SBML Level 3 Package Flux Balance Constraints

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Constraint based modelling

> **Assumes a steady state**

> **Optimise a specific property (e.g. biomass)**

Maximize
biomass

Subject to
NJ = 0

Bounds
$0 \;<= J_{irrev} \;<= inf$
$-inf \;<= J_{rev} \;<= inf$
$l.b <= Jn \;<= u.b$
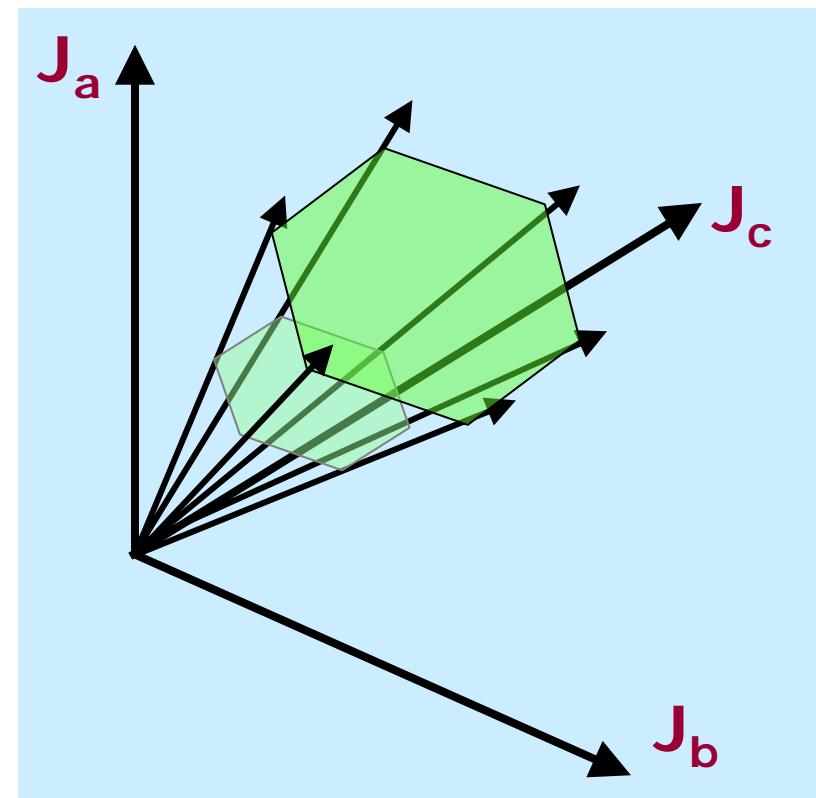
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Glucose

Eschericia coli
1000+ reactions

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Genome scale models

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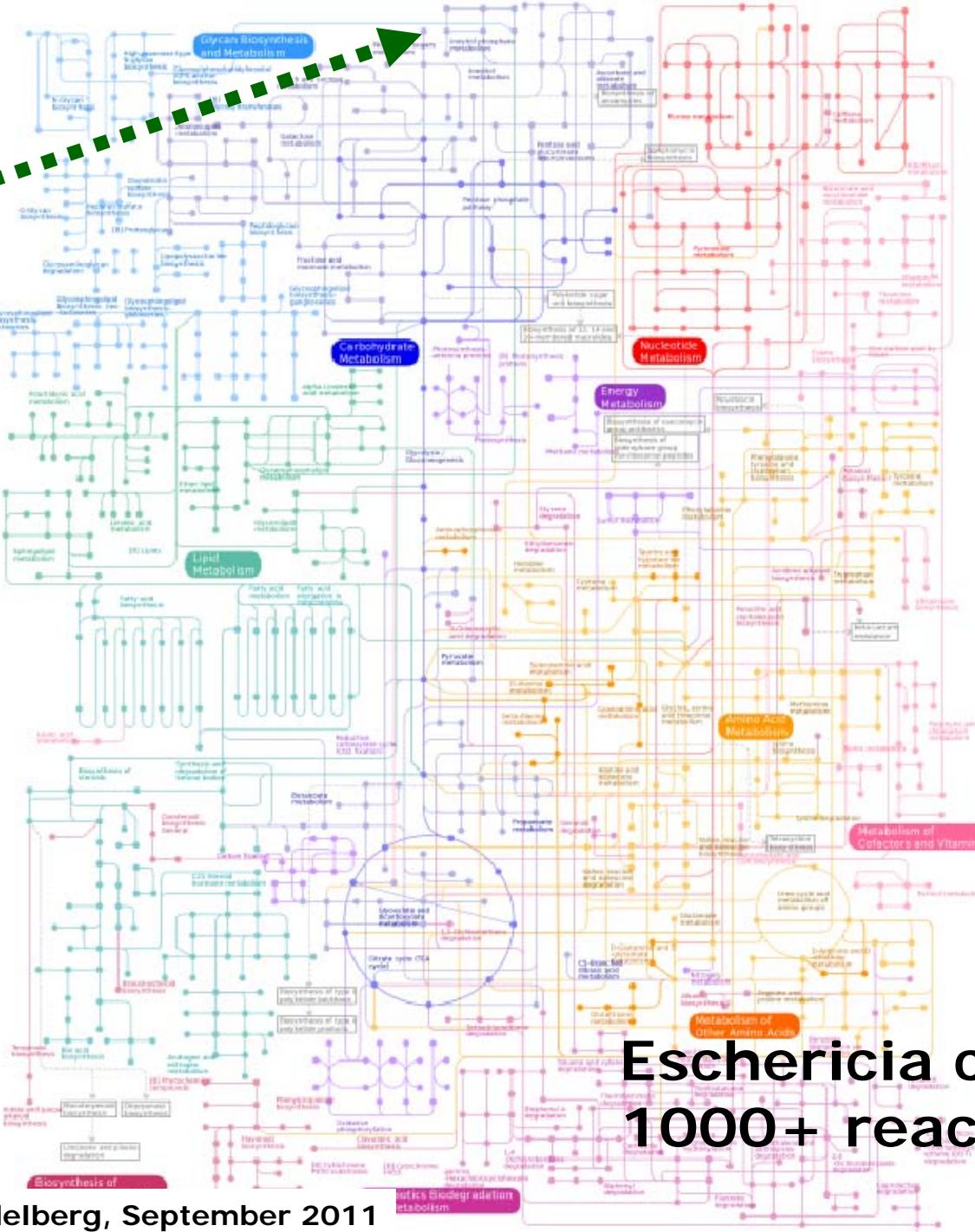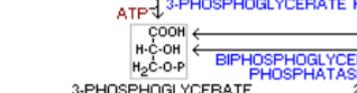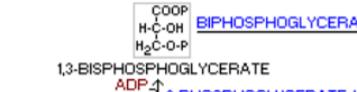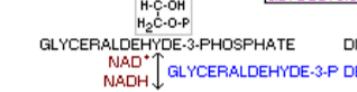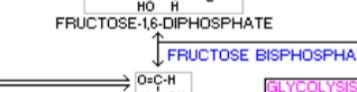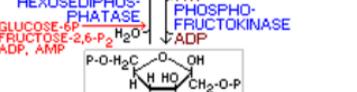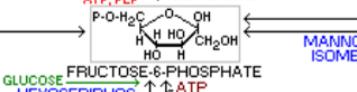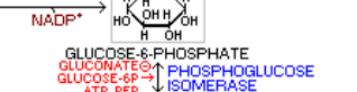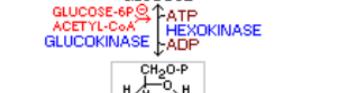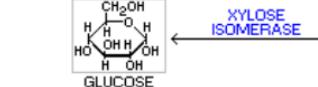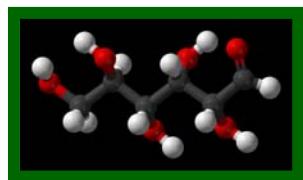
BiGG/COBRA/SEED

> **tool specific SBML L2 dialects**

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Flux Balance Constraints proposal

The outcome of this vote is accept because more than 50% of the votes cast were cast for 'accept'. The following graph presents the results:

Accepted!
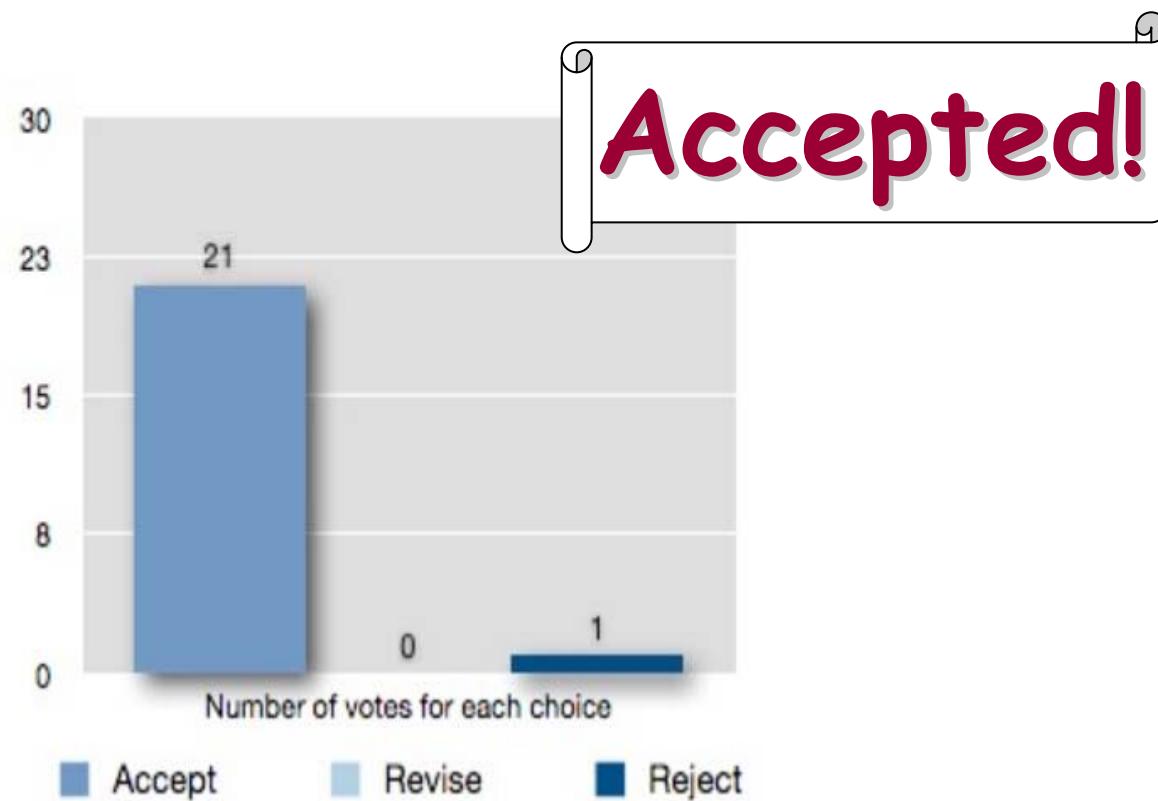
Olivier & Bergmann (2011) SBML Level 3 Package Proposal: Flux

http://sbml.org/Community/Wiki/SBML_Level_3_Proposals/Flux_Constraints

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Flux Bounds

listOfFluxBounds

fluxBound

0

*
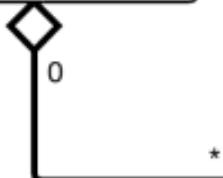
id : SId
reaction : SIdRef
operation : string
value : double

Objectives

listOfObjectives

activeObjective : SIdRef

0

*
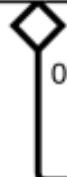
objective

id : SId
type : string

1   1

listOfFluxes

1
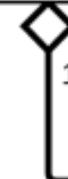
fluxObjective

*

reaction : SIdRef
coefficient : double

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Objectives

```xml
<fbc:listOfObjectives
   fbc:activeObjective="ObjFun1">

 <fbc:objective fbc:id="ObjFun1"
   fbc:type="maximize">

   <fbc:listOfFluxes>

    <fbc:fluxObjective fbc:reaction="PFK"
       fbc:coefficient="1"/>

   </fbc:listOfFluxes>

 </fbc:objective>
</fbc:listOfObjectives>
```

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Flux Bounds

```
<fbc:listOfFluxBounds>

<fbc:fluxBound fbc:id="fb1" fbc:reaction="Glc_i"
  fbc:operation="lessEqual" fbc:value="10"/>

</fbc:listOfFluxBounds>
```

Implementation

Operations
lessEqual, greaterEqual, less, greater, equal

Undefined upper or lower flux bounds
Assumed to be unbound, (i.e. infinite bounds)

Explicit ∞
"Infinity"

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```
<species id="glc" name="D-Glucose"
 compartment="Cytosol"
 fbc:chemicalFormula="??????"
 fbc:charge="0"/>
```

Chemical Formula

Molecular Formula
$C6H12O6$

SMILES
C([C@@H]1[C@H]([C@@H]([C@H]([C@H](O1)O)O)O)O)O

InChI
1S/C6H12O6/c7-1-2-3(8)4(9)5(10)6(11)12-2/h2-11H,1H2/t2-,3-,4+,5-,6+/m1/s1

Chemical Formula

➢ **Chemical Formula is for balancing, not a full annotation!**

➢ **Existing standard: the Hill system**

  ➢ **write carbon and hydrogen atoms first then all remaining atoms in alphabetical order**

  ➢ **if there is no carbon, write all atoms in alphabetical order**

➢ **Pairs of atom and optional number**

➢ **C6H12O6, BrH, BrI, CH3I, C2H5Br, H2O4S, CsS**

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CWI Gene association

```
<listOfGeneAssociations>

    <geneAssociation id="ga3" reaction="R_PFK">
        <association>
            <and>
                <gene>b3916</gene>
                <gene>b1723</gene>
            </and>
        </association>
    </geneAssociation>

</listOfGeneAssociations>
```

Not part of this proposal, some form of annotation ...

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Available as a libSBML 5 module
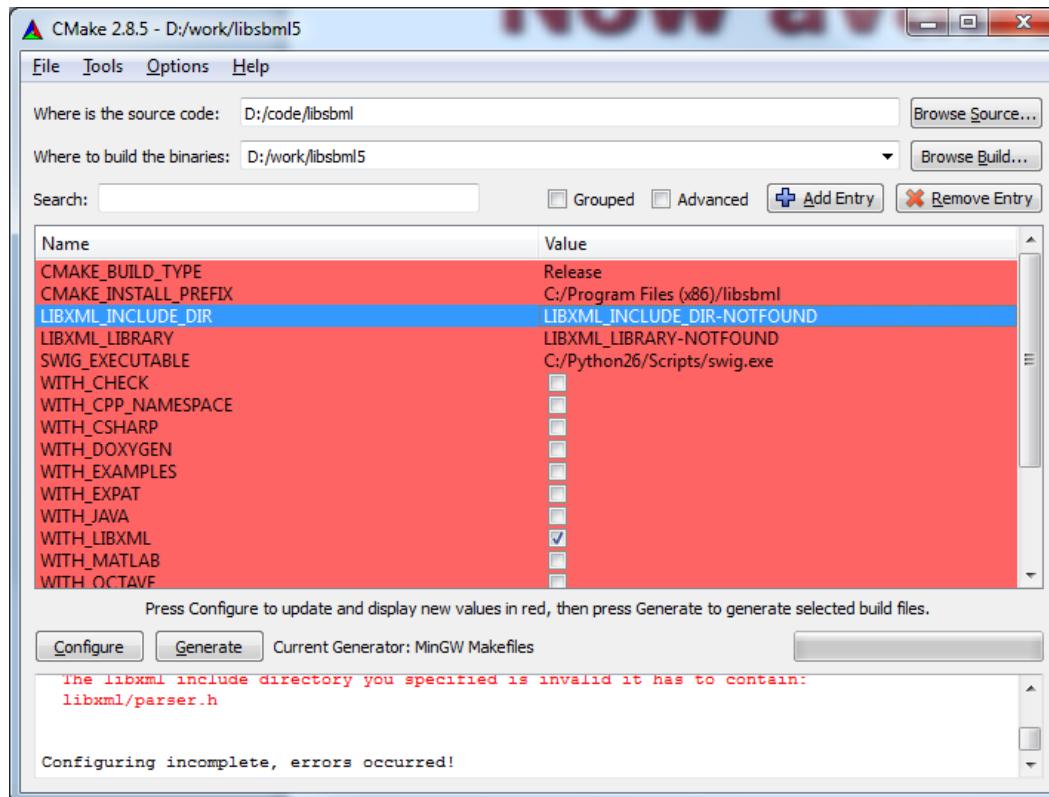
Easy to incorporate into the libSBML 5 source tree using CMAKE

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Windows binaries

For more information about the Flux Balance Constraints package, please have a look at the proposal page. On that page you find a detailed description about the current proposal, as well as links to examples.

Below you find full installers (including C#, Java, Perl and Python bindings) as well as python bindings for specific versions of Python.

- libSBML 5.0.0 + FBC full installer (Win32)
- libSBML 5.0.0 + FBC full installer (Win64)
- libSBML 5.0.0 + FBC python 2.5 (Win32)
- libSBML 5.0.0 + FBC python 2.6 (Win64)

http://frank-fbergmann.blogspot.com/2011/04/flux-balance-constraints-for-libsbml.html

Implementations

Systems Biology WorkBench (**www.sys-bio.org**)

■ **PySCeS-CBM** (**pysces.sourceforge.net/cbm**)

PySCeS
Python Simulator for Cellular Systems

■ **FAME** (**f-a-m-e.org**)

FAME

Available soon, online converters:
COBRA, SEED → SBML L3 FBC

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CWI Package Working Group
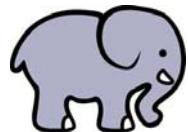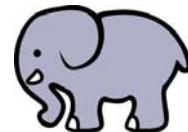
Name	Label	Description	PWG list	Prop. Stat.	Spec. Stat.	libSBML
Level 3 Core	`core`	The core portion of SBML Level 3.	**sbml-discuss** 🔗	🎖	✅	☰
Layout	`layout`	Support for storing the spatial topology of a model's network diagram. Adjunct to the *render* package, below.	**sbml-layout** 🔗	🎖	☀	☰
Flux Balance Constraints	`fbc`	Support for constraint-based (a.k.a. steady-state) models.	**sbml-flux** 🔗	🎖	☀	☰

Join the FBC Package Working Group!

http://lists.sourceforge.net/lists/listinfo/sbml-flux

Issues that require attention:

➢ **Implementation & adoption**

➢ **Annotation (e.g. using "annot")**

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Thanks

CWI

vrije Universiteit   amsterdam

SBML community

- ➢ **Frank Bergmann**
- ➢ **Herbert Sauro**
- ➢ **Neil Swainston**
- ➢ **Kieran Smallbone**
- ➢ **Mike Hucka**
- ➢ **Nicolas Le Novere**
- ➢ **and others …**

CWI/VU

- ➢ **Joost Boele**
- ➢ **Frank Bruggeman**
- ➢ **Bas Teusink**

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NWO
Netherlands Organisation for Scientific Research