

SBML Model Report

Model name: “Martins2013 - True and apparent inhibition of amyloid fibril formation”



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 Villas¹ at December eleventh 2014 at 3:30 p. m. and last time modified at April eighth 2016 at 5:52 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 | 1 |
| events | 0 | constraints | 0 |
| reactions | 0 | function definitions | 0 |
| global parameters | 8 | unit definitions | 3 |
| rules | 3 | initial assignments | 0 |

Model Notes

Martins2013 - True and apparent inhibition of amyloid fibril formation

This model is described in the article: [True and apparent inhibition of amyloid fibril formation](#). Martins PM. Prion 2013 Mar-Apr; 7(2): 136-139

Abstract:

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A possible therapeutic strategy for amyloid diseases involves the use of small molecule compounds to inhibit protein assembly into insoluble aggregates. According to the recently proposed Crystallization-Like Model, the kinetics of amyloid fibrillization can be retarded by decreasing the frequency of new fibril formation or by decreasing the elongation rate of existing fibrils. To the compounds that affect the nucleation and/or the growth steps we call true inhibitors. An apparent inhibition mechanism may however result from the alteration of thermodynamic properties such as the solubility of the amyloidogenic protein. Apparent inhibitors markedly influence protein aggregation kinetics measured in vitro, yet they are likely to lead to disappointing results when tested in vivo. This is because cells and tissues media are in general much more buffered against small variations in composition than the solutions prepared in lab. Here we show how to discriminate between true and apparent inhibition mechanisms from experimental data on protein aggregation kinetics. The goal is to be able to identify false positives much earlier during the drug development process.

This model is hosted on [BioModels Database](#) and identified by: [BIOMD0000000561](#).

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

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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 dimensionless

2.2 Unit time

Name time

Definition dimensionless

2.3 Unit substance

Name substance

Definition dimensionless

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 |
|-------|-------|-----|-----------------------|------|---------------|-------------------------------------|---------|
| Brain | Brain | | 3 | 1 | dimensionless | <input checked="" type="checkbox"/> | |

3.1 Compartment Brain

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

Name Brain

4 Species

This model contains one species. The boundary condition of one of these species is set to `true` so that this 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 |
|---------|---------|-------------|--|--------------------------|-------------------------------------|
| Amyloid | Amyloid | Brain | dimensionless dimensionless ⁻¹ | <input type="checkbox"/> | <input checked="" type="checkbox"/> |

5 Parameters

This model contains eight global parameters.

Table 4: Properties of each parameter.

| Id | Name | SBO | Value | Unit | Constant |
|---------|---------|-----|-------|------|-------------------------------------|
| kb | kb | | 0.001 | | <input checked="" type="checkbox"/> |
| ka | ka | | 0.500 | | <input checked="" type="checkbox"/> |
| sigmao | sigmao | | 1.000 | | <input checked="" type="checkbox"/> |
| V | V | | 1.000 | | <input checked="" type="checkbox"/> |
| C | C* | | 1.000 | | <input checked="" type="checkbox"/> |
| gamma | gamma | | 1.000 | | <input type="checkbox"/> |
| deltamt | deltamt | | 1.000 | | <input type="checkbox"/> |
| C_0 | C | | 2.000 | | <input checked="" type="checkbox"/> |

6 Rules

This is an overview of three rules.

6.1 Rule gamma

Rule gamma is an assignment rule for parameter gamma:

$$\text{gamma} = \frac{C_0 - C}{C} \quad (1)$$

6.2 Rule deltamt

Rule deltamt is an assignment rule for parameter deltamt:

$$\text{deltamt} = \text{sigmao} \cdot V \cdot C \cdot \text{gamma} \quad (2)$$

6.3 Rule Amyloid

Rule Amyloid is an assignment rule for species Amyloid:

$$\text{Amyloid} = \left(1 - \frac{1}{\text{kb} \cdot (\exp(\text{ka} \cdot \text{time}) - 1) + 1} \right) \cdot \text{deltamt} \quad (3)$$

7 Derived Rate Equation

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

7.1 Species `Amyloid`

Name `Amyloid`

Notes `Amyloid` fibril

Initial concentration $0 \text{ dimensionless} \cdot \text{dimensionless}^{-1}$

Involved in rule `Amyloid`

One rule determines the species' quantity.

SBML²TeX 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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