How Low Can You Go? Feature Selection for Drug Discovery

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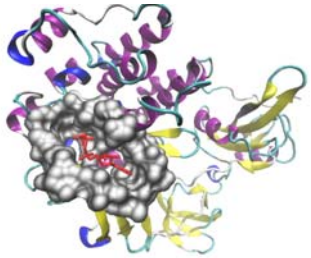
Background and Motivation

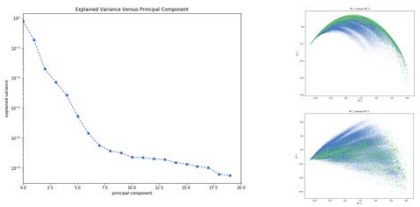
- The cost of bringing a drug to market depends on how quickly a candidate drug can be “discovered” and evaluated to ensure safety and effectiveness
- In this work we develop a method for predicting whether a given drug and protein compound will “bind”.
- Our aim is to select a set of features to predict drug-protein interactions



This study focuses on kinases. Kinase inhibitors are the largest class of new cancer therapies. Selective inhibition is difficult due to high sequence similarity, leading to off-target interactions and side-effects. Pictured here human c-SRC.

Dataset

- **Our dataset consists of 361,786 protein-drug molecule combinations** from the Directory of Useful Decoys Enhanced [4] subset of kinases which includes both known active compounds and generated decoys for 26 kinases. We collected the following features for our dataset:
  - Binding features: Vina MPI [2]
  - Drug features: Dragon [1]
  - Protein features: ExPasy [6], Porter,PaleAle 4.0 [5], & PROFEAT-Protein Feature Server [7]
  - Pocket features* [8]
- **1:50 ratio of positive to negative training examples**
- **5432 features before selection pipeline, reduced to a set of 1260** which are examined using PCA.



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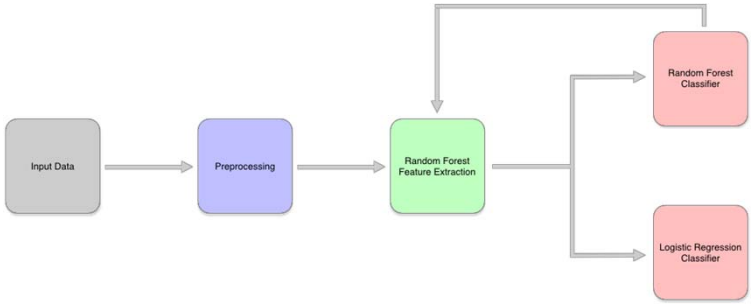
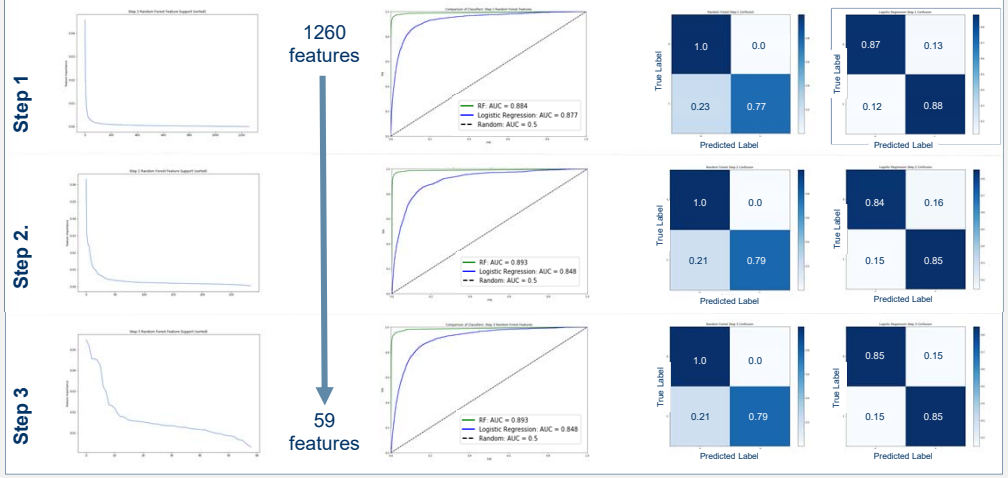
Methods



1. **Preprocessing:** Impute data using mean for each feature, then normalize each feature to unit length
2. **Random Forest Feature Extraction:** train a random forest, using randomized grid search. Using the feature importances of the optimal random forest classifier, create a reduced feature set from the features with above mean importance.
3. **Create 80/20 training and testing stratified split** of the data using only the “relevant” features
4. **Train** classification models on the reduced feature set, using randomized grid search to select the optimal model parameters.
5. **Test** classification models on the reduced feature set
6. **Repeat** until a minimal set of features are selected

Results

Given the initial set of 5432 features, we are able to reduce this set by 2 orders of magnitude while retaining nearly identical performance on the classification task. We evaluate a random forest and logistic regression on each reduced set.



Results cont..

Table 1: Random Forest Performance

Reduction	N Features	Precision	Recall	F1-Score	Positive Precision	Positive
Step 1	1260	0.99	0.99	0.99	0.99	0.87
Step 2	284	0.99	0.99	0.99	0.94	0.86
Step 3	59	0.99	0.99	0.99	0.93	0.85
Step 4	15	0.99	0.99	0.99	0.68	0.74

Table 2: Logistic Regression Performance

Reduction	N Features	Precision	Recall	F1-Score	Positive Precision	Positive
Step 1	1260	0.97	0.87	0.91	0.16	0.26
Step 2	284	0.97	0.84	0.89	0.12	0.22
Step 3	59	0.97	0.85	0.90	0.13	0.22
Step 4	15	0.97	0.79	0.86	0.10	0.17

Conclusions and Future Work

- We are able to significantly reduce the feature set and identify the important properties of the interaction to make accurate prediction
- This work helps lay the foundation for future work that will ask mo specific questions regarding protein-drug molecule interactions
- Can we expand our model to include multiple protein binding pockets to understand more complex interactions?
- Can we develop an effective method to predict adverse drug reactions based upon a drug molecule binding to multiple proteins
- Can we use secondary structure information about the protein to improve our results?

Acknowledgements

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