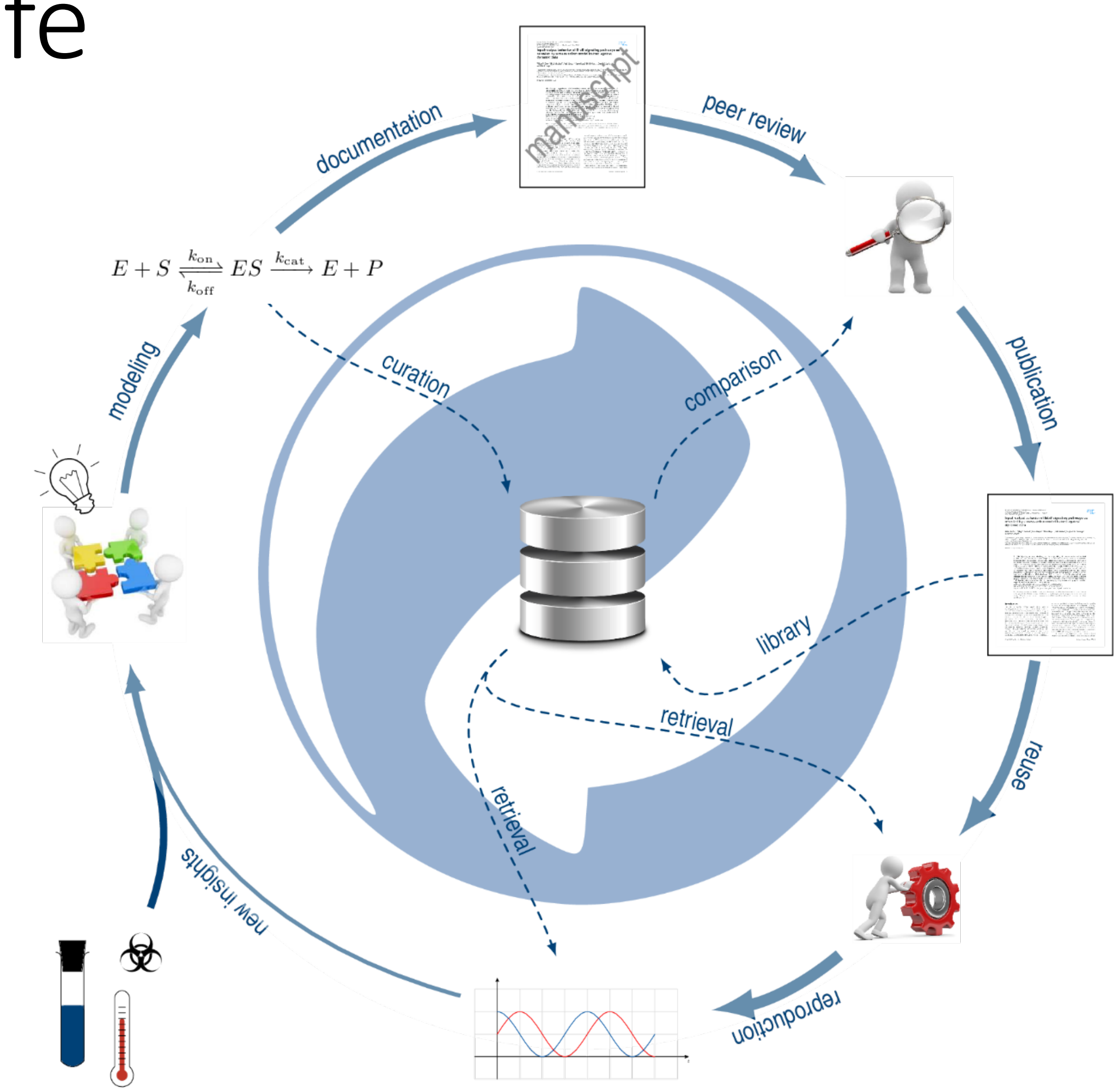
Model Management

Ron Henkel

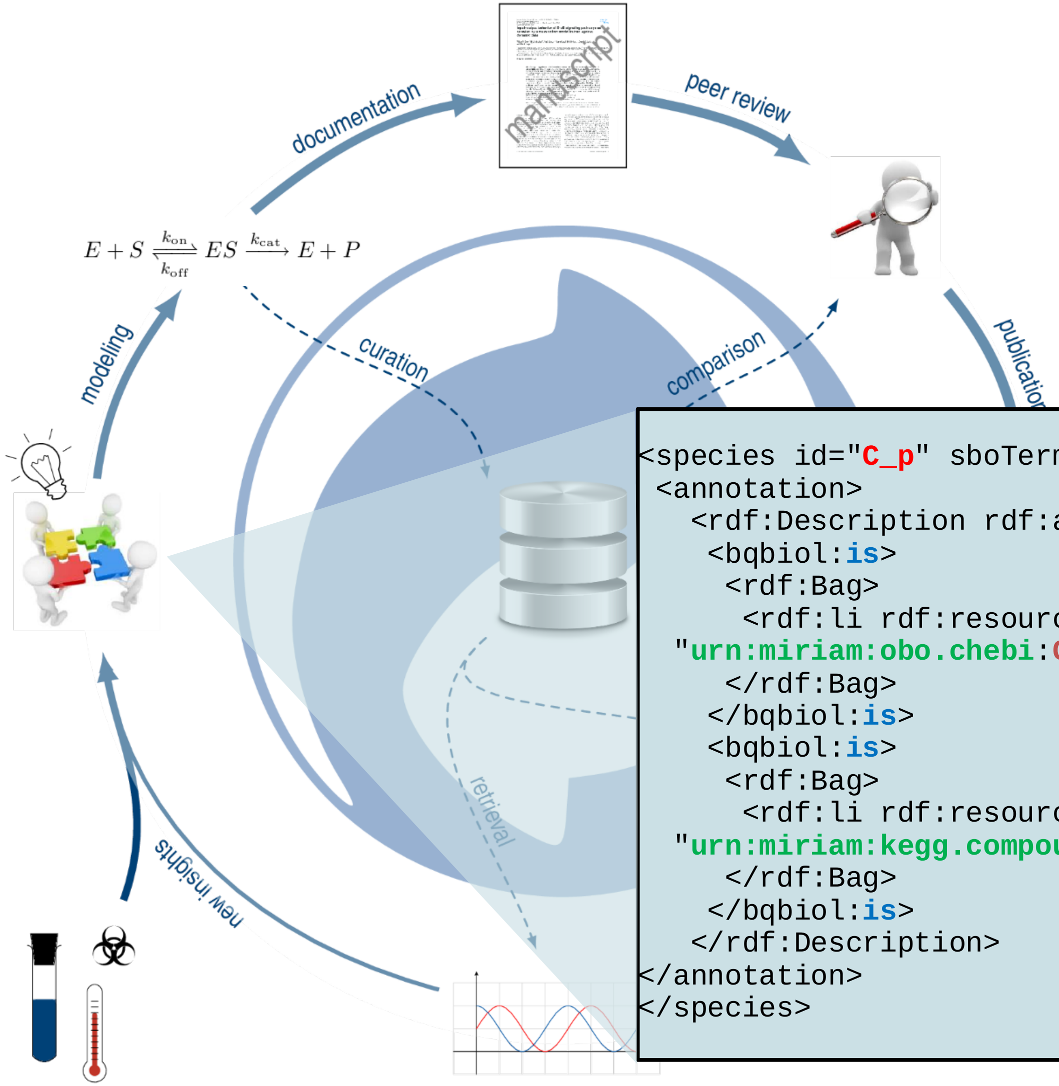
August 6th 2017

Combine Tutorial @ ICSB

Circle of life



Models



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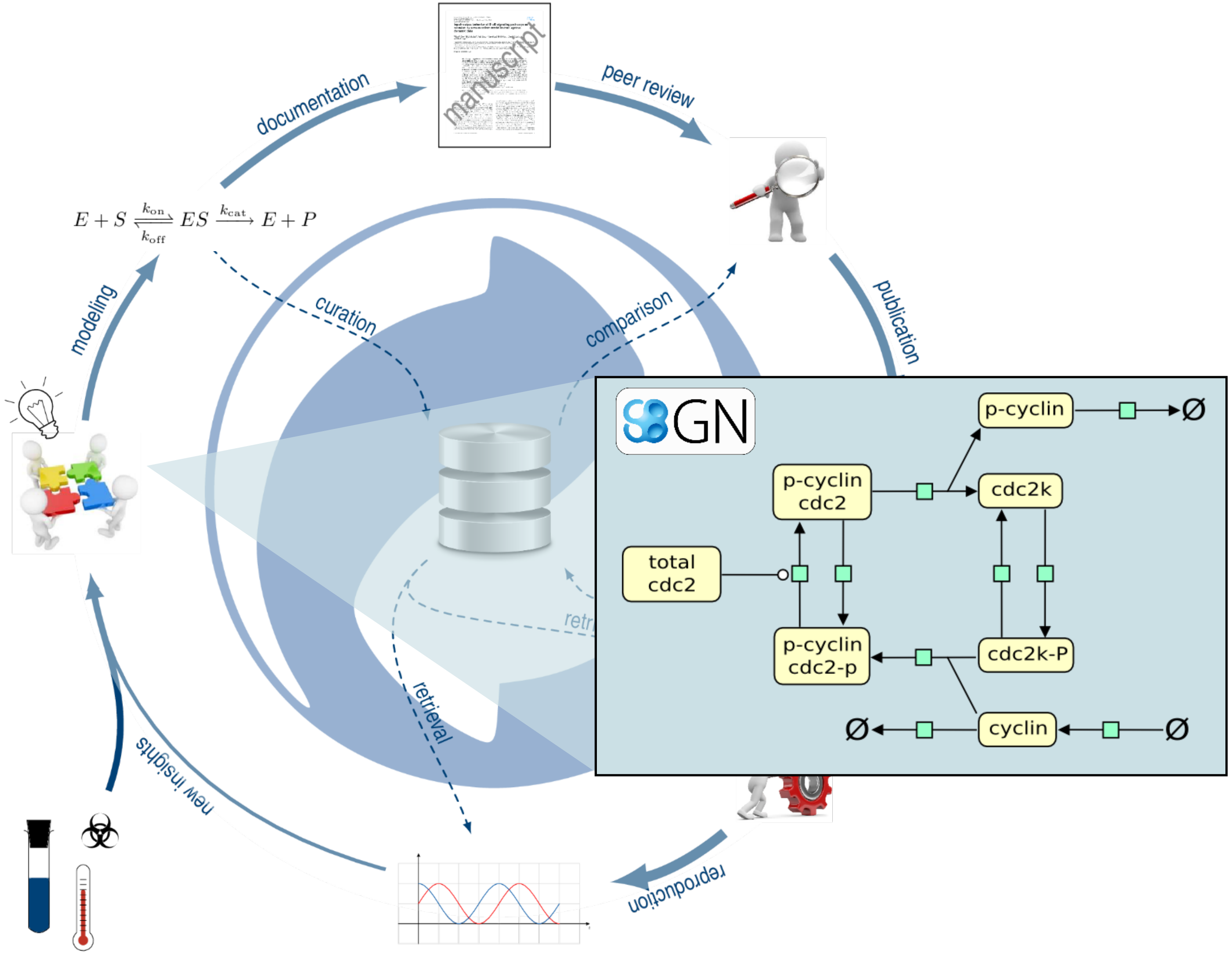
<species id="C_p" sboTerm="SBO:0000247">
 <annotation>
   <rdf:Description rdf:about="C_p">
    <bqbiol:is>
     <rdf:Bag>
      <rdf:li rdf:resource=
  "urn:miriam:obo.chebi:CHEBI%3A27732"/>
     </rdf:Bag>
    </bqbiol:is>
    <bqbiol:is>
     <rdf:Bag>
      <rdf:li rdf:resource=
  "urn:miriam:kegg.compound:C07481"/>
     </rdf:Bag>
    </bqbiol:is>
   </rdf:Description>
</annotation>
</species>
```

MIRIAM compliant
Minimum information required in the annotation of models

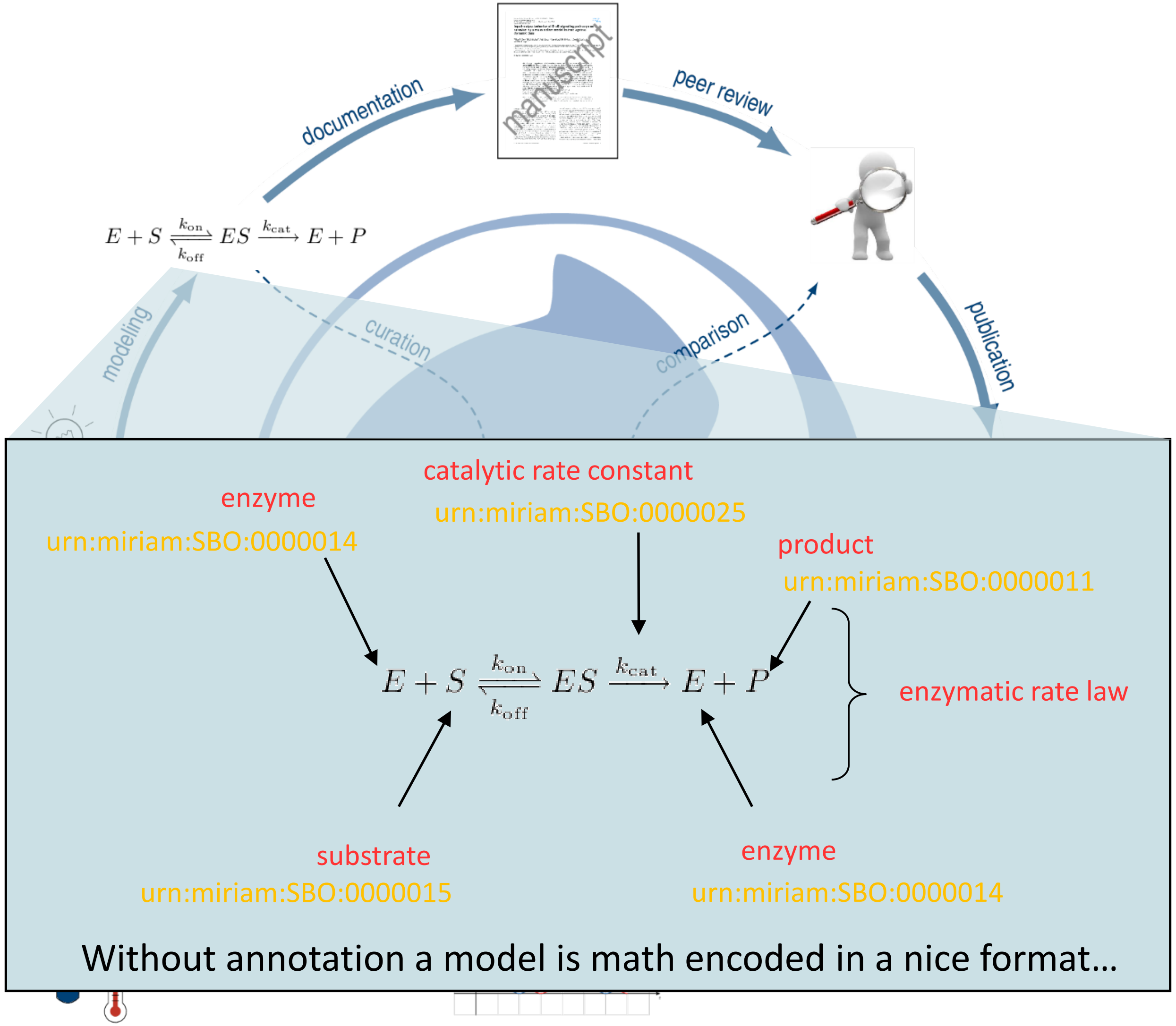
Models

SBML

cellML
biology. math. data. knowledge.



Annotation



catalytic rate constant
urn:miriam:SBO:0000025

enzyme
urn:miriam:SBO:0000014

product
urn:miriam:SBO:0000011

$$E + S \underset{k_{\text{off}}}{\overset{k_{\text{on}}}{\rightleftharpoons}} ES \xrightarrow{k_{\text{cat}}} E + P$$

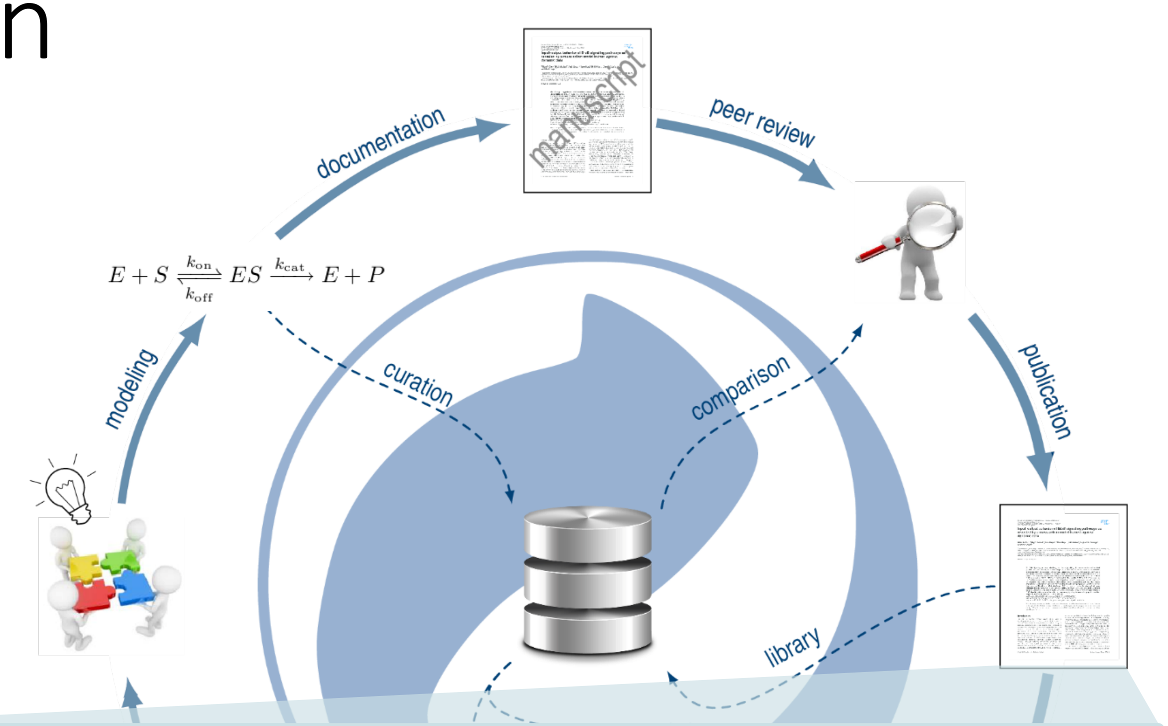
enzymatic rate law

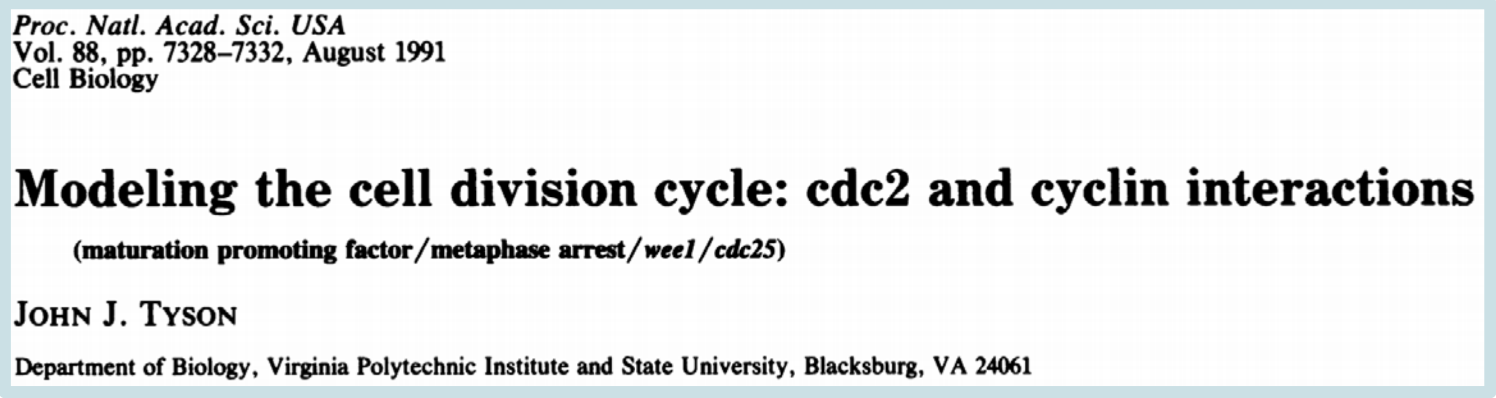
substrate
urn:miriam:SBO:0000015

enzyme
urn:miriam:SBO:0000014

Without annotation a model is math encoded in a nice format…

Publication





Proc. Natl. Acad. Sci. USA
Vol. 88, pp. 7328–7332, August 1991
Cell Biology

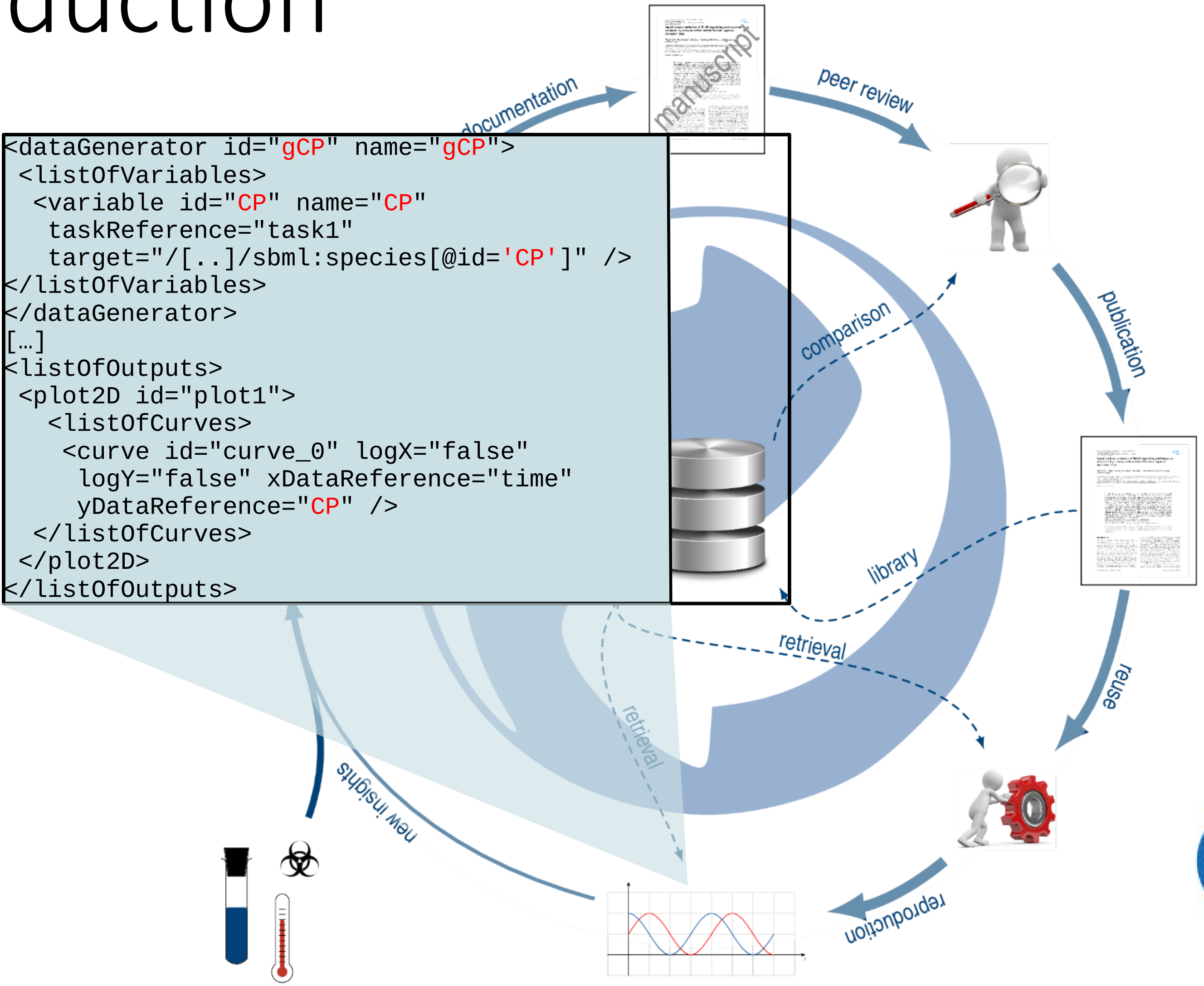
Modeling the cell division cycle: cdc2 and cyclin interactions

(maturation promoting factor/metaphase arrest/*wee1*/*cdc25*)

JOHN J. TYSON

Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061

Reproduction

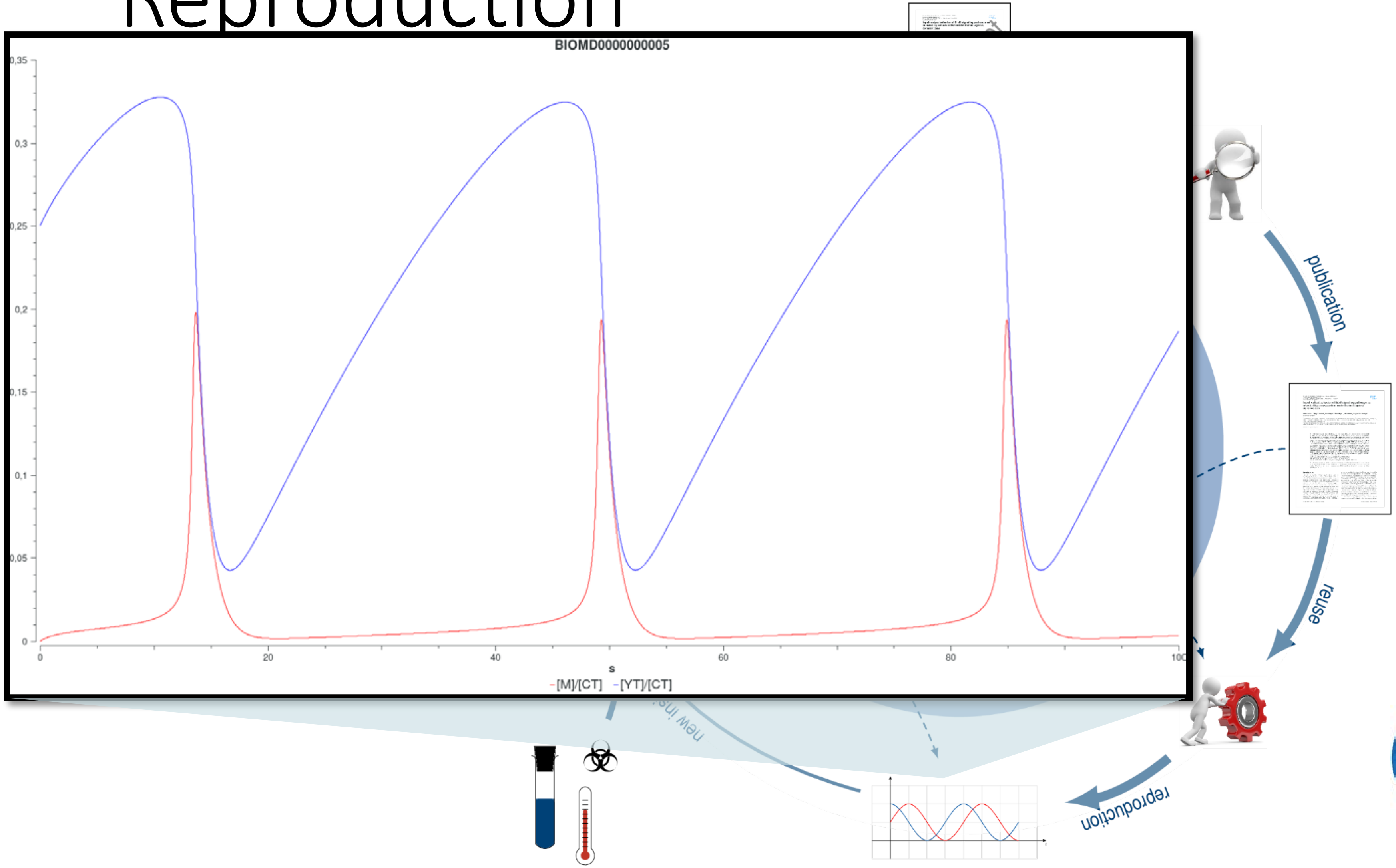


```
<dataGenerator id="gCP" name="gCP">
 <listOfVariables>
  <variable id="CP" name="CP"
   taskReference="task1"
   target="/[..]/sbml:species[@id='CP']" />
</listOfVariables>
</dataGenerator>
[…]
<listOfOutputs>
 <plot2D id="plot1">
   <listOfCurves>
    <curve id="curve_0" logX="false"
     logY="false" xDataReference="time"
     yDataReference="CP" />
  </listOfCurves>
 </plot2D>
</listOfOutputs>
```

MIASE compliant
Minimum Information About a Simulation Experiment

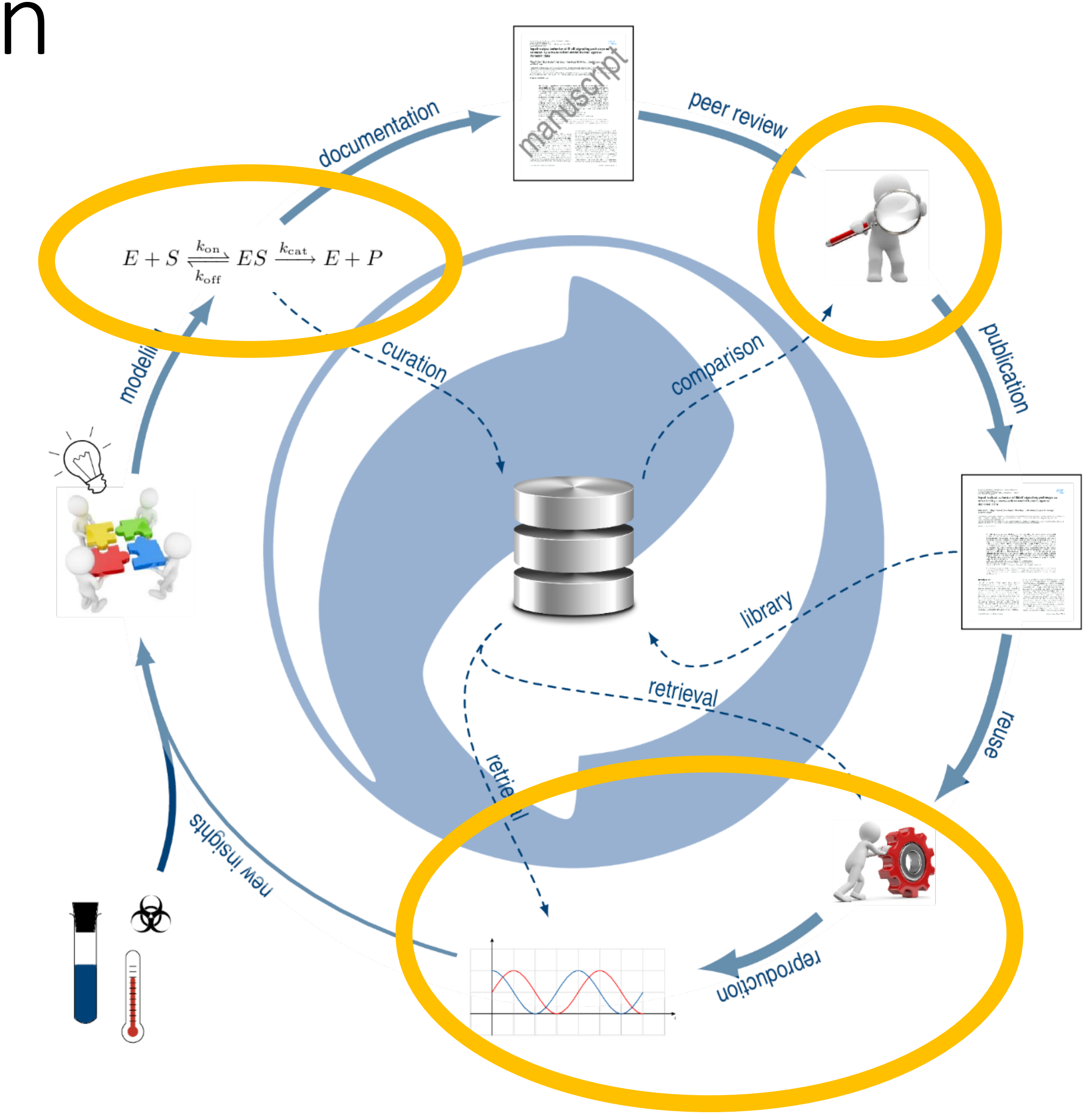
SED ML

Reproduction

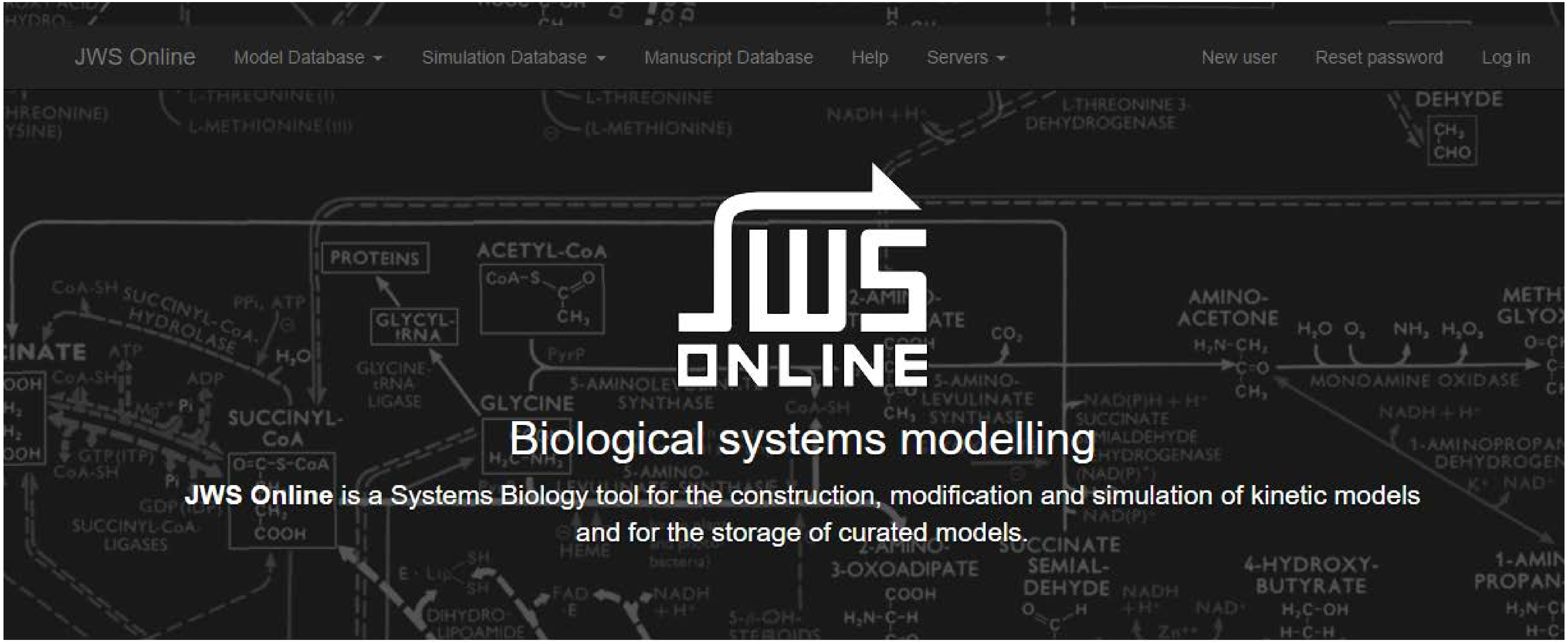


SED ML

Simulation


manuscript
documentation
peer review
$E + S \underset{k_{\text{off}}}{\overset{k_{\text{on}}}{\rightleftharpoons}} ES \xrightarrow{k_{\text{cat}}} E + P$
curation
comparison
publication
modelling
library
retrieval
retrieval
reuse
reproduction
new insights

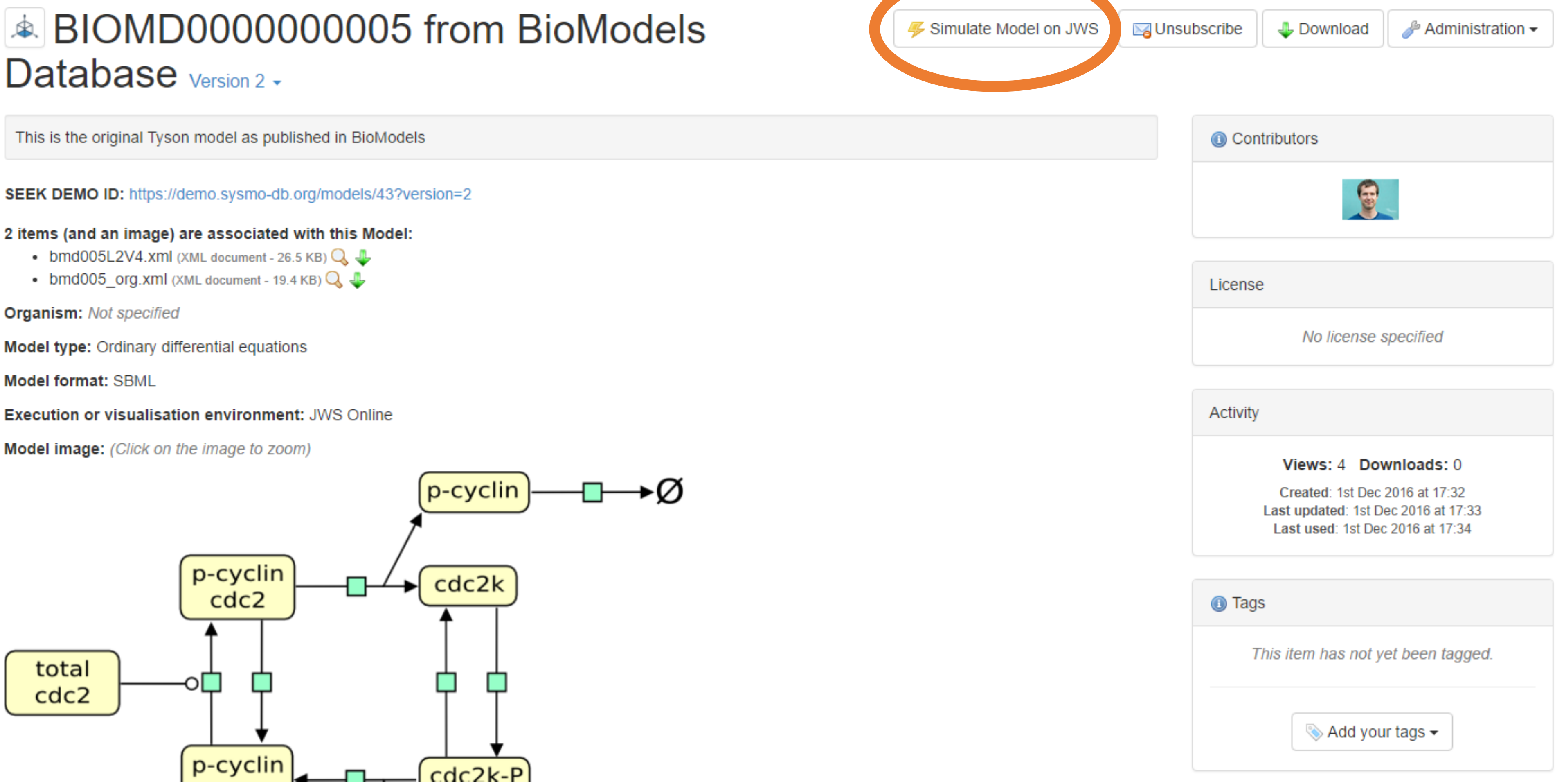
JWS-Online



Biological systems modelling

JWS Online is a Systems Biology tool for the construction, modification and simulation of kinetic models and for the storage of curated models.

SEEK and JWS-Online



BIOMD0000000005 from BioModels Database Version 2

This is the original Tyson model as published in BioModels

SEEK DEMO ID: https://demo.sysmo-db.org/models/43?version=2

2 items (and an image) are associated with this Model:

- bmd005L2V4.xml (XML document - 26.5 KB)
- bmd005_org.xml (XML document - 19.4 KB)

Organism: *Not specified*

Model type: Ordinary differential equations

Model format: SBML

Execution or visualisation environment: JWS Online

Model image: *(Click on the image to zoom)*

Contributors

License

No license specified

Activity

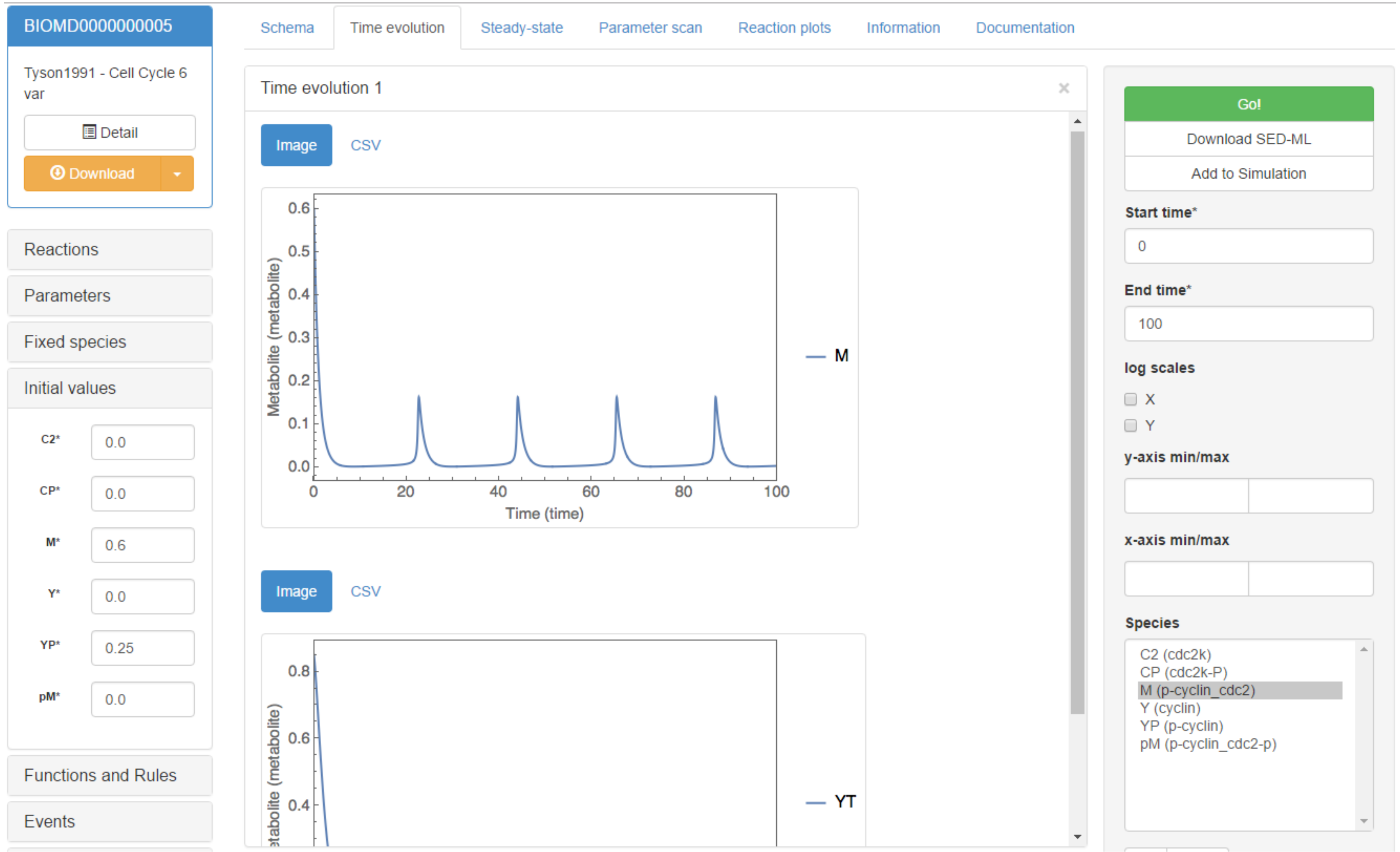
Views: 4 **Downloads:** 0

Created: 1st Dec 2016 at 17:32
Last updated: 1st Dec 2016 at 17:33
Last used: 1st Dec 2016 at 17:34

Tags

This item has not yet been tagged.

Simulation with JWS-Online



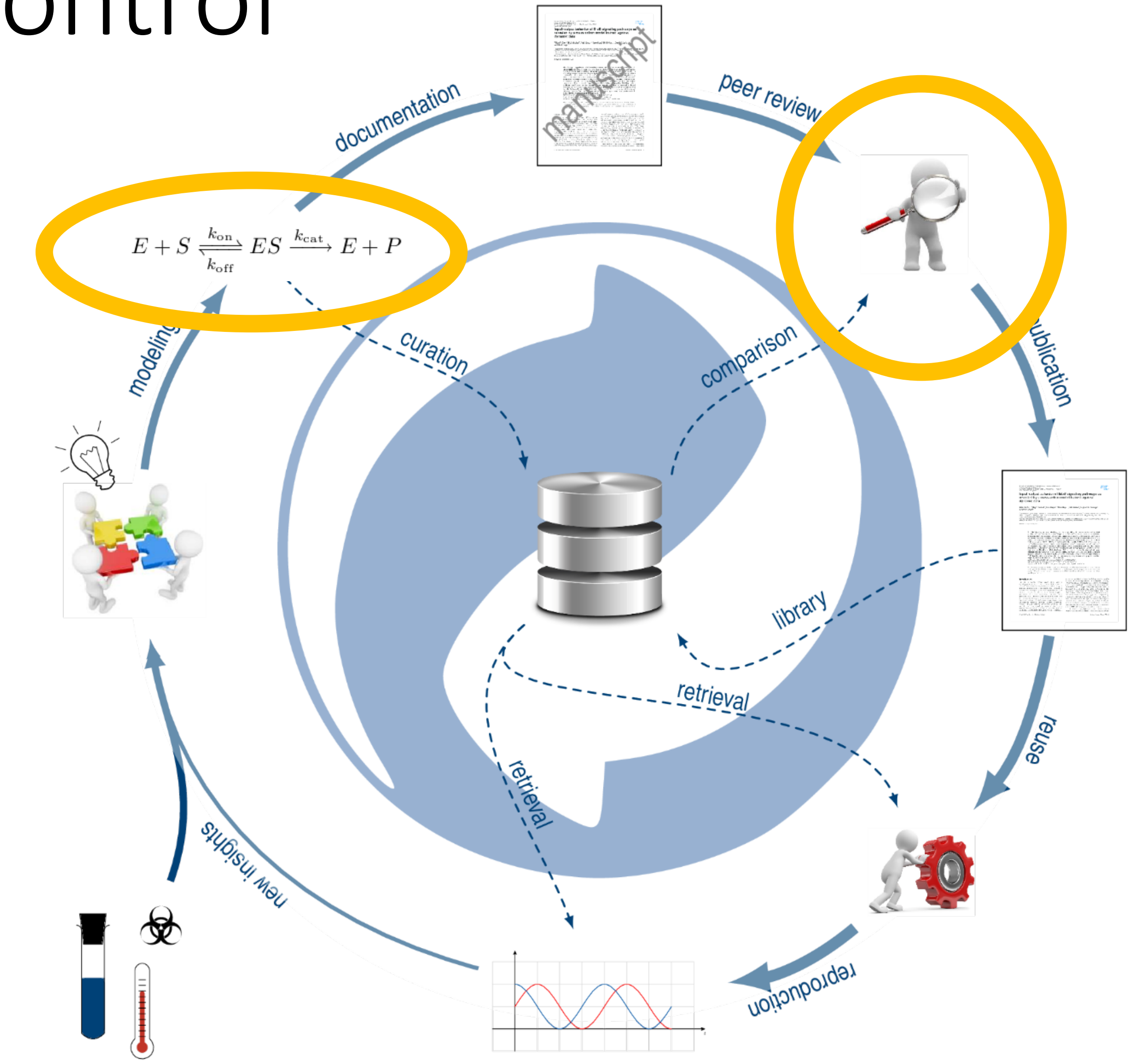
Tyson1991 - Cell Cycle 6 var

C2* 0.0
CP* 0.0
M* 0.6
Y* 0.0
YP* 0.25
pM* 0.0

Start time* 0
End time* 100
log scales
☐ X
☐ Y
y-axis min/max
x-axis min/max

Species
C2 (cdc2k)
CP (cdc2k-P)
M (p-cyclin_cdc2)
Y (cyclin)
YP (p-cyclin)
pM (p-cyclin_cdc2-p)

Version Control



Versioning - Identifying changes

ATP

<species id="~~ADP~~" compartment="cell“/>

- Typo correction
- Change in network
- Change in model nature

ATP

<species id="X" name="~~ADP~~" compartment="cell“/>

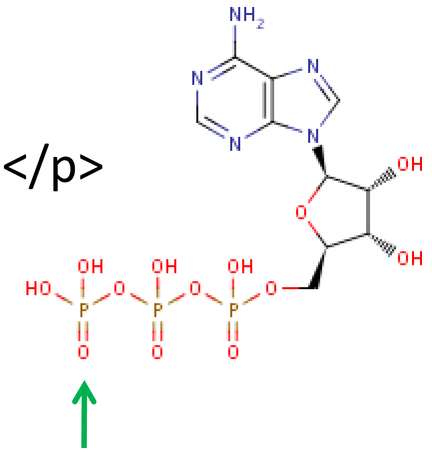
- Not a change in network

Waltemath, Henkel et al. (2013) Oxford Bioinf.

Versioning - Identifying changes

ATP

<species id="X" name="~~ADP~~" compartment="cell">
  <notes>
    <p xmlns=http://www.w3.org/1999/xhtml>this is ATP</p>
  </notes>
  <annotation>
    <rdf:Description rdf:about="X">
      <bqbiol:is>
        <rdf:li rdf:resource="urn:miriam:obo.chebi:CHEBI%3A15422"/>
      </bqbiol:is>
    </rdf:Description>
  </annotation>
</species>



- Including additional information necessary to evaluate a change

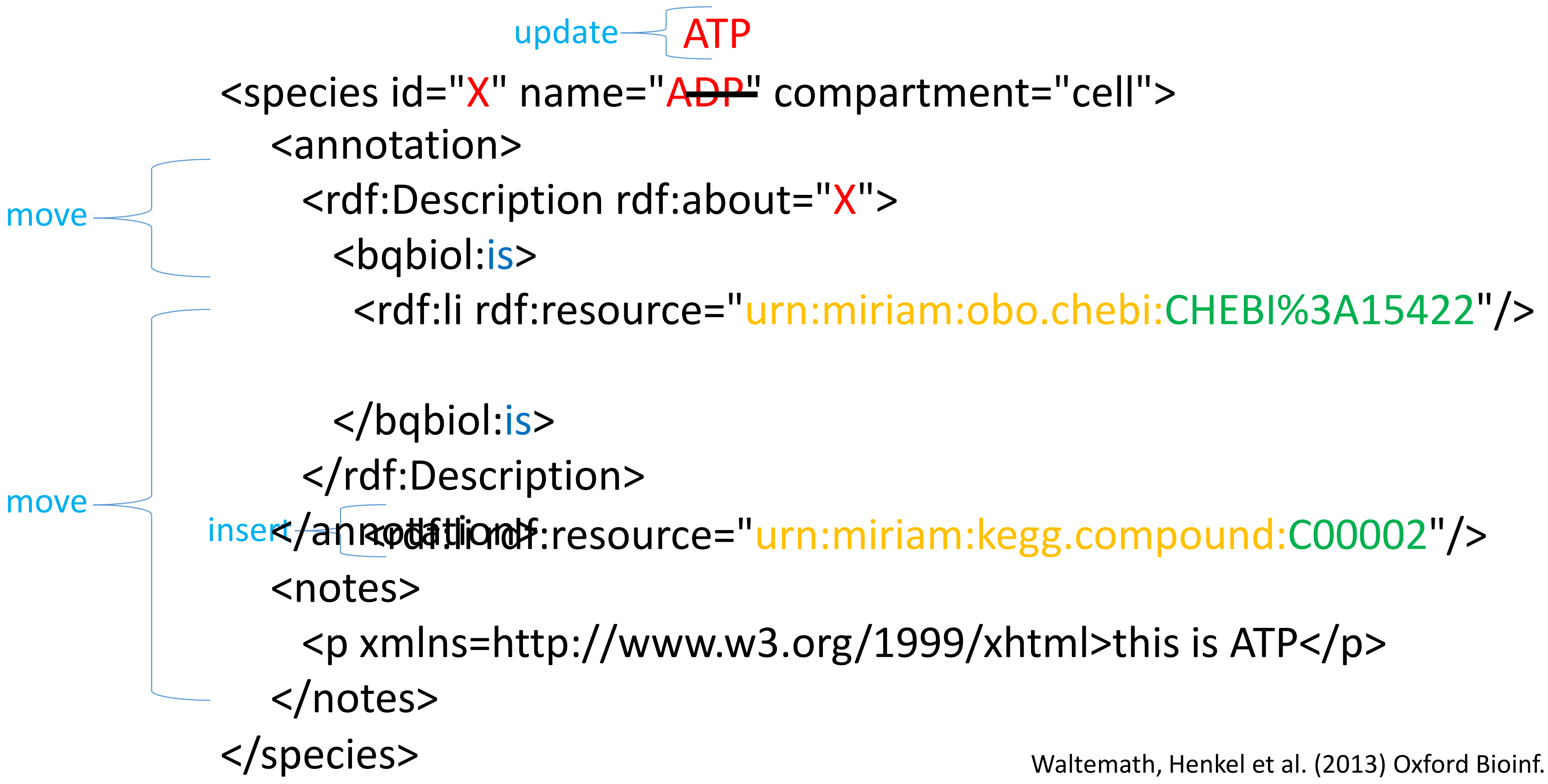
Waltemath, Henkel et al. (2013) Oxford Bioinf.

Universität Rostock Traditio et Innovatio

SEMS simulation experiment management system

Heidelberger Institut für Theoretische Studien HITS

Versioning - Identifying changes (XML level)

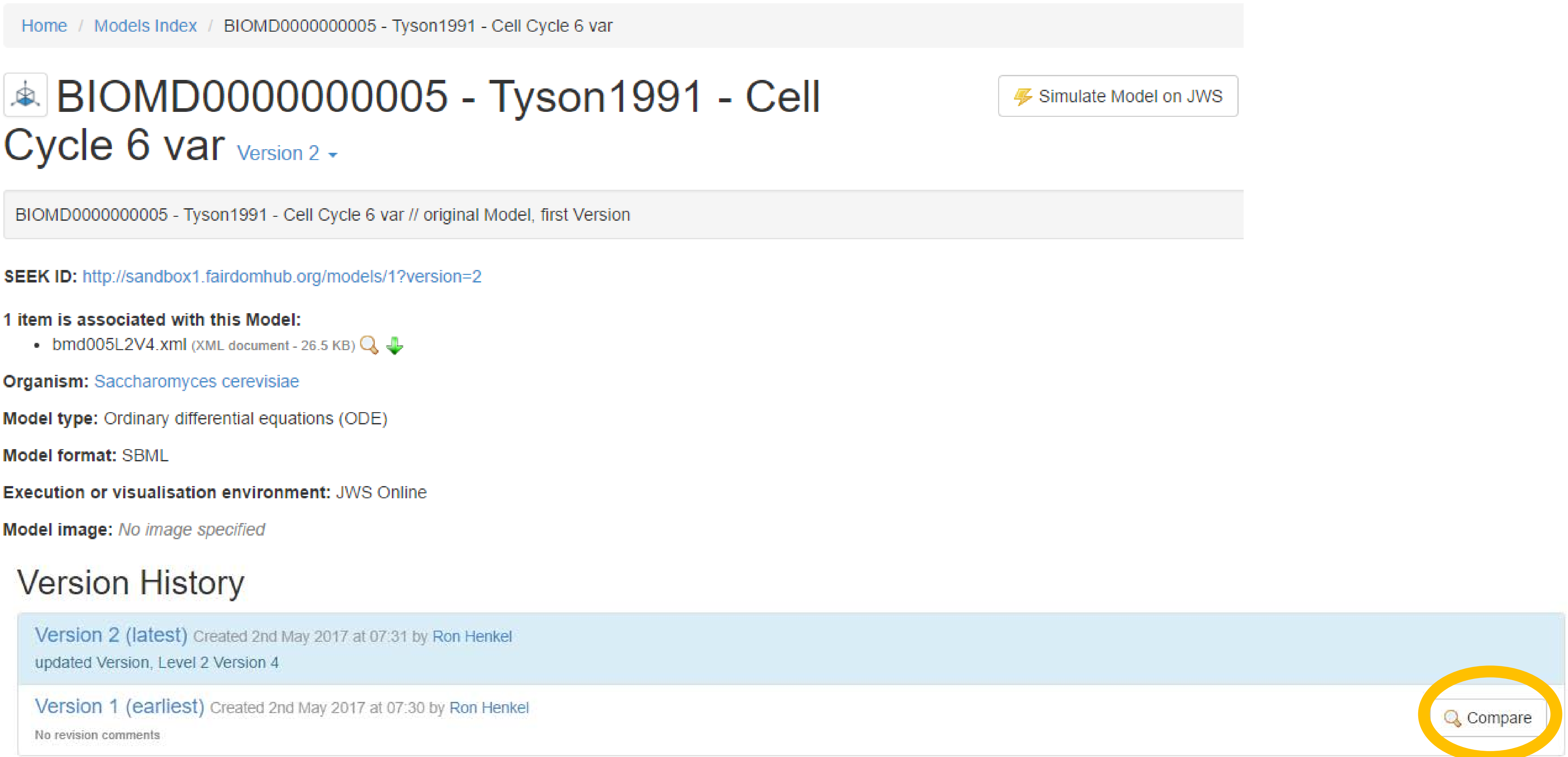


```
<species id="X" name="ADP" compartment="cell">
  <annotation>
    <rdf:Description rdf:about="X">
      <bqbiol:is>
        <rdf:li rdf:resource="urn:miriam:obo.chebi:CHEBI%3A15422"/>
        <rdf:li rdf:resource="urn:miriam:kegg.compound:C00002"/>
      </bqbiol:is>
    </rdf:Description>
  </annotation>
  <notes>
    <p xmlns=http://www.w3.org/1999/xhtml>this is ATP</p>
  </notes>
</species>
```

Waltemath, Henkel et al. (2013) Oxford Bioinf.

de.NBI GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

Version Control in SEEK



Home / Models Index / BIOMD0000000005 - Tyson1991 - Cell Cycle 6 var

BIOMD0000000005 - Tyson1991 - Cell Cycle 6 var Version 2

Simulate Model on JWS

BIOMD0000000005 - Tyson1991 - Cell Cycle 6 var // original Model, first Version

SEEK ID: http://sandbox1.fairdomhub.org/models/1?version=2

1 item is associated with this Model:

- bmd005L2V4.xml (XML document - 26.5 KB)

Organism: Saccharomyces cerevisiae

Model type: Ordinary differential equations (ODE)

Model format: SBML

Execution or visualisation environment: JWS Online

Model image: *No image specified*

Version History

Version 2 (latest) Created 2nd May 2017 at 07:31 by Ron Henkel
updated Version, Level 2 Version 4

Version 1 (earliest) Created 2nd May 2017 at 07:30 by Ron Henkel
No revision comments

Compare

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SEMS simulation experiment management system

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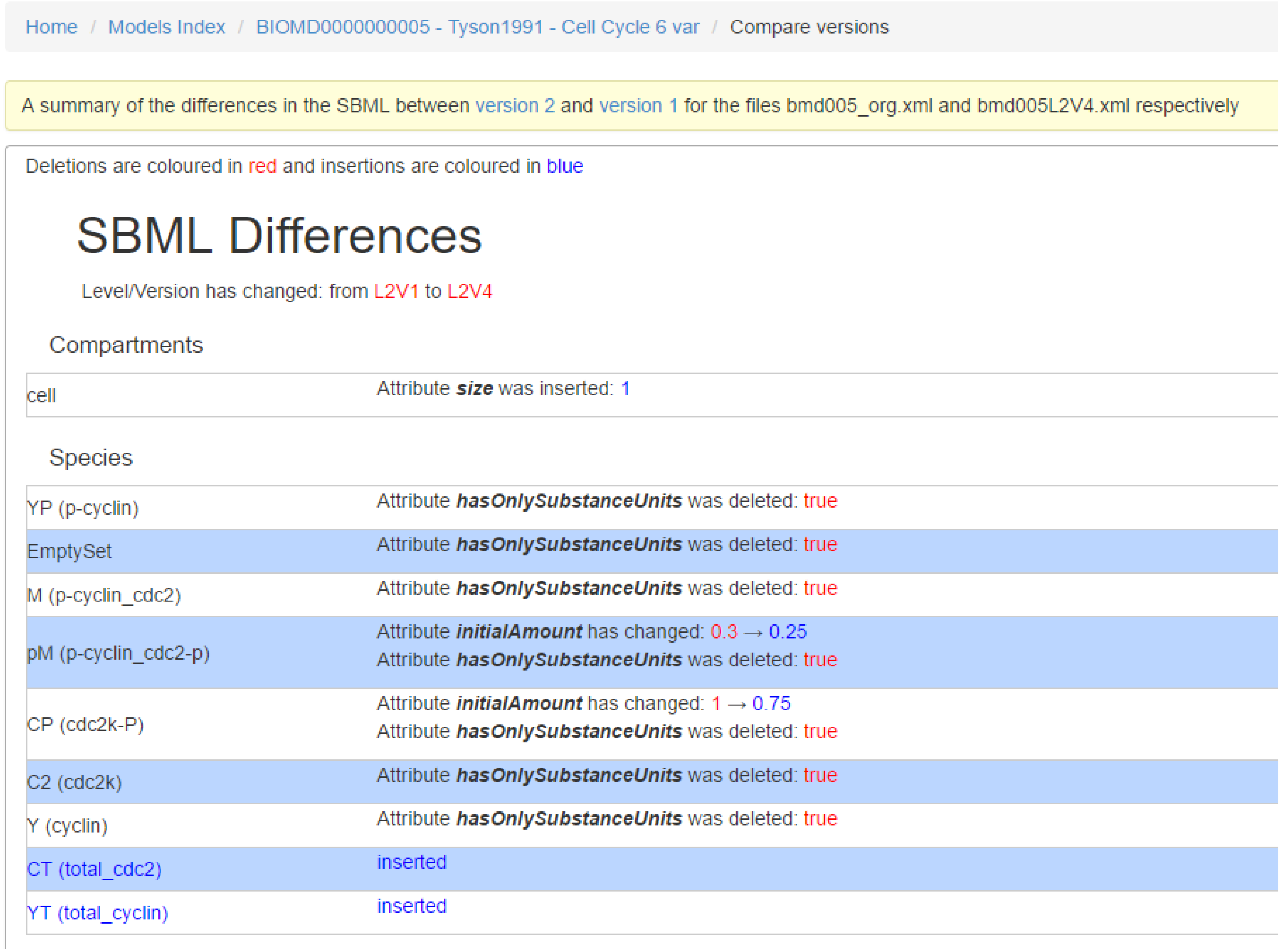


Home / Models Index / BIOMD0000000005 - Tyson1991 - Cell Cycle 6 var / Compare versions

A summary of the differences in the SBML between version 2 and version 1 for the files bmd005_org.xml and bmd005L2V4.xml respectively

Deletions are coloured in red and insertions are coloured in blue

SBML Differences

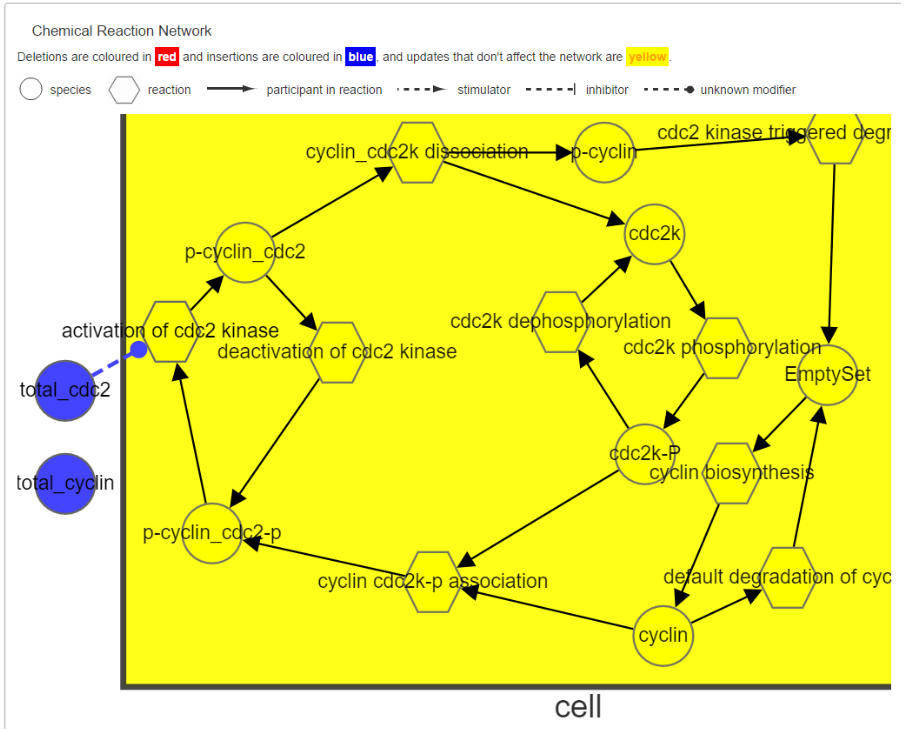
Level/Version has changed: from L2V1 to L2V4

Compartments

cell	Attribute ***size*** was inserted: 1

Species

YP (p-cyclin)	Attribute ***hasOnlySubstanceUnits*** was deleted: true
EmptySet	Attribute ***hasOnlySubstanceUnits*** was deleted: true
M (p-cyclin_cdc2)	Attribute ***hasOnlySubstanceUnits*** was deleted: true
pM (p-cyclin_cdc2-p)	Attribute ***initialAmount*** has changed: 0.3 → 0.25 Attribute ***hasOnlySubstanceUnits*** was deleted: true
CP (cdc2k-P)	Attribute ***initialAmount*** has changed: 1 → 0.75 Attribute ***hasOnlySubstanceUnits*** was deleted: true
C2 (cdc2k)	Attribute ***hasOnlySubstanceUnits*** was deleted: true
Y (cyclin)	Attribute ***hasOnlySubstanceUnits*** was deleted: true
CT (total_cdc2)	inserted
YT (total_cyclin)	inserted

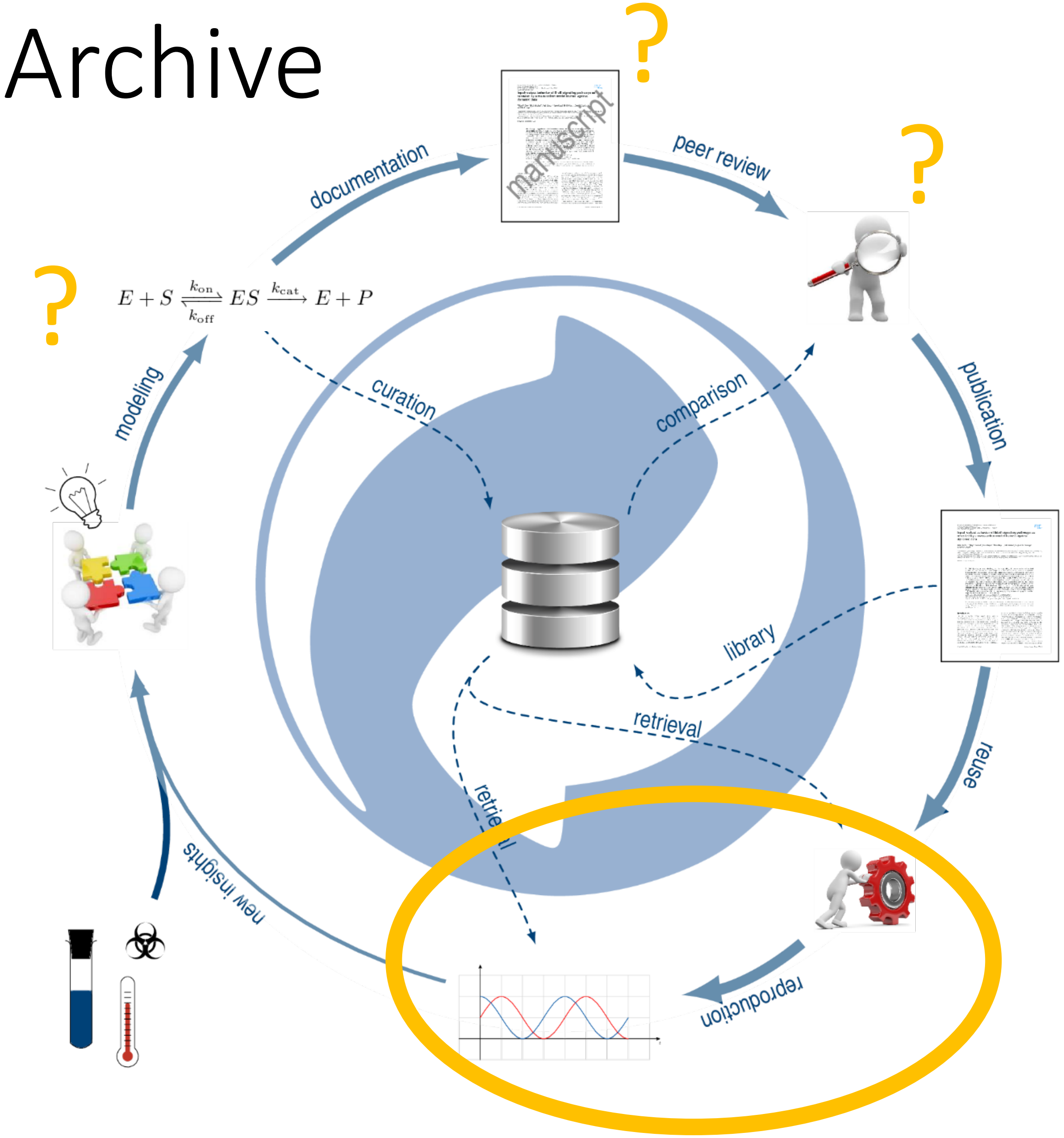


Chemical Reaction Network

Deletions are coloured in red and insertions are coloured in blue, and updates that don't affect the network are yellow.

deNBI GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

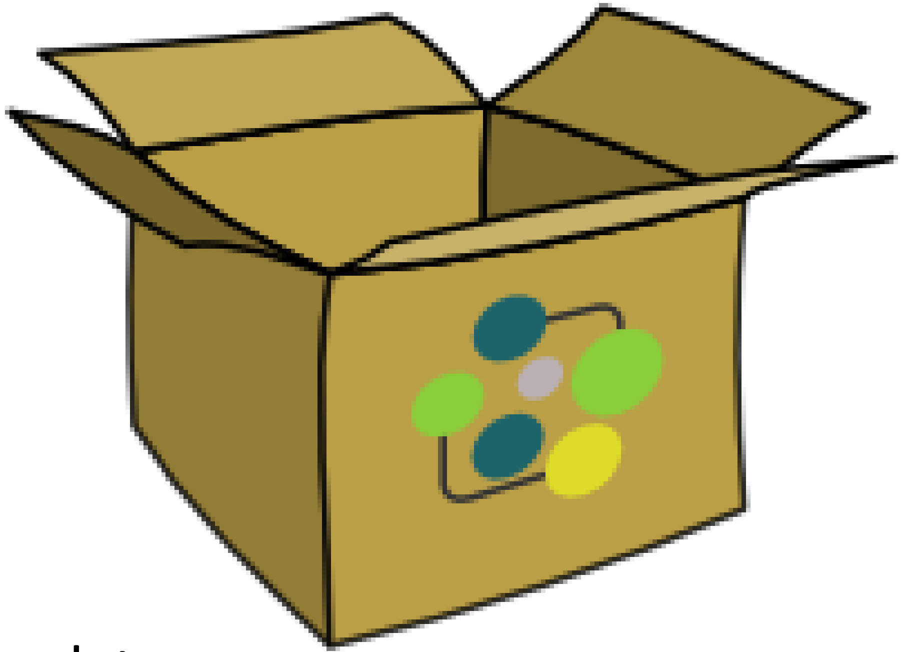
Combine Archive



JWS, BioModels or Physiome Model Repository offer simulation description, graphical representation or publication along with a model

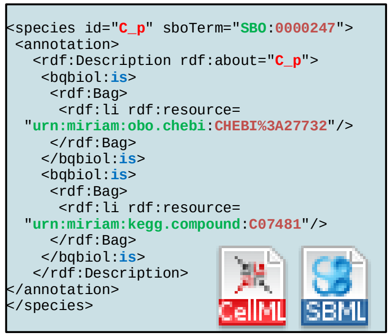
Combine Archive

- Bundling files
- Shipping results
- Exchanging data
- Keeping provenance



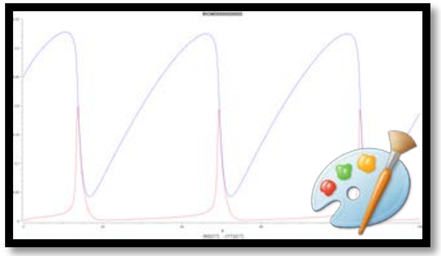
- Encoding: zip-like file with a manifest & meta-data
- Generate, modify & share through WebCAT

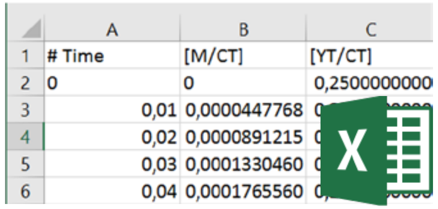
model



```
<species id="C_p" sboTerm="SBO:0000247">
 <annotation>
   <rdf:Description rdf:about="C_p">
    <bqbiol:is>
     <rdf:Bag>
      <rdf:li rdf:resource=
  "urn:miriam:obo.chebi:CHEBI%3A27732"/>
     </rdf:Bag>
    </bqbiol:is>
    <bqbiol:is>
     <rdf:Bag>
      <rdf:li rdf:resource=
  "urn:miriam:kegg.compound:C07481"/>
     </rdf:Bag>
    </bqbiol:is>
   </rdf:Description>
</annotation>
</species>
```

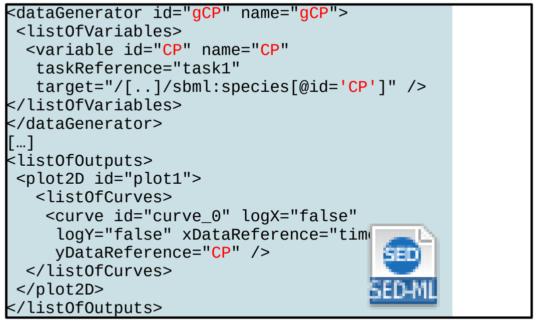
simulation results and data





	A	B	C
1	# Time	[M/CT]	[YT/CT]
2	0	0	0,2500000000
3	0,01	0,0000447768	0
4	0,02	0,0000891215	0
5	0,03	0,0001330460	0
6	0,04	0,0001765560	0,

simulation description



```
<dataGenerator id="gCP" name="gCP">
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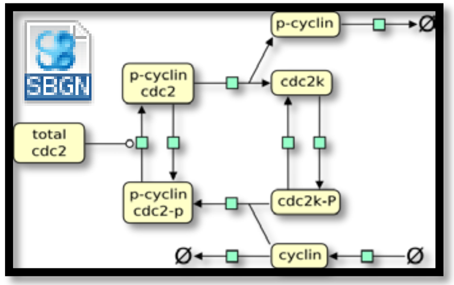
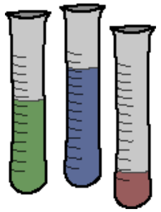
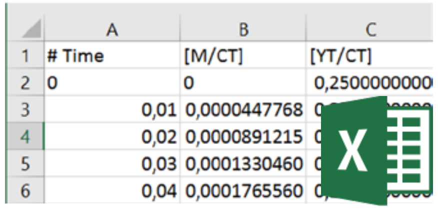
  <variable id="CP" name="CP"
   taskReference="task1"
   target="/[..]/sbml:species[@id='CP']" />
</listOfVariables>
</dataGenerator>
[…]
<listOfOutputs>
 <plot2D id="plot1">
   <listOfCurves>
    <curve id="curve_0" logX="false"
     logY="false" xDataReference="tim
     yDataReference="CP" />
  </listOfCurves>
 </plot2D>
</listOfOutputs>
```

graphical representation



wetlab data





	A	B	C
1	# Time	[M/CT]	[YT/CT]
2	0	0	0,2500000000
3	0,01	0,0000447768	0
4	0,02	0,0000891215	0
5	0,03	0,0001330460	0
6	0,04	0,0001765560	0

manuscript

Proc. Natl. Acad. Sci. USA
Vol. 88, pp. 7328–7332, August 1991
Cell Biology

Modeling the cell division cycle: cdc2 and cyclin interactions

(maturation promoting factor/metaphase arrest/*wee1*/*cdc25*)

JOHN J. TYSON

Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061

BMC Bioinformatics

Software

COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project

Frank T Bergmann[1], Richard Adams[2], Stuart Moodie[3,4], Jonathan Cooper[5], Mihai Glont[3], Martin Golebiewski[6], Michael Hucka[7], Camille Laibe[3], Andrew K Miller[8], David P Nickerson[8], Brett G Olivier[9], Nicolas Rodriguez[10], Herbert M Sauro[11], Martin Scharm[12], Stian Soiland-Reyes[13], Dagmar Waltemath[12], Florent Yvon[3] and Nicolas Le Novère[10,3]*

the current workspace contains the following archives:

::biomd005 showcase

id: 57b5c203-6a00-482e-a371-71b6eae64796

name: BIOMD005 showcase

[Simulate] [Export RO] [Download] [Rename] [Delete]

Archive Content

/
- BIOMD0000000005_SBGN.png
- BIOMD0000000005_SBML2Latex.pdf
- bmd005.cps
- bmd005.png
- **bmd005.sedml**
- model.xml
- pnas01066-0438.pdf

the current workspace contains the following archives:

::biomd005 showcase

id: 57b5c203-6a00-482e-a371-71b6eae64796

name: BIOMD005 showcase

[Simulate] [Export RO] [Download] [Rename] [Delete]

Archive Content

bmd005.sedml

file name: bmd005.sedml
file path: /bmd005.sedml
format: http://identifiers.org/combine.specifications/sed-ml
size: 2.22 KB
master: yes

[Add OMEX meta] [Add RDF/XML meta] [Download] [Edit] [Delete]

OMEX entry

created: 9/15/2016, 10:38:01 AM
modified: [9/15/2016, 10:38:01 AM]
description:
creators:

Ron Henkel *HITS*
ron.henkel@uni-rostock.de

https://cat.bio.informatik.uni-rostock.de/

Universität Rostock
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SEMS
simulation experiment management system

Heidelberger Institut für Theoretische Studien
HITS

CombineArchiveWeb

the current workspace contains the following archives:

::biomd005 showcase

[start] [about] [stats] [create]

id: 57b5c203-6a00-482e-a371-71b6eae64796

name: BI D005 showcase

[Simulate] [Ex ort RO] [Download] [Rename] [Delete]

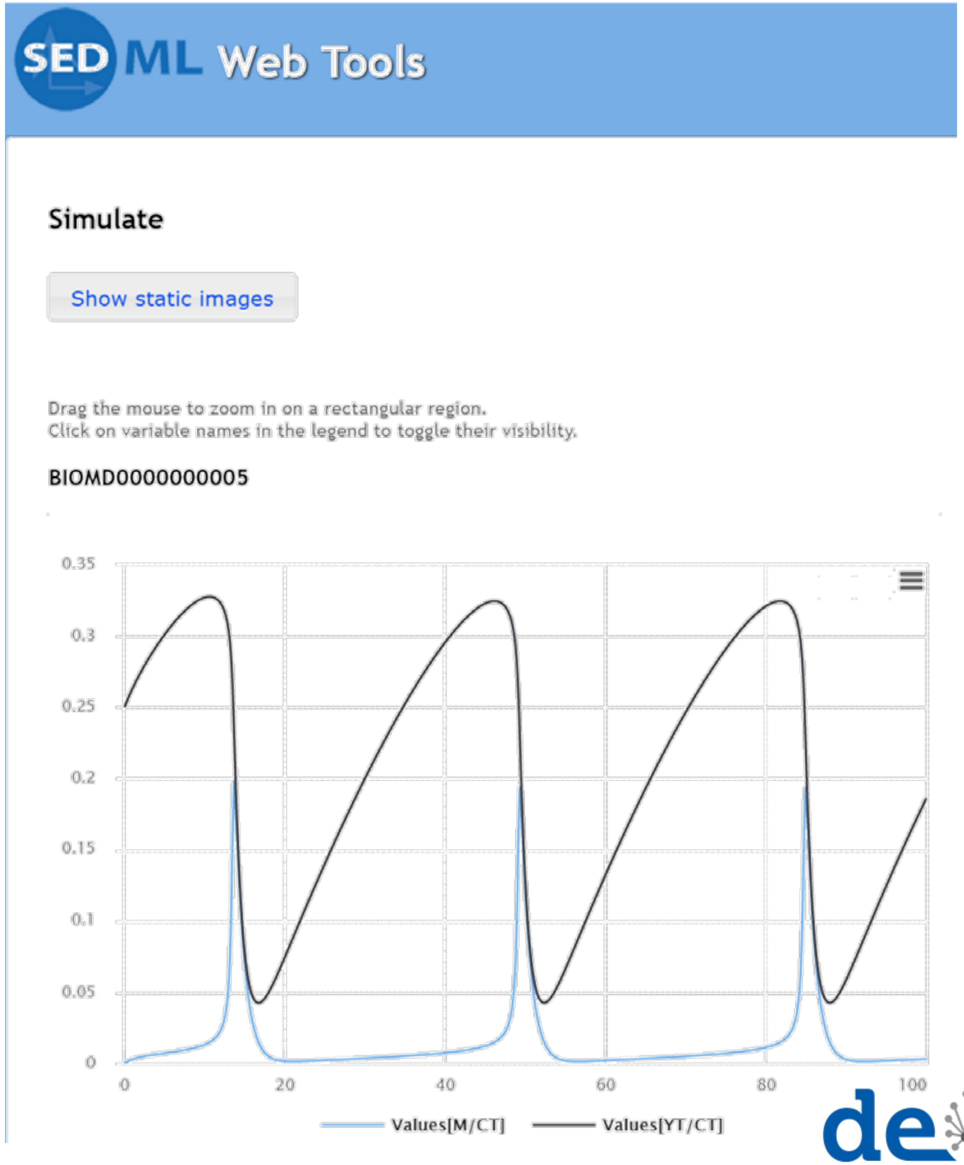
UPLOAD FILES

fetch file from remote url Fetch!

Archive Content

[New folder]

- /
  - BIOMD0000000005_SBGN.png
  - BIOMD0000000005_SBML2Latex.pdf
  - bmd005.cps
  - bmd005.png
  - **bmd005.sedml**
  - model.xml
  - pnas01066-0438.pdf



SEDML Web Tools

Simulate

Show static images

Drag the mouse to zoom in on a rectangular region.
Click on variable names in the legend to toggle their visibility.

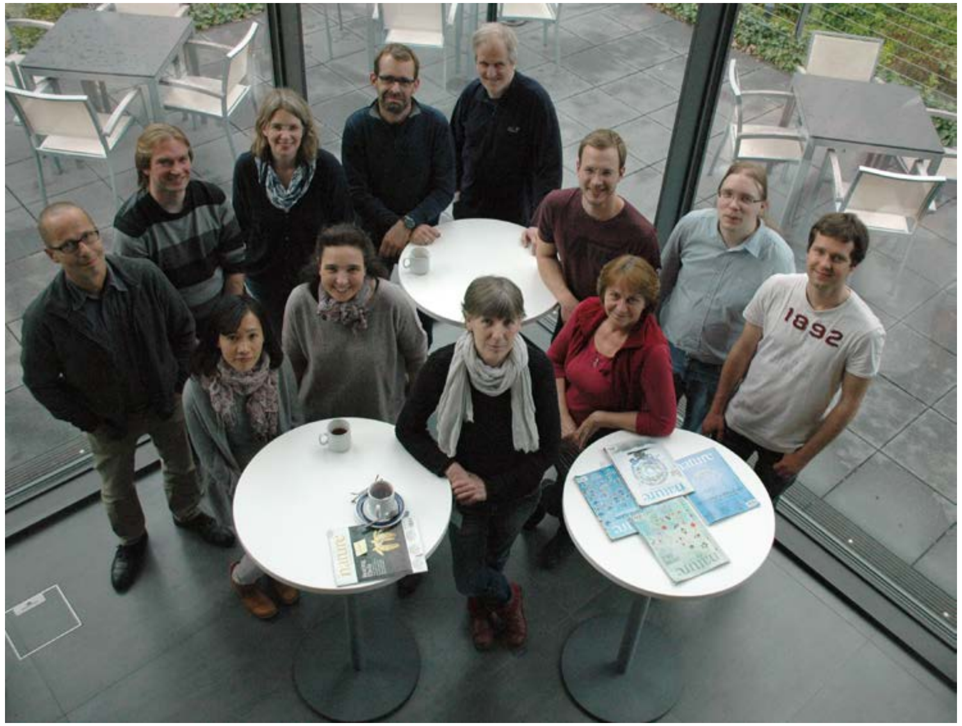
BIOMD0000000005

http://sysbioapps.dyndns.org/SED-ML_Web_Tools

de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

Thank you!

Sems Group Rostock



SDBV Group Heidelberg

Publication

- Waltemath, D., Henkel, R., Hälke, R., Scharm, M., & Wolkenhauer, O. (2013). Improving the reuse of computational models through version control.*Bioinformatics*, *29*(6), 742-748.
- Bergmann, F. T., Adams, R., Moodie, S., Cooper, J., Glont, M., Golebiewski, M., ... & Olivier, B. G. (2014). COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. *BMC bioinformatics*,*15*(1), 1.
- Scharm, M., Wolkenhauer, O., & Waltemath, D. (2015). An algorithm to detect and communicate the differences in computational models describing biological systems. *Bioinformatics*, btv484.