

SBML Model Report

Model name:
“Shen-Orr2002_FeedForward_AND_gate”



May 6, 2016

1 General Overview

This is a document in SBML Level 2 Version 4 format. This model was created by Kieran Smallbone¹ at February eighth 2011 at no o’ clock in the morning. and last time modified at March 16th 2011 at 11:59 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	3
events	4	constraints	0
reactions	4	function definitions	1
global parameters	0	unit definitions	3
rules	0	initial assignments	0

Model Notes

This is the coherent feed forward loop with an AND-gate like control of the response operon described in the article:

Network motifs in the transcriptional regulation network of Escherichia coli

Shai S. Shen-Orr, Ron Milo, Shmoolik Mangan, Uri Alon, *Nat Genet* 2002 31:64-68; PMID: [11967538](#) ; DOI: [10.1038/ng881](#) ;

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Abstract:

Little is known about the design principles of transcriptional regulation networks that control gene expression in cells. Recent advances in data collection and analysis, however, are generating unprecedented amounts of information about gene regulation networks. To understand these complex wiring diagrams, we sought to break down such networks into basic building blocks. We generalize the notion of motifs, widely used for sequence analysis, to the level of networks. We define 'network motifs' as patterns of interconnections that recur in many different parts of a network at frequencies much higher than those found in randomized networks. We applied new algorithms for systematically detecting network motifs to one of the best-characterized regulation networks, that of direct transcriptional interactions in *Escherichia coli*. We find that much of the network is composed of repeated appearances of three highly significant motifs. Each network motif has a specific function in determining gene expression, such as generating temporal expression programs and governing the responses to fluctuating external signals. The motif structure also allows an easily interpretable view of the entire known transcriptional network of the organism. This approach may help define the basic computational elements of other biological networks.

This model reproduces the timecourse presented in Figure 2a. All species and parameters in the model are dimensionless.

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 `substance`

Definition dimensionless

2.2 Unit `time`

Definition dimensionless

2.3 Unit `volume`

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
<code>cell</code>	<code>cell</code>	0000290	3	1	dimensionless	<input checked="" type="checkbox"/>	

3.1 Compartment `cell`

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

Name `cell`

SBO:0000290 physical compartment

4 Species

This model contains three 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 8 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		cell	dimensionless dimensionless ⁻¹	· <input type="checkbox"/>	<input checked="" type="checkbox"/>
Y		cell	dimensionless dimensionless ⁻¹	· <input type="checkbox"/>	<input type="checkbox"/>
Z		cell	dimensionless dimensionless ⁻¹	· <input type="checkbox"/>	<input type="checkbox"/>

5 Function definition

This is an overview of one function definition.

5.1 Function definition F

Arguments $[X], T$

Mathematical Expression

$$\begin{cases} 1 & \text{if } [X] \geq T \\ 0 & \text{otherwise} \end{cases} \quad (1)$$

6 Events

This is an overview of four events. Each event is initiated whenever its trigger condition switches from false to true. A delay function postpones the effects of an event to a later time point. At the time of execution, an event can assign values to species, parameters or compartments if these are not set to constant.

6.1 Event e1

Trigger condition

$$\text{time} \geq 3 \quad (2)$$

Assignment

$$X = 1 \quad (3)$$

6.2 Event e2

Trigger condition

$$\text{time} \geq 3.5 \quad (4)$$

Assignment

$$X = 0 \quad (5)$$

6.3 Event e3

Trigger condition

$$\text{time} \geq 10 \quad (6)$$

Assignment

$$X = 1 \quad (7)$$

6.4 Event e_4

Trigger condition

$$\text{time} \geq 15 \quad (8)$$

Assignment

$$X = 0 \quad (9)$$

7 Reactions

This model contains four reactions. All reactions are listed in the following table and are subsequently described in detail. If a reaction is affected by a modifier, the identifier of this species is written above the reaction arrow.

Table 4: Overview of all reactions

Nº	Id	Name	Reaction Equation	SBO
1	r1		$\emptyset \xrightarrow{X} Y$	0000183
2	r2		$Y \rightleftharpoons \emptyset$	0000179
3	r3		$\emptyset \xrightarrow{X, Y} Z$	0000183
4	r4		$Z \rightleftharpoons \emptyset$	0000179

7.1 Reaction r_1

This is a reversible reaction of no reactant forming one product influenced by one modifier.

SBO:0000183 transcription

Reaction equation



Modifier

Table 5: Properties of each modifier.

Id	Name	SBO
X		

Product

Table 6: Properties of each product.

Id	Name	SBO
Y		

Kinetic Law

Derived unit not available

$$v_1 = F([X], T_y) \quad (11)$$

$$F([X], T) = \begin{cases} 1 & \text{if } [X] \geq T \\ 0 & \text{otherwise} \end{cases} \quad (12)$$

Table 7: Properties of each parameter.

Id	Name	SBO	Value	Unit	Constant
Ty			0.5	dimensionless	<input checked="" type="checkbox"/>

7.2 Reaction r2

This is a reversible reaction of one reactant forming no product.

SBO:0000179 degradation

Reaction equation



Reactant

Table 8: Properties of each reactant.

Id	Name	SBO
Y		

Kinetic Law

Derived unit dimensionless⁻¹

$$v_2 = a \cdot [Y] \quad (14)$$

Table 9: Properties of each parameter.

Id	Name	SBO	Value	Unit	Constant
a			1.0	dimensionless	<input checked="" type="checkbox"/>

7.3 Reaction r3

This is a reversible reaction of no reactant forming one product influenced by two modifiers.

SBO:0000183 transcription

Reaction equation



Modifiers

Table 10: Properties of each modifier.

Id	Name	SBO
X		
Y		

Product

Table 11: Properties of each product.

Id	Name	SBO
Z		

Kinetic Law

Derived unit not available

$$v_3 = F([X], Ty) \cdot F([Y], Tz) \quad (16)$$

$$F([X], T) = \begin{cases} 1 & \text{if } [X] \geq T \\ 0 & \text{otherwise} \end{cases} \quad (17)$$

$$F([X], T) = \begin{cases} 1 & \text{if } [X] \geq T \\ 0 & \text{otherwise} \end{cases} \quad (18)$$

$$F([X], T) = \begin{cases} 1 & \text{if } [X] \geq T \\ 0 & \text{otherwise} \end{cases} \quad (19)$$

$$F([X], T) = \begin{cases} 1 & \text{if } [X] \geq T \\ 0 & \text{otherwise} \end{cases} \quad (20)$$

$$F([X], T) = \begin{cases} 1 & \text{if } [X] \geq T \\ 0 & \text{otherwise} \end{cases} \quad (21)$$

$$F([X], T) = \begin{cases} 1 & \text{if } [X] \geq T \\ 0 & \text{otherwise} \end{cases} \quad (22)$$

Table 12: Properties of each parameter.

Id	Name	SBO	Value	Unit	Constant
Ty			0.5	dimensionless	<input checked="" type="checkbox"/>
Tz			0.5	dimensionless	<input checked="" type="checkbox"/>

7.4 Reaction r4

This is a reversible reaction of one reactant forming no product.

SBO:0000179 degradation

Reaction equation



Reactant

Table 13: Properties of each reactant.

Id	Name	SBO
Z		

Kinetic Law

Derived unit dimensionless⁻¹

$$v_4 = a \cdot [Z] \quad (24)$$

Table 14: Properties of each parameter.

Id	Name	SBO	Value	Unit	Constant
a			1.0	dimensionless	<input checked="" type="checkbox"/>

8 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.

Identifiers for kinetic laws highlighted in gray cannot be verified to evaluate to units of SBML substance per time. As a result, some SBML interpreters may not be able to verify the consistency of the units on quantities in the model. Please check if

- parameters without an unit definition are involved or
- volume correction is necessary because the `hasOnlySubstanceUnits` flag may be set to `false` and `spacialDimensions` > 0 for certain species.

8.1 Species X

SBO:0000252 polypeptide chain

Initial concentration 0 dimensionless · dimensionless⁻¹

Involved in events [e1](#), [e2](#), [e3](#), [e4](#)

This species takes part in two reactions (as a modifier in [r1](#), [r3](#)). Not these but four events influence the species' quantity because this species is on the boundary of the reaction system.

8.2 Species Y

SBO:0000252 polypeptide chain

Initial concentration 0 dimensionless · dimensionless⁻¹

This species takes part in three reactions (as a reactant in [r2](#) and as a product in [r1](#) and as a modifier in [r3](#)).

$$\frac{d}{dt}Y = v_1 - v_2 \quad (25)$$

8.3 Species Z

SBO:0000252 polypeptide chain

Initial concentration 0 dimensionless · dimensionless⁻¹

This species takes part in two reactions (as a reactant in [r4](#) and as a product in [r3](#)).

$$\frac{d}{dt}Z = v_3 - v_4 \quad (26)$$

A Glossary of Systems Biology Ontology Terms

SBO:0000179 degradation: Complete disappearance of a physical entity

SBO:0000183 transcription: Process through which a DNA sequence is copied to produce a complementary RNA

SBO:0000252 polypeptide chain: Naturally occurring macromolecule formed by the repetition of amino-acid residues linked by peptidic bonds. A polypeptide chain is synthesized by the ribosome. CHEBI:1654

SBO:0000290 physical compartment: Specific location of space, that can be bounded or not.
A physical compartment can have 1, 2 or 3 dimensions

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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