

RS-fMRI Classification of Antisocial Personality Disorder Subject's using SVM

K. Nirmala *

PG Student, Dept of ECE,
Sri venkateswara College of Engineering,
Sriperumbudhur,

K. Thaiyalnayaki,

Associate Professor Dept Of ECE,
Sri venkateswara College of Engineering,
Sriperumbudhur,

Abstract- abnormal behaviour state of brain such as ASPD (anti) is identified and classified . Previous attempts using functional connectivity data for diagnostic classification utilized recursive feature elimination and RF. This work implemented the same with several machine learning tools, mostly non-parametric ensemble learning method, to reach high accuracy. The steps in Design Methodology includes input from SIMTb toolbox, simulated sample of 3 healthy person and 2 samples of antisocial personality disorder. Using statistical parametric mapping pre-processing is done, 30 Independent components are separated by ICA which includes amygdala, auditory cortex and visual cortex. The features such as kurtosis, skewness, entropy, autocorrelation are extracted from 30 IC time series of total 5 subjects, 120x5 feature matrix is used for classification using SVM.

Index Terms—Antisocial personality disorder (ASPD), Independent components (IC), Feature extraction, Diagnostic classification, Support vector machine (SVM).

1. INTRODUCTION

Antisocial personality disorder (ASPD) is a highly heterogeneous disorder, diagnosed on the basis of behavioural criteria. From the neurobiological perspective, 'ASD' can be considered an umbrella term that may encompass multiple distinct neurodevelopment etiologies. Since any given cohort is thus likely composed of ill-understood subtypes (whose brain features may vary subtly or even dramatically), it is not surprising that brain markers with perfect sensitivity and specificity remain unavailable. Nonetheless, given the specificity of diagnostic criteria (American psychiatric Association, 2013), the hope that some (potentially complex) patterns of brain features may be unique to the disorder is not unreasonable and worthy of pursuit. Issues of heterogeneity and cohort effects can be partially addressed through the use of large samples, as provide by the recent antisocial personality disorder (ASPD), which incorporates over normal1 data 110×30, normal2 data 110×30, normal3 data 110×30, patient data 64×30, patient data 100×30 datasets from 5 sites. The use of these data for examining functional connectivity matrices for large numbers of ROIs across the entire brain is further promising, as there is growing consensus about ASPD being characterized by aberrant connectivity in numerous functional brain networks. However, the functional connectivity literature in ASD is complex and often inconsistent and data-driven machine learning (ML) techniques provide valuable exploratory tools for uncovering potentially unexpected patterns of aberrant

connectivity that may characterize the disorder. A few previous ASD studies have used intrinsic functional connectivity MRI (fMRI) for diagnostic classification, i.e., for determining whether a dataset is from an ASD or typically developing participant solely based on functional connectivity. , using a large fMRI connectivity matrix, reached an overall diagnostic classification accuracy of 79%, which was however lower in a separate small replication sample used a logistic regression classifier for 10 rs-fMRI based features identified by ICA, which corresponded to previously described functional networks. The classifier achieved accuracies about 60–70% for all but one component identified as salience network, for which accuracy reached 77%[1]. Imperfect accuracy in these studies may be attributed to moderate sample sizes ($N \leq 80$). However, in a recent classification study using the much larger ABIDE dataset, reported an overall accuracy of only 60%, suggesting that the approach selected, a leave one-out classifier using a general linear model, and may not be sufficiently powerful.

In present study, we implement several machine learning methods including, mostly non parametric ensemble to reach high accuracy. The outlines of this research paper are as follows. In section II review of literature is shown; in section III we will see propose approach. In section IV we will see experimental results. and in section V we will see the conclusion.

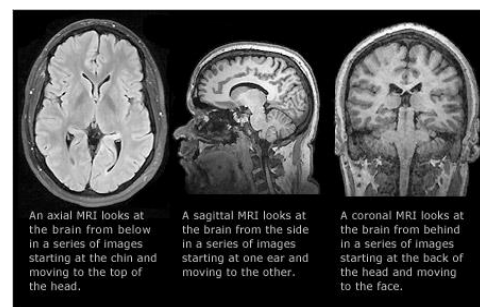


Fig. 1 Brain region

II LITERATURE SURVEY

Colleen P. Chen , Christopher L. Keown [1] Proposed their We first used PSO in combination with a base classifier, a linear support vectore machine. PSO is a biologically inspired, stochastic optimization algorithm that models the behaviour of swarming particles. The PSO

algorithm was utilized as a feature selection tool to obtain a compact and discriminative feature subset for improved accuracy and robustness of the subsequent classifiers. Aiying Zhang^{1,2}, Ping Tang¹ [2] In addition to performing linear classification, SVM can efficiently perform non-linear classification using what is called the Kernel trick, implicitly mapping their inputs into high-dimensional Feature Spaces. Marek Kurzynski, maciej krysmann [3] in these paper the experiments were conducted using two types of ensembles are homogeneous and heterogeneous. Each classifier was trained using randomly selected 70% of objects from the training dataset. Gopika suresh, Graduate student Member, IEEE [4] The classification algorithm must try to resemble the method that the human brain uses to choose between natural oil slicks and L-As. We choose a decision-based classifier that employs an array of classification rules due to its speed and simplicity.

III PROPOSED SYSTEM

Data were selected from the antisocial personality disorder, a collection of over F16-99 inputs. In view of the sensitivity of intrinsic fMRI analyses to motion artifacts and noise, we prioritized data quality over sample size acts. We excluded any datasets exhibiting artifact, signal drop-out, suboptimal registration or standardization, or excessive motion. The Design methodology as shown in fig.2.

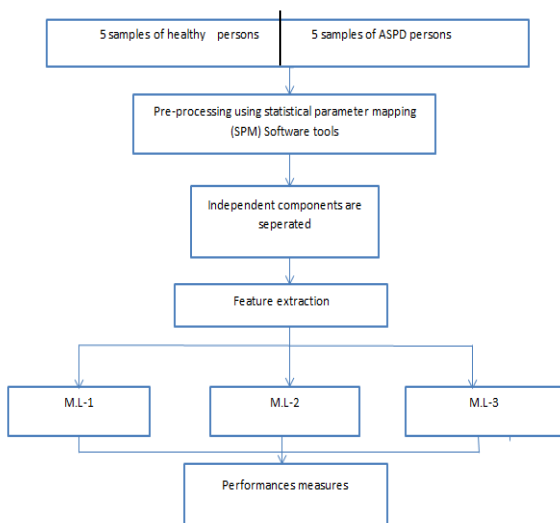


Fig. 2 Design methodology

DATA PRE-PROCESSING

Data were processed using the SPM (Statistical parameter mapping) software tools. SPM is made freely available to the [neuro] imaging community, to promote collaboration and a common analysis scheme across laboratories. The software represents the implementation of the theoretical concepts of Statistical Parametric Mapping in a complete analysis package. The SPM software is a suite of MATLAB functions and subroutines with some externally compiled C routines. SPM was written to organise and interpret our functional neuro imaging data. The distributed version is the same as that we use ourselves. The SPM

software package has been designed for the analysis of brain imaging data sequences. The sequences can be a series of images from different cohorts, or time-series from the same subject. The current release is designed for the analysis of Fmri PET, SPECT, EEG and MEG. SPM12, is a major update to the SPM software, containing substantial theoretical, algorithmic, structural and interface enhancement over previous versions. Statistical parametric mapping (SPM13 software) using preprocessing steps in pre-processing steps the given inputs are F 16-99 inputs.

Preprocessing steps:

1. Image Realignment
2. Co-registration
3. Normalized
4. Smoothing

IMAGE REALIGNMENT

Realign is the most basic function to match images. In image realignment the input data F16-99 are too shown in X, Y, Z translation. The wave form shows from 0 to 83 as the sagittal, axial, and coronal.

CO-REGISTRATION

Co- registration is the process of transforming different sets of data into one co-ordinate systems. Registration is necessary in order to be able to compare or integrate the data obtained from these different measurements. Data are stored in the .hdr files.

NORMALIZED

Normalized is process of those changes the range of pixel intensity values. It is a multi-steps process that puts data into tabular form by removing duplicated data from the relation tables.

SMOOTHING

Smoothing is a process of blurring image. Smoothing may be used in to important ways that can aid in data analysis. The blurring image of brain is called as Smoothing.

STEPS 2 FEATURE EXTRACTION

Feature extraction involves reducing the amount of resources required to describe a large set of data. When performing analysis of complex data one of the major problems stems from the number of variables involved. Analysis with a large number of variables generally requires a large amount of memory and computation power, also it may cause a Classification algorithm to over fit to training samples and generalize poorly to new samples. Feature extraction is a general term for methods of constructing combinations of the variables to get around these problems while still describing the data with sufficient accuracy. In machine learning, pattern recognition and in image processing, feature extraction start from an initial set of measured data and builds derived values (features) intended to be informative and non-redundant, facilitating the subsequent learning and generalisation steps, and in some cases leading to better human interpretations. Feature extraction is related to

dimensionality reduction. When the input data to an algorithm is too large to be processed and it is suspected to be redundant (e.g. the same measurement in both feet and meters, or the repetitiveness of images presented as pixels), then it can be transformed into a reduced set of features (also named a features vector). This process is called feature extraction. The extracted features are expected to contain the relevant information from the input data, so that the desired task can be performed by using this reduced representation instead of the complete initial data. 30 Independent components are separated from the normal data1,2,3 and patient data1&2 to find features like Kurtosis, Skewness, Entropy and Autocorrelation.

FEATURE MEASUREMENT

KURTOSIS: kurtosis is a measure of the sparseness of a distribution; it is zero for gaussian distribution.

$$Kurt_i = \frac{\sum_{k=0}^n Z_{i,k}^4}{N} - 3$$

Where, $z_{i,k}$ represents the value of the k^{th} voxel of the i^{th} component and N is the number of voxels

SKEWNESS: Skewness is a measure of asymmetry distribution, it is zero Gaussian distribution.

$$skew_i = \frac{\sum_{k=1}^N Z_{i,k}^3}{N}$$

ENTROPY: entropy is a measure of information of time course of component.

$$H = \sum_{b=1}^{N_b} ht_i(b) \cdot \log_2(ht_i(b))$$

AUTOCORRELATION: for one, lag of autocorrelation is estimated.

$$r_i = \frac{\frac{1}{T-1} \sum_{t=1}^{T-1} a_i(t) \cdot a_i(t+1)}{\frac{1}{T} \sum_{t=1}^{nT} a_i(t)^2}$$

EXTRACTED FEATURES

4 sets of features are extracted from each IC. The four sets of values denote Kurtosis, skewness, entropy, Autocorrelation.

STEPS-3 CLASSIFIER

SVM TRAINED

The SVM trained values are 4 sets of the 30 values of Kurtosis and skewness. Other SVM trained values are 4 sets of the 30 values of Entropy and Autocorrelation. The output of svm trained as shows in Fig.7 and Fig.8.

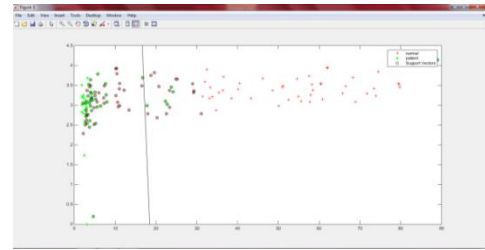


Fig. 7 SVM trained output1

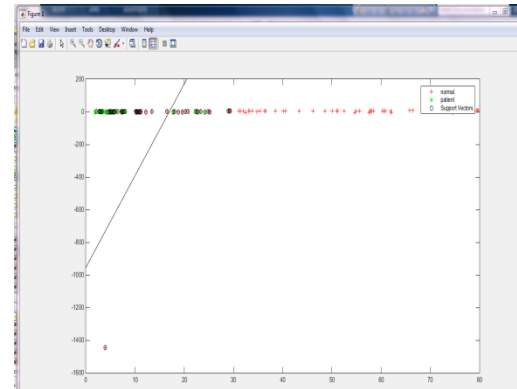


Fig.8 SVM trained output 2

IV CONCLUSION

Independent component analysis (ICA) is one of the common methods used for analyzing Fmri measurements. In this study, Fmri data was simulated by activating various brain regions involved in an ASPD person in comparison with the healthy controls using SPM13 b MATALAB Toolbox. IC automatically separated a time- series waveform representing neural activity associated with a auditory stimulus. Identified the 30 independent components (IC) of 5 subjects and extracted 5 sets of features from each IC. Apply the ensemble classifier to reach high accuracy.

V FUTURE WORK

Apply the classifiers to measure parameters values. Diagnostic classification will be implemented with several machine learning tools, mostly non- parametric ensemble learning method, to reach high accuracy. Finished module can be utilized for any clinical decision support system. This can be futher extended for automatic neurosurgery application.

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