Interpretable and Lightweight Machine Learning Approach for Autism Classification Using Biomarkers Derived from **Multi-trial Resting EEG**

BOSTON

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INTRODUCTION

- Autism Spectrum Disorder (ASD): heterogenous, hard to identify biomarkers for diagnosis
- Electroencephalography (EEG): valuable tool for biomarker identification—non-invasive, high temporal resolution, affordable

1) DATA¹ Age (years) Male/Female Size Group Autism (ASD) 55/39 12.5 ± 2.9 94 Control (CON) 96 12.9 ± 2.8 49/47

3) FEATURE EXTRACTION

Electrodes

frequency band

Within-band features

 $128 \times 5 \times 4 = 2560$ features

Frequency bands

Get Power Spectral Density (PSD) at each electrode and frequency

2) PREPROCESSING

- Low pass (<100 Hz) and Notch (60Hz) filters</p>
- Wavelet threshold and bad segment rejection
- ICA and bad channel rejection¹

4) TRAINING AND TESTING

Four classifiers trained on the two



Subset of EEG signals (Figure from Biopac)

EEG head map (Template from Neuhaus *et. al.*¹)

Coccipital

GOALS

- Predict ASD from EEG using machine learning tools
- Explore distributional features across EEG trials
- Identify important features for ASD diagnosis

band using Welch's estimate {hamming, 512 point}

Two Feature Aggregation Types

| Mean-EEG | | Across-trial |
|--|--|--|
| PSD of Mean EEG (conventional) | | PSD of EEG for each |
| Mean, std. deviation, skew, & kurtosis of PSD in each | | Mean, std. deviation & kurtosis of PSD in |

skew, & kurtosis of PSD in each frequency band

trial

METHODS

Mean and std. deviation of band features <u>across trials</u>

2 x 2560 = 5210 features

standardized feature types separately

- 1. Logistic regression (LR)
- 2. Random forest without bootstrap (RF)
- 3. Kernel-support vector machine (SVM)
- 4. An artificial neural network (ANN)
- Stratified 5-fold cross-validation
 - Repeated 5x
- Evaluation: accuracy, F1 score, precision, recall, specificity, AUROC, AUPRC metrics
- Feature importance: determined by magnitude of mean feature weights in cross-validation across-trial LR models

RESULTS

REPEATED 5-FOLD CROSS-VALIDATION MODEL PERFORMANCE

| Model | Features | Accuracy | F1 score | Precision | Recall | Specificity | AUROC | AUPRC |
|-------|--------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| LR | Across-trial | 0.678±0.083 | 0.678±0.083 | 0.674±0.101 | 0.693±0.108 | 0.664±0.123 | 0.748±0.073 | 0.751±0.086 |

REPEATED 5-FOLD CROSS-VALIDATION ACCURACY



| | Mean-EEG | 0.608±0.060 | 0.597±0.088 | 0.601±0.082 | 0.604±0.117 | 0.61±0.085 | 0.648±0.070 | 0.678±0.084 |
|-----|--------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| RF | Across-trial | 0.660±0.085 | 0.646±0.102 | 0.665±0.112 | 0.649±0.147 | 0.681±0.121 | 0.742±0.082 | 0.744±0.089 |
| | Mean-EEG | 0.614±0.068 | 0.589±0.076 | 0.626±0.095 | 0.571±0.109 | 0.662±0.115 | 0.672±0.092 | 0.693±0.088 |
| SVM | Across-trial | 0.659±0.079 | 0.656±0.089 | 0.659±0.101 | 0.679±0.146 | 0.654±0.106 | 0.734±0.087 | 0.743±0.093 |
| | Mean-EEG | 0.577±0.064 | 0.532±0.087 | 0.608±0.136 | 0.509±0.161 | 0.669±0.146 | 0.608±0.146 | 0.619±0.102 |
| ANN | Across-trial | 0.654±0.088 | 0.682±0.099 | 0.650±0.108 | 0.751±0.156 | 0.590±0.160 | 0.721±0.095 | 0.709±0.084 |
| | Mean-EEG | 0.622±0.079 | 0.616±0.112 | 0.600±0.112 | 0.661±0.160 | 0.564±0.158 | 0.651±0.108 | 0.683±0.098 |

Table 1: Metrics from all experiments. Significant differences (p<0.05) from two-sample t-tests between the two feature types are highlighted in green. (No significant differences between model choices found.)

Fig 1: Accuracy of all models using the two feature types. Across-trial feature models show higher accuracy.



DISTRIBUTION OF TOP 5% MOST IMPORTANT FEATURES

SIGNIFICANTLY DIFFERENT BRAIN REGIONS BETWEEN GROUPS



P-value = 6.38e-14P-value = 5.94e-06

Fig 2: Frequency band distribution (left) and across-trial feature distribution (right) of the top 5% most important features. P-values from chi-square goodness-of-fit tests with the null hypothesis of a uniform distribution.

-log10(P-value) p>0.05 p<0.05 2 3 4

Fig 3: Topological head plots of significant regions based on two-sample t-tests for the difference between ASD and CON in the mean of summed across-trial features adjusted by LR model weights.

DISCUSSION AND CONCLUSION

Features recording variability across trials are more important

- Trial-to-trial variability differs between ASD and CON groups²
- The choice of machine learning model is not significant
- Beta frequency: highest diagnostic value in all brain regions
- Occipital and frontal temporal regions: higher diagnostic value across multiple frequency bands

Future work:

- Incorporate features from task-EEG data
- Use deep learning for feature extraction

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