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An Analysis of Overfitting In Modern QSAR Models

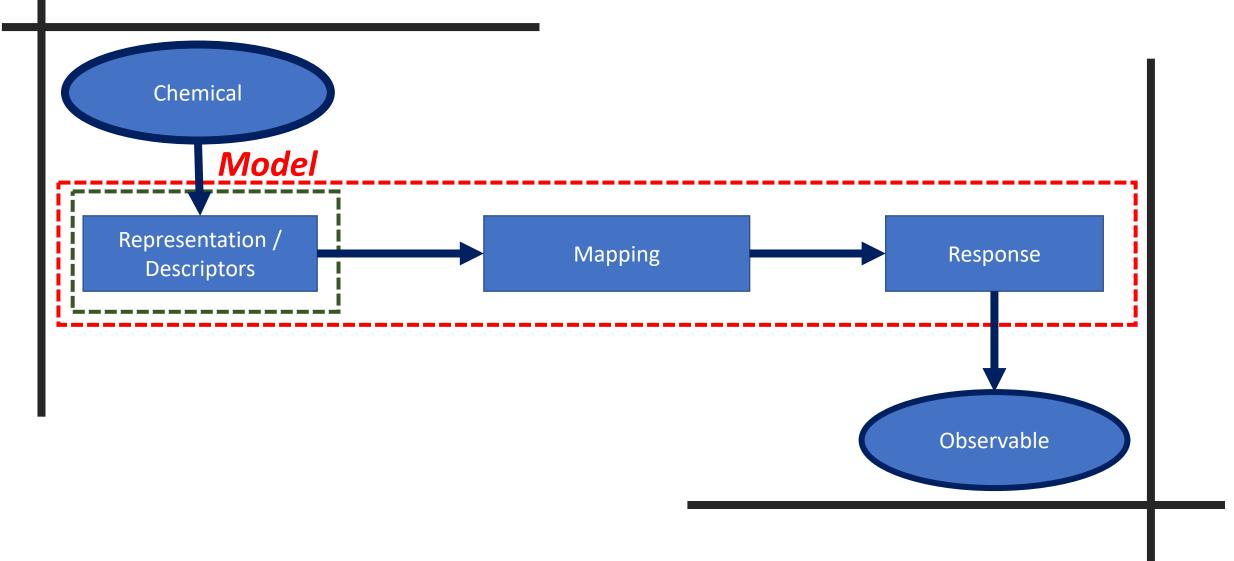
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- 31(000) Flavors...let's go with vanilla
- Interpretability For Regulation
- Global vs. Local
 - Global models theoretically can flag compounds unlike the chemical space of training data
 - Techniques like GenRA or analogue analysis provide local insights
 - Regulators seek abstractions of globally relevant indicators of toxicity, environmental persistence, or other concern

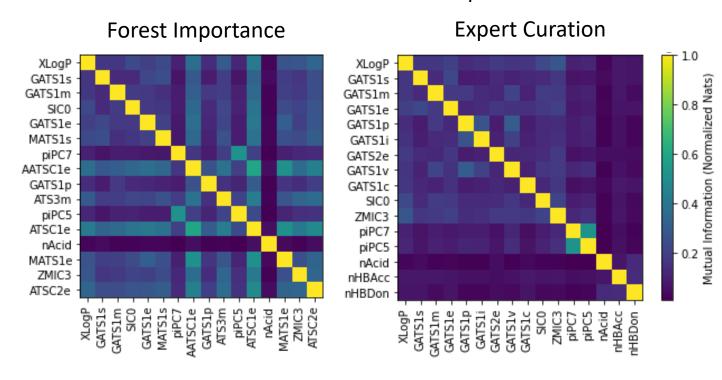


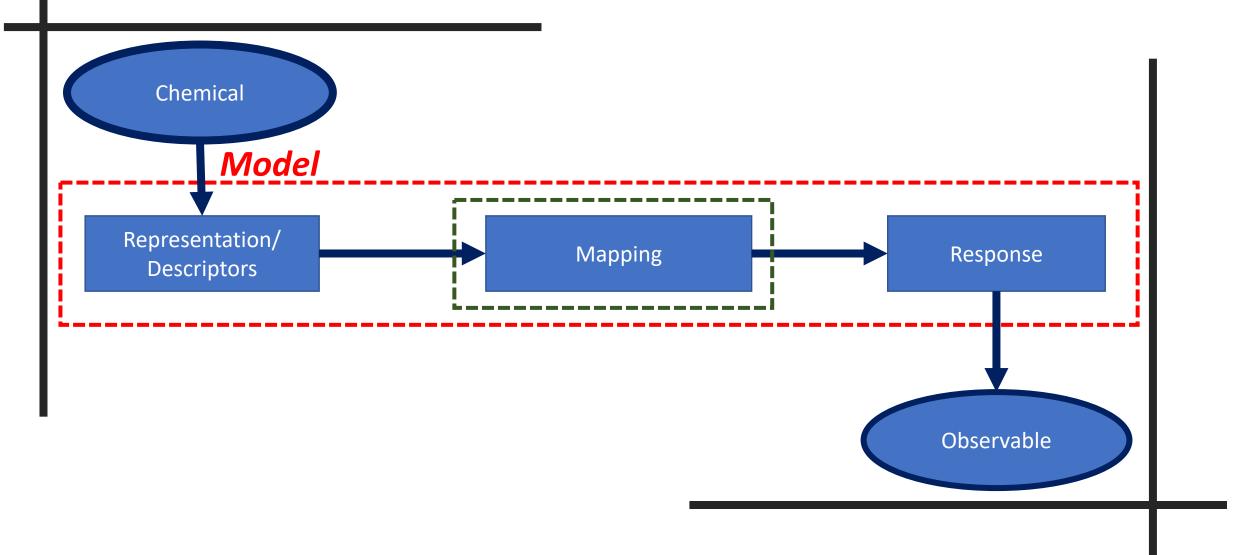
- Representation Matters
- "Descriptors"
 - Structure counts, fingerprints, SMILES, etc.
 - Embeds chemistry as glyphs representing functional groups
 - Physiochemical indices
 - Embeds chemistry as reals representing topology and property
 - Constitutional
 - Embeds chemistry as reals representing global molecular properties
 - Semi-empirical model predictions
 - Embeds chemistry as low-level model predictions

Automated Descriptor Selection

- Algorithmic selection can overrepresent informatically entangled facets of structure
- Depending on the structure of the dataset, this can "over-localize" the mechanisms described by the model

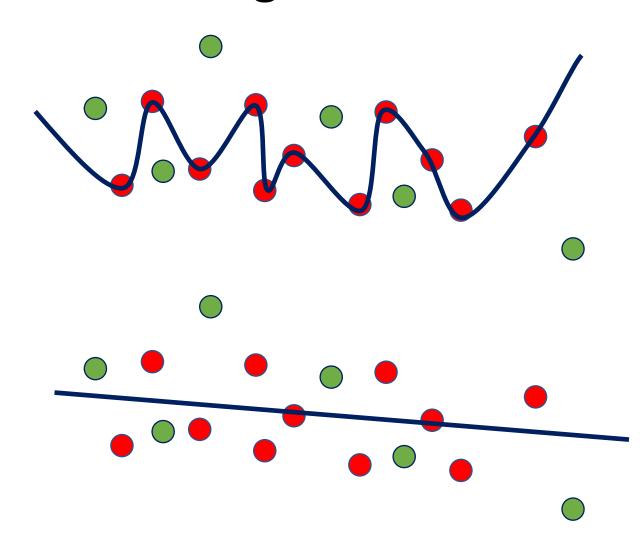
Mutual Information of Descriptors





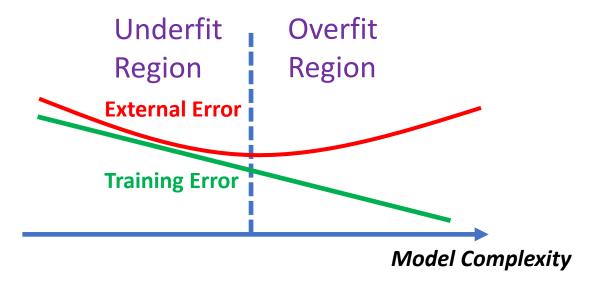
The Traditional Case of Overfitting

- Mappings can overfit because they do not necessarily abstract underlying principles that govern the chemistry or physics
- An 'overfit' model has mapped each training point directly to its response, memorizing the noise and local patterns of the data

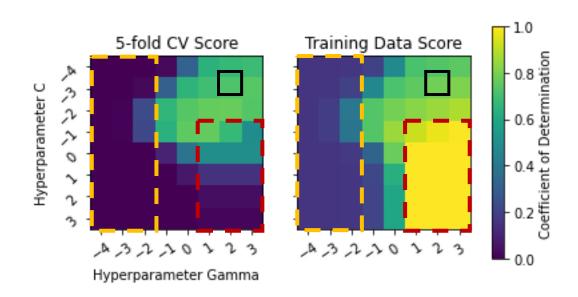


Model Complexity & Fit

- Fitting is a function of model complexity – the more information a model can contain, the more capacity it has to memorize
- With more limited capacity, it learns the data more efficiently
- Efficiency means finding useful, high-level abstractions within the data

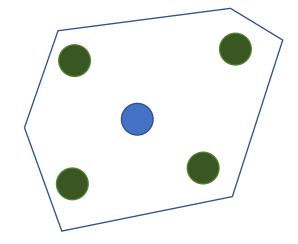


Support Vector Regression



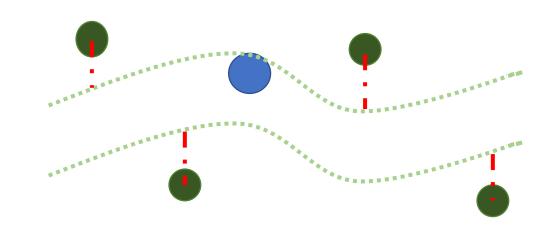
Common Types of Regressor

- "Neighborhood" models
 - K-Nearest Neighbors
 - Decision Trees
 - Random Forests



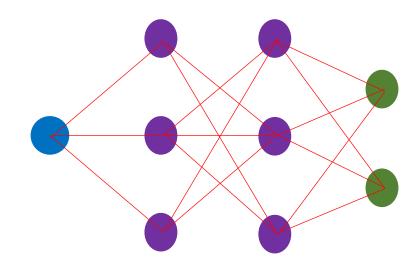
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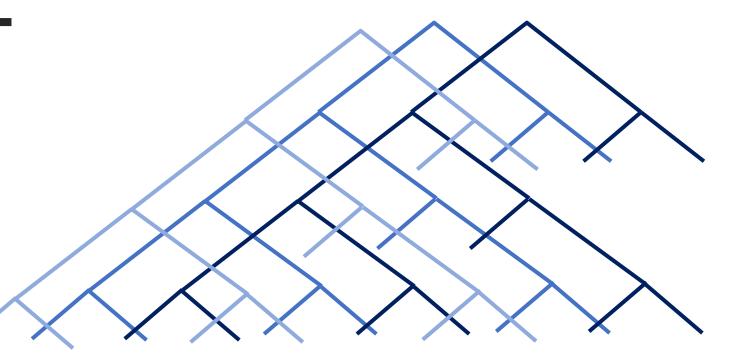
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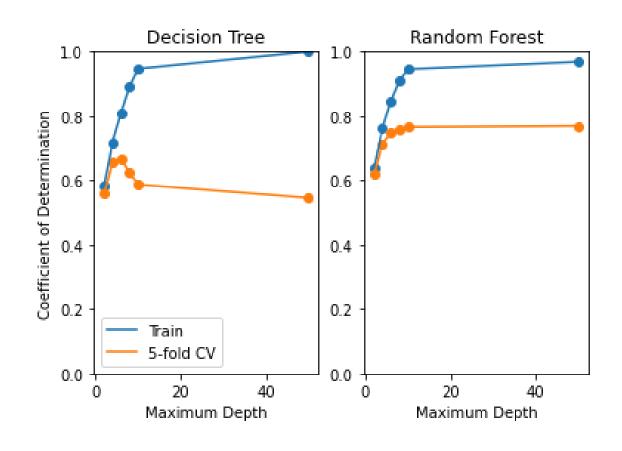
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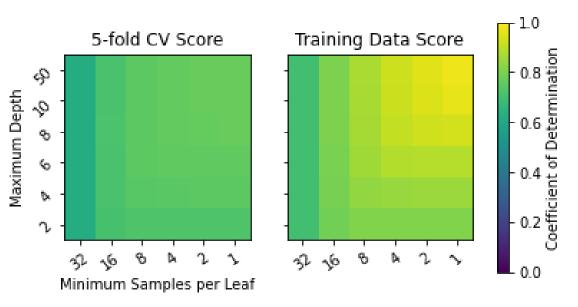
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Random Forests

Random forests are an ensemble of a neighborhood model

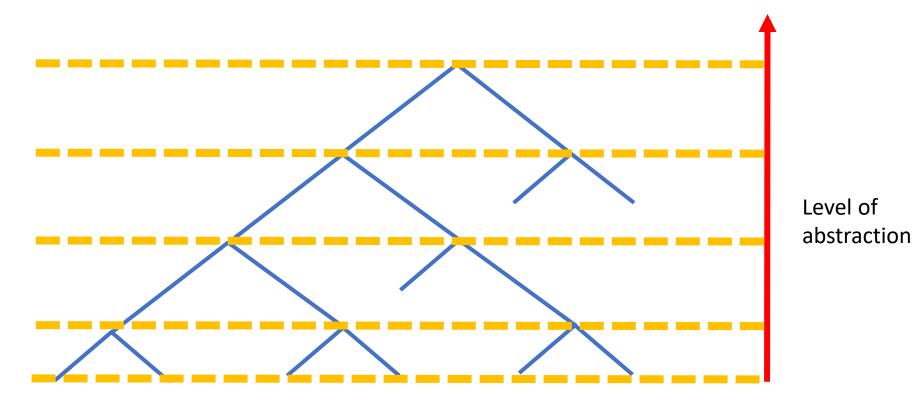




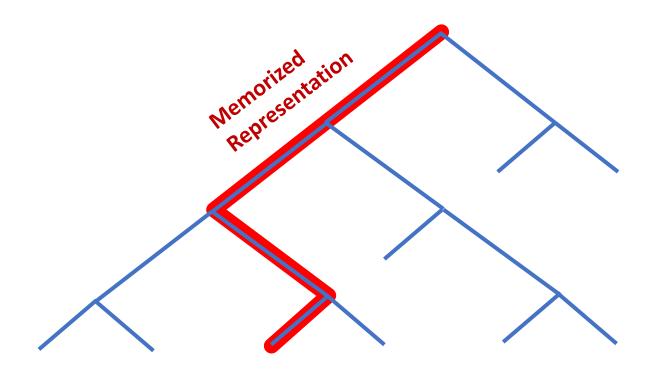
<u>Immunity?</u>

- In one sense
 - Breiman random forests are like k-Nearest Neighbor model in that they
 explicitly store a representation of the data they are trained on
 - Breiman forests grow trees without pruning, which often results in a data point getting its own leaf
 - This is an *explicit* representation of the data

Breiman Tree



Breiman Tree

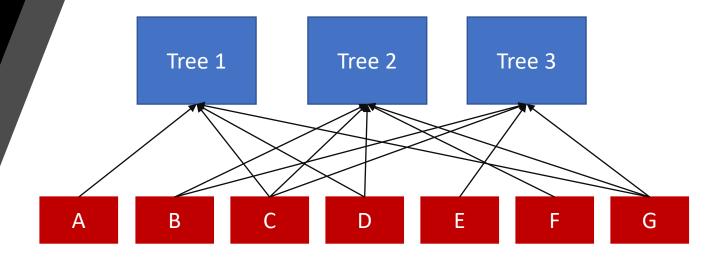


Immunity?

- Breiman forests bootstrap with replacement for each tree so that a given tree does not see the entire training set $(1/e \approx 63\%)$
- Do they "overfit"? Not really, because it memorizes its exposed training set by construction
- The "partially blind" ensemble effect of the bootstraps causes all these memorizations to wash out, so the memorization is "blurred"

"Partially blind" ensemble

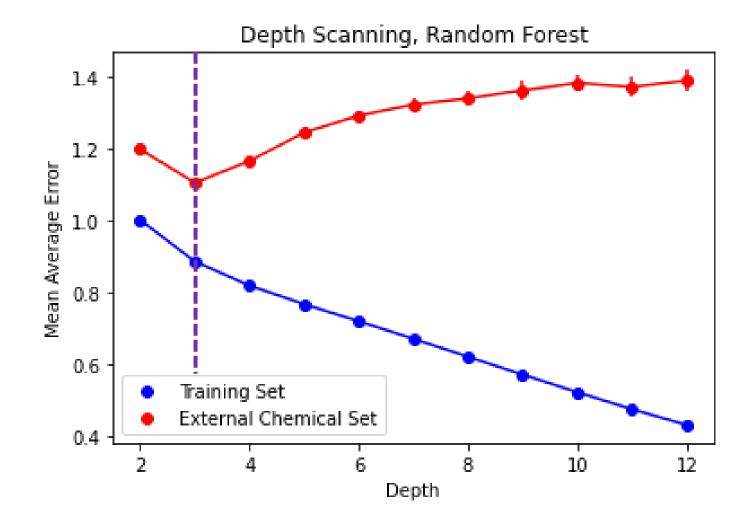
Bootstrapping partially blinds the model



- The partially blind trees "wash out" their predictions, resulting in a more generalized model
- But the model contains a memorized form of the data so the proportional representation of the training set matters a lot!

Limitations

- There is a limit to the overfitting resistance of the random forest the is relevant to "global" modeling
- The high-level abstractions of the shallow trees perform better than the local chemistries of the training domain
- Careful selection of chemical representation can fix this, but short of that it may be savvy to use a more conservative model for highly general chemistries



Conclusions

- Demands for transparency, generality and clarity limit regulatory ability to rely on statistical summaries in model validation
- Idiosyncrasies of public data sets increase concern around overfitting or over-localization
- Due to EPA interest in exotic chemistries (carbon-fluoro bonds, metallics, etc.) we are integrating analysis to combat over-localization to produce more robust theoretical underpinnings for policy decisions