Using fMRI to Diagnose Schizophrenia

Department of Computing Science
University of Alberta

Department of Computing Science
University of Alberta

Department of Computing Science
University of Alberta

Abstract

Diagnosis of schizophrenia is a challenging task that yet to be addressed [6]. Although, in recent years methods which use Functional Magnetic Resonance Imaging (fMRI) for mental disorder diagnosis has become more popular, but in case of schizophrenia it still needs to become more robust and reliable. In similar studies [8][9] have been shown that fMRI can be used in conjunction with Sparse Gaussian Markov Random Field (SGMRF) to produce high accuracy in diagnosis of illness. However having a dataset with homogeneous distribution of illness makes this result less reliable and creates the need for more evidence using heterogeneous dataset in terms of illness. In this work we pursue two path to tackle this problem. First, we evaluate performance of Sparse Gaussian Markov Random Field (SGMRF) on fMRI data obtained through whole brain, and second we work on Regions of Interest (ROI) according to Power *et al.* [7]. We have used 5 fold cross validation for hyper parameter tuning and 20% holdout set for test. Accuracies that we have obtained through mentioned method are: —— for whole brain features and —- for ROI features. While this result are slightly less than the results obtained by Rish *et al.* it is on par with Rosa *et al.* results.

1 Introduction

Schizophrenia is a mental/psychiatric disorder [8, 5] known affect blood flow in the brain [5] where those who are affected can experience hollucinations, delusions and diminished mental capacities to varying extents [4]. While several features of schizophrenia have proven useful for its diagnosis there are current no set of features that have sufficient sensitivity or specificity to be used in diagnostic tests [4]. This effectively means that subjectivity plays a role when a physician is looking to diagnose a patient.

Functional Magnetic Resonance Imaging (fMRI) is a tool for recording functional changes caused by neuron activity[]. When a person is doing a task, neuron activity fluctuates and in order to provide the energy needed for this activity human body increases the blood flow to feed the neurons with the needed glucose which is not stored in the brain[]. More blood flow also brings more oxygen through blood vessels. This change in the level of oxygenated blood known as oxyhemoglobin and deoxyhemoglobin (oxygenated or deoxygenated blood) changes the magnetic susceptibility of blood (BOLD signal) which is the base for detection in MRI machine[].

As a mental disorder, schizophrenia is well suited to be analyzed using fMRI because fMRI is able to detecting changes in the brain caused by Schizophrenia or other neuralogical disease[]. The

only disadvantage is the low resolution of fMRI compared to the scale of those changes. However, fMRI is still one of the most used and efficient tools in the study of psychiatric disorders such as Schizophrenia[]. Another advantage of fMRI is that this method is non-invasive. This means that unlike some other imaging methods that need to use some types of instruments in patient's body, this method operates without using them[].

One of the approaches that has been used for studying schizophrenia is Sparse Gaussian Markov Random Field(SGMRF) [8][9]. A main advantage of using this method is that functional network of the brain can be captured using the precision matrix [8]. By using the resulted network, one can differentiate between healthy subjects and schizophrenic ones, which depends on the functional connectivity in the brain. Currently automated approaches to schizophrenia diagnosis have been able to yeild accuracies of 93% for data that originates from a single location [8] and up to approximately 80% for data that originates from multiple locations [1].

2 Background and Prior Work

2.1 Regions of Interest and Single-Voxel Analysis

Traditionally in fMRI analysis there are two main approaches for extracting information from the fMRI image. The first is a single-voxel approach and the second is to study regions of interest (ROI) [3]. The tradeoff between these two approaches is that a single-voxel approach requires the analysis of every voxel and is subject to the low signal to noise ratios of individual voxels, whereas a region based approach is only as effective as the regions are relevant to the fMRI task [3]. In 2011, Power *et al.* identified 264 putative function regions of interest derived from resting state fMRI, where no specific task being performed during data collection [7]. These regions contain substructures that agree that with known functional brain systems and therefore can be seen as fairly accurate representations [7].

2.1.1 Calculating Degrees

When analyzing fMRI data features such as voxel degrees can be extracted for use with a machine learner. Voxel degrees represent the connectedness of voxels in the brain with the other voxels and are described as "the number of voxel neighbours in a network" [8]. Degrees are calculated by performing multiple Pearson correlation comparisons between the i^{th} voxel and every other voxel. Once correlation values have be determined, a threshold is applied to the correlation matrix. This results in binary matrix where 1 represents a correlation value above the threshold and 0 represents a value below. Finally, for each voxel the number of 1 entries are summed (excluding the comparison against itself) and this becomes the degree of the voxel.

2.2 Multi-site Comparisons

2.3 Principal Component Analysis

2.4 Support Vector Machines

What is an SVM and how does it work

2.5 SGMRF

What is a SGMRF and how does it work

One variation of Markov Random Field is Gaussian Random which is mostly being used for continuous space of variables and has well-defined mathematic properties that can be computed. Multivariate Gaussian density function over set of random variables X is defined as below:

$$p(X) = (2\pi)^{-n/2}|\Sigma|^{-1/2} \exp\left\{-\frac{1}{2}(X-\mu)^t\Sigma^{-1}(X-\mu)\right\}. \quad (1)$$

Where μ is mean and Σ is the covariance matrix. We can set the μ to zero and replace Σ^{-1} with C the equation (1) can be written as the following form.

$$p(X) = (2\pi)^{-n/2}|C|^{1/2} \exp\left\{-\frac{1}{2}(X-\mu)^t\Sigma^{-1}(X-\mu)\right\}. \quad (2)$$

3 Methodology

3.1 Data Set

Turn our slide into this section How do we have? Balance? How we create the holdout set?

3.2 Your Approach? Mario

First, we ran the approach proposed by Rish *et al.* [8] on our data set. Here, we obtained the log degrees of each voxel for each subject. Thus we had a matrix of size 380×28720. However, using all the available voxels resulted in computation difficulties and thus selecting the best voxels to separate the healthy and schizophrenic subjects is very important.

To select the best voxels out of the possible 28720 voxels, we experimented multiple approaches. These include

1. Selecting the voxels based on the t-test.
2. Selecting the voxels based on the absolute differences between the mean degrees of a voxel between schizophrenic and healthy subjects.
3. Selecting the voxels based on the differences between the mean degrees of a voxel between schizophrenic and healthy subjects.
4. Selecting the voxels based on the differences between the mean degrees of a voxel between healthy and schizophrenic subjects.

Out of the above four approaches we obtained the highest accuracy on our cross validation set by the third approach. Also the number of voxels to select k was decided by running the same approach for different k values. And we found the optimum k value as 20 for our cross validation set. By using the selected voxels we obtained the precision matrices for schizophrenic and healthy subjects. Similar to the value of k, the sparsity coefficient λ was also obtained through a hyper parameter serach on our cross validation set.

3.3 Methods using Power *et al.*'s ROIs

3.3.1 ROI with Patient Concatenation

3.3.2 ROI with Fouier Coefficients

3.3.3 Region Degrees and SVMs

3.3.4 Individual MRF Structure Classification

3.4 Your Approach? Farhad

Describe your experiments

4 Results

4.1 Your Approach? Mario

With the Rish et al. code we obtained a 69% cross validation accuracy on our cross validation sets and 75% accuracy on the hold-out set.

4.2 Methods using Power *et al.*'s ROIs

4.2.1 ROI with Patient Concatenation

4.2.2 ROI with Fouier Coefficients

4.2.3 Region Degrees and SVMs

4.2.4 Individual MRF Structure Classification

4.3 Your Approach? Farhad

Report your results

5 Conclusions

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