

Tutorial 1 – Import a GEM, Set Parameters and Run FBA

This is a short introduction that shows how to load a genome-scale metabolic model (GEM), set reaction constraints, objective function and perform an optimization through flux balance analysis (FBA). The resulting fluxes are visualized and exported to a PDF file.

A GEM for the filamentous fungus *Penicillium chrysogenum* is used in this tutorial. The model can be found in a Microsoft Excel file under the name iAL1006 v1.00.xlsx and in SBML file iAL1006 v1.00.xml. Open tutorial1.m file in MATLAB to begin this exercise. To run a section of code in MATLAB, highlight it, press right mouse button on it and choose an option "Evaluate selection".

NOTE: the user must be able to successfully import the GEMs in Excel format with the RAVEN function importExcelModel. Although, this functionality is not necessary for this exercise, the users without such ability would not be able to do Tutorials 2-4, which involve working with GEMs in RAVEN compatible Excel format.

```
In [ ]: setRavenSolver('gurobi')
```

- importExcelModel

function

```
model=importExcelModel(fileName,removeExcMets,printWarnings,ignoreErrors)
```

Imports a constraint-based model from a Excel file

- importModel

function

```
model=importModel(fileName,removeExcMets,isSBML2COBRA,supressWarnings)
```

Import a constraint-based model from a SBML file

removeExcMets: true if exchange metabolites should be removed. This is needed to be able to run simulations, but it could also be done using simplifyModel at a later stage (opt, default true)"

The tutorial file explains:

"The "false" flag imports a model with exchange reactions in their "closed" form. This makes the model unsuited for modelling, but it is useful for some quality control steps."

```
In [ ]: % How to Load a model  
model=importModel('tutorial_data/iAL1006 v1.00.xml',false)
```

The model contains 47 errors.

Error encountered during read.

WARNING: No objective function found. This might be intended, but results in FBCv2 n on-compliant SBML file when exported

WARNING: The composition for the following metabolites could not be parsed:
LPE

```
Out[ ]: model = struct with fields:  
    id: 'iAL1006'  
        name: 'Penicillium chrysogenum genome-scale model'  
    annotation: [1x1 struct]  
        rxns: {1632x1 cell}  
        mets: {1395x1 cell}  
            S: [1395x1632 double]  
            lb: [1632x1 double]  
            ub: [1632x1 double]  
            rev: [1632x1 double]  
            c: [1632x1 double]  
            b: [1395x1 double]  
        comps: {5x1 cell}  
        compNames: {5x1 cell}  
        compMiriams: {5x1 cell}  
            rxnNames: {1632x1 cell}  
            rxnComps: [1632x1 double]  
            grRules: {1632x1 cell}  
            rxnGeneMat: [1632x1006 double]  
            subSystems: {1632x1 cell}  
            eccodes: {1632x1 cell}  
            rxnMiriams: {1632x1 cell}  
            rxnNotes: {1632x1 cell}  
            rxnReferences: {1632x1 cell}  
                genes: {1006x1 cell}  
                geneMiriams: {1006x1 cell}  
                geneShortNames: {1006x1 cell}  
                    metNames: {1395x1 cell}  
                    metComps: [1395x1 double]  
                    inchis: {1395x1 cell}  
                    metFormulas: {1395x1 cell}  
                    metMiriams: {1395x1 cell}  
                    unconstrained: [1395x1 double]
```

```
In [ ]: %The following function prints some properties of the model. The two "true"  
%flags say that it should also list potential problems such as dead-end  
%reactions or unconnected metabolites.
```

- `printModelStats`

```
function printModelStats(model, printModelIssues, printDetails)  
Prints some statistics about a model to the screen
```

```
In [ ]: % Useful for model validation. Notice the two "true" flags.  
printModelStats(model,true,true);
```

Network statistics for iAL1006: Penicillium chrysogenum genome-scale model		
EC-numbers		626
Genes*		1006
Peroxisome	38	
EC-numbers		626
Genes*		1006
Peroxisome	38	
Mitochondria	219	
Cytosol	802	
Extracellular	95	
Boundary	0	
Reactions*		1632
Peroxisome	137	
Mitochondria	324	
Cytosol	1144	
Extracellular	336	
Boundary	161	
Unique reactions**		1449
Metabolites		1395
Peroxisome	105	
Mitochondria	242	
Cytosol	728	
Extracellular	160	
Boundary	160	
Unique metabolites		849

* Genes and reactions are counted for each compartment if any of the corresponding metabolites are in that compartment. The sum may therefore not add up to the total number.

** Unique reactions are defined as being biochemically unique (no compartmentalization)

Short model quality summary for iAL1006: Penicillium chrysogenum genome-scale model

Dead-end reactions 66

r0035

r0036

r0040

r0061

r0071

r0108

r0161

r0162

r0169

r0170

r0174

r0213

r0224

r0235

r0238

r0240

r0356

r0405

r0407

r0424

r0427

r0429

r0447

r0454

r0514

r0515

r0516

r0533

r0534

r0535

r0538

r0539

r0573

r0576

r0577

r0580

r0581

r0582
r0586
r0597
r0602
r0603
r0604
r0612
r0630
r0631
r0641
r0691
r0697
r0707
r0712
r0723
r0726
r0730
r0731
r0732
r0752
r0754
r1166
r1221
r1275
r0234
r0428
r0437
r0517
r0537

Dead-end metabolites 232
(LLACb) (S)-lactate
(MALb) (S)-malate
(13GLUCANb) 1,3-beta-D-glucan
(2HPENGb) 2-hydroxybenzylpenicillin
(AKGb) 2-oxoglutarate
(C40Db) 2-oxy-but-3-enoate
(PABA_b) 4-aminobenzoate
(4HPOAb) 4-hydroxyphenoxyacetate
(4HPENVb) 4-hydroxyphenoxyethylpenicillin
(6APAb) 6-aminopenicillanate
(OPCb) 6-oxopiperidine-2-carboxylate
(8HPA_b) 8-hydroxypenillic acid
(ACb) acetate
(ADb) adenine
(TREb) alpha,alpha-trehalose
(GLCb) alpha-D-glucose
(ARABINb) alpha-L-arabinan
(AMIACEb) aminoacetaldehyde
(ANb) anthranilate
(PENARTb) artificial penicillin
(ARTPROTb) artificial protein
(PENGb) benzylpenicillin
(PENGAb) benzylpenicilloic acid
(bALAb) beta-alanine
(bDGLCb) beta-D-glucose
(BIOMASSb) biomass
(C40b) butyrate
(CB15LCTb) cellobiono-1,5-lactone
(CELLOBb) cellobiose
(CELLUb) cellulose
(CHITb) chitin
(CHIBb) chitobiose
(CHITO_b) chitosan
(CHO_b) choline
(CITb) citrate
(CO2b) CO₂
(CYNEb) cyanate
(CYTSb) cytosine
(AOLb) D-arabinitol
(ARABb) D-arabinose
(C100b) decanoate
(FRUb) D-fructose

(GLACb) D-galactose
(GLCNTb) D-gluconate
(GLCN15LACb) D-glucono-1,5-lactone
(GLCnb) D-glucosamine
(DGLCb) D-glucose
(MNTb) D-mannitol
(MANb) D-mannose
(RIBb) D-ribose
(XYLb) D-xylose
(ETHb) ethanol
(ETHNITb) ethylnitronate
(FMNb) FMN
(FORb) formate
(FUMb) fumarate
(GABA_b) gamma-aminobutyrate
(RGtb) glutathione
(GLb) glycerol
(GLYBETb) glycine betaine
(GLYb) glycine
(GLYCOGENb) glycogen
(GLYAb) glycolate
(GNb) guanine
(H2Ob) H₂O
(H2O2b) H₂O₂
(H2Sb) H₂S
(C170b) heptadecanoate
(C171b) heptadecenoate
(C70b) heptanoate
(C162b) hexadecadienoate
(C161b) hexadecenoate
(C60b) hexanoate
(PENDFb) hexanoylpenicillin
(HYXNb) hypoxanthine
(C200b) icosanoate
(ICITb) isocitrate
(IPNb) isopenicillin N
(AMAb) L-2-amino adipate
(LACTb) lactose
(ALAb) L-alanine
(LAOLb) L-arabinitol
(LARABB) L-arabinose
(ARGb) L-arginine
(ASNb) L-asparagine
(ASPB) L-aspartate
(C120b) laurate
(CITRb) L-citrulline
(CYSB) L-cysteine
(CYSTb) L-cystine
(DOQUIb) L-dopaquinone
(GLUb) L-glutamate
(GLNb) L-glutamine
(HISb) L-histidine
(HCYSb) L-homocysteine
(IDOLb) L-iditol
(ILEb) L-isoleucine
(LEUb) L-leucine
(LYSb) L-lysine
(METb) L-methionine
(ORNb) L-ornithine
(PHEb) L-phenylalanine
(PROb) L-proline
(RLRB) L-ribulose
(SERb) L-serine
(SORb) L-sorbose
(THRb) L-threonine
(TRPb) L-tryptophan
(TYRb) L-tyrosine
(VALb) L-valine
(MLTb) maltose
(MLTIOSEb) maltotriose
(MANNANb) mannans
(MELIB) melibiose
(METHOLb) methanol

(MYO1b) myo-inositol
(C140b) myristate
(NAGb) N-acetyl-D-glucosamine
(NH3b) NH3
(NICDb) nicotinamide
(NICAb) nicotinate
(HNO3b) nitrate
(HNO2b) nitrite
(C90b) nonanoate
(O2b) O2
(C182b) octadecadienoate
(C183b) octadecatrienoate
(C181b) octadecenoate
(C80b) octanoate
(PENKb) octanoylpenicillin
(OXALb) oxalate
(OAb) oxaloacetate
(C160b) palmitate
(C150b) pentadecanoate
(POAb) phenoxyacetate
(PENVb) phenoxyethylpenicillin
(PENVAb) phenoxyethylpenicilloic acid
(PAAb) phenylacetate
(PIb) phosphate
(6CARHEXb) pimelate
(PROPB) propionate
(PYRb) pyruvate
(QUINb) quinolinate
(RAFFb) raffinose
(STARb) starch
(C180b) stearate
(SUCCb) succinate
(SUCb) sucrose
(SLFb) sulfate
(H2SO3b) sulfite
(Sb) sulfur
(THMEb) thiamin
(URAb) uracil
(UREAb) urea
(URIb) uridine
(C50b) valerate
(XANb) xanthine
(XYLANb) xylans
(XOLb) xylitol
(DIDIPC) (S)-2,3-dihydrodipicolinate
(ACPC) 1-aminocyclopropanecarboxylate
(PINS3P) 1-phosphatidyl-1D-myoinositol 3-phosphate
(PINS4P) 1-phosphatidyl-1D-myoinositol 4-phosphate
(D45PI) 1-phosphatidyl-D-myoinositol 4,5-bisphosphate
(ACLAC) 2-acetolactate
(AM6SA) 2-aminomuconic 6-semialdehyde
(2D3DGALT) 2-dehydro-3-deoxy-D-galactonate
(DEXG) 2-deoxy-D-gluconic acid
(DEORIPI) 2-deoxy-D-ribose 5-phosphate
(OXGLY) 2-hydroxy-3-oxosuccinic acid
(KEMYOI) 2-inosose
(PHEETHAL) 2-phenylethanol
(DEHXG) 3-dehydro-2-deoxy-D-gluconate
(APEBU) 4-(2-Aminophenyl)-2,4-dioxobutanoate
(AHMPP) 4-amino-2-methyl-5-diphosphomethylpyrimidine
(AHMP) 4-amino-2-methyl-5-phosphomethylpyrimidine
(THZP) 4-methyl-5-(2-phosphonoxyethyl)thiazole
(THZ) 5-(2-hydroxyethyl)-4-methylthiazole
(ADPR) 5-deoxy-D-ribofuranos-5-yl-ADP
(MTHPTGLU) 5-methyltetrahydropteroyltri-L-glutamate
(ACTP) acetyl phosphate
(AGMT) agmatine
(GLUCRE) beta-D-glucosiduronic acids
(CINNAM) cinnamate
(ARABLAC) D-arabinono-1,4-lactone
(DC) deoxycytidine
(DU) deoxyuridine
(GLCUNT) D-glucuronate

(DPRO) D-proline
(TDP) D-tagatofuranose 1,6-bisphosphate
(DTDP) dTDP
(DTTP) dTTP
(GALOL) galactitol
(PPGPP) guanosine 3',5'-bis(diphosphate)
(PPPGPP) guanosine 3'-diphosphate 5'-triphosphate
(IAD) indole-3-acetamide
(IAC) indole-3-acetate
(ACNL) indole-3-acetonitrile
(PHC) L-1-pyrroline-3-hydroxy-5-carboxylate
(LACT) lactose
(PYTE) myo-inositol hexakisphosphate
(MHIS) N(pi)-methyl-L-histidine
(ACVb) N-[L-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine
(OSLHSER) O-succinyl-L-homoserine
(PROPAL) propanal
(PURI5P) pseudouridine 5'-phosphate
(QT) quinate
(SARC) sarcosine
(SPRM) spermine
(T6P) tagatose 6-phosphate
(TAR) tartrate
(THPTGLU) tetrahydropteroyltri-L-glutamate
(DT) thymidine
(THY) thymine
(HPRO) trans-4-hydroxy-L-proline
(TRPM) tryptamine
(UDPGE) UDP-D-glucuronate
(GALUNTe) D-galacturonate
(PECTATEe) pectate
(PHEETHALm) 2-phenylethanol
(ECYSm) cysteine-[enzyme]
(FALDm) formaldehyde
(PHCm) L-1-pyrroline-3-hydroxy-5-carboxylate
(ALAm) L-alanine
(DIMEGLYm) N,N-dimethylglycine
(NMNm) nicotinamide mononucleotide
(OAHSERm) O-acetyl-L-homoserine
(PHALm) phenylacetaldehyde
(SARCm) sarcosine
(ESULFCYSm) S-sulfanyl cysteine-[enzyme]
(HPROm) trans-4-hydroxy-L-proline
(LYSp) L-lysine

Reactions which could not be elementally balanced 43

r0123
r0144
r0244
r0247
r0248
r0280
r0281
r0282
r0283
r0302
r0303
r0304
r0312
r0313
r0481
r0482
r0514
r1010
r1109
r1119
r1120
r1121
r1125
r1134
r1135
r1261
r1348

r1422
r1453
r1455
r1456
r1459
r1460
r1461
r1462
r1463
r1464
r1465
r1467
r1468
penartOUT
proteinOUT
bmOUT

Reactions which are elementally unbalanced	123
r0065	hydrogen
r0066	hydrogen
r0108	hydrogen
r0118	hydrogen
r0121	hydrogen
r0127	hydrogen
r0134	hydrogen
r0137	oxygen, hydrogen
r0148	carbon, nitrogen, hydrogen, generic group
r0161	generic group
r0174	oxygen, hydrogen, generic group
r0202	oxygen, hydrogen
r0205	oxygen, hydrogen
r0213	hydrogen
r0223	oxygen, hydrogen
r0261	oxygen, hydrogen
r0264	oxygen, hydrogen
r0277	oxygen, hydrogen
r0278	oxygen, hydrogen
r0284	oxygen, hydrogen
r0285	carbon, oxygen, hydrogen
r0286	oxygen, hydrogen
r0287	oxygen, hydrogen
r0288	oxygen, hydrogen
r0289	carbon, oxygen, hydrogen
r0298	hydrogen
r0358	oxygen, hydrogen
r0359	oxygen, hydrogen
r0360	oxygen, hydrogen
r0478	hydrogen, iron
r0479	carbon, oxygen, hydrogen
r0480	oxygen, hydrogen
r0483	iron
r0484	carbon, nitrogen, hydrogen, generic group
r0486	hydrogen
r0491	hydrogen
r0506	carbon, oxygen, phosphorus, hydrogen
r0507	carbon, oxygen, phosphorus, hydrogen
r0519	hydrogen
r0520	hydrogen
r0521	oxygen, hydrogen
r0533	hydrogen
r0534	oxygen, hydrogen
r0561	hydrogen
r0564	hydrogen
r0586	hydrogen
r0629	oxygen, hydrogen
r0654	hydrogen
r0697	hydrogen
r0729	carbon, oxygen, hydrogen
r0745	oxygen
r0769	carbon, nitrogen, hydrogen, generic group
r0771	carbon, nitrogen, hydrogen, generic group
r0772	carbon, nitrogen, hydrogen, generic group
r0773	carbon, nitrogen, generic group

r0774 carbon, nitrogen, hydrogen, generic group
r0775 carbon, nitrogen, hydrogen, generic group
r0781 carbon, nitrogen, hydrogen, generic group
r0782 carbon, nitrogen, hydrogen, generic group
r0783 carbon, nitrogen, hydrogen, generic group
r0784 carbon, nitrogen, hydrogen, generic group
r0786 carbon, nitrogen, hydrogen, generic group
r0787 carbon, nitrogen, hydrogen, generic group
r0788 carbon, nitrogen, hydrogen, generic group
r0789 carbon, nitrogen, hydrogen, generic group
r0790 carbon, nitrogen, hydrogen, generic group
r0792 carbon, nitrogen, hydrogen, generic group
r0822 hydrogen
r0833 hydrogen
r1003 hydrogen
r1004 hydrogen
r1005 hydrogen
r1006 hydrogen
r1007 hydrogen
r1008 hydrogen
r1009 hydrogen
r1011 hydrogen
r1012 hydrogen
r1013 hydrogen
r1014 hydrogen
r1015 hydrogen
r1020 hydrogen
r1029 hydrogen
r1030 hydrogen
r1035 hydrogen
r1036 hydrogen
r1041 hydrogen
r1042 hydrogen
r1046 hydrogen
r1047 hydrogen
r1048 hydrogen
r1049 hydrogen
r1051 hydrogen
r1052 hydrogen
r1056 hydrogen
r1057 hydrogen
r1061 hydrogen
r1062 hydrogen
r1077 hydrogen
r1078 hydrogen
r1082 hydrogen
r1083 hydrogen
r1096 hydrogen
r1097 hydrogen
r1098 hydrogen
r1099 hydrogen
r1104 hydrogen
r1106 hydrogen
r1123 hydrogen
r1127 hydrogen
r1130 hydrogen
r1131 hydrogen
r1146 carbon, hydrogen
r1152 hydrogen
r1153 hydrogen
r1158 hydrogen
r1159 hydrogen
r1161 hydrogen
r1454 carbon, hydrogen, generic group
r1457 carbon, nitrogen, oxygen, phosphorus, hydrogen, generic group
r1458 carbon, nitrogen, oxygen, phosphorus, hydrogen, generic group
freeNADH hydrogen
freeNADPH hydrogen

From the tutorial:

%Most modelling approaches using GEMs are based on the mass balancing around the internal metabolites in the system. However, in order for the system to uptake or excrete metabolites, some metabolites have been defined as "unconstrained". In order to simulate something, those metabolites have to be removed from the model. The function `simplifyModel` is a general-purpose function for making models smaller. This includes the options such as grouping linear reactions and deleting reactions which cannot carry flux. Here it is chosen to delete the exchange metabolites, all reactions that are constrained to zero (mainly uptake of non-standard carbon sources), and all reactions that cannot carry flux (mainly reactions that were dependent on any of those non-standard carbons sources).

- `simplifyModel`

```
function [reducedModel, deletedReactions, deletedMetabolites]=simplifyModel(model,deleteUnconstrained, deleteDuplicates, deleteZeroInterval, deleteInaccessible, deleteMinMax, groupLinear, constrainReversible, reservedRxns, suppressWarnings)
```

Simplifies a model by deleting reactions/metabolites

```
In [ ]: model=simplifyModel(model,true,false,true,true);  
model
```

```
Out[ ]: model = struct with fields:  
    id: 'iAL1006'  
        name: 'Penicillium chrysogenum genome-scale model'  
        annotation: [1x1 struct]  
        rxns: {1305x1 cell}  
        mets: {1037x1 cell}  
            S: [1037x1305 double]  
            lb: [1305x1 double]  
            ub: [1305x1 double]  
            rev: [1305x1 double]  
            c: [1305x1 double]  
            b: [1037x1 double]  
            comps: {4x1 cell}  
            compNames: {4x1 cell}  
            compMiriams: {4x1 cell}  
            rxnNames: {1305x1 cell}  
            rxnComps: [1305x1 double]  
            grRules: {1305x1 cell}  
            rxnGeneMat: [1305x1006 double]  
            subSystems: {1305x1 cell}  
                eccodes: {1305x1 cell}  
                rxnMiriams: {1305x1 cell}  
                rxnNotes: {1305x1 cell}  
            rxnReferences: {1305x1 cell}  
                genes: {1006x1 cell}  
                geneMiriams: {1006x1 cell}  
                geneShortNames: {1006x1 cell}  
                metNames: {1037x1 cell}  
                metComps: [1037x1 double]  
                inchis: {1037x1 cell}  
            metFormulas: {1037x1 cell}  
            metMiriams: {1037x1 cell}
```

- `setParam`

```
function model=setParam(model, paramType, rxnList, params, var)
Sets parameters for reactions
```

```
In [ ]: %%% validating the model using the theoretical yield of carbon dioxide from glucose
% First, set the uptake of carbon to glucose
model=setParam(model,'ub',{'glcIN' 'etohIN'},[1 0]); % remember, the units are mmol
% Second, set the objective for the simulation to maximize CO2 production
model=setParam(model,'obj',{'co2OUT'},1);
```

- solveLP

```
function [solution, hsSolOut]=solveLP(model,minFlux,params,hsSol)
Solves a linear programming problem
```

```
In [ ]: % Third, get the maximum given the setted constrains
sol=solveLP(model);
disp(sol);
```

```
x: [1305x1 double]
f: -6.0000
stat: 1
msg: 'Optimal solution found'
sPrice: [1037x1 double]
rCost: [1305x1 double]
```

- printFluxes

```
function printFluxes(model, fluxes, onlyExchange, cutOffFlux,
outputFile,outputString,metaboliteList)
Prints reactions and fluxes to the screen or to a file.
```

onlyExchange: only print exchange fluxes (opt, default true)

```
In [ ]: % Print the fluxes in console. The true flag indicates to only print exchange fluxes
printFluxes(model, sol.x, true, 10^-7);
```

```
EXCHANGE FLUXES:
co2OUT (production of CO2):    6
h2oOUT (production of H2O):    6
glcIN  (uptake of alpha-D-glucose):    1
co2OUT (production of CO2):    6
h2oOUT (production of H2O):    6
glcIN  (uptake of alpha-D-glucose):    1
o2IN   (uptake of O2):    6
```

```
In [ ]: % Exploring other fluxes. Notice that some are "infinite" (1000)
printFluxes(model, sol.x, false, 10^-7);
```

FLUXES:

r0001 (spontaneous conversion): 333.3333
r0002 (spontaneous conversion): -333.3333
r0004 (ATP:alpha-D-glucose 6-phosphotransferase): 1
r0006 (alpha-D-glucose 6-phosphate ketol-isomerase): -999
r0007 (beta-D-glucose 6-phosphate ketol-isomerase): -1000
r0008 (alpha-D-glucose 6-phosphate ketol-isomerase): 1000
r0009 (phosphofructokinase): 1
r0010 (fructose-bisphosphate aldolase): 1
r0011 (D-glyceraldehyde-3-phosphate aldose-ketose-isomerase): -1
r0012 (glyceraldehyde-3-phosphate dehydrogenase): 2
r0013 (phosphoglycerate kinase): 2
r0014 (phosphoglycerate mutase): 2
r0015 (2-phospho-D-glycerate hydro-lyase (phosphoenolpyruvate-forming)): 2
r0016 (pyruvate kinase): 2
r0019 (ethanol:NADP+ oxidoreductase): 8
r0001 (spontaneous conversion): 333.3333
r0002 (spontaneous conversion): -333.3333
r0004 (ATP:alpha-D-glucose 6-phosphotransferase): 1
r0006 (alpha-D-glucose 6-phosphate ketol-isomerase): -999
r0007 (beta-D-glucose 6-phosphate ketol-isomerase): -1000
r0008 (alpha-D-glucose 6-phosphate ketol-isomerase): 1000
r0009 (phosphofructokinase): 1
r0010 (fructose-bisphosphate aldolase): 1
r0011 (D-glyceraldehyde-3-phosphate aldose-ketose-isomerase): -1
r0012 (glyceraldehyde-3-phosphate dehydrogenase): 2
r0013 (phosphoglycerate kinase): 2
r0014 (phosphoglycerate mutase): 2
r0015 (2-phospho-D-glycerate hydro-lyase (phosphoenolpyruvate-forming)): 2
r0016 (pyruvate kinase): 2
r0019 (ethanol:NADP+ oxidoreductase): 8
r0020 (ethanol:NAD+ oxidoreductase): -1000
r0021 (ethanol:NAD+ oxidoreductase): 992
r0022 (pyruvate:[dihydrolipoyllysine-residue acetyltransferase]-lipoyllysine 2-oxido-reductase (decarboxylating, acceptor-acetylating)): 2
r0023 (acetyl-CoA:enzyme N6-(dihydrolipooyl)lysine S-acetyltransferase): 2
r0024 (dihydrolipoamide:NAD+ oxidoreductase): 4
r0081 ((S)-3-hydroxybutanoyl-CoA:NADP+ oxidoreductase): -2
r0084 (succinate:ubiquinone oxidoreductase): -2
r0085 (acetyl-CoA:oxaloacetate C-acetyltransferase (thioester-hydrolysing)): 2
r0086 (citrate hydro-lyase (cis-aconitate-forming)): -2
r0087 (isocitrate hydro-lyase (cis-aconitate-forming)): 2
r0089 (isocitrate:NADP+ oxidoreductase (decarboxylating)): 2
r0091 (2-oxoglutarate:[dihydrolipoyllysine-residue succinyltransferase]-lipoyllysine 2-oxidoreductase (decarboxylating, acceptor-succinylating)): 2
r0092 (succinyl-CoA:enzyme N6-(dihydrolipooyl)lysine S-succinyltransferase): 2
r0094 (succinate:CoA ligase (GDP-forming)): -998
r0095 (succinate:CoA ligase (ADP-forming)): 1000
r0097 ((S)-malate hydro-lyase (fumarate-forming)): 2
r0098 ((S)-malate:NAD+ oxidoreductase): -998
r0099 ((S)-malate:NAD+ oxidoreductase): 1000
r0116 (ubiquinol oxidase (mitochondrial alternative oxidase (aox))): 5.6646
r0118 (ferrocytochrome-c:oxygen oxidoreductase): 0.1677
r0120 (NADH:ubiquinone oxidoreductase): 4
r0127 (ubiquinol:ferricytochrome-c oxidoreductase): 0.3354
r0128 (H+-transporting two-sector ATPase): 0.14
r0149 (5,10-methylenetetrahydrofolate:glycine hydroxymethyltransferase): -100
0
r0150 (5,10-methylenetetrahydrofolate:glycine hydroxymethyltransferase): 1000
r0175 (D-mannitol:NADP+ 2-oxidoreductase): 8
r0181 (D-mannitol:NAD+ 2-oxidoreductase): -8
r0205 (cellobiose dehydrogenase): -994
r0223 (cellobiose dehydrogenase): 994
r0226 (UTP:alpha-D-galactose-1-phosphate uridylyltransferase): 1000
r0228 (UTP:alpha-D-glucose-1-phosphate uridylyltransferase): -1000
r0230 (UDP-glucose:alpha-D-galactose-1-phosphate uridylyltransferase): -100
0
r0233 (D-galactose:oxygen 6-oxidoreductase): 6
r0236 (D-galactose:NAD+ 1-oxidoreductase): -6
r0237 (D-galactono-1,4-lactone hydroxyacylhydrolase): -6
r0374 (ATP:AMP phosphotransferase): -1000
r0376 (adenylate kinase): 1000
r0377 (adenylate kinase): -998

```

r0378 (adenylate kinase): 998
r0398 (ATP:dADP phosphotransferase): 1000
r0399 (ATP:GDP phosphotransferase): -1000
r0400 (ATP:IDP phosphotransferase): -1000
r0401 (ATP:GMP phosphotransferase): -1000
r0403 (guanylate kinase): -1000
r0416 (GTP:uridine 5'-phosphotransferase): 1000
r0418 (ATP:uridine 5'-phosphotransferase): 1000
r0540 (L-aspartate:2-oxoglutarate aminotransferase): 1000
r0541 (L-aspartate:2-oxoglutarate aminotransferase): -1000
r0735 (hydrogen-peroxide:hydrogen-peroxide oxidoreductase): 3
r0929 (3-hydroxyacyl-CoA dehydrogenase): 2
r1165 ((S)-malate mitochondrial permease): 1000
r1170 (2-oxoglutarate mitochondrial permease): 1000
r1174 (5,10-methylenetetrahydrofolate mitochondrial permease): -1000
r1178 (ADP/ATP/phosphate mitochondrial shuttle): 2.14
r1182 (citrate/isocitrate mitochondrial shuttle): -1000
r1183 (citrate/malate mitochondrial shuttle): -1000
r1194 (glycine mitochondrial permease): -1000
r1200 (isocitrate/malate mitochondrial shuttle): 1000
r1204 (L-aspartate mitochondrial permease): 1000
r1217 (malate/succinate mitochondrial shuttle): -1000
r1230 (phosphate mitochondrial permease): -1000
r1231 (phosphate/malate mitochondrial shuttle): -1000
r1235 (pyruvate mitochondrial permease): 2
r1236 (serine mitochondrial permease): 1000
r1238 (succinate mitochondrial permease): -1000
r1240 (tetrahydrofolate mitochondrial permease): 1000
r1243 (acetaldehyde mitochondrial membrane diffusion): -992
r1246 (CO2 mitochondrial membrane diffusion): -6
r1247 (ethanol mitochondrial membrane diffusion): 992
r1248 (H2O mitochondrial membrane diffusion): 1000
r1251 (O2 mitochondrial membrane diffusion): 3
r1316 (alpha-D-glucose permease): 334.3333
r1322 (beta-D-glucose permease): 666.6667
r1323 (cellobiono-1,5-lactone permease): -994
r1324 (cellobiose permease): 994
r1336 (D-mannose permease): 1000
r1337 (D-mannose permease): -1000
r1342 (glucose permease): -1000
r1424 (CO2 plasma membrane diffusion): 6
r1428 (H2O plasma membrane diffusion): 6
r1441 (O2 plasma membrane diffusion): 1000
r1466 (ATP maintenance): 1
co2OUT (production of CO2): 6
h2oOUT (production of H2O): 6
glcIN (uptake of alpha-D-glucose): 1
o2IN (uptake of O2): 6

```

"Infinite" (± 1000) fluxes suggest and non physiologicla behaviour. The tutorial states:

```

%The results show many reactions that have -1000 or 1000 flux. This is
%because there are loops in the solution. In order to clean up the
%solution
%one can minimize the sum of all the fluxes. This is done by setting the
%third flag to solveLP to true (take a look at solveLP, there are other
%options as well).

```

```

In [ ]: % minFlux = 1 indicates that a second optimization performed to get rid of loops in
% adress to minimize the sum of abs(fluxes).
sol=solveLP(model,1);
printFluxes(model, sol.x, false, 10^-7);

```

FLUXES:

r0003 (D-glucose 1-epimerase): 1
r0006 (alpha-D-glucose 6-phosphate ketol-isomerase): -2.5446
r0011 (D-glyceraldehyde-3-phosphate aldose-ketose-isomerase): 0.37625
r0012 (glyceraldehyde-3-phosphate dehydrogenase): 0.41584
r0013 (phosphoglycerate kinase): 0.41584
r0014 (phosphoglycerate mutase): 0.41584
r0015 (2-phospho-D-glycerate hydro-lyase (phosphoenolpyruvate-forming)): 0.41584
r0022 (pyruvate:[dihydrolipoyllysine-residue acetyltransferase]-lipoyllysine 2-oxido-reductase (decarboxylating, acceptor-acetylating)): 0.20792
r0023 (acetyl-CoA:enzyme N6-(dihydrolipoyl)lysine S-acetyltransferase): 0.20792
r0024 (dihydrolipoamide:NAD+ oxidoreductase): 0.83167
r0027 (glucose-6-phosphate 1-dehydrogenase): 2.5446
r0028 (6-phospho-D-glucono-1,5-lactone lactonohydrolase): 2.5446
r0029 (6-phospho-D-gluconate:NADP+ 2-oxidoreductase (decarboxylating)): 3.5446
r0030 (D-ribulose-5-phosphate 3-epimerase): 2.1683
r0031 (D-ribose-5-phosphate aldose-ketose-isomerase): 1.3762
r0032 (sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glycolaldehyde transferase): 1.3762
r0033 (transketolase): 1.1683
r0034 (sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase): -1.3762
r0038 (ATP:D-gluconate 6-phosphotransferase): 1
r0042 (beta-D-glucose:oxygen 1-oxidoreductase): -1
r0045 (spontaneous conversion): 1
r0059 ((S)-malate:NADP+ oxidoreductase(oxaloacetate-decarboxylating)): 0.20792
r0084 (succinate:ubiquinone oxidoreductase): -0.62375
r0085 (acetyl-CoA:oxaloacetate C-acetyltransferase (thioester-hydrolysing)): 0.62375
r0086 (citrate hydro-lyase (cis-aconitate-forming)): -0.62375
r0087 (isocitrate hydro-lyase (cis-aconitate-forming)): 0.62375
r0090 (isocitrate:NADP+ oxidoreductase (decarboxylating)): 0.62375
r0091 (2-oxoglutarate:[dihydrolipoyllysine-residue succinyltransferase]-lipoyllysine 2-oxidoreductase (decarboxylating, acceptor-succinylating)): 0.62375
r0092 (succinyl-CoA:enzyme N6-(dihydrolipoyl)lysine S-succinyltransferase): 0.62375
r0093 (succinyl-CoA:acetoacetate CoA-transferase): 0.20792
r0095 (succinate:CoA ligase (ADP-forming)): 0.41584
r0097 ((S)-malate hydro-lyase (fumarate-forming)): 0.83167
r0098 ((S)-malate:NAD+ oxidoreductase): 0.62375
r0118 (ferrocytochrome-c:oxygen oxidoreductase): 1.0396
r0119 (NADH:ubiquinone oxidoreductase): 1.4554
r0124 (NADPH:oxygen oxidoreductase): 6.2971
r0127 (ubiquinol:ferricytochrome-c oxidoreductase): 2.0792
r0128 (H+-transporting two-sector ATPase): 4.5162
r0153 (formaldehyde:NAD+ oxidoreductase): 0.37625
r0157 (formate:NAD+ oxidoreductase): 0.37625
r0158 (D-xylulose-5-phosphate:formaldehyde glycolaldehydetransferase): 0.37625
r0242 (sn-glycerol-3-phosphate phosphohydrolase): 0.37625
r0253 (alcohol oxidase): 0.58416
r0254 (alcohol oxidase): 0.37625
r0255 (NAD-dependent alcohol dehydrogenase): 0.58416
r0308 (sn-glycerol-3-phosphate:NAD+ 2-oxidoreductase): 0.37625
r0553 (L-glutamate:NADP+ oxidoreductase (deaminating)): 0.20792
r0693 (phosphoenolpyruvate:D-erythrose-4-phosphate C-(1-carboxyvinyl)transferase (phosphate hydrolysing, 2-carboxy-2-oxoethyl-forming)): 0.20792
r0694 (2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate phosphate-lyase (cyclizing)): 0.20792
r0695 (3-dehydroquinate hydro-lyase): 0.20792
r0696 (shikimate:NADP+ 3-oxidoreductase): 0.20792
r0698 (ATP:shikimate 3-phosphotransferase): 0.20792
r0699 (phosphoenolpyruvate:3-phosphoshikimate 5-O-(1-carboxyvinyl)-transferase): 0.20792
r0700 (5-O-(1-carboxyvinyl)-3-phosphoshikimate phosphate-lyase (chorismate-forming)): 0.20792
r0713 (chorismate pyruvatemutase): 0.20792
r0716 (prephenate hydro-lyase (decarboxylating; phenylpyruvate-forming)): 0.20792

```

r0717 (L-phenylalanine:2-oxoglutarate aminotransferase): -0.20792
r0720 (homogentisate:oxygen 1,2-oxidoreductase (decyclizing)): 0.20792
r0721 (maleylacetoacetate isomerase): 0.20792
r0722 (4-fumarylacetoacetate fumarylhydrolase): 0.20792
r0724 (L-phenylalanine:oxygen oxidoreductase (decarboxylating)): 0.20792
r0725 (2-phenylacetamide amidohydrolase): 0.20792
r0735 (hydrogen-peroxide:hydrogen-peroxide oxidoreductase): 4.1287
r0748 (phenylacetate 2-hydroxylase): 0.20792
r0751 (2-hydroxyphenylacetate hydroxylase): 0.20792
r0930 (acetyl-CoA:acetyl-CoA C-acetyltransferase): 0.20792
r1164 ((S)-malate mitochondrial permease): -0.20792
r1170 (2-oxoglutarate mitochondrial permease): 0.41584
r1178 (ADP/ATP/phosphate mitochondrial shuttle): 4.9321
r1191 (fumarate mitochondrial permease): 0.20792
r1199 (isocitrate mitochondrial permease): 0.62375
r1235 (pyruvate mitochondrial permease): 0.20792
r1245 (acetoacetate mitochondrial membrane diffusion): 0.20792
r1246 (CO2 mitochondrial membrane diffusion): -0.83167
r1248 (H2O mitochondrial membrane diffusion): 0.20792
r1251 (O2 mitochondrial membrane diffusion): 1.0396
r1316 (alpha-D-glucose permease): 1
r1424 (CO2 plasma membrane diffusion): 6
r1428 (H2O plasma membrane diffusion): 6
r1441 (O2 plasma membrane diffusion): 6
r1466 (ATP maintenance): 1
co2OUT (production of CO2): 6
h2oOUT (production of H2O): 6
glcIN (uptake of alpha-D-glucose): 1
o2IN (uptake of O2): 6

```

```
In [ ]: % Lets repeat, but change the objective function to biomass production
% Notice the change in metabolic requirements (exchange IN reactions)
model=setParam(model,'obj',{'bmOUT'},1);
sol=solveLP(model,1);
printFluxes(model, sol.x, true, 10^-7);
```

EXCHANGE FLUXES:

```

c4odOUT (production of 2-oxy-but-3-enoate): 8.4803e-06
bmOUT (production of biomass): 0.084803
co2OUT (production of CO2): 3.061
c4odOUT (production of 2-oxy-but-3-enoate): 8.4803e-06
bmOUT (production of biomass): 0.084803
co2OUT (production of CO2): 3.061
h2oOUT (production of H2O): 5.586
glcIN (uptake of alpha-D-glucose): 1
piIN (uptake of phosphate): 0.027889
nh3IN (uptake of NH3): 0.59384
o2IN (uptake of O2): 2.937
slfIN (uptake of sulfate): 0.022888
thmIN (uptake of thiamin): 8.4803e-06
pimIN (uptake of pimelate): 8.4803e-06

```

```
In [ ]: % To compare carbon flux swapping glucose by ethanol, remembear that
% ethanol have 2 carbons and glucose 6; so, 3 * 2 = carbon number in glucose
modelETH=setParam(model,'eq',{'glcIN' 'ethoIN'},[0 3]);
solETH=solveLP(modelETH,1);
printFluxes(modelETH, solETH.x, true, 10^-7);
```

EXCHANGE FLUXES:

```

c4odOUT (production of 2-oxy-but-3-enoate): 1.0816e-05
bmOUT (production of biomass): 0.10816
co2OUT (production of CO2): 2.2514
c4odOUT (production of 2-oxy-but-3-enoate): 1.0816e-05
bmOUT (production of biomass): 0.10816
co2OUT (production of CO2): 2.2514
h2oOUT (production of H2O): 8.4719
piIN (uptake of phosphate): 0.035572
nh3IN (uptake of NH3): 0.75743
o2IN (uptake of O2): 5.0932
slfIN (uptake of sulfate): 0.029193
thmIN (uptake of thiamin): 1.0816e-05
pimIN (uptake of pimelate): 1.0816e-05
ethoIN (uptake of ethanol): 3

```

To make more clear the comparison between two conditions:

- `followChanged`

```
function followChanged(model,fluxesA,fluxesB, cutOffChange, cutOffFlux,  
cutOffDiff, metaboliteList)
```

Prints fluxes and reactions for each of the reactions that results in different fluxes compared to the reference case (fluxesB).

```
In [ ]: % fluxesA: flux vector for the test case.fluxesB: flux vector for the reference tes  
followChanged(modelETH,sol.x,solETH.x, 50, 0.5, 0.5);
```

These reactions have flux values that differ by more than 50 percent, absolute value s above 0.5, and a total difference above 0.5 (64 reactions)

r0004: alpha-D-glucose[c] + ATP[c] => ADP[c] + alpha-D-glucose 6-phosphate[c]
ATP:alpha-D-glucose 6-phosphotransferase
Flux: 1 Reference flux: 0 Difference: 1

r0006: alpha-D-glucose 6-phosphate[c] <=> beta-D-fructofuranose 6-phosphate[c]
alpha-D-glucose 6-phosphate ketol-isomerase
Flux: 0.91584 Reference flux: -0.10723 Difference: 1.0231

r0009: ATP[c] + beta-D-fructofuranose 6-phosphate[c] => ADP[c] + beta-D-fructofuranose 1,6-bisphosphate[c]
phosphofructokinase
Flux: 0.87408 Reference flux: 0 Difference: 0.87408

r0010: beta-D-fructofuranose 1,6-bisphosphate[c] <=> D-glyceraldehyde 3-phosphate[c]
+ glycerone phosphate[c]
fructose-bisphosphate aldolase
Flux: 0.87408 Reference flux: -0.16057 Difference: 1.0347

r0011: D-glyceraldehyde 3-phosphate[c] <=> glycerone phosphate[c]
D-glyceraldehyde-3-phosphate aldose-ketose-isomerase
Flux: -0.82751 Reference flux: 0.21997 Difference: -1.0475

r0012: D-glyceraldehyde 3-phosphate[c] + NAD(+)c] + phosphate[c] <=> 3-phospho-D-glyceroyl phosphate[c] + NADH[c]
glyceraldehyde-3-phosphate dehydrogenase
Flux: 1.6507 Reference flux: -0.44547 Difference: 2.0962

r0013: 3-phospho-D-glyceroyl phosphate[c] + ADP[c] <=> 3-phospho-D-glycerate[c] + ATP[c]
phosphoglycerate kinase
Flux: 1.6507 Reference flux: -0.44547 Difference: 2.0962

r0014: 3-phospho-D-glycerate[c] <=> 2-phospho-D-glycerate[c]
phosphoglycerate mutase
Flux: 1.608 Reference flux: -0.44565 Difference: 2.0536

r0015: 2-phospho-D-glycerate[c] <=> H2O[c] + phosphoenolpyruvate[c]
2-phospho-D-glycerate hydro-lyase (phosphoenolpyruvate-forming)
Flux: 1.608 Reference flux: -0.44565 Difference: 2.0536

r0016: ADP[c] + phosphoenolpyruvate[c] => ATP[c] + pyruvate[c]
pyruvate kinase
Flux: 1.567 Reference flux: 0 Difference: 1.567

r0019: ethanol[c] + NADP(+)c] <=> acetaldehyde[c] + NADPH[c]
ethanol:NADP+ oxidoreductase
Flux: 0 Reference flux: 1.6348 Difference: -1.6348

r0020: ethanol[c] + NAD(+)c] <=> acetaldehyde[c] + NADH[c]
ethanol:NAD+ oxidoreductase
Flux: 0 Reference flux: 1.3652 Difference: -1.3652

r0022: lipoamide-[enzyme][m] + pyruvate[m] => CO2[m] + S-acetyldihydrolipoamide-[enzyme][m]
pyruvate:[dihydrolipoyllysine-residue acetyltransferase]-lipoyllysine 2-oxidoreductase (decarboxylating, acceptor-acetylating)
Flux: 1.2352 Reference flux: 0 Difference: 1.2352

r0023: coenzyme A[m] + S-acetyldihydrolipoamide-[enzyme][m] => acetyl-CoA[m] + dihydrolipoamide-[enzyme][m]
acetyl-CoA:enzyme N6-(dihydrolipoyl)lysine S-acetyltransferase
Flux: 1.2352 Reference flux: 0 Difference: 1.2352

r0026: acetate[m] + ATP[m] + coenzyme A[m] => acetyl-CoA[m] + AMP[m] + diphosphate [m]
acetate:CoA ligase (AMP-forming)
Flux: 0 Reference flux: 1.8845 Difference: -1.8845

r0053: acetaldehyde[m] + H2O[m] + NAD(+)m] => acetate[m] + NADH[m]
acetaldehyde:NAD+ oxidoreductase

Flux: 0 Reference flux: 1.8845 Difference: -1.8845

r0072: 2-oxobutanoate[m] + lipoamide-[enzyme][m] => CO2[m] + S-propionylidihydrolipoamide-[enzyme][m]

2-oxobutanoate:[dihydrolipoyllysine-residue propionyltransferase]-lipoyllysine 2-oxidoreductase (decarboxylating, acceptor-propionylating)

Flux: 0 Reference flux: 0.88113 Difference: -0.88113

r0073: coenzyme A[m] + S-propionylidihydrolipoamide-[enzyme][m] => dihydrolipoamide-[enzyme][m] + propionyl-CoA[m]

propionyl-CoA:enzyme N6-(dihydrolipoyl)lysine S-propionyltransferase

Flux: 0 Reference flux: 0.88113 Difference: -0.88113

r0074: H2O[m] + oxaloacetate[m] + propionyl-CoA[m] => 2-methylcitrate[m] + coenzyme A[m]

propanoyl-CoA:oxaloacetate C-propanoyltransferase (thioester-hydrolysing, 1-carboxyethyl-forming)

Flux: 0 Reference flux: 0.88098 Difference: -0.88098

r0075: (Z)-but-2-ene-1,2,3-tricarboxylate[m] + H2O[m] <=> 2-methylcitrate[m]

2-hydroxybutane-1,2,3-tricarboxylate hydro-lyase

Flux: 0 Reference flux: -0.88098 Difference: 0.88098

r0076: methylisocitrate[m] <=> pyruvate[m] + succinate[m]

(2S,3R)-3-hydroxybutane-1,2,3-tricarboxylate pyruvate-lyase (succinate-forming)

Flux: 0 Reference flux: 0.88098 Difference: -0.88098

r0079: methylisocitrate[m] <=> (Z)-but-2-ene-1,2,3-tricarboxylate[m] + H2O[m]

(2S,3R)-3-Hydroxybutane-1,2,3-tricarboxylate hydro-lyase

Flux: 0 Reference flux: -0.88098 Difference: 0.88098

r0084: fumarate[m] + ubiquinol[m] <=> succinate[m] + ubiquinone[m]

succinate:ubiquinone oxidoreductase

Flux: -0.91885 Reference flux: -2.5565 Difference: 1.6377

r0085: acetyl-CoA[m] + H2O[m] + oxaloacetate[m] <=> citrate[m] + coenzyme A[m]

acetyl-CoA:oxaloacetate C-acetyltransferase (thioester-hydrolysing)

Flux: 1.1838 Reference flux: 1.8189 Difference: -0.6351

r0086: cis-aconitate[m] + H2O[m] <=> citrate[m]

citrate hydro-lyase (cis-aconitate-forming)

Flux: -1.0313 Reference flux: -1.8189 Difference: 0.78767

r0087: cis-aconitate[m] + H2O[m] <=> isocitrate[m]

isocitrate hydro-lyase (cis-aconitate-forming)

Flux: 1.0313 Reference flux: 1.8189 Difference: -0.78767

r0090: isocitrate[c] + NADP(+)[c] => 2-oxoglutarate[c] + CO2[c] + NADPH[c]

isocitrate:NADP+ oxidoreductase (decarboxylating)

Flux: 0.86372 Reference flux: 0.23939 Difference: 0.62433

r0097: fumarate[m] + H2O[m] <=> (S)-malate[m]

(S)-malate hydro-lyase (fumarate-forming)

Flux: 0.96827 Reference flux: 2.6196 Difference: -1.6513

r0098: (S)-malate[m] + NAD(+)[m] <=> NADH[m] + oxaloacetate[m]

(S)-malate:NAD+ oxidoreductase

Flux: 0.96827 Reference flux: 1.9921 Difference: -1.0239

r0099: (S)-malate[c] + NAD(+)[c] <=> NADH[c] + oxaloacetate[c]

(S)-malate:NAD+ oxidoreductase

Flux: 0 Reference flux: 0.62742 Difference: -0.62742

r0103: isocitrate[p] => glyoxylate[p] + succinate[p]

isocitrate glyoxylate-lyase (succinate-forming)

Flux: 0.055182 Reference flux: 1.0602 Difference: -1.005

r0111: ATP[m] + CO2[m] + H2O[m] + pyruvate[m] => ADP[m] + oxaloacetate[m] + phosphate[m]

pyruvate:carbon-dioxide ligase (ADP-forming)

Flux: 0.16454 Reference flux: 0.70776 Difference: -0.54323

r0115: diphosphate[m] + H2O[m] => 2 phosphate[m]
diphosphate phosphohydrolase
Flux: 0 Reference flux: 1.8845 Difference: -1.8845

r0118: 4 ferrocytochrome c[m] + 8 H(+) (energy metabolism)[m] + O2[m] => 8 H(+) (energy metabolism)[c] + 4 ferricytochrome c[m] + 2 H2O[m]
ferrocytochrome-c:oxygen oxidoreductase
Flux: 2.9049 Reference flux: 5.0523 Difference: -2.1474

r0119: 4 H(+) (energy metabolism)[m] + NADH[m] + ubiquinone[m] => 4 H(+) (energy metabolism)[c] + NAD(+)[m] + ubiquinol[m]
NADH:ubiquinone oxidoreductase
Flux: 3.0878 Reference flux: 5.8294 Difference: -2.7417

r0127: 2 ferricytochrome c[m] + 4 H(+) (energy metabolism)[m] + ubiquinol[m] => 4 H(+) (energy metabolism)[c] + 2 ferrocytochrome c[m] + ubiquinone[m]
ubiquinol:ferricytochrome-c oxidoreductase
Flux: 5.8098 Reference flux: 10.1046 Difference: -4.2947

r0128: 3.88 H(+) (energy metabolism)[c] + ADP[m] + phosphate[m] => ATP[m] + 3.88 H(+) (energy metabolism)[m] + H2O[m]
H+-transporting two-sector ATPase
Flux: 13.4161 Reference flux: 23.5764 Difference: -10.1603

r0377: 2 ADP[m] <=> AMP[m] + ATP[m]
adenylate kinase
Flux: 0 Reference flux: -1.8845 Difference: 1.8845

r0542: 2-oxoglutarate[c] + L-alanine[c] <=> L-glutamate[c] + pyruvate[c]
L-alanine:2-oxoglutarate aminotransferase
Flux: -0.081019 Reference flux: -1.0932 Difference: 1.0122

r0553: 2-oxoglutarate[c] + NADPH[c] + NH3[c] => H2O[c] + L-glutamate[c] + NADP(+)[c]
L-glutamate:NADP+ oxidoreductase (deaminating)
Flux: 0.4735 Reference flux: 1.5394 Difference: -1.0659

r0558: glyoxylate[p] + L-alanine[p] <=> glycine[p] + pyruvate[p]
L-alanine:glyoxylate aminotransferase
Flux: 0.055199 Reference flux: 1.0602 Difference: -1.005

r0625: L-threonine[c] <=> acetaldehyde[c] + glycine[c]
L-threonine acetaldehyde-lyase (glycine-forming)
Flux: -0.031173 Reference flux: -0.92089 Difference: 0.88972

r0633: L-threonine[m] => 2-oxobutanoate[m] + NH3[m]
L-threonine ammonia-lyase (2-oxobutanoate-forming)
Flux: 0.013536 Reference flux: 0.8984 Difference: -0.88486

r1170: 2-oxoglutarate[c] <=> 2-oxoglutarate[m]
2-oxoglutarate mitochondrial permease
Flux: 0.67604 Reference flux: 0 Difference: 0.67604

r1213: L-threonine[m] <=> L-threonine[c]
L-threonine mitochondrial permease
Flux: -0.013536 Reference flux: -0.8984 Difference: 0.88486

r1217: (S)-malate[c] + succinate[m] <=> succinate[c] + (S)-malate[m]
malate/succinate mitochondrial shuttle
Flux: 0 Reference flux: -0.61335 Difference: 0.61335

r1235: pyruvate[c] <=> pyruvate[m]
pyruvate mitochondrial permease
Flux: 1.5123 Reference flux: -0.030007 Difference: 1.5423

r1243: acetaldehyde[c] <=> acetaldehyde[m]
acetaldehyde mitochondrial membrane diffusion
Flux: 0 Reference flux: 1.8845 Difference: -1.8845

r1250: NH3[c] <=> NH3[m]
NH3 mitochondrial membrane diffusion
Flux: -0.013536 Reference flux: -0.95275 Difference: 0.93922

r1251: O2[c] <=> O2[m]

```

O2 mitochondrial membrane diffusion
Flux: 2.905 Reference flux: 5.0523 Difference: -2.1474

r1263: glycine[c] <=> glycine[p]
    glycine peroxisomal permease
    Flux: -0.055199 Reference flux: -1.0602 Difference: 1.005

r1270: isocitrate[c] + (S)-malate[p] <=> (S)-malate[c] + isocitrate[p]
    isocitrate/malate peroxisomal permease
    Flux: 0.055182 Reference flux: 1.0602 Difference: -1.005

r1273: L-alanine[c] <=> L-alanine[p]
    L-alanine peroxisomal permease
    Flux: 0.055199 Reference flux: 1.0602 Difference: -1.005

r1276: (S)-malate[c] <=> (S)-malate[p]
    malate peroxisomal permease
    Flux: 0.055182 Reference flux: 1.0602 Difference: -1.005

r1284: pyruvate[c] <=> pyruvate[p]
    pyruvate peroxisomal permease
    Flux: -0.055182 Reference flux: -1.0602 Difference: 1.005

r1286: succinate[c] <=> succinate[p]
    succinate peroxisomal permease
    Flux: -0.055182 Reference flux: -1.0602 Difference: 1.005

r1316: alpha-D-glucose[e] <=> alpha-D-glucose[c]
    alpha-D-glucose permease
    Flux: 1 Reference flux: 0 Difference: 1

r1426: ethanol[c] <=> ethanol[e]
    ethanol plasma membrane diffusion
    Flux: 0 Reference flux: -3 Difference: 3

r1428: H2O[c] <=> H2O[e]
    H2O plasma membrane diffusion
    Flux: 5.586 Reference flux: 8.4719 Difference: -2.8859

r1441: O2[e] <=> O2[c]
    O2 plasma membrane diffusion
    Flux: 2.937 Reference flux: 5.0932 Difference: -2.1562

h2oOUT: H2O[e] =>
    production of H2O
    Flux: 5.586 Reference flux: 8.4719 Difference: -2.8859

glcIN: => alpha-D-glucose[e]
    uptake of alpha-D-glucose
    Flux: 1 Reference flux: 0 Difference: 1

o2IN: => O2[e]
    uptake of O2
    Flux: 2.937 Reference flux: 5.0932 Difference: -2.1562

etohIN: => ethanol[e]
    uptake of ethanol
    Flux: 0 Reference flux: 3 Difference: -3

```

```
In [ ]: % You can filter using a metabolite list:
followChanged(modelETH,sol.x,solETH.x, 30, 0.4, 0.4,{'ATP'});
```

These reactions have flux values that differ by more than 30 percent, absolute value s above 0.4, and a total difference above 0.4 (10 reactions)

Only prints reactions involving one or more of the following metabolites:
ATP

r0004: alpha-D-glucose[c] + ATP[c] => ADP[c] + alpha-D-glucose 6-phosphate[c]
ATP:alpha-D-glucose 6-phosphotransferase
Flux: 1 Reference flux: 0 Difference: 1

r0009: ATP[c] + beta-D-fructofuranose 6-phosphate[c] => ADP[c] + beta-D-fructofuranose 1,6-bisphosphate[c]
phosphofructokinase
Flux: 0.87408 Reference flux: 0 Difference: 0.87408

r0013: 3-phospho-D-glyceroyl phosphate[c] + ADP[c] <=> 3-phospho-D-glycerate[c] + ATP[c]
phosphoglycerate kinase
Flux: 1.6507 Reference flux: -0.44547 Difference: 2.0962

r0016: ADP[c] + phosphoenolpyruvate[c] => ATP[c] + pyruvate[c]
pyruvate kinase
Flux: 1.567 Reference flux: 0 Difference: 1.567

r0018: ATP[c] + oxaloacetate[c] => ADP[c] + CO2[c] + phosphoenolpyruvate[c]
phosphoenolpyruvate carboxykinase (ATP)
Flux: 0 Reference flux: 0.4979 Difference: -0.4979

r0026: acetate[m] + ATP[m] + coenzyme A[m] => acetyl-CoA[m] + AMP[m] + diphosphate [m]
acetate:CoA ligase (AMP-forming)
Flux: 0 Reference flux: 1.8845 Difference: -1.8845

r0111: ATP[m] + CO2[m] + H2O[m] + pyruvate[m] => ADP[m] + oxaloacetate[m] + phosphate[m]
pyruvate:carbon-dioxide ligase (ADP-forming)
Flux: 0.16454 Reference flux: 0.70776 Difference: -0.54323

r0128: 3.88 H(+) (energy metabolism)[c] + ADP[m] + phosphate[m] => ATP[m] + 3.88 H(+) (energy metabolism)[m] + H2O[m]
H+-transporting two-sector ATPase
Flux: 13.4161 Reference flux: 23.5764 Difference: -10.1603

r0377: 2 ADP[m] <=> AMP[m] + ATP[m]
adenylate kinase
Flux: 0 Reference flux: -1.8845 Difference: 1.8845

r1178: ADP[c] + H(+) (energy metabolism)[c] + phosphate[c] + ATP[m] + H2O[m] => ATP[c] + H2O[c] + ADP[m] + H(+) (energy metabolism)[m] + phosphate[m]
ADP/ATP/phosphate mitochondrial shuttle
Flux: 13.9437 Reference flux: 19.4962 Difference: -5.5525

To understand better the underlying flux distributions the fluxes can be visualized in a map:

- [load](#)

`load(filename,variables)`

Loads the specified variables from the MAT-file filename.

- [drawMap](#)

function

`notMapped=drawMap(title,pathway,modelA,conditionA,conditionB,modelB,filename,`
Imports a previously drawn map of the metabolic network and plots the fluxes on that map.
If the pathway contains expression data the log-fold changes are plotted as well.

```
In [ ]: load('./tutorial_data/pcPathway.mat', "pathway");
drawMap('Glucose vs ethanol',pathway,model,sol.x,solETH.x,modelETH,'./output/tutori
```

File saved as ./output/tutorial1_GLCvsETH.pdf
./output/tutorial1_GLCvsETH.pdf