

Multivariate classification of social anxiety disorder using whole brain functional connectivity

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Abstract Recent research has shown that social anxiety disorder (SAD) is accompanied by abnormalities in brain functional connections. However, these findings are based on group comparisons, and, therefore, little is known about whether functional connections could be used in the diagnosis of an individual patient with SAD. Here, we explored the potential of the functional connectivity to be used for SAD diagnosis. Twenty patients with SAD and 20 healthy controls were scanned using resting-state functional magnetic resonance imaging. The whole brain was divided into 116 regions based on automated anatomical labeling atlas. The functional connectivity between each pair of regions was computed using Pearson's correlation coefficient and used as classification feature. Multivariate pattern analysis was then used to classify patients from healthy controls.

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The pattern classifier was designed using linear support vector machine. Experimental results showed a correct classification rate of 82.5 % ($p < 0.001$) with sensitivity of 85.0 % and specificity of 80.0 %, using a leave-one-out cross-validation method. It was found that the consensus connections used to distinguish SAD were largely located within or across the default mode network, visual network, sensory-motor network, affective network, and cerebellar regions. Specifically, the right orbitofrontal region exhibited the highest weight in classification. The current study demonstrated that functional connectivity had good diagnostic potential for SAD, thus providing evidence for the possible use of whole brain functional connectivity as a complementary tool in clinical diagnosis. In addition, this study confirmed previous work and described novel pathophysiological mechanisms of SAD.

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Introduction

Anxiety disorders, classified by the Diagnostic and Statistical Manual of Mental Disorders IV (DSM-IV) (APA 1994), are among the most common psychiatry disorders. Even so, social anxiety disorder (SAD), one of the most common anxiety disorders (Fink et al. 2009; Fouché et al. 2013; Jefferys 1997), has received relatively little attention. SAD, also termed social phobia (Stein and Stein 2008), is characterized by an excessive and unreasonable fear of social interactions and performance situations wherein the individual fears negative evaluation by others. Patients with SAD typically avoid the feared situations or endure them with intense feelings of anxiety or distress, thus leading to significant functional impairment (Talati et al. 2013). Epidemiological research conducted on the general population has demonstrated that the lifetime prevalence of SAD ranges between 4 and 16 % (Ohayon and Schatzberg 2010). At present, however, SAD is diagnosed mainly based on clinical signs and symptoms, and its pathophysiology remains largely unclear. Undoubtedly, it is important to explore a valid and objective biomarker to distinguish patients with SAD from healthy controls.

In recent years, resting-state functional magnetic resonance imaging (fMRI) has attracted considerable attention. This technique not only overcomes potential limitations associated with task paradigms in fMRI studies but is also relatively easy and more economical to implement than positron emission tomography (PET) and single photon emission computed tomography (SPECT) in clinical studies (Greicius 2008). Moreover, resting-state fMRI is a novel non-invasive imaging technique for measuring spontaneous brain activity as low-frequency fluctuations in blood oxygen level-dependent (BOLD) signals to identify areas of increased or decreased neuronal activity (Biswal et al. 1995; Fox and Greicius 2010; Guo et al. 2011; Liu et al. 2012b). Resting-state functional connectivity has been defined as the identification of correlation patterns between these fluctuations measured in different brain areas and has the potential to greatly increase the translation of fMRI into clinical care (Fox and Greicius 2010). By using resting-state functional connectivity, previous studies focused on the quantitative analysis of the brains in patients with psychiatric and neurological diseases, such as major depression (Guo et al. 2013), Alzheimer's disease (Zhou et al. 2013), and schizophrenia (Liu et al. 2008). In addition, a recent study found decreased functional connectivity

of the left amygdala with the medial orbitofrontal cortex and the posterior cingulate gyrus (PCG)/precuneus (PCUN) in SAD (Hahn et al. 2011). However, little is known about whether the altered functional connectivity could be used in the diagnosis of an individual patient with SAD. For clinical purposes, one must be able to provide predictions at the level of the individual patient (Smith 2012).

As a data-driven technique, multivariate pattern analysis (MVPA) plays an important role in analyzing neuroimaging data. In contrast to conventional approaches that are mainly based on univariate and group-level statistical methods, MVPA method is sensitive to the fine-grained spatial discriminative patterns and exploration of inherent multivariate nature from high-dimensional neuroimaging data (Norman et al. 2006). Furthermore, MVPA could provide novel insight into the differences between two groups because it allows the identification of features which contribute the most to individual classification (Meier et al. 2012). Recently, an increasing number of neuroimaging studies focused on applying MVPA to discriminate psychiatric patients from healthy controls (Anderson et al. 2011; Liu et al. 2012a; Uddin et al. 2011).

To date, no MVPA studies have been published on patients with SAD. Such studies are particularly important, because it can examine whether MVPA and functional connectivity could become a clinical tool for the diagnosis of SAD, with emphasis on early treatment. In the present study, our goal was to determine whether MVPA and whole brain resting-state functional connectivity could help to discriminate, at an individual level, patients with SAD from healthy controls. Specifically, a pattern classifier was designed using linear support vector machine (SVM) to perform classification between the patient and control groups and to identify functional connections with distinct characteristics. Previous findings have revealed functional connectivity differences between patients and controls. Therefore, we hypothesized that functional connectivity could be used as a potential biomarker to distinguish patients from controls. Additionally, we also hypothesized that aberrant functional connections would be observed in the resting-state networks involved in social cognition and emotional processing. We hoped that by thoroughly exploring the whole brain we could finally obtain additional information for advancing our understanding of the pathophysiology of this disorder.

Materials and methods

Subjects

The present study was approved by the Ethics Committee of the Huaxi Hospital, Sichuan University, Chengdu,

China. Written informed consent was obtained from each participant before any study procedure was initiated. Twenty-three patients with SAD were recruited from Mental Health Center of the Huaxi Hospital. All patients did not receive psychiatric and psychotherapy medications. SAD was diagnosed by two attending psychiatrists and a trained interviewer using the Structured Clinical Interview DSM-IV (SCID) Patients Version. Exclusion criteria included participants with ages younger than 18 or older than 40 years, any history of major physical illness, cardiovascular disease, bipolar disorder, neurological illness, or a lifetime history of alcohol or drug use. Twenty age-, sex-, and education-matched healthy controls were recruited from the local community by advertisements. The same psychiatrists and interviewer that used the SCID Non-Patient Version to confirm the current absence of psychiatric and neurological illness screened them as well. None of them had any neurological or psychiatric disorders. There was also no major psychiatric or neurological illness among their first-degree relatives.

All participants were evaluated with the State-Trait Anxiety Inventory (STAI), Hamilton Anxiety Rating Scale (HAMA), Hamilton Depression Rating Scale (HAM-D), and Liebowitz Social Anxiety Scale (LSAS). Specifically, the STAI questionnaire consists of two parts: the STAI-State (STAI-S) score, which gives the level of state anxiety at the time of completing the text, and the STAI-Trait (STAI-T) score, which gives the level of inherent trait anxiety of the subject. The STAI-S questionnaire was completed before and after the MRI scanning (pre-scanning and post-scanning) session (Campbell et al. 2007).

Data acquisition

The MR images were acquired on the 3.0-T GE-Signa MRI scanner (Excite, General Electric, Milwaukee, USA) in Huaxi MR Research Center, Chengdu, China. Foam padding was used to minimize head movement. During data acquisition, the participants were instructed to hold still, relax minds, and move as little as possible. Functional images were performed by a single-shot, gradient-recalled echo-planar imaging (EPI) sequence. Sequence parameters were as follows: repetition time/echo time (TR/TE) = 2,000/30 ms, thickness = 5 mm, no slice gap, field of view (FOV) = 24 cm, flip angle (FA) = 90°, data matrix = 64 × 64, voxel size = 3.75 × 3.75 × 5 mm³. Five dummy scans were discarded to remove the impact of magnetization instability. For each participant, the brain volume comprised 30 axial slices, and each functional run contained 200 image volumes.

Data preprocessing

Image preprocessing was carried out using the statistical parametric mapping (SPM8, <http://www.fil.ion.ucl.ac.uk/spm>) software package. For each participant, EPI images were first corrected for the temporal differences between slices and then realigned to correct head motion. Recent studies demonstrated that head motion had a substantial impact on resting-state functional connectivity (Power et al. 2012; Satterthwaite et al. 2012; Van Dijk et al. 2012). Thus, only participants with head motion less than 2.0 mm in the *x*, *y*, or *z* direction and less than 2.0° rotation in each axis were included. Besides, “Mean motion” was computed and compared between the subject groups to further determine the comparability of head movement across groups, as suggested by Van Dijk et al. (2012). Then, the corrected images were spatially normalized to the Montreal Neurological Institute (MNI) EPI template in SPM8 and resampled to 3 mm cubic voxels. In order to avoid introducing artificial local spatial correlations, no spatial smoothing was applied, as previously suggested (Achard et al. 2006; Wang et al. 2009; Zhang et al. 2011b, c).

Anatomical parcellation

The registered fMRI data were further divided into 116 anatomical regions of interests (ROIs) according to the automated anatomical labeling (AAL) atlas (Tzourio-Mazoyer et al. 2002), which was shown in Figure S1 in Supplement 1. This atlas parcellates the brain into 78 cortical regions (39 in each hemisphere), 12 subcortical regions (6 in each hemisphere), and 26 cerebellar regions (9 in each cerebellar hemisphere and 8 in the vermis). Details of AAL regions can be found in Table S1 in Supplement 1. From a network perspective, these regions belong to several different resting-state networks, such as default mode network (DMN), visual network (VN), sensory-motor network (SMN), and affective network (AN). For the details of the regions in these resting-state networks, see Supplement 1.

Functional connectivity of the whole brain

For each subject, a representative time series in each region was obtained by averaging the fMRI time series of all voxels in each of the 116 regions (Liu et al. 2007; Yu et al. 2008). These representative time series were temporally band-pass filtered (0.01–0.08 Hz) to reduce the effects of low-frequency drift and high-frequency physiological noises (Liao et al. 2010b). Several sources of spurious variance were removed by regression along with their first derivatives: six head motion parameters obtained by rigid body correction, signal from a region centered in the white

matter and signal from a ventricular region of interest. This regression procedure removed variances unlikely to be involved in specific regional correlations of neuronal origin (Fox et al. 2005). Of note, it is still an ongoing controversy of removing the global signal in the preprocessing of resting-state fMRI data (Fox et al. 2009; Murphy et al. 2009; Saad et al. 2012). Therefore, we did not regress out the global signal. The residuals of these regressions were used for the following functional connectivity analysis. Functional connectivity between each pair of regions was evaluated using Pearson's correlation coefficients, resulting in $(116 \times 115)/2 = 6,670$ dimensional functional connectivity feature vectors for each subject. These functional connections were the features used in all subsequent analyses.

Feature selection

Given that some features are uninformative, irrelevant or redundant for classification, reducing a number of features not only speed up computation, but also improve classification performance (Dosenbach et al. 2010; Pereira et al. 2009). Therefore, an initial feature selection step was utilized. In this study, the F score method was employed for feature ranking (Chen and Lin 2006). F score is simple, generally quite effective, and used in previous studies (Akay 2009; Huang et al. 2007).

Given the number of positive instances (i.e., patient subjects) n_+ and negative instances (i.e., control subjects) n_- , the F score of the i th feature is defined as follows (Chen and Lin 2006):

$$F(i) = \frac{(\bar{x}_i^{(+)} - \bar{x}_i)^2 + (\bar{x}_i^{(-)} - \bar{x}_i)^2}{\frac{1}{n_+ - 1} \sum_{k=1}^{n_+} (x_{k,i}^{(+)} - \bar{x}_i^{(+)})^2 + \frac{1}{n_- - 1} \sum_{k=1}^{n_-} (x_{k,i}^{(-)} - \bar{x}_i^{(-)})^2}, \quad (1)$$

where \bar{x}_i , $\bar{x}_i^{(+)}$, $\bar{x}_i^{(-)}$ are the averages of the i th feature of the whole, positive, and negative data sets, respectively; $x_{k,i}^{(+)}$ is the i th feature of the k th positive instance, and $x_{k,i}^{(-)}$ is the i th feature of the k th negative instance. The denominator represents the discrimination within each of the positive and negative sets, while the numerator represents the discrimination between the two sets. Obviously, the larger the F score is, the more discriminative the feature is.

A leave-one-out cross-validation (LOOCV) strategy was used to evaluate the performance of a classifier (see immediately below). For each LOOCV fold, we ranked the features according to their F scores in descending order and retained the 250 highest ranked features (see details in the following subsection of “Overall classifier performance”). It was worth noting that all the procedures of feature

selection were constrained in the training set of each LOOCV fold, without using the information of the testing set, in order to avoid the introduction of bias.

Since feature ranking was based on a slightly different subset of the data in each iteration of LOOCV, the final features (in our case functional connections) used in classification differed for each iteration of LOOCV. Consensus features were introduced here. They were defined as the common features always selected to form the final feature set from each LOOCV iteration. Feature weights (i.e., support vector classification weights) of the consensus functional connections were the average across all folds of LOOCV. To represent the relative contribution of different regions for classification, the weight of each region to the overall ability of the classifier to accurately discriminate between two groups could be evaluated by summing one-half of the consensus feature weights associated with that region (Meier et al. 2012). Of note, if a region did not form any consensus functional connections, it was given a region weight of zero.

Classification and support vector machine

Support vector machine (SVM) classifier was adopted here for classification. This technique works well when the number of training samples is small but the number of features is large (Vapnik 1995). SVM classification is a form of supervised learning because training is accomplished by labeled samples (Burges 1998). A binary label with 1 for patients and -1 for healthy controls was used here. The classification process consists of two steps: training and testing. During the training step, the SVM finds a decision boundary that separates the examples in the input space using their class labels. Once the decision function is determined from the training set, it can be used to predict the class label of a new testing example.

A linear kernel SVM was used to reduce the risk of overfitting the data and to allow direct extraction of the feature weights (Pereira et al. 2009). The linear SVM has only one parameter C that determines the trade-off between allowing misclassifications and training error minimization. The SVM classifier was implemented using LIBSVM toolbox (Chang and Lin 2011), with a default value for the parameter C (i.e., $C = 1$).

Evaluation on the performance of Classifier

Due to our limited number of samples, a LOOCV strategy was employed to evaluate the performance of the classifier (Schölkopf et al. 2001; Wee et al. 2011). In brief, suppose there were n samples in total. In each LOOCV trial, we used $n-1$ samples as the training set and the remaining one was used as the testing set. Classifiers were built for each

training set and tested with its corresponding testing subject. Accuracy, sensitivity, and specificity could be used to quantify the performance of the classifier based on the results of LOOCV.

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{FN} + \text{TN} + \text{FP}} \quad (2)$$

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}} \quad (3)$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}, \quad (4)$$

where TP is the number of true positives: number of patients correctly classified; TN is the number of true negatives: number of normal controls correctly classified; FP is the number of false positives: number of normal controls classified as patients; FN is the number of false negatives: number of patients classified as normal controls.

To assess whether the computed classification accuracy is statistically significant, the statistical significance of the classification results is evaluated using permutation test as proposed by Golland and Fischl (2003). The permutation test is a non-parametric technique which is used to test the null hypothesis that the computed accuracy is obtained by chance (Mourao-Miranda et al. 2005; Wang et al. 2012; Zhu et al. 2008). In the permutation test, the class labels of the original data S are randomly permuted to obtain a set of k randomized versions of data, $\hat{S} = \{S'_1, S'_2, \dots, S'_k\}$. A classifier is then built based on each of the S' and test on the same testing data. The p value of the permutation test is defined as the fraction of the number of classifiers that built based on S' which is better than the classifier that built based on S , which is given as

$$p = \frac{|\{S' \in \hat{S} : \text{acc}(S') \geq \text{acc}(S)\}| + 1}{k + 1}, \quad (5)$$

where $\text{acc}(S)$ represents the accuracy obtained from the original data S and $\text{acc}(S')$ represents the accuracy obtained from the randomized data S' . The p value of Eq. (5) measures how likely the observed accuracy is obtained by chance. The smaller the p value is, the more unlikely it is obtained by chance, and the more reasonable we reject the null hypothesis. In the current analysis, the class labels (i.e., SAD vs. healthy controls) of the training data were permuted 1,000 times at random prior to training and then the same entire classification process including feature selection was carried out with each set of permuted class labels. The accuracies were obtained across all permutations and the p value was calculated as the proportion of accuracies that are equal to or greater than the accuracy obtained by the non-permuted (original) data. If less than 5 % ($p < 0.05$) of the accuracies from all permutations

exceeded the non-permuted value, the result was thought to be significant.

Results

Demographics and clinical characteristics of the participants

Data of three patients with SAD were excluded because translation and rotation exceeded ± 2 mm or $\pm 2^\circ$. Two-sample t tests were performed to assess the differences in age, years of education, head movement, and clinical scores, while Chi-square test was performed to assess the difference in gender. The two groups were matched for gender (14 males for SAD group and 14 males for control group), age (22.90 ± 3.99 years for SAD group; 21.75 ± 3.73 years for healthy controls; $p = 0.313$), years of education (14.10 ± 1.48 years for SAD group; 14.05 ± 1.96 years for healthy controls; $p = 0.928$), and the head motion (0.034 ± 0.012 mm for SAD group; 0.040 ± 0.020 mm for healthy controls; $p = 0.258$). Relative to healthy controls, patients with SAD have significantly higher scores of LSAS, HAMD, HAMA, and significantly higher levels of anxiety assessed by the STAI-T and pre-scanning STAI-S. The detailed demographic and clinical data are presented in Table 1.

Table 1 Demographics and clinical characteristics of patients with SAD and HC

Variables (Mean \pm SD)	SAD	HC	p value
Gender (M/F)	20 (14/6)	20 (14/6)	–
Age (years)	22.90 ± 3.99	21.75 ± 3.73	0.313
Education (years)	14.10 ± 1.48	14.05 ± 1.96	0.928
Illness duration, (months)	45.40 ± 39.78	–	–
LSAS			
Total score	53.90 ± 11.50	20.00 ± 8.27	<0.001
Fear factor	28.00 ± 6.17	8.40 ± 4.81	<0.001
Avoidance factor	25.90 ± 6.93	11.60 ± 5.91	<0.001
HAMD	7.50 ± 6.27	1.30 ± 1.87	<0.001
HAMA	6.20 ± 4.74	1.22 ± 1.80	<0.001
STAI			
STAI-T	48.25 ± 7.02	32.90 ± 4.93	<0.001
STAI-S			
Pre-scanning	41.35 ± 8.31	31.40 ± 4.85	<0.001
Post-scanning	37.65 ± 9.54	33.10 ± 7.08	0.095
Head motion	0.034 ± 0.012	0.040 ± 0.020	0.258

SAD social anxiety disorder, HC healthy controls, LSAS Liebowitz Social Anxiety Scale, HAMA Hamilton Anxiety Rating Scale, HAMD Hamilton Depression Rating Scale, STAI State-Trait Anxiety Inventory

The p values were obtained by two-sample t test

Fig. 1 Schematic diagram illustrating the proposed classification framework

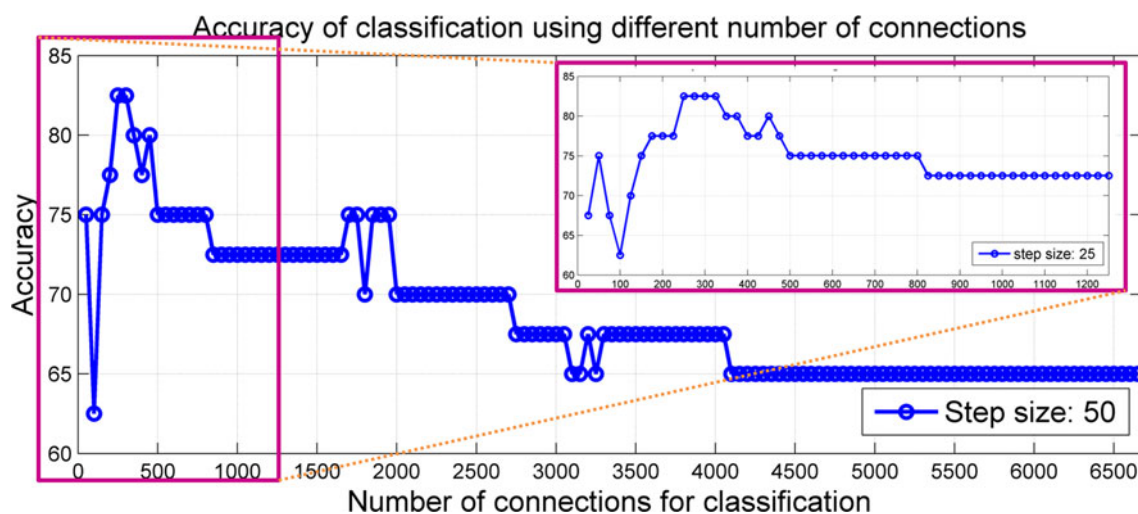
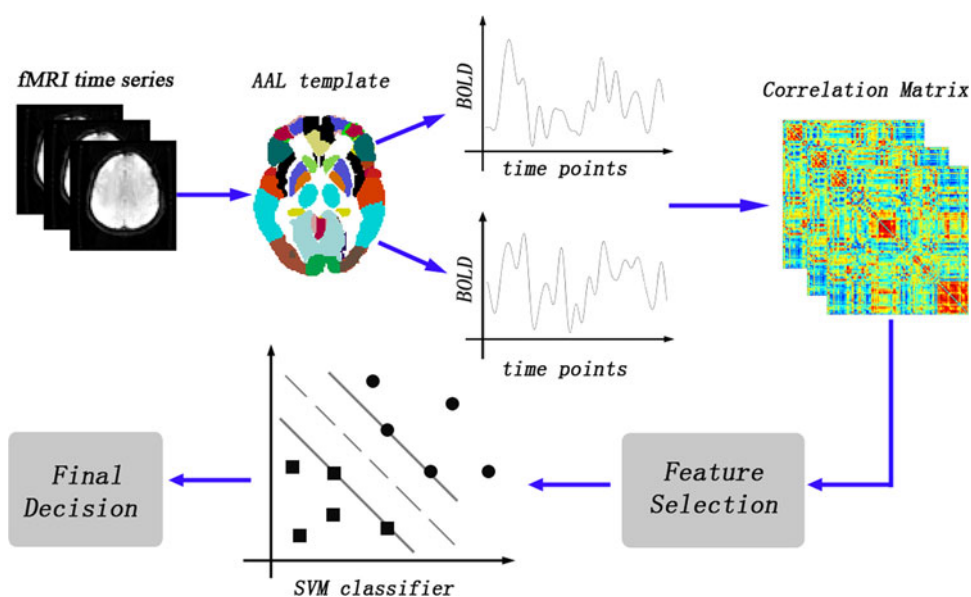


Fig. 2 Predictive accuracy as a function of the number of connections used in the classification process. The connections were ranked according to F scores in descending order

Overall classifier performance

An overview of the proposed MVPA framework was summarized in Fig. 1. As shown in Fig. 2, the linear SVM classifier could reach up to 82.5 % (85 % for sensitivity, 80 % for specificity, $p < 0.001$) by using the 250 highest ranked functional connections. Thus, we selected the top 250 ranked features in each iteration of LOOCV for the classification features. In addition, the discriminative score of each testing subject was acquired by the SVM classifier. Taking each subject's discriminative score as a threshold, the receiver operating characteristic (ROC) curve of the

classifier was yielded, as shown in Fig. 3. The area under the ROC curve (AUC) of the proposed method was 0.852, indicating a good classification power.

Consensus features

In this study, 148 features, known as consensus features, were identified in the cross-validation. The consensus functional connections were mainly located within or across the DMN, VN, SMN, AN, and cerebellum. The consensus functional connections related to these networks are shown in Fig. 4.

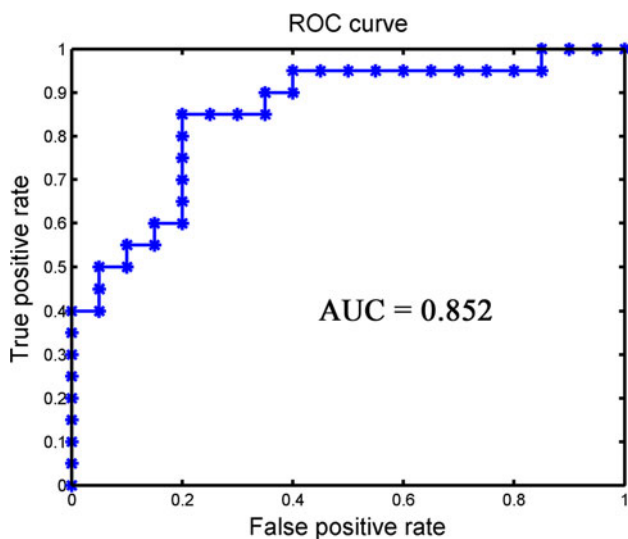


Fig. 3 ROC curve of the classifier. *ROC* receiver operating characteristic

Region weight

Some regions showed greater weights than others. Specifically, we defined a region having significantly higher weight if its weight was at least one standard deviation greater than the average of the weight of all the regions, as used in a previous study (Tian et al. 2011). The regions with the greater weight included the right orbital part of the middle frontal gyrus (MFGorb), the left PCUN, the left lingual gyrus (LING), the right orbital part of the superior frontal gyrus (SFGorb), the right insula (INS), the left postcentral gyrus (PoCG), the left middle part of temporal pole (TPOMid), the left superior occipital gyrus (SOG), the right superior part of temporal pole (TPOsup), the vermis_1&2 (VER 1&2), and the left angular gyrus (ANG). Figure 5 displays these regions.

Comparison between linear and non-linear SVM classifiers

Non-linear SVM classifier (i.e., radial basis function (RBF) kernel SVM) was trained and tested with the same procedure used in the proposed framework to validate the effectiveness of using linear SVM classifier. For fair comparison, default parameters were used for both linear and non-linear SVM classifiers. Figure 6 shows that non-linear SVM classifier achieves the best accuracy of 75 % when the 250 highest ranked functional connections are used. Results in Table 2; Fig. 7 show that linear SVM classifier performs better than non-linear SVM classifier in terms of accuracy, sensitivity, specificity, and AUC value.

Comparison between linear SVM classifier and k -nearest neighbors (k -NN) classifier

To further understand the performance of the linear SVM classifier, we applied k -NN classifier to the same data. In the machine learning field, k -NN method is a non-parametric lazy learning algorithm for classifying testing samples on the basis of the closest training samples in the feature space (Cover and Hart 1967). In addition, k -NN method is one of the simplest machine learning algorithms. This method entailed finding the k nearest neighbors and performing a majority voting of its neighbors. The main advantage of k -NN classifier is that it is more intuitive than SVM and less labor-intensive because no parameter is required except k (i.e., the number of neighbors). In the current study, k -NN was used with the same training and testing procedure in the proposed framework by utilizing the MATLAB R2012a (Mathworks, Natick, Massachusetts) “ClassificationKNN.fit” and “predict” functions. As seen in Table 3, linear SVM classifier outperformed k -NN classifier in SAD classification. Specifically, with default parameter ($k = 1$), the k -NN (i.e., nearest neighbor algorithm) classifier achieved accuracy of 72.5 % (when we used the 850 highest ranked functional connections), with a sensitivity of 75.0 %, and a specificity of 70.0 %. We also performed grid search to determine the best number of neighbors (k) for k -NN classifier. It is found that k -NN classifier achieves the highest accuracy of 80.0 % when $k = 3$ and when 300 highest ranked functional connections are used, as shown in Fig. 6.

Discussion

To the best of our knowledge, the current study is the first to apply MVPA to discriminate patients with SAD from healthy controls. Our study had three main findings: (1) a promising classification performance had been validated by LOOCV: our method achieved a relatively high accuracy (82.5 %) for SAD classification and the AUC value was 0.852, indicating good potential for diagnosis; (2) most of the consensus functional connections were located within or across the DMN, VN, SMN, AN, and cerebellum; (3) the region of the right MFGorb exhibited the highest weight in classification.

Our findings showed that the altered functional connections were related to the DMN. The DMN is thought to be a higher-level cognitive network system and comprises a set of brain regions that typically deactivate during performance of goal-directed tasks and activate during resting state (Raichle et al. 2001). The main function of the DMN is self-referential activity, which is impaired in SAD (Anderson et al. 2008). Abnormality of the DMN in SAD

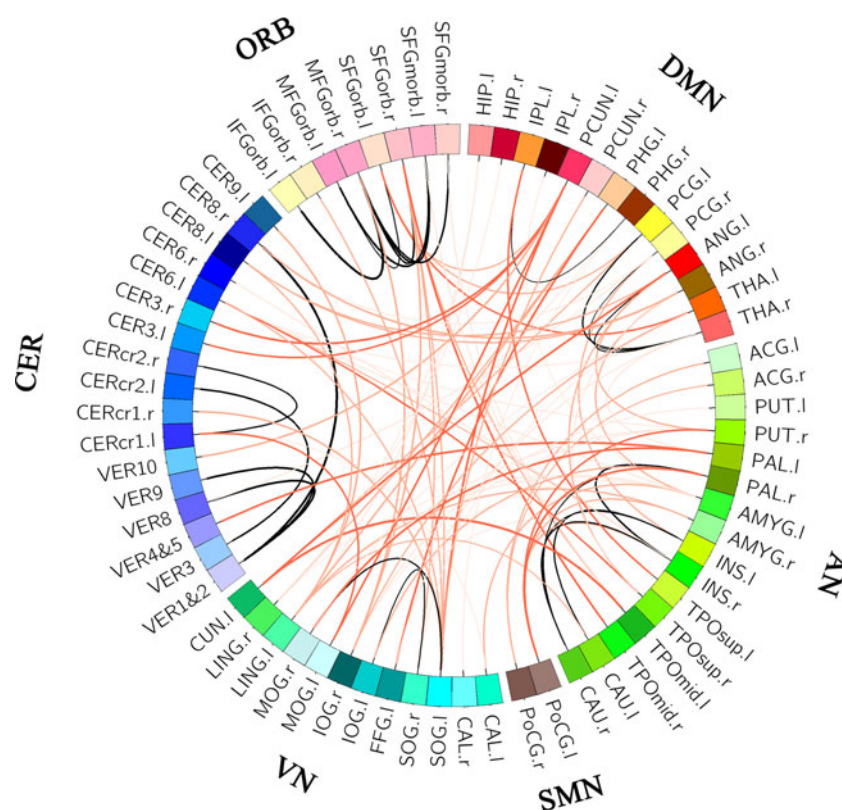


Fig. 4 This is a connectogram that shows the consensus functional connections within or across the default mode network, visual network, sensory-motor network, affective network, orbitalfrontal cortex and cerebellum. The brain region of each cluster is represented by a *square* on the circumference of the big circle. The *lines* connecting two squares represent the connections between the corresponding two brain regions. The thickness of the line represents

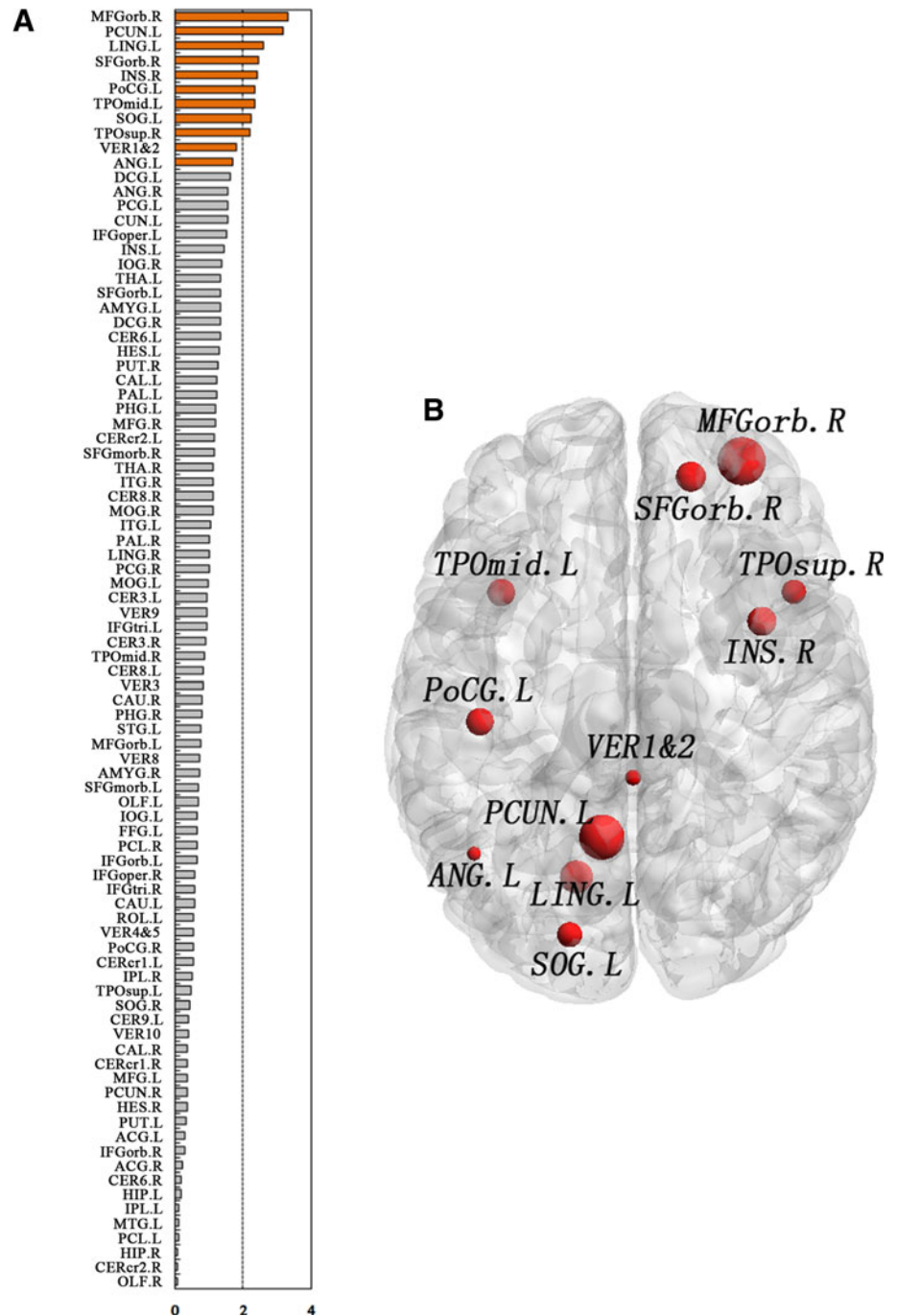
the weight (i.e., support vector classification weight) of the connection. The thicker the line, the larger the weight. The *red lines* represent inter-network connections and the *black lines* represent intra-network connections. *DMN* default mode network, *AN* affective network, *SMN* sensory-motor network, *VN* visual network, *CER* cerebellum, *ORB* orbitalfrontal cortex. This visualization was created using Circos (<http://circo.ca/>)

has been found in previous studies (Gentili et al. 2009; Liao et al. 2010a). Thus, our results supported the notion that DMN played a key role in SAD. Moreover, the left PCUN and the left ANG were shown to have high weights. The PCG/PCUN is not only the critical hub of the DMN involved in social cognition (Gentili et al. 2009; Raichle et al. 2001), but also a core hub of the whole brain network (Hagmann et al. 2008). Patients with SAD showed a lower deactivation in the PCG/PCUN regions during task conditions (Gentili et al. 2009). In addition, Warwick and colleagues found a decreased perfusion of the PCUN in patients with SAD during resting state, indicating that the abnormal functional connectivity in PCUN may be linked with the pathophysiological mechanism underlying SAD (Warwick et al. 2008). The ANG, another hub of DMN, plays a critical role in mental constructs such as thoughts, feelings, and beliefs (Frith and Frith 2003). A recent task-based study reported that the ANG had a greater BOLD response when patients reacted to feelings of negative self-belief (Goldin and Gross 2010). Accumulated evidence demonstrated that SAD was characterized by emotional

biases and distorted negative self-beliefs (Goldin et al. 2009a). Furthermore, Qiu et al. (2011) found a decreased regional homogeneity in bilateral ANG. Thus, our finding was consistent with previous studies and suggested that the connections related to the ANG were abnormal in the resting state.

In addition to the DMN, perceptual networks were shown to be altered in SAD. In contrast to DMN, the perceptual networks can be considered as lower-level cognitive processing. Commonly, the perceptual networks include the VN, SMN and auditory network. Aberrant functional connectivity and high region weight were found in the visual processing network (LING and SOG) and sensory processing network (PoCG), which might contribute to perceptual impairments in SAD. To some extent, this result was in line with previous findings. For example, greater activity was found after treatment in SMN and VN in a social anxiety imagery task (Kilts et al. 2006). Using a social (harsh facial expressions) and physical (violent scenes) threat task, Goldin et al. (2009b) found significantly greater BOLD responses in SAD. Furthermore, a

Fig. 5 The region weight in the classification. **a** Bar plot of the values of mean normalized region weight for the detected brain regions that related to consensus functional connections in descending order. The regions with *orange color* represent the regions having significantly higher weight. **b** Rendering plot of the regions with significantly higher weight in the classification. The size of the node represented the magnitude of the normalized region weight. *L* left, *R* right



pilot structural MRI study showed that patients with SAD had significant bilateral cortical thinning in the visual and sensory regions (Syal et al. 2012). Taken together, these findings indicated that the altered perceptual networks might be related to impaired visual and sensory function in SAD.

The AN, which is involved in emotional processing (Mayberg et al. 1999), is important to fear, vigilance and visceral regulation (Olson et al. 2007). The INS and

temporal pole (TPO) were found to exhibit the high weights. The INS has increasingly become the focus of attention for its role in body representation and subjective emotional experience. Recently, Borg et al. (2012) found impaired emotional processing in patients with an INS lesion. Some evidence further emphasized hyperactivity of the INS of anxiety patients during the processing of negative emotion (Etkin and Wager 2007; Gentili et al. 2008). We speculated that functional abnormality of the INS

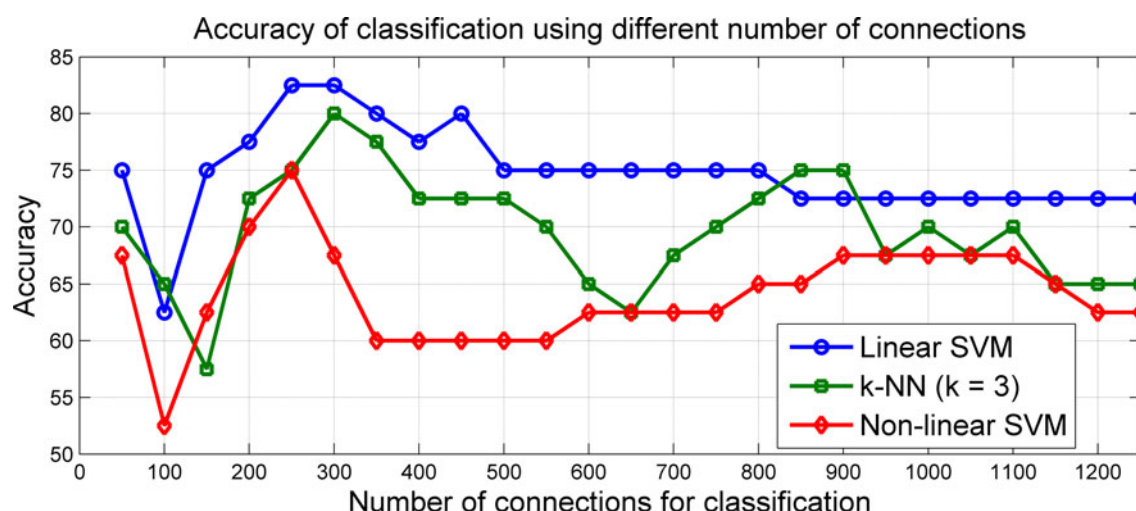


Fig. 6 Predictive accuracy as a function of the number of connections used in the classification process by using linear SVM, non-linear SVM and k -NN classifiers. The connections were ranked according to F scores in descending order

Table 2 Classification performance for linear and non-linear SVM classifiers

SVM classifier	Accuracy	Sensitivity	Specificity	AUC
Non-linear (RBF)	75.0	75.0	75.0	0.805
Linear	82.5	85.0	80.0	0.852

RBF radial basis function

Table 3 Classification performance for linear SVM and k -NN classifiers

Method	Accuracy	Sensitivity	Specificity
k -NN ($k = 1$, default parameter)	72.5	75.0	70.0
k -NN ($k = 3$, best parameter)	80.0	85.0	75.0
Linear SVM	82.5	85.0	80.0

k -NN k -nearest neighbors

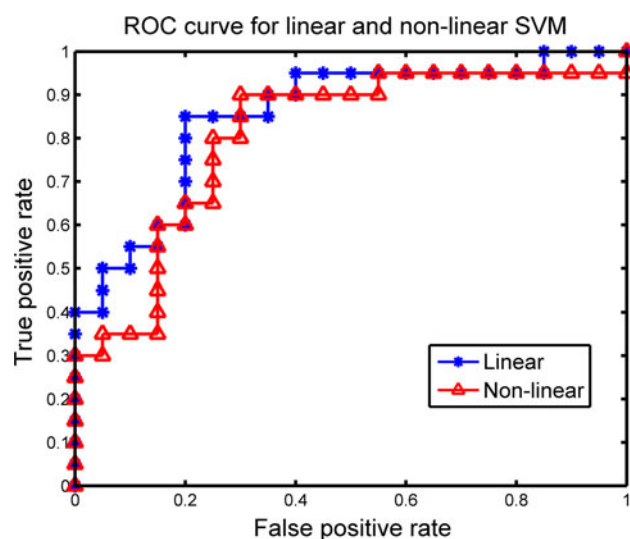


Fig. 7 ROC curves of the linear and non-linear SVM classifier. In this study, non-linear SVM denotes the RBF kernel SVM

would disrupt functional connectivity from INS to other brain systems. Additionally, the TPO region plays an important role in social and emotional processing as a paralimbic region (see the review by Olson et al. (2007)). Moreover, previous study in healthy subjects found

activation in this region during social perception and competition with the mental states of others (Polosan et al. 2011). In contrast, impairment in TPO led to alterations in the ability to characterize social attributes of behavior (Zahn et al. 2007). Tillfors et al. demonstrated that decreased blood flow of the TPO was found during anticipation of public speaking (Tillfors et al. 2002) and stressful speaking tasks (Tillfors et al. 2001). The above-mentioned indicate that altered functional connections in AN may lead to poor emotion regulation which is found in patients with SAD.

It was unexpected that the cerebellar region had relatively high weight. Up to now, a large number of neuroimaging studies have focused on the cerebral cortex in SAD, not really considering the role of the cerebellum in this disorder. The traditional view on cerebellum function is on the acquisition of motor coordination and motor behavior (Stein and Glickstein 1992). However, a recent study found that the cerebellum was involved in emotional control and played a role in the perception of emotional stimuli (Schmahmann 2010). Moreover, both structural and functional studies found changes in the cerebellum in SAD. Warwick et al. (2008) demonstrated both hyper- and

hypo-perfusion in the cerebellum among patients with SAD, and a social situation task-based fMRI study reported significantly decreased activation in the cerebellum (Nakao et al. 2011). In addition, Kilts and colleagues found that inducing anxiety in patients with SAD increased blood flow to the cerebellum (Kilts et al. 2006). Furthermore, patients with SAD had greater gray matter volume in the cerebellum compared with healthy controls (Talati et al. 2013). In spite of the fact that the mechanisms are remaining largely unknown, cerebellar abnormalities may increase vulnerability to anxiety states via modulation of arousal. Many cerebellar subdivisions and the vermis in particular project to the fastigial nucleus and then to the pons and medulla oblongata, which mediate the autonomic responses that are exaggerated in subjects with anxiety (Baldacara et al. 2008). Overall, these findings may provide a basis for the cerebellar regions to participate in emotional processing.

The region of right MFGorb had the highest weight. As shown in literature, SAD is characterized by a hyper-activated right prefrontal cortex (Engel et al. 2009). A previous study demonstrated that a lesion in the orbitofrontal cortex would impair self-insight, which might preclude the generation of helpful emotional information (Beer et al. 2006). According to the orbitofrontal cortex-anger hypothesis, this region is also the core hub of angry emotion [see the review by Lindquist et al. (2012)]. In addition, the orbitofrontal cortex assigns positive and negative stimulus response contingencies and regulates expression of emotion (Blackmon et al. 2011; Milad and Rauch 2007). Taken together, altered functional connectivity associated with the orbitofrontal region may contribute to emotional dysregulation exhibited by SAD.

From a local scale viewpoint, the brain is organized into multiple resting-state networks (Damoiseaux et al. 2006; Sorg et al. 2007) as mentioned above. From a global scale viewpoint, the human brain is a complex network which continuously integrates information across different brain networks (Bullmore and Sporns 2012; Jiang 2013). In addition to the aberrant intra-network connectivity, we also found altered inter-network connectivity. Investigation of the intra-network connectivity may advance our understanding of the functional specialization of the brain, while investigation on inter-network connectivity may increase our understanding of the functional integration within the brain (Friston 2004; Sporns 2011). Inter-network connectivity may provide additional information to understand the pathophysiology underlying the symptoms of SAD. Relative to intra-network connectivity, which is low on the level of the hierarchy, inter-network connectivity is higher in the hierarchy (Luo et al. 2011). Thus, the changed inter-network connectivity might disrupt the high-level complex function which integrates information from multi-networks, such as impression formation and revision (Haker

et al. 2013), learning (Gross-Isseroff et al. 2010) and emotion processing (Bruhl et al. 2011, 2013; Hattingh et al. 2012).

MRI-related classification is a challenging task due to the high dimensionality of MRI features but small number of available training samples. The consequence of this is that it is possible to find a decision function which has good classification performance for the samples in the training set, but has poor predictive performance in the testing set: this phenomenon is called overfitting (Mitchell 1997). One way of alleviating the danger of overfitting lies in the choice of the classifier. The advantage of linear SVM is that the model is simple. In addition, it can reduce the risk of overfitting and allow direct extraction of the feature weights. We performed an experiment for comparison between the linear and non-linear SVM classifiers. The results revealed that linear SVM outperformed non-linear SVM for our SAD classification purpose, the rationale for which might be twofold: first, the non-linear SVM may overfit the data in the training set due to the “small sample size, large feature size” problem; second, for fair comparison, we used default parameters in both linear and non-linear SVM classifiers which may degenerate the classification performance of non-linear SVM classifier. We also performed a comparison between the linear SVM and k -NN method. As one of the simplest classification methods, nearest-neighbor method does not involve explicit learning of a classification function. Classification of a testing sample is done by finding the most similar training sample and assigning the label of this nearest neighbor to the testing sample. The theory of k -NN method (a variant of nearest-neighbor method) is that a testing sample is classified by a majority vote of its k neighbors, with the sample being assigned to the label most common amongst its k nearest neighbors (k is an odd positive integer). The results of Table 3 demonstrate linear SVM classifier performs better than k -NN classifier, even though k -NN uses the best neighbor size. In addition, we also perform a two-sample t test between all the classification accuracies of linear SVM and k -NN (i.e., the accuracies corresponding to different number of features). The p value obtained is smaller than 0.001, indicating a significant difference between linear SVM and k -NN methods. However, we would like to emphasize that the main contribution of this study is to discriminate patients with SAD from healthy controls by using MVPA. Though linear SVM outperforms k -NN and non-linear SVM in this study, it is actually based on a small sample size of dataset. In the future, we would like to test our framework using larger dataset to verify whether linear SVM still outperforms other classifiers.

A LOOCV method was used to evaluate the performance of the classifier. Since the selected features for

constructing SVM model were different in each iteration of LOOCV, the SVM models were different across LOOCV folds. Thus, we had forty different SVM models for SAD classification. In the real life application, it would be definitely more suitable to generate only one SVM model, which is used to predict all patients in the future. Ideally, if the sample size was large enough (thousands or tens of thousands of samples), there is no doubt that we can construct a robust and reliable model for predicting new samples. However, in practice, it is too difficult to obtain the MRI data from thousands of patients with SAD and matched healthy controls. For our case, we can use a weighted majority vote strategy to combine different SVM models. Specifically, in the SVM theory, given a new testing sample x , the decision function $F_j(x)$ of j th linear SVM model for predicted label is

$$D_j(x) = \sum_{i=1}^n y_i \alpha_{ij} x_i^T x + b_j \quad (6)$$

$$F_j(x) = \text{sign}(D_j(x)) \quad (7)$$

where $x_i (i = 1, \dots, n)$, represents a feature vector of the i th subject and $y_i \in \{1, -1\}$ represents the corresponding class label. α denotes the Lagrange multiplier and b denotes the bias term. Thus, for multiple SVM models, the final decision function $F(x)$ of SVM model for predicted label can be written as

$$F(x) = \text{sign}\left(\sum_{j=1}^m D_j(x)\right), \quad (8)$$

where m is the total number of SVM models. Using this method, we finally generated one SVM model, which could be utilized to predict new subjects in the future. Alternatively, it *seems* that we can use the consensus features to build a SVM model to test unseen samples. If we used consensus features as final classification features, the two groups could be discriminated with accuracy of 92.5 %. However, this will introduce a bias because of “double dipping” which used the same dataset for selection and analysis (Kriegeskorte et al. 2009). In fact, the consensus features were obtained from all the samples which included training and testing samples. Subsequently, these features were used to build a SVM classifier and LOOCV method was used to evaluate the performance of the classifier. In the feature selection procedure, we cannot include the subjects from testing set. Thus, the result obtained by using consensus features as final classification features did not make sense.

As shown in Fig. 2, the accuracy is 75 % using the 50 highest ranked features. It momentarily drops down to 62.5 % using top 100 features, increases back to 75 % using top 150 features, and reaches its maximum at 82.5 %

using top 250 features. This looks like a strange phenomenon, but we observe that previous neuroimaging studies have reported similar results as well (Fan et al. 2008; Shi et al. 2007; Su et al. 2012; Tang et al. 2013; Zhang et al. 2011a). The possible reason for this phenomenon may be the fact that, in our study and aforementioned studies, the features are selected based on their rankings of discriminative power which are computed individually and independently. We do not select features based on the discriminative power of the combination of features, as there are too many possible combinations (i.e., $2^{6670}-1$). The application of feature selection based on the individual ranking implies that there is no guarantee on the performance of their combinations, e.g., the discriminative power of the combination of the top 100 features might not be better than the combination of the top 50 features for SAD classification. This might be the limitation of this kind of commonly used feature selection method (i.e., select features based on their individual discriminative power rather than select features based on their combination discriminative power). In fact, as shown in Fig. 6, all the comparison methods (non-linear SVM and k -NN) show the similar phenomenon, which indicates that the phenomenon is caused by the feature selection method and not the type of classifier. To overcome this limitation, we will investigate other feature selection methods [e.g., recursive feature elimination (RFE) (Guyon et al. 2002) or sparse representation (Wee et al. 2013)] for SAD classification in the future.

Several limitations should be noted in this study. First of all, our sample size was relatively small. Although the findings were remarkable, the small sample size might limit the translational value of our results. Larger, independent and multi-center imaging datasets will be necessary to confirm our findings. Second, in the current study, the AAL atlas was used to parcellate the whole brain into 116 regions. However, recent studies demonstrated that different parcellation schemes or different spatial scales generated different results (Hayasaka and Laurienti 2010; Wang et al. 2009; Zalesky et al. 2010). Thus, further studies should determine which brain parcellation strategy or spatial scale is more appropriate to discriminate patients with SAD from healthy controls. Third, although we controlled for head motion, we could not fully eliminate this effect. This issue still requires systematic methodological work in the future. Fourth, a total of 250 features were used while we only have 40 subjects; this may lead to the problem of overfitting. However, as described before, linear SVM works well when the number of training samples is small and the number of features is large. Finally, a relatively low sampling rate ($TR = 2$ s) was used for multislice acquisitions. Under this sampling rate, some inevitable physiological noises, such as respiratory and

cardiac fluctuations of the subject during scanning were reduced but could not be completely removed. Future studies should use a more rigorous approach to correct such physiological noises.

In summary, this study used an MVPA method, which is based on the whole brain resting-state functional connectivity, to distinguish patients with SAD from healthy controls. The current study provided evidence that functional connections have good diagnostic potential. Moreover, the identified altered functional connectivity and high weight regions might provide a complementary method of the clinical diagnosis of SAD. Although functional connectivity was used as feature, the MVPA method is not confined by this kind of feature. Future studies may benefit from the integration of functional connectivity with graph network measures or other imaging modality measurements.

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Conflict of interest All authors declare that they have no conflicts of interest.

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