

# Fingerprinting using Machine Learning on fMRI Data

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# What is fingerprint?

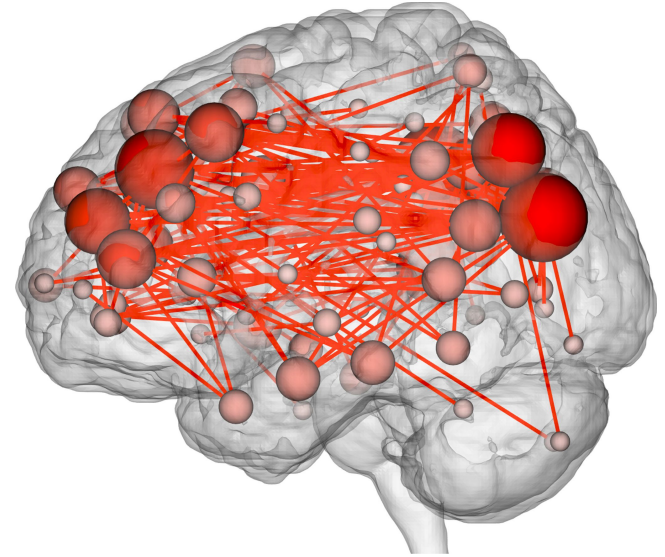
## Examples:



Hand based Fingerprint



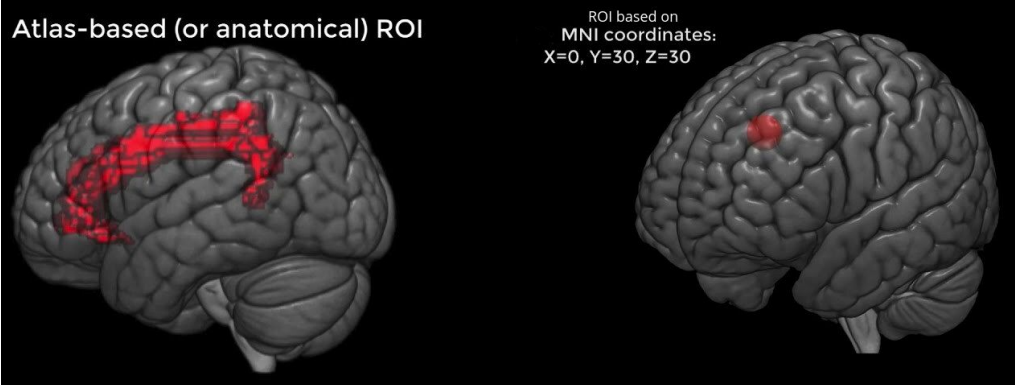
DNA Fingerprinting -  
Unique DNA patterns



Brain fingerprint - Unique brain  
connectivity graph

# What is fMRI Fingerprint?

- **Region of Interests(ROI):** a voxel or a cluster of voxels in the same vicinity defining some functionality of brain.
- Functional connectivity is defined as the temporal dependency of spatially separated brain regions or as a correlation between two ROI's in mathematical terms.
- A set of carefully chosen ROI's and their Functional Connectivity defines a matrix or a graph.
- Hypothesis: This graph represents a fingerprint and can uniquely identify individuals from a group.



# Literature Review

[1] employed an SVM based approach for fingerprinting.

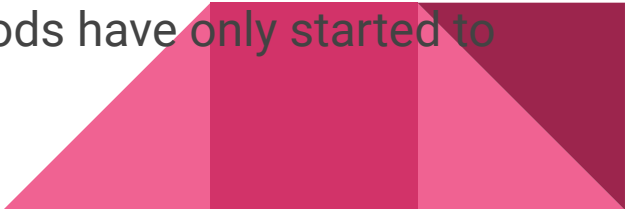
[1] made further remarks that Fingerprints are quite stable from childhood to adulthood and that fingerprints vary with decreasing genetic similarity.

[2] employed a Deep Learning based pipeline for Fingerprinting.

[3] Proposed using an SVM based approach for task-state fMRI.

[4] utilized an autoencoder based approach to enhance the inter subject variability by attempting to remove shared neural activities.

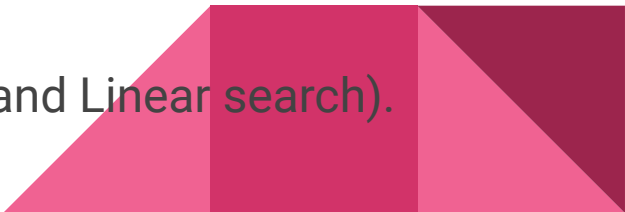
SVM's efficiency is well established, Deep Learning methods have only started to occur recently, hence I used SVM as our classifier..



# Machine Learning Pipeline for identification using Fingerprint

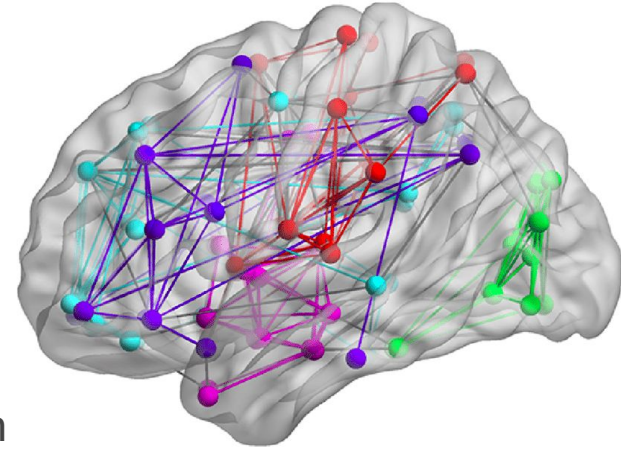
## Preprocessing

All bold images preprocessed using FSL which includes

- removing first 10 volumes
  - Band-pass filtering (0.0009 Hz, 0.08 Hz)
  - Motion Correction
  - Spatial Smoothing ( 4 mm fwhm)
  - Intensity normalization
  - Registration to 2mm MNI atlas space (using 12DOF and Linear search).
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# Feature Extraction

- <sup>1</sup> defines 264 most putative functionally connected Regions of Interests(ROI) as 264 MNI co-ordinates.
- For each Bold image, a sphere of 10 mm radius is drawn
- Within each sphere, all time series are averaged giving a total of 264 time series.
- Pearson Correlation is calculated for each of these time series pair which can be put in a 264x264 matrix.
- This matrix is called a Functional Connectivity(FC) matrix giving a total of 264x264 features for each bold image.
- Can represent this matrix as a graph called the Brain connectivity graph.



# Feature Selection and Classification

- FC matrices are symmetric and diagonal entries are always one.
- Variable and useful features are  $[264 \times 264 - 264(\text{diagonal})] / 2 = 34716$  features
- Then top k features from 34716 are selected using ANOVA feature selection.
- A  $n \times k$  data matrix is formed where n is the number of samples and divided into train-test splits or trained with LeaveOneOut Cross Validation.
- A Linear SVM is trained on the data.

```
anova_filter = SelectKBest(f_classif, k='top k features')
clf = LinearSVC()
anova_svm = make_pipeline(anova_filter, clf)
anova_svm.fit(X_train, y_train)
```

```
cv = LeaveOneOut()
anova_filter = SelectKBest(f_classif, k='top k features')
clf = LinearSVC()
model = make_pipeline(anova_filter, clf)
scores = cross_val_score(model, X, y, scoring='accuracy', cv=cv, n_jobs=-1)
```

# Training and Testing Data Set Used

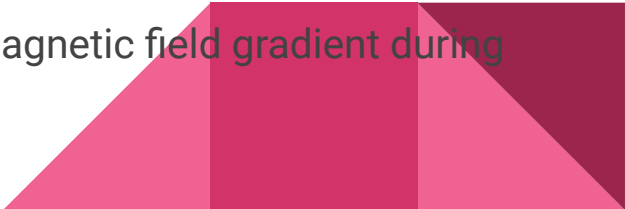
## 1) **Midnight Scan Club Data**

Description- 10 subjects, 10 sessions, 1 rfMRI image + some tfMRI image per session.

## 2) **HCP Data**

1200 subjects, each subject has 4 rfMRI image(rfMRI\_REST1\_LR, rfMRI\_REST1\_RL, rfMRI\_REST2\_LR, rfMRI\_REST2\_RL), 14 tfMRI images (tfMRI\_EMOTION\_LR, tfMRI\_EMOTION\_RL, tfMRI\_MOTOR\_LR, tfMRI\_MOTOR\_RL, tfMRI\_GAMBLING\_LR, tfMRI\_RELATIONAL\_LR, tfMRI\_RELATIONAL\_RL, tfMRI\_LANGUAGE\_LR, tfMRI\_LANGUAGE\_RL, tfMRI\_SOCIAL\_LR, tfMRI\_SOCIAL\_RL, tfMRI\_WM\_LR, tfMRI\_WM\_RL)

LR and RL are two different directions of phase encoding of magnetic field gradient during fMRI scan.





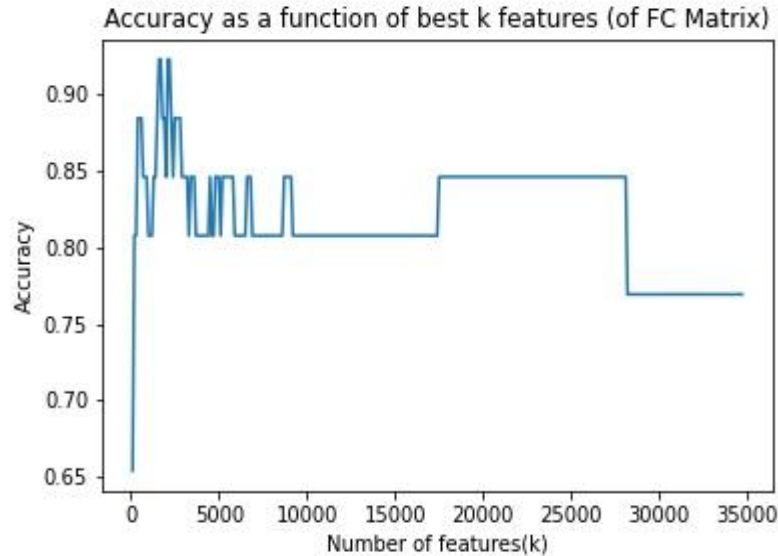
# Results

## Midnight Scan Club Data (ds000224/version 00001)

- 10 subjects, each underwent 10 sessions, each session recorded 1 resting state fMRI giving  $10 \times 10 = 100$  samples.
- Erroneous samples reduced the sample size to 84 and 9 subjects.
- LeaveOneOut Cross Validation gives a mean accuracy of 0.905 with a mean standard deviation of 0.294 in accuracy.



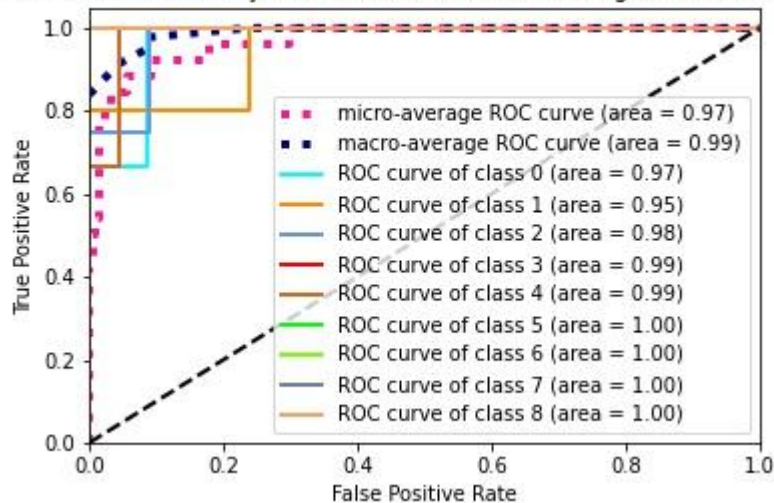
# Accuracy vs. best k-features plot



Using ANOVA feature selection and selecting k best features, and ranging k from 1 to 34716 features, the following plot is obtained, where max mean leave one out cross validation accuracy was found at  $k = 1600$ .

# ROC Curve

ROC Curve for 9 Subjects (or 9 classes) from Midnight Scan Club Data



Area Under Curve (AUC) score:

AUC = 1 implies an excellent model.

AUC = 0.5 implies that the model has no power than a random guess.

AUC = 0 implies that the model is poor, and reciprocating results.

High AUC indicates a good sensitivity or True Positive rate and a good specificity or True Negative rate at various thresholds.

All ROC values have area under curve (AUC) in the range (0.9, 1) indicating the classifier is efficient.

# HCP Data (100 Subjects)

Used 100 Subjects, 48 males, 52 females- used task images tfMRI\_EMOTION\_LR, tfMRI\_EMOTION\_RL, tfMRI\_MOTOR\_LR, tfMRI\_MOTOR\_RL, tfMRI\_LANGUAGE\_LR, tfMRI\_LANGUAGE\_RL, tfMRI\_WM\_LR, tfMRI\_WM\_RL .

Each subject represents a class.

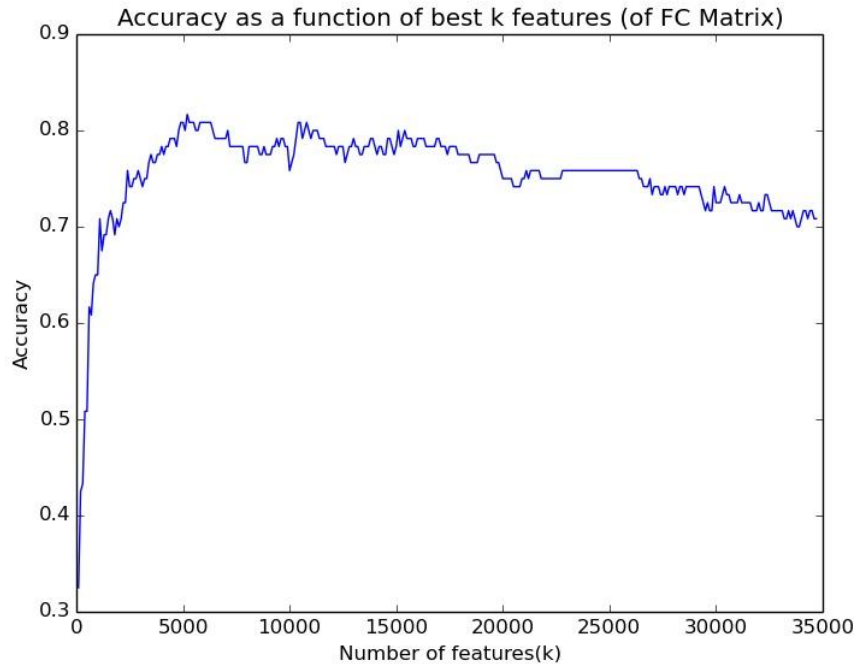
Giving  $n = 100 \times 8 = 800$  samples, i.e., 8 samples per class.

Accuracy at 30% test split is 0.68.

LeaveOneOut Cross Validation gives a mean accuracy of 0.83 with a mean standard deviation of 0.376 in accuracy.

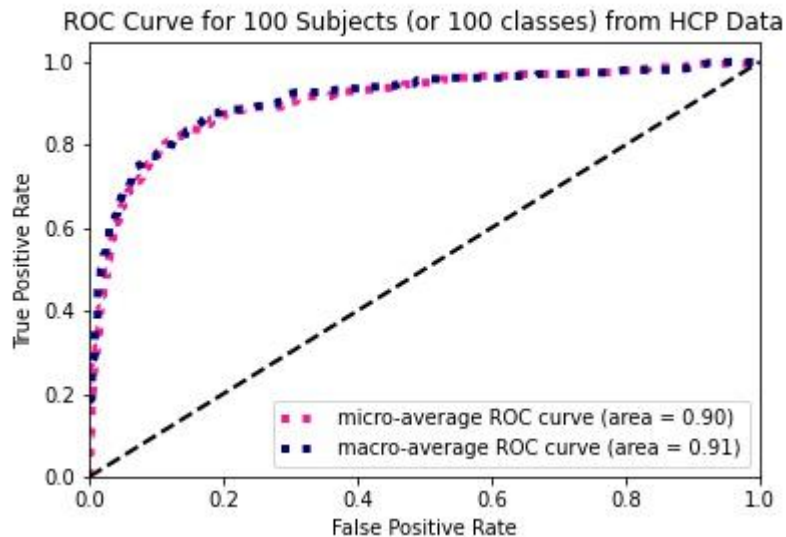


# Accuracy vs. best k-features plot



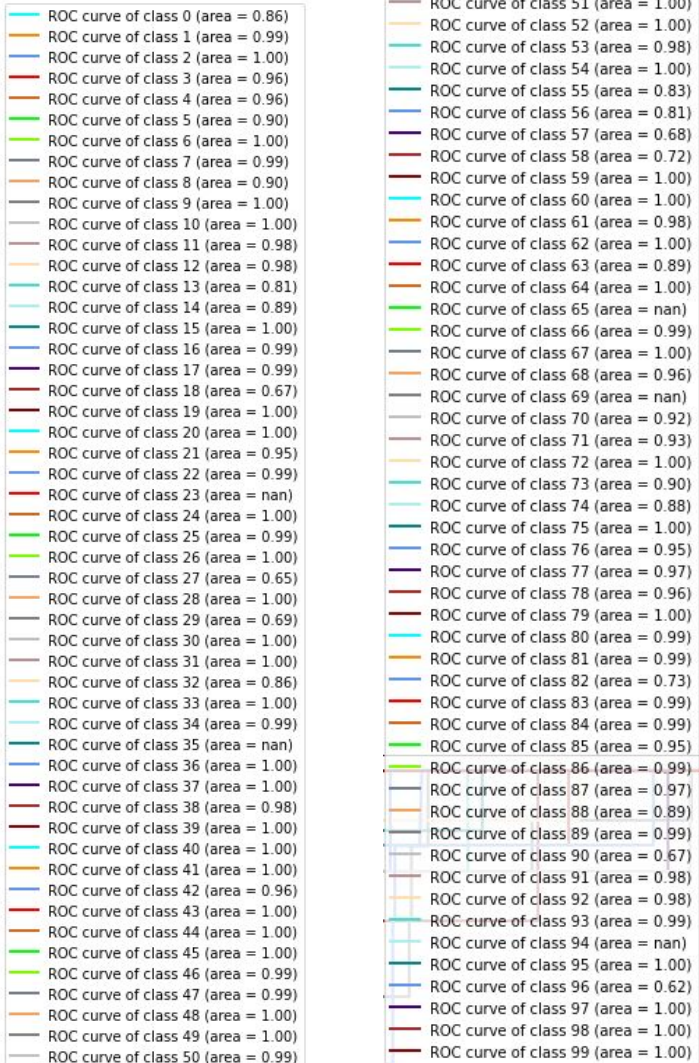
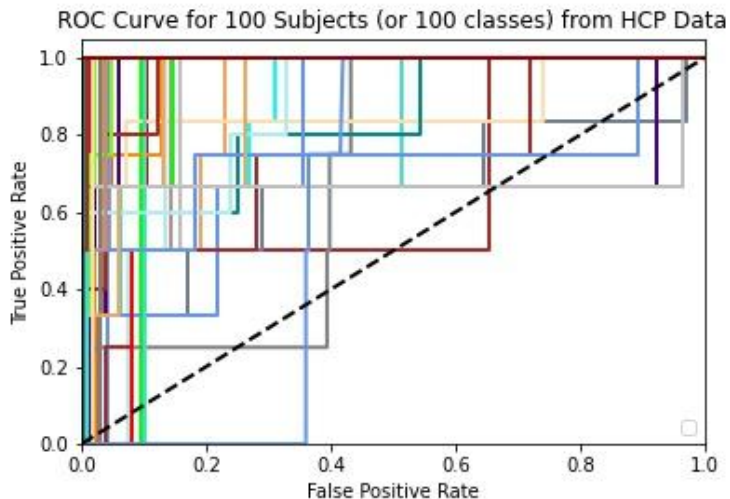
Using ANOVA feature selection and selecting k best features, and ranging k from 1 to 34716 features, the following plot is obtained, where max mean leave one out cross validation accuracy was found at  $k = 5200$ .

# ROC Curve



AUC values are close to 1 for micro-average and macro-average plus for individual classes (except some are in range 0.6 - 0.9) indicating a powerful classifier.

# ROC Curve




# Inference

Good classification results indicate that the 264 ROIs indicate regions of neural firings that are most unique.

Good AUC scores indicate the classifier is powerful enough to be used for fingerprint identification.

Since only tfMRI were used in HCP Data, indicates that the underlying fingerprint is retained to a large extent when scans are changed from rest to task.

More ROIs can be explored in future and better classifiers to eliminate common neural activities making the fingerprint more unique.





# Tools used

FSL for preprocessing.

Utilized fslroi command line tool for creating ROI 10mm radius masks.

Nilearn python library for creating FC matrices.

Scikit-learn python library for ANOVA F-test, LeaveOneOut Cross Validation and SVM Classification.



# References

- [1] Functional Connectivity Fingerprints at Rest Are Similar across Youths and Adults and Vary with Genetic Similarity- Damion V. Demeter et al., iScience 23, 2020
- [2] Deep Learning Based Pipeline for Fingerprinting Using Brain Functional MRI Connectivity Data- Nicolas F. Lori et al., Elsevier, 2018.
- [3] Support Vector Machine for Analyzing Contributions of Brain Regions During Task-State fMRI- Mengyue Wang et al., frontiers in Neuroinformatics, 2019.
- [4] Functional connectome fingerprinting: Identifying individuals and predicting cognitive function via deep learning- Biao Cai et al., 2020.

