SBML Model Report

Model name: "Chaouiya2013 - EGF and TNFalpha mediated signalling pathway"

May 5, 2016

1 General Overview

This is a document in SBML Level 3 Version 1 format. This model was created by the following two authors: Vijayalakshmi Chelliah[1] and Thomas Cokelaer[2] at December twelveth 2014 at 5:21 p. m. and last time modified at January 21st 2015 at 11:01 a. m. Table 1 gives an overview of the quantities of all components of this model.

Table 1: Number of components in this model, which are described in the following sections.

Element	Quantity	Element	Quantity
compartment types	0	compartments	1
species types	0	species	0
events	0	constraints	0
reactions	0	function definitions	0
global parameters	0	unit definitions	0
rules	0	initial assignments	0

Model Notes

Chaouiya2013 - EGF and TNFalpha mediated signalling pathway

This model is described in the article:SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools.Chaouiya C, Brenguier D, Keating SM, Naldi A, van Iersel MP, Rodriguez N, Drger A,

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Bchel F, Cokelaer T, Kowal B, Wicks B, Gonalves E, Dorier J, Page M, Monteiro PT, von Kamp A, Xenarios I, de Jong H, Hucka M, Klamt S, Thieffry D, Le Novre N, Saez-Rodriguez J, Helikar T.BMC Syst Biol 2013; 7: 135

Abstract:

BACKGROUND: Qualitative frameworks, especially those based on the logical discrete formalism, are increasingly used to model regulatory and signalling networks. A major advantage of these frameworks is that they do not require precise quantitative data, and that they are well-suited for studies of large networks. While numerous groups have developed specific computational tools that provide original methods to analyse qualitative models, a standard format to exchange qualitative models has been missing. RESULTS: We present the Systems Biology Markup Language (SBML) Qualitative Models Package („qual„), an extension of the SBML Level 3 standard designed for computer representation of qualitative models of biological networks. We demonstrate the interoperability of models via SBML qual through the analysis of a specific signalling network by three independent software tools. Furthermore, the collective effort to define the SBML qual format paved the way for the development of LogicalModel, an open-source model library, which will facilitate the adoption of the format as well as the collaborative development of algorithms to analyse qualitative models. CONCLUSIONS: SBML qual allows the exchange of qualitative models among a number of complementary software tools. SBML qual has the potential to promote collaborative work on the development of novel computational approaches, as well as on the specification and the analysis of comprehensive qualitative models of regulatory and signalling networks.

This model is hosted on BioModels Database and identified by: BIOMD0000000562.

To cite BioModels Database, please use: BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models.

2 Unit Definitions

This is an overview of five unit definitions which are all predefined by SBML and not mentioned in the model.

2.1 Unit `substance`

Notes Mole is the predefined SBML unit for `substance`.

Definition mol

2.2 Unit `volume`

Notes Litre is the predefined SBML unit for `volume`.

Definition l

Produced by SBML2LATEX

2.3 Unit `area`

Notes Square metre is the predefined SBML unit for `area` since SBML Level 2 Version 1.

Definition m^2

2.4 Unit `length`

Notes Metre is the predefined SBML unit for `length` since SBML Level 2 Version 1.

Definition m

2.5 Unit `time`

Notes Second is the predefined SBML unit for `time`.

Definition s

3 Compartment

This model contains one compartment.

Table 2: Properties of all compartments.

Id	Name	SBO	Spatial Dimensions	Size	Unit	Constant	Outside
main			3	1	litre	☑	

3.1 Compartment `main`

This is a three dimensional compartment with a constant size given in litre.