SBML Model Report

Model name: “Steckmann2012 - Amyloid beta-protein fibrillogenesis (kinetics of secondary structure conversion)”

May 6, 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 July 30th 2014 at 2:14 p. m. and last time modified at September 24th 2014 at 1:16 p. 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	11
events	0	constraints	0
reactions	0	function definitions	0
global parameters	7	unit definitions	3
rules	11	initial assignments	0

Model Notes

Steckmann2012 - Amyloid beta-proteinfibrillogenesis (kinetics of secondary structure conversion)

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This model is described in the article:Kinetics of peptide secondary structure conversion during amyloid ?-protein fibrillogenesis.Steckmann T, Awan Z, Gerstman BS, Chapagain PP.J. Theor. Biol. 2012 May; 301: 95-102

Abstract:

Amyloid fibrils are a common component in many debilitating human neurological diseases such as Alzheimer's (AD), Parkinson's, and Creutzfeldt-Jakob, and in animal diseases such as BSE. The role of fibrillar ?? proteins in AD has stimulated interest in the kinetics of ?? fibril formation. Kinetic models that include reaction pathways and rate parameters for the various stages of the process can be helpful towards understanding the dynamics on a molecular level. Based upon experimental data, we have developed a mathematical model for the reaction pathways and determined rate parameters for peptide secondary structural conversion and aggregation during the entire fibrillogenesis process from random coil to mature fibrils, including the molecular species that accelerate the conversions. The model and the rate parameters include different molecular structural stages in the nucleation and polymerization processes and the numerical solutions yield graphs of concentrations of different molecular species versus time that are in close agreement with experimental results. The model also allows for the calculation of the time-dependent increase in aggregate size. The calculated results agree well with experimental results, and allow differences in experimental conditions to be included in the calculations. The specific steps of the model and the rate constants that are determined by fitting to experimental data provide insight on the molecular species involved in the fibril formation process.

This model is hosted on BioModels Database and identified by: BIOMD0000000533.

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

2.1 Unit `volume`

Name volume

Definition ml

2.2 Unit `time`

Name time

Definition 86400 s

2.3 Unit substance

Name substance

Definition mmol

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 ml.

Name cell

4 Species

This model contains eleven species. The boundary condition of eleven 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
RCT0	RCT0	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
alpha	alpha	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
BN1	BN1	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
BN2	BN2	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
BN3	BN3	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
BN4	BN4	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
BTX	BTX	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
BM	BM	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
RCT1	RCT1	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
RC	RC	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑
beta	beta	cell	$\mathrm{mmol} \cdot \mathrm{ml}^{-1}$	⊟	☑

5 Parameters

This model contains seven global parameters.

Table 4: Properties of each parameter.

Id	Name	SBO	Value	Unit	Constant
k0	k0		0.590		☑
k1	k1		0.672		☑
k2	k2		0.678		☑
k3	k3		0.039		☑
k4	k4		0.554		☑
q	q		2.000		☑
epsilon	epsilon		0.000		☑

6 Rules

This is an overview of eleven rules.

6.1 Rule RC

Rule RC is an assignment rule for species RC:

$$\mathrm{RC} = [\mathrm{RCT0}] + [\mathrm{RCT1}] \tag{1}$$

Derived unit $\mathrm{mmol} \cdot \mathrm{ml}^{-1}$

6.2 Rule beta

Rule beta is an assignment rule for species beta:

$$\mathrm{beta} = [\mathrm{BM}] + [\mathrm{BN1}] + [\mathrm{BN2}] + [\mathrm{BN3}] + [\mathrm{BN4}] + [\mathrm{BTX}] \tag{2}$$

Derived unit $\mathrm{mmol} \cdot \mathrm{ml}^{-1}$

6.3 Rule RCT0

Rule RCT0 is a rate rule for species RCT0:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{RCT0} = \mathrm{k0} \cdot (\mathrm{epsilon} + [\mathrm{BM}]) \cdot [\mathrm{RCT0}] - \mathrm{k1} \cdot [\mathrm{BTX}] \cdot [\mathrm{RCT0}] \tag{3}$$

6.4 Rule alpha

Rule alpha is a rate rule for species alpha:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{alpha} = \mathrm{k1} \cdot [\mathrm{BTX}] \cdot [\mathrm{RCT0}] - \mathrm{k2} \cdot [\mathrm{BTX}]^{\mathrm{q}} \cdot [\mathrm{alpha}] \tag{4}$$

6.5 Rule BN1

Rule BN1 is a rate rule for species BN1:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{BN1} = \mathrm{k2} \cdot [\mathrm{BTX}]^{\mathrm{q}} \cdot [\mathrm{alpha}] - 4 \cdot \mathrm{k3} \cdot [\mathrm{BN1}] \tag{5}$$

6.6 Rule BN2

Rule BN2 is a rate rule for species BN2:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{BN2} = 4 \cdot \mathrm{k3} \cdot [\mathrm{BN1}] - 4 \cdot \mathrm{k3} \cdot [\mathrm{BN2}] \tag{6}$$

6.7 Rule BN3

Rule BN3 is a rate rule for species BN3:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{BN3} = 4 \cdot \mathrm{k3} \cdot [\mathrm{BN2}] - 4 \cdot \mathrm{k3} \cdot [\mathrm{BN3}] \tag{7}$$

6.8 Rule BN4

Rule BN4 is a rate rule for species BN4:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{BN4} = 4 \cdot \mathrm{k3} \cdot [\mathrm{BN3}] - 4 \cdot \mathrm{k3} \cdot [\mathrm{BN4}] \tag{8}$$

6.9 Rule BTX

Rule BTX is a rate rule for species BTX:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{BTX} = 4 \cdot \mathrm{k3} \cdot [\mathrm{BN4}] - \mathrm{k4} \cdot [\mathrm{BTX}] \tag{9}$$

6.10 Rule BM

Rule BM is a rate rule for species BM:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{BM} = \mathrm{k4} \cdot [\mathrm{BTX}] \tag{10}$$

6.11 Rule RCT1

Rule RCT1 is a rate rule for species RCT1:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{RCT1} = \mathrm{k0} \cdot (\mathrm{epsilon} + [\mathrm{BM}]) \cdot [\mathrm{RCT0}] \tag{11}$$

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 RCT0

Name RCT0

Initial concentration $88.1\ \mathrm{mmol} \cdot \mathrm{ml}^{-1}$

Involved in rule RCT0

One rule determines the species' quantity.

7.2 Species alpha

Name alpha

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

Involved in rule alpha

One rule determines the species' quantity.

7.3 Species BN1

Name BN1

Initial concentration $11.9\ \mathrm{mmol} \cdot \mathrm{ml}^{-1}$

Involved in rule BN1

One rule determines the species' quantity.

7.4 Species BN2

Name BN2

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

Involved in rule BN2

One rule determines the species' quantity.

7.5 Species BN3

Name BN3

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

Involved in rule BN3

One rule determines the species' quantity.

7.6 Species BN4

Name BN4

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

Involved in rule BN4

One rule determines the species' quantity.

7.7 Species BTX

Name BTX

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

Involved in rule BTX

One rule determines the species' quantity.

7.8 Species BM

Name BM

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

Involved in rule BM

One rule determines the species' quantity.

7.9 Species RCT1

Name RCT1

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

Involved in rule RCT1

One rule determines the species' quantity.

7.10 Species RC

Name RC

Initial concentration $88.1\ \mathrm{mmol} \cdot \mathrm{ml}^{-1}$

Involved in rule RC

One rule determines the species' quantity.

7.11 Species beta

Name beta

Initial concentration $11.9\ \mathrm{mmol} \cdot \mathrm{ml}^{-1}$

Involved in rule beta

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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