SBML Model Report

Model name: “Sneppen2009 - Modeling proteasome dynamics in Parkinson’s disease”

May 5, 2016

1 General Overview

This is a document in SBML Level 2 Version 4 format. This model was created by Audald Lloret i Villas[1] at September tenth 2014 at 11:17 a. m. and last time modified at October 30th 2014 at 1:25 p. m. Table 1 shows 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	3
events	0	constraints	0
reactions	0	function definitions	0
global parameters	4	unit definitions	2
rules	3	initial assignments	0

Model Notes

Sneppen2009 - Modeling proteasome dynamics inParkinson’s disease

This model is described in the article:Modeling proteasome dynamics in Parkinson’s disease.Sneppen K, Lizana L, Jensen MH, Pigolotti S, Otzen D.Phys Biol 2009; 6(3): 036005

Abstract:

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In Parkinson's disease (PD), there is evidence that alpha-synuclein (alphaSN) aggregation is coupled to dysfunctional or overburdened protein quality control systems, in particular the ubiquitin-proteasome system. Here, we develop a simple dynamical model for the on-going conflict between alphaSN aggregation and the maintenance of a functional proteasome in the healthy cell, based on the premise that proteasomal activity can be titrated out by mature alphaSN fibrils and their protofilament precursors. In the presence of excess proteasomes the cell easily maintains homeostasis. However, when the ratio between the available proteasome and the alphaSN protofilaments is reduced below a threshold level, we predict a collapse of homeostasis and onset of oscillations in the proteasome concentration. Depleted proteasome opens for accumulation of oligomers. Our analysis suggests that the onset of PD is associated with a proteasome population that becomes occupied in periodic degradation of aggregates. This behavior is found to be the general state of a proteasome/chaperone system under pressure, and suggests new interpretations of other diseases where protein aggregation could stress elements of the protein quality control system.

This model is hosted on BioModels Database and identified by: BIOMD0000000548.

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 of which three are predefined by SBML and not mentioned in the model.

2.1 Unit `volume`

Name volume

Definition ml

2.2 Unit `substance`

Name substance

Definition mmol

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
`Brain`	Brain		3	1	litre	☑	

3.1 Compartment `Brain`

This is a three dimensional compartment with a constant size of one ml.

Name Brain

4 Species

This model contains three species. The boundary condition of three of these species is set to `true` so that these species' amount cannot be changed by any reaction. Section 7 provides further details and the derived rates of change of each species.

Table 3: Properties of each species.

Id	Name	Compartment	Derived Unit	Constant	Boundary Condition
F	F	Brain	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
P	P	Brain	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
C	C	Brain	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑

5 Parameters

This model contains four global parameters.

Table 4: Properties of each parameter.

Id	Name	SBO	Value	Unit	Constant
m	m		25.0		☑
gamma	gamma		1.0		☑
nu	nu		1.0		☑
sigma	sigma		1.0		☑

6 Rules

This is an overview of three rules.

6.1 Rule F

Rule F is a rate rule for species F:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{F} = \frac{\mathrm{m}}{1 + [\mathrm{P}]} - \mathrm{gamma} \cdot [\mathrm{F}] \cdot [\mathrm{P}] \tag{1}$$

6.2 Rule P

Rule P is a rate rule for species P:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{P} = \mathrm{sigma} - [\mathrm{P}] - \mathrm{gamma} \cdot [\mathrm{F}] \cdot [\mathrm{P}] + \mathrm{nu} \cdot [\mathrm{C}] \tag{2}$$

6.3 Rule C

Rule C is a rate rule for species C:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{C} = \mathrm{gamma} \cdot [\mathrm{F}] \cdot [\mathrm{P}] - \mathrm{nu} \cdot [\mathrm{C}] \tag{3}$$

7 Derived Rate Equations

When interpreted as an ordinary differential equation framework, this model implies the following set of equations for the rates of change of each species.

7.1 Species F

Name F

Notes Mature -synuclein fibrils

Initial concentration $135\ \mathrm{mmol} \cdot \mathrm{ml}^{-1}$

Involved in rule F

One rule determines the species' quantity.

7.2 Species P

Name P

Notes Proteasome

Initial concentration $0\ \mathrm{mmol} \cdot \mathrm{ml}^{-1}$

Involved in rule P

One rule determines the species' quantity.

7.3 Species C

Name C

Notes Complex mature -synuclein fibrils - proteasome

Initial concentration $18\ \mathrm{mmol} \cdot \mathrm{ml}^{-1}$

Involved in rule C

One rule determines the species' quantity.

SBML2LaTeX was developed by Andreas Dräger[a], Hannes Planatscher[a], Dieudonné M Wouamba[a], Adrian Schröder[a], Michael Hucka[b], Lukas Endler[c], Martin Golebiewski[d] and Andreas Zell[a]. Please see http://www.ra.cs.uni-tuebingen.de/software/SBML2LaTeX for more information.

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