





# Strategies for integrated management of computational biology models and associated simulations

Ron Henkel

Department of Systems Biology and Bioinformatics
The University of Rostock

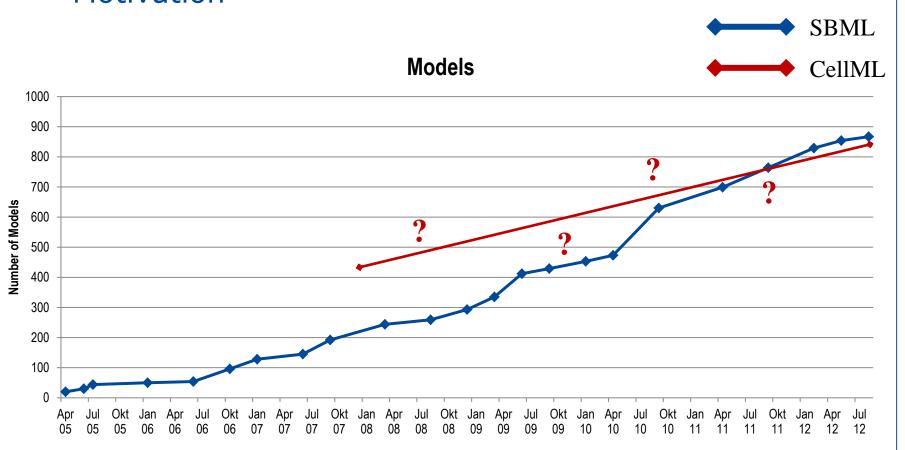








## **Motivation**



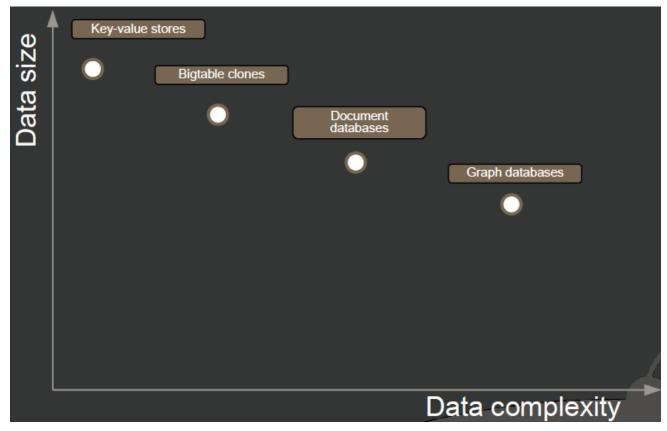
SBML Data from BioModels Database, CellML data from Tommy Yu







# NoSQL Data Models



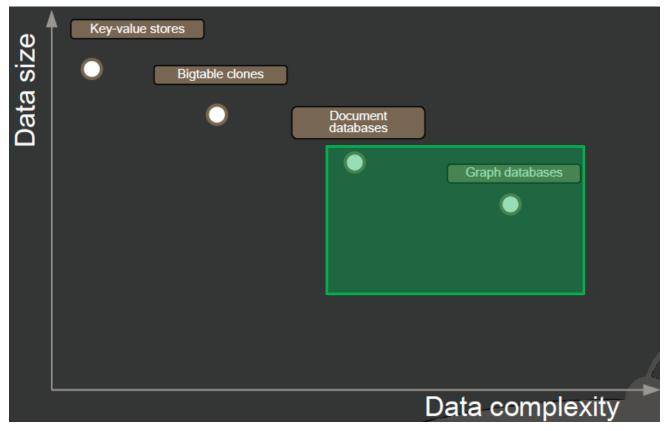
Taken from: http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.174.8830&rep=rep1&type=pdf







# NoSQL Data Models



Taken from: http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.174.8830&rep=rep1&type=pdf







## Available Data

### Model and Simulation



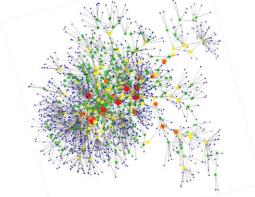
- Constituent names
- XML encoded representation







## Annotation & Ontologies



- Biochemical background
- Synonyms









## A model's network

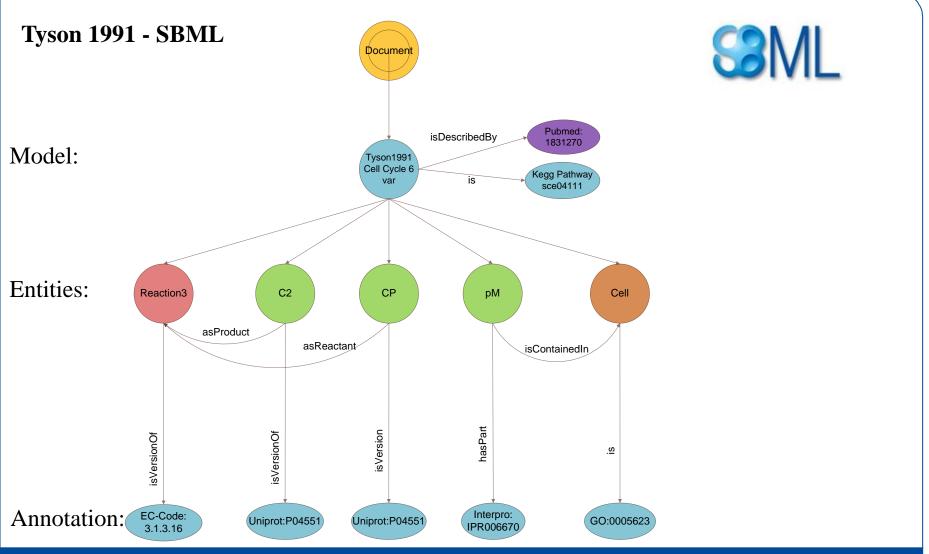


- Model structure
- Aggregation values
- Model related data





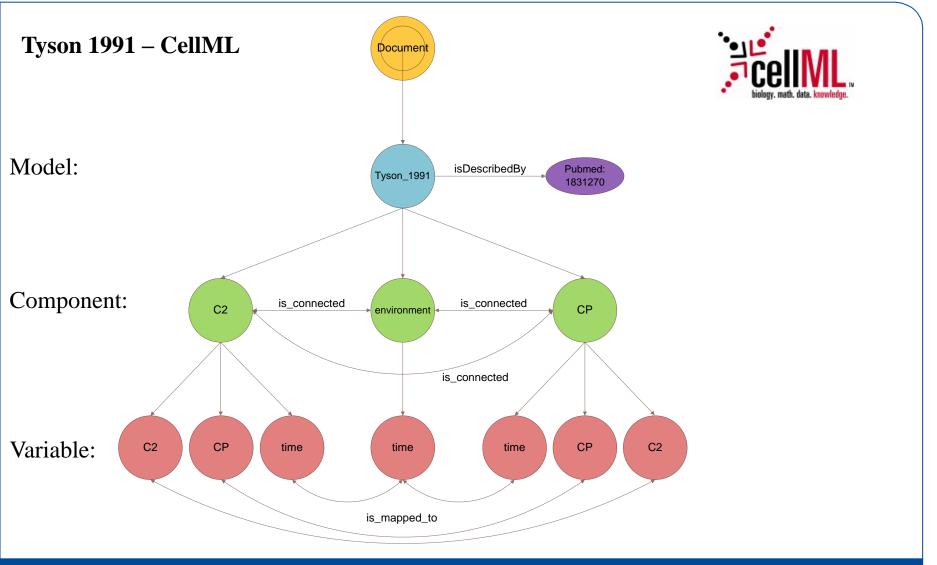








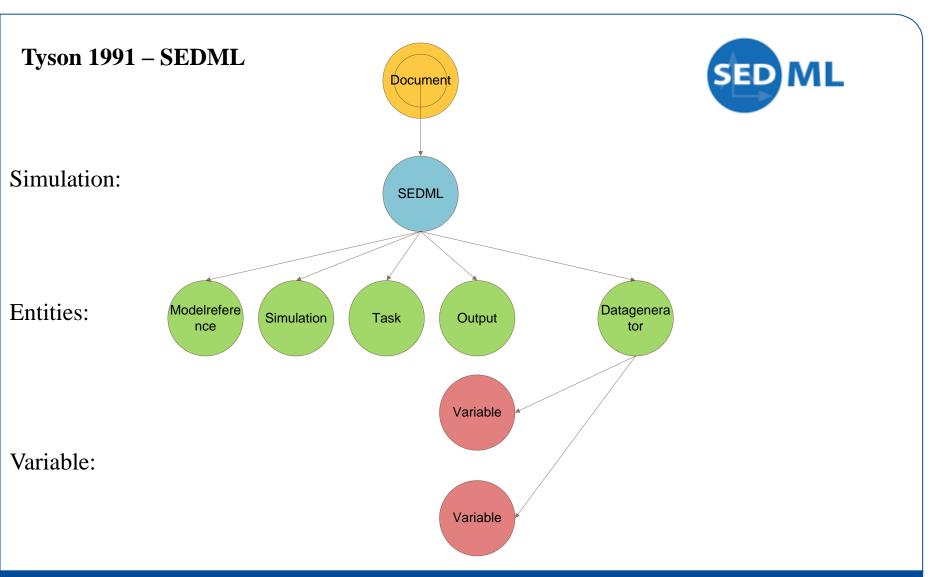








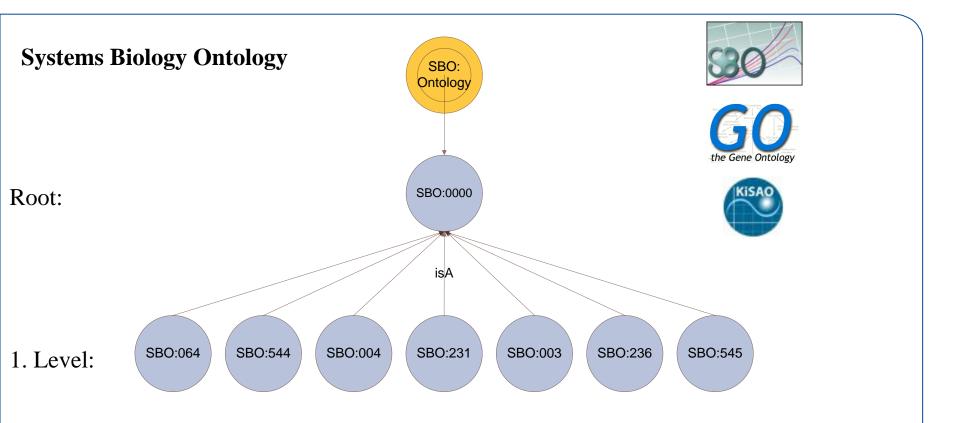












All Ontologies available in OWL can be added easily











19.09.2013





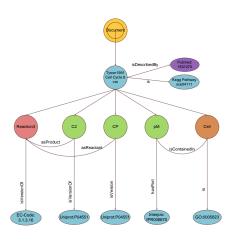


















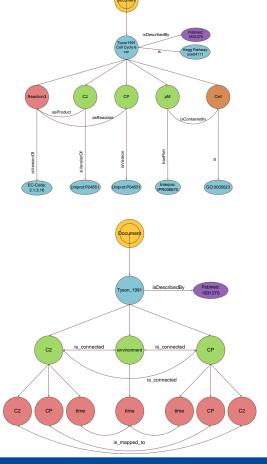
















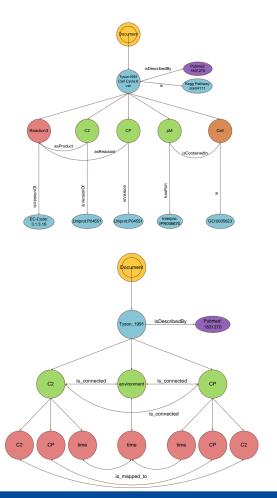


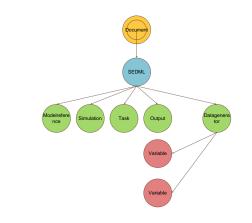














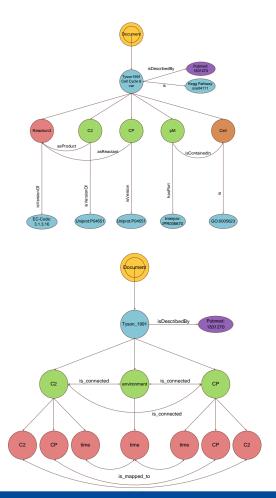


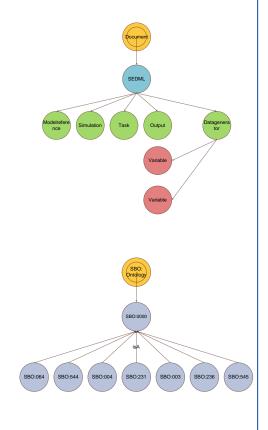








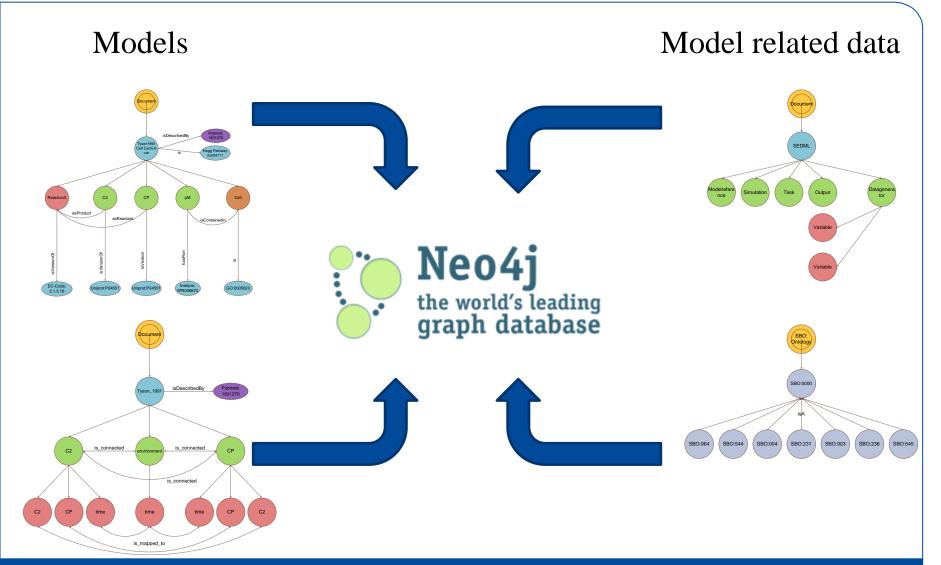










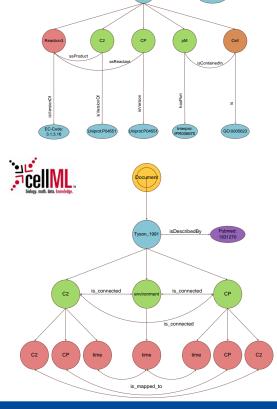




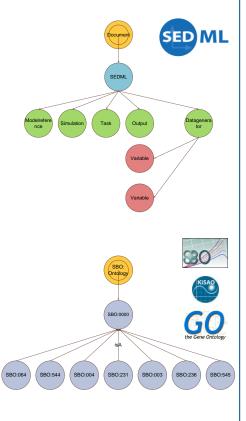




SML



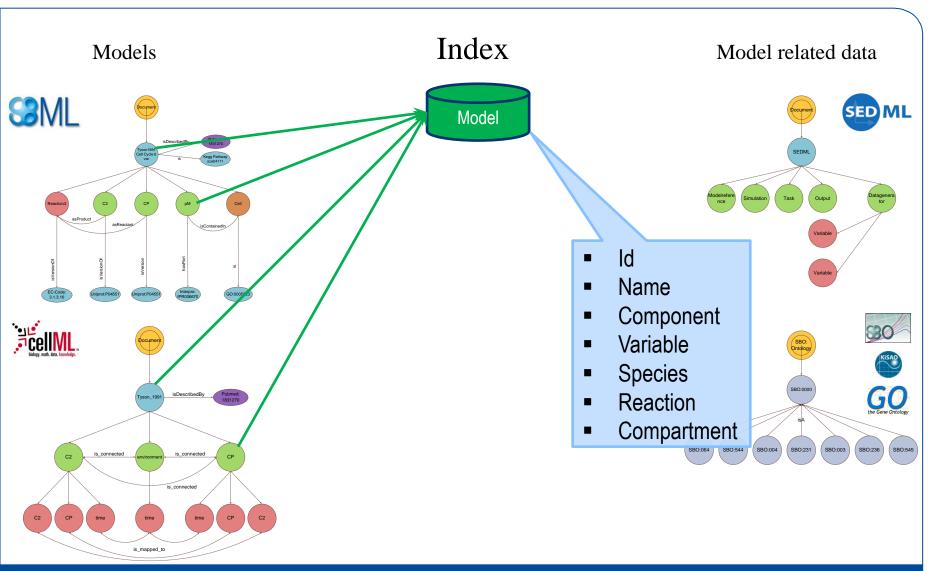
# Index







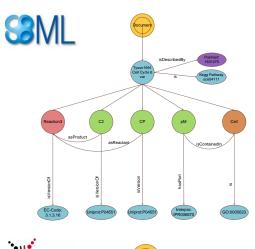


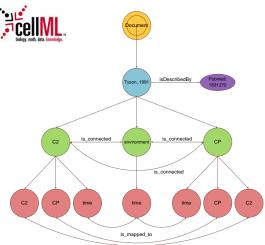




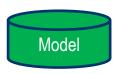


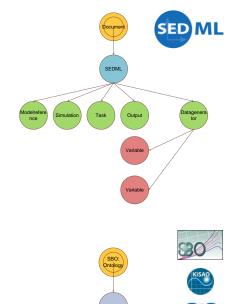


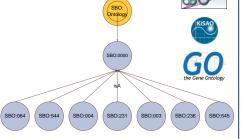




## Index



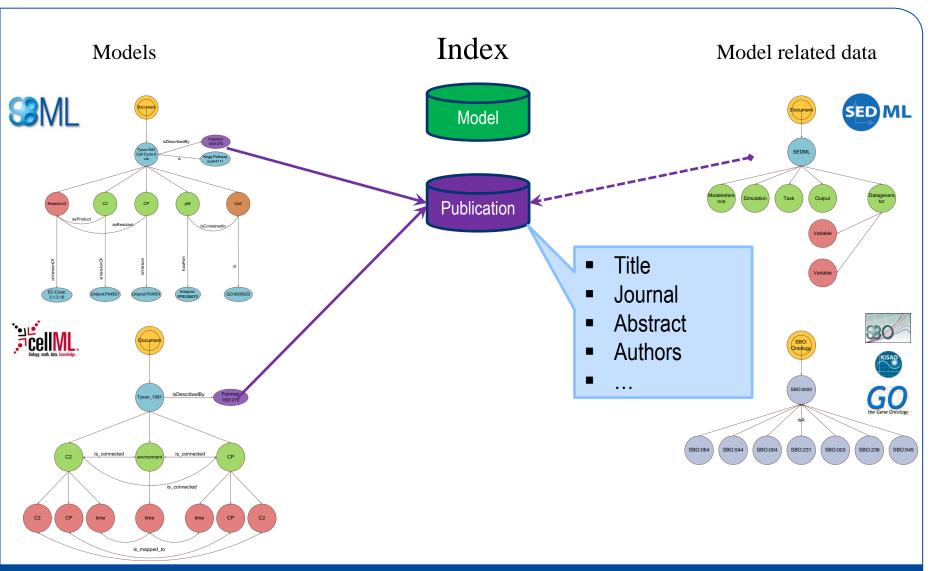








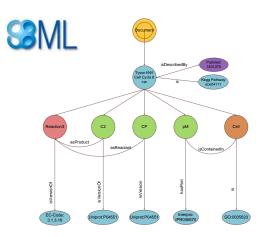


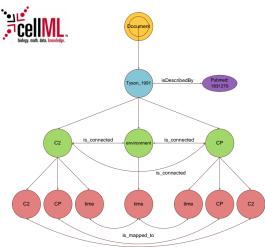




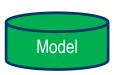




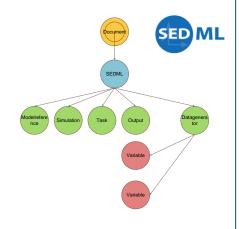


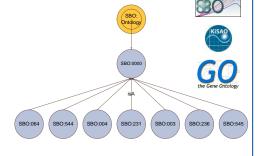


## Index





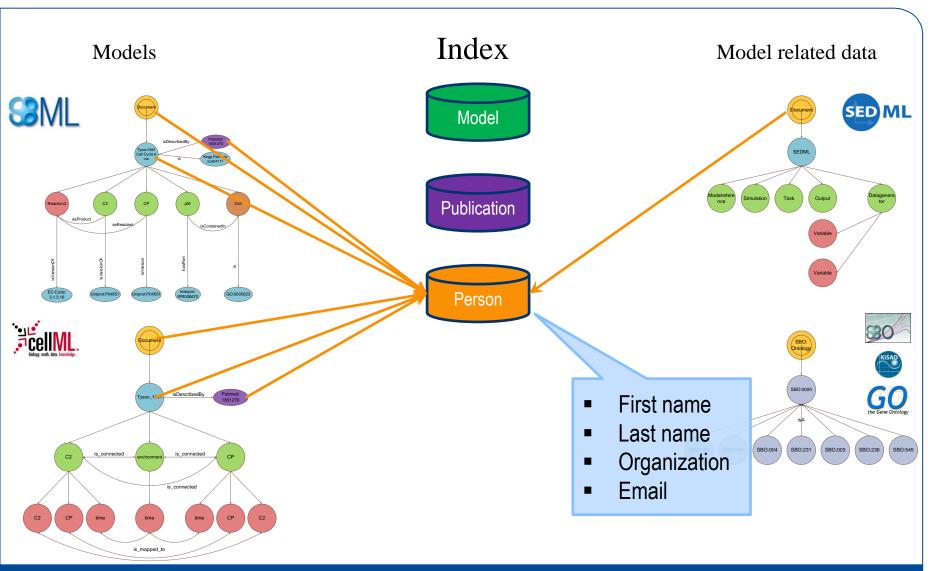








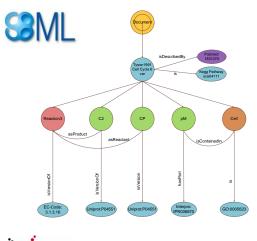


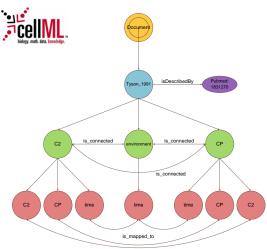




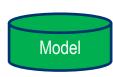






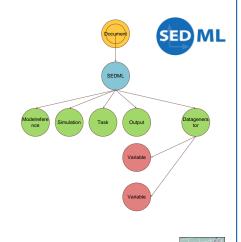


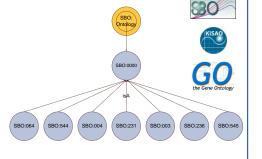
## Index







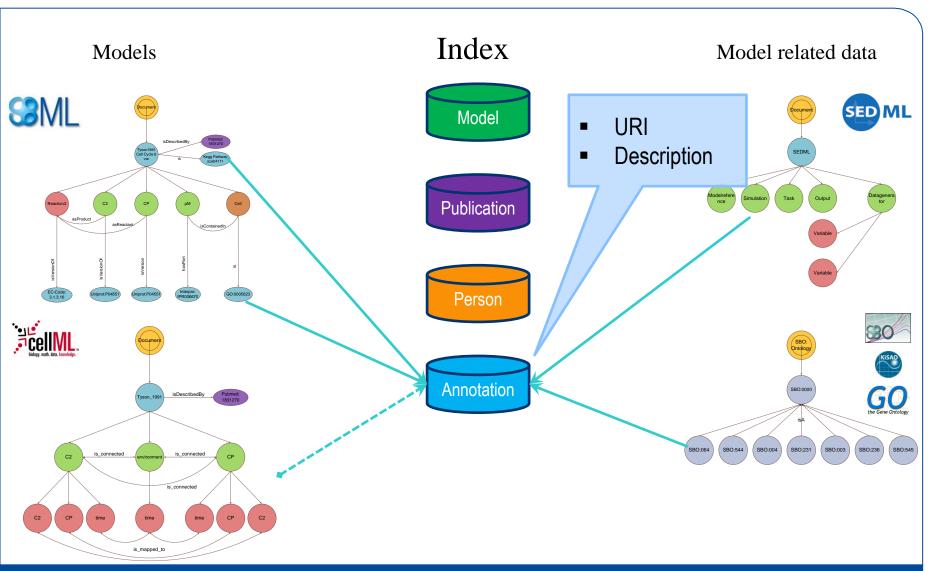








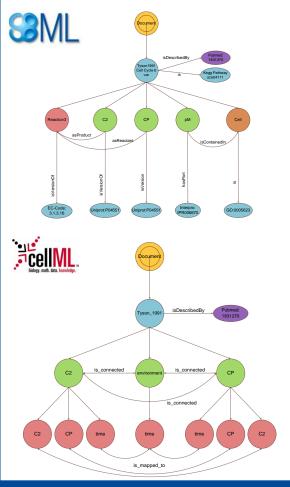




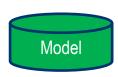








## Index

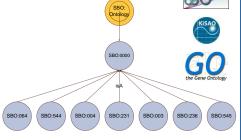








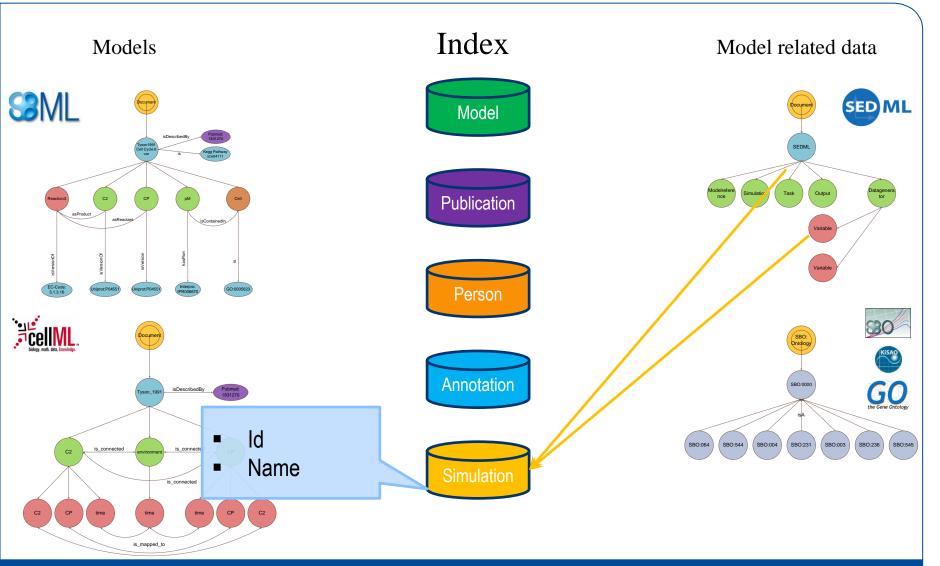








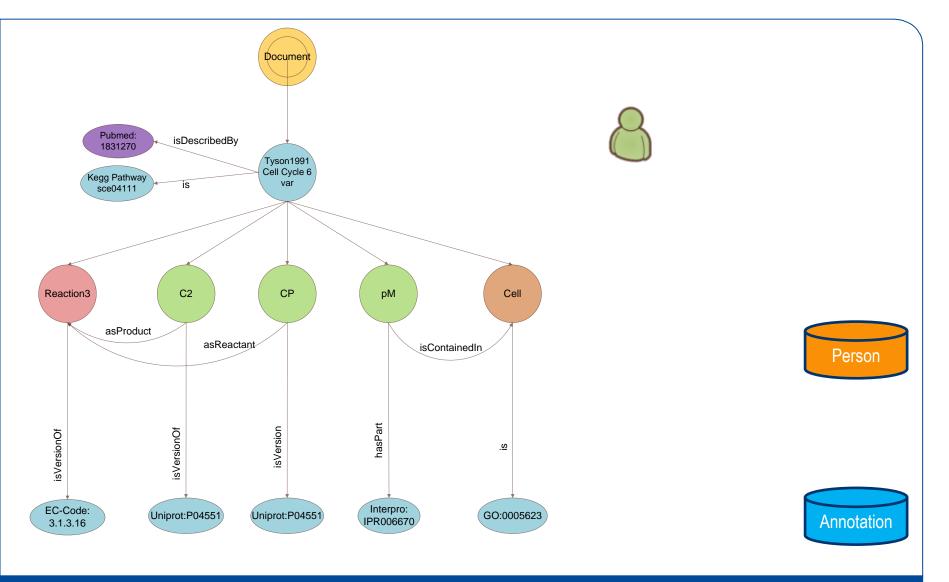








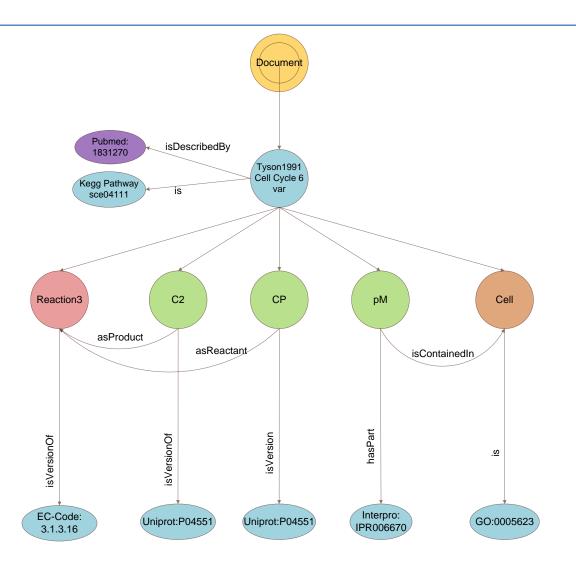














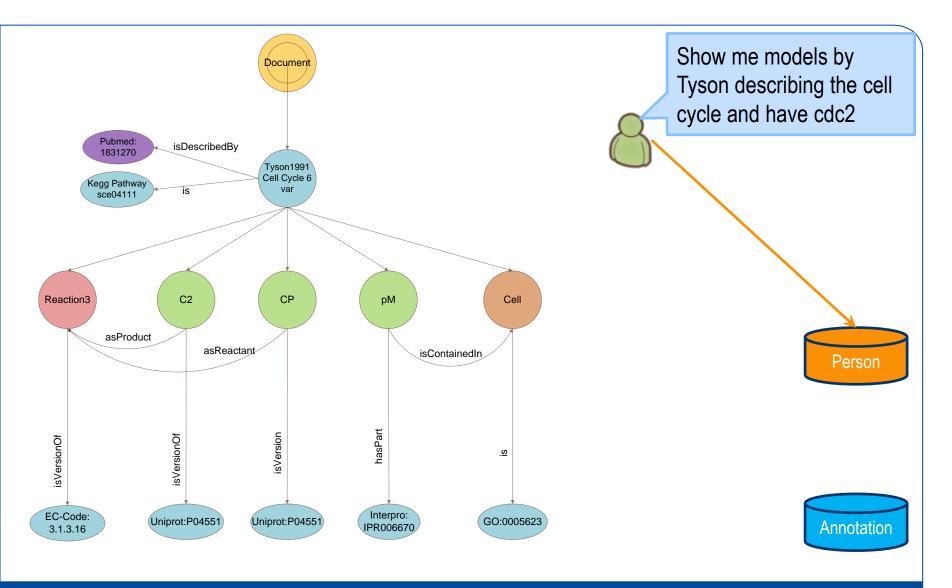


19.09.2013







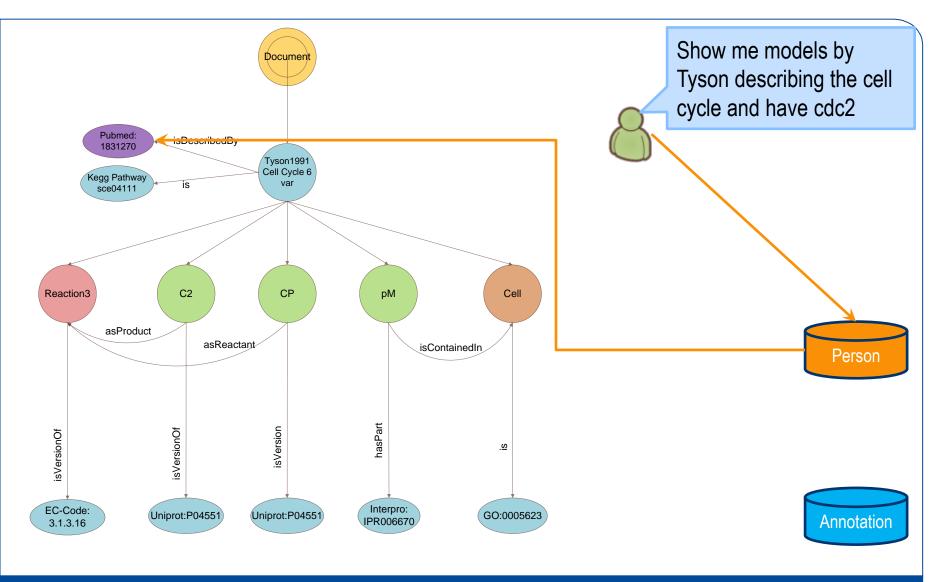








12

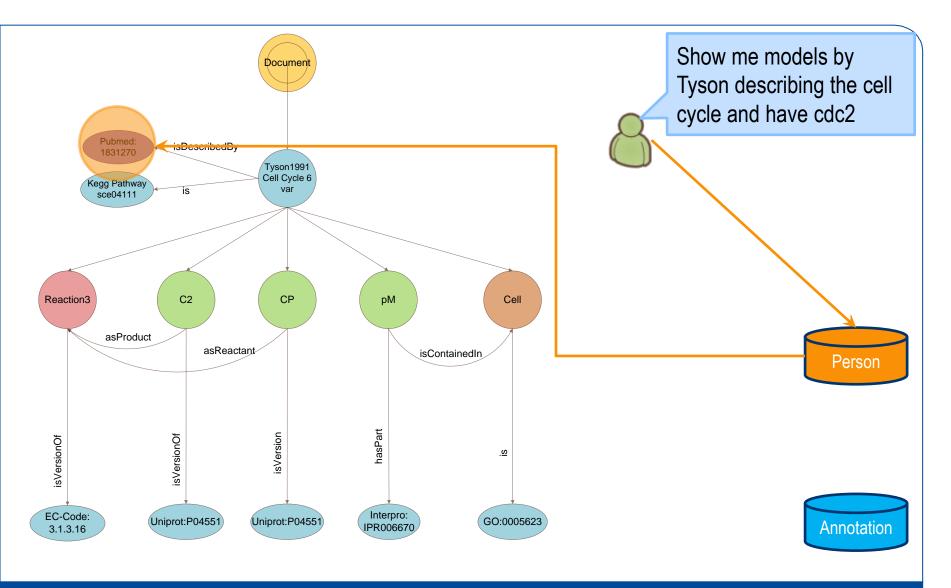


19.09.2013





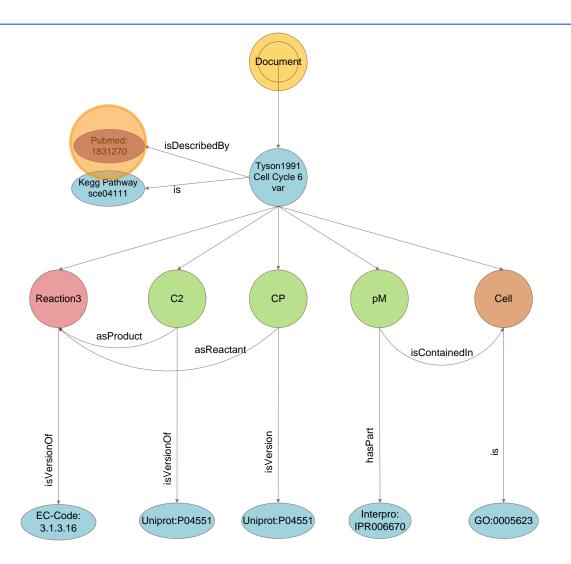












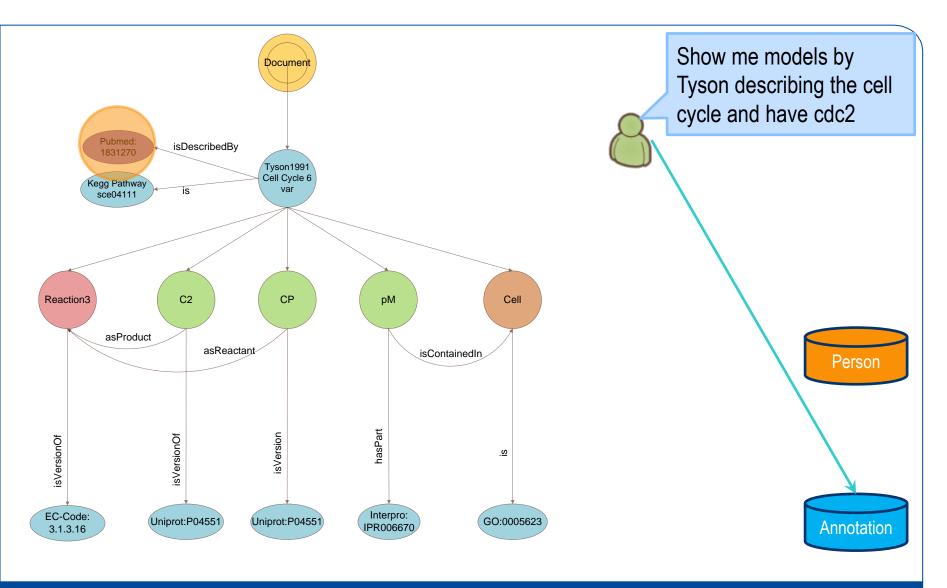








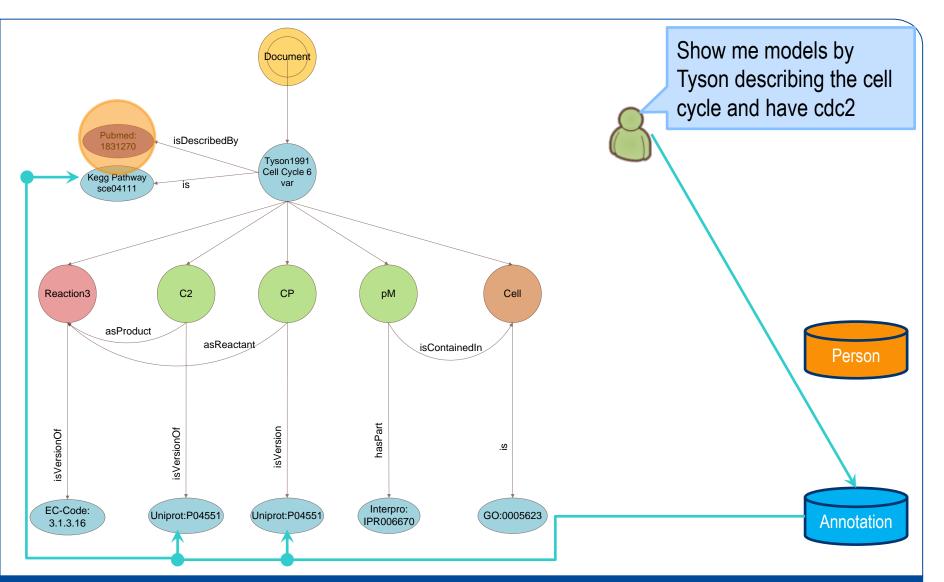








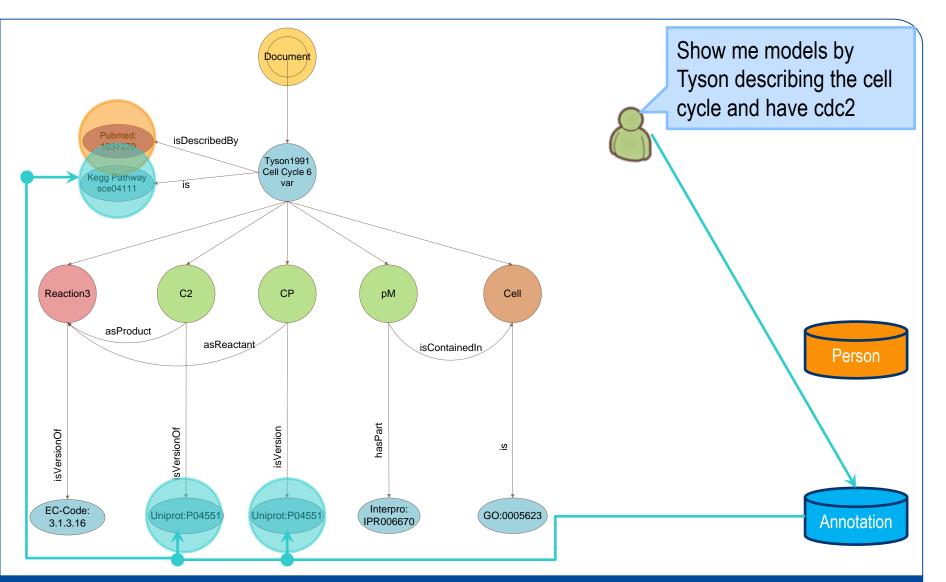








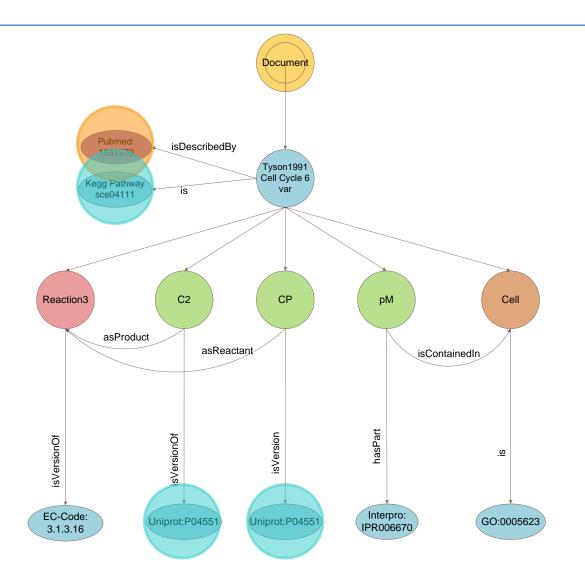












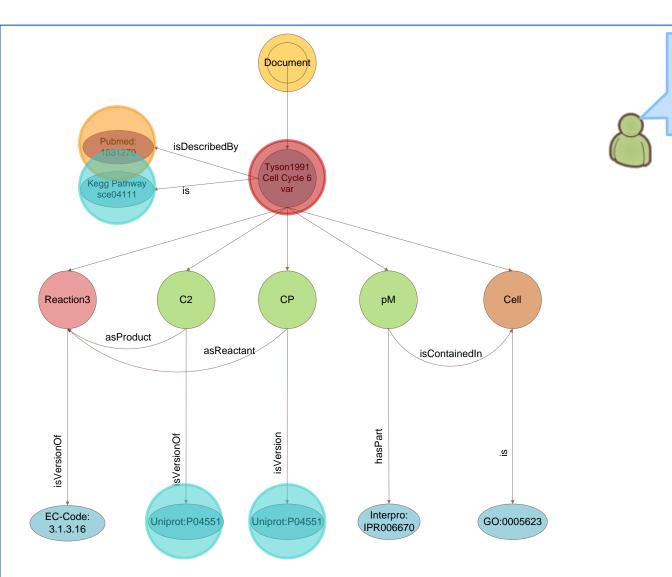












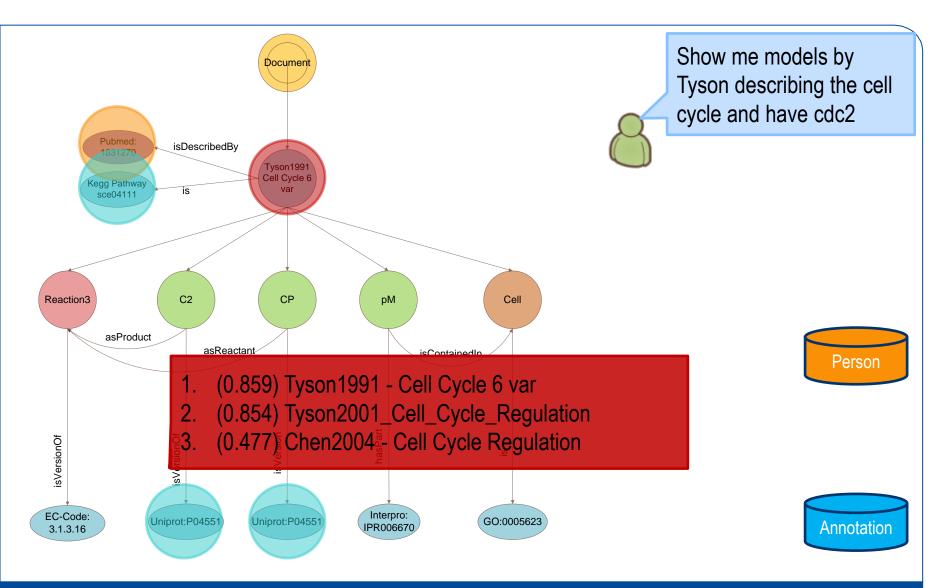








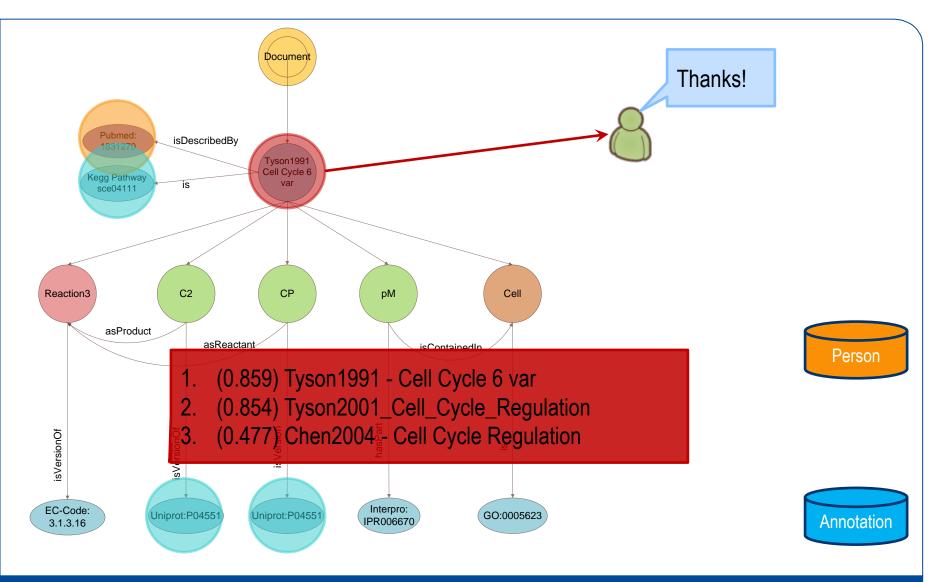


















## **Preliminary Results**

- Dataset 1:
  - curated models available in Biomodels DB
  - 841 exposed CellML Models from Physiome Model Repository
  - 38 SED-ML files (from our Cell-Cycle side project Uni Rostock)

- Webpage explaining the web service:
  - http://sems.uni-rostock.de/projects/morre/
- Pmr2 staging machine already implements the web service:
  - http://staging.physiomeproject.org/morre\_pmr2\_search
  - CellML only!







## **Preliminary Results**

- Dataset 2:
  - 140.811 models from path2models project
- Database statistics:
  - 45,534,192 nodes
  - **31,784,961** properties

- 492,296,146 relationships
- 81GB database disk usage

- Currently no annotation index...
  - Downloading the content of 4,583,240 unique URIs is beyond the capability of my desktop or laptop machine





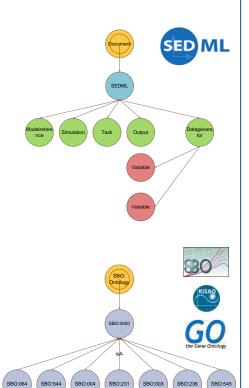


### Models

SML

# Links

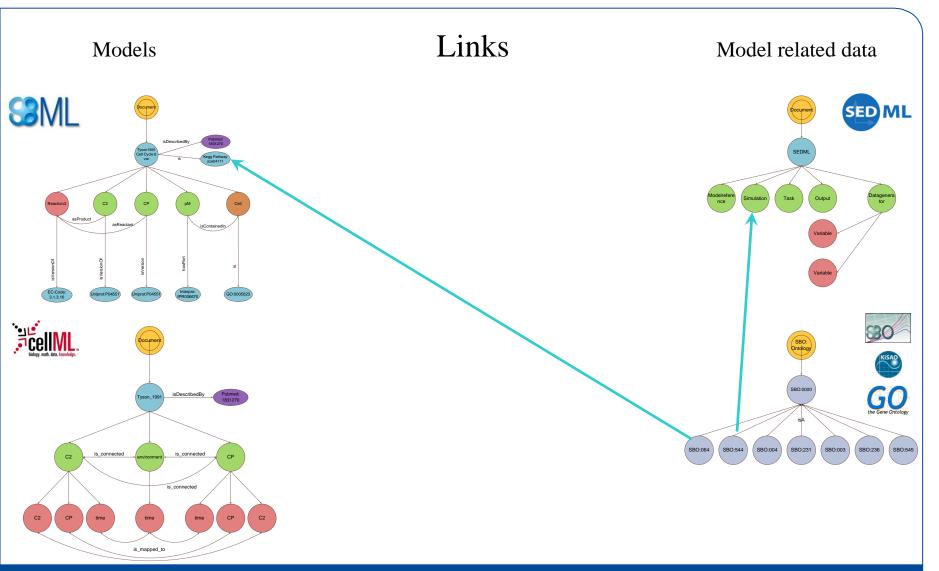
### Model related data







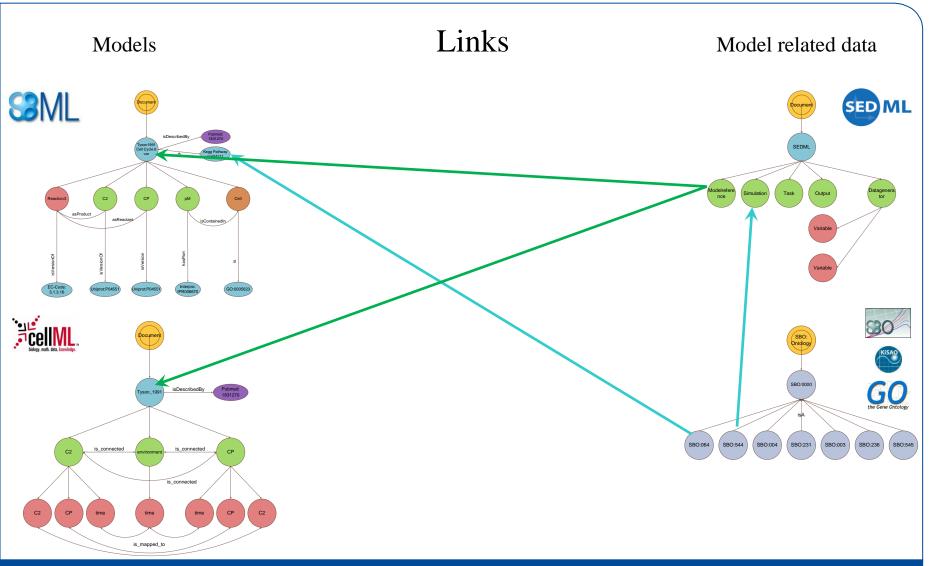








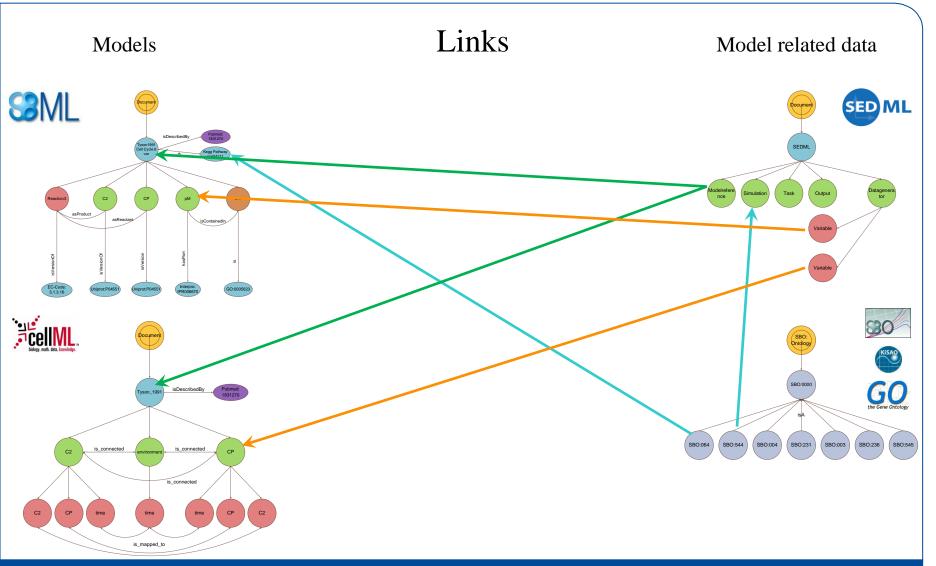
















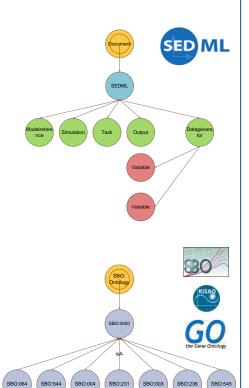


### Models

SML

# Links

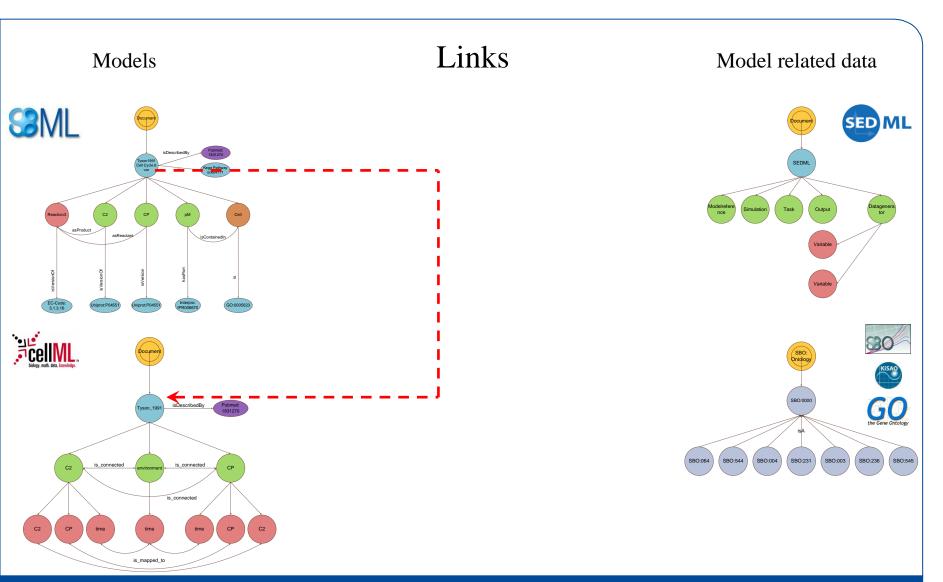
### Model related data

















MATCH o:GOOntology RETURN count(o);

MATCH o:GOOntology WHERE o<-[:IS\_ONTOLOGY\_ENTRY]-() RETURN count(o);







MATCH o:GOOntology RETURN count(o);

==> 39787

MATCH o:GOOntology WHERE o<-[:IS\_ONTOLOGY\_ENTRY]-() RETURN count(o);







MATCH o:GOOntology RETURN count(o);

==> 39787

MATCH o:GOOntology WHERE o<-[:IS\_ONTOLOGY\_ENTRY]-() RETURN count(o);

==> 1097







Retrieve the three most used annotations:

MATCH r:RESOURCE, r-[rel:BELONGS\_TO]->()

WITH r, count(rel) AS numOfRelations

ORDER BY numOfRelations DESC LIMIT 3

RETURN r.URI, numOfRelations;







Retrieve the three most used annotations:

MATCH r:RESOURCE, r-[rel:BELONGS\_TO]->()
WITH r, count(rel) AS numOfRelations
ORDER BY numOfRelations DESC LIMIT 3
RETURN r.URI, numOfRelations;

r.URI	numOfRelations
urn:miriam:biomodels.sbo:SBO:0000009	1127
urn:miriam:biomodels.sbo:SBO:0000252	509
http://identifiers.org/obo.go/GO:0043241	484







### **Tools**

- All java based:
  - Neo4J a graph database
  - Lucene an index and search tool
  - Jetty a web server
  - A parser for each format
    - CellML Api (java bindings)
    - jLibSBML
    - jSedML







## Take Home Message

Models and related data grow in size and complexity

 Ranked retrieval is a necessary feature for model databases.

 Linking models, simulation and other model related data allows to query the spanned network







Thanks for your attention.

Questions?

ron.henkel@uni-rostock.de