



# Schizophrenia Identification Using Multi-View Graph Measures of Functional Brain Networks

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Schizophrenia (SZ) is a functional mental disorder that seriously affects the social life of patients. Therefore, accurate diagnosis of SZ has raised extensive attention of researchers. At present, study of brain network based on resting-state functional magnetic resonance imaging (rs-fMRI) has provided promising results for SZ identification by studying functional network alteration. However, previous studies based on brain network analysis are not very effective for SZ identification. Therefore, we propose an improved SZ identification method using multi-view graph measures of functional brain networks. Firstly, we construct an individual functional connectivity network based on Brainnetome atlas for each subject. Then, multi-view graph measures are calculated by the brain network analysis method as feature representations. Next, in order to consider the relationships between measures within the same brain region in feature selection, multi-view measures are grouped according to the corresponding regions and Sparse Group Lasso is applied to identify discriminative features based on this feature grouping structure. Finally, a support vector machine (SVM) classifier is employed to perform SZ identification task. To evaluate our proposed method, computational experiments are conducted on 145 subjects (71 schizophrenic patients and 74 healthy controls) using a leave-one-out cross-validation (LOOCV) scheme. The results show that our proposed method can obtain an accuracy of 93.10% for SZ identification. By comparison, our method is more effective for SZ identification than some existing methods.

**Keywords:** Schizophrenia identification, fMRI, functional brain networks, multi-view graph measures, SVM

## 1. INTRODUCTION

Schizophrenia (SZ) is a functional mental disorder which caused by genetic factors and environmental effects. Patients with SZ (SZs) share some common symptoms which include depression, hallucinations, cognitive dysfunction and disorganized thinking (Marín, 2012). Impairments of this disorder cover multiple cognitive areas, including memory (He et al., 2012), attention and executive function (Heinrichs and Zakzanis, 1998). One percent of the population is affected by the serious psychiatric disease worldwide (Ripke et al., 2013). The clinical diagnosis of SZ relies mainly on mental state examination rather than any biomarker (Arbabshirani et al., 2013; Liu et al., 2017d) since the cause and mechanism of the disease are not clearly revealed. However, this diagnosis method is usually subjective and not completely effective. Therefore, it is urgent to find an objective method to realize the automatic diagnosis of SZ and improve the accuracy of recognition.

Nowadays, Magnetic resonance imaging technology has been widely used in various studies related to brain disease diagnosis (Nieuwenhuis et al., 2012; Liu et al., 2016, 2017b,c, 2018a; Yang and Wang, 2018). Since SZ is reported to be a functional disease, functional magnetic resonance imaging (fMRI) is increasingly used to study brain dysfunction in patients with mental illness (Castro et al., 2011; Huang et al., 2018; Liu et al., 2018b; Moghimi et al., 2018; Chen et al., 2019). In addition, fMRI provides a database for functional analysis of these brain diseases owing to its massive spatial and temporal information.

In recent years, the number of neurobiological literatures using fMRI to study SZ disease has increased significantly. fMRI is usually applied to discover anomalous patterns present in activation maps [i.e., Regional Homogeneity (REHO), Amplitude of Low Frequency Fluctuations (ALFF), fractional Amplitude of Low Frequency Fluctuations (FALFF)] (Guo et al., 2014; Chyzyk et al., 2015; Huang et al., 2018) of SZ. These activation maps are widely used as potential clinical biomarkers for the diagnosis of SZ. For example, Huang et al. (2018) used tree-guided group sparse learning method to perform feature selection on fALFF data in multi-frequency bands, and then used multi-kernel learning (MKL) method to achieve an accuracy of 91.10% on 34 subjects. Chyzyk et al. (2015) combined these activation maps by using extreme learning machines and successfully distinguished SZs from healthy controls (HCs). However, these methods focus on the voxel-wise information in these maps rather than the connectivity between regions of interest (ROIs).

Functional connectivity has been reported to analyze the differences in the functional organization of brain networks between patients and HCs (Lynall et al., 2010; Pettersson-Yeo et al., 2011). Functional connectivity networks are usually derived from fMRI data (Van Den Heuvel and Pol, 2010; Craddock et al., 2013). Nodes of a functional brain network could be the voxels of fMRI data, ROIs defined by brain atlas or the discrete regions with similar size by randomly parcellating the brain (Fornito et al., 2013). Links of a functional brain network could be determined by the correlations estimated from time courses between pairs of nodes (Liu et al., 2017a). For example, Yu et al. (2015) created functional brain network using group ICA and Pearson correlation coefficient, and they found the new evidence about altered dynamic brain graphs in SZ. Abraham et al. (2017) investigated the most predictive biomarkers for Autism spectrum disorders (ASD) by building participant-specific connectomes from functionally-defined brain areas. For these methods, the connections between all pairs of nodes in a brain network are employed as features, but the topological measures of connectivity networks are not considered.

To quantitatively analyze functional brain networks, graph theoretical analysis is employed for investigating the topological organization of functional connectivity (Anderson and Cohen, 2013; Brier et al., 2014). The most commonly used graph measures include betweenness centrality, degree, local efficiency, participation coefficient, average clustering coefficient, average path length, global efficiency, and small-worldness (Liu et al., 2017a). These topological measures have been applied in the brain disease classifications (Cheng et al., 2015; Khazaei et al., 2015, 2017; Moghimi et al., 2018). For example, Moghimi et al.

(2018) calculated a set of 25 graph measures including global and local measures for each subject and obtained a classification accuracy of 80% with a double-cross validation scheme. Cheng et al. (2015) achieved an accuracy of 79% by using betweenness centrality measure in SZ identification, and they found that changes in functional hubs were associated with SZ. Overall, these methods using graph measures for SZ identification have not achieved a good classification performance.

In this paper, we propose an improved method based on multi-view graph measures to identify SZs from HCs. Functional brain networks are constructed based on fMRI scans. Nodes of functional brain network are brain regions parcellated with the Brainnetome atlas (Fan et al., 2016), and edges of functional brain networks are determined by Pearson's correlation coefficients. Five local graph measures are calculated from functional brain networks by graph theoretical approach as features. The five local graph measures include betweenness centrality, nodal clustering coefficient, local efficiency, degree and participation coefficient. In order to consider the relationship of features within the same region, firstly we need to group graph measures according to brain regions defined by Brainnetome atlas. Then Sparse Group Lasso feature selection method is employed to select the most important regions as well as discriminative features within the selected regions. Finally, support vector machine (SVM) is trained for SZ identification. Our experiments are conducted on 145 samples with fMRI data, including 74 HCs and 71 SZs. Our proposed method achieves a mean classification accuracy of 93.10% using a leave-one-out cross-validation (LOOCV) scheme. The overall framework of our proposed method is shown in **Figure 1**, which consists of four main components include image preprocessing, feature representation, feature selection, and classification with SVM classifier. The code for this classification framework is available for download at <https://github.com/xyxzj/SZClassification>.

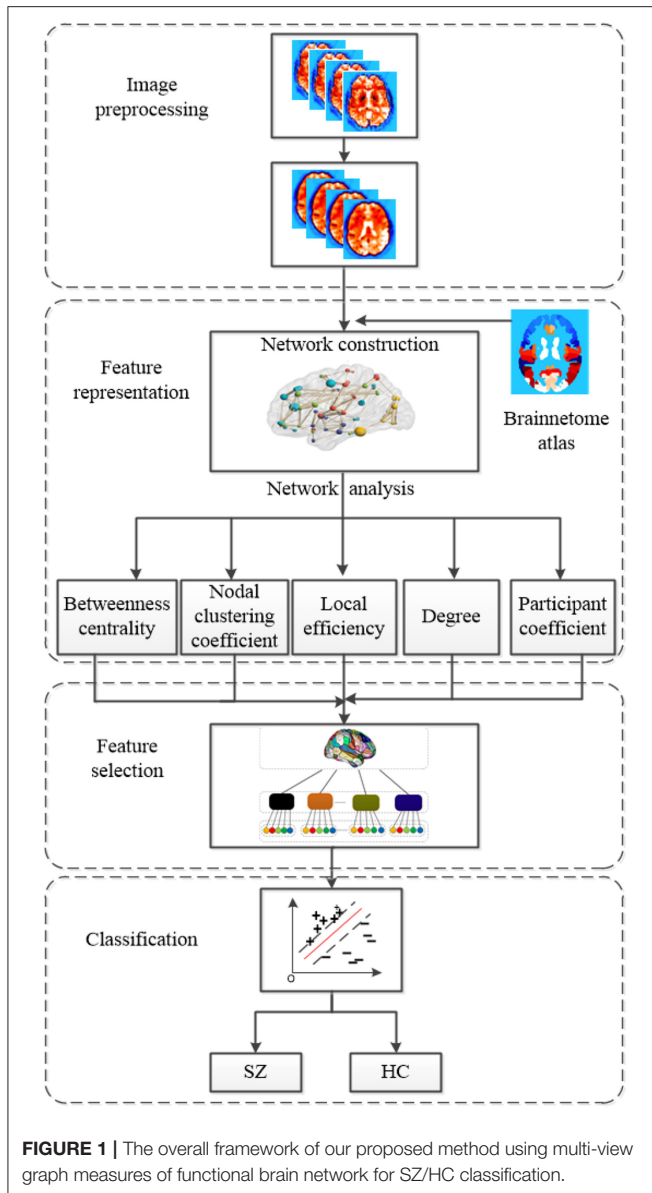
## 2. MATERIALS AND METHODS

### 2.1. Subject Description and Image Preprocessing

The data involved in this study is collected by the Center for Biomedical Research Excellence (COBRE). COBRE<sup>1</sup> dataset consists of 148 subjects with functional and anatomical MRI data. 74 HCs and 71 SZs of the dataset are employed for our subsequent experiments owing to the class labels of the other three subjects are not given. During the scan, all participants are asked to remain relaxed and keep their eyes open. A brief summary of demographic information of subjects is listed in **Table 1**.

All of the fMRI images are preprocessed by using Data Processing & Analysis for Brain Imaging (DPABI) (Yan et al., 2016). The preprocessing procedure is as follows: the first 10 volumes of functional runs are removed owing to the fMRI signal instability. Then, the rest volumes are performed slice time correction, head-motion correction, and co-registration of T1-weighted MRI images and fMRI images. After that, the fMRI images are normalized to Montreal Neurological Institute (MNI)

<sup>1</sup>[http://fcon\\_1000.projects.nitrc.org/indi/retro/cobre.html](http://fcon_1000.projects.nitrc.org/indi/retro/cobre.html)



space and resampled to  $3 \times 3 \times 3 \text{ mm}^3$  voxels. Smooth (4-mm FWHM) and band-pass filter (0.01–0.1Hz) are applied to the images which are transformed to MNI space.

In order to construct time series matrices for all subjects, first all brain images are parcellated into 246 regions by registering images to the Brainnetome atlas after fMRI data preprocessing. Then we extract the averaged time series for each of 246 brain regions for each subject. The time series of each brain region is derived from averaging fMRI signals of all voxels within the region. Finally, a time series matrix consists of 246 regional time series.

## 2.2. Feature Representation

### 2.2.1. Brain Network Construction

A network is composed of a collection of nodes and links. It can be described as a graph  $G = (V, E)$ , where  $V$  denotes

**TABLE 1** | Demographic information of 145 subjects from COBRE dataset.

| Type | Number | Age             | Gender (M/F) |
|------|--------|-----------------|--------------|
| SZ   | 71     | $38.1 \pm 13.9$ | 57/14        |
| HC   | 74     | $35.8 \pm 11.5$ | 51/23        |

the set of nodes and  $E$  is the set of links. There are four types of network topology, including weighted undirected, weighted directed, binary undirected and binary directed. In this study, the functional connectivity network is represented by an weighted undirected graph. The nodes in functional connectivity network usually are defined by brain regions, and links can represent temporal correlation in activity between pairs of nodes. Given a time series matrix, we can construct a functional connectivity network by calculating Pearson correlation coefficients (Pedersen et al., 2018) between signals of all pairs of regions. The generated functional brain network has  $246 \times (246 - 1)/2 = 30,315$  weighted edges under the condition of 246 brain regions and the strength of each edge is the Pearson correlation coefficient between a pair of connected nodes.

### 2.2.2. Brain Network Analysis

A great deal of functional connections in the network may lead to feature redundancy. A threshold  $t$  is employed in the dense network to keep a certain proportion of edges with the highest correlation. Graph-theoretic measures can quantify topological organization of network. Thus, we can extract some measures which can characterize the global or local functional connectivity from the threshold network. We compute 5 local graph measures using brain network analysis as feature representations, including degree, betweenness centrality, nodal clustering coefficient, local efficiency, and participation coefficient.

Degree is the most fundamental and important measure to characterize the centrality of nodes. In general, nodes with a higher degree are more important in networks. Betweenness centrality can also reflect the centrality of nodes. The betweenness centrality of a brain region can measure its ability on information transmission. Nodal clustering coefficient represents the possibility that any two neighbors of a given node are also neighbors of each other. It measures the ability of the node on functional segregation. Local efficiency measures the efficiency of a subnetwork formed by a given node and all its direct neighbors to transfer information. Local efficiency is related to the shortest path length of the node, the shorter the shortest path length, the greater the local efficiency of the node, the faster the information transmission in the subnetwork. Participation coefficient of a node measures its diversity of intermodular interconnections. The nodes with low participation coefficient but high degree in the module are regarded as provincial hubs, it indicates that the hubs are likely to have a great impact on the modular segregation. These five local measures play an important role in information exchange of functional networks. They can be calculated as follow:

$$K(i) = \sum_{j \in N} a_{ij} \quad (1)$$

$$B(i) = \frac{1}{(N-1)(N-1)} \sum_{m \neq j \neq i} \frac{n_{mj}(i)}{n_{mj}} \quad (2)$$

$$C(i) = \frac{2sw_i}{(K_i(K_i-1))} \quad (3)$$

$$E_{loc}(i) = \frac{1}{N_{G_i}(N_{G_i}-1)} \sum_{j \neq h \neq G_i} \frac{1}{l_{jh}} \quad (4)$$

$$PC(i) = 1 - \sum_{m \in M} \left( \frac{k_i(m)}{k_i} \right)^2 \quad (5)$$

where  $K(i)$ ,  $B(i)$ ,  $C(i)$ ,  $E_{loc}(i)$ , and  $PC(i)$  are the degree, betweenness centrality, clustering coefficient, local efficiency, and participation coefficient of node  $i$ , respectively.  $N$  is the number of nodes in a network,  $a_{ij} = 1$  if node  $i$  and node  $j$  are connected,  $a_{ij} = 0$  otherwise;  $n_{mj}(i)$  is the number of shortest paths between  $m$  and  $j$  that pass through node  $i$ , and  $n_{mj}$  is the number of shortest paths between  $m$  and  $j$ ;  $sw_i$  is the sum of the weights of all the connected edges between the neighbors of node  $i$ ;  $G_i$  is the subnetwork that contains node  $i$  and its all direct neighbors,  $N_{G_i}$  is the number of nodes in the subnetwork  $G_i$ ,  $l_{jh}$  is the length of shortest path between node  $j$  and node  $h$  in the subgraph;  $M$  denotes the set of modules,  $k_i$  is determined as the number of links between  $i$  and the nodes within module  $m$ .

In this study, we adopt the Brain Connectivity Toolbox (<http://www.brain-connectivity-toolbox.net>) (Rubinov and Sporns, 2010) to calculate these five local graph measures. For each local graph measure (gm), we compute 246 values corresponding to the 246 brain regions. Therefore, the dimension of the final feature vector for each subject is 1,230.

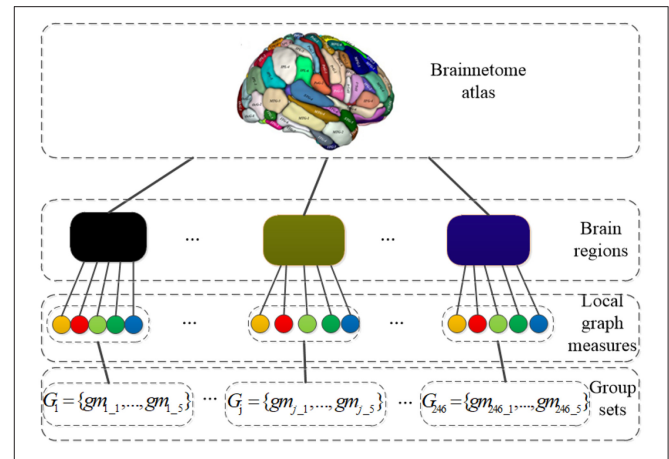
### 2.3. Feature Selection

The raw feature matrices have high dimension, multiple redundancy and multi-noise characteristics. Thus, applying a suitable feature selection algorithm to identify features related to SZ/HC identification and remove unnecessary information appears especially important. Least absolute shrinkage and selection operator (Lasso) (Chan et al., 2015) is widely used in various areas due to the very low data requirements. In addition, lasso can filter variables and reduce the complexity of the model. It aims to select the most important features from dense data matrix by using  $l_1$  norm constraint. The optimization problem can be formulated as follow:

$$\min_{\alpha} \|y - X\alpha\|^2 + \lambda_1 \|\alpha\|_1 \quad (6)$$

where  $X$  denotes an  $n \times p$  feature matrix, and  $n$  is the number of subjects,  $p$  represents the dimension of a feature vector.  $y$  is defined as a class label,  $\alpha$  is a coefficient vector, and  $\lambda_1$  is a regularization parameter.

Graph measures within the same region usually have a certain correlation. However, Lasso has not consider the relationship between graph measures derived in the same brain region. Hence we use the priori information of brain regions to group measures and then perform feature selection based on this feature grouping structure. Group Lasso (GLasso) (Yuan and Lin, 2006), a group variable selection method, is the extension of Lasso. It can select



**FIGURE 2 |** The grouping structure: the nodes in the third layer represent local graph measures and the blocks in the second layer represent brain regions;  $G_j = \{gm_{j_1}, \dots, gm_{j_5}\}$  is a group set which consists of 5 local graph measures calculated for  $j$ -th region.

the most important groups by grouping all the variables and penalizing the  $l_2$  norm of each group. The effect is that we can eliminate the entire set of coefficients into zero at the same time and then this set of features are excluded. The objective function of GLasso is as follow:

$$\min_{\alpha} \|y - X\alpha\|^2 + \lambda_2 \sum_{j=1}^M w_j \|\alpha_{G_j}\|_2 \quad (7)$$

where  $\alpha_{G_j}$  denotes the set of coefficients of all features in the group  $G_j$ ,  $w_j$  is a weight for group  $G_j$ .

Actually, there are also many redundant features in the important groups selected by GLasso. It is necessary to perform another feature selection to choose the most important features from these selected groups. Sparse Group Lasso (SGLasso) (Liu et al., 2009) is introduced to select the most significant groups as well as the discriminative features within the selected groups by adding  $l_1$  and  $l_2$  penalties. The objective function of the SGLasso can be written as:

$$\min_{\alpha} \|y - X\alpha\|^2 + \lambda_1 \|\alpha\|_1 + \lambda_2 \sum_{j=1}^M w_j \|\alpha_{G_j}\|_2 \quad (8)$$

Before performing SGLasso, 1230-dimensional feature vector for each subject is grouped as  $G = \{G_1, \dots, G_j, \dots, G_M\}$  according the brain regions defined by Brainnetome atlas.  $M$  is the number of groups.  $G_j = \{gm_{j_1}, gm_{j_2}, gm_{j_3}, gm_{j_4}, gm_{j_5}\}$  is a group consists of 5 local graph measures calculated for  $j$ -th region. The grouping structure is shown in **Figure 2**. In addition, z-score transformation is used to normalize the feature matrix before feature selection. It is worth noting that, after feature selection, those features are kept with corresponding regression coefficients greater than the mean value of absolute values of all elements in coefficient vectors.

## 2.4. Classification

SVM (Chang and Lin, 2011) is widely applied in various fields such as natural language processing, target detection, pattern classification due to its good performance as a supervised machine learning approach. The choice of SVM kernel functions is critical to their performance. In this study, we choose the linear kernel SVM (LSVM) to identify SZs from HCs. Linear kernel is mainly used in linear separability cases, and the dimension of the feature space and input space is the same. It performs good classification in most linear separable problems owing to the less parameters and fast calculation. The formulation of SVM model and linear kernel function are as follows:

$$\max_{\lambda} -\frac{1}{2} \sum_{i=1}^N \sum_{j=1}^N \lambda_i \lambda_j y_i y_j K(x_i, x_j) + \sum_{i=1}^N \lambda_i \quad (9)$$

$$\begin{aligned} \text{s.t. } & \sum_{i=1}^N \lambda_i y_i = 0 \\ & 0 \leq \lambda_i \leq C, i = 1, 2, \dots, N \\ & K(x_i, x_j) = \langle x_i, x_j \rangle \end{aligned} \quad (10)$$

where  $\lambda$  is the Lagrange multiplier,  $N$  is the number of samples,  $x_i$  represents the feature vector of the  $i$ -th sample, and  $y_i$  is the label corresponding to  $x_i$ ,  $K(\cdot, \cdot)$  denotes the kernel function,  $C$  is determined as the soft margin parameter.

After feature selection, the optimal feature set  $X = \{x_1, \dots, x_i, \dots, x_n\}$  is used as the input to SVM classifier,  $i = 1, \dots, n$ . Giving a test subject  $x$ , the trained SVM will predict its label based on a decision function  $P(x)$  as follows:

$$P(x) = \text{sign}\left(\sum_{i=1}^N \lambda_i y_i K(x_i, x)\right) \quad (11)$$

## 3. EXPERIMENTS AND RESULTS

### 3.1. Experiment Settings

In our study, the classification performance of our proposed method is estimated by adopting LOOCV scheme. LOOCV scheme is not affected by the random sample partitioning because  $n$  samples are only divided into  $n$  subsets in a unique way, each subset contains one sample. Each subset will be tested as a test data in turn while remaining subjects as the training data. In addition, we usually adopt the LIBSVM library (Chang and Lin, 2011) to solve SVM classification. We further calculate classification accuracy (ACC), sensitivity (SEN), specificity (SPE) to measure the performance of the method. These three metrics can be written as follows:

$$ACC = \frac{TP + TN}{TP + FP + FN + TN} \quad (12)$$

$$SPE = \frac{TN}{TN + FP} \quad (13)$$

$$SEN = \frac{TP}{TP + FN} \quad (14)$$

where true positive (TP), true negative (TN), false negative (FN), and false positive (FP) are defined as the number of correctly classified SZs, HCs and misidentified SZs, HCs, respectively.

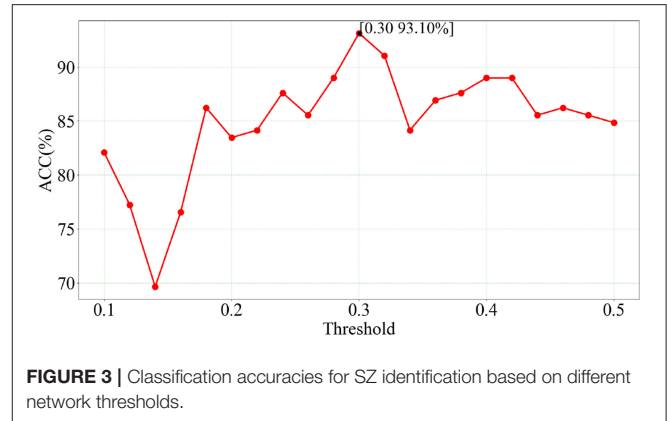


FIGURE 3 | Classification accuracies for SZ identification based on different network thresholds.

In addition, the area under receiver operating characteristic (ROC) curve (AUC) is also used to evaluate overall classification performance of our method.

At the stage of feature representation, we set  $t = [0.1, 0.12, \dots, 0.48, 0.5]$  to represent a collection of threshold values from 0.1 to 0.5 by the step of 0.02, and then calculate the 5 local graph measures at these 21 thresholds. The two regularization parameters for SGLasso are set as  $\lambda_1 = [1, 2, 3, 4, 5, 6, 7, 8, 9, 10]$  and  $\lambda_2 = [0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0]$ , which are optimized with the grid search algorithm.

### 3.2. Identification Performance for SZ

We use LSVM to perform SZ/HC classification on the optimal feature set obtained from feature selection of SGLasso at each of 21 thresholds. The classification results corresponding to 21 thresholds are showed in Figure 3.

According to Figure 3, we can see that the best accuracy (93.10%) is achieved at  $t = 0.30$ . Furthermore, the classification accuracies at these 21 thresholds are all higher than 70%. In addition, the number of selected features is 55 and SEN, SPE, AUC values are 92.96%, 93.24%, 0.950, respectively. The experimental results indicate that the feature combination of five local measures extracted at  $t = 0.30$  has a relatively strong correlation with SZ identification.

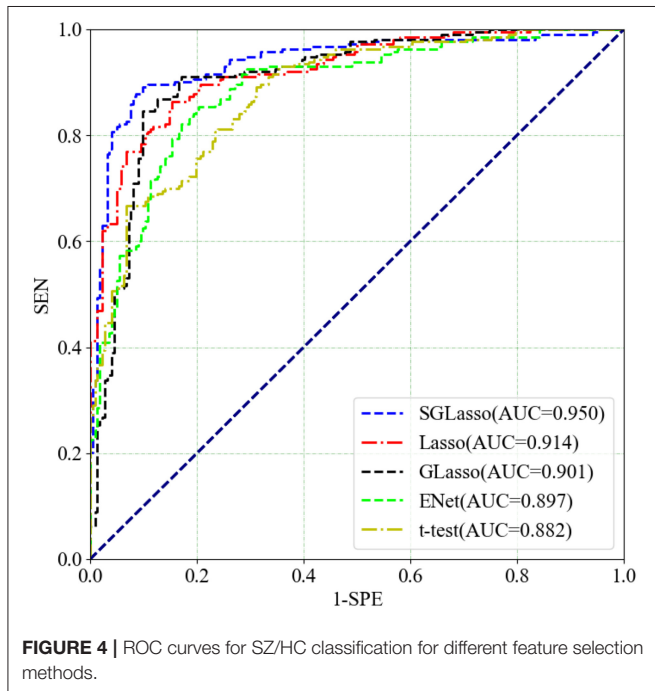
## 4. DISCUSSION

### 4.1. Comparison With Different Feature Selection Methods

In order to demonstrate the SGLasso method is more effective than the common feature selection methods based on these five local measures for SZ classification, we compare four feature selection methods. The first one is  $t$ -test which is the one of the most basic feature selection method and the most critical part of this method is selecting features based on the  $p$ -value (i.e., 0.05). The rest methods are Lasso, GLasso and Elastic Net (Enet). These three methods are based on linear sparse models. GLasso and Enet are the extension of Lasso. GLasso is used to solve  $l_1/l_q$ -norm regularized problem. Enet is used for the situations

**TABLE 2** | Classification with different feature selection methods.

| Methods | Number of selected features | ACC (%) | SEN (%) | SPE (%) |
|---------|-----------------------------|---------|---------|---------|
| t-test  | 153                         | 78.62   | 80.28   | 77.03   |
| Lasso   | 123                         | 83.45   | 88.73   | 78.38   |
| GLasso  | 225                         | 86.21   | 85.92   | 86.49   |
| ENet    | 64                          | 85.52   | 84.51   | 86.19   |
| SGLasso | 55                          | 93.10   | 92.96   | 93.24   |



**FIGURE 4** | ROC curves for SZ/HC classification for different feature selection methods.

where features are related to each other and always produce valid solution.

These four feature selection methods perform the same experimental procedure as SGLasso for the sake of fairness. It's worth noting that the five local graph measures are extracted at the threshold of 0.30. **Table 2** shows the experimental results of the above mentioned four methods and SGLasso feature selection method. As we can see that SGLasso method selects the least features (55) but achieves the best ACC (93.10%), SEN (92.96%), SPE (93.24%). The ROC curves for SZ/HC classification for different feature selection methods as shown in **Figure 4**. We notice that SGLasso achieves the highest AUC (0.950) than other four feature selection methods. Experimental result shows that considering within- and between- group sparsity is likely helpful for selecting significant features that are effective for SZ identification.

### 4.2. Comparison With Different Classifiers

In order to prove that LSVM is optimal to conduct classification in this context, a series of comparative experiments using several SVMs with different kernels including Radial Basis Function kernel (RBF), Polynomial kernel (Poly), Sigmoid kernel (Sigm)

**TABLE 3** | Comparison with other SVMs using different kernels.

| Methods  | ACC (%)      | SEN (%)      | SPE (%)      | AUC          |
|----------|--------------|--------------|--------------|--------------|
| RBF-SVM  | 80.00        | 76.06        | 83.78        | 0.8601       |
| Poly-SVM | 82.07        | 77.46        | 86.49        | 0.8506       |
| Sigm-SVM | 87.59        | 83.10        | 91.89        | 0.9393       |
| LSVM     | <b>93.10</b> | <b>92.96</b> | <b>93.24</b> | <b>0.950</b> |

*Bold text indicates that the best result is obtained on a certain evaluation metric.*

**TABLE 4** | Comparison with other commonly used classifiers.

| Methods | ACC (%)      | SEN (%)      | SPE (%)      | AUC          |
|---------|--------------|--------------|--------------|--------------|
| KNN     | 82.07        | 74.65        | 89.19        | 0.7912       |
| RForest | 77.93        | 74.65        | 81.08        | 0.8378       |
| NBayes  | 84.83        | 83.10        | 86.49        | 0.9069       |
| LDA     | 90.34        | 87.32        | 93.24        | 0.9418       |
| LSVM    | <b>93.10</b> | <b>92.96</b> | <b>93.24</b> | <b>0.950</b> |

*Bold text indicates that the best result is obtained on a certain evaluation metric.*

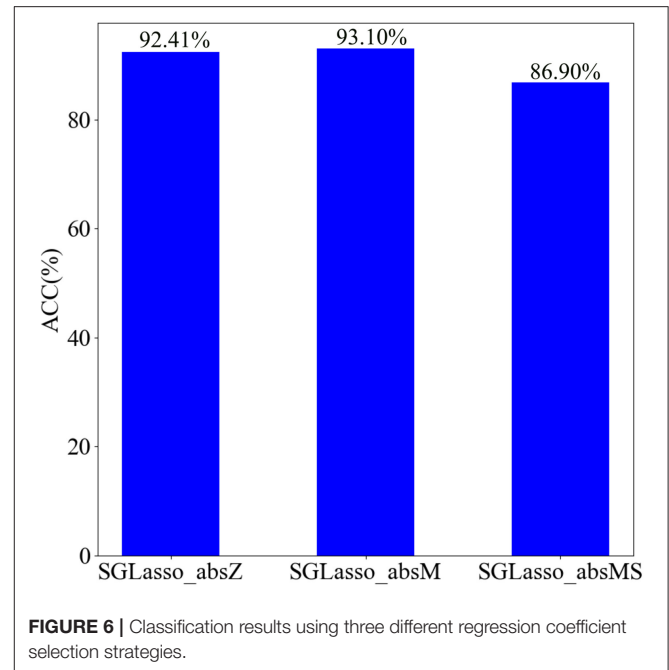
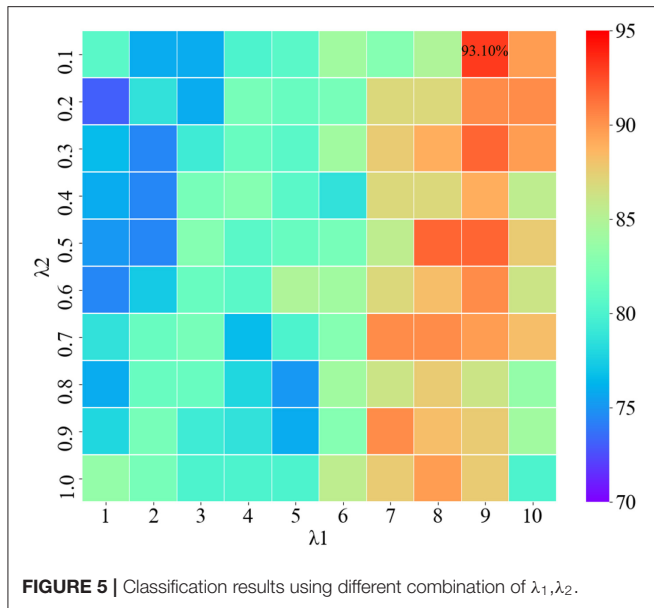
under the same condition as the LSVM have been performed. These SVMs are denoted as RBF-SVM, Poly-SVM, Sigm-SVM, respectively. The experimental results of SVMs with different kernels are shown in **Table 3**. It is worth mentioning that bold text indicates that the best result is obtained on a certain evaluation metric.

In addition, we also compare four commonly used classifiers, such as k-nearest neighbors (KNN), Random Forest (RForest), NaiveBayes (NBayes), and Linear Discriminant Analysis (LDA). These classifiers are all implemented on the platform of Matlab2016a. We evaluate the performance of the above four classifiers under the same conditions as LSVM. The experimental results of these five classifiers are shown in **Table 4**. As can be seen from **Tables 3, 4**, LSVM can achieve the best classification performance than other classifiers.

### 4.3. Regularization Parameter Selection

The regularization parameters of SGLasso have a great influence on the results of feature selection. Using different regularization parameters, the selected features are also different. It affects not only the feature dimension, but also the final classification performance. Therefore, selecting the appropriate regularization parameters can improve the efficiency of SGLasso method and obtain more effective features associated with the labels.

The two regularization parameters of SGLasso are  $\lambda_1$  and  $\lambda_2$ .  $\lambda_1$  is used to control the model sparseness, and  $\lambda_2$  can control the sparse constraint of each feature group. We use the grid search algorithm to find the optimal combination of regularization parameters. **Figure 5** shows the classification results using different combination of  $\lambda_1$ ,  $\lambda_2$ . According to **Figure 5**, when the parameter combination is ( $\lambda_1=9$ ,  $\lambda_2=0.1$ ), the features obtained from SGLasso feature selection method are the most effective for SZ/HC classification.



#### 4.4. Regression Coefficient Selection

In general, the non-zero elements in the coefficient vector  $\alpha$  generated from the SGLasso feature selection algorithm indicate that the corresponding features are selected. In order to retain the least but most informative features according to  $\alpha$ , we test the impact of the three coefficient selection strategies on classification performance. We named these three strategies as SGLasso\_absZ, SGLasso\_absM, and SGLasso\_absMS. The description of these three strategies is as follows:

- SGLasso\_absZ is a common strategy to retain non-zero coefficients of  $\alpha$ .
- SGLasso\_absM strategy is to retain those coefficients which are greater than the mean value of absolute values of all elements in  $\alpha$ .
- SGLasso\_absMS strategy is more strict for selecting coefficients, since it retains the coefficients which are larger than the mean value of absolute values of all non-zero coefficients in  $\alpha$ .

We apply the above mentioned three strategies to feature selection, and then select the corresponding features according to the retained coefficients in  $\alpha$ . SVM performs SZ identification using these selected features. The classification results using three different regression coefficient selection strategies are shown in **Figure 6**. According to **Figure 6**, the classification accuracy is the best when using SGLasso\_absM strategy. Experimental result indicates that using SGLasso\_absM strategy in feature selection can select the most effective features for SZ/HC classification. Therefore, we finally choose the SGLasso\_absM strategy to select the regression coefficients.

#### 4.5. Classification Comparison Using Different Feature Combinations

In order to explore the impact of different feature combinations on SZ/HC identification, we combine these five local measures

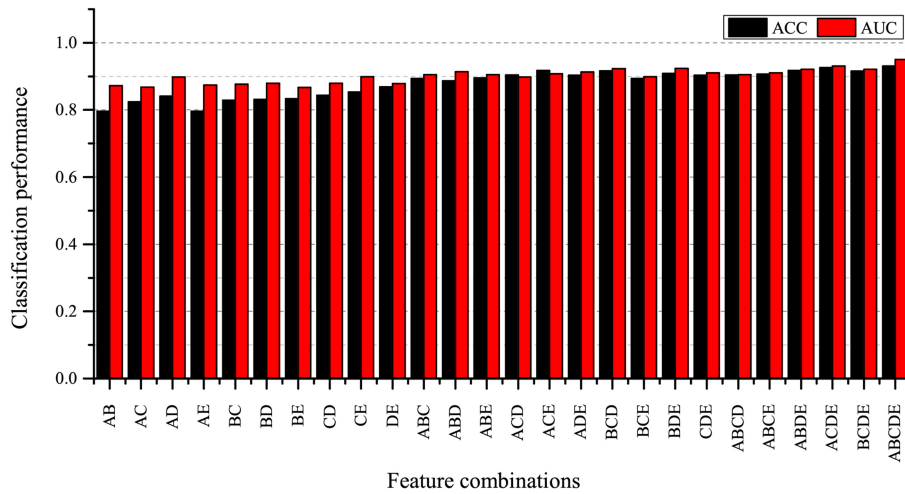
extracted at the threshold of 0.30 in  $C_5^2 + C_5^3 + C_5^4 + C_5^5 = 26$  ways. Furthermore, we don't consider individual graph measure because we only investigate multiple measures in this study. We evaluate these 26 feature sets under the same experimental settings. The classification results are shown in **Figure 7**.

As can be seen from **Figure 7**, the combination of 5 local graph measures achieves the best classification performance compared to other feature sets. At the same time, we also find that the classification accuracies obtained by using feature sets including two measures are lower than the classification accuracies obtained by using feature sets including three measures, four measures and five measures. It indicates that using fewer measures may not be enough to characterize brain network alteration, and we find that the combination of five local measures can provide more useful information for SZ identification.

#### 4.6. Comparison With Existing Classification Methods

To verify the effectiveness of our proposed classification method, we compare some recently proposed methods for SZ classification using fMRI in the literature. Huang et al. (2018) proposed a tree-guided group sparse learning method to select the most important information from FALFF data in four frequency bands and get a classification accuracy of 91.1% by using multi-kernel SVM. Cheng et al. (2015) calculated only betweenness centrality measure to characterize the network. They used the rank of betweenness centrality of all nodes as feature representations and used SVM to classify SZs from HCs.

The two above mentioned methods are performed on the COBRE dataset. The classification results and ROC curves for SZ/HC classification of the two methods and our proposed method are shown in **Table 5** and in **Figure 8**, respectively.



**FIGURE 7 |** Classification result for different feature combinations. A: betweenness centrality, B: nodal clustering coefficient, C: local efficiency, D: degree, E: participation coefficient.

**TABLE 5 |** Comparison with some existing methods for SZ/HC classification.

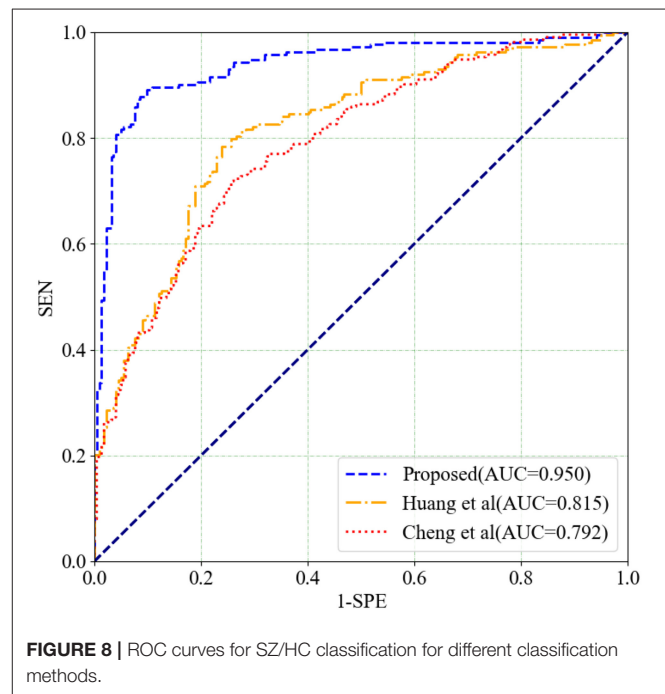
| Methods             | ACC (%)      | SEN (%)      | SPE (%)      | AUC          |
|---------------------|--------------|--------------|--------------|--------------|
| Huang et al. (2018) | 77.24        | 77.46        | 76.58        | 0.815        |
| Cheng et al. (2015) | 74.48        | 73.53        | 69.12        | 0.792        |
| Proposed            | <b>93.10</b> | <b>92.96</b> | <b>93.24</b> | <b>0.950</b> |

*Bold text indicates that the best result is obtained on a certain evaluation metric.*

According to **Table 5** and **Figure 8**, Our proposed method gets the best ACC (93.10%), SEN (92.96%), SPE (93.24%), and AUC (0.950) values. The experimental result illustrates that our proposed method has made a significant improvement in classification performance on the COBRE dataset.

### 4.7. Analysis of Discriminative Graph Measures and Corresponding Regions

The graph measures selected in the feature selection stage are considered to be related to their corresponding brain regions. Our method can select the most discriminative brain regions as the biomarkers to guide the disease-induced interpretation. There is a total of 145 experiments in the LOOCV scheme due to 145 subjects. And the number of feature occurrence in 145 experiments is introduced to indicate the contribution of the feature to classification. We assume that if the occurrence number of a local graph measure extracted from a certain brain region is greater than 140 in a total of 145 experiments, the brain region is considered to have the most discriminative power to distinguish between SZs and HCs. Based on this hypothesis, 21 salient brain regions have been found. These significant brain regions are shown in **Table 6**. Five brain regions include left superior frontal gyrus (SFG\_L\_7\_2), right inferior temporal gyrus (ITG\_R\_7\_7), right inferior parietal lobule (IPL\_R\_6\_4), right postcentral gyrus (PoG\_R\_4\_1), and



**FIGURE 8 |** ROC curves for SZ/HC classification for different classification methods.

right thalamus (Tha\_R\_8\_7) are related to more than one local graph measure.

These findings on discriminative brain regions are in agreement with the following studies: superior frontal gyrus, cingulate gyrus, postcentral gyrus (Szeszko et al., 1999; Gur et al., 2000; Arbabshirani et al., 2013; Chyzhyk et al., 2015), parahippocampal gyrus (Shenton et al., 1992; Chyzhyk et al., 2015), middle temporal gyrus, fusiform gyrus and thalamus (Chyzhyk et al., 2015; Li et al., 2019), inferior parietal lobule, inferior temporal gyrus (Peng et al., 1994; Goldstein et al., 1999; Li et al., 2019). However, we cannot report agreement with these



**TABLE 6 |** The most discriminative graph measures and corresponding Brainnetome regions.

| Graph measures               | Hemisphere | Brainnetome regions      | Occurrence number |
|------------------------------|------------|--------------------------|-------------------|
| Nodal clustering coefficient | SFG_L_7_2  | Superior Frontal Gyrus   | 144               |
| Degree                       | SFG_L_7_2  | Superior Frontal Gyrus   | 145               |
| Nodal clustering coefficient | SFG_R_7_2  | Superior Frontal Gyrus   | 140               |
| Participation coefficient    | SFG_R_7_7  | Superior Frontal Gyrus   | 144               |
| Betweenness centrality       | IFG_L_6_3  | Inferior Frontal Gyrus   | 143               |
| Betweenness centrality       | OrG_L_6_2  | Orbital Gyrus            | 143               |
| Betweenness centrality       | OrG_R_6_6  | Orbital Gyrus            | 145               |
| Betweenness centrality       | PrG_L_6_3  | Precentral Gyrus         | 142               |
| Degree                       | MTG_L_4_4  | Middle Temporal Gyrus    | 145               |
| Betweenness centrality       | MTG_L_4_1  | Middle Temporal Gyrus    | 141               |
| Participation coefficient    | ITG_R_7_7  | Inferior Temporal Gyrus  | 145               |
| Betweenness centrality       | ITG_R_7_7  | Inferior Temporal Gyrus  | 145               |
| Betweenness centrality       | FuG_R_3_3  | Fusiform Gyrus           | 145               |
| Betweenness centrality       | PhG_L_6_3  | Parahippocampal Gyrus    | 144               |
| Degree                       | PhG_L_6_5  | Parahippocampal Gyrus    | 145               |
| Local efficiency             | IPL_R_6_4  | Inferior Parietal Lobule | 145               |
| Participation coefficient    | IPL_R_6_4  | Inferior Parietal Lobule | 145               |
| Degree                       | IPL_R_6_2  | Inferior Parietal Lobule | 145               |
| Degree                       | PCun_L_4_3 | Precuneus                | 145               |
| Nodal clustering coefficient | PoG_R_4_1  | Postcentral Gyrus        | 145               |
| Betweenness centrality       | PoG_R_4_1  | Postcentral Gyrus        | 145               |
| Local efficiency             | PoG_R_4_1  | Postcentral Gyrus        | 143               |
| Degree                       | PoG_R_4_1  | Postcentral Gyrus        | 145               |
| Participation coefficient    | CG_L_7_4   | Cingulate Gyrus          | 145               |
| Betweenness centrality       | CG_R_7_3   | Cingulate Gyrus          | 145               |
| Participation coefficient    | LOcC_L_4_3 | lateral Occipital Cortex | 145               |
| Degree                       | BG_R_6_1   | Basal Ganglia            | 145               |
| Betweenness centrality       | BG_R_6_4   | Basal Ganglia            | 145               |
| Participation coefficient    | Tha_L_8_8  | Thalamus                 | 145               |
| Degree                       | Tha_L_8_5  | Thalamus                 | 145               |
| Degree                       | Tha_R_8_8  | Thalamus                 | 145               |
| Nodal clustering coefficient | Tha_R_8_7  | Thalamus                 | 140               |
| Local efficiency             | Tha_R_8_7  | Thalamus                 | 141               |

regions:inferior frontal gyrus, orbital gyrus, precentral gyrus, precuneus, lateral occipital cortex and basal ganglia.

## 5. CONCLUSION

In this paper, we propose a method to classify SZs from HCs using multi-view graph measures of functional brain

## REFERENCES

- Abraham, A., Milham, M. P., Di Martino, A., Craddock, R. C., Samaras, D., Thirion, B., et al. (2017). Deriving reproducible biomarkers from multi-site resting-state data: an autism-based example. *Neuroimage* 147, 736–745. doi: 10.1016/j.neuroimage.2016.10.045
- Anderson, A., and Cohen, M. S. (2013). Decreased small-world functional network connectivity and clustering across resting state networks in schizophrenia: an fMRI classification tutorial. *Front. Hum. Neurosci.* 7:520. doi: 10.3389/fnhum.2013.00520

networks. We get five local network measures using graph theoretical approach from multiple views. These measures play an important role in the information exchange of brain networks. Our proposed method achieves a good classification performance on the COBRE dataset. Experimental results demonstrate that this approach is efficient for the clinical diagnosis of SZ. Furthermore, multiple measures have the potential to be used as clinical biomarkers to differentiate SZs from HCs.

## DATA AVAILABILITY STATEMENT

The imaging data and phenotypic information was collected and shared by the Mind Research Network and the University of New Mexico funded by a National Institute of Health Center of Biomedical Research Excellence (COBRE) grant 1P20RR021938-01A2. The dataset for this study can be found in this website: [http://fcon\\_1000.projects.nitrc.org/indi/retro/cobre.html](http://fcon_1000.projects.nitrc.org/indi/retro/cobre.html).

## AUTHOR CONTRIBUTIONS

JW and JL conceived the project. YX, GT, F-XW, and JL designed the experiments. YX and GT performed the experiments. YX and JL wrote the paper. All authors read and approved the final manuscript.

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- Arbabshirani, M. R., Kiehl, K., Pearlson, G., and Calhoun, V. D. (2013). Classification of schizophrenia patients based on resting-state functional network connectivity. *Front. Neurosci.* 7:133. doi: 10.3389/fnins.2013.00133
- Brier, M. R., Thomas, J. B., Fagan, A. M., Hassenstab, J., Holtzman, D. M., Benzinger, T. L., et al. (2014). Functional connectivity and graph theory in preclinical Alzheimer's disease. *Neurobiol. Aging* 35, 757–768. doi: 10.1016/j.neurobiolaging.2013.10.081
- Castro, E., Martínez-Ramón, M., Pearlson, G., Sui, J., and Calhoun, V. D. (2011). Characterization of groups using composite kernels and multi-source

- fMRI analysis data: application to schizophrenia. *Neuroimage* 58, 526–536. doi: 10.1016/j.neuroimage.2011.06.044
- Chan, M., Krebs, M., Cox, D., Guest, P., Yolken, R. H., Rahmoune, H., et al. (2015). Development of a blood-based molecular biomarker test for identification of schizophrenia before disease onset. *Transl. Psychiatry* 5:e601. doi: 10.1038/tp.2015.91
- Chang, C.-C., and Lin, C.-J. (2011). Libsvm: a library for support vector machines. *ACM Trans. Intell. Syst. Technology* 2:27. doi: 10.1145/1961189.1961199
- Chen, Q., Lai, D., Lan, W., Wu, X., Chen, B., Chen, Y.-P. P., et al. (2019). ILDMSF: inferring associations between long non-coding RNA and disease based on multi-similarity fusion. *IEEE/ACM Trans. Comput. Biol. Bioinformatics*. doi: 10.1109/TCBB.2019.2936476. [Epub ahead of print].
- Cheng, H., Newman, S., Goñi, J., Kent, J. S., Howell, J., Bolbecker, A., et al. (2015). Nodal centrality of functional network in the differentiation of schizophrenia. *Schizophrenia Res.* 168, 345–352. doi: 10.1016/j.schres.2015.08.011
- Chyzyk, D., Savio, A., and Graña, M. (2015). Computer aided diagnosis of schizophrenia on resting state fMRI data by ensembles of ELM. *Neural Netw.* 68, 23–33. doi: 10.1016/j.neunet.2015.04.002
- Craddock, R. C., Jabdi, S., Yan, C.-G., Vogelstein, J. T., Castellanos, F. X., Di Martino, A., et al. (2013). Imaging human connectomes at the macroscale. *Nat. Methods* 10:524. doi: 10.1038/nmeth.2482
- Fan, L., Li, H., Zhuo, J., Zhang, Y., Wang, J., Chen, L., et al. (2016). The human brainnetome atlas: a new brain atlas based on connectonal architecture. *Cereb. Cortex* 26, 3508–3526. doi: 10.1093/cercor/bhw157
- Fornito, A., Zalesky, A., and Breakspear, M. (2013). Graph analysis of the human connectome: promise, progress, and pitfalls. *Neuroimage* 80, 426–444. doi: 10.1016/j.neuroimage.2013.04.087
- Goldstein, J. M., Goodman, J. M., Seidman, L. J., Kennedy, D. N., Makris, N., Lee, H., et al. (1999). Cortical abnormalities in schizophrenia identified by structural magnetic resonance imaging. *Arch. Gen. Psychiatry* 56, 537–547. doi: 10.1001/archpsyc.56.6.537
- Guo, W., Su, Q., Yao, D., Jiang, J., Zhang, J., Zhang, Z., et al. (2014). Decreased regional activity of default-mode network in unaffected siblings of schizophrenia patients at rest. *Eur. Neuropsychopharmacol.* 24, 545–552. doi: 10.1016/j.euroneuro.2014.01.004
- Gur, R. E., Cowell, P. E., Latshaw, A., Turetsky, B. I., Grossman, R. I., Arnold, S. E., et al. (2000). Reduced dorsal and orbital prefrontal gray matter volumes in schizophrenia. *Arch. Gen. Psychiatry* 57, 761–768. doi: 10.1001/archpsyc.57.8.761
- He, H., Sui, J., Yu, Q., Turner, J. A., Ho, B.-C., Sponheim, S. R., et al. (2012). Altered small-world brain networks in schizophrenia patients during working memory performance. *PLoS ONE* 7:e38195. doi: 10.1371/journal.pone.0038195
- Heinrichs, R. W., and Zakzanis, K. K. (1998). Neurocognitive deficit in schizophrenia: a quantitative review of the evidence. *Neuropsychology* 12:426. doi: 10.1037/0894-4105.12.3.426
- Huang, J., Zhu, Q., Hao, X., Shi, X., Gao, S., Xu, X., and Zhang, D. (2018). Identifying resting-state multifrequency biomarkers via tree-guided group sparse learning for schizophrenia classification. *IEEE J. Biomed. Health Informatics* 23, 342–350. doi: 10.1109/JBHI.2018.2796588
- Khazaei, A., Ebrahimzadeh, A., and Babajani-Feremi, A. (2015). Identifying patients with Alzheimer's disease using resting-state fMRI and graph theory. *Clin. Neurophysiol.* 126, 2132–2141. doi: 10.1016/j.clinph.2015.02.060
- Khazaei, A., Ebrahimzadeh, A., Babajani-Feremi, A., for the Alzheimer's Disease Neuroimaging Initiative (2017). Classification of patients with mci and ad from healthy controls using directed graph measures of resting-state fMRI. *Behav. Brain Res.* 322, 339–350. doi: 10.1016/j.bbr.2016.06.043
- Li, J., Sun, Y., Huang, Y., Bezerianos, A., and Yu, R. (2019). Machine learning technique reveals intrinsic characteristics of schizophrenia: an alternative method. *Brain Imaging Behav.* 13, 1386–1396. doi: 10.1007/s11682-018-9947-4
- Liu, J., Ji, S., and Ye, J. (2009). *Slep: Sparse Learning With Efficient Projections*. Arizona State University, 7.
- Liu, J., Li, M., Lan, W., Wu, F.-X., Pan, Y., and Wang, J. (2016). Classification of Alzheimer's disease using whole brain hierarchical network. *IEEE/ACM Trans. Comput. Biol. Bioinformatics* 15, 624–632. doi: 10.1109/TCBB.2016.26.35144
- Liu, J., Li, M., Pan, Y., Lan, W., Zheng, R., Wu, F.-X., and Wang, J. (2017a). Complex brain network analysis and its applications to brain disorders: a survey. *Complexity* 2017:8362741. doi: 10.1155/2017/8362741
- Liu, J., Li, M., Pan, Y., Wu, F.-X., Chen, X., and Wang, J. (2017b). Classification of schizophrenia based on individual hierarchical brain networks constructed from structural MRI images. *IEEE Trans. Nanobiosci.* 16, 600–608. doi: 10.1109/TNB.2017.2751074
- Liu, J., Pan, Y., Li, M., Chen, Z., Tang, L., Lu, C., et al. (2018a). Applications of deep learning to MRI images: a survey. *Big Data Mining Analyt.* 1, 1–18. doi: 10.26599/BDMA.2018.9020001
- Liu, J., Wang, J., Hu, B., Wu, F.-X., and Pan, Y. (2017c). Alzheimer's disease classification based on individual hierarchical networks constructed with 3-D texture features. *IEEE Trans. Nanobiosci.* 16, 428–437. doi: 10.1109/TNB.2017.2707139
- Liu, J., Wang, J., Tang, Z., Hu, B., Wu, F.-X., and Pan, Y. (2017d). Improving Alzheimer's disease classification by combining multiple measures. *IEEE/ACM Trans. Comput. Biol. Bioinformatics* 15, 1649–1659. doi: 10.1109/TCBB.2017.2731849
- Liu, J., Wang, X., Zhang, X., Pan, Y., Wang, X., and Wang, J. (2018b). MMM: classification of schizophrenia using multi-modality multi-atlas feature representation and multi-kernel learning. *Multimedia Tools Appl.* 77, 29651–29667. doi: 10.1007/s11042-017-5470-7
- Lynall, M.-E., Bassett, D. S., Kerwin, R., McKenna, P. J., Kitzbichler, M., Muller, U., et al. (2010). Functional connectivity and brain networks in schizophrenia. *J. Neurosci.* 30, 9477–9487. doi: 10.1523/JNEUROSCI.0333-10.2010
- Marín, O. (2012). Interneuron dysfunction in psychiatric disorders. *Nat. Rev. Neurosci.* 13:107. doi: 10.1038/nrn3155
- Moghimi, P., Lim, K. O., and Netoff, T. I. (2018). Data driven classification of fMRI network measures: application to schizophrenia. *Front. Neuroinform.* 12:71. doi: 10.3389/fninf.2018.00071
- Nieuwenhuis, M., van Haren, N. E., Pol, H. E. H., Cahn, W., Kahn, R. S., and Schnack, H. G. (2012). Classification of schizophrenia patients and healthy controls from structural MRI scans in two large independent samples. *Neuroimage* 61, 606–612. doi: 10.1016/j.neuroimage.2012.03.079
- Pedersen, M., Omidvarnia, A., Zalesky, A., and Jackson, G. D. (2018). On the relationship between instantaneous phase synchrony and correlation-based sliding windows for time-resolved fMRI connectivity analysis. *Neuroimage* 181, 85–94. doi: 10.1016/j.neuroimage.2018.06.020
- Peng, L. W., Lee, S., Federman, E. B., Chase, G. A., Barta, P. E., and Pearlson, G. D. (1994). Decreased regional cortical gray matter volume in schizophrenia. *Am. J. Psychiatry* 151:843. doi: 10.1176/ajp.151.6.842
- Pettersson-Yeo, W., Allen, P., Benetti, S., McGuire, P., and Mechelli, A. (2011). Dysconnectivity in schizophrenia: where are we now? *Neurosci. Biobehav. Rev.* 35, 1110–1124. doi: 10.1016/j.neubiorev.2010.11.004
- Ripke, S., O'Dushlaine, C., Chambert, K., Moran, J. L., Kähler, A. K., Akterin, S., et al. (2013). Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nat. Genet.* 45, 1150–1159. doi: 10.1038/ng.2742
- Rubinov, M., and Sporns, O. (2010). Complex network measures of brain connectivity: uses and interpretations. *Neuroimage* 52, 1059–1069. doi: 10.1016/j.neuroimage.2009.10.003
- Shenton, M. E., Kikinis, R., Jolesz, F. A., Pollak, S. D., LeMay, M., Wible, C. G., et al. (1992). Abnormalities of the left temporal lobe and thought disorder in schizophrenia: a quantitative magnetic resonance imaging study. *N. Engl. J. Med.* 327, 604–612. doi: 10.1056/NEJM199208273270905
- Szeszko, P. R., Bilder, R. M., Lencz, T., Pollack, S., Alvir, J. M. J., Ashtari, M., et al. (1999). Investigation of frontal lobe subregions in first-episode schizophrenia. *Psychiatry Res. Neuroimaging* 90, 1–15. doi: 10.1016/S0925-4927(99)00002-5
- Van Den Heuvel, M. P., and Pol, H. E. H. (2010). Exploring the brain network: a review on resting-state fMRI functional connectivity. *Eur. Neuropsychopharmacol.* 20, 519–534. doi: 10.1016/j.euroneuro.2010.03.008
- Yan, C.-G., Wang, X.-D., Zuo, X.-N., and Zang, Y.-F. (2016). *Dpabi: data processing & analysis for (resting-state) brain*

- imaging. *Neuroinformatics* 14, 339–351. doi: 10.1007/s12021-016-9299-4
- Yang, Y., and Wang, H. (2018). Multi-view clustering: a survey. *Big Data Mining and Analyt.* 1, 83–107. doi: 10.26599/BDMA.2018.9020003
- Yu, Q., Erhardt, E. B., Sui, J., Du, Y., He, H., Hjelm, D., et al. (2015). Assessing dynamic brain graphs of time-varying connectivity in fMRI data: application to healthy controls and patients with schizophrenia. *Neuroimage* 107, 345–355. doi: 10.1016/j.neuroimage.2014.12.020
- Yuan, M., and Lin, Y. (2006). Model selection and estimation in regression with grouped variables. *J. R. Stat. Soc. Ser. B* 68, 49–67. doi: 10.1111/j.1467-9868.2005.00532.x

**Conflict of Interest:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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