MATLAB-COBRA codes (function name & description)

calculateMetTurnover.m	calculates metabolite turnover
cellularizeCellString.m	converts a cell array into a cell
changeReversibility.m	changes the reversibility of desired reactions
convert4Mapping.m	converts model to a more presentable form for Cell Designer
convertCOBRA2XML.m	converts a COBRA model to SBML file
createCircularNetwork.m	creates a network in the shape of a circle
createMET4mRXNS.m	creates a list of metabolites from given set of reactions
createNetwork4CellDesigner. m	creates a network for cell designer for better view
epistaticInteractions.m	calculate epistatic interactions
extractSubsystem.m	creates a new model with only one particular subsystem/pathway
fast_gcd.m	calculates greatest common denominator in a vector
findCmptmtGeneDistribution. m	calculates and lists subsystem/pathway-gene distribution of the model or desired genes in the model
findCmptmtRxnDistribution. m	calculates and lists subsystem/pathway-reaction distribution of the model or desired reactions in the model
findCompartmentInteraction s.m	calculates interactions within a subsystem/pathway: positive, negative and null
findCompartmentOfGenes.m	lists subsystem/pathway of genes
findCompartmentRelationshi p.m	lists subsystem/pathway relationships
findEssentialGenes.m	calculates essential genes - iterative methods
findEssentialRxns.m	calculates essential reactions - iterative method
findNegativeInteractions.m	finds all the negative interactions
findNoInteractions.m	finds all the null interactions
findPositiveInteractions.m	finds all the positive interactions
findRxns.m	generates information about metabolite from a given model, i.e. all the reactions it is involved in
findRxnsConstrained.m	finds the list of reactions that gene is involved with
findStringIn2OrderCellArray.m	finds a string in a cell array with list elements
findSyntheticLethalDyads.m	finds synthetic lethal dyads - iterative method
findUniqueGeneDeletions.m	finds the unique set of genes, such that each gene will have a unique set of reactions it constrains
geneAssociationHistogram.m	calculates the histogram of gene-reaction association of the model
linearizeCellString.m	linearizes a cell array such that it has no list elements
mapGenesOnModelB.m	maps a desired set of genes belonging to model 1 and maps them unto model 2 using EC number comparison
mapMutantFluxDifference.m	compares the flux difference between two mutants or mutant and wildtype, so it can be used for graphic visualization