

Flux Balance Analysis

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INTRODUCTION

In this practical, the use of Flux Balance Analysis (FBA) is introduced using the E. coli core model, with functions in the COBRA Toolbox v3.0 [2].

Flux balance analysis is a solution to the optimisation problem

$$\begin{aligned} \max \quad & c^T v \\ \text{s.t.} \quad & Sv = b \\ & l \leq v \leq u \end{aligned}$$

where c is a vector of linear objective coefficients, S is an m times n matrix of stoichiometric coefficients for m molecular species involved in n reactions. l and u are n times 1 vectors that are the lower and upper bounds on

the n times 1 variable vector v of reaction rates (fluxes). The optimal objective value is $c^T v^*$ is always unique, but the optimal vector v^* is usually not unique.

In summary, the data is $\{c, S, l, u\}$ and the variable being optimised is v .

TIMING

< 1 hrs

E. coli core model

A map of the E. coli core model is shown in Figure 1.

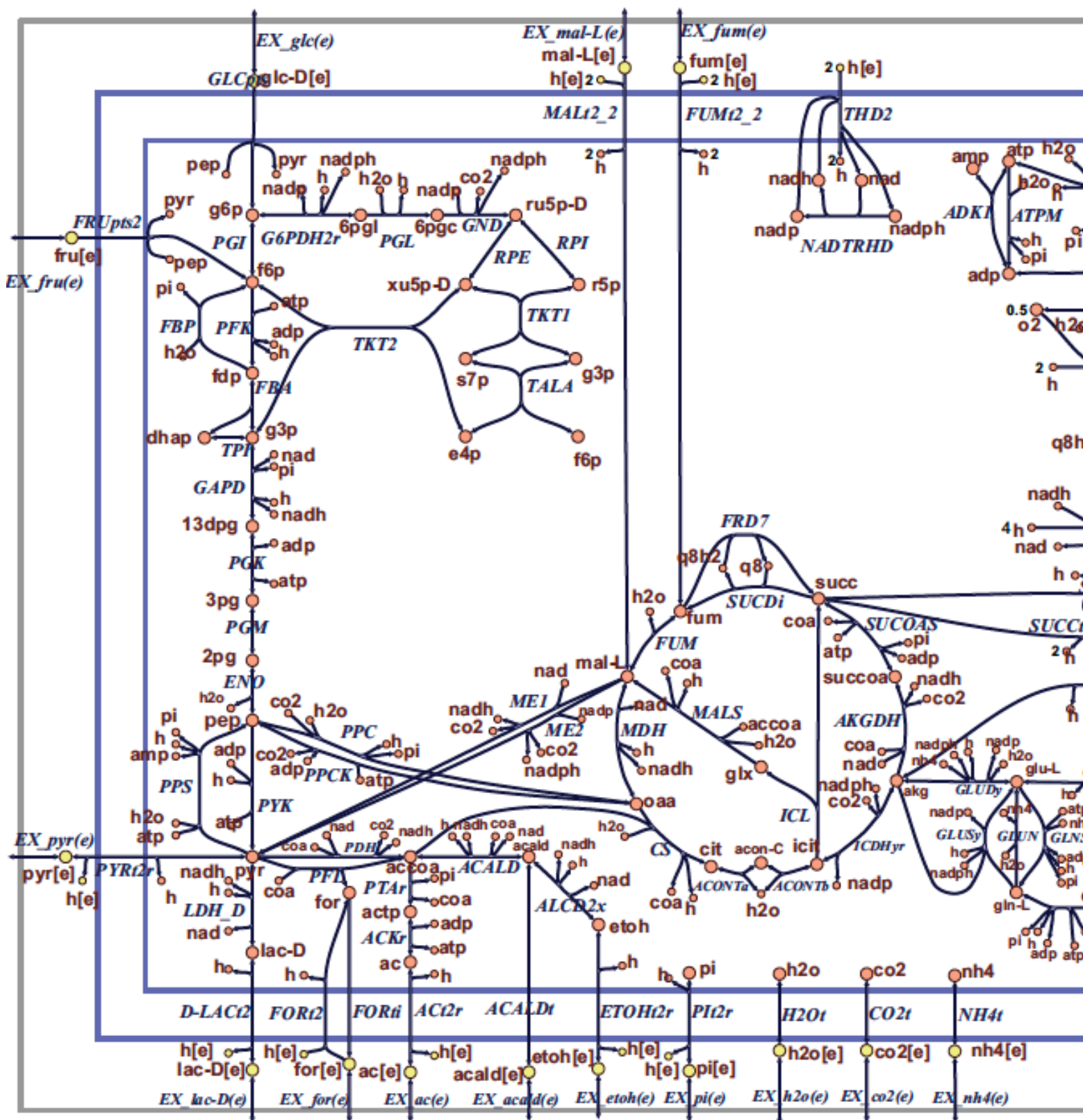


Figure 1 Map of the core *E. coli* metabolic network. Orange circles represent cytosolic metabolites, yellow circles represent extracellular metabolites, and the blue arrows represent reactions. Reaction name abbreviations are uppercase (blue) and metabolite name abbreviations are lowercase (rust colour). This flux map was drawn using SimPheny and edited for clarity with Adobe Illustrator.

MATERIALS - EQUIPMENT SETUP

Please ensure that all the required dependencies (e.g. , `git` and `curl`) of The COBRA Toolbox have been properly installed by following the installation guide [here](#). Please ensure that the COBRA Toolbox has been initialised (`tutorial_initialize.mlx`) and verify that the pre-packaged LP and QP solvers are functional (`tutorial_verify.mlx`).

PROCEDURE


























Load E. coli core model

The most appropriate way to load a model into The COBRA Toolbox is to use the `readCbModel` function.

```
fileName = 'ecoli_core_model.mat';  
if ~exist('modelOri','var')  
    modelOri = readCbModel(fileName);  
end  
%backward compatibility with primer requires relaxation of upper bound on  
%ATPM  
modelOri = changeRxnBounds(modelOri,'ATPM',1000,'u');  
model = modelOri;
```

model

1x1 struct with 28 fields

Field ▲	Value	Size
 S	72x95 sparse do...	72x95
 mets	72x1 cell	72x1
 b	72x1 double	72x1
 csense	72x1 char	72x1
 rxns	95x1 cell	95x1
 lb	95x1 double	95x1
 ub	95x1 double	95x1
 c	95x1 double	95x1
 osenseStr	'max'	1x3
 genes	137x1 cell	137x1
 rules	95x1 cell	95x1
 metCharges	72x1 int32	72x1
 metFormulas	72x1 cell	72x1
 metNames	72x1 cell	72x1
 metInChIString	72x1 cell	72x1
 metKEGGID	72x1 cell	72x1
 metChEBIID	72x1 cell	72x1
 metPubChemID	72x1 cell	72x1
 grRules	95x1 cell	95x1
 rxnGeneMat	95x137 sparse d...	95x137
 rxnConfidence...	95x1 double	95x1
 rxnNames	95x1 cell	95x1
 rxnNotes	95x1 cell	95x1
 rxnECNumbers	95x1 cell	95x1
 rxnReferences	95x1 cell	95x1
subSystems	95x1 cell	95x1

The meaning of each field in a standard model is defined in the [standard COBRA model field definition](#).

In general, the following fields should always be present:

- **S**, the stoichiometric matrix
- **mets**, the identifiers of the metabolites
- **b**, Accumulation (positive) or depletion (negative) of the corresponding metabolites. 0 Indicates no concentration change.
- **csense**, indicator whether the b vector is a lower bound ('G'), upper bound ('L'), or hard constraint 'E' for the metabolites.
- **rxns**, the identifiers of the reactions
- **lb**, the lower bounds of the reactions
- **ub**, the upper bounds of the reactions
- **c**, the linear objective
- **genes**, the list of genes in your model
- **rules**, the Gene-protein-reaction rules in a computer readable format present in your model.
- **osenseStr**, the objective sense either 'max' for maximisation or 'min' for minimisation

Checking the non-trivial constraints on a model

What are the default constraints on the model?

Hint: `printConstraints`

Example 1: Calculating growth rates

Growth of *E. coli* on glucose can be simulated under aerobic conditions.

What is the growth rate of *E. coli* on glucose (uptake rate = 18.5 mmol/gDW/h) under aerobic conditions?

Hint: `changeRxnBounds`, `changeObjective`, `optimizeCbModel`, `printFluxVector`

What are the main fields to check in the `FBA solution` structure?

Hint: `help optimizeCbModel`

What does `FBA solution.stat` mean?

Example 2: Display an optimal flux vector on a metabolic map

Which reactions/pathways are in use (look at the flux vector and flux map)?

Hint: `drawFlux`

```
if exist('FBA solution','var')
```

```

outputFormatOK = changeCbMapOutput('matlab');
map=readCbMap('ecoli_core_map');
options.zeroFluxWidth = 0.1;
options.rxnDirMultiplier = 10;
drawFlux(map, model, FBAsolution.v, options);
end

```

Example 3: Anerobic growth

Growth of *E. coli* on glucose can be simulated under anaerobic conditions.

What is the optimal growth rate under anaerobic conditions?

Hint: `changeRxnBounds`

What reactions of oxidative phosphorylation are active in anaerobic conditions?

Hint: `printFluxVector` `drawFlux`

Example 3: Growth on alternate substrates

Just as FBA was used to calculate growth rates of *E. coli* on glucose, it can also be used to simulate growth on other substrates. The core *E. coli* model contains exchange reactions for 13 different organic compounds, each of which can be used as the sole carbon source under aerobic conditions.

What is the growth rate of *E. coli* on succinate?

Hint: `changeRxnBounds`

REFERENCES

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