SBML Level 3 Package Flux Balance Constraints

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![CWI] # Constraint based modelling

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

Maximize
 biomass

Subject to
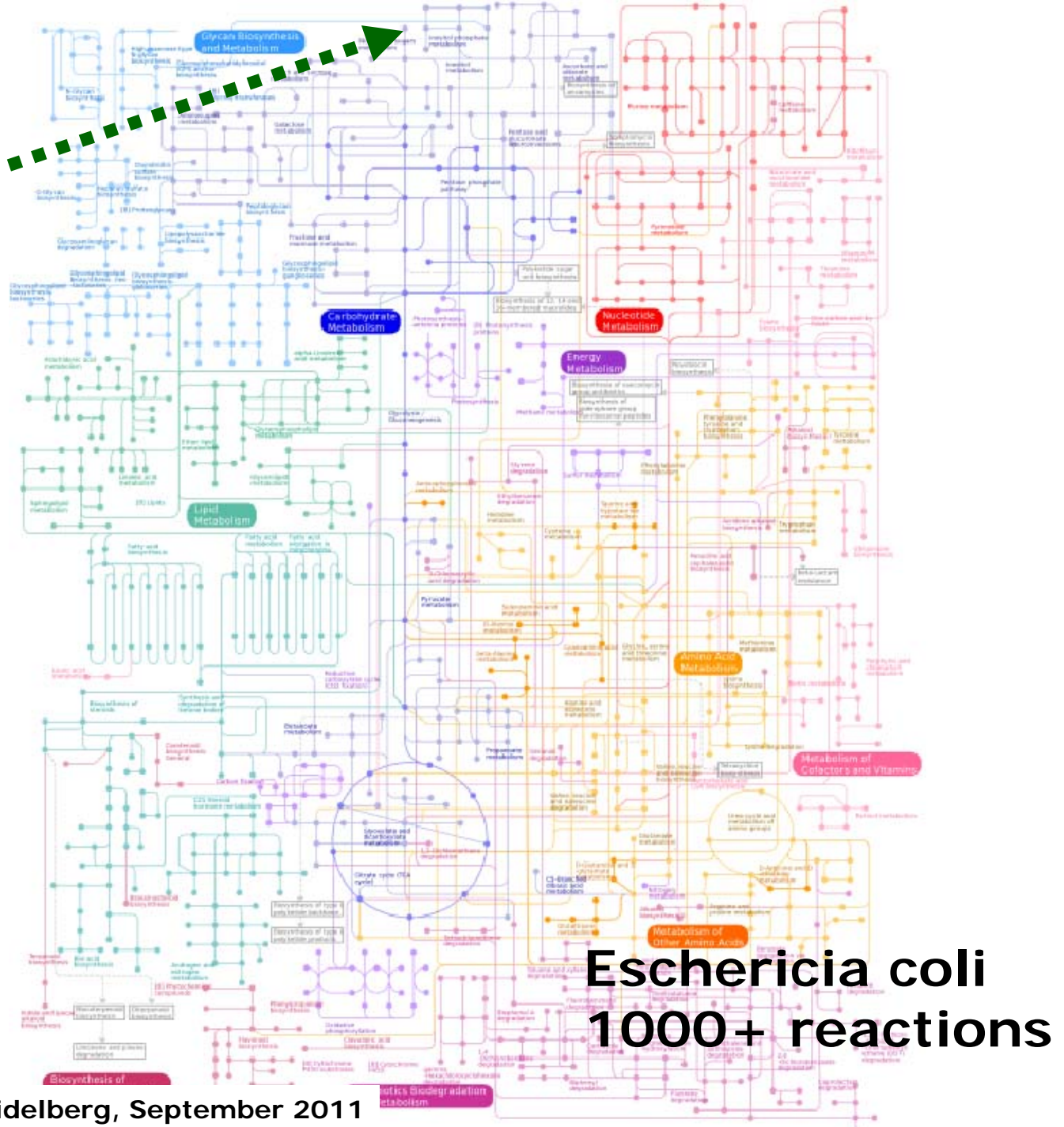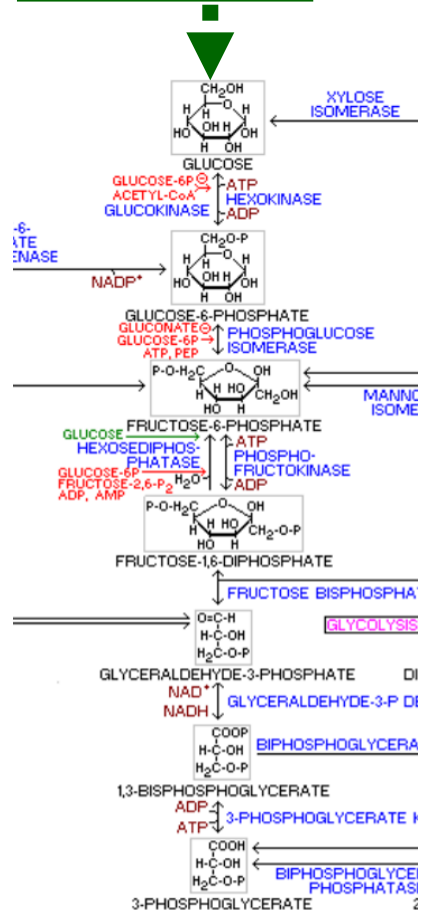 NJ = 0

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

J_a

J_c

J_b
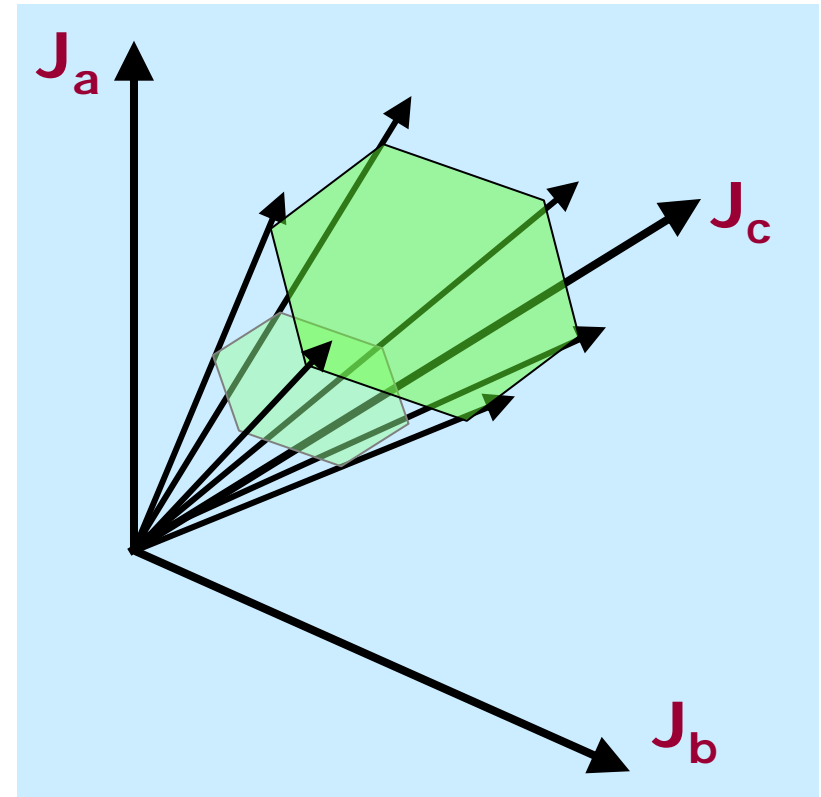
Glucose
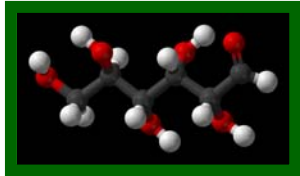
Eschericia coli

1000+ reactions

Genome scale models

BiGG/COBRA/SEED

> tool specific **SBML** L2 dialects

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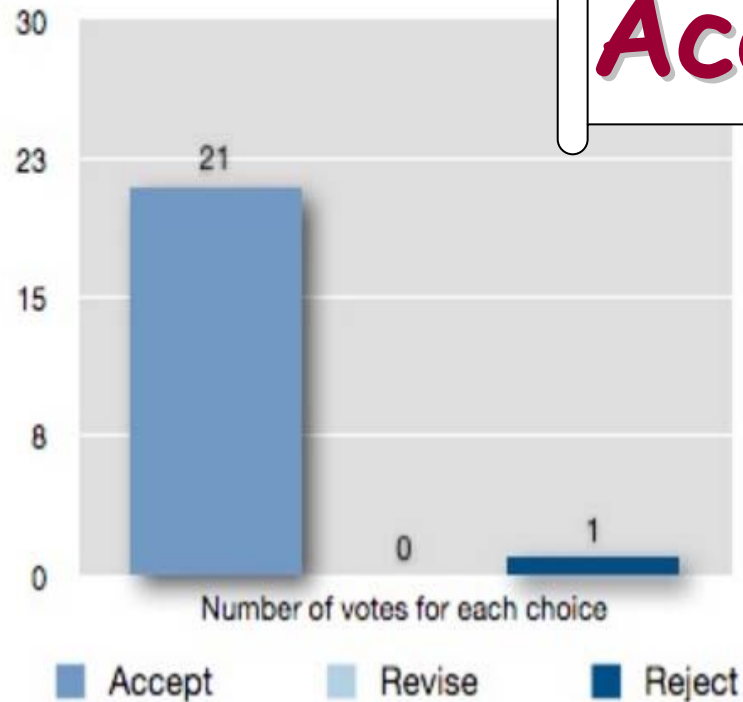
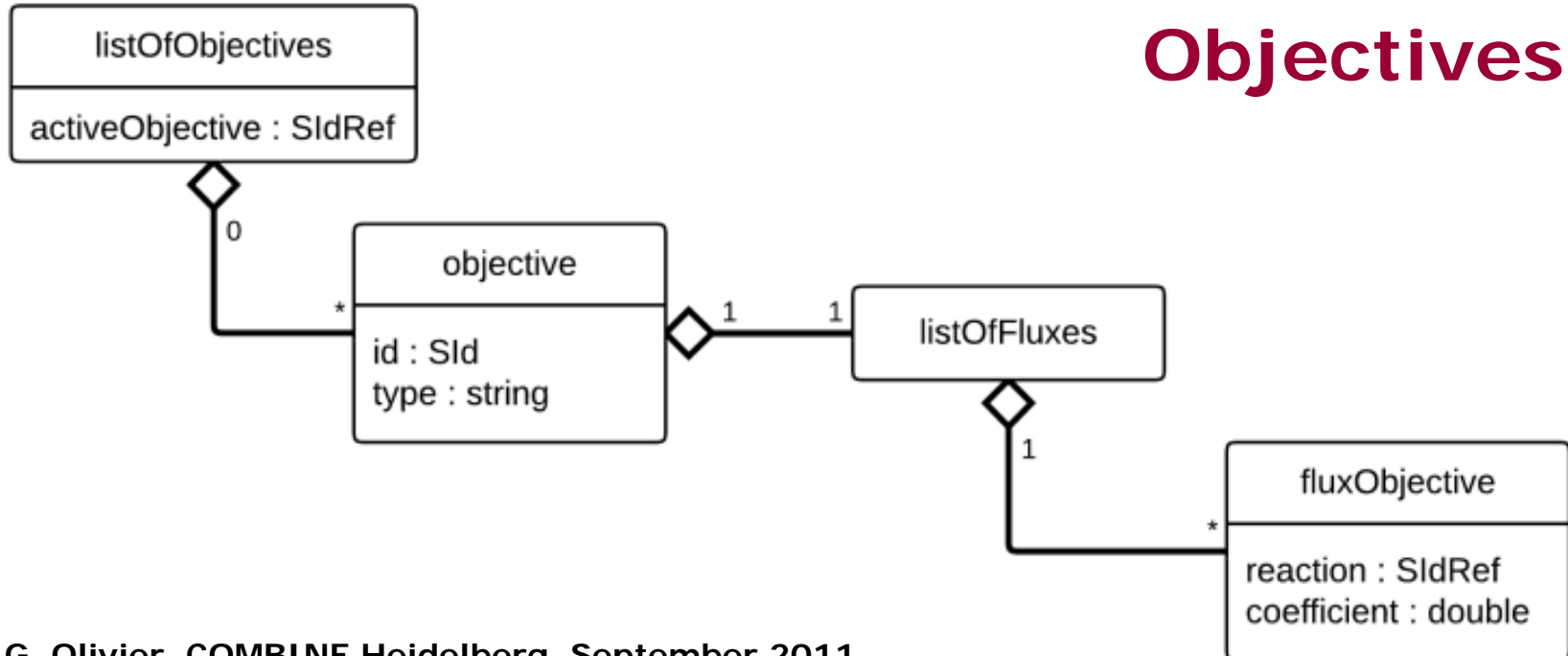Olivier & Bergmann (2011) SBML Level 3 Package Proposal: Flux

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

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FBC Package overview

Flux Bounds
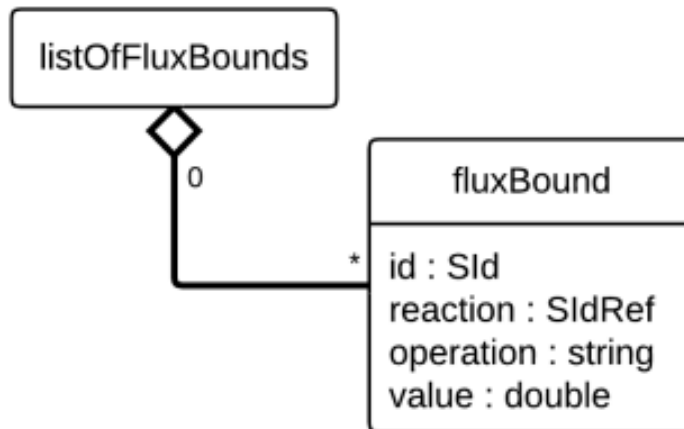
Objectives

Objectives

```
<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>
```

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"

```
<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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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 …

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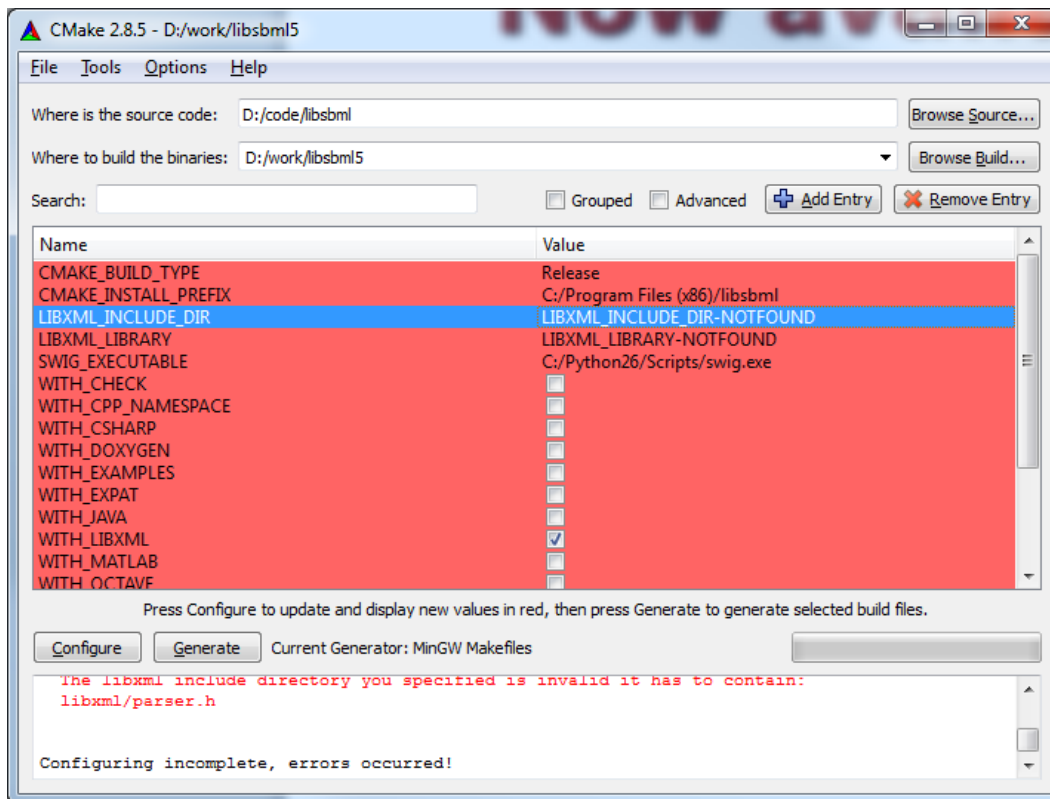
Easy to incorporate into the libSBML 5 source tree using CMAKE

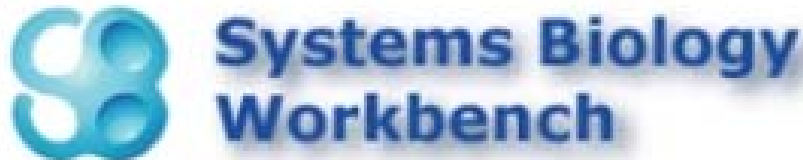Brett G. Olivier, COMBINE Heidelberg, September 2011

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

CWI **Implementations**

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

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

- **FAME** (**f-a-m-e.org**)

  FAME

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

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Package Working Group

CWI

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

SBML community
- Frank Bergmann
- Herbert Sauro
- Neil Swainston
- Kieran Smallbone
- Mike Hucka
- Nicolas Le Novere
- and others ...

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- Frank Bruggeman
- Bas Teusink

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NWO
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