

## SBML Model Report

# Model name: “Owen1998 - tumour growth model”



May 17, 2018

## 1 General Overview

This is a document in SBML Level 2 Version 4 format. This model was created by Emma Fairbanks<sup>1</sup> at June thirteenth 2017 at 9:19 a. m. and last time modified at June thirteenth 2017 at 9:19 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	3
events	0	constraints	0
reactions	0	function definitions	0
global parameters	8	unit definitions	0
rules	3	initial assignments	0

## Model Notes

Owen1998 - tumour growth modelDeterministic model for the early, avascular growth of a tumour, concentrating on the inhibitory effect of macrophages.

This model is described in the article: [Modelling the macrophage invasion of tumours: effects on growth and composition](#). Owen MR, Sherratt JA. IMA J Math Appl Med Biol 1998 Jun; 15(2): 165-185

Abstract:

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Even in the early stages of their development, tumours are not simply a homogeneous grouping of mutant cells; rather, they develop in tandem with normal tissue cells, and also recruit other cell types including lymphatic cells and the endothelial cells required for the development of a blood supply. It has been repeatedly seen that macrophages form a significant proportion of the tumour mass, and that they can have a variety of effects upon the tumour, leading to a delicate balance between growth promotion and inhibition. This paper develops a model for the early, avascular growth of a tumour, concentrating on the inhibitory effect of macrophages due to their cytolytic activity. It is shown that such an immune response is not sufficient to prevent growth, due to it being a second-order process with respect to the density of the tumour cells present. However, the presence of macrophages does have important effects on the tumour composition, and the authors perform a detailed bifurcation analysis of their model to clarify this. An extended model is also considered which incorporates addition of exogenous chemical regulators. In this case, the model admits the possibility of tumour regression, and the therapeutic implications of this are discussed.

This model is hosted on [BioModels Database](#) and identified by: [BIOMD0000000670](#).

To cite BioModels Database, please use: [Chelliah V et al. BioModels: ten-year anniversary. Nucl. Acids Res. 2015, 43\(Database issue\):D542-8.](#)

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## 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

### 2.3 Unit `area`

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

**Definition** m<sup>2</sup>

## 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
<code>cell</code>	Tumor Microenvironment		3	1	litre	<input checked="" type="checkbox"/>	

## 3.1 Compartment `cell`

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

**Name** Tumor Microenvironment

## 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
l	macrophage	cell	$\text{mol} \cdot \text{l}^{-1}$	<input type="checkbox"/>	<input checked="" type="checkbox"/>
n	normal cell	cell	$\text{mol} \cdot \text{l}^{-1}$	<input type="checkbox"/>	<input checked="" type="checkbox"/>
m	mutated cell	cell	$\text{mol} \cdot \text{l}^{-1}$	<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
A	A		0.025		✓
N	N		1.000		✓
I	I		0.010		✓
K_l	K_l		17.857		✓
delta_l	delta_l		0.100		✓
K_m	K_m		25.000		✓
xi	xi		2.000		✓
S	S		62.500		✓

## 6 Rules

This is an overview of three rules.

### 6.1 Rule l

Rule l is a rate rule for species l:

$$\frac{d}{dt}l = \frac{A \cdot [l] \cdot [m] \cdot (N + 1)}{N + [l] + [m] + [n]} + I \cdot (1 + S \cdot [m]) - K_l \cdot [l] \cdot [m] \cdot [m] - \text{delta}_l \cdot [l] \quad (1)$$

### 6.2 Rule n

Rule n is a rate rule for species n:

$$\frac{d}{dt}n = \frac{[n] \cdot (N + 1)}{N + [l] + [m] + [n]} - [n] \quad (2)$$

### 6.3 Rule m

Rule m is a rate rule for species m:

$$\frac{d}{dt}m = \frac{\text{xi} \cdot [m] \cdot (N + 1)}{N + [l] + [m] + [n]} - [m] - K_m \cdot [l] \cdot [m] \cdot [m] \quad (3)$$

## 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 <sub>l</sub>

**Name** macrophage

**Initial concentration**  $0.0999999999999985 \text{ mol} \cdot \text{l}^{-1}$

**Involved in rule** <sub>l</sub>

One rule determines the species' quantity.

## 7.2 Species <sub>n</sub>

**Name** normal cell

**Initial concentration**  $0.8999999999999988 \text{ mol} \cdot \text{l}^{-1}$

**Involved in rule** <sub>n</sub>

One rule determines the species' quantity.

## 7.3 Species <sub>m</sub>

**Name** mutated cell

**Initial concentration**  $0.8999999999999988 \text{ mol} \cdot \text{l}^{-1}$

**Involved in rule** <sub>m</sub>

One rule determines the species' quantity.

SBML<sub>2</sub>TeX was developed by Andreas Dräger<sup>a</sup>, Hannes Planatscher<sup>a</sup>, Dieudonné M Wouamba<sup>a</sup>, Adrian Schröder<sup>a</sup>, Michael Hucka<sup>b</sup>, Lukas Endler<sup>c</sup>, Martin Golebiewski<sup>d</sup> and Andreas Zell<sup>a</sup>. Please see <http://www.ra.cs.uni-tuebingen.de/software/SBML2LaTeX> for more information.

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