Sex classification models based on temporal complexity features

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INTRODUCTION

Sex Difference in the Brain

Though sex chromosomes, and, in turn, sex hormones, are known to influence brain organization to some degree, it is difficult to conclude that the male and female brains are distinct organs. Although male and female brains differ on average in a handful of regions, a "mosaic model" of structural differences suggests that there are very few individuals who lie on the male or female end of the spectrum for every brain region in which a sex difference has been identified [8]. Sex-differences, though commonly misunderstood [5], still have clinical relevance because of the difference in prevalence, severity, and survival of neurological conditions like autism spectrum disorders, Parkinson's Disease, and schizophrenia [3].

Classification Models

With the advent of large imaging datasets like the Human Connectome Project, it has become possible to achieve better separation of males and females though higher-dimensional machine learning classification models. To date, a host of signal features– including parcel-wise connectivity [10], Hurst Exponent [4], and dynamic functional connectivity [6]-- have been employed to build these models. The aim of this study is to investigate the relationship between sex and temporal complexity features through the construction and evaluation of classification models. The signal features of interest are regional sample entropy (SampEn), a measure of temporal complexity that has been linked to individual differences [12], and fractional amplitude of low frequency fluctuations, (fALFF), which has shown a sex difference in studies involving shyness [11], and conduct disorder [2].

METHODS

Dataset

Subjects were selected from the S500 release of the Young Adult Human Connectome Project; subjects were included if all four resting scans were available and head motion was below a threshold value of 0.14 mm [7]. Randomly selecting a sex balanced subset of the data yielded 340 subjects (170 males), which were split into groups of 272 and 68 for training and out-of-sample prediction.

Preprocessing

Data were preprocessed using the FIX-denoising pipeline [1] and parcellated using the 90 region of interest (ROI) map from Stanford's FIND Lab [9].

Classification Models

- Support vector machine, Logistic regression

METHODS CONTINUED

Signal Features

- Sample Entropy: calculated for subseries lengths m=2 and m=5
- fALFF: Each ROI time series was transformed to the frequency domain using fast-Fourier transform (FFT), and the corresponding power spectrum was calculated as the square of the magnitude. A low-frequency cutoff of 0.1 Hz was used when calculating the ratio of the power spectrum in the low-frequency range to the full power spectrum. [12]

Training

For each model and input feature combination (e.g., support vector machine with sample entropy calculated at m=2), hyperparameters for the model were selected through a grid search using a 10-fold cross-validation. Trained models were assessed by calculating prediction accuracy, and area under the curve (AUC) scores from the receiver operating characteristic (ROC) curves in Figure 1.

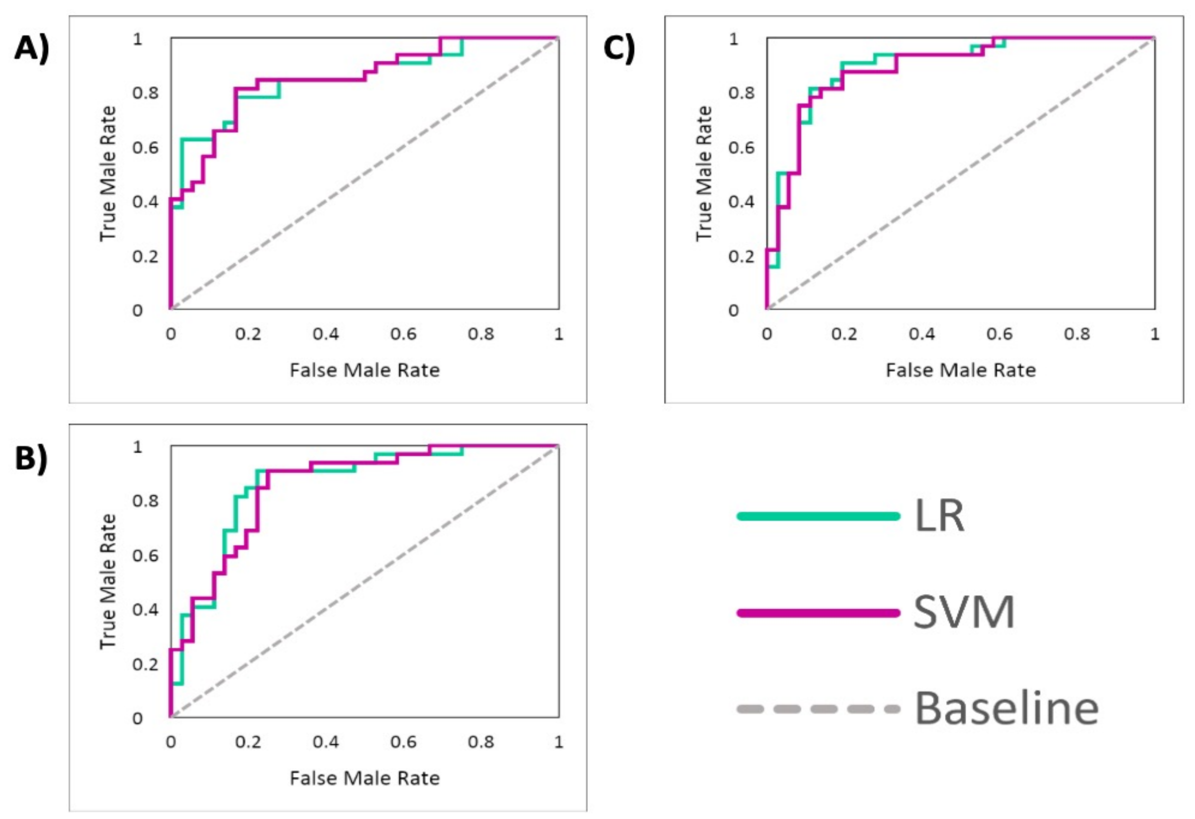

Fig. 1: Receiver operating characteristic (ROC) curves for each data type: A) sample entropy at m=2; B) sample entropy at m=5; C) fALFF and each model type: LR) logistic regression; SVM) support vector machine.

RESULTS

Data	Model Type	Classification Accuracy	AUC (area under curve)
Sample entropy (m=2)			
	Logistic Regression	0.76	0.85
	Support Vector Machine	0.79	0.85
Sample Entropy (m=5)			
	Logistic Regression	0.84	0.86
	Support Vector Machine	0.82	0.85
fALFF			
	Logistic Regression	0.82	0.90
	Support Vector Machine	0.82	0.89

Table 1. Summary of performance statistics for input feature and model type combinations, where classification accuracy is the percentage of correctly-predicted instances in the test set and AUC is the area under the receiver operating characteristic curves shown in Figure 1.

CONCLUSIONS

- Range of prediction accuracies was consistent with other reported resting fMRI classification accuracies ([10], [4], [6])
- Accuracy was not as high as with FC-based methods, possibly due to the smaller number of features used here (90 regional measures rather than 71,824 pairwise correlations)
- Results indicate the potential for temporal complexity features to carry information about sex difference, though high prediction accuracies do not necessarily imply a clear sex dimorphism [10]
- Future work will compare these results with existing understanding of structural and functional sex differences and explore different classification model types.

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