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

\[ \text{biomass} \]

Subject to

\[ NJ = 0 \]

Bounds

\[
\begin{align*}
0 & \leq J_{irrev} \leq \infty \\
-\infty & \leq J_{rev} \leq \infty \\
l.b & \leq J_n \leq u.b
\end{align*}
\]
Eschericia coli
1000+ reactions
Genome scale models

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:

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

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<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

<\texttt{fbc:}listOfFluxBounds>

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

</\texttt{fbc:}listOfFluxBounds>

Implementation

Operations

lessEqual, greaterEqual, less, greater, equal

Undefined upper or lower flux bounds

Assumed to be unbound, (i.e. infinite bounds)

Explicit \(\infty\), "Infinity"

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Extended species

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

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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

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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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<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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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)**


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Implementations

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

- PySCeS-CBM (pysces.sourceforge.net/cbm)
- FAME (f-a-m-e.org)

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

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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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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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