



QUANTITATIVE MEDICINE

Transforming Drug Discovery™

Technical Discussion

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Open Question

How can we more effectively utilize *all* publicly available screening results improve prediction accuracy?

New prediction methods utilizing all historical data

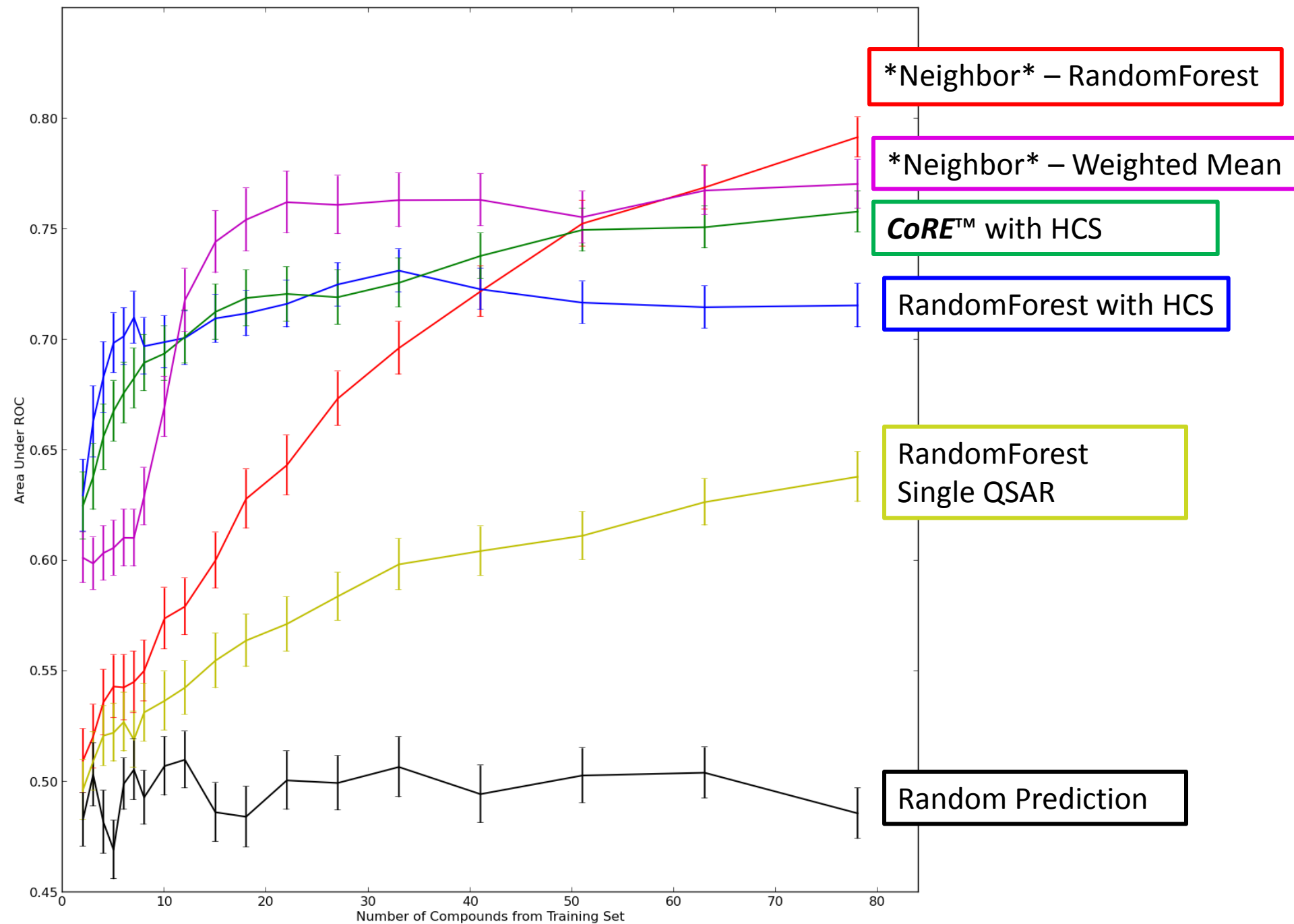
- For each assay in the historical data, learn a QSAR model using all available data (10-200,000 discrete observations)
- These models only predict what was measured in the experiment (not necessarily hepatotoxicity).
- Make predictions for all compounds “observed” and to be predicted.
- These predictions form the basis of a feature matrix describing each compound.
- Learn a model to predict hepatotoxicity from the resulting feature matrix where observations are available

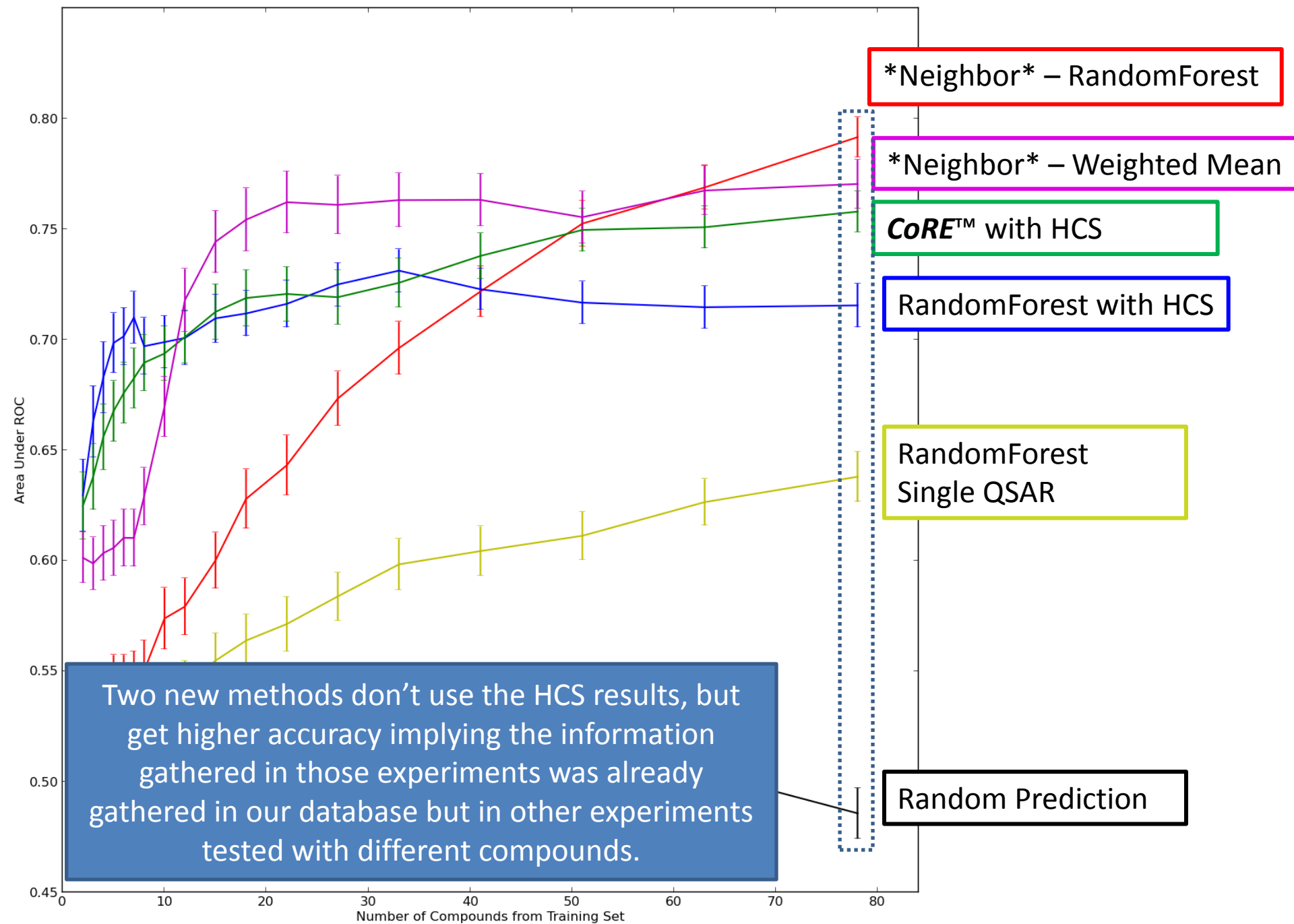
New prediction methods utilizing all historical data

- Random Forest – use random forest to learn a model to predict hepatotoxicity from prediction based features
- Weighted mean – for each assay, determine the correlation between model predictions and observations. Weight that assays predictions for held out set by $-\log(p)$ where p is the probability of seeing a higher correlation in a permutation test.

Prediction Simulations

- Selection Method: Random
- Batch size: 20% of what had been previously observed (cuts down on run time in generally uninteresting phases when there are a lot of observations)





Other considerations

- Experiment direction
- Types of model predictions
 - Neighbor approach with RF can use any types of predictions (discrete or continuous)
 - Weighted mean neighbor approach can only use two-class discrete predictions unless predictions are scaled from 0 – 1.
- Next steps?



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