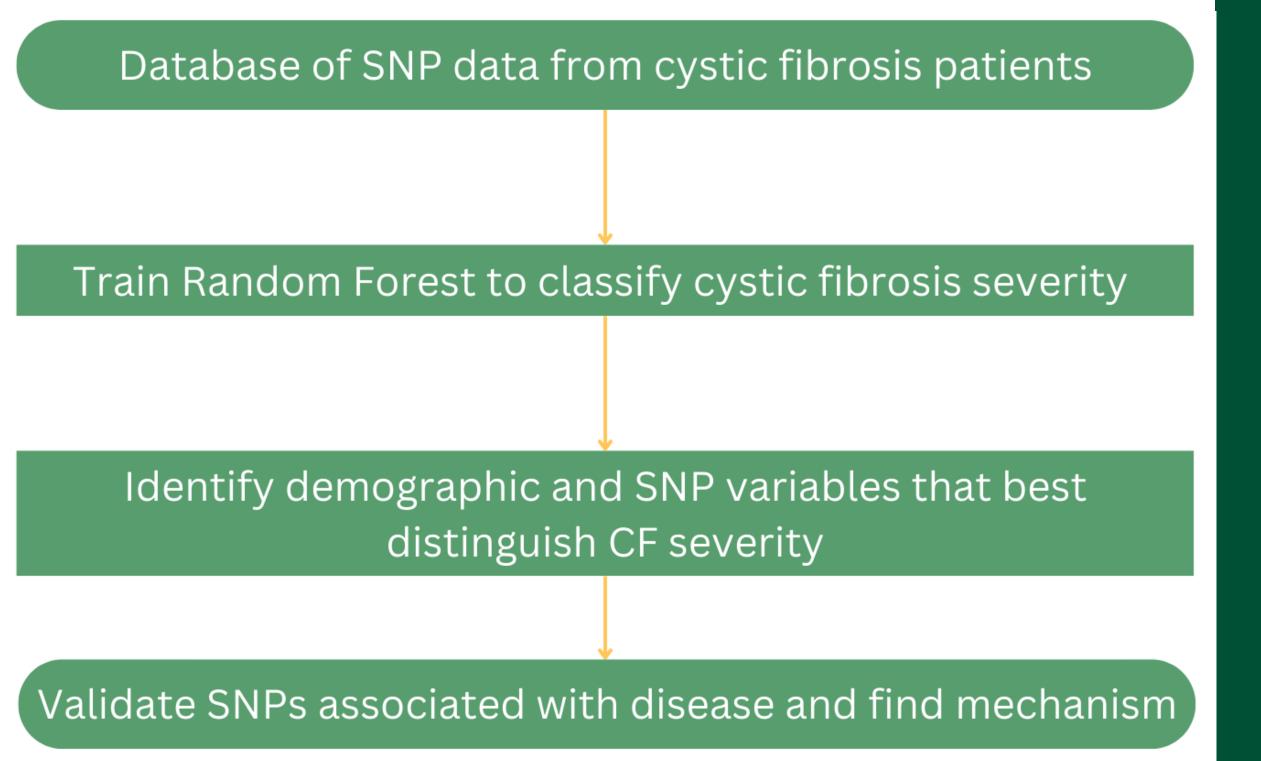
Louie Alexander

BACKGROUND:

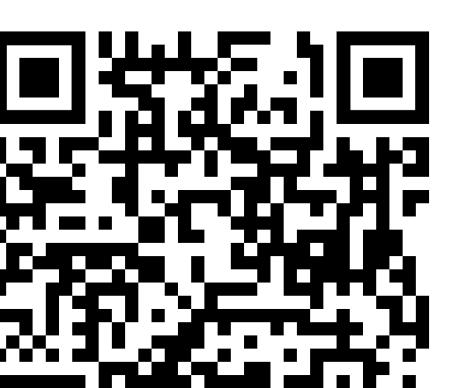
Cystic fibrosis is a disease characterized by poor lung function due to mutations in the cystic fibrosis transmembrane conductance regulator (CFTR.) The effects of mutations in CFTR have been described; however, individuals with the same CFTR genotype can have differing symptoms and severity.

Other regulatory and functional genetic elements likely contribute to these differing phenotypes. However, it can be hard to identify all genes or SNPs that contribute to the disease and *in-vitro* research on one gene or SNP is time-intensive.

Random forest can direct *in-vitro* research by identifying features that contribute strongly to distinguishing between phenotypes of cystic fibrosis severity.



Tutorial of randomForest in R:

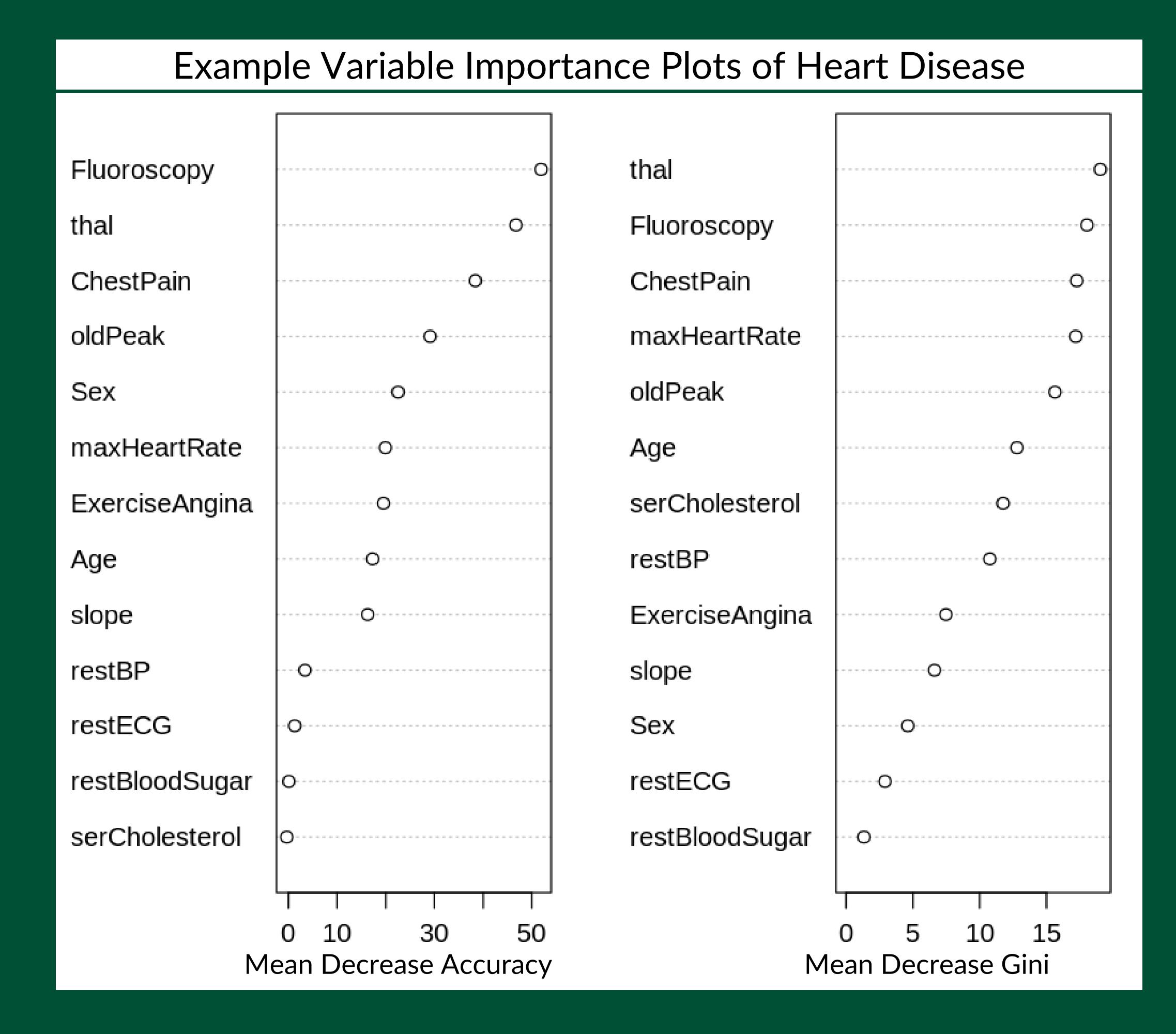


Can also use

- randomForest (R)
- cForest (R)
- Caret (R)
- RandomForest (python)
 - scikit-learn (python)

Random Forest can Identify Variables

that Affect Cystic Fibrosis Severity



Other Applications:

- Classification or Regression
- Diagnostic aid
- Improve sedative use for veterinary surgery
- ID molecular/genetic biomarkers contributing to disease
- ID variables that differ markedly between pheno/genotypes
- The relationship between "important variable" and trait can be researched

Results:

- Presence/Absence of SNP would be binary
- Can use VIM to determine impactful SNPs
- Need to consider whether SNPs are correlated
 - Linkage disequilibrium
 - Could select 1 SNP per block
 - Could use permutation VIM
- Permutation VIM can better separate correlated predictors
- If traditional VIM are used, correlated SNPs may still show high importance and point to functional significance or a functional block

VIP of Sedation in Animals

