Towards an automatic conversion from SBML core to SBML qual
Athénaïs Vaginay, Malika Smail-Tabbone, Taha Boukhobza

To cite this version:
Athénaïs Vaginay, Malika Smail-Tabbone, Taha Boukhobza. Towards an automatic conversion from SBML core to SBML qual. Journées Ouvertes Biologie, Informatique et Mathématiques, JOBIM 2019, Jul 2019, Nantes, France. hal-02407443

HAL Id: hal-02407443
https://hal.archives-ouvertes.fr/hal-02407443
Submitted on 12 Dec 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
Towards an automatic conversion from SBML core to SBML qual

Athénaïs Vaginay(1, 2), Malika Smail-Tabbone(1), Taha Boukhobza(2)
(1)LORIA (Université de Lorraine, CNRS, Inria); (2)CRAN (Université de Lorraine, CNRS)
Contact: <athenais.vaginay@inria.fr>

Abstract: The SBML format is the de facto standard to encode biological model in different formalisms. It was first developed to encode quantitative models like Differentials Equations (DEs), but the current release allows the definition of packages extending the core format. One of these packages, named qual, encodes qualitative models like Boolean Networks (BNs). To the best of our knowledge, there is no automatic pipeline to convert a quantitative model encoded in SBML core into a qualitative model encoded with the qual package. Here, we explore such a pipeline on a relatively simple system: the cell division of fission yeast, which has been studied both with a set DEs [1] and with a BN [2]. Our approach consists in extracting the model topology from the set of DEs and in solving them numerically in order to retrieve the time course data of species' concentrations on which we apply a discretization. Then we extract from these data a scarce state transition table. We are currently investigating ways to synthesize a BN fitting both topology knowledge and state transitions.

References: