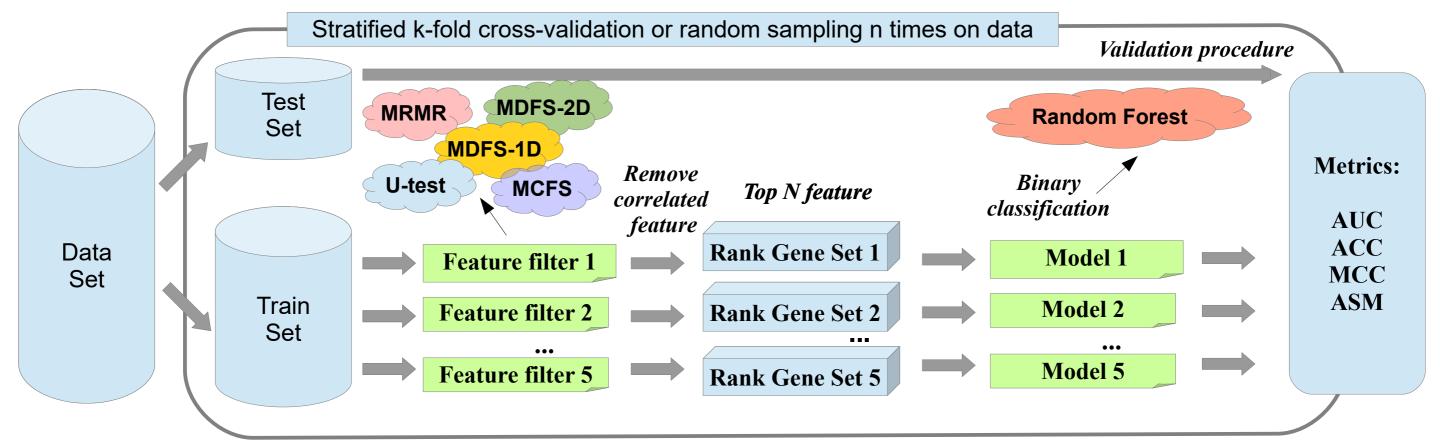
Feature Selection



U-test **Ensemble Feature Selection** Feature Selection MDFS-1D in n resampling steps MDFS-2D MRMR Union or intersection of **MCFS** feature subsets with up to five Data Set filters *Five* Majority voting feature procedure **U-test** filters Top N features MDFS-1D **Informative Gene Set 1** n-rank gene subsets Feature filter **Informative Gene Set 2** n-rank gene subsets 2 MRMR **MCFS Informative Gene Set 5** n-rank gene subsets 5 Filter results MDFS-2D

Gene Information

information Data bases Union or intersection of Transfac regulatory motif feature subsets with up to five **Gene Ontology** filters miRNA targets miRTarBase **U-test** MDFS-1D Reactome **WikiPathways** pathways MRMR **KEGG MCFS Human Protein Atlas** MDFS-2D CORUM

Human Phenotype Ontology

Biological Cellular component Molecular function

> Biological process

tissue specificity

protein complexes

human disease phenotypes

Feature Selection module functionalities

Load input file (*.csv, *.txt)

Select feature filter and set hyparameters

Set the cut off value of correlation coefficient

Set the method of evaluating predictive models and set it's parametes

Generate model outputs

> Learn model

Table of:

- 1. Feature
- 2. Feature-importance
- 3. Feature filter

Table of:

- 1. N-top
- 2. ASM
- 3. Feature filter

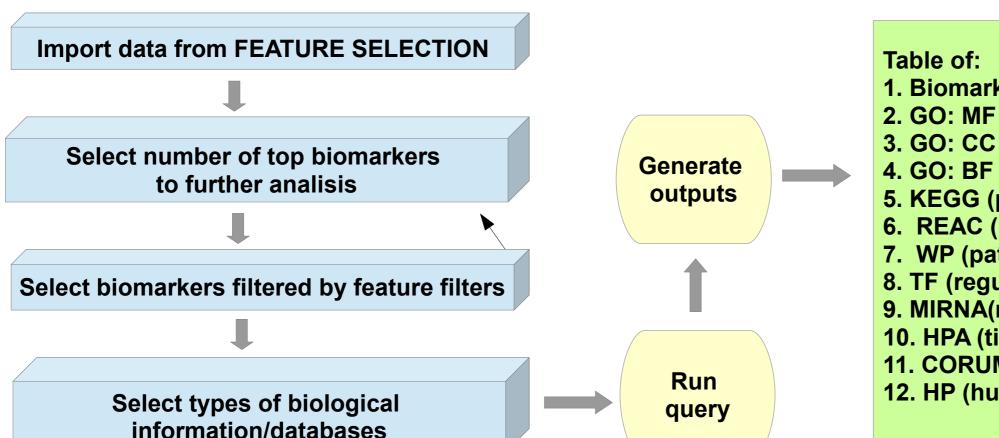
Table of:

- 1. N-top
- 2. mean AUC
- 3. mean ACC
- 4. mean MCC
- 5. MSE AUC
- 6. MSE ACC
- 7. MSE MCC
- 8. Feature filter

Plots:

- 1. mean AUC (N)
- 2. mean ACC (N)
- 3. mean MCC (N)
- 4. ASM (N)
- N is top N features

Gene Information module functionalities



- 1. Biomarker
- 2. GO: MF (molecular function)
- 3. GO: CC (cellular function)
- 4. GO: BF (biological function)
- 5. KEGG (pathways)
- 6. REAC (pathways)
- 7. WP (pathways)
- 8. TF (regulatory motif)
- 9. MIRNA(miRNA targets)
- 10. HPA (tissue specificity)
- 11. CORUM (protein complexes)
- 12. HP (human disease phenotypes)