



Shobeir Fakhraei, Hamid Soltanian-Zadeh, Farshad Fotouhi, Kost Elisevich

• **Effect of Classifiers in  
Consensus Feature Ranking  
for Biomedical Datasets**

# ➔ Dimension Reduction

- Prediction accuracy of practical machine learning algorithms **degrades** when faced with many features that are **not necessary** for predicting the desired output.
- Feature Construction / Extraction
  - Construct new features based on the original data  
e.g. PCA and ISOMAP.
- Feature Selection / Ranking
  - Choose features from the original feature set.  
e.g. Filter and Wrapper methods.

## ➔ Feature Selection / Ranking

- Improves the prediction performance.
- Eases understanding of the underlying process that generated the data.
- Reduces measurement and storage requirements.
- Facilitates data visualization.
- Reduces training and utilization times.

## ➔ Feature Ranking

- The output of the process is a ranked list of features according to a criteria.
- $f_{R1}, f_{R2}, \dots, f_{Rn}$
- Variable ranking is not necessarily used to build predictors:
  - Understanding of the underlying data.
  - e.g. which medical test is more accurate or reliable than the others in a diagnosis.

# ➔ Consensus Feature Ranking

- Ensemble (consensus) methods have been used to mitigate the problems of traditional methods such as poor accuracy, bias, and stability.
- $FinalScore(f_i) = Combination(score_1(f_i), \dots, score_n(f_i))$

# ➔ Motivation

- $FinalScore(f_i) = Combination(score_1(f_i), \dots, score_n(f_i))$
- $score_i$  is a Single Variable Classifier
- Feature score is the predictive performance of a classifier build based on only that single feature.



# ➔ Motivation

- $FinalScore(f_i) =$   
 $Combination(score_1(f_i), \dots, score_n(f_i))$
- The effect of inclusion of classifiers in the combination (ensemble function) has been studied to see which classifier plays a positive/negative role.
  - Logistic-Regression
  - Support Vector Machines (SVM)
  - K-nearest Neighbors
  - Naïve Bayes
  - Bagging

# ➔ Biomedical Datasets

- When applying Feature Ranking methods on medical datasets, one has to consider the common characteristics of medical datasets:
  - Class-imbalanced data
  - Missing values

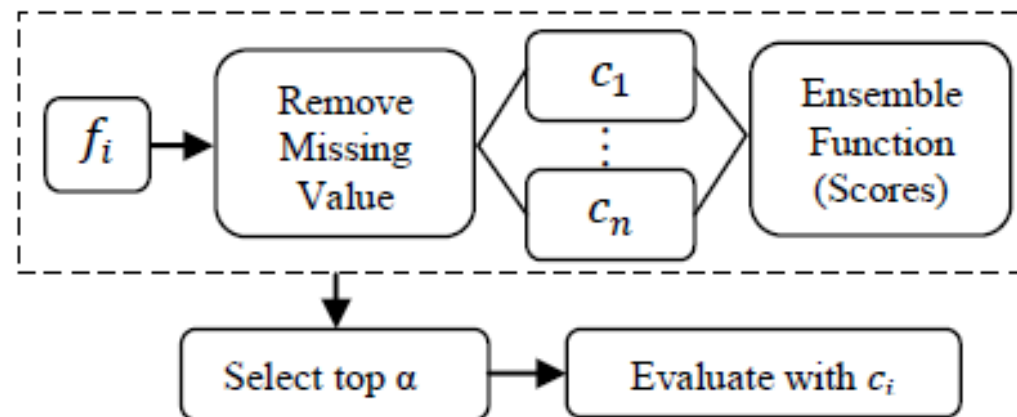


# ➔ Missing Value / Class-Imbalance

- Missing value estimation and imputation negatively affects the reliability of the model.
- We performed the study only based on properly recorded values and missing values were **eliminated**.
  - Adversely affecting the imbalance distribution
- We used the area under receiver operating characteristic (ROC) curve (AUC) as a performance evaluator for individual features, to address the balance problem.

# ➔ Framework

- Experimental Framework:



# → Evaluation

- $\alpha$  **features from the top** of the ranked features were selected and the predictive power of this feature subset was tested with a classifier via cross validation.
- To use the maximum possible instances for each feature subset, we used the samples that have all the values for **only the features in the subset** being evaluated.
- The **number of instances varies** for each feature subset, making the comparison of the ranking methods with different feature subsets difficult.

# ➔ Performance Index

- To mitigate the mismatching number of instances.

$$PI(n, c) = \sum_{i=1}^n \left( \frac{F_{i\_ins}}{i} \cdot AUC(c(F_i)) \right) / \sum_{i=1}^n \left( \frac{F_{i\_ins}}{i} \right)$$

- ***n*** is the number of features considered in the calculation.
- ***c*** is the evaluating classifier.
- ***F<sub>i</sub>*** is the set of ***i*** features with the highest score
- ***F<sub>i</sub>\_ins*** is the numbers of instances that have all the values for features in ***F<sub>i</sub>***.
- ***AUC(c(F<sub>i</sub>))*** represents the average AUC of ROC for evaluation of on ***c***, using the leave-one-out technique.

## ➔ Performance Index

$$PI(n, c) = \sum_{i=1}^n \left( \frac{F_{i\_ins}}{i} \cdot AUC(c(F_i)) \right) / \sum_{i=1}^n \left( \frac{F_{i\_ins}}{i} \right)$$

- A consideration in this formula is that the ranking methods that achieve a **higher accuracy with fewer features and more instances** are preferable.
- For this reason, the number of features appears in the weight factor as  **$1/i$**  and the number of instances as  **$F_{i\_ins}$** .

# → Experiments Environment

- The dataset used in the experiments is from Human Brain Image Database System (HBIDS), developed in the Radiology Department of Henry Ford Health System (Detroit, Michigan USA).
- The main task in this dataset is a binary classification that predicts the patients' lateralization (side of abnormality).
- The database contains 197 medical features and 145 patients.



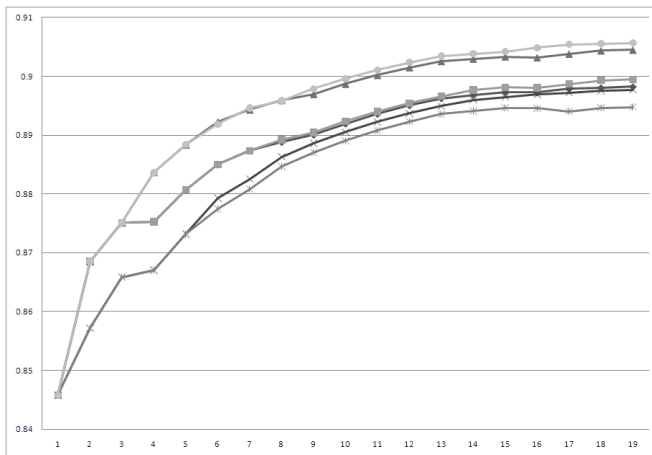
# ➔ Some features in HBIDS

- Semiology,
- Pre- and postoperative neuropsychological profiles
- Location of surgery,
- Surgery outcome according to the Engel classification.
- Interictal waveforms, their location and predominance as well as ictal onset location.
- Both magnetic resonance (MR) and single photon emission computed tomography (SPECT) (ictal and interictal) imaging is included with the provision for quantitative semi-automated assessment of compartmental volume, fluid-attenuated inversion recovery (FLAIR) mean signal and standard deviation and texture analysis
- Compartmentalized ictal SPECT subtraction image analysis is also available.

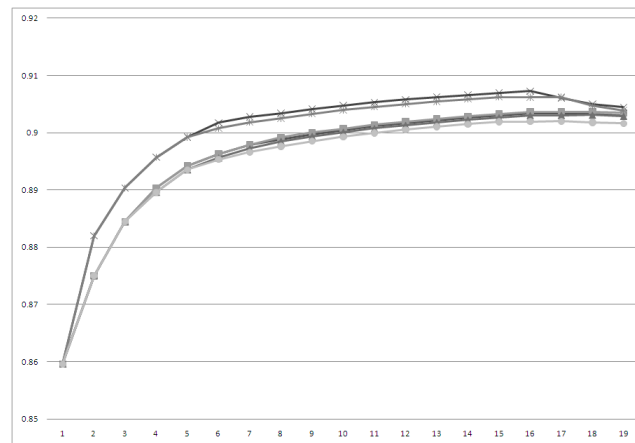
# → HBIDS Missing Values

- Missing values were identified for:
  - EEG features in 21% of cases
  - Wada studies in 31% of cases
  - Imaging features in 46% of cases
  - The remaining features in about 20% of cases on average.

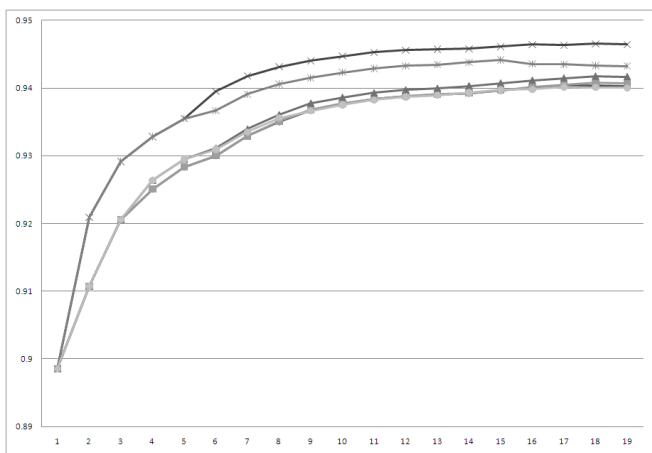
# ➔ Experimental Results



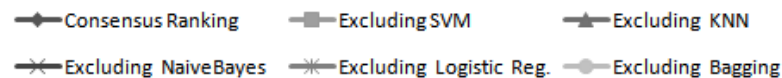
Evaluation with SVM



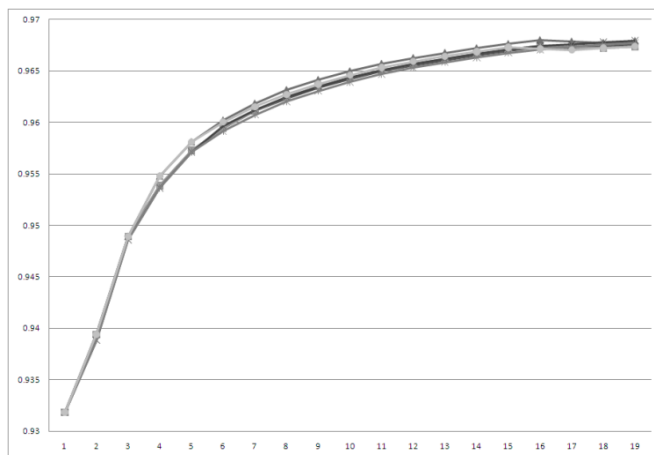
Evaluation on Bagging



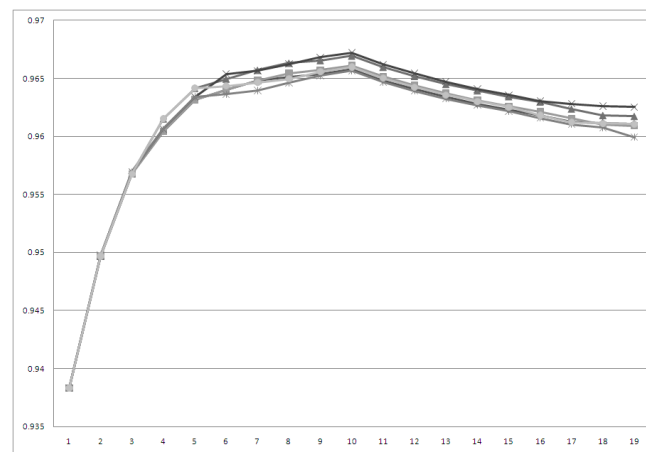
Evaluation on K-Nearest-Neighbors



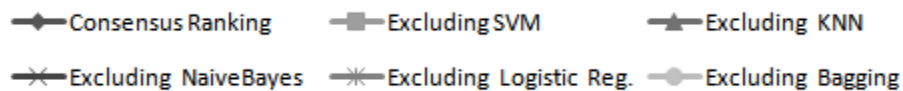
# ➔ Experimental Results



Evaluation on Logistic-Regression



Evaluation on Naïve-Bayes



# ➔ Observations

- Evaluation with SVM:
  - SVM: Neutral
  - Naïve-Bayes: Positive
  - K-Nearest Neighbors: Negative
  - Bagging: Negative
  - Logistic Regression: Positive
- Evaluation with Bagging:
  - SVM: Neutral
  - Naïve-Bayes: Negative
  - K-Nearest Neighbors: Neutral
  - Bagging: Neutral
  - Logistic Regression: Negative
- Evaluation with K-NN:
  - SVM: Neutral
  - Naïve-Bayes: Negative
  - K-Nearest Neighbors: Neutral
  - Bagging: Neutral
  - Logistic Regression: Negative
- Evaluation with Naïve-Bayes:
  - SVM: Neutral
  - Naïve-Bayes: Negative
  - K-Nearest Neighbors: Negative
  - Bagging: Neutral
  - Logistic Regression: Neutral

## ➔ Observations

- Performance of the consensus feature ranking with a classifier is **not highly dependent on inclusion of that classifier** itself in the fusion.
- Therefore, features ranked based on ensemble of scores from multiple classifiers are likely to perform well on **unseen classifiers**.
- This ranking plays an important role in **data-warehousing**, where data are gathered with the possibility to be used with **new emerging classifiers** in the future.





# ➔ References

1. Y. Saeys, I. Inza, P. Larranaga, "A review of feature selection techniques in bioinformatics," *Bioinformatics*, vol. 23, p. 2507, 2007.
2. I. Guyon, A. Elisseeff, "An introduction to variable and feature selection," *Journal of Machine Learning Research*, vol. 3, pp. 1157-82, 2003.



• **Thank you**

If you are interested to get more details about this research please contact  
Shobeir Fakhraei {[shobeir@wayne.com](mailto:shobeir@wayne.com)}