Readme

Prerequisites:

1. COBRA toolbox installed
2. Basic knowledge of model manipulation and FBA

Step 1: Initialize the COBRA Toolbox using “initCobraToolbox()”.

Step 2: Prepare your inputs (model and expression data) as described in the documentation of “extract\_mCADRE\_models.m”. The model must NOT be the original genome-scale model but must be pre-treated to be fully flux consistent. Refer to (Gopalakrishnan et al, 20xx/ Manuscript #1) for specific details.

Step 3: Execute “extract\_mCADRE\_models.m” with the required inputs.

Step 4: To get the final reduced model, remove all reactions with a value of 0 in the output results structure. Assign this to a variable “remove\_rxns”

Step 5: Execute the following lines of code to get the final model:

Reduced\_model = removeRxns(genome\_scale\_model,remove\_rxns);

Reduced\_model = removeUnusedGenes(Reduced\_model);