

Formal description and visual modeling of complex biological systems using BioUML workbench and BioUML Network Edition



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Institute of Systems Biology
(spin-off of DevelopmentOnTheEdge.com)

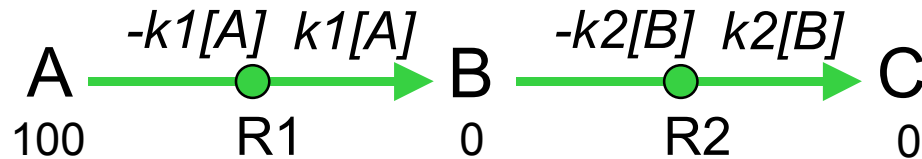
Laboratory of Bioinformatics,
Design Technological Institute of Digital Techniques

Novosibirsk, Russia

Main BioUML concepts and ideas

- Visual modeling
 - Diagram type concept – formally defines graphical notation and provides its incorporation into BioUML workbench (as Java classes or **XML document**)
 - Meta model – problem domain neutral level of abstraction that describes system as compartmentalized graph
 - Automated code generation for model simulation.
- Module concept - allows developer to incorporate databases on biological pathways into BioUML workbench taking into account database peculiarities.
- Plug-in based architecture (Eclipse platform runtime from IBM company).

Meta-model: example of formal description of system from two chemical reactions



ID	A
CC	..
...	..
//	..

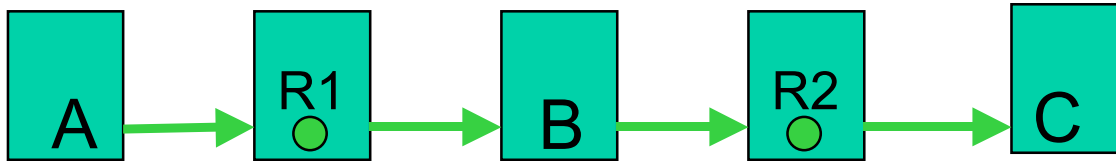
ID	R1
CC	A->B
...	..
//	..

ID	B
CC	..
...	..
//	..

ID	R2
CC	B->C
...	..
//	..

ID	C
CC	..
...	..
//	..

Description of system components in the database

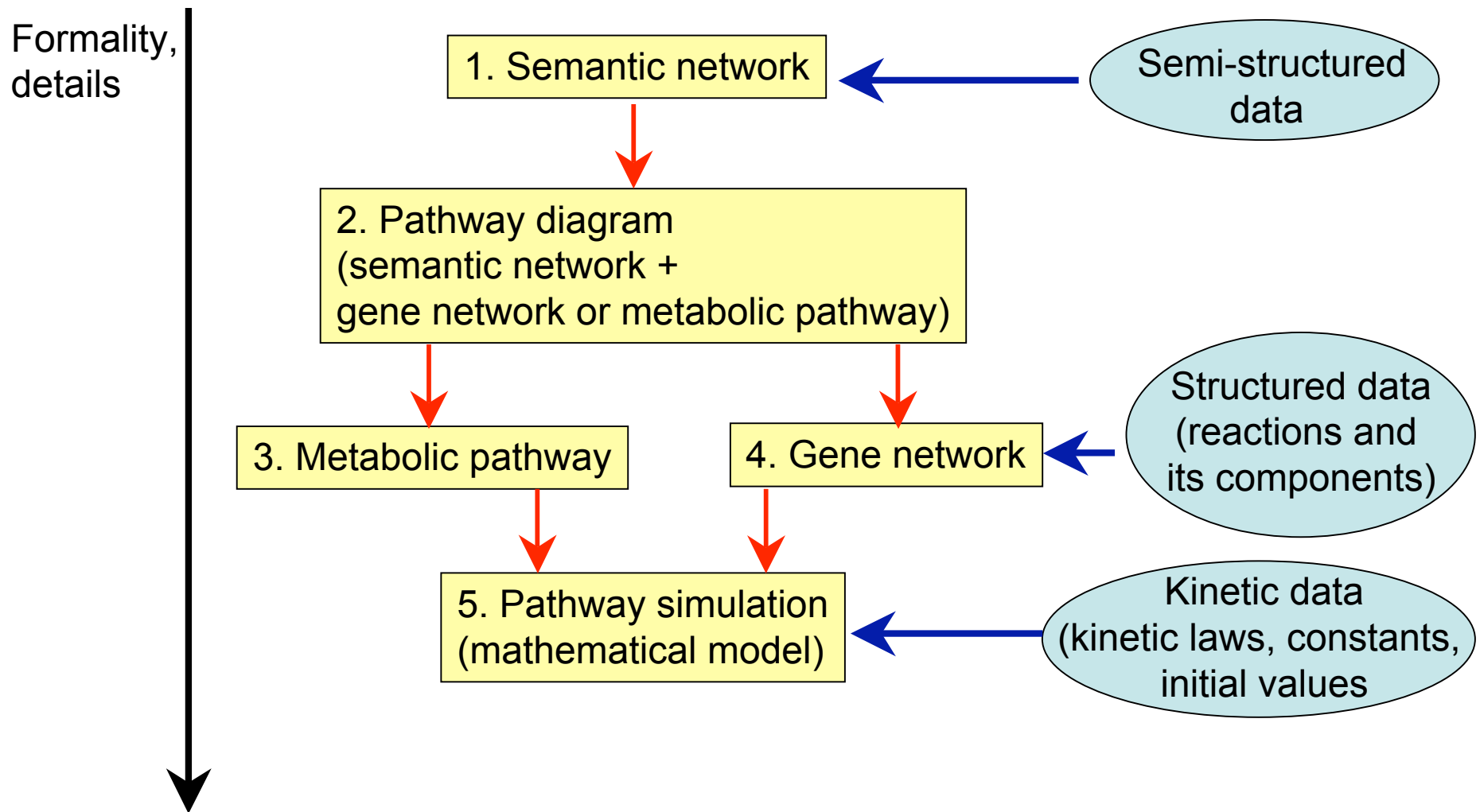


System structure is described as a **compartmentalized attributed graph**

100	$-k_1[A]$	$k_1[A]$	0	$-k_2[B]$	$k_2[B]$	0
-----	-----------	----------	---	-----------	----------	---

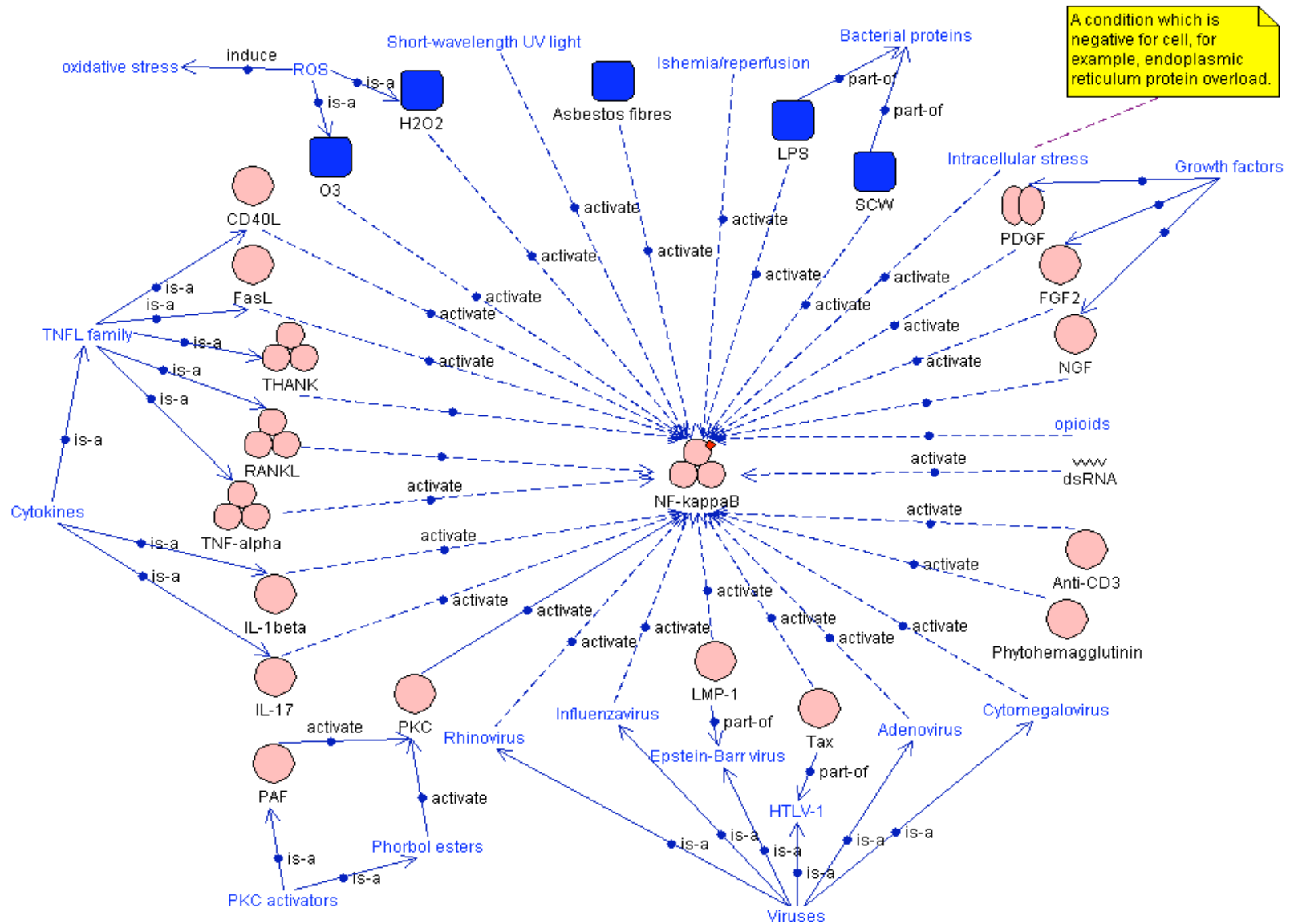
Mathematical model of the system

Reconstruction and formal description of biological systems using different diagram types



Stimulus activating NF-kappaB

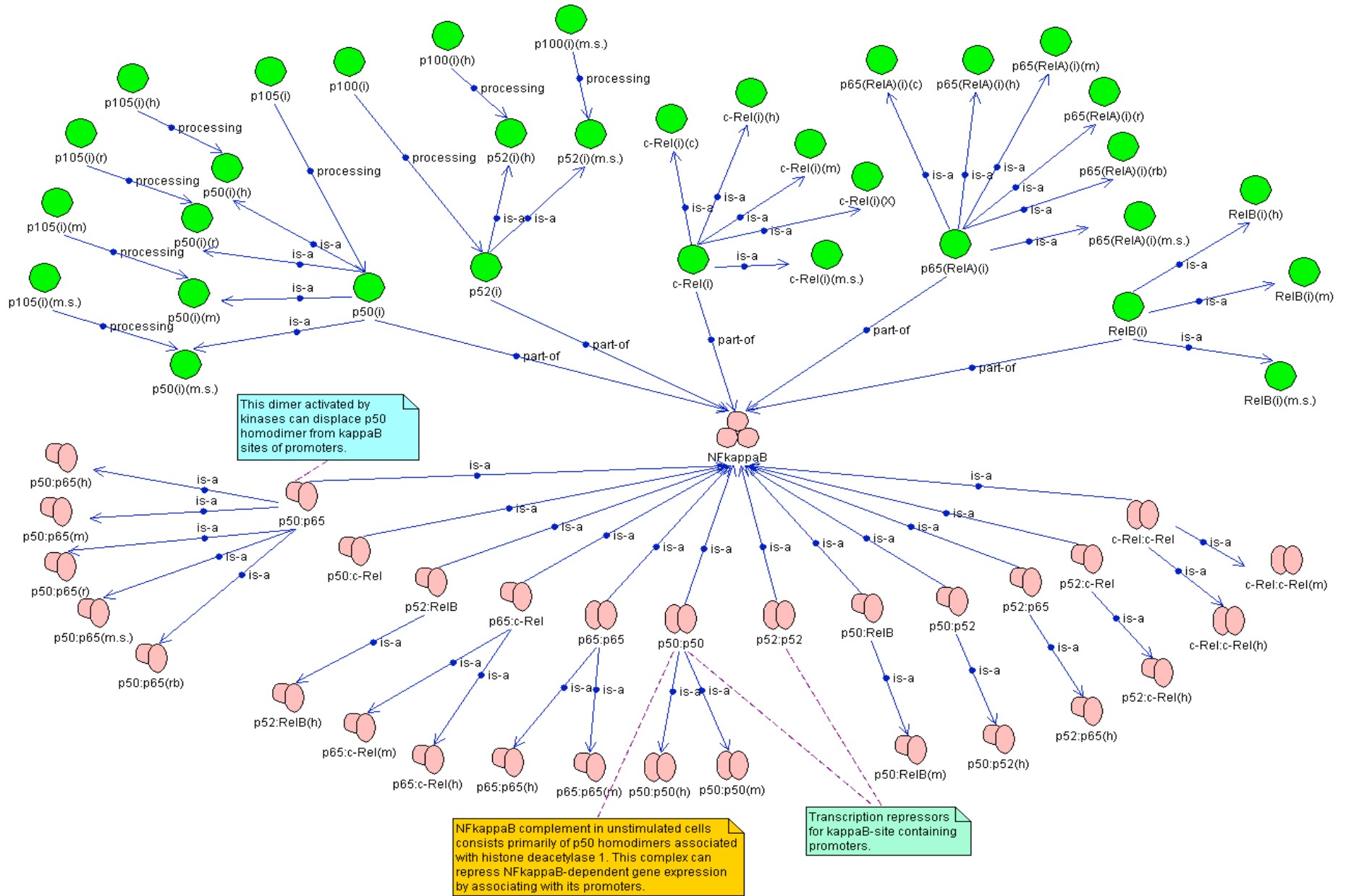
(semantic network, ontology)



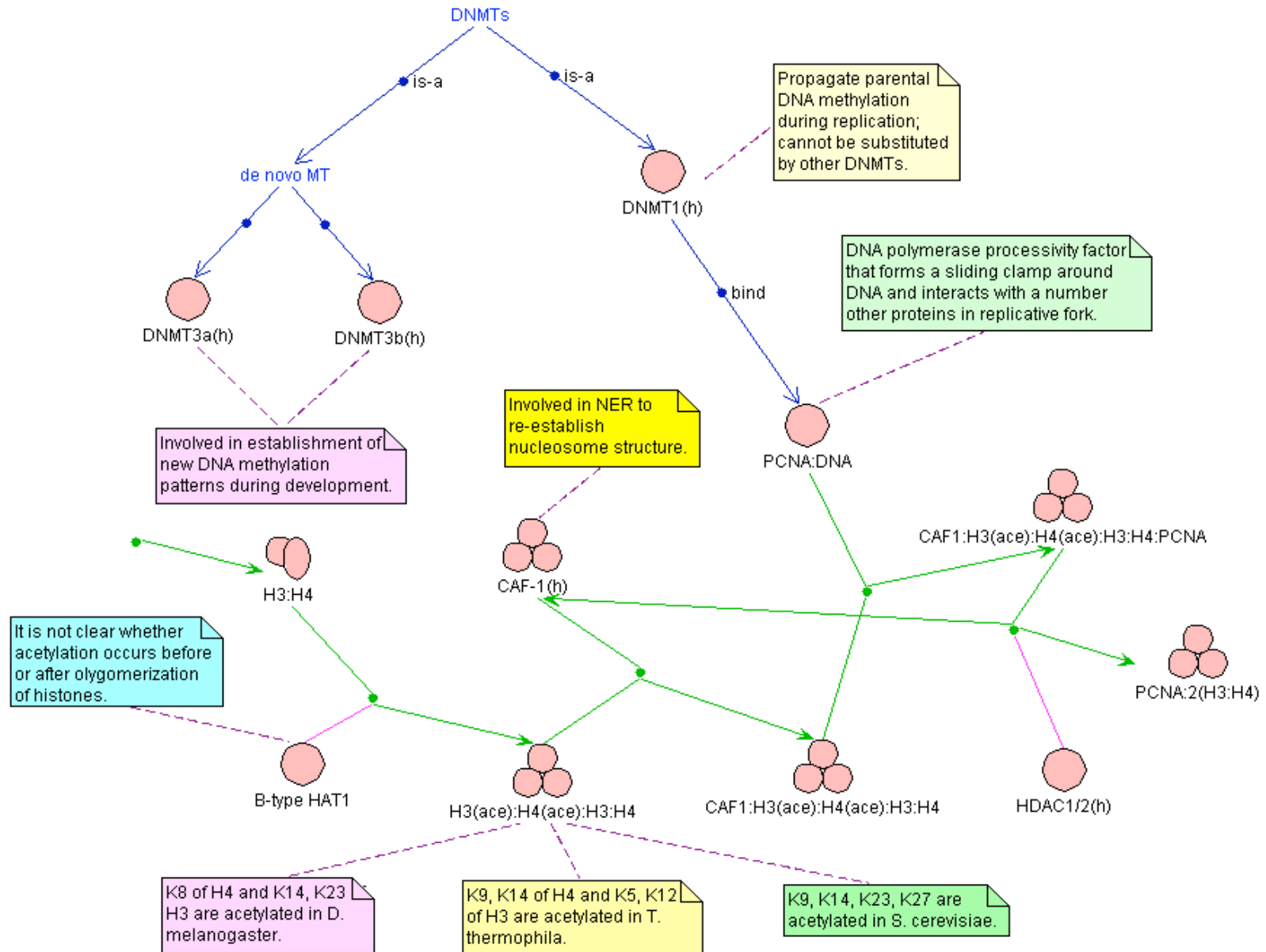
A condition which is negative for cell, for example, endoplasmic reticulum protein overload.

NF-kappaB family

(semantic network, ontology)

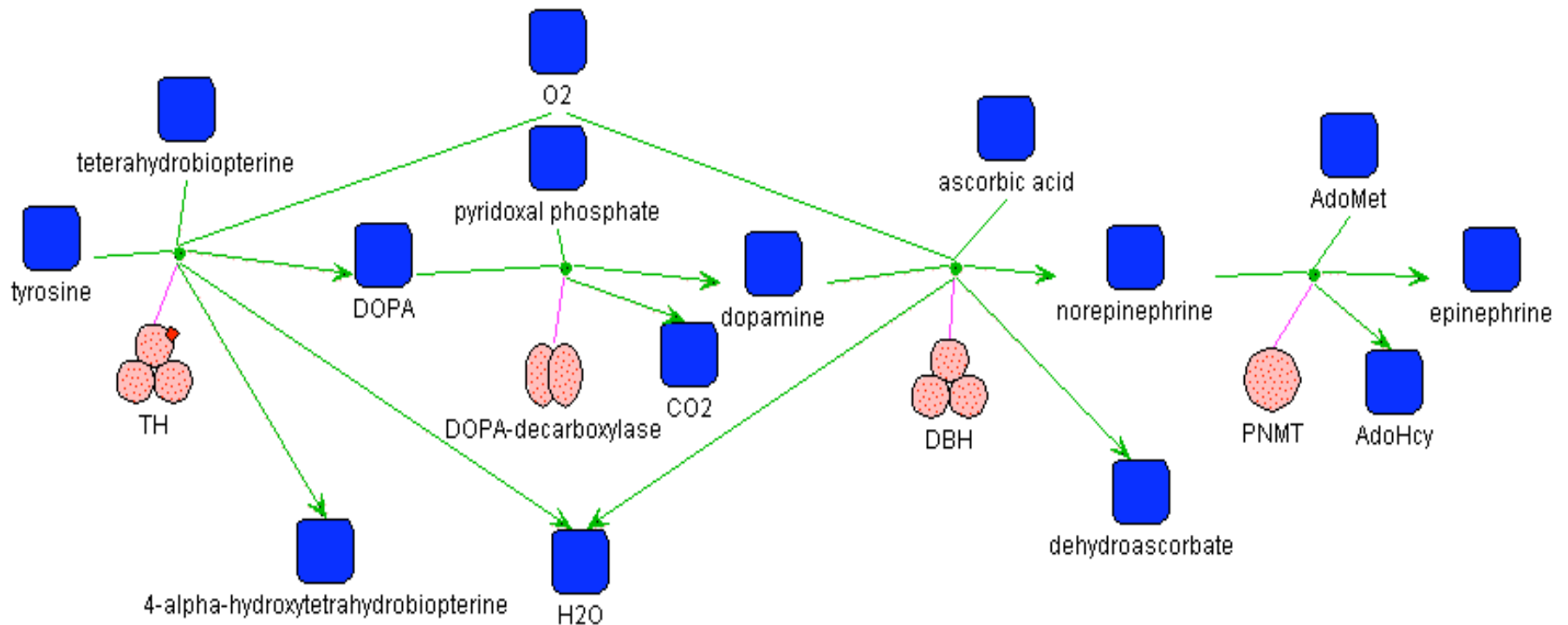


Function of human DNA methyltransferases (pathway diagram)



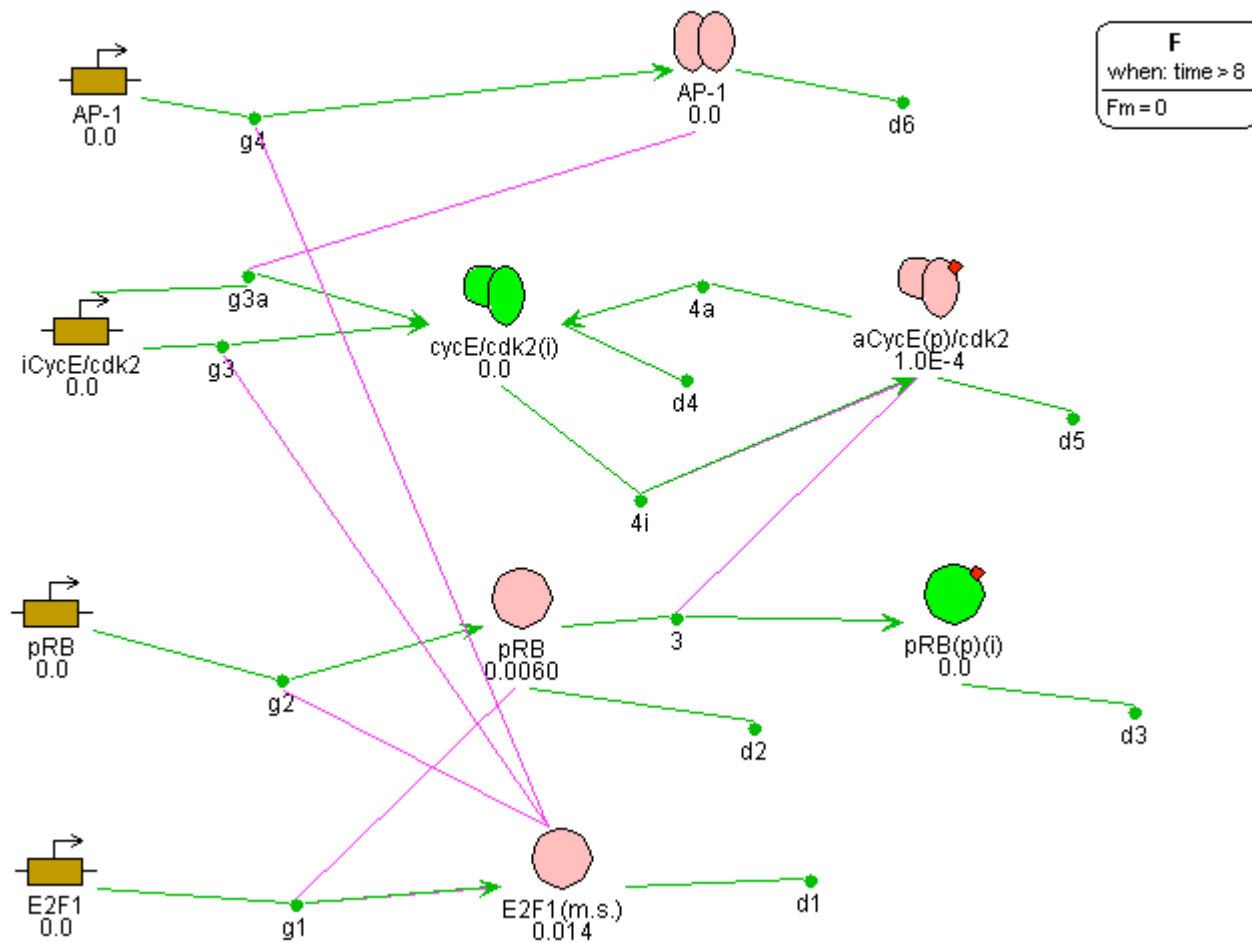
The biosynthesis of catecholamines

(metabolic pathway)



Cell cycle model of mammalian G1/S transition control with E2F feedback loops

(pathway simulation diagram)



BioUML modules

BioUML standard module

Databases

- **BioModels** (<http://www.ebi.ac.uk/biomodels>)
- BMOND (<http://biopath.biouml.org>)
- GeneNet (<http://www.mgs.bionet.nsc.ru>)
- KEGG/Ligand (<http://www.kegg.com>)
- TRANSPATH (<http://www.biobase.de>)

Formats

- SBML – Systems Biology Markup Language, level 1, 2
- **BioPax – Biological Pathways Exchange**
- **OBO - Open Biomedical Ontologies, a collection of freely available well-structured controlled vocabularies** (<http://obofoundry.org>)
- CellML – Cell Markup Language
- GXL - Graph eXchange Language (<http://www.gupro.de/GXL>)
- GinML – extension of GXL for description regulatory networks (<http://gin.univ-mrs.fr/GINsim>)



The SBML Wiki

Semantic Test Suite

You can edit these Wiki pages from within your browser. [Click here to learn how.](#)

The semantic test suite is set of test models with given time series behaviour data. The aims of the suite are described in more detail in the [Test Suite Introduction](#).

The test suite is downloadable with documentation and test automation scripts in 2 versions one for [windows cygwin](#) and the other for [unix](#). Documentation on the general structure of the test suite, file formats and automation scripts is available separately [here](#)

The suite is under development. A test is either:

- complete - it has times series behaviour data and supporting documentation
- under development - the model exists but no times series data is available
- planned - a model to cover more of the specification is required

The suite is currently divided into the following categories:

[Basic Reaction Semantic Tests](#) 19 complete tests

[Complex Reaction Semantic Tests](#) 6 complete tests

[Parameter Scope Semantic Tests](#) 4 complete tests

[Discontinuity and Delays Semantic Tests](#) 14 complete tests + 2 planned tests

[Compartment and Transport Reaction Semantic Tests](#) 3 tests under development

[Stoichiometry Semantic Tests](#) 2 completed Tests

[Basic Rule Semantic Tests](#) 16 complete tests

[Algebraic Rule Semantic Tests](#) 2 complete tests

Results of SBML semantic tests

BioUML workbench - validation using SBML Semantic Test Suite - Microsoft Internet Explorer

Файл Правка Вид Избранное Сервис Справка

Адрес: http://biouml.org/sbml_tests/overview.html Переход Ссылки

Simulation engine	Details	Tests	Successful	Failed	Errors	Needs tuning	CSV error	Result differs	Success rate	Time (s)
<i>SBML level 1</i>										
Java	details	53	49	0	0	0	4	0	100.00 %	21
MATLAB	details	53	49	0	0	0	4	0	100.00 %	444
<i>SBML level 2</i>										
Java	details	141	120	0	0	0	21	0	100.00 %	41
MATLAB	details	141	120	0	0	0	21	0	100.00 %	1598

Готово Интернет

Main new features

- Full text search engine (use Apache Lucene)
- Improved graph search
- BioPAX import/export
- OBO import/export
- Chemical structures support and visualization (use CDK – Chemical Development Kit library)
- Any image can be used as node view
- BioUML network edition

Full text search (uses Lucene engine)

Text search _ □ ×

	Name	title	description	databaseReferences	literatur...	syn
0	ENSG00000042286	AIFM2	Apoptosis-inducing factor	GO (0): GO:0030261		
1	ENSG00000055163	CYFIP2	cytoplasmic FMR1	EMBL (0): AL136549		
2	ENSG00000067369	TP53BP1	Tumor suppressor	GO (0): GO:0005654		
3	ENSG00000078804	TP53INP2	Tumor protein	UniGene (0): Hs.516994		
4	ENSG00000088356	PDRG1	p53 and DNA	EMBL (0): BC001856		
5	ENSG00000088808	PPP1R13B	Apoptosis-stimulating of	Codelink (0): GE53478		
6	ENSG00000105327	BBC3	Bcl-2-binding component 3	GO (0): GO:0045926		
7	ENSG00000111554	MDM1	Mdm4, transformed 3T3	CCDS (1): CCDS8983.1		
8	ENSG00000112378	PERP	p53 apoptosis effector	protein id (0):		
9	ENSG00000115129	TP53I3	Putative quinone	Illumina V1 (0):		
10	ENSG00000125686	PPARBP	Peroxisome	AFFY HG U133 Plus 2		
11	ENSG00000134222	PSRC1	Proline/serine-rich coiled	Uniprot/SPTREMBL (0):		
12	ENSG00000135679	MDM2	Ubiquitin-protein ligase E3	protein id (0):		
13	ENSG00000141510	TP53	Cellular tumor antigen p53	GO (0): GO:0006350		
14	ENSG00000143514	TP53BP2	Apoptosis-stimulating of	Uniprot/SWISSPROT		
15	ENSG00000149480	MTA2	Metastasis-associated	EntrezGene		
16	ENSG00000163743	RCHY1	RING finger and CHY zinc	AgilentProbe (0):		
17	ENSG00000164938	TP53INP1	Tumor protein	EMBL (0): AB062056		
18	ENSG00000167543	TP53I13	tumor protein p53 inducible	Codelink (0): GE88221		
19	ENSG00000170836	PPM1D	Protein phosphatase 2C	Uniprot/SPTREMBL (0):		
20	ENSG00000172167	MTBP	Mdm2, transformed 3T3	GO (0): GO:0005515		
21	ENSG00000172638	EFEMP2	EGF-containing fibulin-like	Illumina V2 (0):		
22	ENSG00000172667	ZMAT3	p53 target zinc finger	RefSeq dna (1):		
23	ENSG00000173226	IQCB1	IQ calmodulin-binding	CCDS (1): CCDS3005.1		
24	ENSG00000175274	TP53I11	p53-induced protein	protein id (0):		
25	ENSG00000175866	BALAP2	Brain-specific angiogenesis	EMBL (0): U70669		
26	ENSG00000185101	TMEM16J	tumor protein p53 inducible	Codelink (0): GE85790		
27	ENSG00000198625	MDM4	Mdm4 protein (p53-binding	RefSeq peptide (2):		

Search \ Table columns \

Data collection: Data/gene ▾

Search:

Alternative view:

Variable row height:

Start
Close

Gene

ID: ENSG00000042286

ED: 01-яHB-0001

TI: AIFM2

DE: Apoptosis-inducing factor 2 (EC 1.-.-.) (Apoptosis-inducing factor- like mitochondrion-associated inducer of death) (Apoptosis-inducing factor-homologous mitochondrion-associated inducer of death) (p53- responsive gene 3 protein). [Source:Uniprot/SWISSPROT;Acc: Q9BRQ8]

View
Edit

Graph search engine

Search form - New Diagram 8

Search options | Layout options

Search options

Property	Value
GraphSearchOptions	
QueryOptions	
Direction	Both
Depth	1
Cell	<input checked="" type="checkbox"/>
Concept	<input checked="" type="checkbox"/>
Gene	<input checked="" type="checkbox"/>
RNA	<input checked="" type="checkbox"/>
Protein	<input checked="" type="checkbox"/>

Protein

ID: PRT000074

Title: NIK

Search Cancel

Save Open

Incremental search | Clipboard

	Add	Id	Title	Type
0	<input type="checkbox"/>	RLT002188		relation-semantic
1	<input type="checkbox"/>	RCT000627	PRT000217 + PRT000...	reaction
2	<input type="checkbox"/>	CEL0013	human monocytes	compartment-cell
3	<input type="checkbox"/>	RLT002181	induce	relation-semantic
4	<input type="checkbox"/>	RLT003107	increase	relation-semantic
5	<input type="checkbox"/>	CEL0010	human macrophages	compartment-cell
6	<input type="checkbox"/>	CEL0011	human VSMC	compartment-cell

Diagram

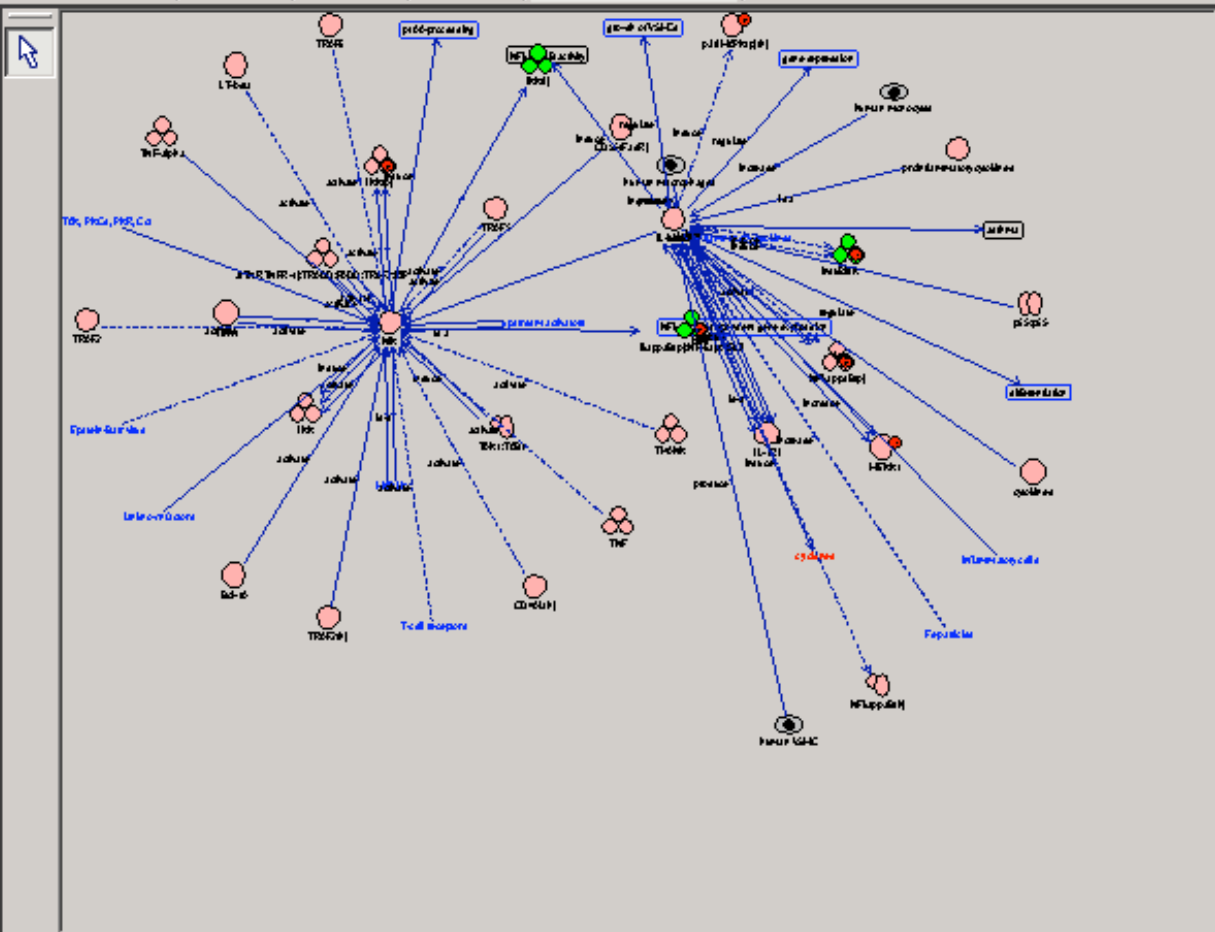
Title: New Diagram 8

Diagram type: Semantic network

Layouter: "...forceDirectedLayout..."

Data:

View Edit



Incremental search | Clipboard

Search options | Layout options

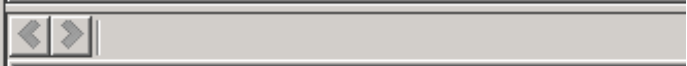
Search options

Property	Value
GraphSearchOptions	
QueryOptions	
Direction	Both
Depth	1
Cell	<input checked="" type="checkbox"/>
Concept	<input checked="" type="checkbox"/>
Gene	<input checked="" type="checkbox"/>
RNA	<input checked="" type="checkbox"/>
Protein	<input checked="" type="checkbox"/>

Protein

ID:

Title:



Diagram

Title: New Diagram 8

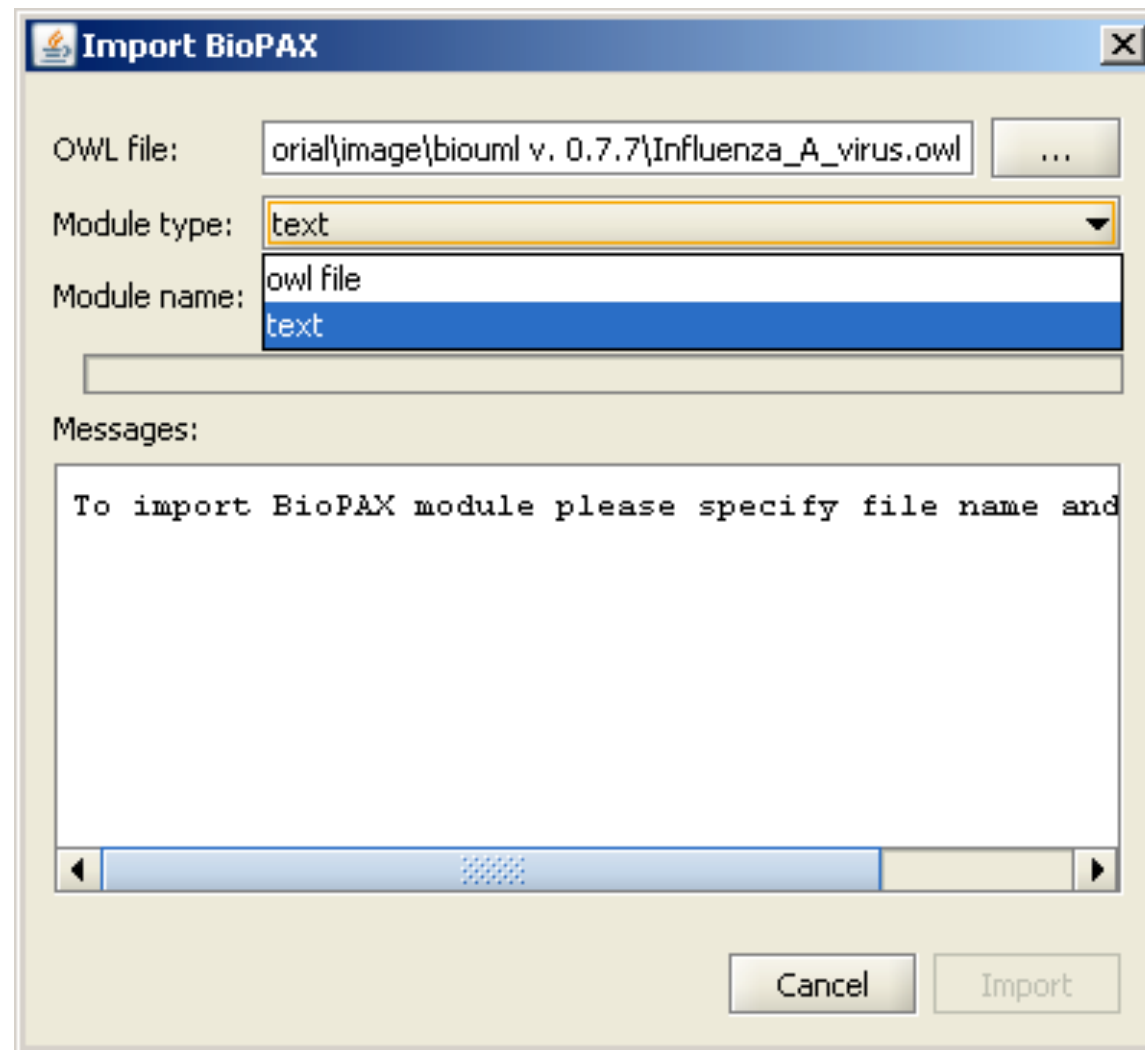
Diagram type: Semantic network

Layouter: "...forceDirectedLayout..."

Data:

View

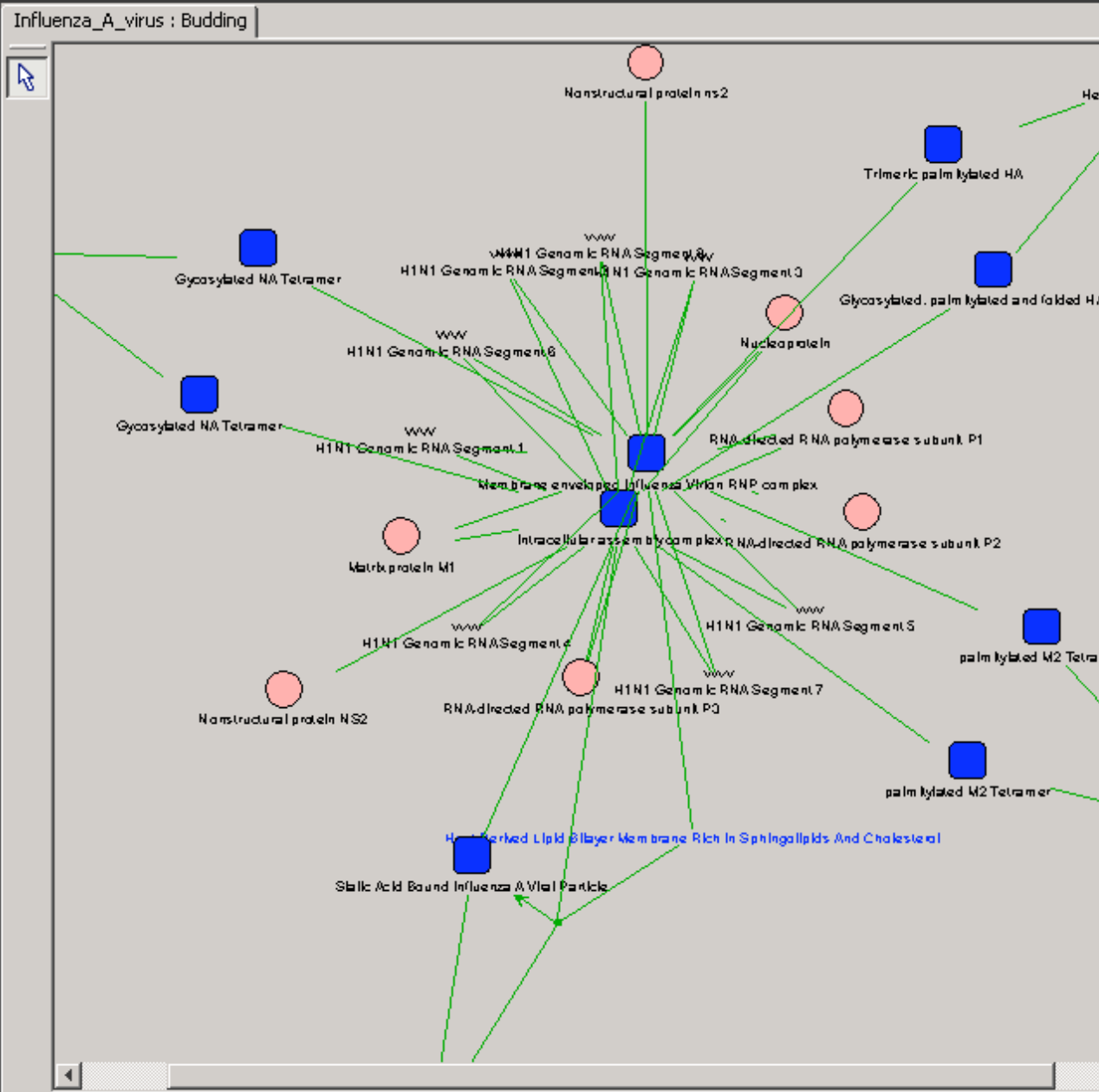
BioPAX import dialog



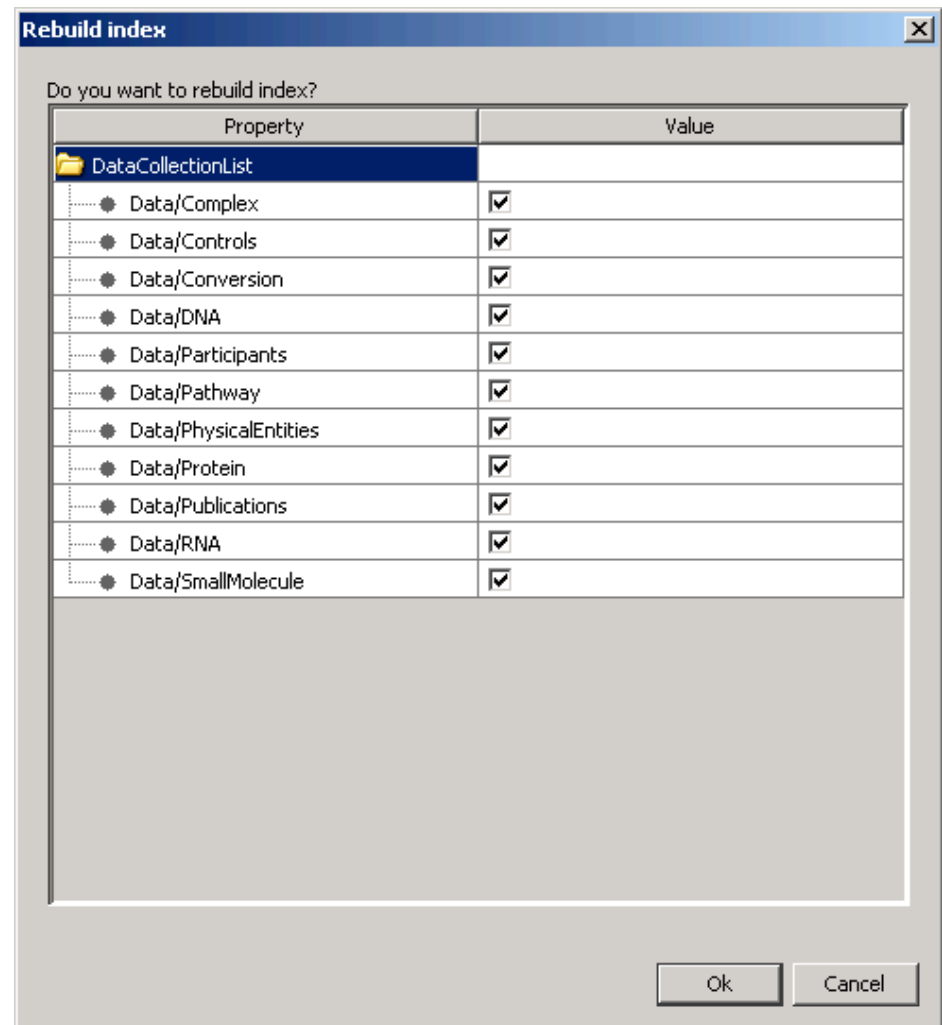
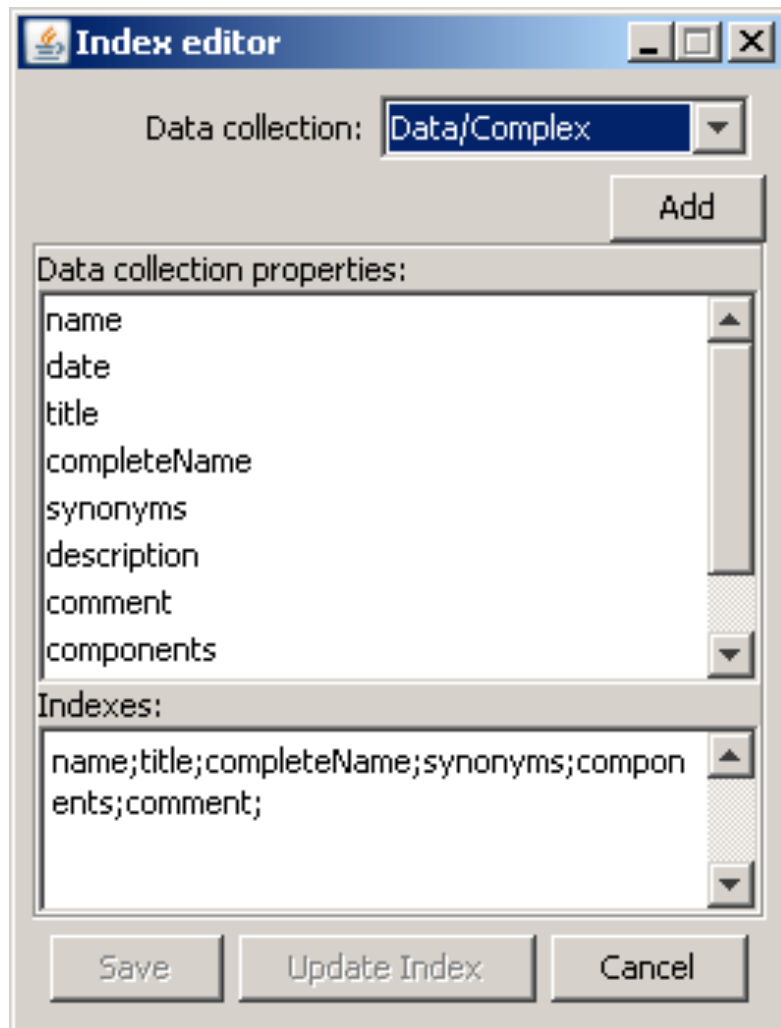


Modules | Data | Plugins

- modules
 - Biopath
 - Biopath (local)
 - CellML models
 - GeneNet
 - Influenza_A_virus
 - Data
 - Complex
 - Controls
 - Conversion
 - DNA
 - Participants
 - Pathway
 - PhysicalEntities
 - Protein
 - Publications
 - RNA
 - SmallMolecule
 - _7_Methylguanosine_5__phosphate_C
 - NTP__nucleoplasm_1
 - ChEBI_21622_N_acetylneuraminic_acids
 - GTP__ChEBI_15996_
 - GDP__ChEBI_17552_
 - H__ChEBI_15378_
 - Orthophosphate__ChEBI_18367_
 - Diagrams
 - Assembly_of_Viral_Components_at_the_Buc
 - Budding**
 - Entry_of_Influenza_Virion_into_Host_Cell_y
 - Export_of_Viral_Ribonucleoproteins_from_N
 - Fusion_and_Uncoating_of_the_Influenza_Vi
 - Fusion_of_the_Influenza_Virion_to_the_Hos
 - Host_Interactions_with_Influenza_Factors
 - Influenza_Infection
 - Influenza_Life_Cycle
 - Influenza_Viral_RNA_Transcription_and_Rep
 - Influenza_Virus_Induced_Apoptosis



Dialogs to create text indexes for BioPAX module



Text search

	Name	Field	Field data	Score
0	Glycosylated_NA_Tetramer__Golgi_lumen_1	relativeName	Data/Complex/ Glycosylated _NA_Tetramer__Golgi_lumen_1	1.0
1	Glycosylated_NA_Tetramer__Golgi_lumen_1	name	Glycosylated _NA_Tetramer__Golgi_lumen_1	1.0
2	Glycosylated_NA_Tetramer__Golgi_lumen_1	title	Glycosylated NA Tetramer	1.0
3	Glycosylated_NA_Tetramer__Golgi_lumen_1	completeName	Glycosylated _NA_Tetramer__[Golgi_lumen_1]	1.0
4	Glycosylated_NA_Tetramer__Golgi_lumen_1	components	Data/Participants/ Glycosylated _NA__Golgi_lumen_1	1.0
5	Glycosylated_NA_Tetramer__ER_to_Golgi_transport	relativeName	Data/Complex/ Glycosylated _NA_Tetramer__ER_to_Golgi_transport	1.0
6	Glycosylated_NA_Tetramer__ER_to_Golgi_transport	name	Glycosylated _NA_Tetramer__ER_to_Golgi_transport	1.0
7	Glycosylated_NA_Tetramer__ER_to_Golgi_transport	title	Glycosylated NA Tetramer	1.0
8	Glycosylated_NA_Tetramer__ER_to_Golgi_transport	completeName	Glycosylated _NA_Tetramer__[ER_to_Golgi_transport]	1.0
9	Glycosylated_NA_Tetramer__ER_to_Golgi_transport	components	Data/Participants/ Glycosylated _NA__ER_to_Golgi_transport	1.0
10	Glycosylated_NA_Tetramer__extracellular_virion	components	Data/Participants/ Glycosylated _NA__extracellular_virion	1.0
11	Glycosylated__palmitylated_and_folded_HA_trimer	relativeName	Data/Complex/ Glycosylated __palmitylated_and_folded_HA_trimer	1.0
12	Glycosylated__palmitylated_and_folded_HA_trimer	name	Glycosylated __palmitylated_and_folded_HA_trimer	1.0
13	Glycosylated__palmitylated_and_folded_HA_trimer	title	Glycosylated , palmitylated and folded HA trimer:Lipid Raft	1.0

Search | Available properties | Columns

Data collection:

Search:

Alternative view:

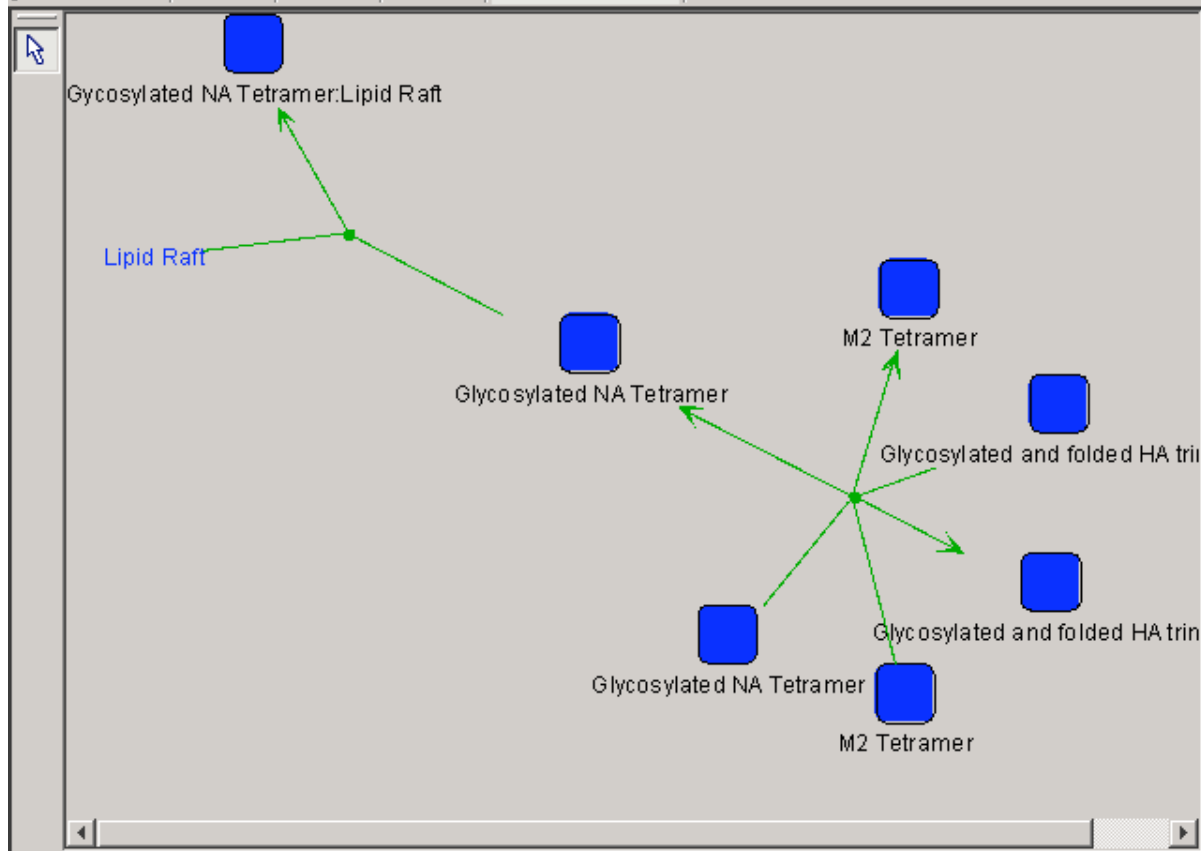
Variable row height:

Start Close

Complex

ID: Glycosylated_NA_Tetramer__Golgi_lumen_1
TI: Glycosylated NA Tetramer
NM: Glycosylated_NA_Tetramer__[Golgi_lumen]
CP:
[0]: Data/Participants/Glycosylated_NA__Golgi_lumen_1
AT:
Organism:
 Dictionaries/Organisms/Influenza_A_virus__A_Puerto_Rico/02/99/HK/0599
DR:
Database reference:
DN: Reactome
ID: REACT_10176
CM: (1) Reactome stable identifier. Use this URL page of this instance in Reactome:
http://www.reactome.org/cgi-bin/eventbrowser_...

View Edit



Search options | Layout options

Search options

Property	Value
GraphSearchOptions	
QueryOptions	
Direction	Both
Depth	1
Concept	<input checked="" type="checkbox"/>
Substance	<input checked="" type="checkbox"/>
Complex	<input checked="" type="checkbox"/>
RNA	<input checked="" type="checkbox"/>
DNA	<input checked="" type="checkbox"/>

Complex:

ID:

Title:

Search Cancel Save Open

Incremental search | Clipboard

	Add	Id	Title	Type
0	<input type="checkbox"/>	Glycosylated_NA_Tetram...	Glycosylated NA Tetramer	molecule-substance
1	<input type="checkbox"/>	Palmitoylation_of_cystein...	Palmitoylation of cysteine ...	reaction
2	<input type="checkbox"/>	palmitylated_M2_Tetrame...	palmitylated M2 Tetramer	molecule-substance
3	<input type="checkbox"/>	Fusion_of_vesicle_contai...	Fusion of vesicle containin...	reaction
4	<input type="checkbox"/>	Glycosylated_NA_Tetram...	Glycosylated NA Tetramer	molecule-substance
5	<input type="checkbox"/>	Glycosylated_and_folded...	Glycosylated and folded H...	molecule-substance
6	<input type="checkbox"/>	M2_Tetramer__ER_to_Go...	M2 Tetramer	molecule-substance
7	<input type="checkbox"/>	M2_Tetramer__Golgi_Jum...	M2 Tetramer	molecule-substance
8	<input type="checkbox"/>	Glycosylated_and_folded...	Glycosylated and folded H...	molecule-substance

Node

Title: M2 Tetramer

Size: Dimension (width = 50, height = 50)

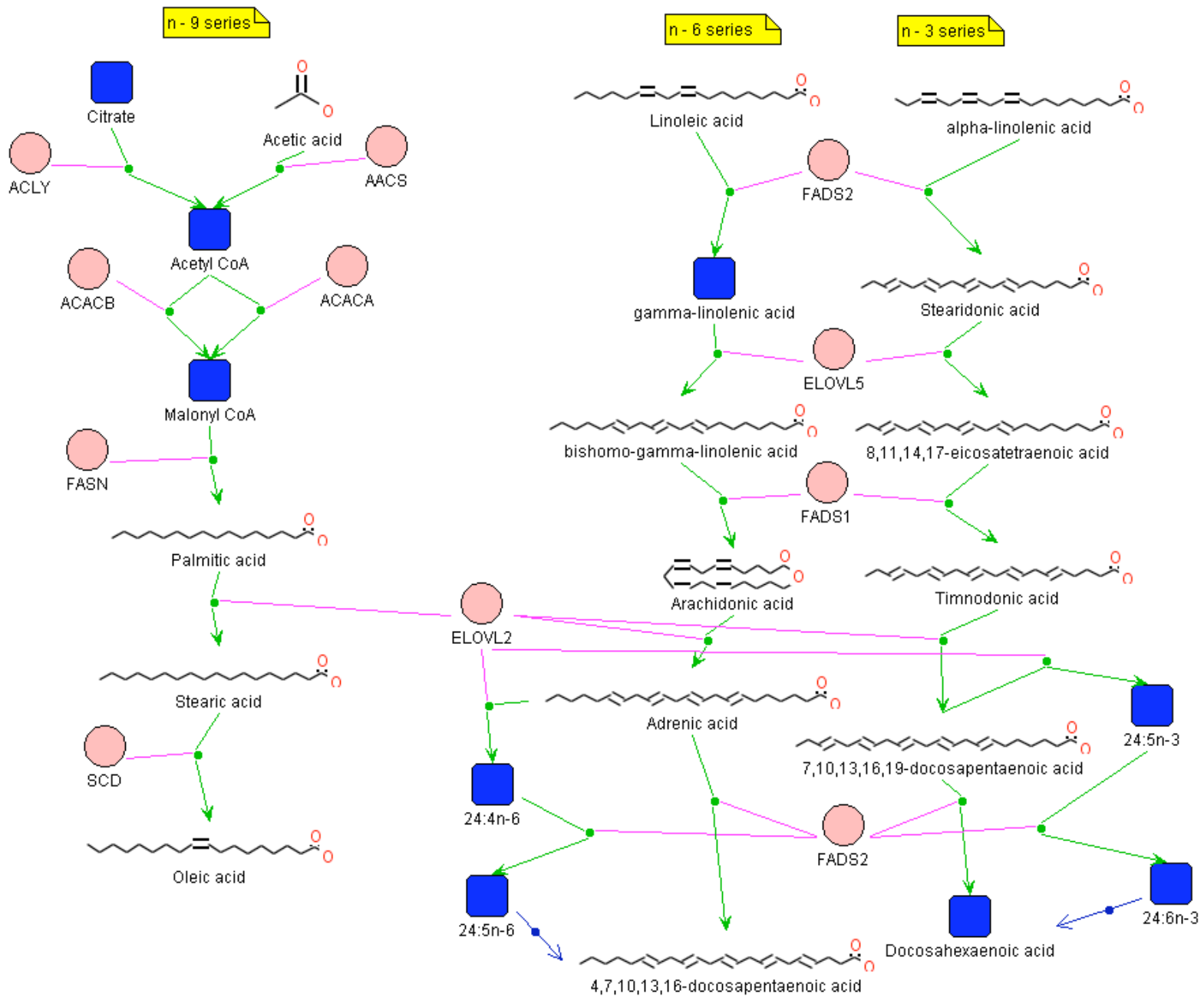
Data:

ID: M2_Tetramer__Golgi_lumen_1

TI: M2 Tetramer

NM: M2 Tetramer [Golgi lumen]

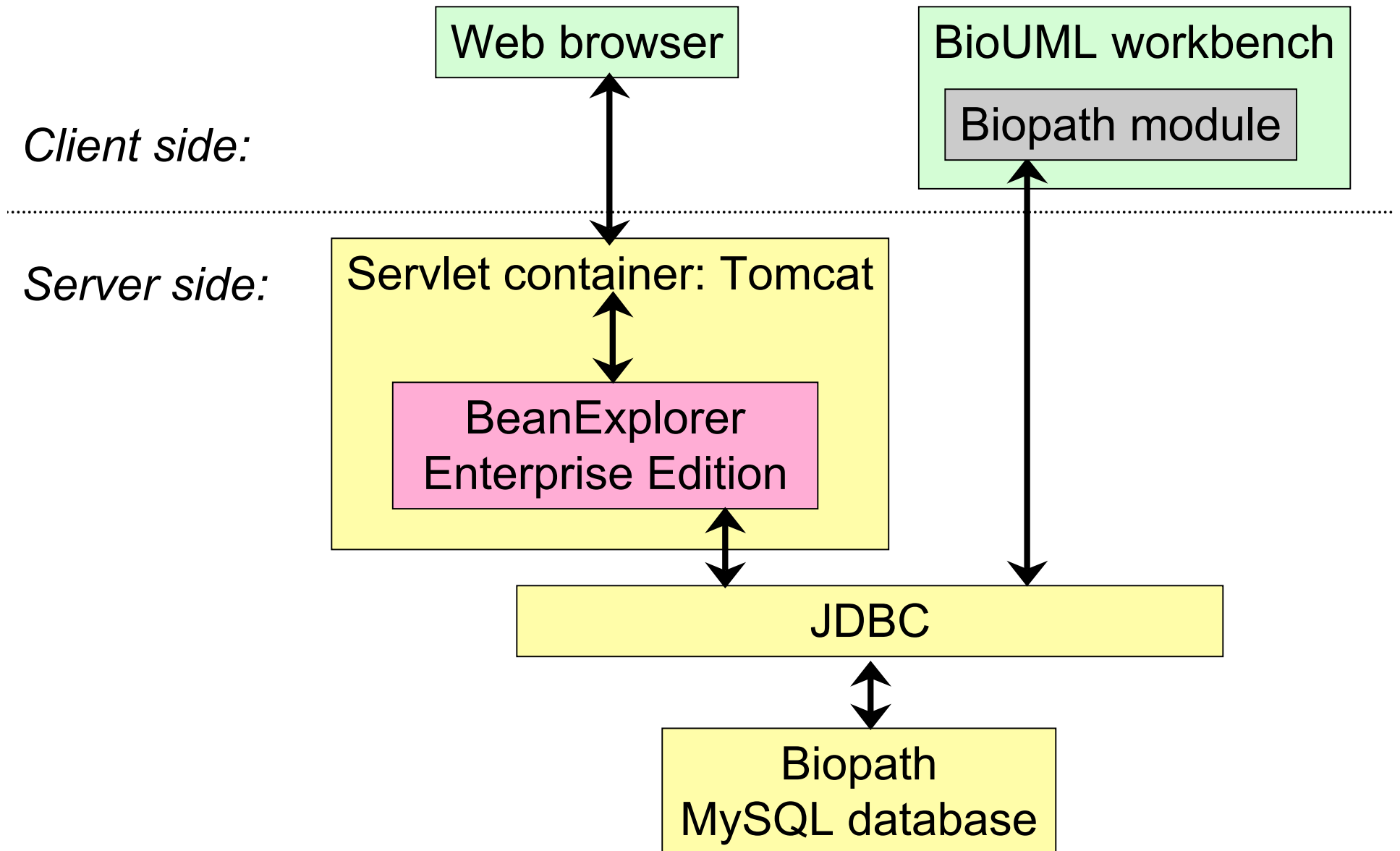
View Edit



BMOND
Biological MOdels aNd Diagrams
database

<http://bmond.biouml.org>

BMOND system architecture



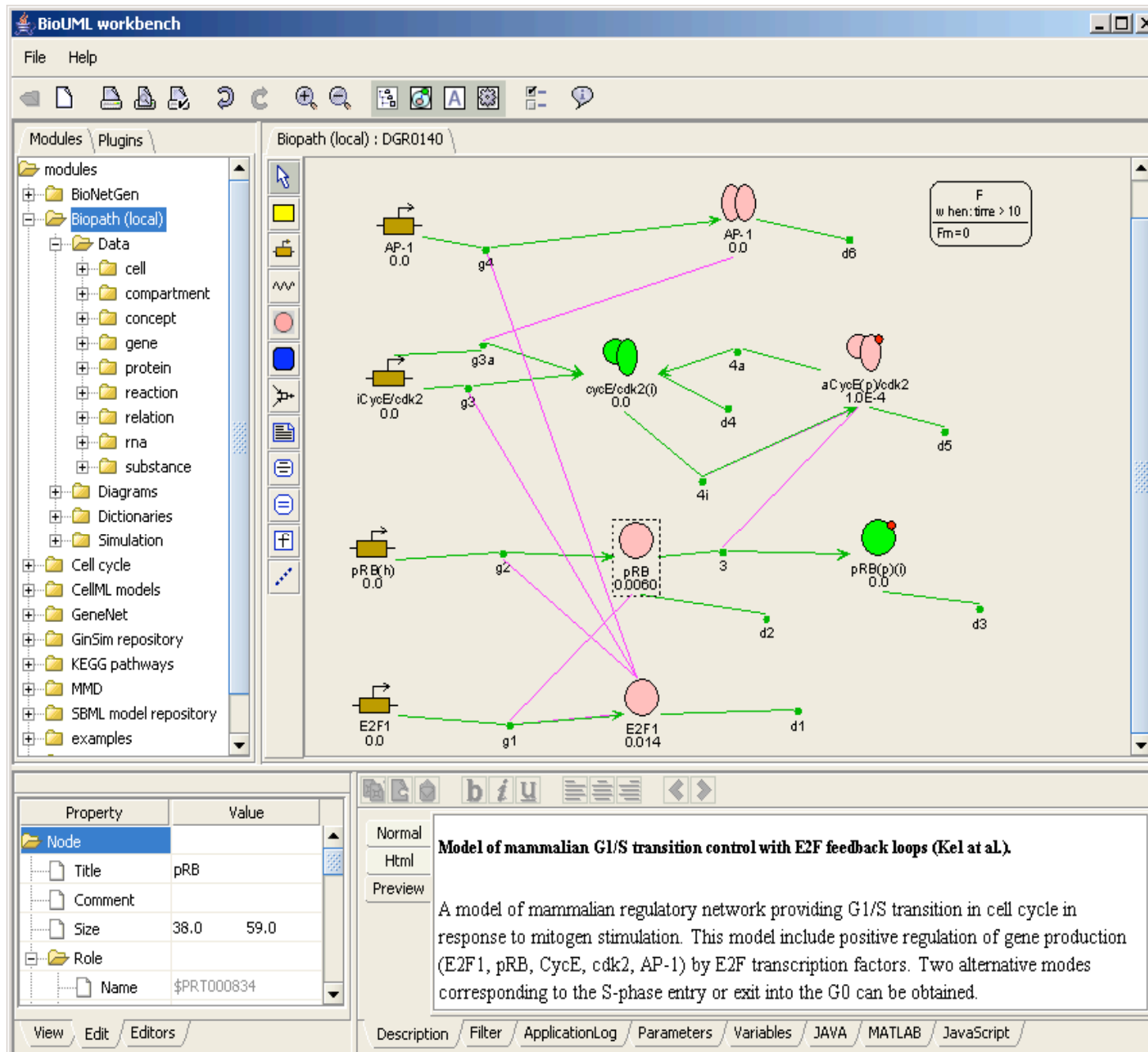
















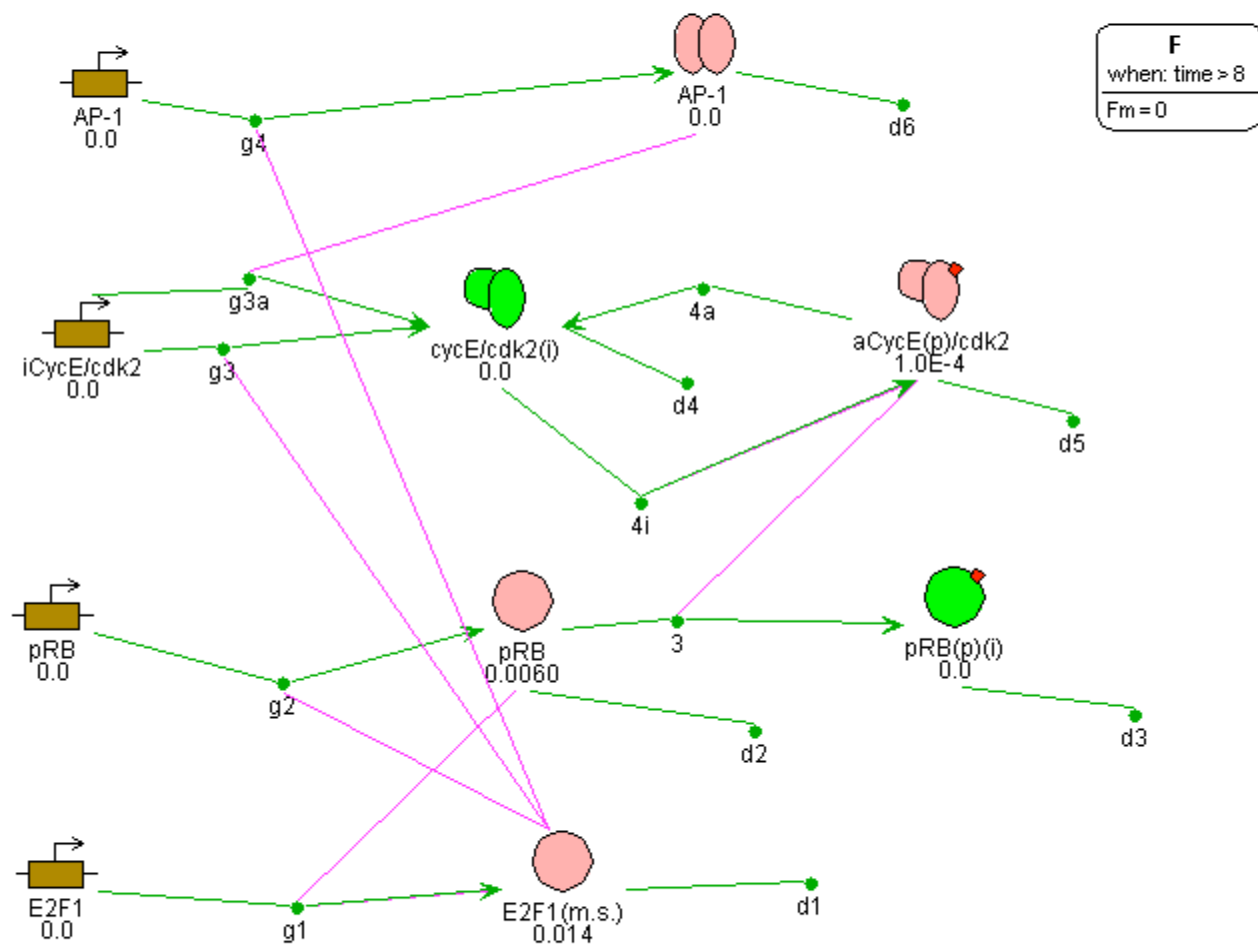


Figure 4. G1/S entry model (Kel et al., 2000) described using BioUML technology

- [-] About
- [-] Diagrams 
- [-] Components
 - Compartments 
 - Cells 
 - Concepts 
 - Genes 
 - Proteins 
 - RNAs 
 - Relations 
 - Substances 
- [-] Literature
 - Compact view 
 - Detailed view 
 - for BioUML data 
- [-] Dictionaries
 - Databases 
 - Relation types 
 - Species 
 - Units 

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Kel et al. Model of mammalian G1/S transition control with E2F feedback loops.



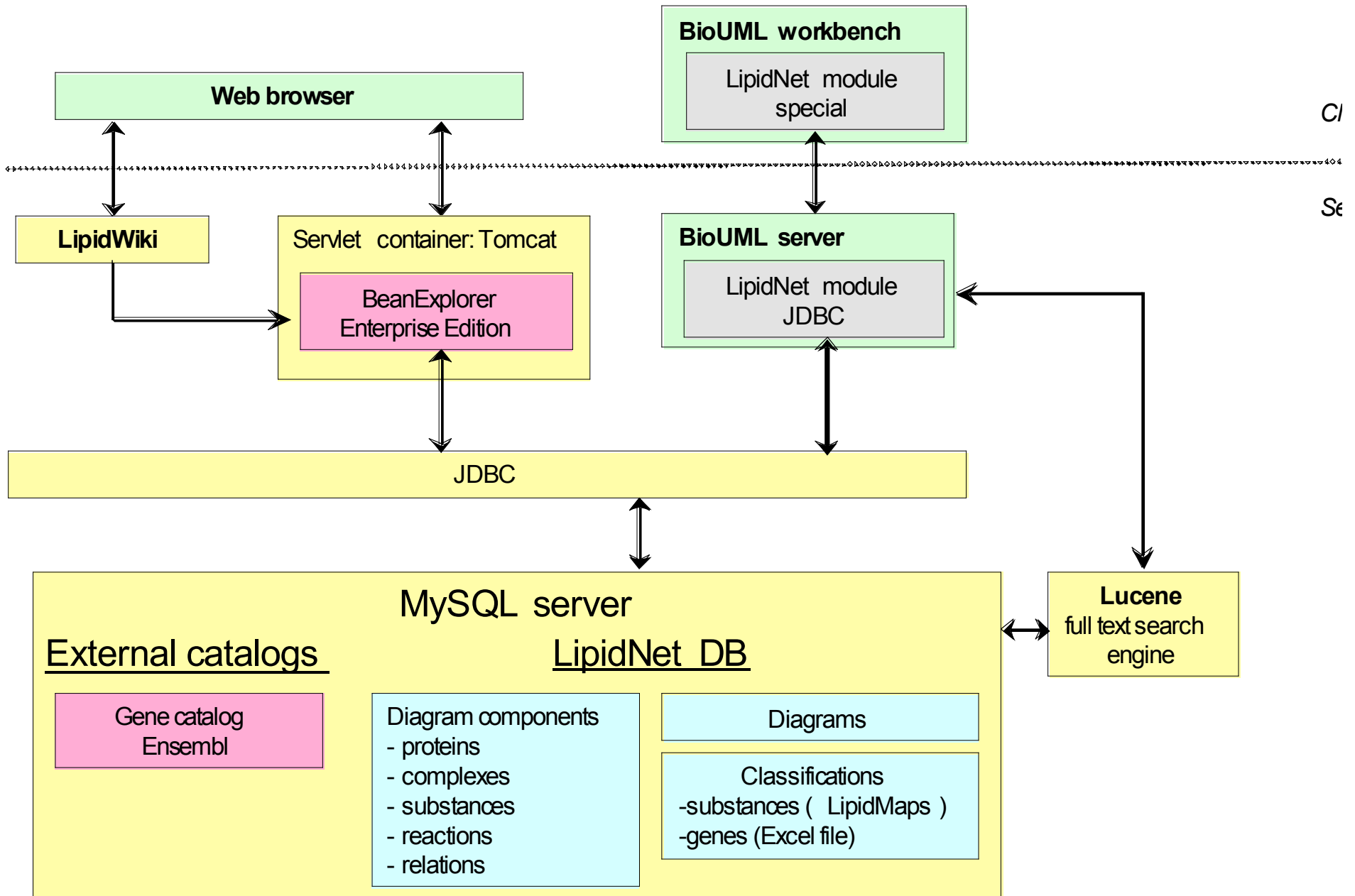
Genes

***LipidomicsNet - integrated
project on metabolomics.
Demo version for FP 7 grant.***

External catalogs.

<http://demo.developmentontheedge.com/lipidnet>

Current architecture of LipidomicsNet project



BioUML workbench

File Help

Modules Plugins

modules

- Lipid Network (client, N-sk)
 - Data
 - cell
 - compartment
 - concept
 - gene
 - ENSG000000000003
 - ENSG000000000005
 - ENSG0000000000419
 - ENSG0000000000457
 - ENSG0000000000460
 - ENSG0000000000938
 - ENSG0000000000971
 - ENSG0000000001036
 - ENSG0000000001084
 - ENSG0000000001167
 - ENSG0000000001460
 - ENSG0000000001461
 - ENSG0000000001497
 - ENSG0000000001561
 - ENSG0000000001617
 - ENSG0000000001626
 - ENSG0000000001629
 - ENSG0000000001630
 - ENSG0000000001631

Lipid Network (client, N-sk) : figure6a

Diagram

Title: Elongation and desaturation of fatty acids

Data:

ID: figure6a

TI: Elongation and desaturation of fatty acids

DE:

Elongation and desaturation of n-3, n-6 and n-9 fatty acids

The text will be added.

CC:

Normal Elongation and desaturation of n-3, n-6 and n-9 fatty acids

Html The text will be added.

Preview

View Edit Editors

Description Text search Filter ApplicationLog JavaScript

BioUML workbench

File Help

Modules Plugins

modules

- Lipid Network
 - Data
 - cell
 - compartment
 - concept
 - gene
 - protein
 - reaction
 - relation
 - rna
 - structure
 - substance
 - Diagrams
 - AS_retinoids
 - AS_ster_horm
 - cholesterol metabolism
 - cholesterol sulfate
 - eicosanoids biosynthesis pathway
 - figure 12_2
 - figure 14
 - figure 5

Lipid Network : figure6

Node

Title: AIFM2

Size: java.awt.Dimension[width=40,height=43]

Data:

ID: ENSG00000042286

ED: 01-январь-0001

TI: AIFM2

Data collection: Data/gene Search: p53 Search Alternative view:

name	Collecti...	Name	Field	Field d...	Title	Score
title	0	Data/gene	ENSG00000042286	description	Apoptosis-inhibitor 2	1.0
synonyms	1	Data/gene	ENSG00000042286	databaseRef	GO (0): GO:0005508	1.0
description	2	Data/gene	ENSG00000042286	databaseRef	EMBL (0): CYFIP2	1.0
chromosome	3	Data/gene	ENSG00000042286	databaseRef	GO (0): GO:0005508	1.0
comment	4	Data/gene	ENSG00000042286	databaseRef	UniGene (0): TP53INP2	1.0
databaseReferences	5	Data/gene	ENSG00000042286	description	p53 and DN PDRG1	1.0
literatureReferences						

View Edit Editors

Description Text search Filter ApplicationLog Clipboard JavaScript

BMOND database - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Address <http://demo.developmentontheedge.com/lipidnet/protected.html> Go Links >>

LipidNet

Hello **Administrator!**

- [-] [About](#)
- [-] [Diagrams](#)
 - [Diagrams with categories](#)
- [-] [Components](#)
 - [Cells](#)
 - [Compartments](#)
 - [Concepts](#)
 - [-] [Genes](#)
 - [Genes](#)
 - [Cross references](#)
 - [Proteins](#)
 - [Relations](#)
 - [RNAs](#)
 - [-] [Substances](#)
 - [Substances](#)
 - [Cross references](#)
- [-] [Literature](#)
 - [for BioUML data](#)
 - [Compact view](#)
 - [Compact view](#)
 - [Quick view](#)
 - [Detailed view](#)
 - [Detailed view](#)
- [-] [Dictionaries](#)
 - [Databases](#)
 - [Relation types](#)
 - [Species](#)
 - [Units](#)

Registered users ([Insert](#))

- [Logout](#)
- [Change password](#)

- [-] [Dictionaries](#)
 - [Categories](#)

Genes

[Root](#) <- [Lipid genes](#) <- [Insulin](#) / [Glucose](#) / [Glutathione](#) / [Glucuronides](#) / [Energy](#) / [b-Oxidation](#) / [Fucose](#) ->

[CITRATE CYCLE](#)
[GLUCOSE AND INSULIN SIGNALLING](#)
[GLUCOSE METABOLISM AND GLUTATHIONE AND](#)
[GLUCURONIDE](#)
[GLUCOSE TRANSPORTERS](#)
[GLYCOLYSE-GLUCONEOGENESE](#)
[MITOCHONDRUM](#)
[PENTOSE-PHOSPATE CYCLE](#)

Show columns: [Diagrams](#)

#	Ensembl ID	Gene symbol	Description	Details
<input type="checkbox"/> 1	ENSG00000165029	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	Click
<input type="checkbox"/> 2	ENSG00000085563	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	Click
<input type="checkbox"/> 3	ENSG00000073734	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	Click
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<input type="checkbox"/> 5	ENSG00000115657	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	Click
<input type="checkbox"/> 6	ENSG00000131269	ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	Click
<input type="checkbox"/> 7	ENSG00000197150	ABCB8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	Click
<input type="checkbox"/> 8	ENSG00000150967	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	Click
<input type="checkbox"/> 9	ENSG00000103222	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Click
<input type="checkbox"/> 10	ENSG00000023839	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	Click

Result Pages: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [11](#) ▶ ◀ **Total records:** 254

Check all records

Local intranet

BioUML versions

- Version 0.7.6, May 2005 – last public release
- 2006 -2007 – many special releases for partners
- October 1, 2007 – BioUML tutorial at ICSB-2007
- December, 2007 – BioUML 1.0 release candidate

Current works

- Library of predefined kinetic laws
- Microarray support
- Spatial models support
 - 1D model for blood flow
- Graphic notation
 - formal definition using XML
 - user friendly editor
 - SBGN, CellDesigner 3.5 graphic notations implementation
- New diagram types:
 - sequence map
 - Sequence map + pathway network
- Composite diagram
- Performance improvements, bug fixing

Library of predefined kinetic laws

- SBO – Systems Biology Ontology is used
- BioUML supports import data in OBO format and SBO was imported
- BioUML supports MathML parsing

Current work:

- using SBML annotations
- new reaction dialog with SBO kinetic laws

Add/remove reaction component:

Component: Role:

Variable name:

Reaction components:

	Identifier	Name	Role	Stoichio...	Modifier...	Partisip...	Title
0	CMP0175/C...	PRT002678	reactant	1		direct	PRT002678
1	CMP0175/C...	PRT002678	product	1		direct	PRT002678

Reaction rate:

It will be replaced by reaction editor

Microarray plug-in

- Import microarray data in tab delimited format (the same as Cytoscape)
- Show data as a table
- Binding with diagram nodes by ID
- Coloring diagrams

Further work:

- Powerful user interface for coloring diagrams
- Support of other formats for microarray data and results of analyses
- Sophisticated binding algorithm using different database references and ID
- Server module that will provide access to ArrayExpress data

BiOPath Workbench

File Help

Modules Data Plugins

data

- classifications
- colorschemes
- factors
- graphic notations
- matrices
- microarray
 - galExpData
 - m1
 - m2
 - m3
- profiles
- results
- sequences
- test

Biopath (local) : DGR0003a

Microarray: m2

Experiment	
v1	<input checked="" type="checkbox"/>
v2	<input checked="" type="checkbox"/>
v3	<input checked="" type="checkbox"/>

MicroarrayElement

experiments:
empty: false
name: galExpData

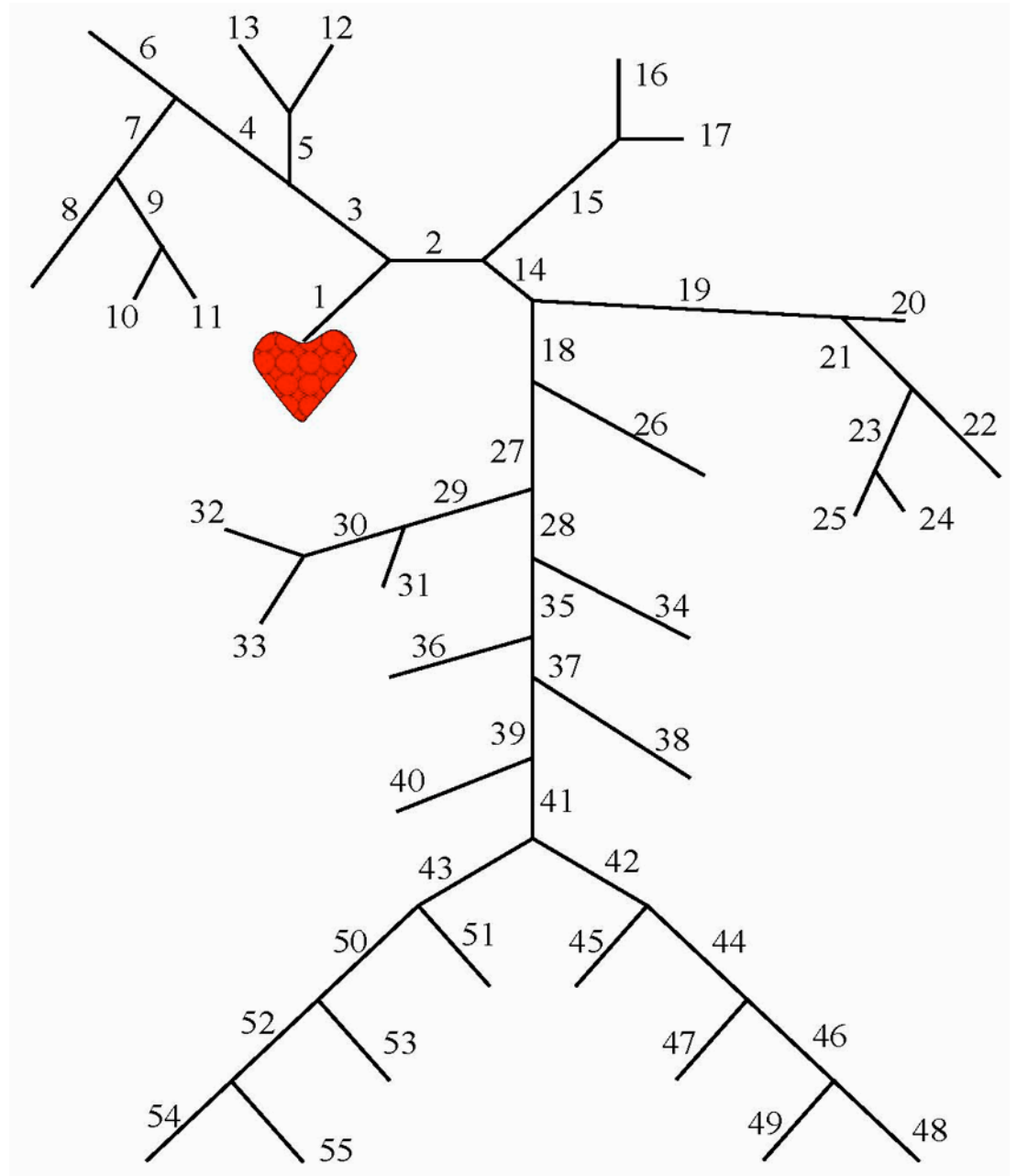
Data collection:
Name: microarray

View Edit Editors

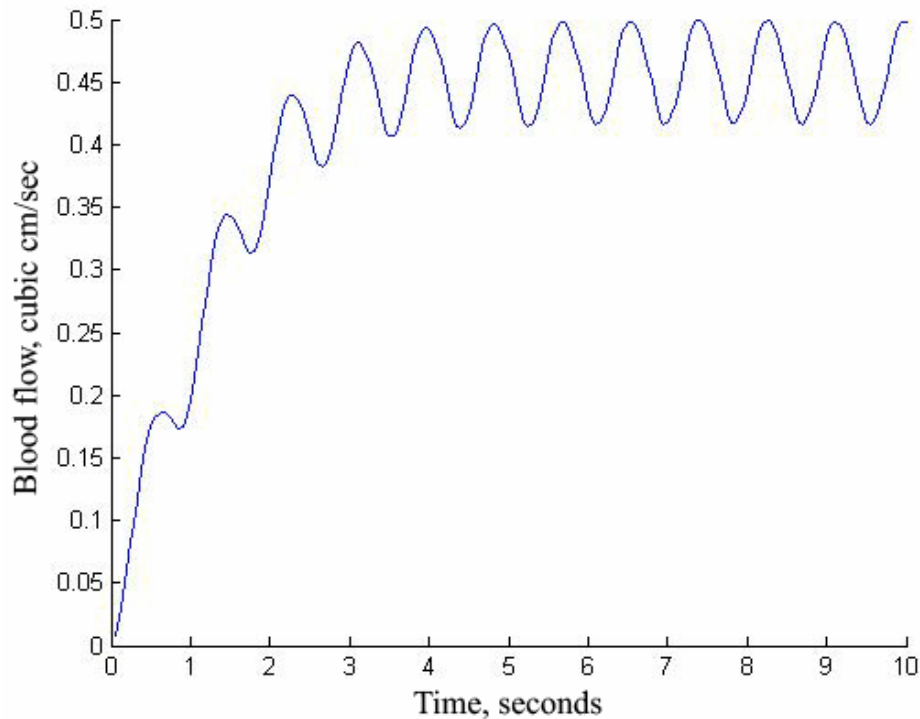
Description Microarray Application Log Clipboard Layouter pane JavaScript Search linked

Arterial tree diagram

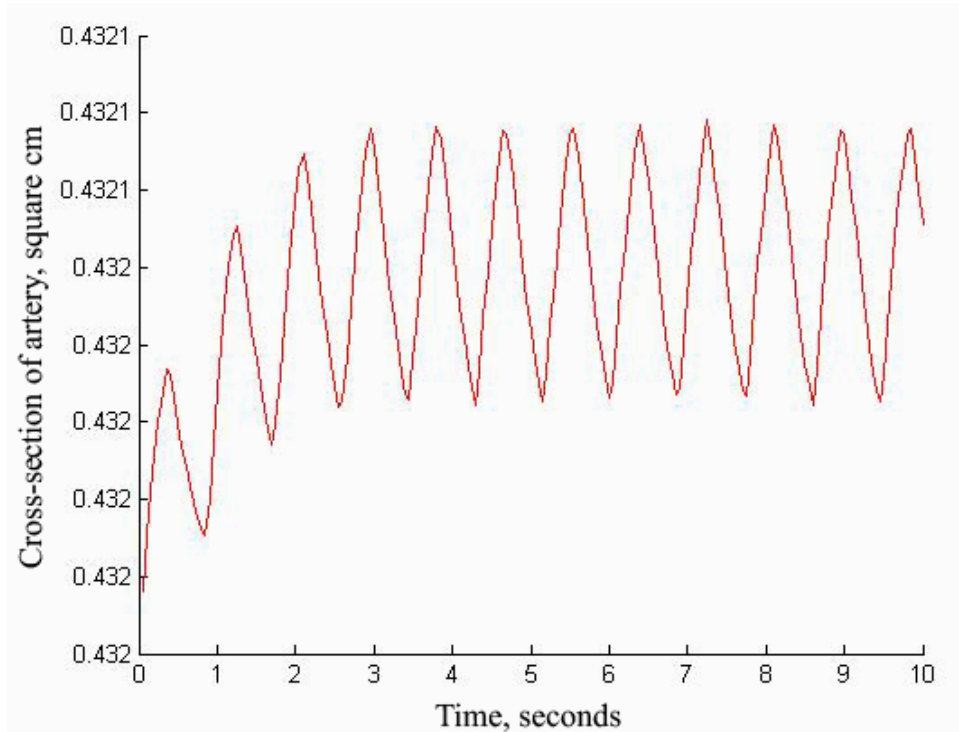
Daniele N. Lamponi. One dimensional and multiscale models for blood flow circulation. Pour l'obtention du grade de docteur es sciences. Ecole Polytechnique Federale De Lausanne, 2004.



Results of Matlab simulation



Oscillations of blood flow in artery №5 of hemodynamic tree



Oscillations of cross-section in artery №5 of hemodynamic tree

Further work: reproduce Matlab simulation engine functionality in Java simulation engine.

Further development of diagram types:

- Formal definition of graphic notation as XML document
- Graphic notation editor – friendly user interface for editing XML document
- New diagram types:
 - sequence map
 - sequence map + pathway diagram
 - composite diagram
 - agent based model

BioUML workbench

File Help

Modules Data Plugins

SBML model repository : kitanoExample.xml

CircClock-1999Lel_pe
 CircClock-2001Ued.x
 CircClock-2002Vil.xml
 ElectroPhys-1952Hod
 Genetic-2000Elo.xml
 Genetic-2003Mar.xml
 Heliobacter-pylori-26
 MAPKcasc-2000Kho.x
 MAPKcasc-2000Kho_
 MAPKcasc-2000Lev-2
 MAPKcasc-2000Lev.x
 Metabolism-2000Poo
 Metabolism-2000Teu
 Metabolism-2001Hel.
 Metabolism-2001Kon
 Metabolism-2002Hoe
 Metabolism-2002Hoe
 Metabolism-2002Lam
 Miscellaneous-1963Lo
 Miscellaneous-1974Fi
 MolMotors-2003Kol.x
 Mycobacterium_tuber

protein1 gene1 rna1 phenotype1 substance1
 protein2 gene2 rna2 phenotype2 C1
 protein3 gene3 rna3 phenotype3 substance3
 protein4 gene4 rna4 unknown1 unknown2
 protein5 gene5 rna5 C3
 protein6 gene6 rna6 C2
 gene7 rna7 substance5 compartment2
 compartment3

Node

Title: compartment3

Comment:

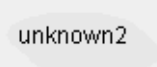
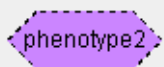
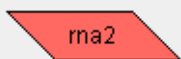
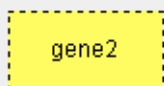
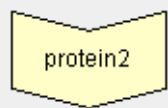
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Role:

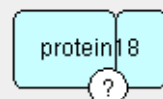
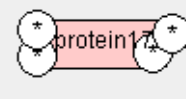
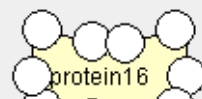
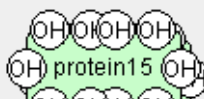
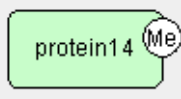
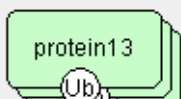
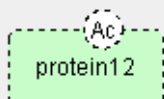
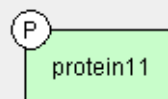
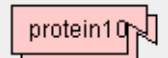
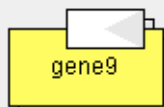
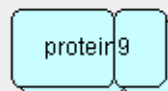
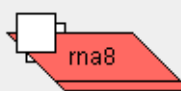
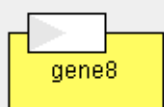
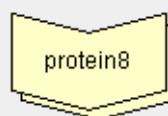
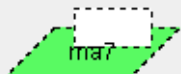
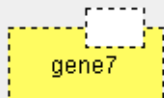
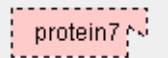
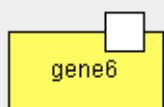
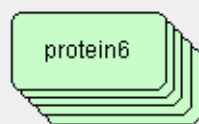
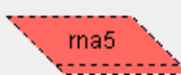
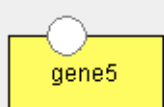
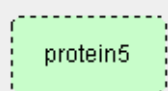
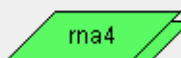
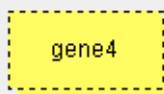
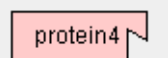
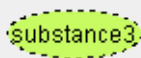
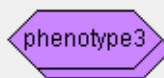
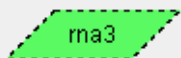
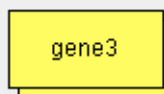
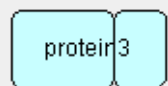
View Edit Editors

WARN : Could not recover graph node edges after transform
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 WARN : Could not recover graph node edges after transform

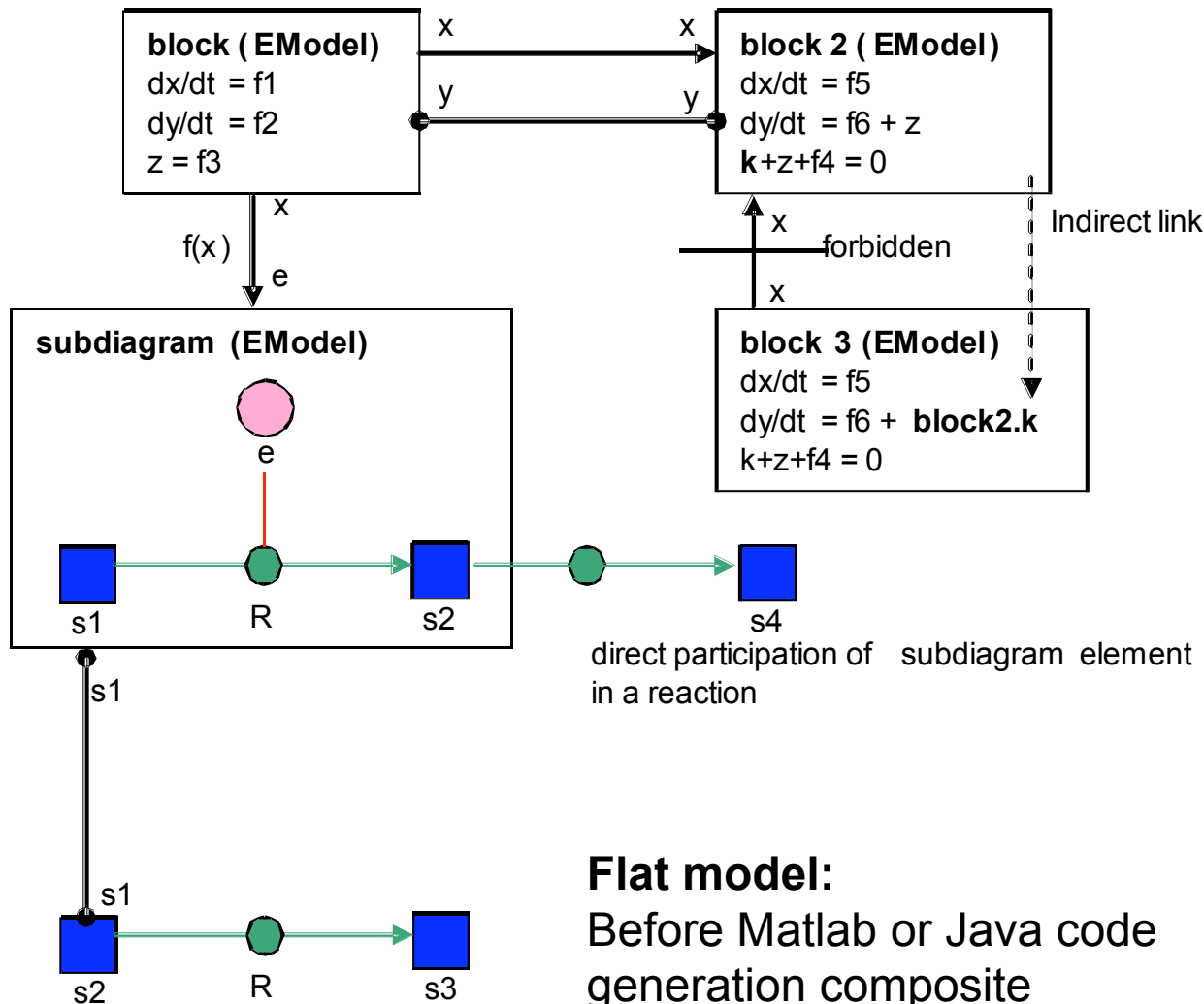
Description Microarray Application Log Clipboard Layout
 Parameters Variables JAVA MATLAB JavaScript



comple



Composite diagram: main concepts



Block types:

- 1) block – only mathematical equations. Used mainly for physiological models;
- 2) subdiagram – other diagram

Connection types:

- 1) directed – input \rightarrow output. Transformation function can be used;
- 2) undirected – contact. Indicates that 2 nodes in mode are the same entity.

Flat model:

Before Matlab or Java code generation composite model is transformed into flat model and usual generation routines are used.

Semantic constraints:

There are semantic constraints, for example: block can have only one input for each variable. Two inputs are forbidden for the same variable.

Further works

- Sequence analyses and visualization
- Agent based modeling
- SBML layout extension
- Improvements BioUML workbench for multiuser mode
- Development of distributed information environment for systems biology
 - PSI-MI format support
 - Reactome – MySQL db support
 - BioCyc support
 - ChEBI support

Availability

BioUML workbench (including source code) is freely available at <http://www.biouml.org>

BMOND (Biopath) database – <http://biopath.biouml.org>



<http://www.biouml.org>

BioSoft.Ru
logo

BioUML - framework for systems biology

Site Content

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 - [Conferences](#)

- Documentation
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 - [Presentations](#)
 - [Architecture overview](#)
 - [BioUML API \(javadoc\)](#)
 - [BioUML meta model](#)

Welcome to BioUML world

What is BioUML?

BioUML is Java framework for systems biology. It spans the comprehensive range of capabilities including access to databases with experimental data, tools for formalized description of biological systems structure and functioning, as well as tools for their visualization and simulations.

Currently BioUML framework consists from following parts:

- Meta model - provides an abstract layer to present structure of any biological system as a clustered graph.
- Viewer - a universal viewer to visualize graphs of biological systems structure as diagrams.
- Editor - universal diagram editor.
- Search engine - provides searching of components with the specified properties in biological pathway databases. The search result can be presented as graph and further edited by a user using BioUML editor.
- Modeler - allows a user to model/simulate dynamics of biological systems using block diagrams.

Version 0.7.6

BioUML workbench version 0.7.6 was released.
[More...](#)

Please support BioUML

If you find BioUML workbench useful and would like it to remain free please [support it](#).

SBML tests passed 100%

Both simulation engines (Java and MATLAB) provided by BioUML workbench version 0.7.5 passed 100% SBML semantic test suite.
[Test details](#)

ICSB workshop materials

BioUML workshop was held at

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- European Committee grant №037590 “Net2Drug”
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- Volkswagen-Stiftung (I/75941),
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