#############################

**Matlab code**

**#############################**



Bi\_RandomWalk.m is for the BiRW method based on comprehensive similarity measure.

Bi\_RW\_Many.m is for the BiRW method (run 500 times) based on comprehensive similarity measure.



RandomWalk.m is for general random walk method.

RW\_Many.m is for general random walk method (run 500 times).



Set the parameter of logistics regression function, value of c



ClusterONE Cluster

#################################

**Python Code**

#############################



Generate the drug-drug and miRNA-miRNA similarity matrix.

Read the miRNA-drug effect associations matrix.

Run the randow walk method by matlab code.



Compute the distribution of prediction results.



Five-fold cross-validation.



Compute the AUC.



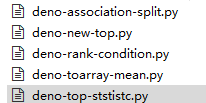
Calculate the probability of miRNA-drug with no relationship.



Compute the distribution of AUC results with different methods.



Compare the top 500 miRNA-drug associations with different methods.



De novo validation