define@key

SBML Model Report

Model name: "Vazquez2014 - Chemical inhibition from amyloid protein aggregation kinetics"

September 9, 2014

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 July 30th 2014 at 1:46 p. m. and last time modified at September eighth 2014 at 1:27 p. m. Table 1 provides 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	4
events	0	constraints	0
reactions	0	function definitions	0
global parameters	13	unit definitions	1
rules	4	initial assignments	0

Model Notes

Vazquez2014 - Chemical inhibition fromamyloid protein aggregation kinetics

This model is described in the article:Modeling of chemical inhibition from amyloid protein aggregation kinetics.Vzquez JA.BMC Pharmacol Toxicol 2014; 15(1): 9

Abstract:

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BACKGROUNDS: The process of amyloid proteins aggregation causes several human neuropathologies. In some cases, e.g. fibrillar deposits of insulin, the problems are generated in the processes of production and purification of protein and in the pump devices or injectable preparations for diabetics. Experimental kinetics and adequate modelling of chemical inhibition from amyloid aggregation are of practical importance in order to study the viable processing, formulation and storage as well as to predict and optimize the best conditions to reduce the effect of protein nucleation. RESULTS: In this manuscript, experimental data of insulin, A?42 amyloid protein and apomyoglobin fibrillation from recent bibliography were selected to evaluate the capability of a bivariate sigmoid equation to model them. The mathematical functions (logistic combined with Weibull equation) were used in reparameterized form and the effect of inhibitor concentrations on kinetic parameters from logistic equation were perfectly defined and explained. The surfaces of data were accurately described by proposed model and the presented analysis characterized the inhibitory influence on the protein aggregation by several chemicals. Discrimination between true and apparent inhibitors was also confirmed by the bivariate equation. EGCG for insulin (working at pH?=?7.4/T?=?37C) and taiwaniaflavone for A?42 were the compounds studied that shown the greatest inhibition capacity. CONCLUSIONS: An accurate, simple and effective model to investigate the inhibition of chemicals on amyloid protein aggregation has been developed. The equation could be useful for the clear quantification of inhibitor potential of chemicals and rigorous comparison among them.

This model is hosted on BioModels Database and identified by: BIOMD0000000532.

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 four are predefined by SBML and not mentioned in the model.

2.1 Unit `time`

Name time

Definition 3600 s

2.2 Unit `substance`

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

Definition mol

2.3 Unit `volume`

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

Definition l

2.4 Unit `area`

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

Definition m^2

2.5 Unit `length`

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

Definition m

3 Compartment

This model contains one compartment.

Table 2: Properties of all compartments.

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

3.1 Compartment `cell`

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

Name cell

4 Species

This model contains four species. The boundary condition of four 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
`X`	X	`cell`	$\mathrm{mol} \cdot \mathrm{l}^{-1}$	⊟	☑
`Xm`	Xm	`cell`	$\mathrm{mol} \cdot \mathrm{l}^{-1}$	⊟	☑
`Vm`	Vm	`cell`	$\mathrm{mol} \cdot \mathrm{l}^{-1}$	⊟	☑
`Lambda`	Lambda	`cell`	$\mathrm{mol} \cdot \mathrm{l}^{-1}$	⊟	☑

5 Parameters

This model contains 13 global parameters.

Table 4: Properties of each parameter.

Id	Name	SBO	Value	Unit	Constant
xm	xm		1.00		☑
vm	vm		0.25		☑
lambda	lambda		3.00		☑
kx	kx		1.00		☑
mx	mx		5.00		☑
ax	ax		2.00		☑
kv	kv		1.00		☑
mv	mv		4.00		☑
av	av		2.00		☑
klambda	klambda		1.00		☑
mlambda	mlambda		2.00		☑
alambda	alambda		2.00		☑
C	C		1.00		☑

6 Rules

This is an overview of four rules.

6.1 Rule Xm

Rule Xm is an assignment rule for species Xm:

$$\mathrm{Xm} = \mathrm{xm} \cdot \left(1 - \mathrm{kx} \cdot \left(1 - \exp\left((\ln 2) \cdot \left(\frac{\mathrm{C}}{\mathrm{mx}}\right)^{\mathrm{ax}}\right)\right)\right) \tag{1}$$

6.2 Rule Vm

Rule Vm is an assignment rule for species Vm:

$$\mathrm{Vm} = \mathrm{vm} \cdot \left(1 - \mathrm{kv} \cdot \left(1 - \exp\left((\ln 2) \cdot \left(\frac{\mathrm{C}}{\mathrm{mv}}\right)^{\mathrm{av}}\right)\right)\right) \tag{2}$$

6.3 Rule Lambda

Rule Lambda is an assignment rule for species Lambda:

$$\mathrm{Lambda} = \mathrm{lambda} \cdot \left(1 + \mathrm{klambda} \cdot \left(1 - \exp\left((\ln 2) \cdot \left(\frac{\mathrm{C}}{\mathrm{mlambda}}\right)^{\mathrm{alambda}}\right)\right)\right) \tag{3}$$

6.4 Rule X

Rule X is an assignment rule for species X:

$$\mathrm{X} = \frac{[\mathrm{Xm}]}{1 + \exp\left(2 + \frac{4 \cdot [\mathrm{Vm}]}{[\mathrm{Xm}]} \cdot ([\mathrm{Lambda}] - \mathrm{time})\right)} \tag{4}$$

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 X

Name X

Notes Amyloid aggregation growth measured as absorbance at 600 nm, relative ThT fluoresce

Initial concentration $0.00427219370168501\ \mathrm{mol} \cdot \mathrm{l}^{-1}$

Involved in rule X

One rule determines the species' quantity.

7.2 Species Xm

Name Xm

Notes Maximum aggregation growth. Units: Au or %

Initial concentration $0.972654947412286\ \mathrm{mol} \cdot \mathrm{l}^{-1}$

Involved in rule Xm

One rule determines the species' quantity.

7.3 Species Vm

Name Vm

Notes Maximum aggregation rate. Units: AU h-1, Au d-1 or % h-1

Initial concentration $0.239400820174643\ \mathrm{mol} \cdot \mathrm{l}^{-1}$

Involved in rule Vm

One rule determines the species' quantity.

7.4 Species Lambda

Name Lambda

Notes `Lag phase. Units: h or d`

Initial concentration $3.47731075423886\ \mathrm{mol} \cdot \mathrm{l}^{-1}$

Involved in rule Lambda

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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