

# Differences in optimal community structure in brain connectivity organization in major depressive disorder

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**Abstract**—We analyzed fMRI data from healthy control subjects (94 subjects) and patients with major depressive episode (70 patients). The preprocessed activity signals extracted with statistical parametric mapping from fMRI were divided into parcellations according to the anatomical labeling atlas. Our findings indicate that patients with major depressive disorder exhibit network organization that is both less locally specialized and less globally integrated. Specifically, our research reveals differences in network segregation rather than integration in patients. The discrepancies between our results and previous studies may be attributed to differences in methodology, depression diversity, sample sizes, and co-occurring factors such as stress and anxiety.

**Index Terms**—fMRI; functional analysis; brain networks; connectivity; optimal community analysis; major depressive disorder;

## I. INTRODUCTION

Integrating the concepts of brain functional networks and complex network theory offers a potent tool for studying brain processes in both healthy individuals and those with various pathologies [1]–[3]. Brain functional connectivity networks refer to statistical associations between neural activities in distinct and distant brain regions [4], [5]. The inherent properties of brain functional networks can pose challenges in applying and analyzing them using traditional statistical [6], [7] and machine learning methods [7], [8].

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The field of psychiatry faces a significant challenge in producing nomothetic networks that represent standard cognitive structures within the medical discipline. Our research contributes to this cross-disciplinary effort by providing results that can be integrated into larger-scale nomothetic networks [9]–[11].

## II. SUBJECTS AND EXPERIMENTAL SETUP

We recruited a total of 164 participants for the study, divided into two groups: 94 healthy individuals without known psychiatric conditions (the Healthy Controls, HC group) and 70 patients diagnosed with major depressive disorder (the MDD group). Each participant underwent thorough evaluations led by experienced psychiatrists, which included the administration of the Mini International Neuropsychiatric Interview [12] and the Montgomery–Åsberg Depression Rating Scale (MADRS) [13], [14]. Exclusion criteria for both groups comprised a history of comorbidities, autoimmune diseases, neurological disorders, prior head trauma, or the presence of metal implants incompatible with MRI procedure.

The MR scanning process was carried out on a 3T MRI system the GE Discovery 750w model with the same parameters as in the Refs. [9], [15].

The data were preprocessed using the SPM12 statistical software package [16]. The preprocessing procedure involved three main steps: motion correction, co-registration of structural data, and normalization to the Montreal Neurological Institute (MNI) standard space. To calculate the connectivity

between diverse brain regions, we computed and detrended the average time series for each node included in the Automated Anatomical Labeling (AAL3) atlas [17].

### III. METHODS AND RESULTS

To assess the connectivity between the regions of interest, we calculated the average BOLD time series  $x_i(t)$  (across voxels in each parcellation  $i$ ) and the corresponding metrics for all pairs of average activities of each region. The analysis of the relationship between the sequence was based on the established Pearson's correlation.

To analyze the topology and larger-scale features of the functional network, we calculated the network measure of optimal community structure [18]. T-test between the groups (HC>MDD) on the communities structure revealed difference close to the significant:  $T_{2,165} = 1.9097$ ,  $p = 0.0579$ . The distributions of communities across nodes are presented in the Fig. 1 and Fig. 2.

We did not use any initial community affiliation vector and used the Louvain community detection algorithm with the resolution parameter was set to 0.05, objective function type or custom objective matrix was set to symmetric treatment of negative weights [19]. For the network calculations we used the Brain Connectivity Toolbox [20].

To assess the similarity between the considered subnetwork and the large-scale brain network, we calculated the ratio of shared nodes between them to the total number of nodes in the large-scale network. This yielded the percentage of similarity between the two networks. The composition of nodes (brain regions) included in the large-scale brain networks was determined based on a literature review [21]–[23]. Difference in the correspondence of community nodes belonging to the large scale networks are following:

- Default Mode Network MDD>HC 20%;
- Central Executive Network HC>MDD 20%;
- Dorsal Attention Network — no difference;
- Salience Network HC>MDD 66%.

Analysis of the optimal community networks revealed that Healthy Controls (HC) tended to have greater Central Executive Network (CEN) and Salience Network (SN) overlap, while Major Depressive Disorder (MDD) demonstrated more overlap with the Default Mode Network (DMN).

### IV. CONCLUSIONS

Our analysis revealed that Major Depressive Disorder (MDD) patients exhibited reduced correspondence to the salience and executive networks, suggesting a less specialized local network organization and impaired global integration. Conversely, we did not find significant differences between the global efficiency of MDD patients and healthy controls. We interpret this to indicate that the divergence lies in network segregation rather than integration. Possible explanations for these distinctive findings may include differences in methodological approaches, MDD variability, sample sizes, and comorbidities, such as stress and anxiety. Conversely, we observed significant

overlap with Default Mode Network (DMN) nodes in the consensus networks specific to MDD patients. The DMN is often implicated in self-referential thoughts and rumination, which are common in depressive states.

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