

Towards model version control

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Versions of models

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JOURNAL ARTICLES

Numerical analysis of a comprehensive model of M-phase control in *Xenopus* oocyte extracts and intact embryos

B. Novak and J.J. Tyson

Author Affiliations

Summary

To contribute to a deeper understanding of M-phase control in eukaryotic cells, we have constructed a model based on the biochemical properties of M-phase promoting factor (MPF) in *Xenopus* oocyte extracts, where there is evidence for two positive feedback loops (MPF

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Proceedings of the National Academy of Sciences of the United States of America

PNAS

Modeling the control of DNA replication in fission yeast

Bela Novak* and John J. Tyson†

Author Affiliations

Edited by Paul Nurse, Imperial Cancer Research Fund, London, United Kingdom, and approved May 21, 1997 (received for review December 31, 1996)

A central event in the eukaryotic cell cycle is the decision to commence DNA replication (S phase). Strict controls normally operate to prevent repeated rounds of DNA replication without intervening mitoses ("endoreplication") or initiation of mitosis before DNA is fully replicated ("mitotic catastrophe"). Some of the genetic interactions involved in these controls have recently been identified in yeast. From this evidence we propose a molecular mechanism of "Start" control in *Schizosaccharomyces pombe*. Using established principles of biochemical kinetics, we compare the properties of this model in detail with the observed behavior of various mutant strains of fission yeast: *wee1⁻* (size control at Start), *cdc13Δ* and *rum1^{OP}* (endoreplication), and *wee1⁻ rum1Δ* (rapid division cycles of diminishing cell size). We discuss essential features of the mechanism that are responsible for characteristic properties of Start control in fission yeast, to expose our proposal to crucial experimental tests.

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PNAS August 19, 1997 vol. 94 no. 17 9147-9152

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Figures Only
Full Text
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Classifications

Biological Sciences
Cell Biology

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This Week's Issue
August 14, 2012, 109 (33)

From the Cover

- Aurora kinase C in mouse oocytes
- Slippery biofilm-resistant surfaces
- Dissecting receptor tyrosine kinase signaling
- Molecular targets of γ-hydroxybutyric acid
- Nitrate transport in salivary glands

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1993

1997

Novak, Tyson, 1993

Numerical analysis of a comprehensive model of M-phase control in *Xenopus* oocyte extracts and intact embryos: parameter values have been taken from the original published paper to reproduce figure 4A.

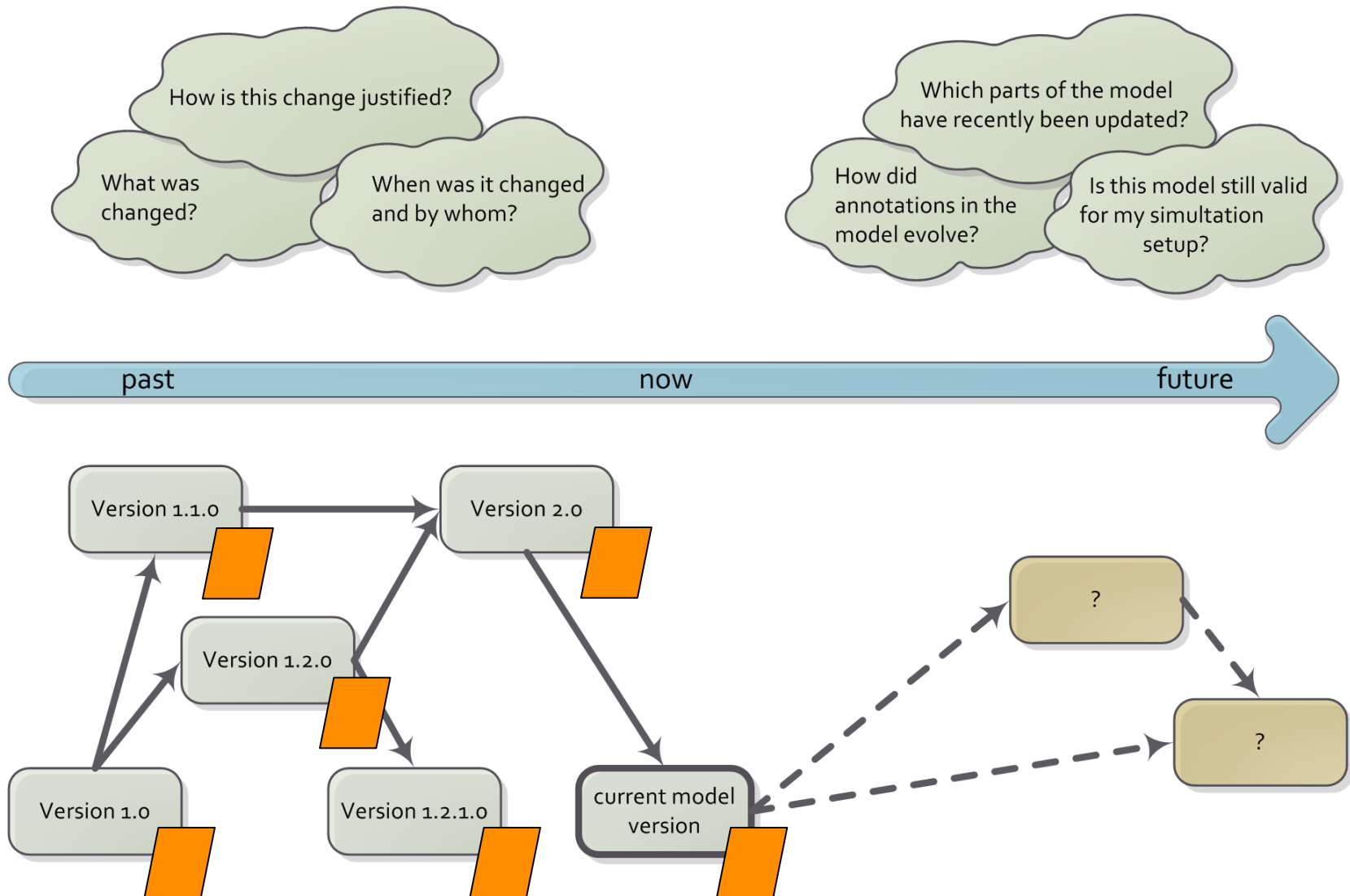
Novak, Tyson, 1993

Numerical analysis of a comprehensive model of M-phase control in *Xenopus* oocyte extracts and intact embryos: parameter values have been taken from the SBML model in the BioModels Database and the model simulates the synthesis and degradation of cyclin.

PMR2

BMDB

Evolution of a model over time



Waltemath et al. (submitted)



Directly accessible from the repository:

- Original model file (any format)
- Current model file
- Date of creation and last modification

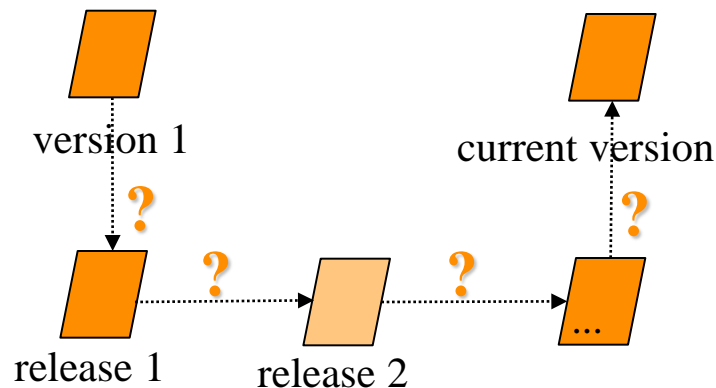
Download SBML
|
Other formats (auto-generated)
|
Actions

Model	Overview	Math	Physical entities	...
<p> Publication ID: P12697 </p> <p> Novak B, Tyson JJ J Cell Sci 1993 Dec;106 (Pt 4):1153-68. Department of Biology, Virginia Polytechnic Institute and State University </p>				
<p> Original Model: BCHMD000000G07.xml url email </p> <p> Submitter: Harish Dhurup </p> <p> Submission ID: MODEL5876465734 </p> <p> Submission Date: 09 Apr 2007 19:29:15 UTC </p> <p> Last Modification Date: 05 Jul 2012 14:43:05 UTC </p> <p> Creation Date: 05 Apr 2007 08:42:03 UTC </p> <p> Encoders: Nicolas Le Novâtre Harish Dhurup </p>				

logical conventions?
[@reactome](#)
[React](#)
[_152](#)

set #1:
logical in version C?
[Gene Ontology](#)
[ontologic](#)
[cycle](#)
[cycle](#)

logical occurs in:
[Taxonomy](#)
[Amphibia](#)



Implicitly accessible:

- Model file(s) at each BioModels Database release

Index of <http://ftp.ebi.ac.uk/pub/databases/bi>

[Up to higher level directory](#)

Name	
2005-04-11	
2005-06-01	
2005-07-28	
2005-01-31	
2006-04-05	
2006-10-03	
2007-01-05	
2007-06-05	
2007-09-25	
2008-03-28	
2008-08-21	
2008-12-03	
2009-03-25	
2009-06-16	
2009-09-02	
2010-01-26	
2010-04-07	
2010-08-30	
2011-04-15	
2011-09-01	
2012-02-08	
2012-05-20	
latest	
	02/08/2012 05:36:00
	02/04/2012 05:35:00
	02/08/2012 05:36:00
	02/08/2012 05:31:00
	02/08/2012 05:27:00
	07/30/2012 03:17:00
	08/02/2012 09:58:00

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Numerical analysis of a comprehensive model of M-phase control in *Xenopus* oocyte extracts and intact embryos: parameter values have been taken from the original published paper to reproduce figure 4A.





Model Status

This CellML version of the model has been checked in COR and OpenCell. This variant of the model runs to replicate the original published results as depicted in figure 4A of the paper. Please note that actual concentrations are displayed by this model, instead of the percentage concentrations used in the paper. The units have been checked and they are consistent.

Model Structure

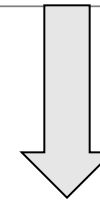
ABSTRACT: To contribute to a deeper understanding of M-phase control in eukaryotic cells, we have constructed a model

Model Curation

Curation Status: 
OpenCell: 
JSim: 
COR: 

Source

Derived from workspace [Novak, Tyson, 1993](#) at changeset [a39b4d26855a](#).



You are here: [Home](#) > [Workspaces](#) > [Novak, Tyson, 1993](#)

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Changelog Entries

- [\(0\)](#)
- [tip](#)

Date	Author	Log
2010-07-05 22:14 +1200		Updated documentation and added meaningful names to the two model variants.
2010-07-05 14:24 +1200		Tidied session file
2009-11-25 14:00 +1300		Added images in ai svg and png format
2009-11-10 10:39 +1300		Removed non pub med reference
2009-11-10 09:32 +1300		Added keyword
2009-06-17 15:26 +1200		committing version02 of novak_tyson_1993
2009-01-14 04:19 +1300		committing version01 of novak_tyson_1993

- CellML metadata specification
 - <http://www.cellml.org/specifications/metadata/>
 - Elements from rdf, dc, dcterms, vcard
 - Trivial vs substantial changes
- SBML History concept
 - dc:creator *model creators*
 - dcterms:created *creation date*
 - dcterms:modified *modification date*

Version information is not propagated to the users.

Currently used algorithms are not suitable for difference detection in XML models (SBML, CellML, NeuroML).

- Find the difference between two model versions,
- understand what a change is about,
- and understand why a model update had been necessary.

1. XML-aware algorithm for difference detection
2. Transparent changes
3. Justification for changes

1. XML difference detection: DiffList

```
1 @@ -661,13 +661,11 @@
2 [...]
3 -     <rdf:Description rdf:about="#_905882">
4 -         <bqbiol:isVersionOf>
5 -             <rdf:Bag>
6 -                 <rdf:li rdf:resource="urn:miriam:obo.go:GO%3A0043037" />
7 -             </rdf:Bag>
8 -         </bqbiol:isVersionOf>
9 -     </rdf:Description>
10 +<rdf:Description rdf:about="#_905882">
11 +<bqbiol:isVersionOf><rdf:Bag>
12 +<rdf:li rdf:resource="urn:miriam:obo.go:GO%3A0043037" />
13 +</rdf:Bag></bqbiol:isVersionOf>
14 +</rdf:Description>
15 [...]
```

- Detects all diffs
 - insert, delete, update, move
 - for two model files,
 - typically two versions of the same model
- Adaptation of *XyDiff*,
 - entity-based
 - ignores XML formatting
 - <http://leo.saclay.inria.fr/software/XyDiff/>

Diff:

```
<updates>
  <attribute attributeName="reversible" value="true" oldValue="false"
    path="[@id='Cdc25_Reaction']" elementName="reaction"/>
  <attribute attributeName="reversible" value="true" oldValue="false"
    path="[@id='Cdc2Phos']" elementName="reaction"/>
  <attribute attributeName="reversible" value="true" oldValue="false"
    path="[@id='G1R_Binding']" elementName="reaction"/>
  <attribute attributeName="reversible" value="true" oldValue="false"
    path="[@id='G2R_Creation']" elementName="reaction"/>
  <attribute attributeName="reversible" value="true" oldValue="false"
    path="[@id='IE_Reaction']" elementName="reaction"/>
  <attribute attributeName="reversible" value="true" oldValue="false"
    path="[@id='PG2R_Creation']" elementName="reaction"/>
  <attribute attributeName="reversible" value="true" oldValue="false"
    path="[@id='UbE2_Reaction']" elementName="reaction"/>
  <attribute attributeName="reversible" value="true" oldValue="false"
    path="[@id='UbE_Reaction']" elementName="reaction"/>
  <attribute attributeName="reversible" value="true" oldValue="false"
    path="[@id='Wee1_Reaction']" elementName="reaction"/>
</updates>
```

Waltemath et al. (submitted)

2. Transparent changes: model history

Table 1: Version information about model BIOM007

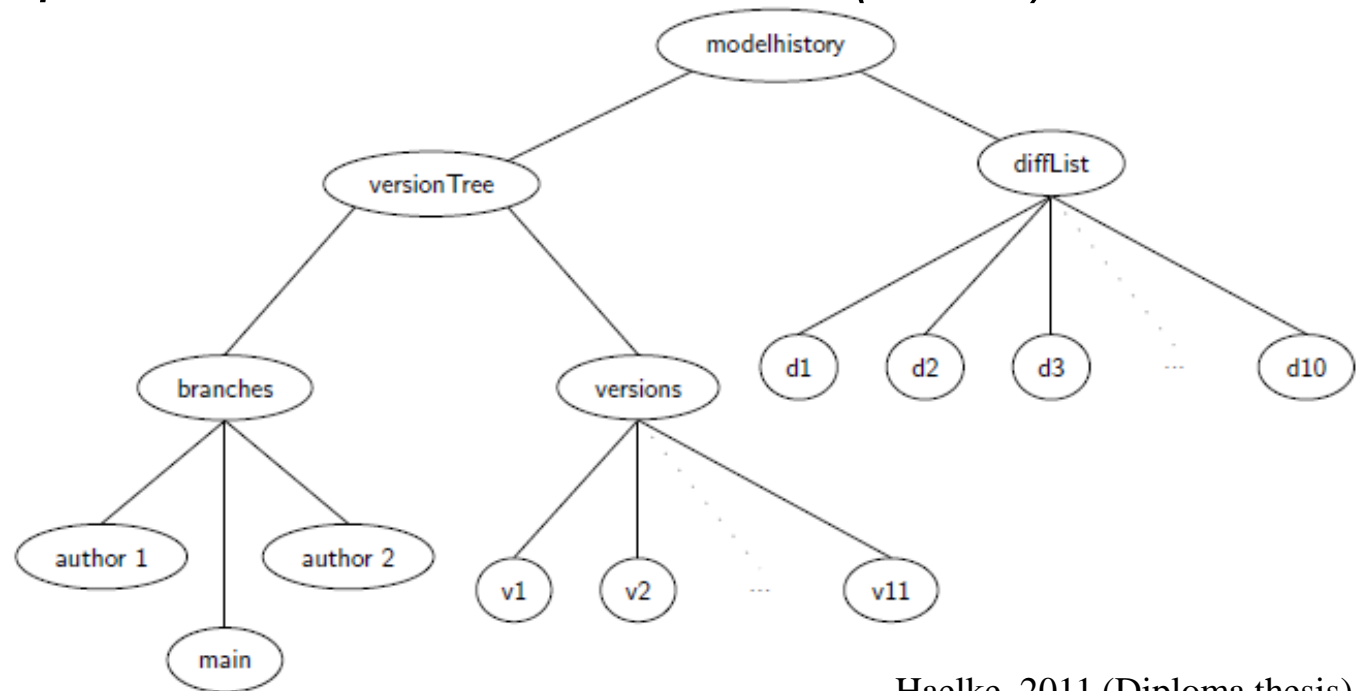
Revision	Date	SVN Comment
R2* initial	06/16/2009	original models.
R3*	06/16/2009	the latest version when implementing revision control
R37	07/29/2009	four assignment rules (k2, k6, kwee and k25) were changed to function definitions.
R51	08/10/2009	converted to SBML Level2 Version 4 and curated. Attributes 'spatialSizeUnits' in element, and 'timeUnits' and 'substanceUnits' in element, which are not part of SBML Level 2 Version 4 element are eliminated.
R57	08/13/2009	The model should remain in SBML L2V1. The model was integrated and simulated using Mathematica 6.0 - MathSBML 2.7.1, which does not support SBML L2V4.
R194	10/15/2009	corrected one error in a kinetic law (Ube1 activation) and changed the file a bit to get it to l2v3 [line break] recurated it, but still problems with the initial conditions

Waltemath et al. (submitted)

2. Transparent changes: model history

Model history (version tree)

- Diff list
- *adapted from Rosado et al., 2009 (EDBT)*



Haelke, 2011 (Diploma thesis)

3. Justification of changes: Ontology

Controlled vocabulary for annotation of the diff file

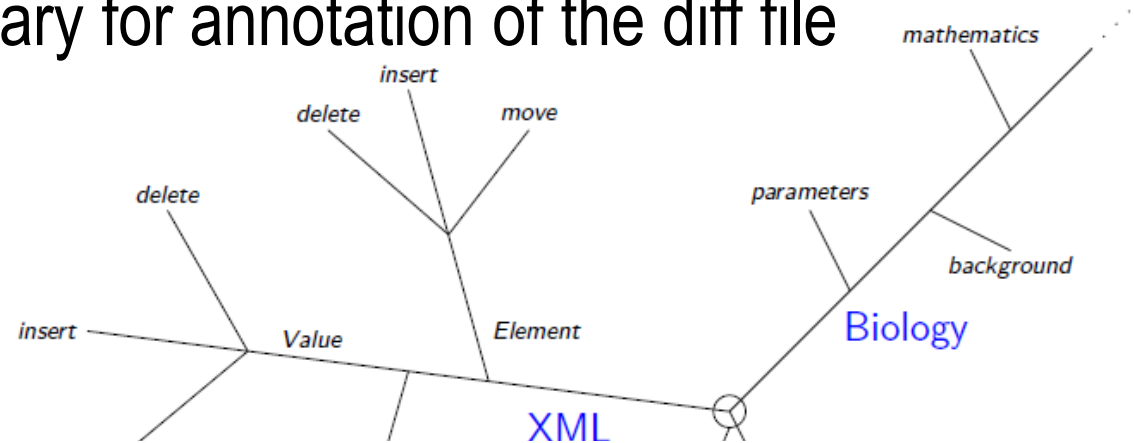


Table 2: Controlled vocabulary for types of changes.

Location		Type	Operation
XML	Annotation	mathematics	update
element	qualifier	biology	insert
attribute	URI	parameter	delete
value		typo	move
		...	

Haelke, 2011 (Diploma thesis)

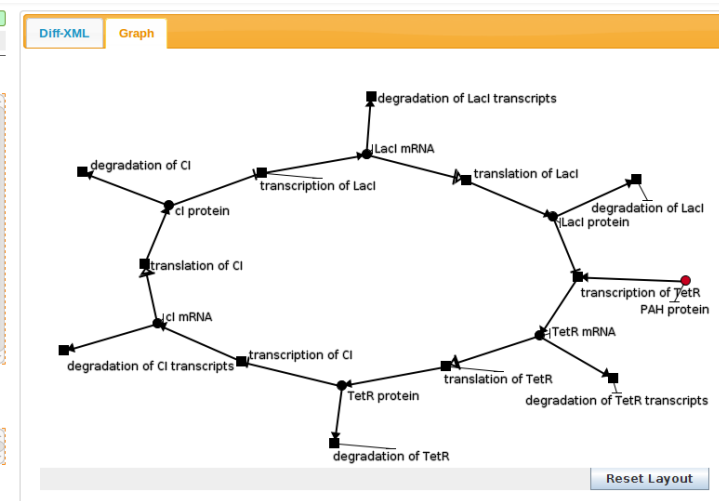
Waltemath et al. (submitted)

Biochemical Model Versioning System (BiVeS)

Waltemath et al. (submitted)

- Java library for **diffList** and **model history**
- Can be used on top of SVN/Mercurial systems to store differences between two model versions, and maintain a history of versions
- Tested on: SBML@BioModels Database
- <https://bitbucket.org/rhaelke/bives.fwk/overview>

- Tree-based view of model versions (history)
- Difference between two models
- XML representation (diff format)
- Graphical representation (GraphViz)



<http://www.sbi.uni-rostock.de/budhat>

- Targeting single versions of a model (model version IDs), e.g. to build the model history
- Change annotation
- Detecting merges in models
- Support of CellML, NeuroML, SED-ML etc in the diff tool

