

Fine-grained prediction of Huntington's disease progression using a stacked ensemble approach

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We applied a *stacked ensemble* based approach for predictive-classification of 184 HD gene positive subjects from TRACK-HD dataset. Our model sets a new benchmark for fine-grained classification of HD, & thus sets the ground for clinically useful future work such as prediction of onset

1. Background

- Classification of individual disease state in Huntington's disease (HD) is key for stratification of patients in clinical trials
- However, there has been no coordinated effort to assess benefits of using Machine learning (ML) based Stacking ensemble approach for making patient-specific & data-driven predictions of disease state in HD

2. Objectives

- We developed a novel ML framework that facilitates predictive-classification of individual-level HD disease state; the framework classifies subjects according to:
 - binary HD disease state (i.e., Pre-manifest HD (PreHD); manifest HD)
 - fine-grained disease state (i.e., PreHD A; PreHD B; HD1; HD2)

3. Methods

- ML framework comprises of:
 - Tier 1 (Base models): array of 6* standard ML models; trained & fit on actual training-data using repeated 10-fold cross-validation
 - Tier 2 (meta-model): trained on predictions made by Tier 1 models; learns how to best combine these predictions to reduce variance & generalisation error
- Data** : baseline cross-sectional data from 184 HD gene-positive participants from the TRACK-HD dataset, which includes clinical, imaging & genetic data

- Subjects**: Details about how subjects were grouped in various classes can be found at - Tabrizi et al., 2013**

No. of subjects in each group		
PreHD A	58	PreHD 104
PreHD B	46	
HD1	49	HD 80
HD2	31	

Figure 2: No. of subjects in each class/group

4. Results

Binary classification (PreHD vs HD)

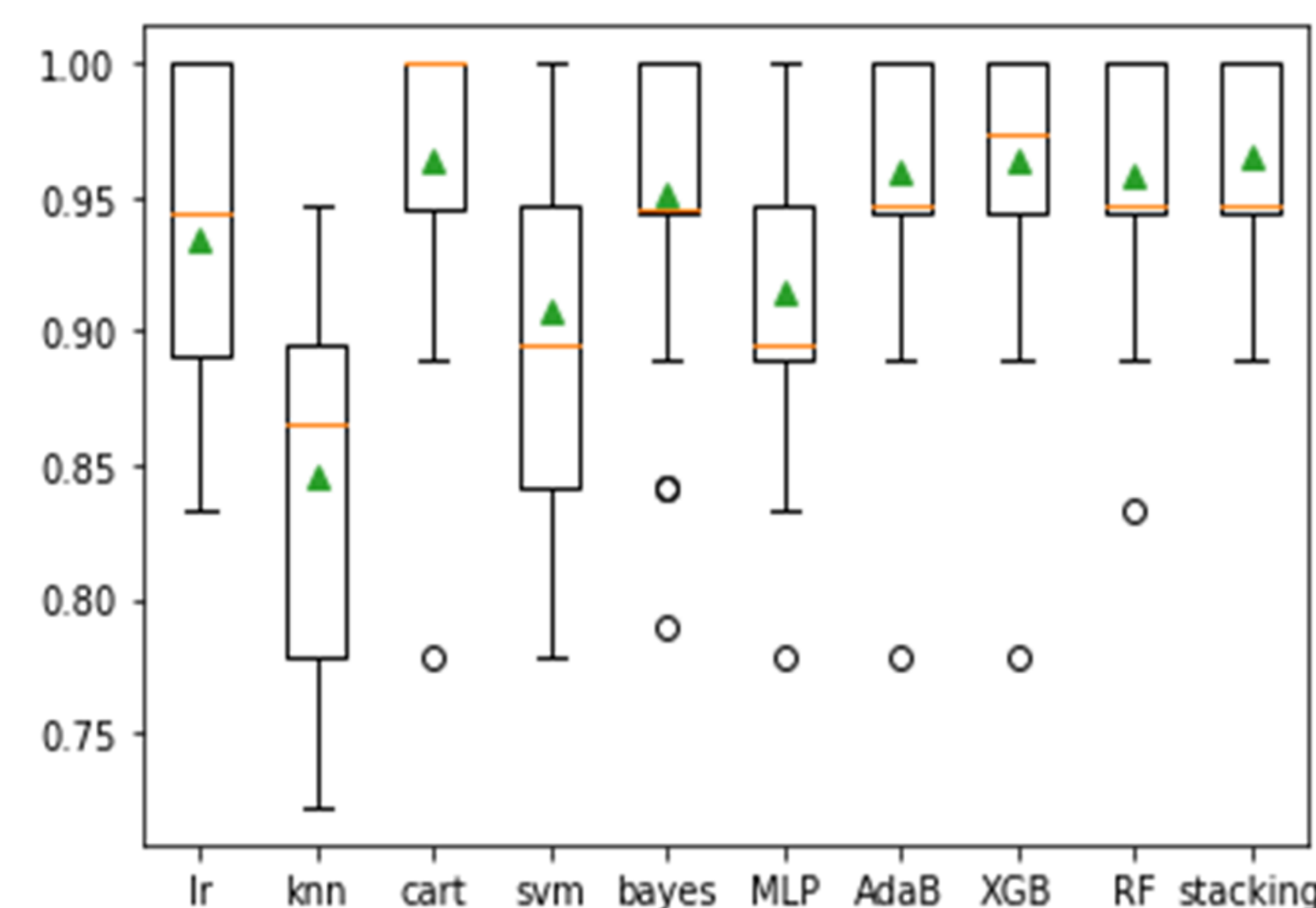


Figure 3: Binary classification accuracy

- Stacked ensemble model achieved an accuracy of $96.5\% \pm 3.6$ in binary-classification task
- It also performed better than base-models & comparative ensemble models albeit non-significantly

Fine-grained classification (PreHD A; PreHD B; HD1; HD2)

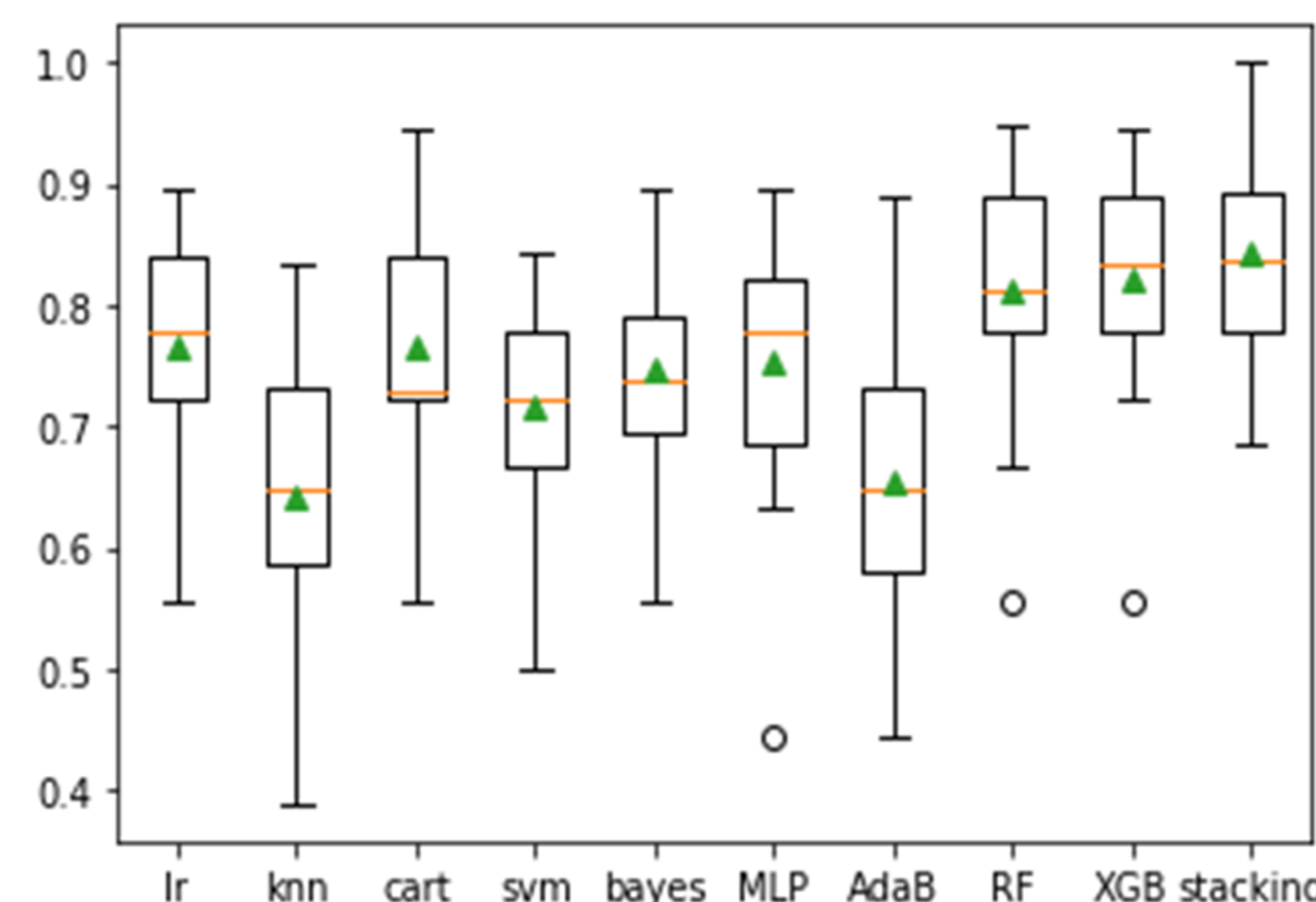


Figure 4: Fine-grained classification accuracy

- Stacked model achieved an accuracy of $85.2\% \pm 8.0$ in fine-grained classification task
- It also performed significantly (>9%) better than base-models & comparative ensemble models

Our Stacked ensemble approach sets a new benchmark for fine-grained classification task

Imaging → Caudate; Pallidum; Putamen;

Genetic → CAG Repeat Length

Clinical → SDMT; SWRT; TMS; TFC

General → Age; Sex

Figure 1: Input Features used for classification

*ML models used

Base-models → lr = logistic regression; knn = k nearest neighbour; cart = decision trees; svm = support vector machine; bayes = Gaussian Naïve Bayes; MLP = multi-layer perceptron
Meta-model (Stacking) → Gaussian Naïve Bayes
Comparative ensemble methods → ; AdaB = adaboost; XGB = extreme gradient boosting; RF = random forest

5. Conclusion

- Our stacked model achieved best predictive-classification fine-grained classification tasks
- These encouraging results indicate that the Stacked ensemble approach might potentially be a powerful tool for making clinically useful predictions such as time-to-onset → Future work

*Data: Full list of Imaging input Features used:

(1.) Caudate; (2.) Pallidum; (3.) Putamen; (4.) Accumbens area; (5.) Lateral vents; (6.) Thalamus proper; (7.) Temporal; (8.) Frontal; (9.) Occipital; (10.) Parietal; (11.) Sensory Motor; (12.) Insula; (13.) Cingulate; (14.) Insula white matter

*Full forms of clinical input Features used:

SDMT → symbol digit modality test; SWRT → stroop word reading test; TMS → total motor score; TFC → total functional capacity

**Tabrizi, Sarah J., et al. "Predictors of phenotypic progression and disease onset in premanifest and early-stage Huntington's disease in the TRACK-HD study: analysis of 36-month observational data." *The Lancet Neurology* 12.7 (2013): 637-649.



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