

SBML Level 3 Package: Flux Balance Constraints version 2

Brett G. Olivier^{1,2,3} and Frank T. Bergmann^{2,3}

¹Systems Bioinformatics, AIMMS, Vrije Universiteit Amsterdam, The Netherlands

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

³Department 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 [1] 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.

Keywords: SBML, constraint-based modeling, standards

References

- [1] Olivier BG, Bergmann FT. The Systems Biology Markup Language (SBML) Level 3 package: Flux Balance Constraints. *J Integr Bioinform.* 2015;12(2):660–690.