

1. Scrape raw data from the Tox21 Public database
[Google drive link to raw data](#)
2. Generate outcome matrix and feature matrix using RDKit
File [outcome matrix](#) [feature matrix](#)
-> **208 features**
3. Feature selection using R file preprocessing -> **114 features**
 - a. [define functions to remove features and run models](#)
 - b. [run defined functions on tox21](#)
4. **Perform lasso regression to select top 40 features**
File [lasso regression](#)
Output of 40 features, bal_acc for 5, 10, 15, 20, 25, 30, 40, 50, 60, 114
5. Generate DS1 -> assay by assay with 40 features
6. Generate DS2 -> stacked 50 assays with 40 features
7. Generate DS3 -> stacked 50 assays with 40 features and gender and organism
8. Run ridge, naïve Bayesian and HBM for three datasets
 - a. Ridge
 - i. [DS1](#)
 - ii. [DS2](#)
 - iii. [DS3](#)
 - b. Naive Bayes
 - i. [DS1](#)
 - ii. [DS2](#)
 - iii. [DS3](#)
 - c. HBM
 - i. DS1
 1. [training](#)
 2. [testing + validation](#)
 - ii. [DS2](#)
 - iii. [DS3](#)
9. Use histogram to look at feature importance
 - a. [Ridge DS1](#)
 - b. [Ridge DS2](#)
 - c. [Ridge DS3](#)
 - d. [Naive DS1](#)
 - e. [Naive DS2](#)
 - f. [Naive DS3](#)
 - g. [HBM DS1](#)
 - h. [HBM DS2](#)
 - i. [HBM DS3](#)