

High Performance GP-Based Approach for fMRI Big Data Classification

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Abstract

We consider resting-state functional Magnetic Resonance Imaging (fMRI) of two classes of patients: one that took the drug N-acetylcysteine (NAC) and the other one a placebo before and after a smoking cessation treatment. Our goal was to classify the relapse in nicotine-dependent patients as treatment or non-treatment based on their fMRI scans. 74% accuracy was obtained using Principal Component Analysis (PCA) along with Genetic Programming (GP) classifier using High Performance Computing (HPC) which we consider significant enough to suggest that there is a difference in the resting-state fMRI images of a smoker that undergoes this smoking cessation treatment compared to a smoker that receives a placebo.

Results



Introduction

As a new approach for classifications, Genetic Programming (GP) has been applied to analyze data from a smoking cessation treatment, where subjects take a drug to reduce their nicotine dependence while still being allowed to smoke in order to keep off the effects of withdrawal. This is the preferred method as more people are likely to try it if they do not have to quit smoking immediately. The goal is to reduce the nicotine dependency to the point that it is easier for the subject to stop. Functional Magnetic Resonance Imaging (fMRI) is a set of noninvasive techniques for functional brain mapping. Areas of high activity are defined to be those where more oxygen-rich blood is flowing and the fMRI is able to map these areas. We have compared some machine learning algorithms with Genetic Programming to classify the subjects on whether or not they underwent the treatment. The accuracy of classification will rely heavily on how the data is reduced.

Table: Classification Accuracy for Different Numbers of Independent Components (ICs)

ICs	LR	Bernoulli NB	Gaussian NB	KNN	GP
5	38.46%	66.66%	41.02%	61.53%	64.10%
10	35.89%	38.46%	48.71%	61.53%	64.10%
15	38.46%	48.71%	41.02%	51.28%	68.71%



Table: Classification Accuracy for Different Numbers of Principal Components (PCs)

PCs	LR	Bernoulli NB	Gaussian NB	KNN	GP
5	61.53%	58.97%	46.15%	61.53%	58.97%
10	46.15%	51.28%	43.58%	61.53%	73.46%
15	53.84%	61.53%	43.58%	58.97%	64.10%

Subjects & Data Acquisition

- Collaboration with the Amsterdam Center for Addiction and Research.
- 3.0 T Intera MRI. scanner, Philips Health care with a SENSE eight-channel receiver head coil.
- 39 subjects: 19 the drug NAC, 20 a placebo.
- 200 3-dimensional temporal images of BOLD signal.
- 3-dimensional anatomical data of size $240 \times 240 \times 220$ with a voxel size of 1mm.
- 3-dimensional functional data was of size $80 \times 80 \times 37$ with a voxel size of 3mm.

Data Pre-Processing

Data Reduction

1 Motion Correction OSlice-Timing Correction Segmentation & Realignment A Normalization & Smoothing **5**Co-Registration

1 Independent Component Analysis 2 Principal Component Analysis





Conclusion

We have compared an evolutionary approach, Genetic Programming model, with multivariate machine learning methods along with 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 out-



Figure: Functional MRI Data

Figure: Correlation Matrices for ICA

Figure: Correlation Matrices for PCA

performed the other methods.

References

[1] Amirhessam Tahmassebi, Amir H. Gandomi, Ian McCann, Mieke HJ Schulte, Lianne Schmaal, Anna E. Goudriaan, and Anke Meyer-Baese. An evolutionary approach for fmri big data classification. IEEE Congress on Evolutionary Computation, 2017.

Classifications

GP Parameters

1 Logistic Regression

• Naive-Bayes (Gaussian & Bernoulli) **3**K-Nearest Neighbors 4 Genetic Programming

- Population: 500, Generation: 2000
- Hall of fame: 300, Tournament: 20
- Function set: add, sub, mul, div, log, inv, abs

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