 1) lower intrinsic connectivity with the right Precuneus; and 2) lower extrinsic connectivity with the left Somatosensory Cortex, left inferior Frontal Gyrus, and left Precentral Gyrus. Broadly speaking, diminished Precuneal integration with the DMN may reflect impaired inhibition of internal mentation, particularly given the role of the Precuneus as a core parietal hub for maintaining conscious self-awareness[117]. Conversely, greater segregation from frontal cognitive control modules and somatosensory areas in DR may indicate globally dysregulated self-referential processing that may also be detached from sensory experience[20,118,119].

710 *fECN*

711 Higher DR severity was also associated with greater extrinsic functional connectivity
712 between the fECN and the left Amygdala – a finding that replicated closely across samples and
713 might be explained in a number of ways. One interpretation stems from the premise that DR might
714 be construed as maladaptive coping strategy for avoiding the negative affective states experienced
715 in depression. For example, severe ruminators might repetitively reflect on their own cognitions as a
716 short-term attempt to ward off negative affect, but at the cost of maintaining a dysphoric mood in
717 the long term[13,92]. If DR were to accordingly operate *as though* it were adaptive, we might therefore
718 expect that it be accompanied by higher fECN-amygdala functional connectivity as a self-regulatory
719 measure[120]. This explanation also aligns with our multimodal findings that indicated that the
720 microstructure of the right SLFT may, to a certain extent, reinforce this pattern in a perseverative
721 manner. Nevertheless, functional connectivity of the fECN, in particular, proved to be the least
722 susceptible triple-network RSN to the impact of WM microstructure.

723 *coSN*

724 DR was also associated with functional connectivity of the coSN, and particularly with
725 clusters corresponding to Broca's area bilaterally. Although anatomically consistent across samples,
726 the direction of the relationship with DR and the specific sub-regions of Broca's area implicated
727 differed across samples. As one explanation for this discrepancy, emerging research offers a
728 compelling case that Broca's area has two distinct functional subunits: the first supports selective
729 language comprehension and the second is responsible for domain-general cognition[121]. Whereas the
730 selective language sub-region activates upon the presentation of salient semantic information, the
731 domain-general sub-region activates during more demanding multi-tasking scenarios. Not only can
732 these sub-regions operate more or less independently in response to multiple demands, their precise
733 anatomical boundaries appear to vary considerably across individuals[121,122]. Consequently, the
734 variable functional connectivity between the coSN and each of these versatile sub-regions might
735 indicate two potential "routes" to DR—excessive negative salience tagging of inner speech and/or
736 deficient positive salience toward reflective problem-solving. Accordingly, the multimodal findings
737 of the present study indicated that global microstructural deficits of the right SLFT predicted both of
738 these cases. Supportively, our exploratory tractography also revealed that the SLFT fibers actually
739 terminated in the vicinity of these coSN clusters in the majority of subjects.

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742 ***Between-Network Functional Connectivity and Depressive Rumination***

743 Upon discovering spatially-overlapping patterns of aberrant extrinsic functional connectivity
744 among the triple-network RSNs, we further found that DR was associated with patterns of between-
745 network functional connectivity. Specifically, higher DR severity was associated with greater
746 inverse correlation between the pDMN-fECN in both discovery and replication samples, greater
747 inverse correlation between the coSN-pDMN in the discovery sample, and greater direct correlation
748 between the coSN-fECN in the replication sample.

749 *pDMN-fECN*

750 Not only did the pDMN-fECN findings replicate those of prior work[29,50], they also replicated
751 across both our initial and replication samples. Ultimately, this finding in particular underscores a
752 highly consistent pattern of antagonism between self-referential and cognitive control systems as a
753 defining feature of DR[103]. Since the pDMN is functionally coupled with the hippocampus during
754 memory retrieval[123], a greater pDMN-fECN inverse correlation associated with higher DR severity
755 could reflect a failure to regulate the episodic memory refreshing that is believed to occur during
756 self-referential processing[124]. More broadly, however, greater DMN-ECN coupling likely occurs
757 during task-related autobiographical planning[125]—a pattern that would appear to be antithetical to
758 DR. Ergo, greater pDMN-fECN inverse correlation associated with DR might conversely implicate
759 the decoupling of cortical midline hubs such as the PCC and ACC, whose synchrony is likely vital
760 to steering self-referential thought in the service of goal-directed cognition[46,104]. When the
761 integration and segregation patterns of these hubs become desynchronized, negatively-biased
762 internal mentation may in turn become increasingly difficult to regulate[50].

763 As with the multimodal relationships discovered when exploring each triple-network RSN
764 separately, tractography also revealed that right SLF microstructure alone predicted the pDMN-
765 fECN inverse correlation in both samples. This finding was surprising, given that the CCG also
766 supplies direct WM connections between ACC and PCC hubs of both networks. Nevertheless, a
767 recent study found that a disrupted SLF microstructure precluded efficient information transfer
768 between frontoparietal networks in hypertension patients[126]. In fact, the right SLF
769 neuroanatomically supplies lateral frontoparietal WM connections that could very well impact
770 pDMN-fECN synchronization patterns beyond the influence of more 'direct' cortical midline WM
771 pathways[52,127,128].

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774 *coSN-pDMN and coSN-fECN*

775 Given that the SN is important for switching attention between externally and internally
776 salient stimuli[46,127], it is also known to interact with the DMN and ECN across contexts[52,127,128].
777 Accordingly, our findings indicated that abnormal between-network relationships with the pDMN
778 and fECN may confer variable risks for DR. As in the case of our within-network connectivity
779 findings, however, between-network connectivity patterns of the coSN also varied across samples,
780 which prevents us from forming hard interpretations about its precise role in DR (*See* **Appendix,**
781 **Results: Sections C, D, & E** *for exploratory analyses*). Interestingly, Hamilton et al. (2011)
782 observed a similar pattern of direction reversal with respect to the association DR severity and
783 between-network activation patterns of the SN as a function of depression severity[50]. Specifically,
784 their state-change analysis showed that relative to healthy controls, depressed participants displayed
785 increased SN activation at the onset of increases in ECN activation relative to the DMN; in contrast,
786 healthy controls exhibited increased SN response at the onset of increases in DMN activation
787 relative to the ECN. Thus, prior evidence suggests that we should expect variable directionality in
788 the relationship between DR severity and the SN's connectivity profile among the triple-network
789 RSN's. Along these lines, coSN-fECN and coSN-pDMN between-network functional connectivity
790 patterns proved to be clearly involved in DR, since they were also associated with localized deficits
791 of the right medial SLFT – a multimodal finding that *was* consistent across samples.

792 ***Limitations and Generalizability***

793 One limitation of the present study may be that the neural biomarkers that it uncovered are
794 not purely attributable DR. Given how closely the theoretical constructs of DR and depression
795 severity are intertwined[80,129], however, there are fundamental theoretical and statistical obstacles to
796 establishing specificity of DR biomarkers in this context. Nevertheless, the majority of participants
797 included in our replication sample were dysphoric and/or depression-remitted, thereby enabling us
798 to at least infer that the replicated DR biomarkers are reproducibly observable across multiple
799 depressive disorder subtypes and at varying levels of depression severity.

800 By validating our initial findings with a replication sample, our study not only has the
801 advantage of contributing verifiably generalizable biomarkers to the larger corpus of depressive
802 rumination literature, it has the unique advantage of contributing verifiable theoretical *models* as
803 well. Specifically, our study proposes a unified view of DR's neural pathophysiology that is both
804 sensitive to multiple network functional connectivity mechanisms and conditional on
805 microstructural connectivity risk factors[85,130,131]. Although twenty findings replicated fully or

806 partially, almost half of our findings did not. On the one hand, that level of discrepancy across
807 samples echoes often-cited concerns regarding reproducibility when working with sub-optimal
808 sample sizes[132,133]. On the other hand, those findings that did fully-replicate consisted only of large
809 effects that were sufficiently powered to generalize as such. And despite unavoidable limitations on
810 the interpretability of the discovered smaller effects, reported here only in supplement, the large
811 effects included ten multimodal relationships that fully replicated across samples. Thus, regardless
812 of sample size, one inalienable fact is clear—the neurobiology of trait rumination has a network
813 connectivity basis that is jointly structural and functional in nature.

814 **CONCLUSION**

815 In the present study, we aimed to identify functional and microstructural connectivity
816 biomarkers of Depressive Rumination (DR), which we achieved in the form of twenty fully
817 replicated findings across two independent samples. Our results from both datasets demonstrated
818 that DR severity is associated with disorganized patterns of within-network and between-network
819 functional connectivity of the 'triple-network', comprising the pDMN, coSN, and fECN. Further,
820 DR severity is associated with microstructural dysconnectivity in the form of global WM deficits of
821 the right Superior Longitudinal Fasciculus, along with deficits in localized primary-fiber and
822 secondary-fiber WM clusters distributed throughout the cortex. Perhaps most strikingly, however,
823 these WM biomarkers multimodally predicted the abnormal functional connectivity patterns of the
824 triple-network. Collectively, our findings corroborate our initial hypotheses and imply that
825 emotionally dysregulated self-referential processing, perpetuated by inefficient attentional and
826 language pathways, confers a set of multidimensional risk factors for trait DR.

827 Supported by initial discovery and replication, our study significantly unifies and extends
828 research on the neurobiological substrates of trait rumination in depression by contributing a new
829 framework for its etiological interpretation. Ultimately, we demonstrate that neural
830 pathophysiological models of trait DR are fundamentally multivariate, and should not, therefore, be
831 reduced to singular or unimodal mechanisms as the field progresses. Rather, a precise and
832 reproducible neurobiology of DR implores 'rethinking' it as a multimodal system of joint
833 microstructural-functional triple-network brain mechanisms, whose whole is greater than the sum of
834 its parts.
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ACKNOWLEDGMENTS

The authors would first like to thank the technical staff at the Texas Advanced Computing Center (TACC) for supplying the computational resources and consulting that would have otherwise rendered our neuroimaging analyses computationally intractable. We would also like to thank Ryan Hammonds for assistance with quality control of neuroimaging data. Additionally, the first author would also like to thank Ari Cohen for her incredible patience and support throughout drafting of the manuscript.

FUNDING

This work was supported by the R21 MH092430 award to Christopher G. Beevers.

COMPETING INTERESTS

We wish to confirm that there are no known conflicts of interest associated with this manuscript and there has been no significant financial support for this work that could have influenced its outcome.

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