Readme text:

1. \ DepMapModels\_Recon
   1. PrepareDepMapData.m to extract the transcriptomics data from the CCLE database into .mat structures. The data is stored in DepMapData.mat
   2. modGenesIDConv.m to convert the gene ids provided in the UpdatedRecon3D.mat in the form of Recon 3D id format into official gene names. The updated model is consRecon3DGeneSymbol.mat
   3. BuildDepMapModels.m to build the models using fastcore, swiftcore and sprintcore using consRecon3DGeneSymbol.mat and DepMapData.mat
2. \ coverage\_core
   1. Cancerrxnscoverage.m to calculate the proportion of generic core cancer reactions in each of the models built using fastcore, swiftcore and sprintcore
   2. core\_coverage\_find.m to compare the results core cancer reactions coverage results of sprintcore derived models with the models built using fastcore and swiftcore
3. \ flux\_results
   1. models\_name.m contains the model names for cancerous and non-cancerous contexts
   2. readfva.m extracts the flux variability results from the excel for all models
   3. fsranalysis\_ccle\_sprint.m to calculate the flux span ratios and flux enrichment ratios across the 10 contexts