MATLAB-COBRA codes (function name & description)

m reactions in the model findCompartmentInteraction substitute interactions within a subsystem/pathway: positive, negative and null subsystem/pathway of genes findCompartmentOfGenes.m lists subsystem/pathway of genes findCompartmentRelationshi p.m lists subsystem/pathway relationships calculates essential genes - iterative methods findEssentialRxns.m calculates essential reactions - iterative method findNegativeInteractions.m finds all the negative 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 findStringIn2OrderCellArray.m finds a string in a cell array with list elements findSynheticLethalDyads.m finds synthetic lethal dyads - iterative method findUniqueGeneDeletions.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 compares the flux difference between two mutants or mutant and wildtype, so it can		
changeReversibility.m changes the reversibility of desired reactions convert4Mapping.m convertCOBRAZMIL.m converts a COBRA model to 3 Man file createCircularNetwork.m creates a network in the shape of a circle createCircularNetwork.m creates a list of metabolites from given set of reactions createNetwork4CellDesigner. m epistaticInteractions.m calculate epistatic interactions extractSubsystem.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 findCmptmtGeneDistribution. m calculates greatest common denominator in a vector findCmptmtRxnDistribution. m calculates and lists subsystem/pathway-reaction distribution of the model or desired genes in the model findCompartmentInteraction s.m findCompartmentOfGenes.m findCompartmentRelationshi p.m findEssentialGenes.m calculates interactions within a subsystem/pathway: positive, negative and null sits subsystem/pathway of genes findEssentialGenes.m calculates essential genes - iterative methods findSesnetialRxns.m calculates essential genes - iterative methods findSesnetialRxns.m findSall the negative interactions findRynheticLethalDyads.m finds subsystem/pathway treations that gene is involved with findStringIn2OrderCellArray.m finds string in a cell array with list elements findSynheticLethalDyads.m finds string in a cell array with list elements findSynheticLethalDyads.m finds the list of reactions that gene is involved with and the positive interaction association of the model finds the list of reactions that gene is involved with findsynheticLethalDyads.m finds string in a cell array with list elements findSynheticLethalDyads.m finds the list of reactions that gene is involved with findsynheticLethalDyads.m finds the list of genes belonging to model 1 and maps them unto model 2 using EC number comparison maps a desired set of genes belonging to model 1 and maps them unto model 2 using EC number comparison	calculateMetTurnover.m	calculates metabolite turnover
convert4Mapping.m convertCOBRA2XML.m convertCOBRA2XML.m createCircularNetwork.m creates a list of metabolites from given set of reactions createNetwork4CellDesigner. m epistaticInteractions.m epistaticInteractions.m calculate epistatic interactions extractSubsystem.m calculates greatest common denominator in a vector findCmptmtGeneDistribution. m findCmptmtRxnDistribution. m findCmptmtRxnDistribution. m findCompartmentInteraction s.m findCompartmentRelationshi p.m findCompartmentRelationshi p.m findSesentialGenes.m findSompartmentOfGenes.m findSesentialGenes.m findSesen	cellularizeCellString.m	converts a cell array into a cell
convertCOBRAZXML.m createCircularNetwork.m creates a network in the shape of a circle createMET4mRXNS.m createNetwork4CellDesigner. mepistaticInteractions.m 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 findCmptmtRxnDistribution. m calculates and lists subsystem/pathway-gene distribution of the model or desired genes in the model findCompartmentInteraction s.m findCompartmentOfGenes.m lists subsystem/pathway of genes findCompartmentOfGenes.m lists subsystem/pathway relationships p.m findEssentialGenes.m calculates essential genes - iterative methods findNegativeInteractions.m finds all the negative interactions findSompartmentCompartmentOfGenes.m findSompartmentCompartmentOfGenes.m findSompartmentRelationships p.m findEssentialGenes.m calculates essential genes - iterative methods findAmpagativeInteractions.m finds all the negative interactions findSompartmentCompartmentOfGenes.m findSompartmentCompart	changeReversibility.m	changes the reversibility of desired reactions
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 depistaticInteractions.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 findComptmtRxnDistribution.m calculates and lists subsystem/pathway-reaction distribution of the model or desired genes in the model findCompartmentInteraction calculates and lists subsystem/pathway-reaction distribution of the model or desired genes in the model findCompartmentOfGenes.m lists subsystem/pathway repathway-reaction distribution of the model or desired genes in the model findCompartmentOfGenes.m lists subsystem/pathway of genes findCompartmentRelationship lists subsystem/pathway relationships p.m calculates essential genes - iterative methods findEssentialRxns.m calculates essential reactions - iterative method findMoInteractions.m finds all the negative interactions	convert4Mapping.m	converts model to a more presentable form for Cell Designer
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 findCompartmentInteraction calculates and lists subsystem/pathway-reaction distribution of the model or desired genes in the model findCompartmentOfGenes.m lists subsystem/pathway pathway-reaction distribution of the model or desired genes in the model findCompartmentOfGenes.m lists subsystem/pathway relationships findCompartmentRelationshi lists subsystem/pathway of genes findEssentialGenes.m calculates essential genes - iterative methods findEssentialRxns.m calculates essential reactions - iterative method 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	convertCOBRA2XML.m	converts a COBRA model to SBML file
creates a network for cell designer for better view epistaticInteractions.m 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 findComptmtRxnDistribution. m calculates and lists subsystem/pathway-gene distribution of the model or desired genes in the model findCompartmentInteraction s.m findCompartmentOfGenes.m lists subsystem/pathway pathway: positive, negative and null s.m findCompartmentRelationshi p.m calculates essential genes - iterative methods findEssentialGenes.m calculates essential genes - iterative method findNegativeInteractions.m finds all the null interactions findSoll the null interactions findRonoitiveInteractions.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 findSynheticLethalDyads.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 geneAssociationHistogram.m calculates es ell array such that it has no list elements mapGenesOnModelB.m mapMutantFluxDifference.m calculates the fitou difference between two mutants or mutant and wildtype, so it can	createCircularNetwork.m	creates a network in the shape of a circle
epistaticInteractions.m extractSubsystem.m creates a new model with only one particular subsystem/pathway fast_gcd.m calculates greatest common denominator in a vector findCmptmtGeneDistribution. m findCmptmtGeneDistribution. m findCompartmentInteraction s.m calculates and lists subsystem/pathway-gene distribution of the model or desired genes in the model calculates and lists subsystem/pathway-reaction distribution of the model or desired genes in the model findCompartmentInteraction s.m dindCompartmentOfGenes.m lists subsystem/pathway of genes findCompartmentRelationshi p.m lists subsystem/pathway of genes findCompartmentRelationshi p.m dindEssentialGenes.m calculates essential genes - iterative methods findEssentialRxns.m calculates essential reactions - iterative method findNegativeInteractions.m finds all the negative 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 findSynheticLethalDyads.m finds string in a cell array with list elements findSynheticLethalDyads.m finds string in a cell array with list elements findSynheticLethalDyads.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 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	createMET4mRXNS.m	creates a list of metabolites from given set of reactions
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 findCompartmentInteraction s.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 sts subsystem/pathway of genes findCompartmentRelationshi p.m lists subsystem/pathway of genes findEssentialGenes.m calculates essential genes - iterative methods findRessentialRxns.m calculates essential reactions - iterative method findNegativeInteractions.m finds all the negative interactions findPositiveInteractions.m finds all the positive 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 findStringIn2OrderCellArray.m finds the list of reactions that gene is involved with findSynheticLethalDyads.m finds synthetic lethal dyads - iterative method findSynheticLethalDyads.m finds the unique set o		creates a network for cell designer for better view
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 state interactions within a subsystem/pathway: positive, negative and null state state interactions within a subsystem/pathway: positive, negative and null state interactions within a subsystem/pathway: positive, negative and null state interactions within a subsystem/pathway: positive, negative and null state interactions hips findCompartmentOfGenes.m lists subsystem/pathway of genes findCompartmentRelationshi lists subsystem/pathway of genes findCompartmentRelationshi lists subsystem/pathway relationships findEssentialGenes.m calculates essential genes - iterative method findBEssentialRxns.m calculates essential reactions - iterative method 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 involved in finds the list of reactions that gene is involved with findSynheticLethalD	epistaticInteractions.m	calculate epistatic interactions
findCmptmtRxnDistribution. 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 findCompartmentOfGenes.m lists subsystem/pathway of genes findCompartmentRelationshi p.m lists subsystem/pathway relationships calculates essential genes - iterative methods findEssentialRxns.m calculates essential reactions - iterative method findNoInteractions.m findSall the negative interactions findRxns.m generates information about metabolite from a given model, i.e. all the reactions it is involved in findStringIn2OrderCellArray.m findStringIn2OrderCellArray.m findSynheticLethalDyads.m findSynheticLethalDyads.m findSynheticLethalDyads.m findSthe unique set of genes, such that each gene will have a unique set of reactions geneAssociationHistogram.m calculates the histogram of gene-reaction association of the model linearizeCellString.m mapGenesOnModelB.m calculates and lists subsystem/pathway-reaction distribution of the model of the model of the model linearizeCellString.m mapMutantFluxDifference.m calculates and lists subsystem/pathway-reaction distribution of the model of the model of genes belonging to model 1 and maps them unto model 2 using EC number comparison compares the flux difference between two mutants or mutant and wildtype, so it can	extractSubsystem.m	creates a new model with only one particular subsystem/pathway
m genes in the model findCmptmtRxnDistribution. calculates and lists subsystem/pathway-reaction distribution of the model or desired reactions in the model findCompartmentInteraction s.m lists subsystem/pathway: positive, negative and null s.m lists subsystem/pathway of genes 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 findPositiveInteractions.m finds all the null interactions findRxns.m generates information about metabolite from a given model, i.e. all the reactions it is involved in findStringIn2OrderCellArray.m finds a string in a cell array with list elements findSynheticLethalDyads.m finds the list of reactions that gene is involved with findStynheticLethalDyads.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 mapSenesOnModelB.m maps a desired set of genes belonging to model 1 and maps them unto model 2 using EC number comparison compares the flux difference between two mutants or mutant and wildtype, so it can	fast_gcd.m	calculates greatest common denominator in a vector
m reactions in the model findCompartmentInteraction substitute interactions within a subsystem/pathway: positive, negative and null s.m 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 findNoInteractions.m finds all the negative 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 findStringIn2OrderCellArray.m finds a string in a cell array with list elements findSynheticLethalDyads.m finds synthetic lethal dyads - iterative method findUniqueGeneDeletions.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 compares the flux difference between two mutants or mutant and wildtype, so it can	-	
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 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 findSynheticLethalDyads.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 comparison compares the flux difference between two mutants or mutant and wildtype, so it can	-	calculates and lists subsystem/pathway-reaction distribution of the model or desired reactions in the model
findCompartmentRelationshi p.m findEssentialGenes.m calculates essential genes - iterative methods findNegativeInteractions.m findNoInteractions.m findS all the negative interactions findPositiveInteractions.m findRxns.m generates information about metabolite from a given model, i.e. all the reactions involved in findStringIn2OrderCellArray.m finds a string in a cell array with list elements findSynheticLethalDyads.m finds synthetic lethal dyads - iterative method findUniqueGeneDeletions.m geneAssociationHistogram.m calculates the histogram of gene-reaction association of the model linearizeCellString.m mapGenesOnModelB.m mapGenesOnModelB.m calculates the flux difference between two mutants or mutant and wildtype, so it can campametationships calculates the flux difference between two mutants or mutant and wildtype, so it can		calculates interactions within a subsystem/pathway: positive, negative and null
p.m findEssentialGenes.m calculates essential genes - iterative methods findSesentialRxns.m calculates essential reactions - iterative method findNegativeInteractions.m finds all the negative 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 findStringIn2OrderCellArray.m finds a string in a cell array with list elements findSynheticLethalDyads.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 mapGenesOnModelB.m mapGenesOnModelB.m calculates the flux difference between two mutants or mutant and wildtype, so it can	findCompartmentOfGenes.m	lists subsystem/pathway of genes
findEssentialRxns.m findNegativeInteractions.m finds all the negative interactions findNoInteractions.m findPositiveInteractions.m findRxns.m findRxns.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 findStringIn2OrderCellArray.m finds a string in a cell array with list elements findSynheticLethalDyads.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 mapGenesOnModelB.m mapGenesOnModelB.m calculates the flux difference between two mutants or mutant and wildtype, so it can compares the flux difference between two mutants or mutant and wildtype, so it can		lists subsystem/pathway relationships
findNegativeInteractions.mfinds all the negative interactionsfindNoInteractions.mfinds all the null interactionsfindPositiveInteractions.mfinds all the positive interactionsfindRxns.mgenerates information about metabolite from a given model, i.e. all the reactions it is involved infindStringIn2OrderCellArray.mfinds the list of reactions that gene is involved withfindSynheticLethalDyads.mfinds a string in a cell array with list elementsfindUniqueGeneDeletions.mfinds synthetic lethal dyads - iterative methodfinds the unique set of genes, such that each gene will have a unique set of reactions it constrainsgeneAssociationHistogram.mcalculates the histogram of gene-reaction association of the modellinearizeCellString.mlinearizes a cell array such that it has no list elementsmapGenesOnModelB.mmaps a desired set of genes belonging to model 1 and maps them unto model 2 using EC number comparisonmapMutantFluxDifference.mcompares the flux difference between two mutants or mutant and wildtype, so it can	findEssentialGenes.m	calculates essential genes - iterative methods
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 findStringIn2OrderCellArray.m finds a string in a cell array with list elements findSynheticLethalDyads.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 compares the flux difference between two mutants or mutant and wildtype, so it can	findEssentialRxns.m	calculates essential reactions - iterative method
findPositiveInteractions.mfinds all the positive interactionsfindRxns.mgenerates information about metabolite from a given model, i.e. all the reactions it is involved infindRxnsConstrained.mfinds the list of reactions that gene is involved withfindStringIn2OrderCellArray.mfinds a string in a cell array with list elementsfindSynheticLethalDyads.mfinds synthetic lethal dyads - iterative methodfindUniqueGeneDeletions.mfinds the unique set of genes, such that each gene will have a unique set of reactions it constrainsgeneAssociationHistogram.mcalculates the histogram of gene-reaction association of the modellinearizeCellString.mlinearizes a cell array such that it has no list elementsmapGenesOnModelB.mmaps a desired set of genes belonging to model 1 and maps them unto model 2 using EC number comparisonmapMutantFluxDifference.mcompares the flux difference between two mutants or mutant and wildtype, so it can	findNegativeInteractions.m	finds all the negative 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 findSynheticLethalDyads.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 compares the flux difference between two mutants or mutant and wildtype, so it can	findNoInteractions.m	finds all the null interactions
findRxnsConstrained.m finds the list of reactions that gene is involved with findStringIn2OrderCellArray.m finds a string in a cell array with list elements findSynheticLethalDyads.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	findPositiveInteractions.m	finds all the positive interactions
findSynheticLethalDyads.m finds a string in a cell array with list elements 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	findRxns.m	generates information about metabolite from a given model, i.e. all the reactions it is involved in
findSynheticLethalDyads.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	findRxnsConstrained.m	finds the list of reactions that gene is involved with
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	findStringIn2OrderCellArray.m	finds a string in a cell array with list elements
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	findSynheticLethalDyads.m	finds synthetic lethal dyads - iterative method
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	findUniqueGeneDeletions.m	
mapGenesOnModelB.mmaps a desired set of genes belonging to model 1 and maps them unto model 2using EC number comparisonusing EC number comparisonmapMutantFluxDifference.mcompares the flux difference between two mutants or mutant and wildtype, so it can	geneAssociationHistogram.m	calculates the histogram of gene-reaction association of the model
using EC number comparisonmapMutantFluxDifference.mcompares the flux difference between two mutants or mutant and wildtype, so it can	linearizeCellString.m	linearizes a cell array such that it has no list elements
	mapGenesOnModelB.m	
be used for graphic visualization	mapMutantFluxDifference.m	compares the flux difference between two mutants or mutant and wildtype, so it can be used for graphic visualization