Prediction of Autism Treatment Response from Baseline fMRI using Random Forests and Tree Bagging

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Autism Spectrum Disorder (ASD)

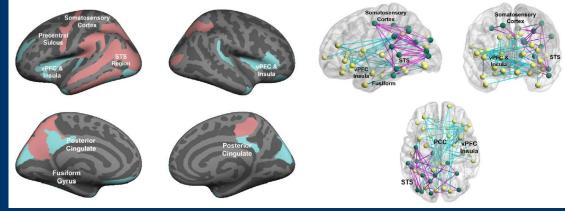
- Neurological developmental disorders characterized by impaired social interactions, difficulties in communication, and repetitive behaviors
- Promising treatment: Intensive behavioral therapies
 - e.g., Pivotal Response Therapy
 - Large commitment from patient and families
 - Early intervention is important
- However, ASD is complex!
 - No "one size fits all" treatment
 - Currently, choose therapy by trial and error
- \rightarrow Need for *precision medicine*



www.autismspeaks.org

Goal: Predict Autism Treatment Outcome from Baseline fMRI

fMRI has aided understanding of ASD pathophysiology

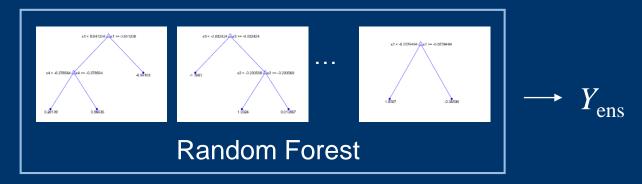


Venkataraman et al., TMI 2016

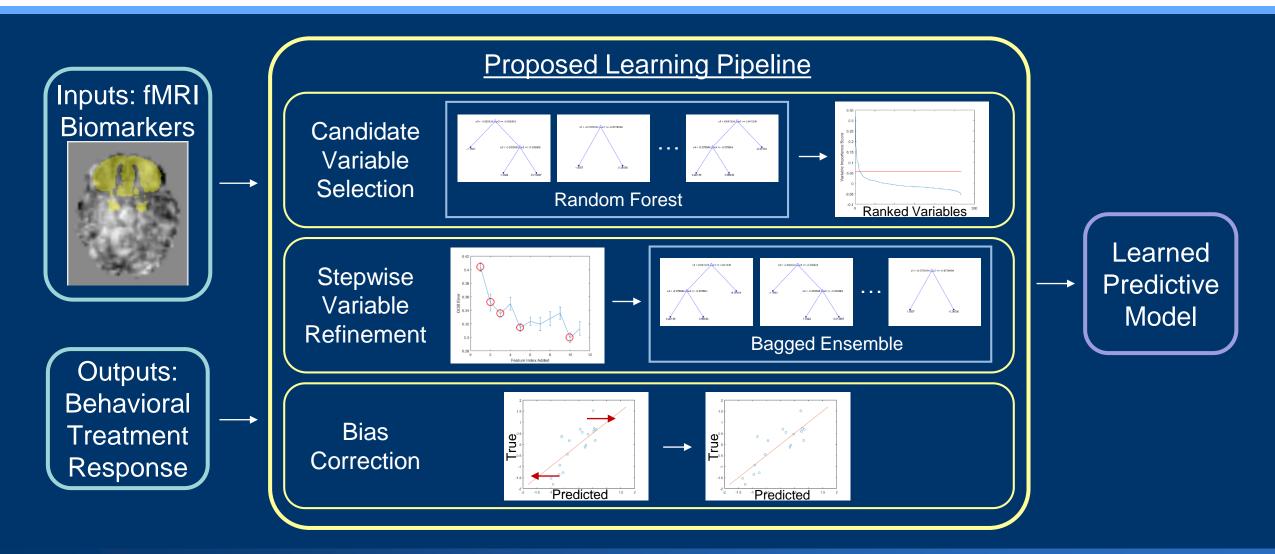
- fMRI for prediction
 - Changes in autistic traits [Plitt et al., PNAS 2015]
 - Treatment outcomes in other brain disorders [Ball et al., Neuropsych 2014]
 - \rightarrow We propose first use of fMRI for predicting ASD treatment response

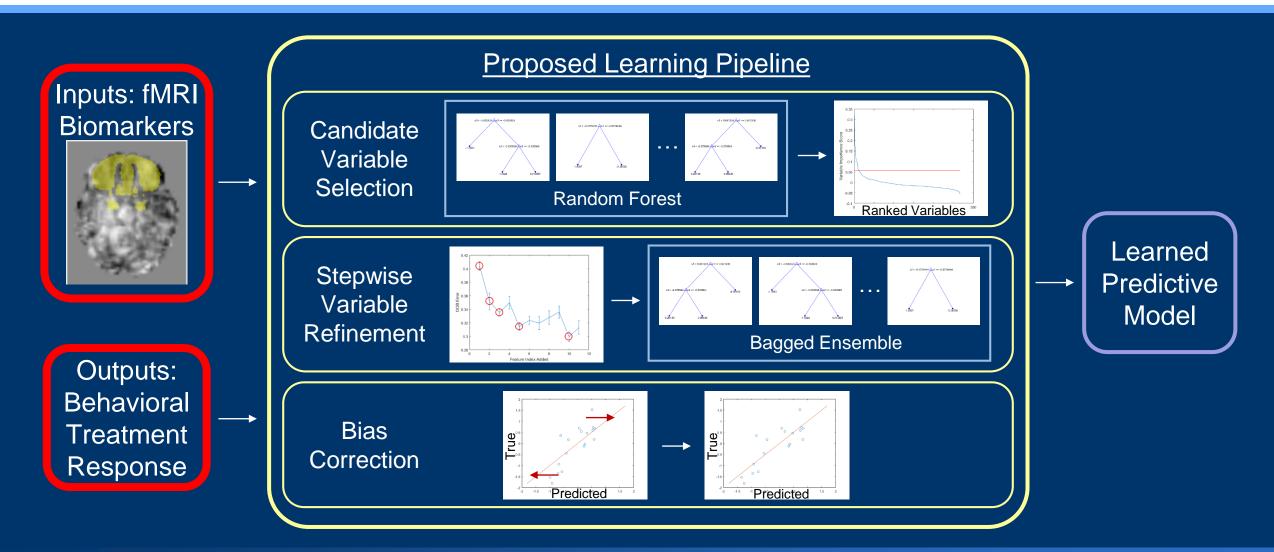
Goal: Predict Autism Treatment Outcome from Baseline fMRI

- Challenge: "large *p*, small *n*"
 - Large number of possible fMRI-derived inputs
 - Small number of subjects in autism studies
- Good candidate for Random Forests



- However...
 - Very noisy inputs degrade prediction accuracy
 - Small samples reduce strength of each tree





Inputs: Baseline fMRI-Derived Parameters

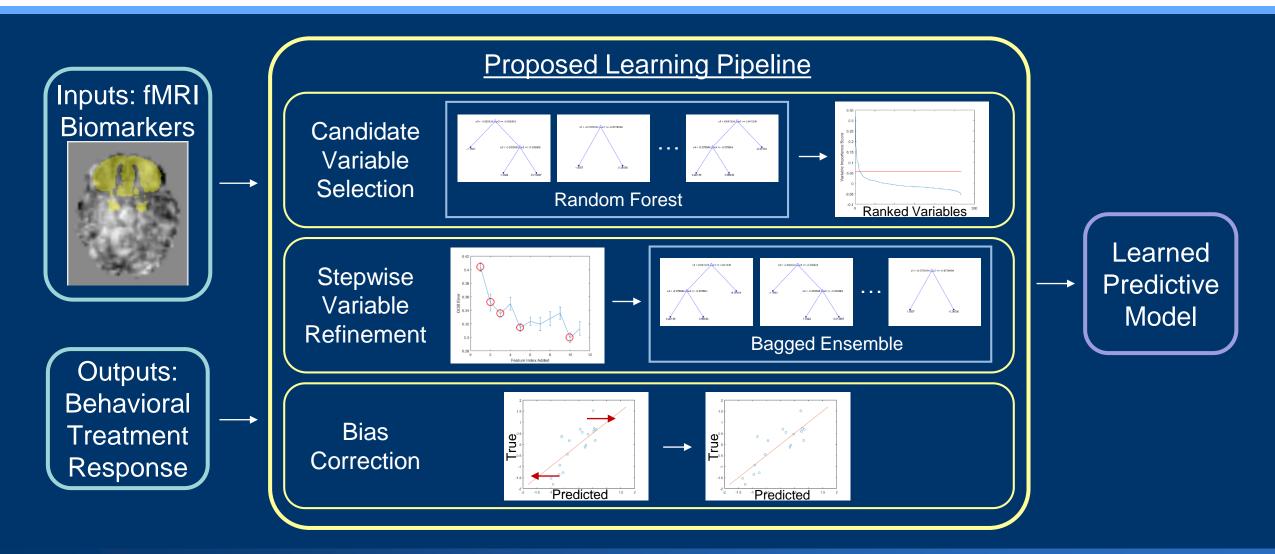
Biopoint: Biological motion perception paradigm

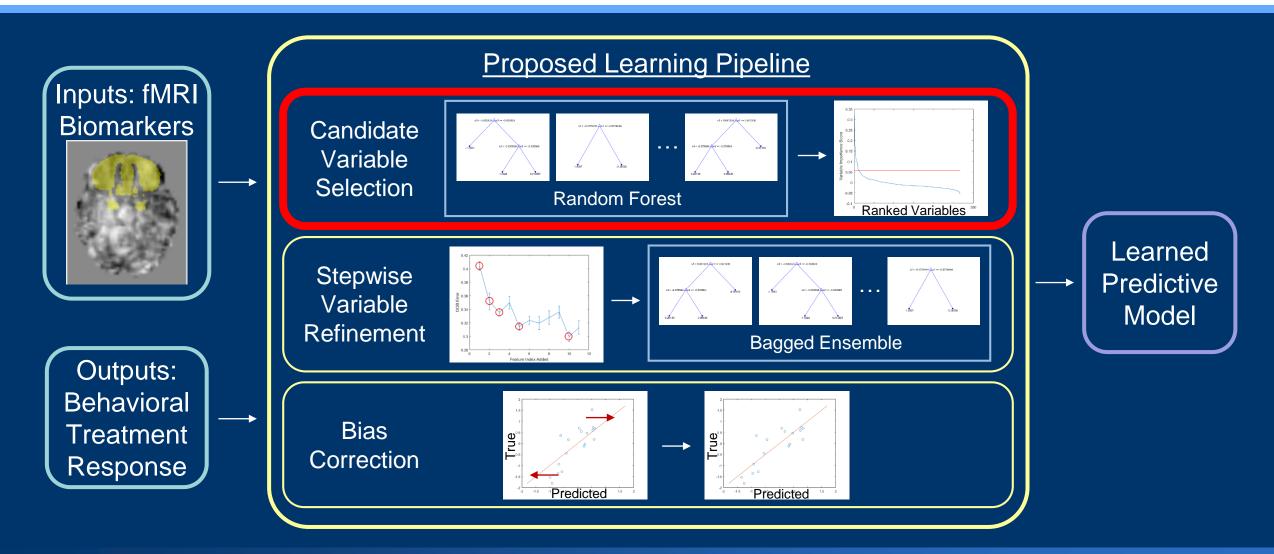


- Focus on brain regions associated with social motivation: Orbitofrontal cortex, ventromedial prefrontal cortex, amygdala, and ventral striatum
- \rightarrow Inputs: t-statistics for biological motion > scrambled motion contrast

Outputs: Behavioral Treatment Outcome

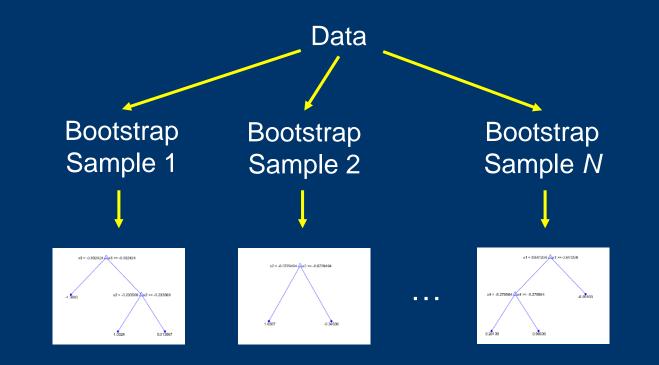
- Social Responsiveness Scale, Second Edition (SRS) Score
 - Measures severity of social impairment in ASD
 - Lower SRS score \rightarrow Better function
- Measure SRS score at baseline and post-treatment
- \rightarrow Outputs: Normalized change in SRS Score (Δ SRS)





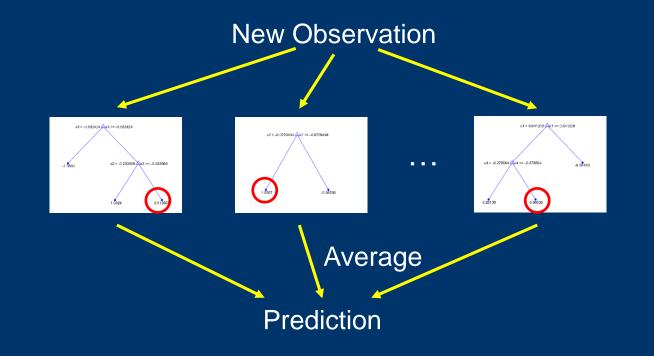
Random Forests for Regression Review

- Ensemble learning method that uses
 - Bagging



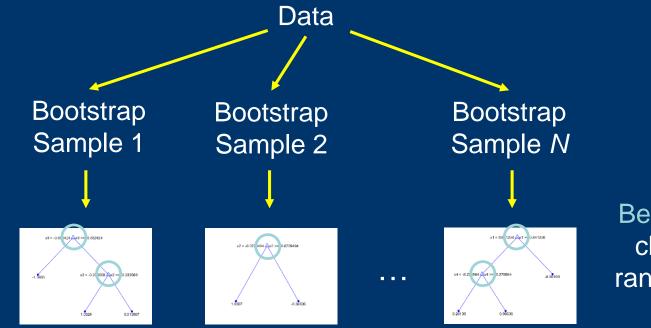
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Random Forests for Regression Review

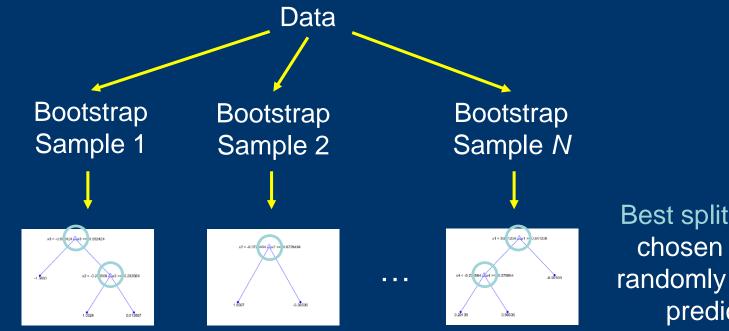
- Ensemble learning method that uses
 - Bagging
 - Random subset sampling of predictors



Best split variable chosen from *m* randomly selected predictors

Random Forests for Regression Advantages

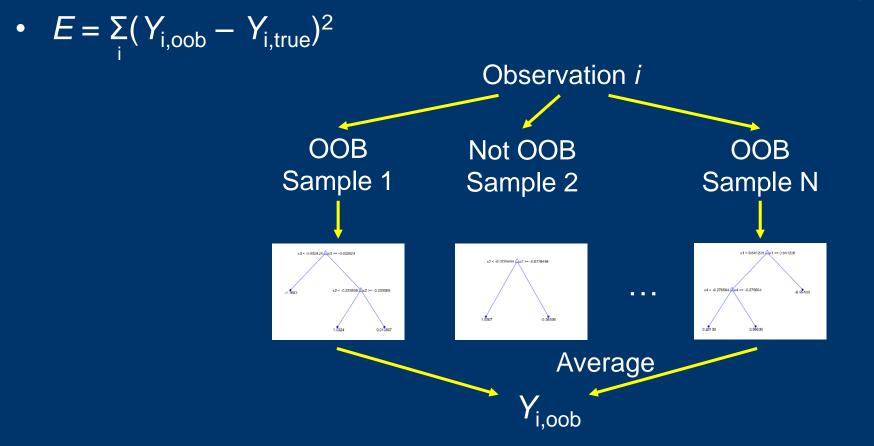
- Reduced correlation of trees \rightarrow Reduced variance of estimate ullet
- Efficient exploration of high dimensional inputs •



Best split variable chosen from *m* randomly selected predictors

Random Forests for Regression Out-of-bag (OOB) Error

• Internal estimate of test error rate estimated by out-of-bag (OOB) error

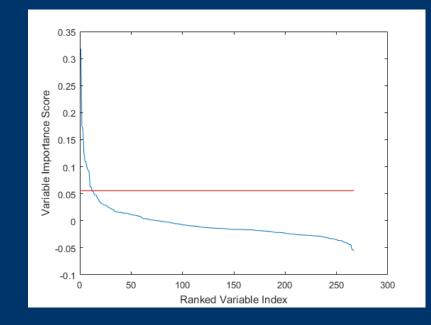


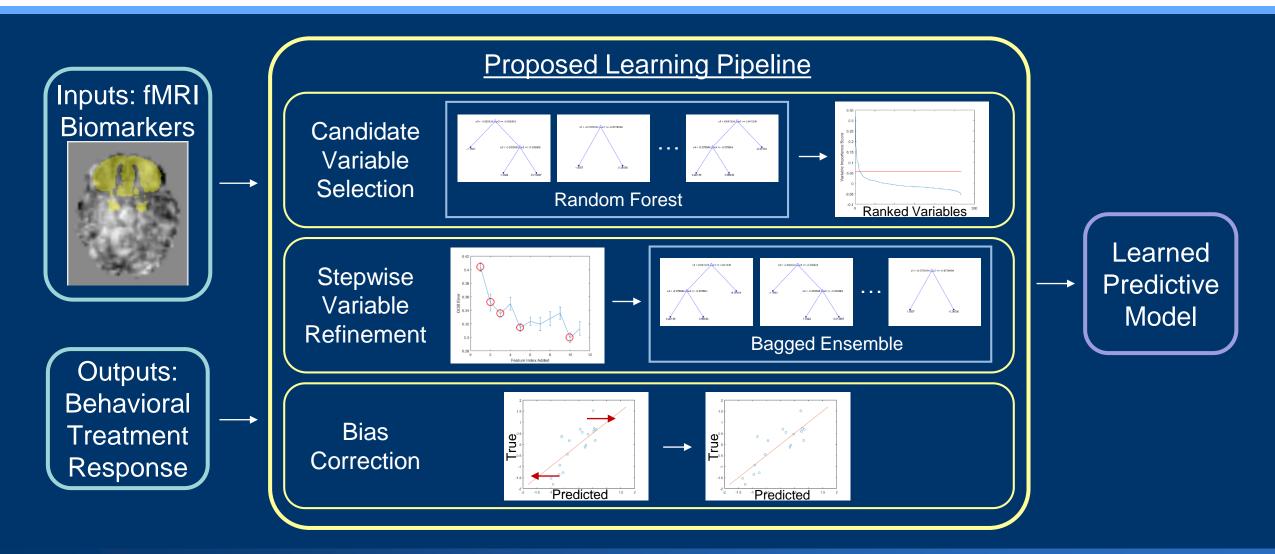
Random Forests for Regression Variable Importance

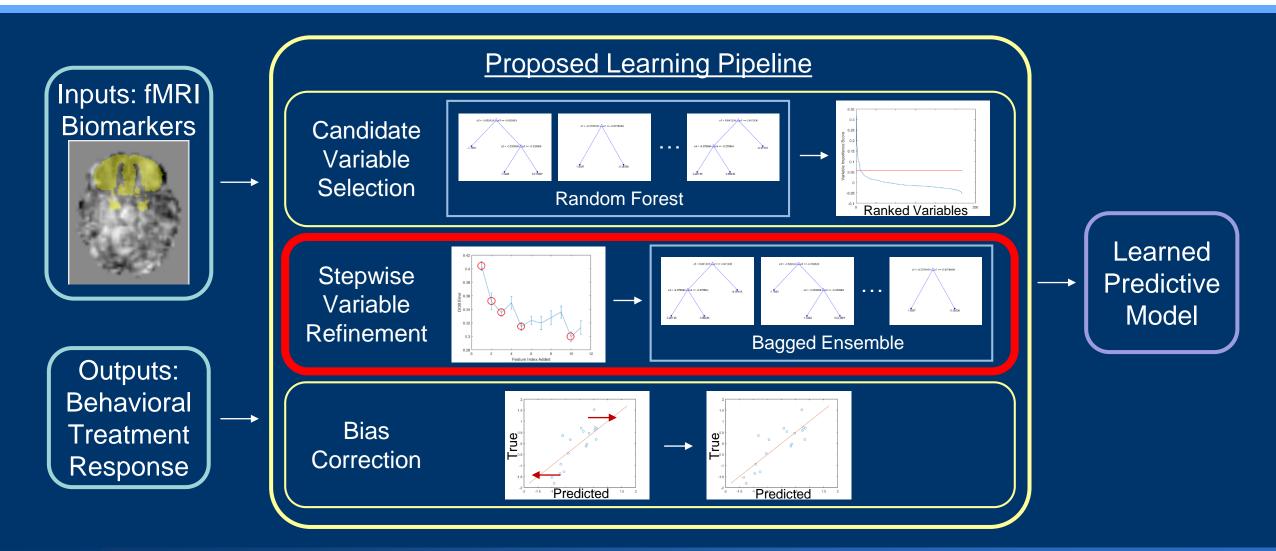
- For each tree and variable
 - Randomly permute values for the OOB samples
 - Calculate change in prediction error
- Importance score: Average change in error over all trees
- Bigger increase in error \rightarrow higher variable importance
- Note: small negative scores possible due to randomness

Candidate Variable Selection Using Variable Importance

- Run random forests to obtain variable importance scores
- Retain voxels with score > absolute value of lowest negative score
 - Intuition: Irrelevant variables have low scores that fluctuate around 0

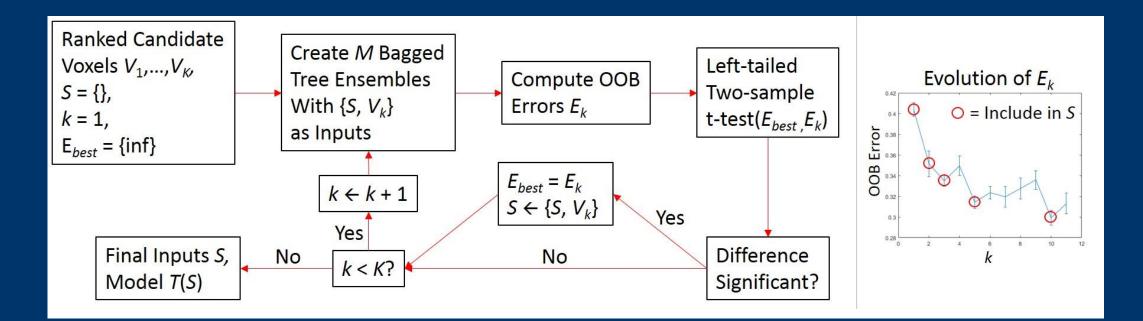


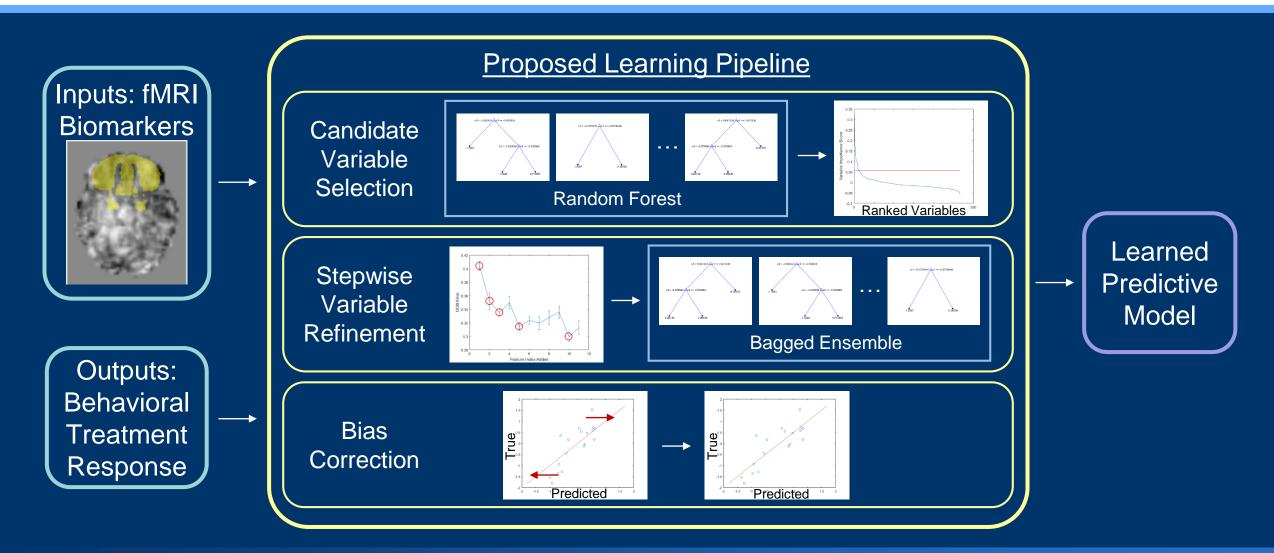


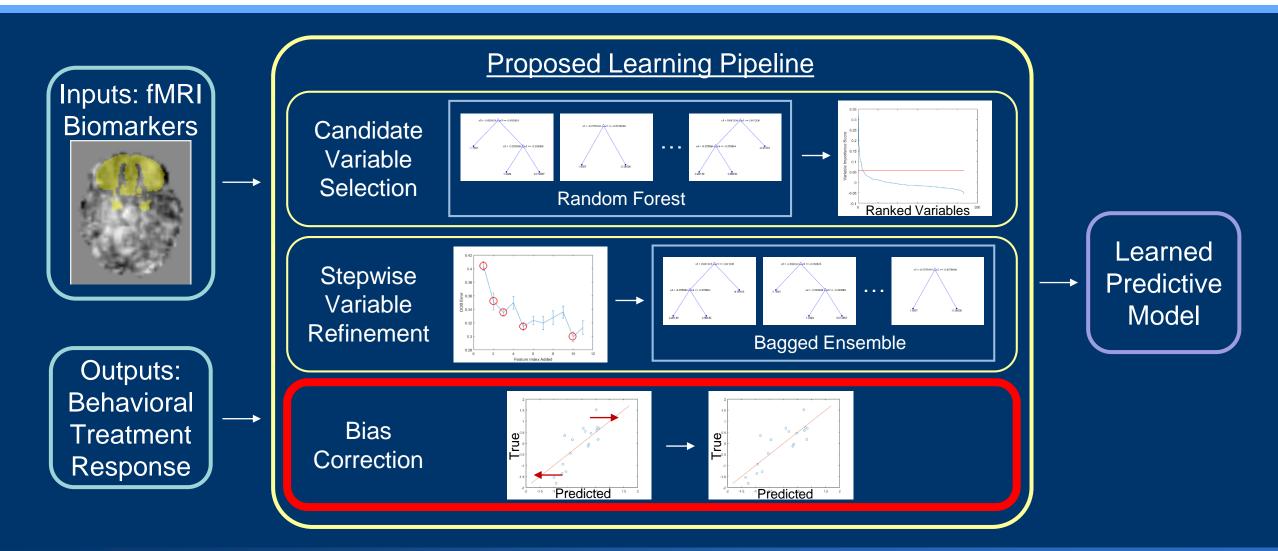


Stepwise Variable Refinement

- Iteratively refine candidate input variables for bagged tree ensemble
- $V_i = i$ th ranked candidate voxel, S = Set of best voxel inputs, E = OOB Error

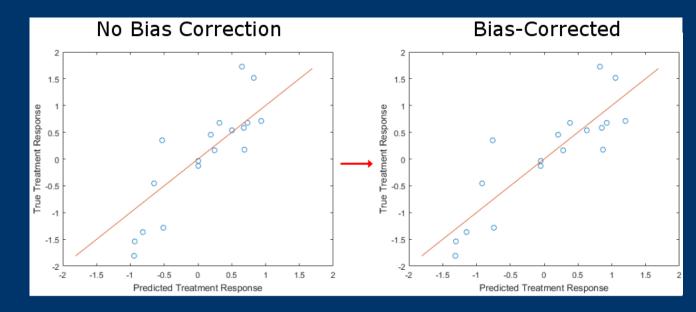


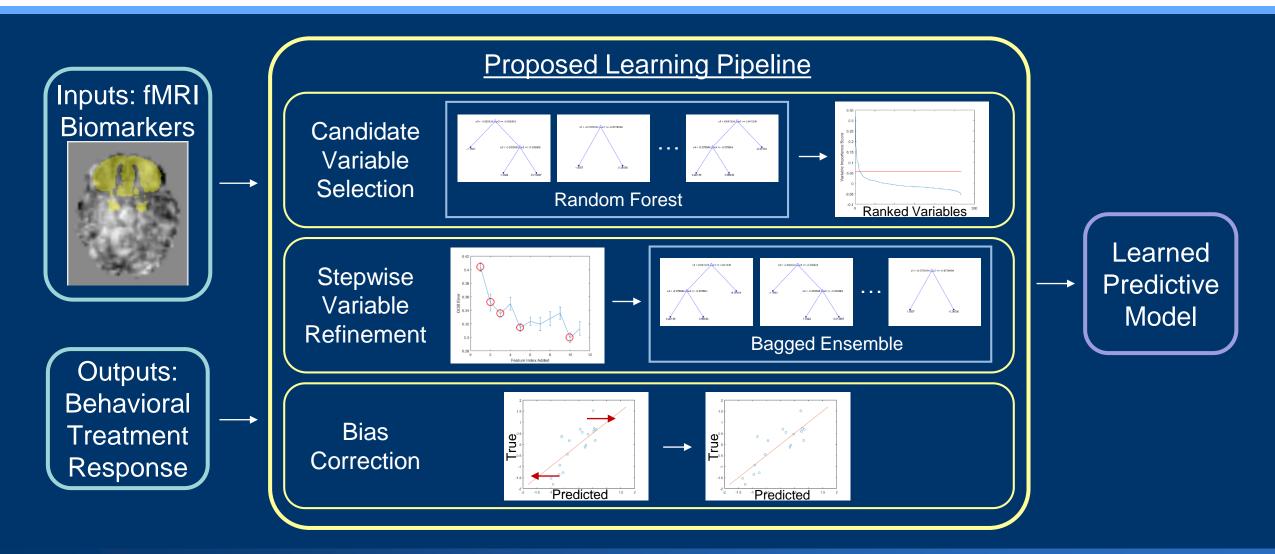




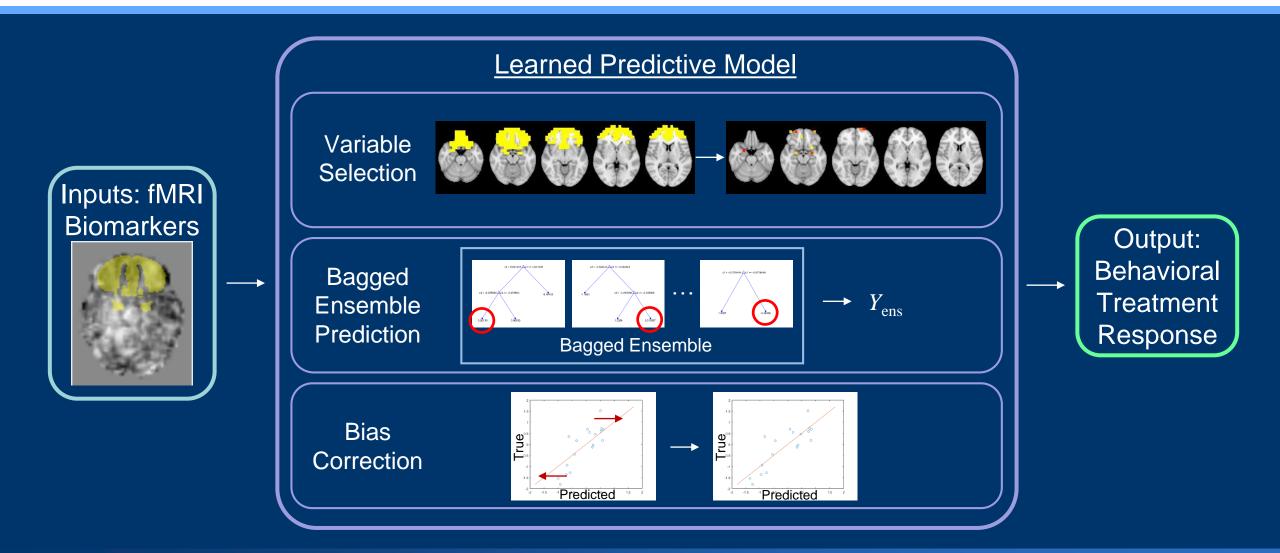
Bias Correction

- Regression tree ensembles underestimate high values and overestimate low values
- Linear model: $Y_{true} = \beta_1 Y_{ens} + \beta_0$
- Estimate parameters using OOB predictions



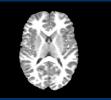


Predictions from New Data



Data

- 19 ASD children underwent 16 weeks Pivotal Response Therapy, 7 hrs/week
- Imaging at baseline:
 - T1-weighted MP-RAGE structural MRI



1 x 1 x 1 mm³

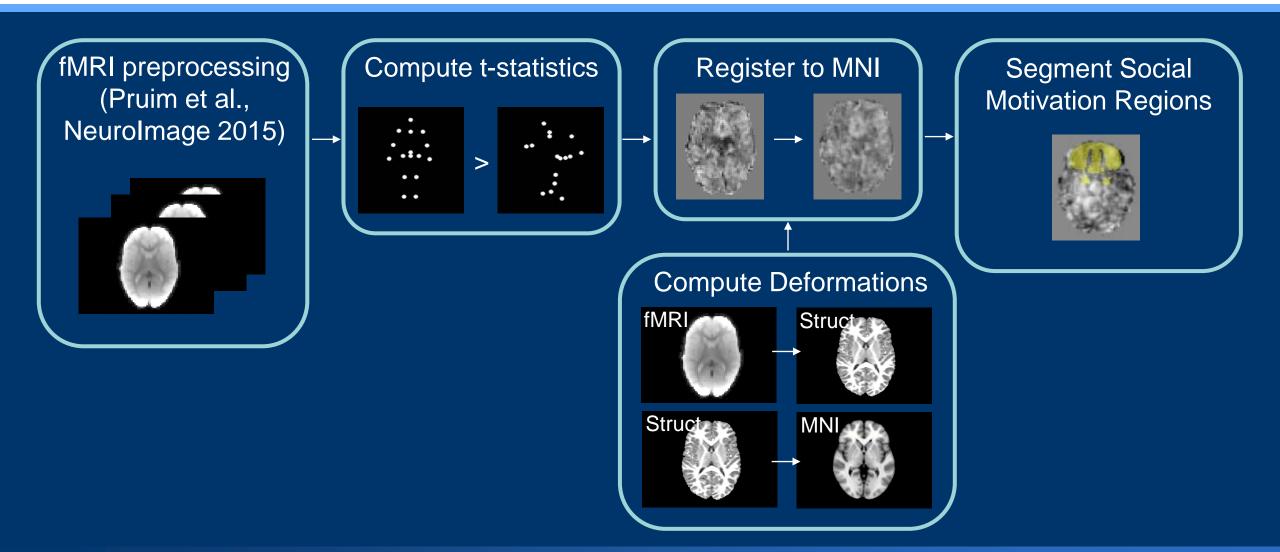
 BOLD T2*-weighted fMRI with Biopoint paradigm



164 volumes 3.44 x 3.44 x 4.00 mm³

• Note: Data collection involved > 2200 hours

Image Preprocessing



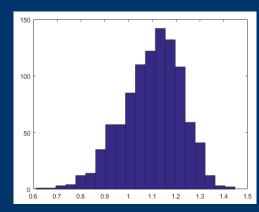
Methods Compared

- 1. Standard random forest
- 2. Standard support vector machine with linear kernel
- 3. Random forest variable selection \rightarrow random forest
- 4. Random forest variable selection \rightarrow bagging
- 5. Random forest variable selection \rightarrow stepwise variable refinement
- Random forest variable selection → stepwise variable refinement → bias correction (Proposed approach)
- MATLAB implementation with default parameters, except
 - 5000 trees for variable selection
 - 1000 trees for final models

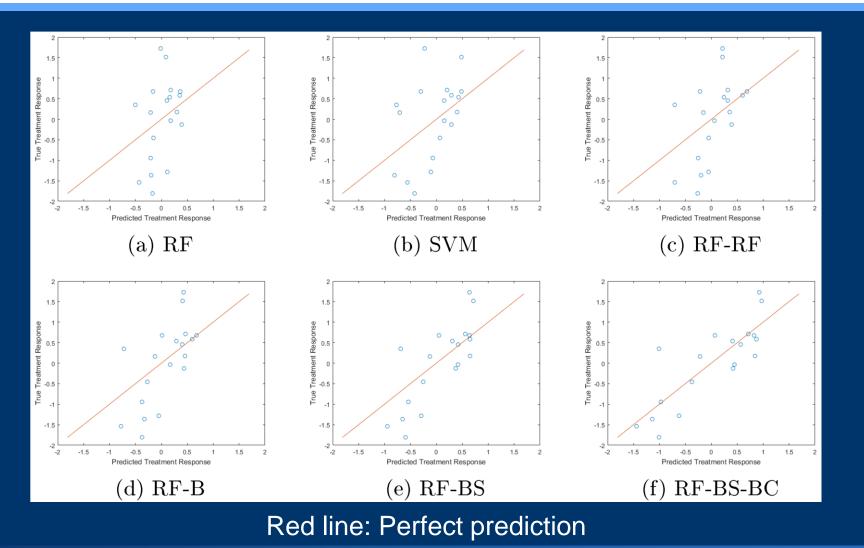
Evaluation Criteria

- Leave-one-out cross-validation
- Accuracy measures for
 - Outputs (ΔSRS)
 - Mean squared error
 - Pearson's correlation coefficient

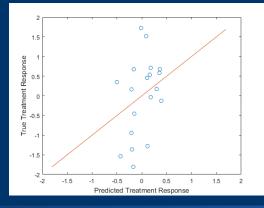
- Predicted outcomes (Post SRS)
 - Relative absolute error
 - Mean absolute percentage error
- Significance assessed using permutation tests
 - p = (# runs with values more extreme than observed statistic) / 1000



True vs. Predicted Response

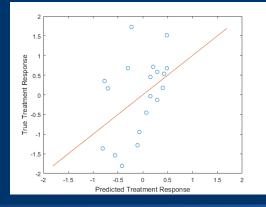


Algorithm	$MSE \pm SD$	p_{MSE}	r	p_r	RAE	p_{RAE}	$MAPE \pm SD$	p_{MAPE}
\mathbf{RF}	0.82 ± 0.96	0.019	0.39	0.038	0.63	0.044	0.24 ± 0.26	0.043
SVM	0.75 ± 0.93	0.037	0.46	0.040	0.60	0.051	0.22 ± 0.22	0.051
RF-RF	0.69 ± 0.80	0.024	0.54	0.023	0.56	0.026	0.21 ± 0.25	0.030
RF-B	0.57 ± 0.67	0.012	0.68	0.006	0.50	0.012	0.20 ± 0.23	0.025
RF-BS	0.40 ± 0.45	0.001	0.80	0.001	0.44	0.005	0.17 ± 0.19	0.013
RF-BS-BC	0.29 ± 0.43	0.001	0.83	0.001	0.35	0.001	0.13 ± 0.15	0.001



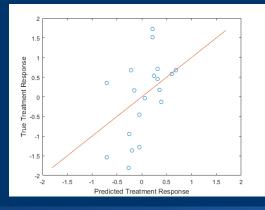
Random forest: Worst prediction accuracy

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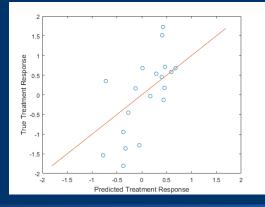
Support vector machine: Similar errors as random forest

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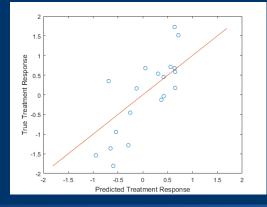
Select top variables \rightarrow random forest: Variable selection improves prediction

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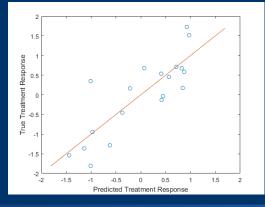
Select top variables \rightarrow bagging: Stronger trees reduce errors

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Stepwise variable refinement: Improved over bagging top variables

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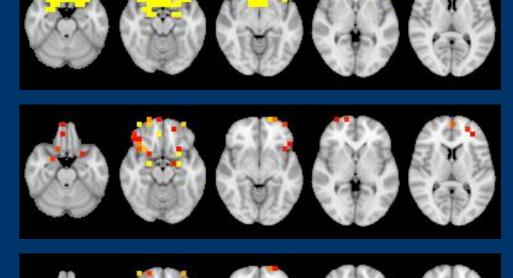


Proposed approach: Highest prediction accuracy

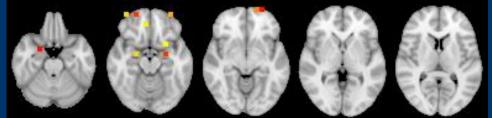
Variable Selection Results

Social motivation regions (original inputs): Orbitofrontal cortex, ventromedial prefrontal cortex, amygdala, ventral striatum

Random forest candidate variable selection



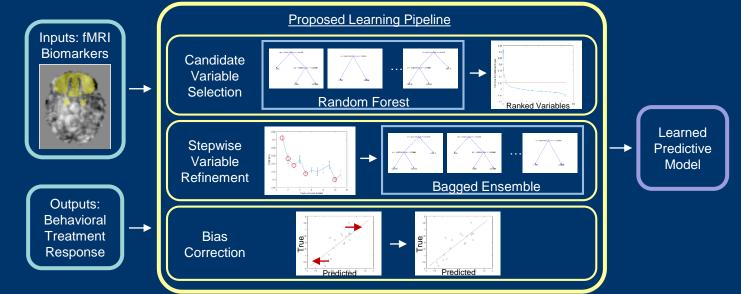
Stepwise variable refinement (final inputs)



Red \rightarrow Yellow: More frequently selected across trials

Conclusions

- Developed learning pipeline to predict response to autism behavior therapy from baseline fMRI
- Move toward personalized treatment



- Future work
 - Explore other biomarkers for prediction, e.g., functional connectivity
 - More data, assess generalization

Thank You!

- Dr. Pamela Ventola (Data collection)
- Dr. Daniel Yang (fMRI preprocessing)
- NIH grants T32 MH18268 and R01 NS035193
- Contact: nicha.dvornek@yale.edu