

# Entropic flux balance analysis: trade off between entropy maximisation and additional information

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**Reviewer(s): Ronan Fleming, University of Galway**

In the context of FBA, an objective function is a mathematical representation of a cellular process that the model attempts to optimize. In entropic flux balance analysis [1], eFBA, the objective is to to maximize the Shannon entropy of the flux distribution, subject to constraints ensuring the feasibility and thermodynamic consistency of the fluxes. Shannon entropy measures the degree of disorder or randomness in a system. In entropic Flux Balance Analysis, maximizing the unnormalised entropy of the (separate forward and reverse) flux distribution. This corresponds to the least biased distribution, given the constraints [1]. This tutorial builds on tutorial\_entropicFluxBalanceAnalysis and examines the ways in which one can (a) trade off between maximisation of a linear combination of net fluxes with maximisation of unidirectional flux entropy, (b) how to set this trade off so that growth rate matches experimentally measured growth rate, and (c) how omics data, e.g., gene expression data, can be used to bias the magnitude of internal net flux.

## Toy model

```
reactionFormulas = {'4 A -> 4 B',...
                    '2 A -> 2 B',...
                    'A -> B',...
                    'A <=> ',...
                    'B <=> '};
reactionNames = {'R1', 'R2', 'R3', 'R4', 'R5'};
lowerBounds = [ -10, -10, -10, -10, 10];
upperBounds = [ 10, 10, 10, -10, 10];
model = createModel(reactionNames, reactionNames, reactionFormulas,...
                    'lowerBoundList', lowerBounds,
                    'upperBoundList', upperBounds);
```

Adding the following Metabolites to the model:

A[c]

B[c]

addMultipleReactions: Adding the following reactions to the model:

R1 4 A[c] <=> 4 B[c]

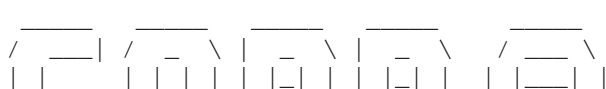
R2 2 A[c] <=> 2 B[c]

R3 A[c] <=> B[c]

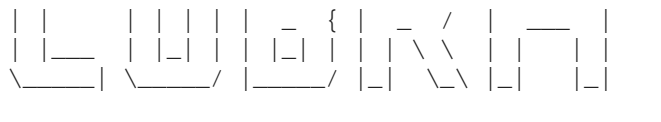
R4 A[c] <=>

R5 B[c] ->

```
initCobraToolbox;
```



COntstraint-Based Reconstruction and Analysis  
The COBRA Toolbox - 2024



Documentation:  
<http://opencobra.github.io/cobratoolbox>

```
> Checking if git is installed ... Done (version: 2.25.1).
> Checking if the repository is tracked using git ... Done.
> Checking if curl is installed ... Done.
> Checking if remote can be reached ... Done.
> Initializing and updating submodules (this may take a while)... Done.
> Adding all the files of The COBRA Toolbox ... Done.
> Define CB map output... set to svg.
> TranslateSBML is installed and working properly.
> Configuring solver environment variables ...
- [ *--- ] ILOG_CPLEX_PATH: /opt/ibm/ILOG/CPLEX_Studio1210/cplex/matlab/x86-64_linux
- [ *--- ] GUROBI_PATH: /opt/gurobi1003/linux64/matlab
- [ *--- ] TOMLAB_PATH: --> set this path manually after installing the solver ( see instructions )
- [ *--- ] MOSEK_PATH: /opt/mosek/10.1/
Done.
> Checking available solvers and solver interfaces ... 0
```

0

Check osense\*c - A'\*lam - w = 0 (stationarity):

0  
0

```
> [gurobi] Primal optimality condition in solveCobraLP satisfied.
> [gurobi] Dual optimality condition in solveCobraLP satisfied.
Version identifier: 12.10.0.0 | 2019-11-26 | 843d4de
CPXPARAM_Output_WriteLevel          3
CPXPARAM_Output_CloneLog             -1
Found incumbent of value 0.000000 after 0.00 sec. (0.00 ticks)
```

Root node processing (before b&c):

```
Real time          = 0.00 sec. (0.00 ticks)
Parallel b&c, 12 threads:
Real time          = 0.00 sec. (0.00 ticks)
Sync time (average) = 0.00 sec.
Wait time (average) = 0.00 sec.
```

```
-----
Total (root+branch&cut) = 0.00 sec. (0.00 ticks)
Could not find installation of tomlab_cplex, so it cannot be tested
GLPK Simplex Optimizer, v4.42
1 row, 2 columns, 1 non-zero
Preprocessing...
~ 0: obj = 0.000000000e+00 infeas = 0.000e+00
OPTIMAL SOLUTION FOUND BY LP PREPROCESSOR
```

```
> [glpk] Primal optimality condition in solveCobraLP satisfied.
> [mosek] Primal optimality condition in solveCobraLP satisfied.
> [mosek] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of matlab, so it cannot be tested
```

```
-----
pdco.m                      Version pdco5 of 15 Jun 2018
Primal-dual barrier method to minimize a convex function
subject to linear constraints Ax + r = b,  bl <= x <= bu
```

Michael Saunders            SOL and ICME, Stanford University  
Contributors:            Byunggyoo Kim (SOL), Chris Maes (ICME)  
                 Santiago Akle (ICME), Matt Zahr (ICME)  
                 Aekaansh Verma (ME)

-----  
The objective is linear  
The matrix A is an explicit sparse matrix

```
m          =          1      n          =          2      nnz(A) =          1
max |b|    =          0      max |x0| = 1.0e+00      xsize = 1.0e+00
max |y0|    =          1      max |z0| = 1.0e+00      zsize = 1.0e+00

x0min      =          1      featol    = 1.0e-06      dlmax   = 1.0e-04
z0min      =          1      opttol    = 1.0e-06      d2max   = 5.0e-04
mu0        = 1.0e-01      steptol   = 0.99      bigcenter= 1000
```

LSMR/MINRES:

```
atoll      = 1.0e-10      atol2    = 1.0e-15      btol     = 0.0e+00
conlim     = 1.0e+12      itnlim   = 10      show     = 0
```

Method = 2 (1 or 11=chol 2 or 12=QR 3 or 13=LSMR 4 or 14=MINRES 21=SQD(LU) 22=SQD(MA57))  
Eliminating dy before dx

Bounds:

```
[0,inf] [-inf,0] Finite bl Finite bu Two bnds Fixed Free
      0      0      0      0      0      2      0
[0, bu] [bl, 0] excluding fixed variables
      0      0
```

Itn	mu	stepx	stepz	Pinf	Dinf	Cinf	Objective	nf	center	QR
0				-6.6	-99.0	-Inf	1.2500000e-07		1.0	
1	-1.0	1.000	1.000	-99.0	-99.0	-Inf	0.0000000e+00	1	1.0	1
2	-3.0	1.000	1.000	-99.0	-99.0	-Inf	0.0000000e+00	1	1.0	
3	-5.0	1.000	1.000	-99.0	-99.0	-Inf	0.0000000e+00	1	1.0	
4	-7.0	1.000	1.000	-99.0	-99.0	-Inf	0.0000000e+00	1	1.0	

Converged

```
max |x| = 0.000      max |y| = 0.000      max |z| = 0.000 scaled
max |x| = 0.000      max |y| = 0.000      max |z| = 0.000 unscaled
max |x| and max |z| exclude fixed variables
PDitns = 4      QRitns = 0      cputime = 0.0
```

```
Distribution of vector      x      z
[      1,      10 )      0      2
[     0.1,      1 )      0      0
[     0.01,     0.1 )      0      0
[     0.001,     0.01 )      0      0
[     0.0001,     0.001 )      0      0
[     1e-05,     0.0001 )      0      0
[     1e-06,     1e-05 )      0      0
[     1e-07,     1e-06 )      0      0
[     1e-08,     1e-07 )      0      0
[      0,     1e-08 )      2      0
```

Elapsed time is 0.021359 seconds.

```
> [pdco] Primal optimality condition in solveCobraLP satisfied.
> [pdco] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of quadMinos, so it cannot be tested
Could not find installation of dqgMinos, so it cannot be tested
Could not find installation of cplex_direct, so it cannot be tested
```

```
> [cplexlp] Primal optimality condition in solveCobraLP satisfied.
> [cplexlp] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of tomlab_snopt, so it cannot be tested
Done.
```

```
> Setting default solvers ...Could not find installation of matlab, so it cannot be tested
```

Done.

> Saving the MATLAB path ... Done.  
 - The MATLAB path was saved as ~/pathdef.m.

> Summary of available solvers and solver interfaces

	Support	LP	MILP	QP	MIQP	NLP	EP	
gurobi	active		1	1	1	1	-	-
ibm_cplex	active		1	1	1	1	-	-
tomlab_cplex	active		0	0	0	0	-	-
glpk	active		1	1	-	-	-	-
mosek	active		1	-	1	-	-	1
matlab	active		0	-	-	-	0	-
pdco	active		1	-	1	-	-	1
quadMinos	active		0	-	-	-	-	-
dqqMinos	active		0	-	0	-	-	-
cplex_direct	active		0	0	0	-	-	-
cplexlp	active		1	-	-	-	-	-
qpnp	passive		-	-	1	-	-	-
tomlab_snopt	passive		-	-	-	-	0	-
lp_solve	legacy		1	-	-	-	-	-
Total	-		7	3	5	2	0	2

+ Legend: - = not applicable, 0 = solver not compatible or not installed, 1 = solver installed.

> You can solve LP problems using: 'gurobi' - 'ibm\_cplex' - 'glpk' - 'mosek' - 'pdco' - 'cplexlp'  
 > You can solve MILP problems using: 'gurobi' - 'ibm\_cplex' - 'glpk'  
 > You can solve QP problems using: 'gurobi' - 'ibm\_cplex' - 'mosek' - 'pdco'  
 > You can solve MIQP problems using: 'gurobi' - 'ibm\_cplex'  
 > You can solve NLP problems using:  
 > You can solve EP problems using: 'mosek' - 'pdco'

> Checking for available updates ...

> You cannot update your fork using updateCobraToolbox() because this is a development branch.  
 > The current branch is: master  
 > The last commit to the current branch is: 097dc1  
 > You can use MATLAB.devTools (<https://github.com/opencobra/MATLAB.devTools>) to update your fork.  
 removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/componentContribution/new  
 removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/groupContribution/new  
 removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/inchi/new  
 removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/molFiles/new  
 removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/protons/new  
 removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/trainingModel/new

```
FBAsolution = optimizeCbModel(model, 'max');
```

The flux distribution is shown in figure 1:



Figure1: Flux distribution calculated using FBA in model1.

As you can see, reactions 'R1' and 'R2' or 'R1' and 'R3' have created a cycle within the network. A cycle means the system is not following the laws of thermodynamics and, therefore, is not occurring in reality. Let's look at eFBA results:

```
param.solver = 'mosek';
param = mosekParamSetEFBA(param);
[solution,~] = entropicFluxBalanceAnalysis(model,param);
```

And illustration using escher is shown in figure2:

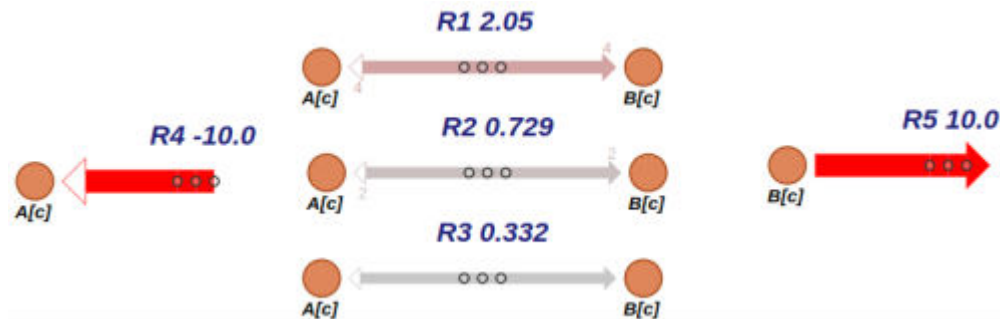
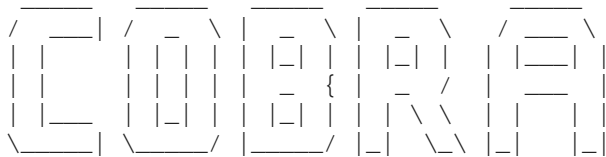


Figure2: Flux distribution calculated using eFBA in model1.

```
plotyy_eFBA(model, 'R1', 20, 20, 1);
```



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```
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> Checking if curl is installed ... Done.
> Checking if remote can be reached ... Done.
> Initializing and updating submodules (this may take a while)... Done.
> Adding all the files of The COBRA Toolbox ... Done.
> Define CB map output... set to svg.
```

```

> TranslateSBML is installed and working properly.
> Configuring solver environment variables ...
- [ *---] ILOG_CPLEX_PATH: /opt/ibm/ILOG/CPLEX_Studio1210/cplex/matlab/x86-64_linux
- [ *---] GUROBI_PATH: /opt/gurobi1003/linux64/matlab
- [ *---] TOMLAB_PATH: --> set this path manually after installing the solver ( see instructions )
- [ *---] MOSEK_PATH: /opt/mosek/10.1/
Done.
> Checking available solvers and solver interfaces ...      0

```

0

```
Check osense*c - A'*lam - w = 0 (stationarity):
```

0

0

```

> [gurobi] Primal optimality condition in solveCobraLP satisfied.
> [gurobi] Dual optimality condition in solveCobraLP satisfied.
Version identifier: 12.10.0.0 | 2019-11-26 | 843d4de
CPXPARAM_Output_WriteLevel          3
CPXPARAM_Output_CloneLog            -1
Found incumbent of value 0.000000 after 0.00 sec. (0.00 ticks)

```

```
Root node processing (before b&c):
```

```

Real time          =      0.00 sec. (0.00 ticks)
Parallel b&c, 12 threads:
Real time          =      0.00 sec. (0.00 ticks)
Sync time (average) =      0.00 sec.
Wait time (average) =      0.00 sec.

```

```

-----
Total (root+branch&cut) =      0.00 sec. (0.00 ticks)
Could not find installation of tomlab_cplex, so it cannot be tested
GLPK Simplex Optimizer, v4.42
1 row, 2 columns, 1 non-zero
Preprocessing...
~      0: obj =      0.000000000e+00   infeas =      0.000e+00
OPTIMAL SOLUTION FOUND BY LP PREPROCESSOR

```

```

> [glpk] Primal optimality condition in solveCobraLP satisfied.
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Could not find installation of matlab, so it cannot be tested

```

```

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pdco.m                      Version pdco5 of 15 Jun 2018
Primal-dual barrier method to minimize a convex function
subject to linear constraints Ax + r = b,  bl <= x <= bu

```

```

Michael Saunders           SOL and ICME, Stanford University
Contributors:              Byunggyoo Kim (SOL), Chris Maes (ICME)
                           Santiago Akle (ICME), Matt Zahr (ICME)
                           Aekaansh Verma (ME)
-----

```

```

The objective is linear
The matrix A is an explicit sparse matrix

```

```

m          =          1          n          =          2          nnz(A) =          1
max |b|    =          0          max |x0|    =      1.0e+00          xsize  =      1.0e+00
max |y0|    =          1          max |z0|    =      1.0e+00          zsize  =      1.0e+00

x0min      =          1          featol     =      1.0e-06          dlmax   =      1.0e-04
z0min      =          1          opttol     =      1.0e-06          d2max   =      5.0e-04
mu0        =      1.0e-01          steptol   =          0.99          bigcenter=      1000

```

```

LSMR/MINRES:
atoll   = 1.0e-10      atol2   = 1.0e-15      btol   = 0.0e+00
conlim  = 1.0e+12      itnlim  = 10          show  = 0

Method   = 2          (1 or 11=chol  2 or 12=QR  3 or 13=LSMR  4 or 14=MINRES 21=SQD(LU) 22=SQD(MA57))
Eliminating dy before dx

```

```

Bounds:
[0,inf] [-inf,0] Finite bl Finite bu Two bnds Fixed Free
      0      0      0      0      0      2      0
[0, bu] [bl, 0] excluding fixed variables
      0      0

```

```

Itn  mu stepx stepz Pinf Dinf Cinf Objective nf center QR
  0      -6.6 -99.0 -Inf 1.2500000e-07 1.0
  1 -1.0 1.000 1.000 -99.0 -99.0 -Inf 0.0000000e+00 1 1.0 1
  2 -3.0 1.000 1.000 -99.0 -99.0 -Inf 0.0000000e+00 1 1.0
  3 -5.0 1.000 1.000 -99.0 -99.0 -Inf 0.0000000e+00 1 1.0
  4 -7.0 1.000 1.000 -99.0 -99.0 -Inf 0.0000000e+00 1 1.0
Converged

```

```

max |x| = 0.000 max |y| = 0.000 max |z| = 0.000 scaled
max |x| = 0.000 max |y| = 0.000 max |z| = 0.000 unscaled
max |x| and max |z| exclude fixed variables
PDitns = 4 QRitns = 0 cputime = 0.0

```

```

Distribution of vector x z
[ 1, 10 ) 0 2
[ 0.1, 1 ) 0 0
[ 0.01, 0.1 ) 0 0
[ 0.001, 0.01 ) 0 0
[ 0.0001, 0.001 ) 0 0
[ 1e-05, 0.0001 ) 0 0
[ 1e-06, 1e-05 ) 0 0
[ 1e-07, 1e-06 ) 0 0
[ 1e-08, 1e-07 ) 0 0
[ 0, 1e-08 ) 2 0

```

Elapsed time is 0.009168 seconds.

```

> [pdco] Primal optimality condition in solveCobraLP satisfied.
> [pdco] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of quadMinos, so it cannot be tested
Could not find installation of dqgMinos, so it cannot be tested
Could not find installation of cplex_direct, so it cannot be tested

```

```

> [cplexlp] Primal optimality condition in solveCobraLP satisfied.
> [cplexlp] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of tomlab_snopt, so it cannot be tested
Done.

```

```

> Setting default solvers ...Could not find installation of matlab, so it cannot be tested
Done.

```

```

> Saving the MATLAB path ... Done.
- The MATLAB path was saved as ~/pathdef.m.

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> Summary of available solvers and solver interfaces

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gurobi	active			1	1	1	1	-	-
ibm_cplex	active			1	1	1	1	-	-
tomlab_cplex	active			0	0	0	0	-	-
glpk	active			1	1	-	-	-	-

mosek	active	1	-	1	-	-	1
matlab	active	0	-	-	-	0	-
pdco	active	1	-	1	-	-	1
quadMinos	active	0	-	-	-	-	-
dqqMinos	active	0	-	0	-	-	-
cplex_direct	active	0	0	0	-	-	-
cplexlp	active	1	-	-	-	-	-
qpng	passive	-	-	1	-	-	-
tomlab_snopt	passive	-	-	-	-	0	-
lp_solve	legacy	1	-	-	-	-	-
-----							
Total	-	7	3	5	2	0	2

+ Legend: - = not applicable, 0 = solver not compatible or not installed, 1 = solver installed.

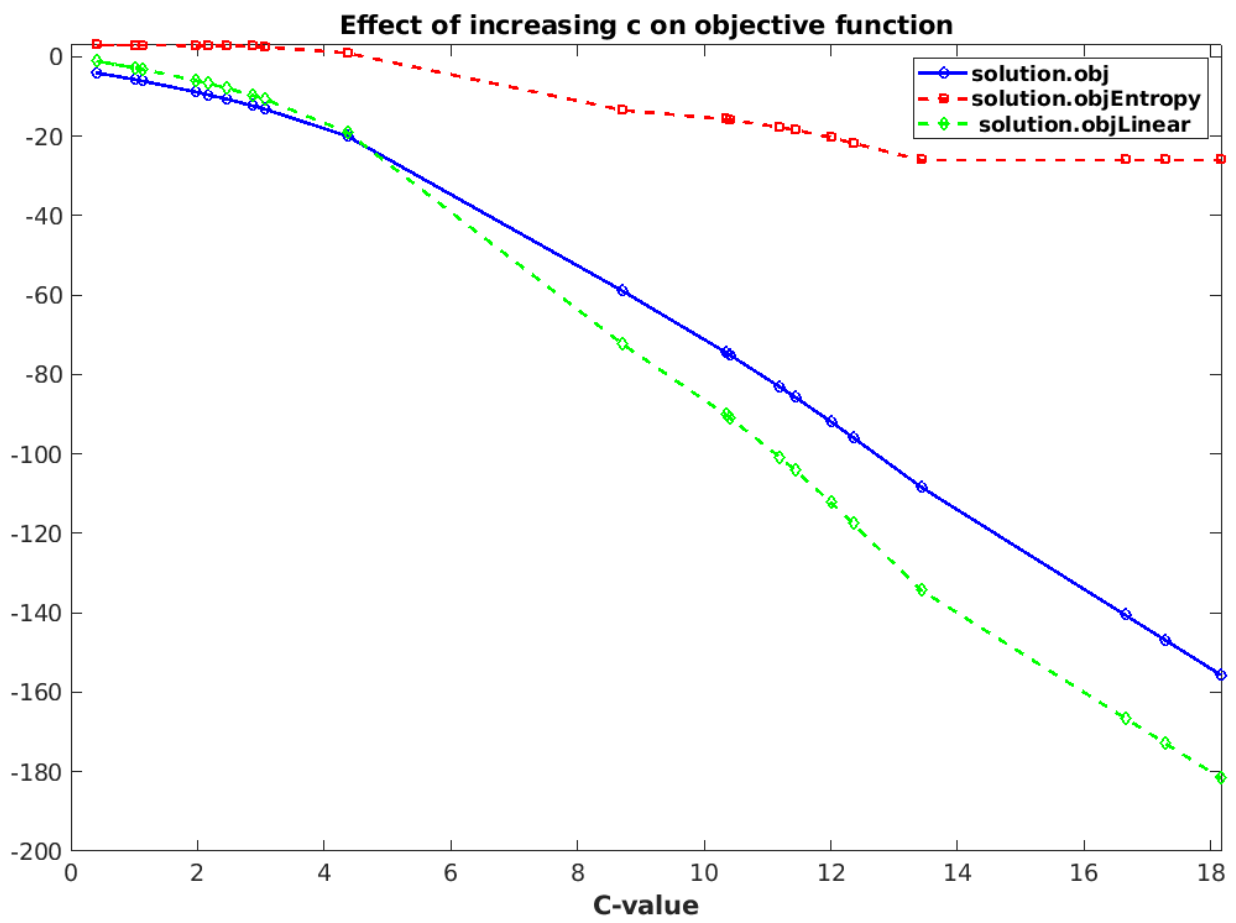
```

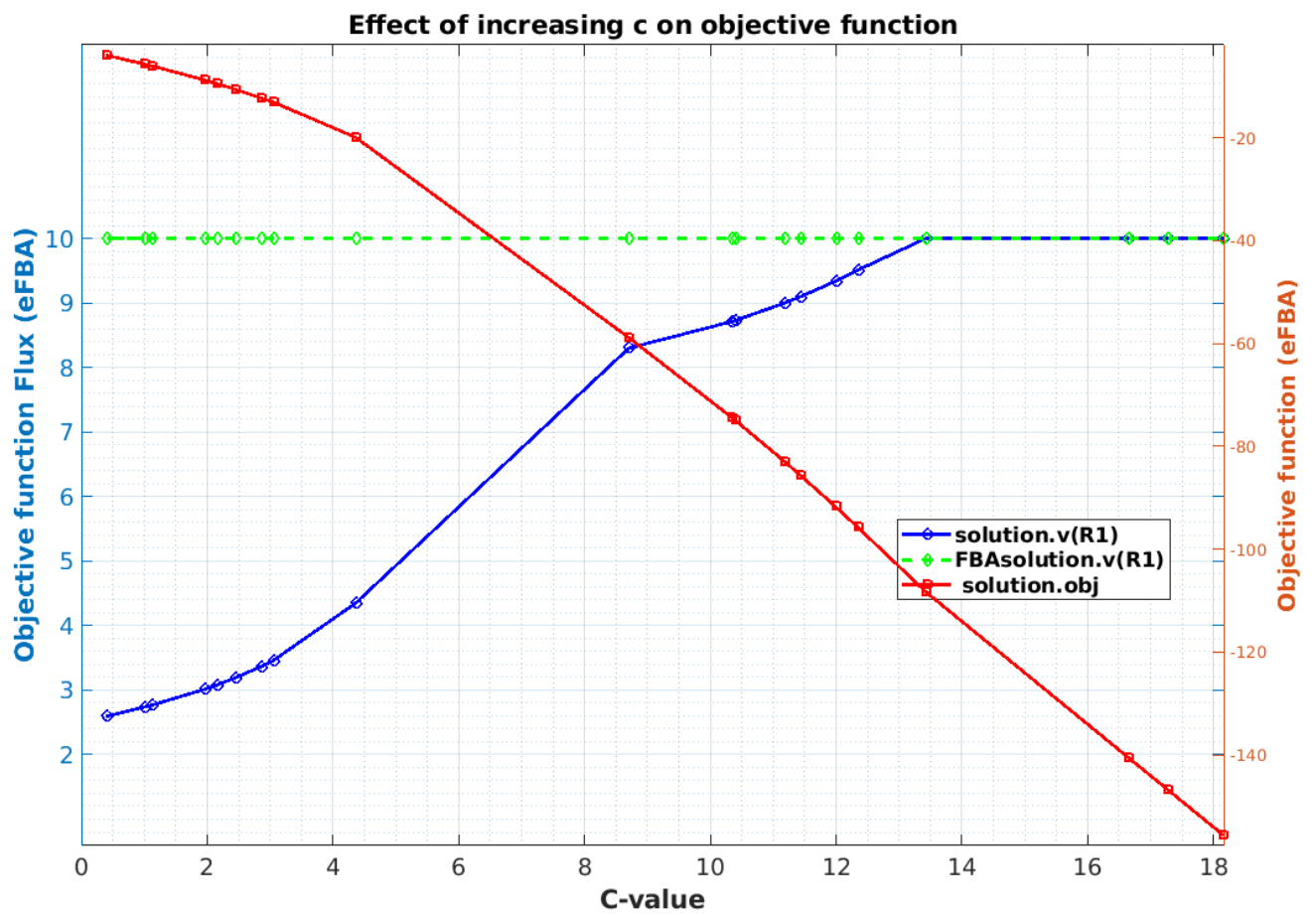
> You can solve LP problems using: 'gurobi' - 'ibm_cplex' - 'glpk' - 'mosek' - 'pdco' - 'cplexlp'
> You can solve MILP problems using: 'gurobi' - 'ibm_cplex' - 'glpk'
> You can solve QP problems using: 'gurobi' - 'ibm_cplex' - 'mosek' - 'pdco'
> You can solve MIQP problems using: 'gurobi' - 'ibm_cplex'
> You can solve NLP problems using:
> You can solve EP problems using: 'mosek' - 'pdco'

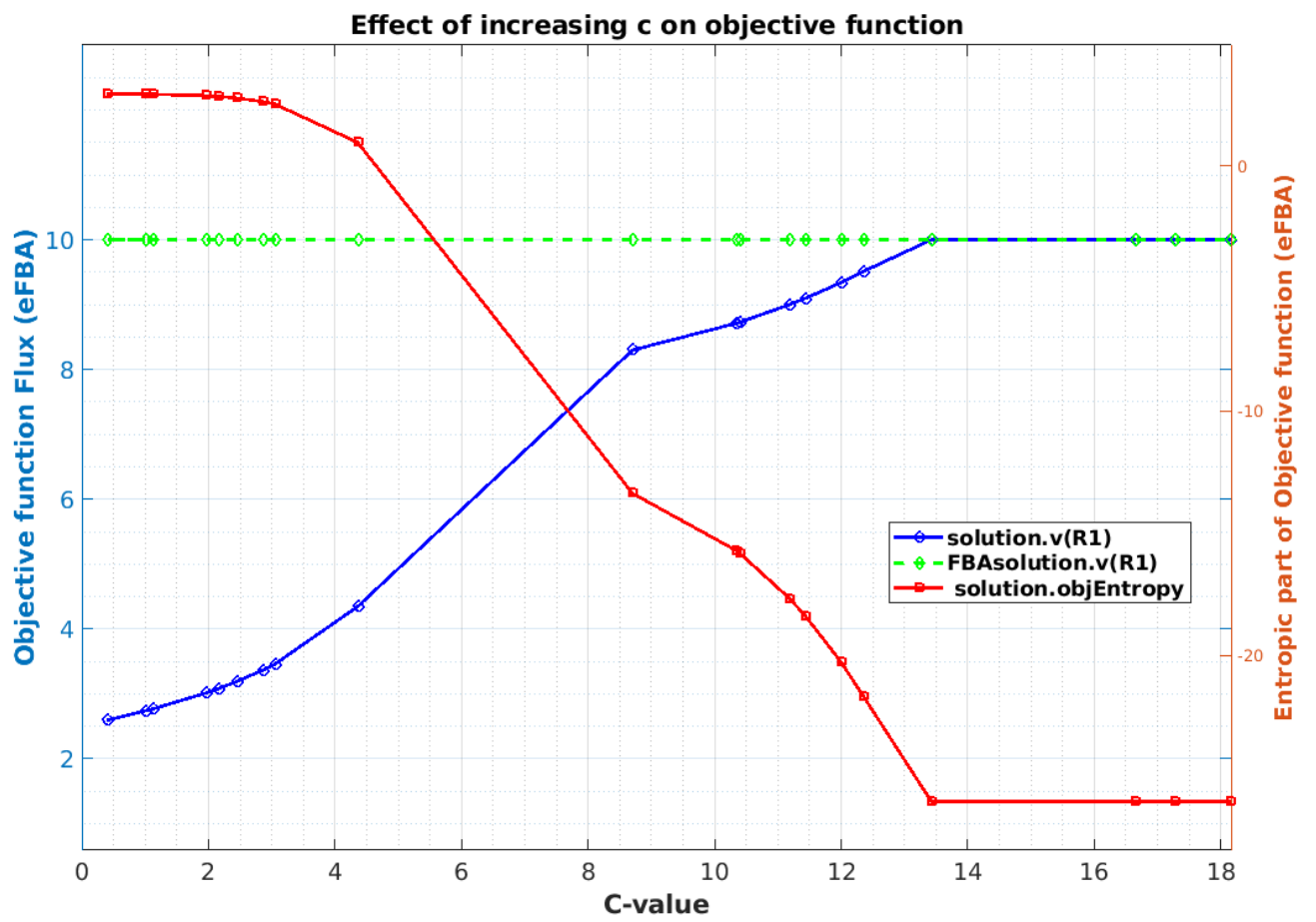
> Checking for available updates ...
> You cannot update your fork using updateCobraToolbox() because this is a development branch.
> The current branch is: master
> The last commit to the current branch is: 097dc1
> You can use MATLAB.devTools (https://github.com/opencobra/MATLAB.devTools) to update your fork.
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/componentContribution/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/groupContribution/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/inchi/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/molFiles/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/protons/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/trainingModel/new

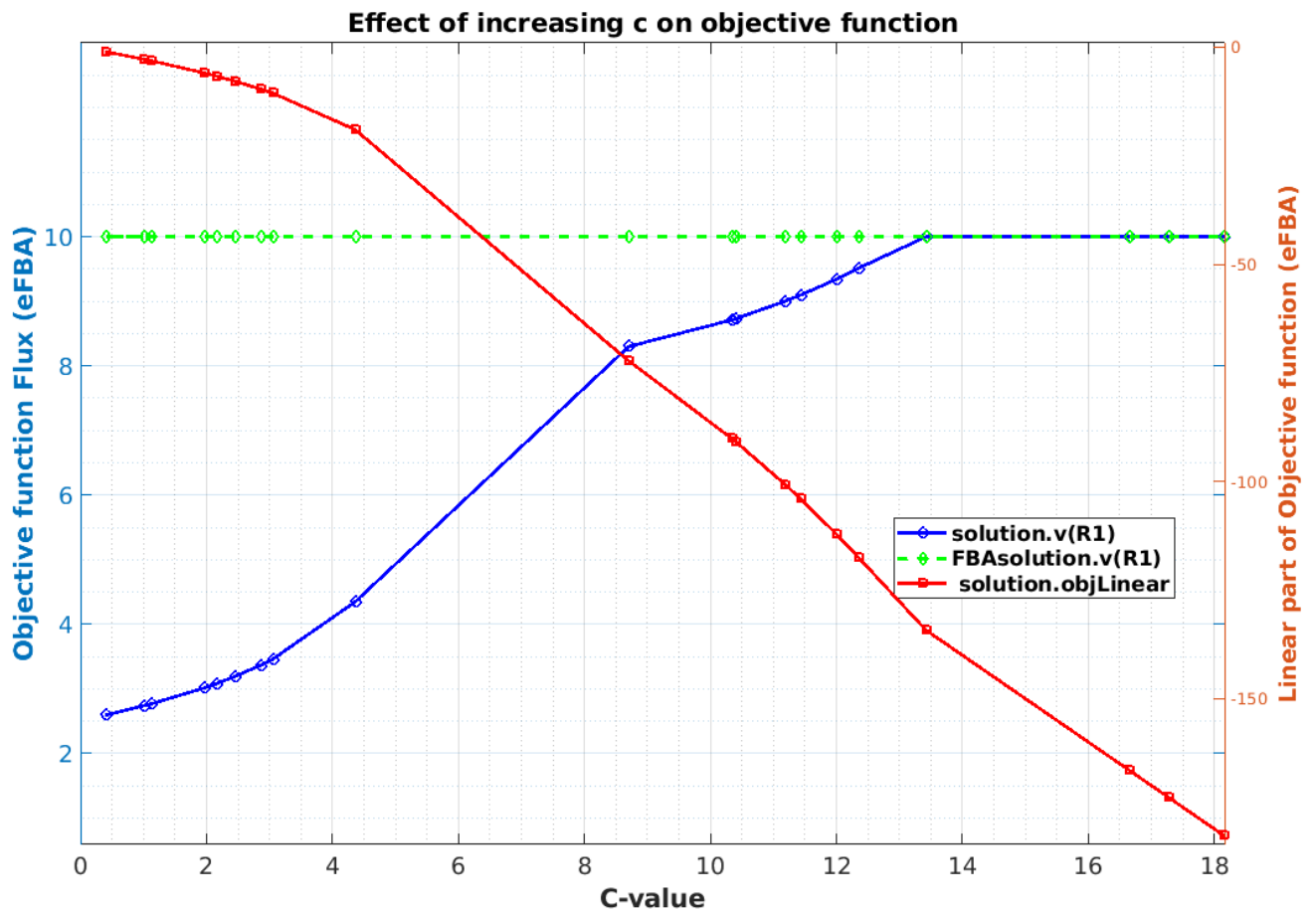
```











Use **tmorous mesenchymal** as an example:

```
clear all
warning('off', 'all')
load('~\drive\glioblastoma/results\csf_media/defaultModels/absolute/-2/
TCmesnh/scRecon3D_mesnh.mat')
model = scRecon3D_mesnh;
param.solver = 'mosek';
param = mosekParamSetEFBA(param);
[solution,~] = entropicFluxBalanceAnalysis(model,param);
```

Using existing internal net flux bounds without modification.

MOSEK Version 10.1.15 (Build date: 2023-10-12 20:25:19)  
 Copyright (c) MOSEK ApS, Denmark WWW: mosek.com  
 Platform: Linux/64-X86

```
Problem
  Name           :
  Objective sense : minimize
  Type           : CONIC (conic optimization problem)
  Constraints     : 3821
  Affine conic cons. : 4532 (13596 rows)
  Disjunctive cons. : 0
```

```

Cones                : 0
Scalar variables     : 9329
Matrix variables     : 0
Integer variables    : 0

Optimizer started.
Presolve started.
Linear dependency checker started.
Linear dependency checker terminated.
Eliminator started.
Freed constraints in eliminator : 0
Eliminator terminated.
Eliminator - tries          : 1          time           : 0.00
Lin. dep. - tries          : 1          time           : 0.00
Lin. dep. - primal attempts : 1          successes        : 1
Lin. dep. - dual attempts  : 0          successes        : 0
Lin. dep. - primal deps.   : 46         dual deps.       : 0
Presolve terminated. Time: 0.01
Optimizer - threads        : 6
Optimizer - solved problem : the primal
Optimizer - Constraints     : 3559
Optimizer - Cones          : 4532
Optimizer - Scalar variables : 15966      conic            : 13596
Optimizer - Semi-definite variables: 0      scalarized       : 0
Factor - setup time        : 0.02
Factor - dense det. time   : 0.00         GP order time    : 0.00
Factor - nonzeros before factor : 2.07e+04   after factor     : 3.29e+04
Factor - dense dim.        : 0           flops            : 1.35e+06

ITE PFEAS   DFEAS   GFEAS   PRSTATUS   POBJ          DOBJ          MU          TIME
0   1.0e+04  1.0e+00  9.6e+03  0.00e+00  3.751763625e+03 -5.850484381e+03 1.0e+00  0.04
1   6.1e+03  6.1e-01  7.5e+03 -1.00e+00  8.313076808e+03 -1.287894680e+03 6.1e-01  0.05
2   5.0e+03  5.0e-01  6.8e+03 -1.00e+00  1.112763764e+04 1.527382355e+03 5.0e-01  0.06
3   1.7e+03  1.7e-01  4.0e+03 -1.00e+00  4.148339684e+04 3.189078369e+04 1.7e-01  0.07
4   6.2e+02  6.2e-02  2.4e+03 -9.99e-01  1.292870514e+05 1.197149432e+05 6.2e-02  0.07
5   2.4e+02  2.4e-02  1.5e+03 -9.97e-01  3.572449862e+05 3.477239896e+05 2.4e-02  0.08
6   1.5e+02  1.5e-02  1.2e+03 -9.91e-01  5.777499688e+05 5.682774441e+05 1.5e-02  0.09
7   5.7e+01  5.7e-03  7.1e+02 -9.86e-01  1.568819718e+06 1.559568322e+06 5.7e-03  0.09
8   2.4e+01  2.4e-03  4.5e+02 -9.59e-01  3.574612144e+06 3.565849568e+06 2.4e-03  0.11
9   1.5e+01  1.5e-03  3.3e+02 -8.84e-01  5.333036825e+06 5.324856390e+06 1.5e-03  0.12
10  9.7e+00  9.7e-04  2.5e+02 -7.64e-01  6.797962076e+06 6.790586654e+06 9.7e-04  0.13
11  6.1e+00  6.1e-04  1.6e+02 -5.53e-01  7.360832852e+06 7.354732475e+06 6.1e-04  0.14
12  5.7e+00  5.7e-04  1.5e+02 -1.74e-01  7.092266424e+06 7.086435891e+06 5.7e-04  0.15
13  3.4e+00  3.4e-04  8.1e+01 -9.66e-02  5.426427962e+06 5.422241669e+06 3.4e-04  0.16
14  1.9e+00  1.9e-04  3.5e+01  3.30e-01  3.319803309e+06 3.317220350e+06 1.9e-04  0.17
15  1.0e+00  1.0e-04  1.5e+01  6.45e-01  2.038763664e+06 2.037238923e+06 1.0e-04  0.17
16  6.1e-01  6.1e-05  7.1e+00  8.15e-01  1.298751555e+06 1.297829593e+06 6.1e-05  0.18
17  5.7e-01  5.7e-05  6.4e+00  9.01e-01  1.205250834e+06 1.204391739e+06 5.7e-05  0.19
18  3.4e-01  3.4e-05  3.0e+00  9.09e-01  7.451237743e+05 7.446090848e+05 3.4e-05  0.20
19  1.1e-01  1.1e-05  6.3e-01  9.52e-01  2.722482999e+05 2.720739261e+05 1.1e-05  0.20
20  7.1e-02  7.1e-06  3.2e-01  9.89e-01  1.739122982e+05 1.738033011e+05 7.1e-06  0.21
21  4.1e-02  4.1e-06  1.4e-01  9.94e-01  1.006840270e+05 1.006219591e+05 4.1e-06  0.22
22  2.0e-02  2.0e-06  4.7e-02  9.98e-01  4.701830842e+04 4.698871132e+04 2.0e-06  0.22
23  1.1e-02  1.1e-06  1.9e-02  1.00e+00  2.425817555e+04 2.424215085e+04 1.1e-06  0.23
24  4.6e-03  4.6e-07  5.6e-03  1.00e+00  8.973177465e+03 8.966243553e+03 4.6e-07  0.24
25  1.5e-03  1.5e-07  1.1e-03  1.00e+00  1.516039780e+03 1.513786029e+03 1.5e-07  0.24
26  5.7e-04  5.7e-08  2.4e-04  1.00e+00  -5.284016613e+02 -5.292396071e+02 5.7e-08  0.25
27  3.9e-04  3.9e-08  1.4e-04  1.00e+00  -8.805553505e+02 -8.811355183e+02 3.9e-08  0.26
28  1.9e-04  1.9e-08  4.6e-05  1.00e+00  -1.299360601e+03 -1.299635631e+03 1.9e-08  0.26
29  6.4e-05  6.4e-09  9.3e-06  1.00e+00  -1.544003826e+03 -1.544097855e+03 6.4e-09  0.27
30  2.1e-05  2.1e-09  1.7e-06  1.00e+00  -1.628423008e+03 -1.628453078e+03 2.1e-09  0.28
31  7.8e-06  7.8e-10  4.0e-07  1.00e+00  -1.652572166e+03 -1.652583634e+03 7.8e-10  0.29
32  5.5e-06  5.5e-10  2.3e-07  1.00e+00  -1.657062117e+03 -1.657070094e+03 5.5e-10  0.30
33  1.9e-06  1.9e-10  4.8e-08  1.00e+00  -1.663672571e+03 -1.663675361e+03 1.9e-10  0.31
34  1.3e-06  1.3e-10  2.7e-08  1.00e+00  -1.664786582e+03 -1.664788498e+03 1.3e-10  0.31

```

```

35  7.0e-07  7.0e-11  1.1e-08  1.00e+00  -1.665911928e+03  -1.665912949e+03  7.0e-11  0.32
36  2.1e-07  2.1e-11  1.8e-09  1.00e+00  -1.666811683e+03  -1.666811992e+03  2.1e-11  0.33
37  5.1e-08  5.1e-12  2.1e-10  1.00e+00  -1.667106905e+03  -1.667106980e+03  5.1e-12  0.34
38  1.7e-08  1.7e-12  4.0e-11  1.00e+00  -1.667171007e+03  -1.667171032e+03  1.7e-12  0.35
39  4.3e-09  4.3e-13  5.1e-12  1.00e+00  -1.667194344e+03  -1.667194350e+03  4.3e-13  0.35
40  9.2e-10  9.2e-14  5.1e-13  1.00e+00  -1.667200707e+03  -1.667200709e+03  9.2e-14  0.36
41  2.2e-10  2.2e-14  5.9e-14  1.00e+00  -1.667202042e+03  -1.667202042e+03  2.2e-14  0.37
42  2.2e-10  5.7e-15  6.4e-15  1.00e+00  -1.667202362e+03  -1.667202362e+03  5.0e-15  0.38
Optimizer terminated. Time: 0.38

```

#### Interior-point solution summary

```

Problem status : PRIMAL_AND_DUAL_FEASIBLE
Solution status : OPTIMAL
Primal.  obj: -1.6672023624e+03  nrm: 1e+00  Viol.  con: 7e-07  var: 0e+00  acc: 9e-08
Dual.    obj: -1.6672023624e+03  nrm: 2e+03  Viol.  con: 8e-12  var: 1e-11  acc: 0e+00

```

#### Optimizer summary

```

Optimizer          -          time: 0.38
  Interior-point    - iterations : 42    time: 0.38
    Basis identification -          time: 0.00
      Primal        - iterations : 0      time: 0.00
      Dual          - iterations : 0      time: 0.00
      Clean primal   - iterations : 0      time: 0.00
      Clean dual     - iterations : 0      time: 0.00
    Simplex         -          time: 0.00
      Primal simplex - iterations : 0      time: 0.00
      Dual simplex   - iterations : 0      time: 0.00
    Mixed integer    - relaxations: 0      time: 0.00

```

```

> [mosek] Primal optimality condition in solveCobraEP satisfied.
> [mosek] Dual   optimality condition in solveCobraEP satisfied.

```

#### Optimality conditions (biochemistry)

```

7.2e-07 || N*(vf - vr) + B*ve - b ||_inf
7.6e-12 || cf + ci + N'*y_N + y_vi + Qv*vf + k_vf + z_vf ||_inf
7.6e-12 || cr - ci - N'*y_N - y_vi + Qv*vf + k_vr + z_vr ||_inf
1.1e-11 || ce + B'*y_N + z_ve ||_inf
0       || k_e_1 + z_e_1 ||_inf
1.6e-12 || -g + k_e_vf + z_e_vf ||_inf
1.6e-12 || -g + k_e_vr + z_e_vr ||_inf
1.7e-07 || e_vf + vf*log(vf) ||_inf
1.1e-07 || e_vr + vr*log(vr) ||_inf

```

#### Derived optimality conditions (biochemistry)

```

2.3e-05 || g.*log(vf) + g - k_vf ||_inf
3e-05   || g.*log(vr) + g - k_vr ||_inf
2.3e-05 || cf + ci + N'*y_N + y_vi + Qv*vf + g.*log(vf) + g + z_vf ||_inf
3e-05   || cr - ci - N'*y_N - y_vi + Qv*vf + g.*log(vr) + g + z_vr ||_inf

```

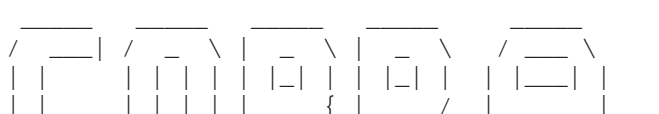
#### Thermo conditions

```

2 || g.*log(vr/vf) - 2*N'*y_N ||_inf
3.5e-05 || g.*log(vr/vf) + cr - cf - 2*ci - 2*N'*y_N - 2*y_vi ||_inf
3.5e-05 || g.*log(vr/vf) + cr - cf - 2*ci - 2*N'*y_N - 2*y_vi - z_vr + z_vf ||_inf
2.6e-11 min(slack)
7.2e-07 max(slack)

```

```
plotyy_eFBA(model, 'biomass_reaction', 1500, 30, 0);
```



CONstraint-Based Reconstruction and Analysis  
The COBRA Toolbox - 2024

_           \ \	Documentation:
\ _ _   \ _ _ /   _ _ /   _ \ \   _	<a href="http://opencobra.github.io/cobratoolbox">http://opencobra.github.io/cobratoolbox</a>

```
> Checking if git is installed ... Done (version: 2.25.1).
> Checking if the repository is tracked using git ... Done.
> Checking if curl is installed ... Done.
> Checking if remote can be reached ... Done.
> Initializing and updating submodules (this may take a while)... Done.
> Adding all the files of The COBRA Toolbox ... Done.
> Define CB map output... set to svg.
> TranslateSBML is installed and working properly.
> Configuring solver environment variables ...
- [ *---] ILOG_CPLEX_PATH: /opt/ibm/ILOG/CPLEX_Studio1210/cplex/matlab/x86-64_linux
- [ *---] GUROBI_PATH: /opt/gurobi1003/linux64/matlab
- [ *---] TOMLAB_PATH: --> set this path manually after installing the solver ( see instructions )
- [ *---] MOSEK_PATH: /opt/mosek/10.1/
Done.
> Checking available solvers and solver interfaces ... 0
```

0

```
Check osense*c - A'*lam - w = 0 (stationarity):
0
0
```

```
> [gurobi] Primal optimality condition in solveCobraLP satisfied.
> [gurobi] Dual optimality condition in solveCobraLP satisfied.
Version identifier: 12.10.0.0 | 2019-11-26 | 843d4de
CPXPARAM_Output_WriteLevel 3
CPXPARAM_Output_CloneLog -1
Found incumbent of value 0.000000 after 0.00 sec. (0.00 ticks)
```

```
Root node processing (before b&c):
Real time = 0.00 sec. (0.00 ticks)
Parallel b&c, 12 threads:
Real time = 0.00 sec. (0.00 ticks)
Sync time (average) = 0.00 sec.
Wait time (average) = 0.00 sec.
-----
Total (root+branch&cut) = 0.00 sec. (0.00 ticks)
Could not find installation of tomlab_cplex, so it cannot be tested
GLPK Simplex Optimizer, v4.42
1 row, 2 columns, 1 non-zero
Preprocessing...
~ 0: obj = 0.000000000e+00 infeas = 0.000e+00
OPTIMAL SOLUTION FOUND BY LP PREPROCESSOR
```

```
> [glpk] Primal optimality condition in solveCobraLP satisfied.
> [mosek] Primal optimality condition in solveCobraLP satisfied.
> [mosek] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of matlab, so it cannot be tested
```

```
-----
pdco.m Version pdco5 of 15 Jun 2018
Primal-dual barrier method to minimize a convex function
subject to linear constraints Ax + r = b, bl <= x <= bu

Michael Saunders SOL and ICME, Stanford University
Contributors: Byunggyoo Kim (SOL), Chris Maes (ICME)
Santiago Akle (ICME), Matt Zahr (ICME)
Aekaansh Verma (ME)
-----
```

The objective is linear  
The matrix A is an explicit sparse matrix

```
m          =          1      n          =          2      nnz(A) =          1
max |b|    =          0      max |x0|   =  1.0e+00      xsize  =  1.0e+00
max |y0|   =          1      max |z0|   =  1.0e+00      zsize  =  1.0e+00

x0min     =          1      featol    =  1.0e-06      dlmax   =  1.0e-04
z0min     =          1      opttol    =  1.0e-06      d2max   =  5.0e-04
mu0       =  1.0e-01      steptol   =          0.99      bigcenter=  1000
```

LSMR/MINRES:

```
atoll      =  1.0e-10      atol2    =  1.0e-15      btol     =  0.0e+00
conlim     =  1.0e+12      itnlim   =          10      show     =          0
```

Method = 2 (1 or 11=chol 2 or 12=QR 3 or 13=LSMR 4 or 14=MINRES 21=SQD(LU) 22=SQD(MA57))  
Eliminating dy before dx

Bounds:

```
[0,inf]  [-inf,0]  Finite bl  Finite bu  Two bnds  Fixed  Free
      0      0      0      0      0      2      0
[0, bu]  [bl, 0]  excluding fixed variables
      0      0
```

```
Itn  mu stepx stepz  Pinf  Dinf  Cinf  Objective  nf  center  QR
  0      -6.6 -99.0 -Inf  1.2500000e-07      1.0
  1 -1.0 1.000 1.000 -99.0 -99.0 -Inf  0.0000000e+00  1      1.0      1
  2 -3.0 1.000 1.000 -99.0 -99.0 -Inf  0.0000000e+00  1      1.0
  3 -5.0 1.000 1.000 -99.0 -99.0 -Inf  0.0000000e+00  1      1.0
  4 -7.0 1.000 1.000 -99.0 -99.0 -Inf  0.0000000e+00  1      1.0
```

Converged

```
max |x| =          0.000      max |y| =          0.000      max |z| =          0.000      scaled
max |x| =          0.000      max |y| =          0.000      max |z| =          0.000      unscaled
max |x| and max |z| exclude fixed variables
PDitns  =          4      QRitns =          0      cputime =          0.0
```

```
Distribution of vector      x      z
[      1,      10 )      0      2
[      0.1,      1 )      0      0
[      0.01,      0.1 )      0      0
[      0.001,      0.01 )      0      0
[      0.0001,      0.001 )      0      0
[      1e-05,      0.0001 )      0      0
[      1e-06,      1e-05 )      0      0
[      1e-07,      1e-06 )      0      0
[      1e-08,      1e-07 )      0      0
[      0,      1e-08 )      2      0
```

Elapsed time is 0.026625 seconds.

```
> [pdco] Primal optimality condition in solveCobraLP satisfied.
> [pdco] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of quadMinos, so it cannot be tested
Could not find installation of dqgMinos, so it cannot be tested
Could not find installation of cplex_direct, so it cannot be tested
```

```
> [cplexlp] Primal optimality condition in solveCobraLP satisfied.
> [cplexlp] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of tomlab_snopt, so it cannot be tested
Done.
```

```
> Setting default solvers ...Could not find installation of matlab, so it cannot be tested
Done.
```



```
> Saving the MATLAB path ... Done.
- The MATLAB path was saved as ~/pathdef.m.
```

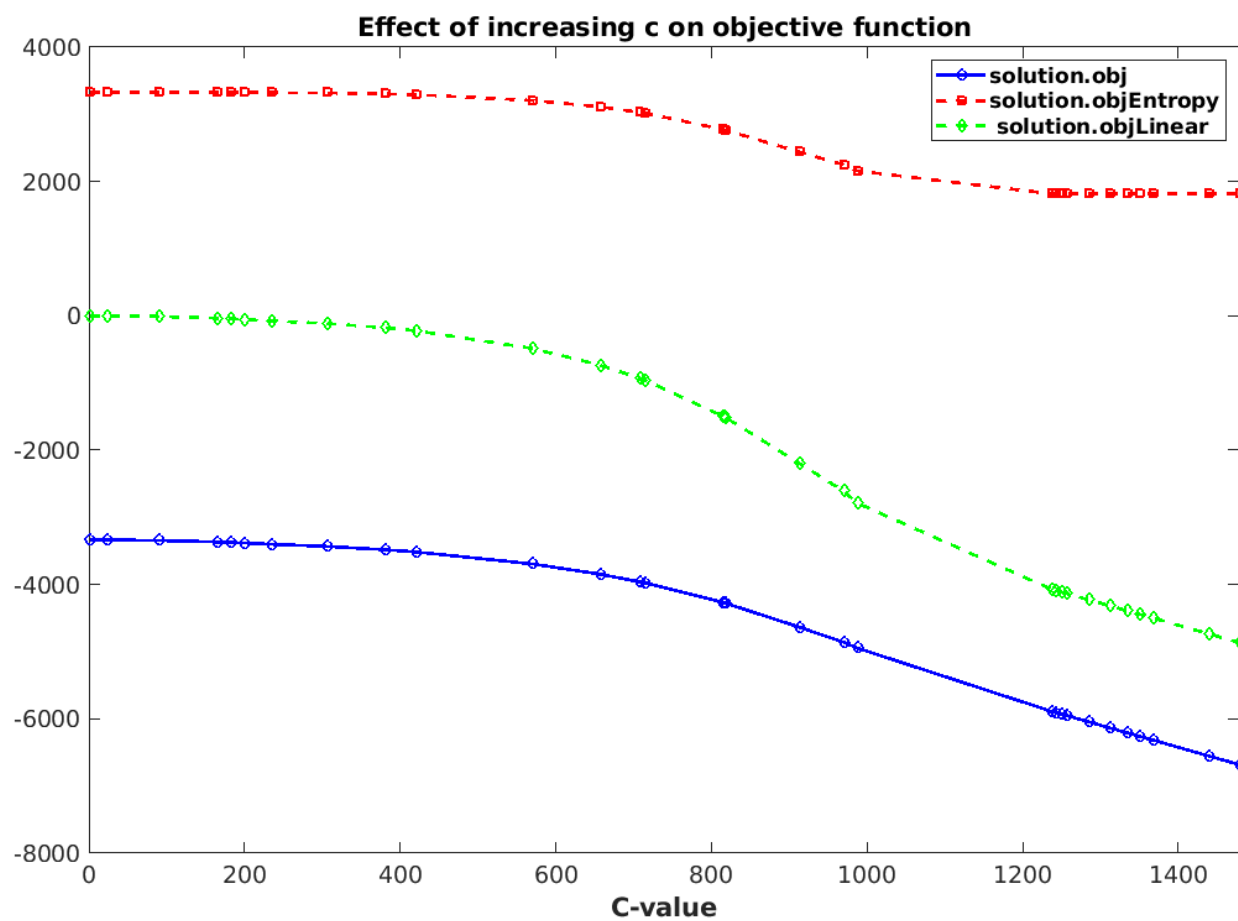
```
> Summary of available solvers and solver interfaces
```

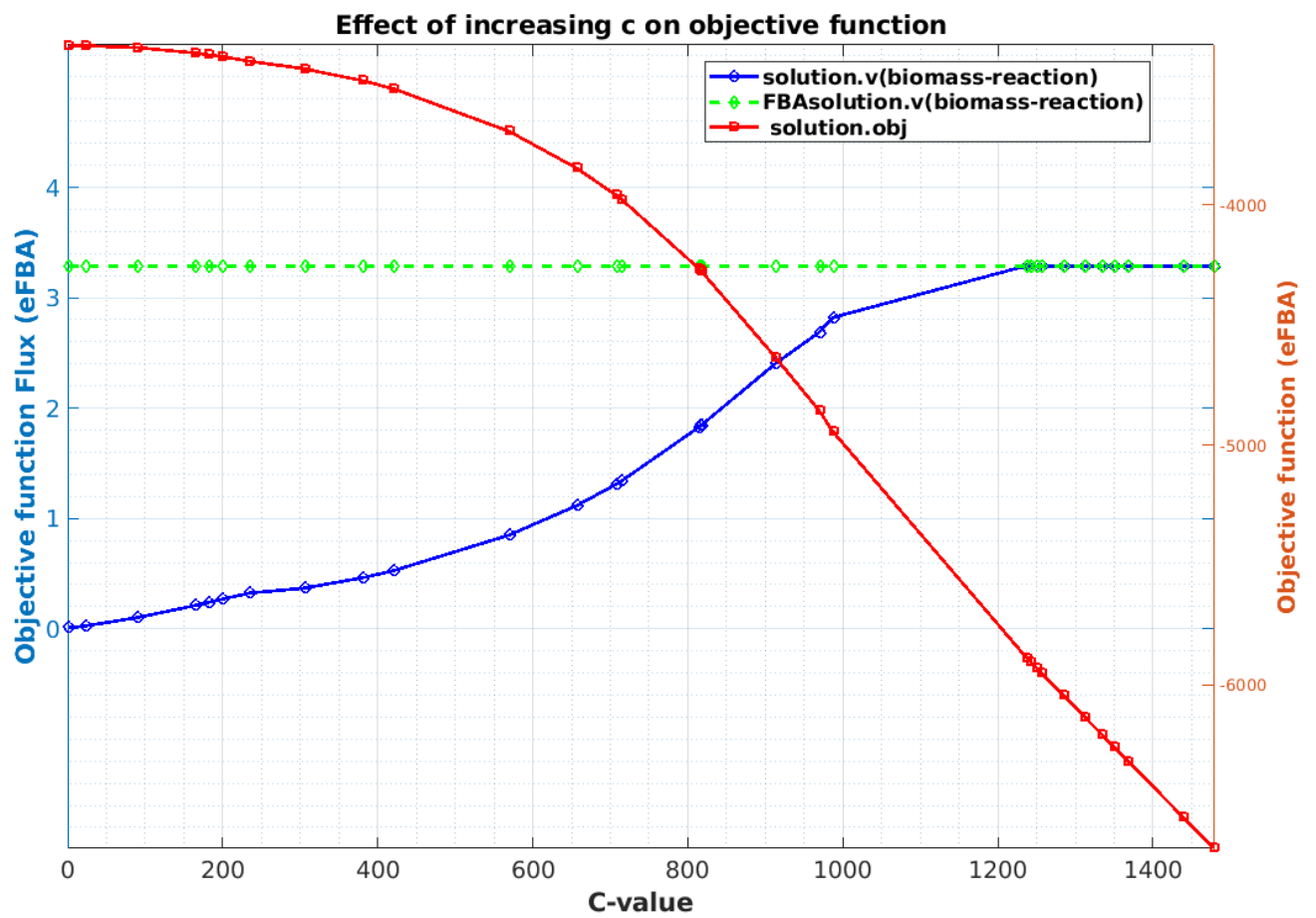
	Support	LP	MILP	QP	MIQP	NLP	EP	
gurobi	active		1	1	1	1	-	-
ibm_cplex	active		1	1	1	1	-	-
tomlab_cplex	active		0	0	0	0	-	-
glpk	active		1	1	-	-	-	-
mosek	active		1	-	1	-	-	1
matlab	active		0	-	-	-	0	-
pdco	active		1	-	1	-	-	1
quadMinos	active		0	-	-	-	-	-
dqqMinos	active		0	-	0	-	-	-
cplex_direct	active		0	0	0	-	-	-
cplexlp	active		1	-	-	-	-	-
qpng	passive		-	-	1	-	-	-
tomlab_snopt	passive		-	-	-	-	0	-
lp_solve	legacy		1	-	-	-	-	-
Total	-		7	3	5	2	0	2

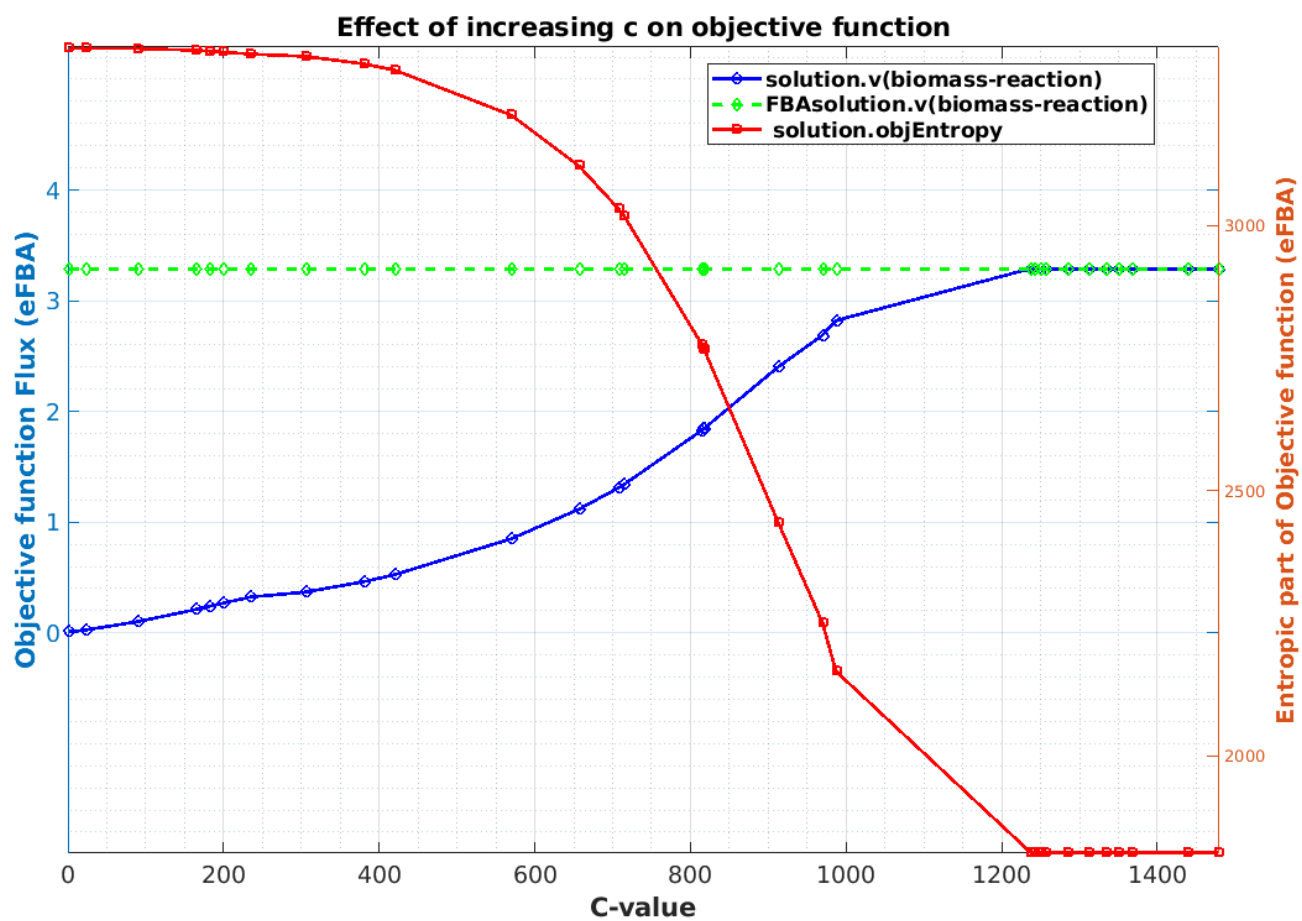
```
+ Legend: - = not applicable, 0 = solver not compatible or not installed, 1 = solver installed.
```

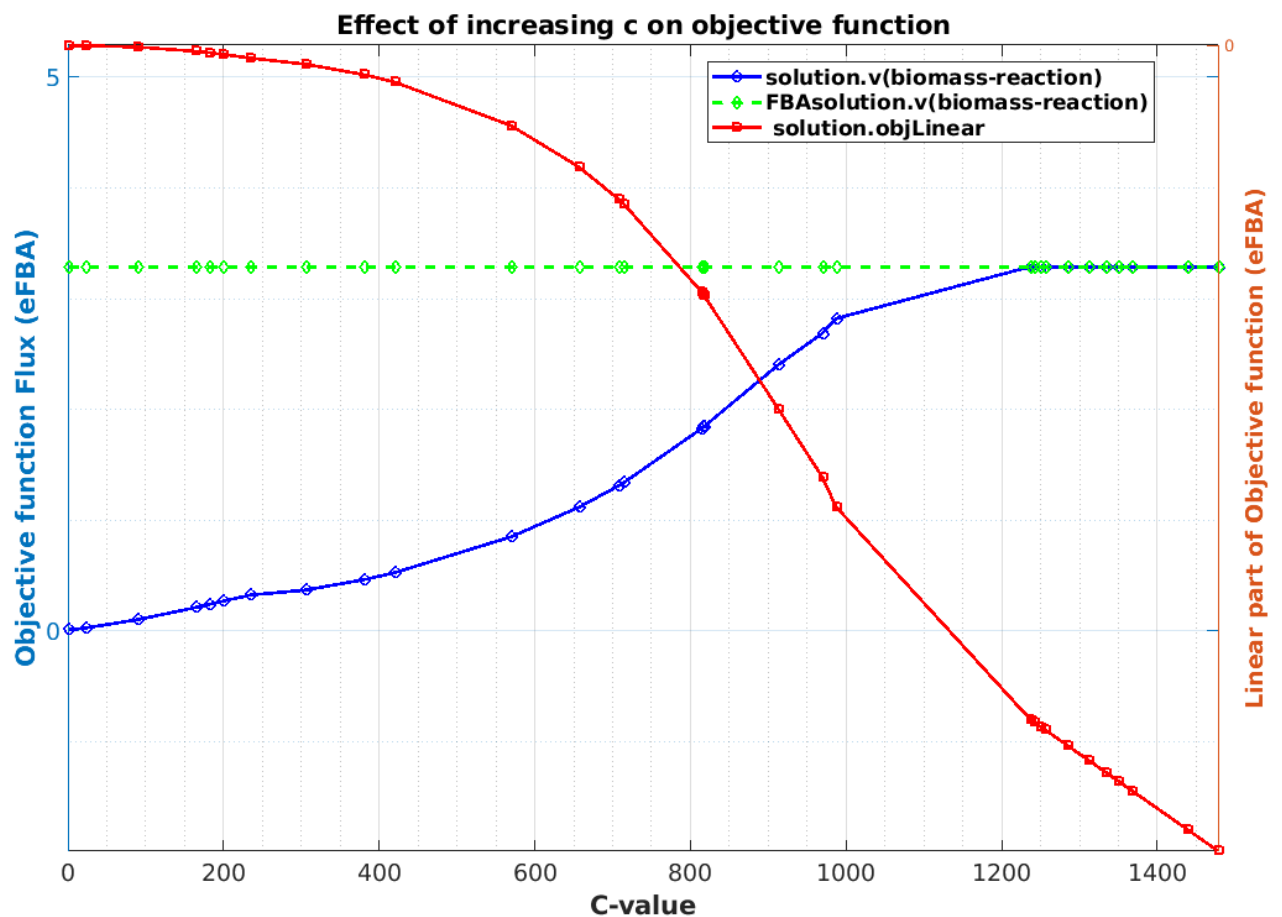
```
> You can solve LP problems using: 'gurobi' - 'ibm_cplex' - 'glpk' - 'mosek' - 'pdco' - 'cplexlp'
> You can solve MILP problems using: 'gurobi' - 'ibm_cplex' - 'glpk'
> You can solve QP problems using: 'gurobi' - 'ibm_cplex' - 'mosek' - 'pdco'
> You can solve MIQP problems using: 'gurobi' - 'ibm_cplex'
> You can solve NLP problems using:
> You can solve EP problems using: 'mosek' - 'pdco'
```

```
> Checking for available updates ...
> You cannot update your fork using updateCobraToolbox() because this is a development branch.
> The current branch is: master
> The last commit to the current branch is: 097dc1
> You can use MATLAB.devTools (https://github.com/opencobra/MATLAB.devTools) to update your fork.
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/componentContribution/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/groupContribution/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/inchi/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/molFiles/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/protons/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/trainingModel/new
```









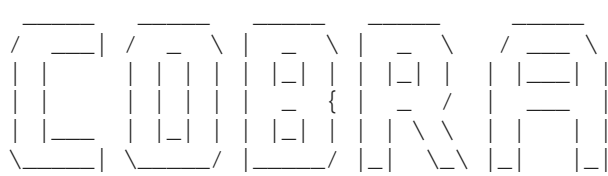
## Estimation of C (coefficient of objective function)

After understanding the behavior of flux in the objective function as a function of C, the question becomes: which value of C is the best for modeling? The value of flux changes between zero and the maximum value calculated in FBA. The C at the maximum value is not the best, since our model will never meet that value. It is important to know what is expected from the model in reality. The answer to this question comes from experiments. For example, in the case of biomass, we know that the growth rate is related to doubling time according to the equation below. If we know the doubling time of the cell, we can find the C value corresponding to that value in modeling.

```
clear all
warning('off', 'all')
load('~\drive\glioblastoma/results\csf_media/defaultModels/absolute/-2/
TCmesnh/scRecon3D_mesnh.mat');
model = scRecon3D_mesnh;
```

```
solution_vals(:,1) = 0:50:1400;
param.printLevel = 0;
```

```
param.solver = 'mosek';
%model
initCobraToolbox
```



COntstraint-Based Reconstruction and Analysis  
The COBRA Toolbox - 2024

Documentation:  
<http://opencobra.github.io/cobratoolbox>

```
> Checking if git is installed ... Done (version: 2.25.1).
> Checking if the repository is tracked using git ... Done.
> Checking if curl is installed ... Done.
> Checking if remote can be reached ... Done.
> Initializing and updating submodules (this may take a while)... Done.
> Adding all the files of The COBRA Toolbox ... Done.
> Define CB map output... set to svg.
> TranslateSBML is installed and working properly.
> Configuring solver environment variables ...
- [*---] ILOG_CPLEX_PATH: /opt/ibm/ILOG/CPLEX_Studio1210/cplex/matlab/x86-64_linux
- [*---] GUROBI_PATH: /opt/gurobi1003/linux64/matlab
- [----] TOMLAB_PATH: --> set this path manually after installing the solver ( see instructions )
- [*---] MOSEK_PATH: /opt/mosek/10.1/
Done.
> Checking available solvers and solver interfaces ...      0
```

0

```
Check osense*c - A'*lam - w = 0 (stationarity):
0
0
```

```
> [gurobi] Primal optimality condition in solveCobraLP satisfied.
> [gurobi] Dual optimality condition in solveCobraLP satisfied.
Version identifier: 12.10.0.0 | 2019-11-26 | 843d4de
CPXPARAM_Output_WriteLevel      3
CPXPARAM_Output_CloneLog        -1
Found incumbent of value 0.000000 after 0.00 sec. (0.00 ticks)
```

Root node processing (before b&c):

```
Real time      = 0.00 sec. (0.00 ticks)
Parallel b&c, 12 threads:
Real time      = 0.00 sec. (0.00 ticks)
Sync time (average) = 0.00 sec.
Wait time (average) = 0.00 sec.
```

```
-----
Total (root+branch&cut) = 0.00 sec. (0.00 ticks)
Could not find installation of tomlab_cplex, so it cannot be tested
GLPK Simplex Optimizer, v4.42
1 row, 2 columns, 1 non-zero
Preprocessing...
~ 0: obj = 0.000000000e+00 infeas = 0.000e+00
OPTIMAL SOLUTION FOUND BY LP PREPROCESSOR
```

```
> [glpk] Primal optimality condition in solveCobraLP satisfied.
> [mosek] Primal optimality condition in solveCobraLP satisfied.
> [mosek] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of matlab, so it cannot be tested
```

pdco.m

Version pdco5 of 15 Jun 2018

Primal-dual barrier method to minimize a convex function  
subject to linear constraints  $Ax + r = b$ ,  $bl \leq x \leq bu$

Michael Saunders            SOL and ICME, Stanford University  
Contributors:            Byunggyoo Kim (SOL), Chris Maes (ICME)  
                         Santiago Akle (ICME), Matt Zahr (ICME)  
                         Aekaansh Verma (ME)

-----

The objective is linear  
The matrix A is an explicit sparse matrix

m	=	1	n	=	2	nnz(A)	=	1
max  b	=	0	max  x0	=	1.0e+00	xsize	=	1.0e+00
max  y0	=	1	max  z0	=	1.0e+00	zsize	=	1.0e+00
x0min	=	1	featol	=	1.0e-06	dlmax	=	1.0e-04
z0min	=	1	opttol	=	1.0e-06	d2max	=	5.0e-04
mu0	=	1.0e-01	steptol	=	0.99	bigcenter	=	1000

LSMR/MINRES:

atoll	=	1.0e-10	atol2	=	1.0e-15	btol	=	0.0e+00
conlim	=	1.0e+12	itnlim	=	10	show	=	0

Method = 2 (1 or 11=chol 2 or 12=QR 3 or 13=LSMR 4 or 14=MINRES 21=SQD(LU) 22=SQD(MA57))  
Eliminating dy before dx

Bounds:

[0,inf]	[-inf,0]	Finite bl	Finite bu	Two bnds	Fixed	Free
0	0	0	0	0	2	0
[0, bu]	[bl, 0]	excluding fixed variables				
0	0					

Itn	mu	stepx	stepz	Pinf	Dinf	Cinf	Objective	nf	center	QR
0				-6.6	-99.0	-Inf	1.2500000e-07		1.0	
1	-1.0	1.000	1.000	-99.0	-99.0	-Inf	0.0000000e+00	1	1.0	1
2	-3.0	1.000	1.000	-99.0	-99.0	-Inf	0.0000000e+00	1	1.0	
3	-5.0	1.000	1.000	-99.0	-99.0	-Inf	0.0000000e+00	1	1.0	
4	-7.0	1.000	1.000	-99.0	-99.0	-Inf	0.0000000e+00	1	1.0	

Converged

max  x	=	0.000	max  y	=	0.000	max  z	=	0.000	scaled
max  x	=	0.000	max  y	=	0.000	max  z	=	0.000	unscaled
max  x  and max  z  exclude fixed variables									
PDitns	=	4	QRitns	=	0	cputime	=	0.1	

Distribution of vector

	x	z
[ 1, 10 )	0	2
[ 0.1, 1 )	0	0
[ 0.01, 0.1 )	0	0
[ 0.001, 0.01 )	0	0
[ 0.0001, 0.001 )	0	0
[ 1e-05, 0.0001 )	0	0
[ 1e-06, 1e-05 )	0	0
[ 1e-07, 1e-06 )	0	0
[ 1e-08, 1e-07 )	0	0
[ 0, 1e-08 )	2	0

Elapsed time is 0.025806 seconds.

> [pdcol] Primal optimality condition in solveCobraLP satisfied.  
> [pdcol] Dual optimality condition in solveCobraLP satisfied.  
Could not find installation of quadMinos, so it cannot be tested  
Could not find installation of dqgMinos, so it cannot be tested

Could not find installation of cplex\_direct, so it cannot be tested

```
> [cplexlp] Primal optimality condition in solveCobraLP satisfied.
> [cplexlp] Dual optimality condition in solveCobraLP satisfied.
Could not find installation of tomlab_snopt, so it cannot be tested
Done.
> Setting default solvers ...Could not find installation of matlab, so it cannot be tested
Done.
> Saving the MATLAB path ... Done.
- The MATLAB path was saved as ~/pathdef.m.
```

> Summary of available solvers and solver interfaces

	Support	LP	MILP	QP	MIQP	NLP	EP	
gurobi	active		1	1	1	1	-	-
ibm_cplex	active		1	1	1	1	-	-
tomlab_cplex	active		0	0	0	0	-	-
glpk	active		1	1	-	-	-	-
mosek	active		1	-	1	-	-	1
matlab	active		0	-	-	-	0	-
pdco	active		1	-	1	-	-	1
quadMinos	active		0	-	-	-	-	-
dqqMinos	active		0	-	0	-	-	-
cplex_direct	active		0	0	0	-	-	-
cplexlp	active		1	-	-	-	-	-
qpng	passive		-	-	1	-	-	-
tomlab_snopt	passive		-	-	-	-	0	-
lp_solve	legacy		1	-	-	-	-	-
Total	-		7	3	5	2	0	2

+ Legend: - = not applicable, 0 = solver not compatible or not installed, 1 = solver installed.

```
> You can solve LP problems using: 'gurobi' - 'ibm_cplex' - 'glpk' - 'mosek' - 'pdco' - 'cplexlp'
> You can solve MILP problems using: 'gurobi' - 'ibm_cplex' - 'glpk'
> You can solve QP problems using: 'gurobi' - 'ibm_cplex' - 'mosek' - 'pdco'
> You can solve MIQP problems using: 'gurobi' - 'ibm_cplex'
> You can solve NLP problems using:
> You can solve EP problems using: 'mosek' - 'pdco'
```

```
> Checking for available updates ...
> You cannot update your fork using updateCobraToolbox() because this is a development branch.
> The current branch is: master
> The last commit to the current branch is: 097dc1
> You can use MATLAB.devTools (https://github.com/opencobra/MATLAB.devTools) to update your fork.
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/componentContribution/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/groupContribution/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/inchi/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/molFiles/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/protons/new
removing: /home/samira/fork-cobratoolbox/src/analysis/thermo/trainingModel/new
```

```
FBAsolution = optimizeCbModel(model,'max');
for nr = 1:length(solution_vals)
    model.c(ismember(model.rxns, 'biomass_reaction')) = solution_vals(nr,1);
    [solution,~] = entropicFluxBalanceAnalysis(model,param);
    solution_vals(nr,2) = solution.v(ismember(model.rxns,
'biomass_reaction'));
end
```



```

sub_solution_vals(:,1) = 0:0.1:15;
param.printLevel = 0;
for nr = 1:length(sub_solution_vals)
    model.c(ismember(model.rxns, 'biomass_reaction')) =
sub_solution_vals(nr,1);
    [solution,~] = entropicFluxBalanceAnalysis(model,param);
    sub_solution_vals(nr,2) = solution.v(ismember(model.rxns,
'biomass_reaction'));
end

```

```

figure('Renderer', 'painters', 'Position', [10 10 1600 800]);
% Define subplot positions
pos1 = [0.1, 0.1, 0.4, 0.8]; % [left, bottom, width, height]
pos2 = [0.65, 0.4, 0.30, 0.5]; % [left, bottom, width, height]
experimental_value = log(2)/60; % it is an example in case that doubling
time is considered to be 600 hourse
% Subplot 1
subplot('Position', pos1);
plot(solution_vals(:,1), solution_vals(:,2), 'red', ...
solution_vals(:,1), FBAsolution.f, '*', 'LineWidth', 2);

legend('Biomass(eFBA)', 'Biomass(FBA)', "FontSize", 12, 'Location', 'West')
ylabel('Biomass (umol/gDwh)', "FontSize", 14, "FontWeight", "bold");
xlabel('C-value', "FontSize", 14, "FontWeight", "bold");
xlim([0 max(solution_vals(:,1))])
rectangle('Position', [0, 0, 40, 0.1], 'EdgeColor', 'black', 'LineWidth',
2, 'LineStyle', '-.');
```

% Draw lines from rectangle to the next subplot

```

x1 = pos1(1) + pos1(3);
y1 = pos1(2) + pos1(4) / 2;
x2 = pos2(1);
y2 = pos2(2) + pos2(4) / 2;
set(gca, 'XTickLabel', get(gca, 'XTickLabel'), 'FontWeight', 'bold',
'FontSize', 14);

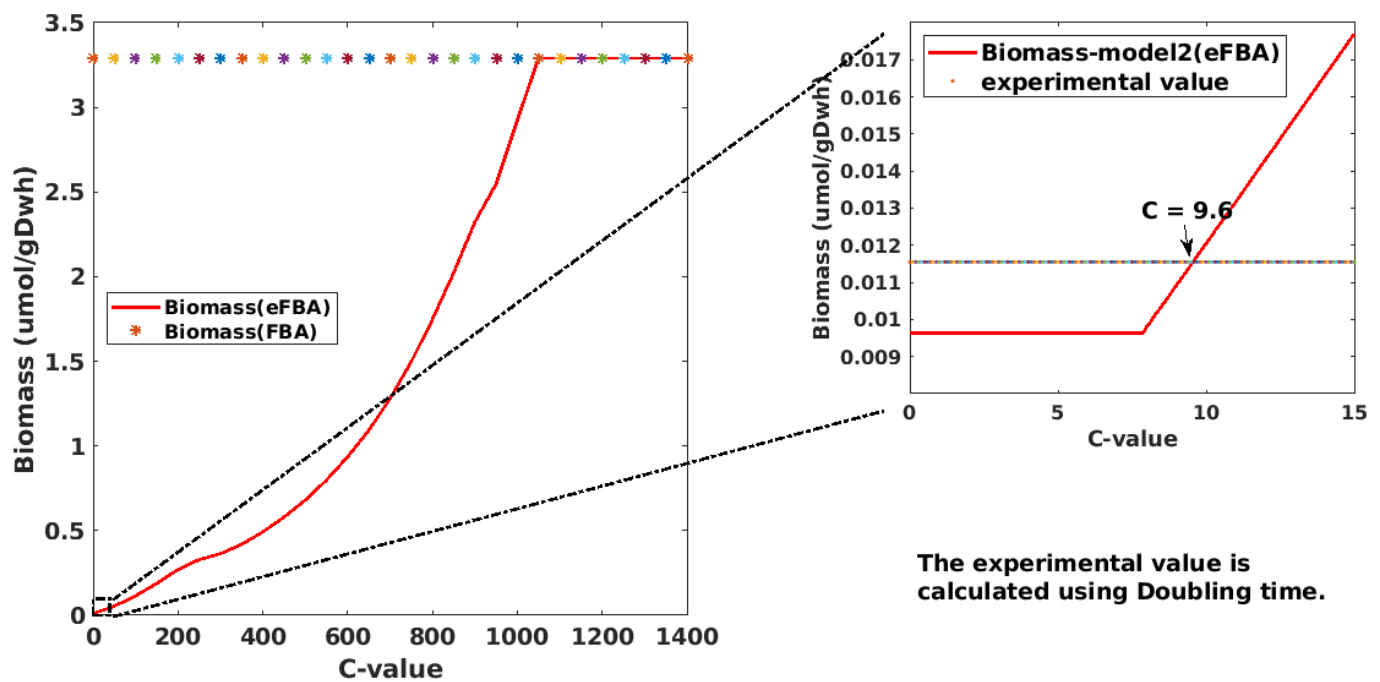
% Subplot 2
subplot('Position', pos2);
plot(sub_solution_vals(:,1), sub_solution_vals(:,2), 'red', ...
sub_solution_vals(:,1), experimental_value, '.', 'LineWidth', 2)
legend('Biomass-model2(eFBA)', 'experimental value', "FontSize", 14,
'Location', "NorthWest")
ylabel('Biomass (umol/gDwh)', "FontSize", 14, "FontWeight", "bold");
xlabel('C-value', "FontSize", 14, "FontWeight", "bold");
xlim([0 max(sub_solution_vals(:,1))])
% ylim([0.009 0.02])
% xticks(0:1:15);

%add crossing point box

```

```
[~,index] = min(abs(sub_solution_vals(:,2) - experimental_value));
% the closest intersection is:
[sub_solution_vals(index,1) experimental_value];
annotation("textarrow", [0.835 0.8385], [0.6263 0.5854], "String", ['C =', num2str(sub_solution_vals(index,1))], 'FontWeight', 'bold', 'FontSize', 14)

% text
annotation('textbox', [pos2(1), 0.1, pos2(3), 0.1], 'String', ['The experimental value is calculated using Doubling time.',...
    'HorizontalAlignment', 'left', 'VerticalAlignment', 'middle',
    'FontWeight', 'bold', 'FontSize', 14, 'EdgeColor', 'none']);
set(gca, 'XTickLabel', get(gca, 'XTickLabel'), 'FontWeight', 'bold', 'FontSize', 12);
annotation("line", [0.113 0.6328], [0.1211 0.8845], 'Color', 'black', 'LineWidth', 2, 'LineStyle', '-.')
annotation("line", [0.113 0.6328], [0.09871 0.3762], 'Color', 'black', 'LineWidth', 2, 'LineStyle', '-.')
% axes 1
% Property editing
positionPropObjs = findobj(gcf, "-property", "Position");
positionPropObjs(1).Position = [0 0 1212.0000, 606.0000];
```



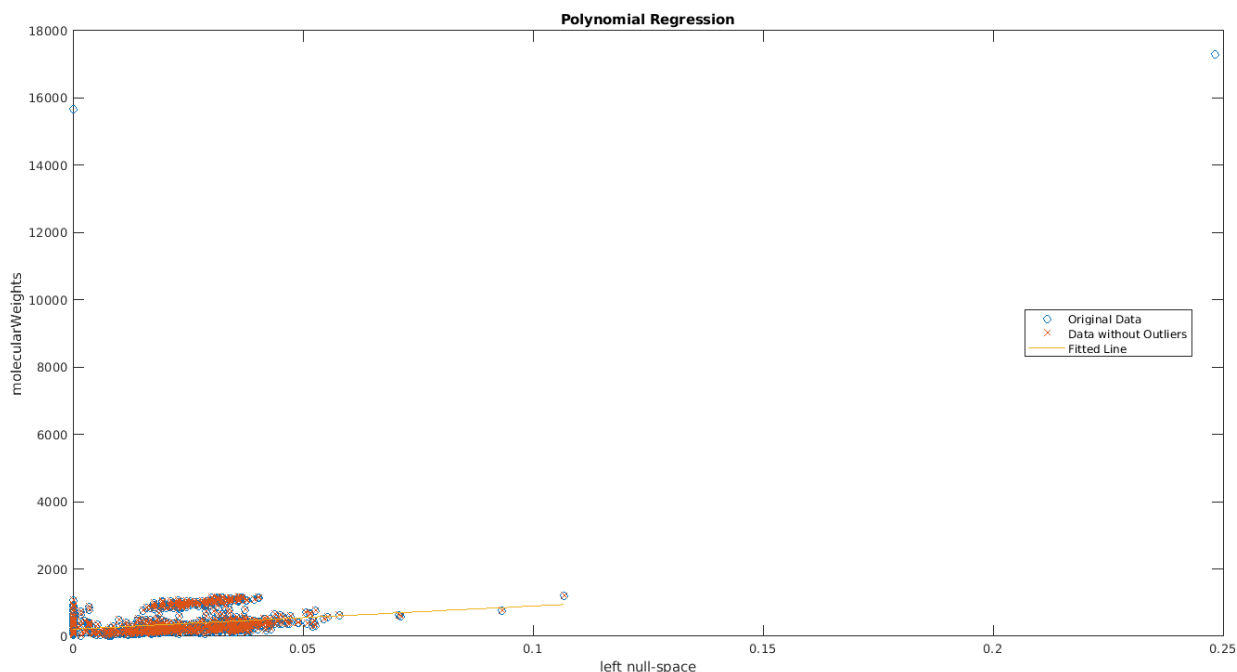
The experimental value is calculated using Doubling time.

Putting weight on cr and cf to unbiased transport of massive molecules

### 1. Using Mass

```
[substratesMass, productsMass] = calculateReactionMasses(model);
```

All reactions that do not include an R-group are mass-balanced.  
LeftNullSpace\_nonzero = 1498



Fitted Polynomial Equation:  
 $y = 6897.7526 * x^1 + 208.665$

```
ave_mass = (substratesMass + productsMass) / 2;
c_mass = ave_mass / sum(ave_mass); % normalize to avoid too aggressive results
```

## 2. Using Gene expression

```
T = readtable('~drive/glioblastoma/data/input/csf_media/
scRef_celltypeAvg.csv');
geneWeight=calculateGeneWeight(model,T(:,[2,51]), 0.1);
```

```
% check to put weight only on internal reactions
j = 1;
for i = 1: numel(model.rxns)
    if model.SConsistentRxnBool(i)
        SCReactionWeight(i) = geneWeight(j);
        SCReactionMass(i) = c_mass(j);
        j = j+1;
    elseif ~model.SConsistentRxnBool(i)
        SCReactionWeight(i) = 0;
        SCReactionMass(i) = 0;
    end
end
c_gene = -log(SCReactionWeight + 1);
c_Mass = SCReactionMass ;
```

```

% weight on objective function
model.c(findRxnIDs(model, 'biomass_reaction')) = 9.6;%rec1
[solution,~] = entropicFluxBalanceAnalysis(model,param);
% changing cr and cf according to geneweight
modell = model;
modell.cr = -log(SCReactionWeight + 1);%- min(-log(SCReactionWeight));
modell.cf = -log(SCReactionWeight + 1); %- min(-log(SCReactionWeight));

[solution1,~] = entropicFluxBalanceAnalysis(modell,param);
% changing cr and cf according to mass
model2 = model;
model2.cr = SCReactionMass;
model2.cf = SCReactionMass;

[solution2,~] = entropicFluxBalanceAnalysis(model2,param);

model3 = model;
model3.cr = modell.cr + model2.cr;
model3.cf = modell.cf + model2.cf;

[solution3,~] = entropicFluxBalanceAnalysis(model3,param);
% initCobraToolbox
FBAsolution = optimizeCbModel(model, 'max');
FBAsolution1 = optimizeCbModel(modell, 'max');
FBAsolution2 = optimizeCbModel(model2, 'max');
FBAsolution3 = optimizeCbModel(model3, 'max');

```

see the effect of different weights on net flux value in some subsystems:

```

subSystem = unique(model.subSystems);

for i = 1:10:length(subSystem)

    figure('Renderer', 'painters', 'Position', [10 10 1600 800])
    ID = findRxnIDs(model,findRxnsFromSubSystem(model,subSystem(i)));
    [sortGeneWeight, idxgeneWeight] = sort(ID, 'descend');

    % findRxnsFromSubSystem(model,subSystem(i));
    % printRxnFormula(model,model.rxns(ID))

    subplot(4,2,1)
    bar(solution.v(ID(idxgeneWeight)),1)
    legend('mesnhFlux-eFBA','FontSize',12)
    % set(gca,'XTick',
    [1:length(model.rxns(ID(contains(findRxnsFromSubSystem(model,subSystem(i)),'r
    ec1')))), 'xticklabel', regexprep(model.rxns(ID(contains(findRxnsFromSubSyste
    m(model,subSystem(i)),'rec2'))), '\[[^\]]*\]', ''))
    % set(gca,'XTickLabelRotation',60, 'FontSize',12)

```

```

title(char(subSystem(i)))
xlabel('rxn ID', 'FontSize',14,'FontWeight','bold');
ylabel('umol/gDWh', 'FontSize',14,'FontWeight','bold');

subplot(4,2,2)
[sortgenWeight, idxgeneWeight] = sort(SCReactionWeight(ID),'descend');
bar(sortgenWeight,1)
legend('mesnhGeneExp', 'FontSize',12)
% set(gca,'XTick',
[1:length(model.rxns(ID(contains(findRxnsFromSubSystem(model,subSystem(i)),'r
ec1')))), 'xticklabel',regexprep(model.rxns(ID(contains(findRxnsFromSubSyste
m(model,subSystem(i)),'rec2'))),'\\[[^\\]]*\\'],''))
% set(gca,'XTickLabelRotation',60, 'FontSize',12)
xlabel('rxn ID', 'FontSize',14,'FontWeight','bold');
ylabel('umol/gDWh', 'FontSize',14,'FontWeight','bold');

subplot(4,2,3)
bar(solution1.v(ID(idxgeneWeight)),1)
legend('mesnhFlux-eFBA(gene)', 'FontSize',12)
xlabel('rxn ID', 'FontSize',14,'FontWeight','bold');
ylabel('umol/gDWh', 'FontSize',14,'FontWeight','bold');

subplot(4,2,4)
bar(model1.cf(ID(idxgeneWeight)))
legend('cf = cr(gene)', 'FontSize',12)
% set(gca,'XTick',
[1:length(model.rxns(ID(contains(findRxnsFromSubSystem(model,subSystem(i)),'r
ec1')))), 'xticklabel',regexprep(model.rxns(ID(contains(findRxnsFromSubSyste
m(model,subSystem(i)),'rec2'))),'\\[[^\\]]*\\'],''))
% set(gca,'XTickLabelRotation',60, 'FontSize',12)
% title('Gene expression in', char(subSystem(i)))
xlabel('rxn ID', 'FontSize',14,'FontWeight','bold');
ylabel('umol/gDWh', 'FontSize',14,'FontWeight','bold');

subplot(4,2,5)
bar(solution2.v(ID(idxgeneWeight)),1)
legend('mesnhFlux-eFBA(mass)', 'FontSize',12)
xlabel('rxn ID', 'FontSize',14,'FontWeight','bold');
ylabel('umol/gDWh', 'FontSize',14,'FontWeight','bold');

subplot(4,2,6)
bar(model2.cf(ID(idxgeneWeight)))
legend('cf = cr(mass)', 'FontSize',12)
xlabel('rxn ID', 'FontSize',14,'FontWeight','bold');
ylabel('umol/gDWh', 'FontSize',14,'FontWeight','bold');

subplot(4,2,7)
bar(solution3.v(ID(idxgeneWeight)),1)
legend('mesnhFlux-eFBA(mass + gene)', 'FontSize',12)

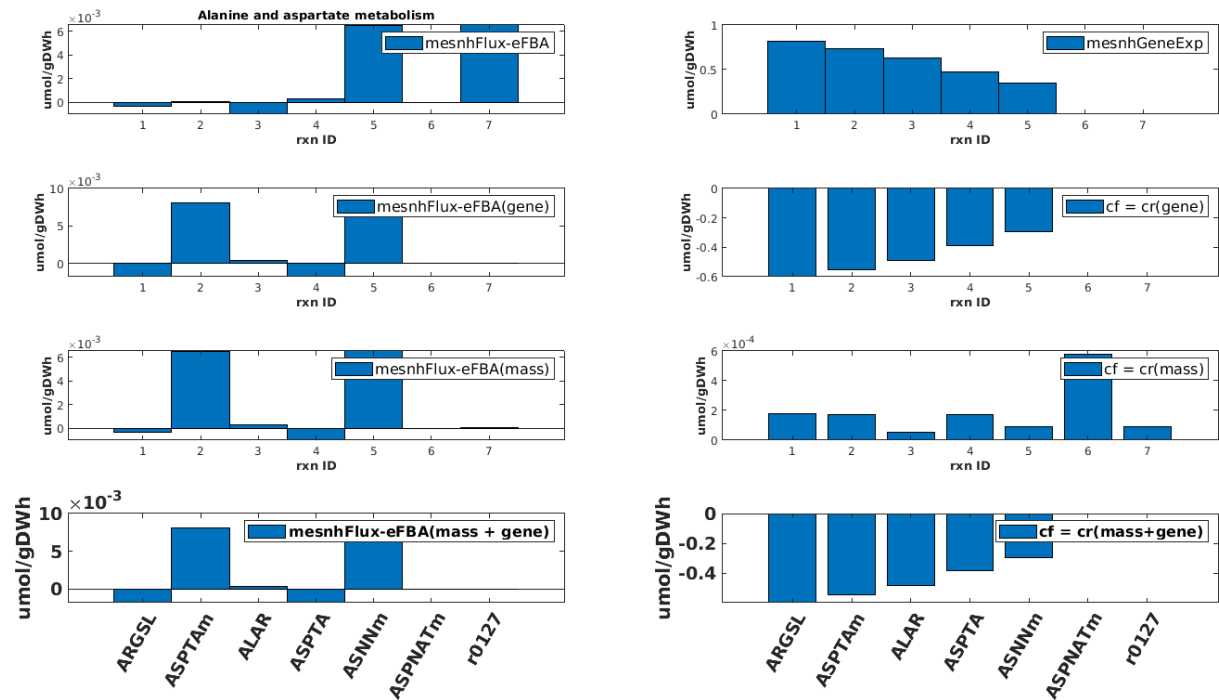
```

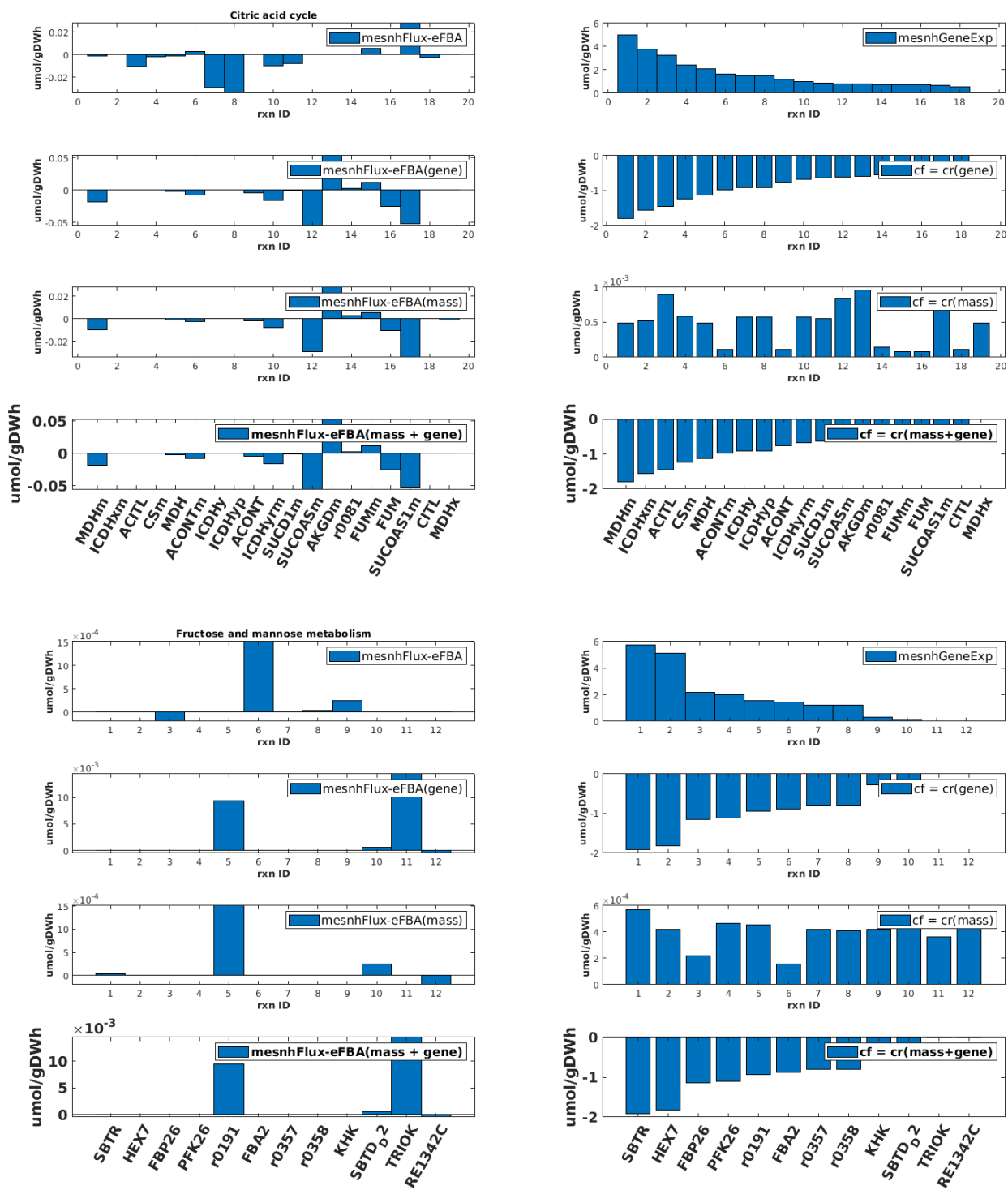
```

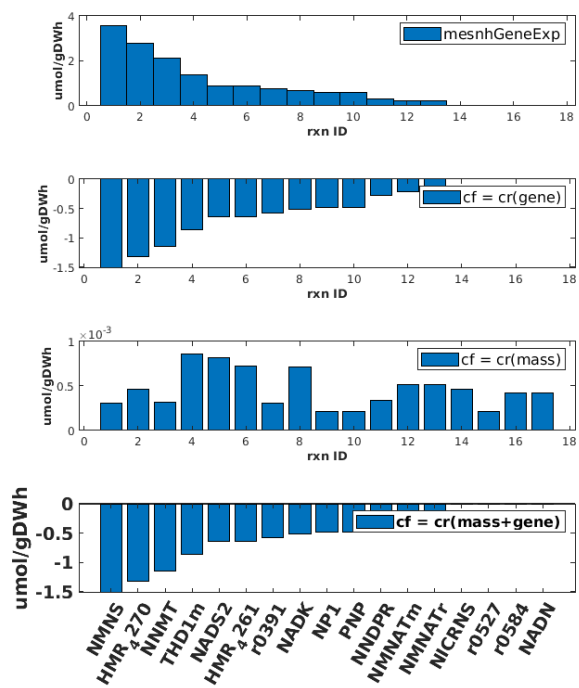
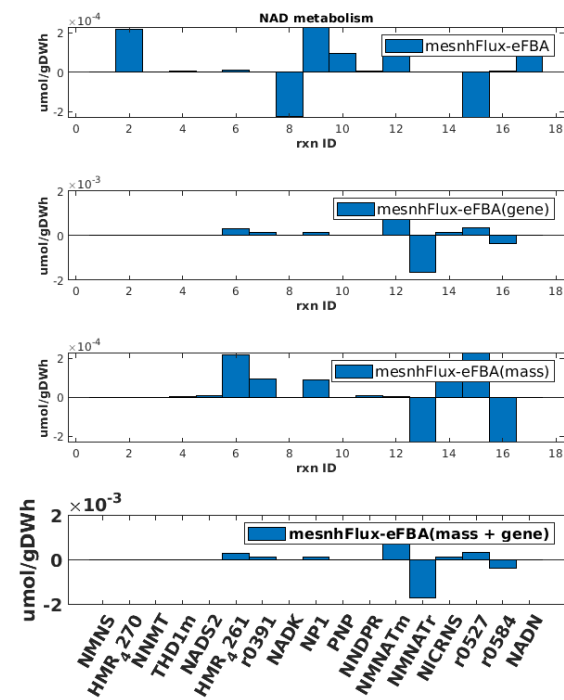
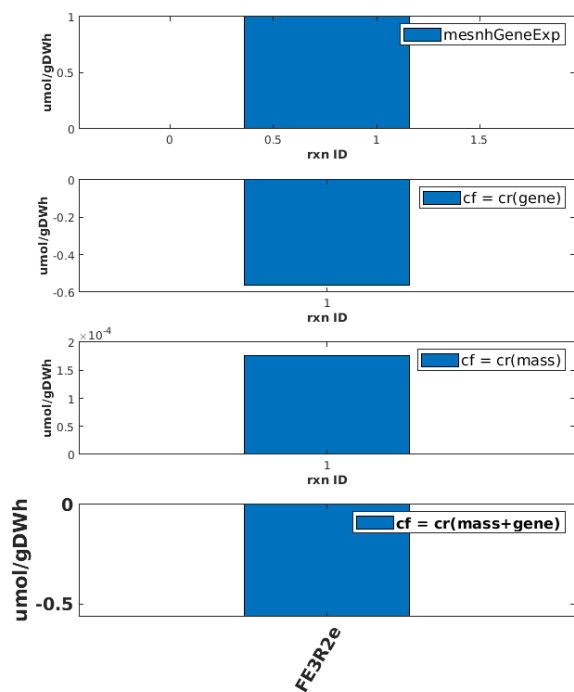
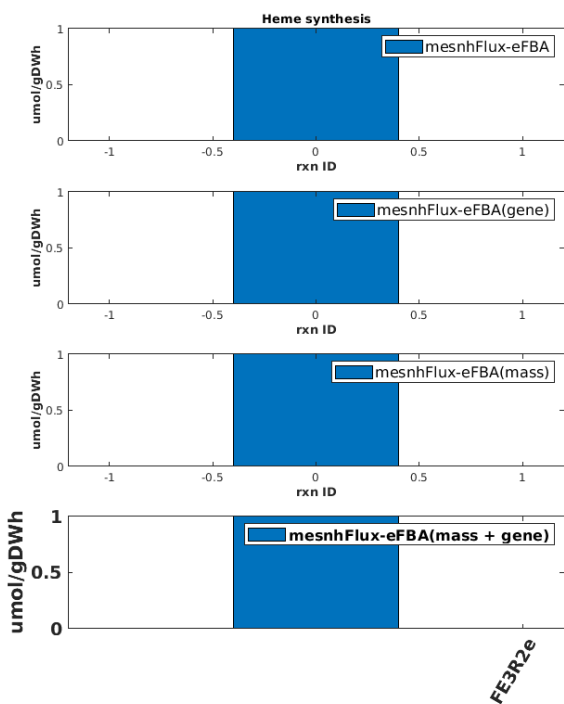
set(gca,'XTick',
[1:length(model1.rxns(ID))],'xticklabel',regexprep(model1.rxns(ID(idxgeneWeigh
ht)),'\[[^\]]*\'],''))
set(gca,'XTickLabelRotation',60,'FontSize',14,'FontWeight','bold')
ylabel('umol/gDWh','FontSize',14,'FontWeight','bold');

subplot(4,2,8)
bar(model3.cf(ID(idxgeneWeight)))
legend('cf = cr(mass+gene)','FontSize',12)
set(gca,'XTick',
[1:length(model1.rxns(ID))],'xticklabel',regexprep(model1.rxns(ID(idxgeneWeigh
ht)),'\[[^\]]*\'],''))
set(gca,'XTickLabelRotation',60,'FontSize',14,'FontWeight','bold')
ylabel('umol/gDWh','FontSize',14,'FontWeight','bold');
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
end

```

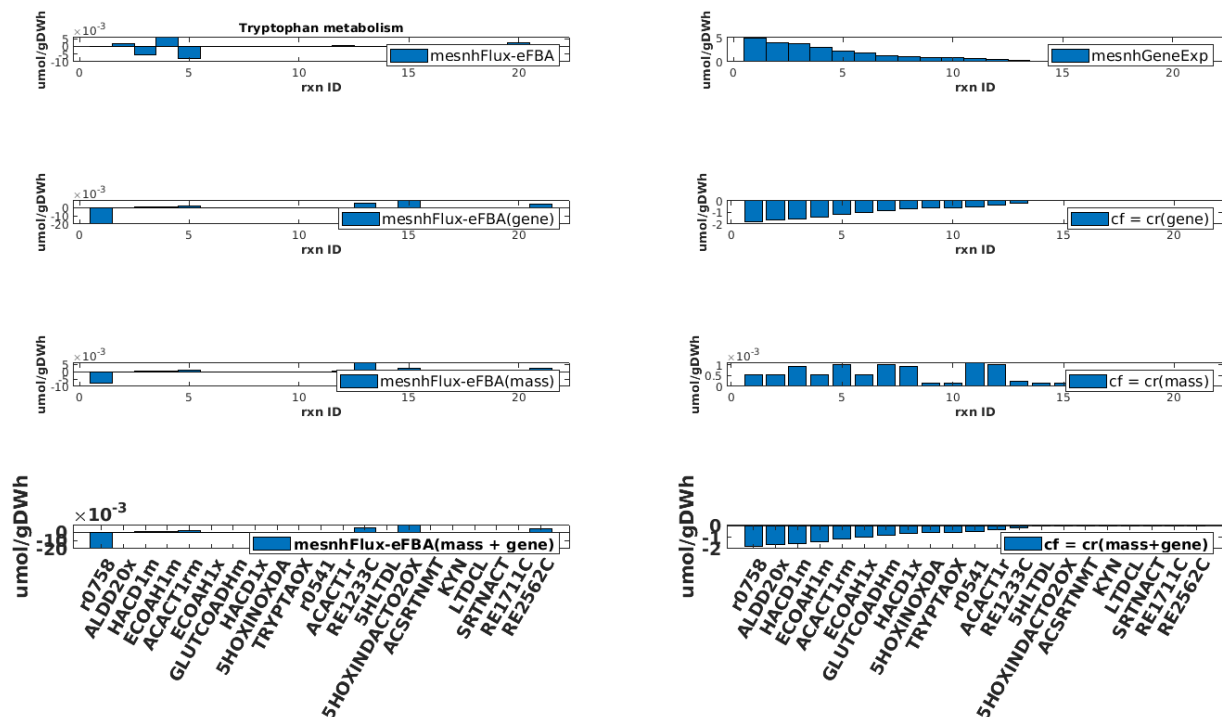












## Acknowledgments

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## REFERENCES

- [1] Fleming, R. M. T., Maes, C. M., Saunders, M. A., Ye, Y., and Palsson, B. O., "A variational principle for computing nonequilibrium fluxes and potentials in genome-scale biochemical networks", *Journal of Theoretical Biology* 292 (2012), pp. 71--77.