

# **SBML Level 3 Package: Flux Balance Constraints version 2**

**Brett G. Olivier<sup>1,2,3</sup> and Frank T. Bergmann<sup>2,3</sup>**

<sup>1</sup>Systems Bioinformatics, AIMMS, Vrije Universiteit Amsterdam, The Netherlands

<sup>2</sup>Modelling of Biol. Processes, BioQUANT/COS, Heidelberg University, Germany

<sup>3</sup>Department of Computing and Mathematical Sciences, California Institute of  
Technology, Pasadena, CA, USA

## **Abstract**

Constraint-based modeling is a well established modeling methodology used to analyze and study biological networks on both a medium and genome scale. Due to their large size and complexity such steady-state flux models are, typically, analyzed using constraint-based optimization techniques, for example, Flux Balance Analysis (FBA).

The Flux Balance Constraints (FBC) Package extends SBML Level 3 and provides a standardized format for the encoding, exchange and annotation of constraint-based models. It includes support for modeling concepts such as objective functions, flux bounds and model component annotation that facilitates reaction balancing. Version two expands on the original release by adding official support for encoding gene-protein associations and their associated elements. In addition to providing the elements necessary to unambiguously encode existing constraint-based models, the FBC Package provides an open platform facilitating the conti-

nued, cross-community development of an interoperable, constraint-based model encoding format.