An Evolutionary Approach for fMRI Big Data Classification

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How does fMRI work?

(A) Normal, random atoms' spins

(B) Magnet aligns atoms' spins

(C) Radio frequency pulse knocks over spins

(D) Spins "recover" to (B), how quickly depending on tissue type

(E) Neural activity computed from recovery time in (D)
Subjects & Data Acquisition

- In collaboration with Amsterdam Center for Addiction, Netherlands
- MRI Scanner: 3.0 T Philips Achieva 3.2.1
- 39 Patients: 19 (NAC), 20 (Placebo)
- Resting States
- Functional Image Size: 80×80×37 with a voxel size of 3mm
  - 200 MRI picture before and 200 MRI picture after two weeks
- Anatomical Image Size: 240×240×220 with a voxel size of 1mm
  - 1 MRI before and 1 MRI after two weeks
Anatomical

Functional
Data Pre-Processing

- Slice Time Correction
- Voxel Realignment
- Co-Registration: change scale
- Segmentation
- Normalization
- Smoothing
Raw Data                         Pre-Processed Data

Pre-Processing
Data Reduction

- Independent Component Analysis (ICA)
- Principal Component Analysis (PCA)
ICA

3D image flattened, all voxels at $T = 1$

FMRI data

$n \times m$

$n$ time points

$m$ voxels

Components spatial map

$n \times n$

$n \times m$

spatial maps
Correlation Matrices with ICA

ICA With 5 Components

ICA With 10 Components

ICA With 15 Components
- Suppose $x_1, x_2, \ldots, x_M$ are $N \times 1$ vectors

**Step 1:**

$$\bar{x} = \frac{1}{M} \sum_{i=1}^{M} x_i$$

**Step 2:** subtract the mean: \( \Phi_i = x_i - \bar{x} \)

**Step 3:** form the matrix \( A = [\Phi_1 \Phi_2 \cdots \Phi_M] \) (\( N \times M \) matrix), then compute:

$$C = \frac{1}{M} \sum_{n=1}^{M} \Phi_n \Phi_n^T = AA^T$$

(sample covariance matrix, \( N \times N \), characterizes the scatter of the data)

**Step 4:** compute the eigenvalues of \( C \): \( \lambda_1 > \lambda_2 > \cdots > \lambda_N \)

**Step 5:** compute the eigenvectors of \( C \): \( u_1, u_2, \ldots, u_N \)
Correlation Matrices with PCA
Classification

- Logistic Regression
- K-Nearest Neighbors
- Gaussian Naïve-Bayes
- Bernoulli Naïve-Bayes
- Genetic Programming
Leave-One-Out Cross-Validation

Total number of available examples

\( K = 0 \)

\( K = 1 \)

\( K = 2 \)

\( K = N \)
Start

Input Raw fMRI Data

Pre-Processing

Data Reduction Feature Selection

Initialize Population

Fitness Evaluation

Termination

Cross-Validation

End

Selection

Reproduction
# GP Parameters

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<th>Parameter</th>
<th>Setting</th>
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GP Evolutions
ROC Curves for GP Classifier
### Classification Accuracies

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<tr>
<th>IC</th>
<th>LR</th>
<th>Bernoulli NB</th>
<th>Gaussian NB</th>
<th>KNN</th>
<th>GP</th>
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Conclusions

- Compared an evolutionary approach, Genetic Programming model, with multivariate machine learning methods along.
- Used ICA and PCA to conduct analyses on high activity regions in the limbic system of the fMRI data.
- Due to the power of GP methods in classifications and flexible heuristic techniques, GP outperformed the other methods.
Thank you!
References


