

Building virtual cell using BioUML platform

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BioUML platform

- Open source integrated platform for systems biology that spans the comprehensive range of capabilities including access to databases with experimental data, tools for formalized description, visual modeling and analyses of complex biological systems.
- Due to scripts (R, JavaScript) and workflow support it provides powerful possibilities for analyses of high-throughput data.
- Plug-in based architecture (Eclipse run time from IBM is used) allows to add new functionality using plug-ins.

BioUML platform consists from 3 parts:

- BioUML server – provides access to biological databases;
- BioUML workbench – standalone application.
- BioUML web edition – web interface based on AJAX technology;

BioUML main features

- Supports access to main biological databases:
 - *catalogs*: Ensembl, UniProt, ChEBI, GO...
 - *pathways*: KEGG, Reactome, EHMN, BioModels, SABIO-RK, TRANSPATH, EndoNet, BMOND...
- Supports main standards used in systems biology: SBML, SBGN, CellML (1.0), BioPAX, OBO, PSI-MI...
- database search:
 - full text search using Lucene engine
 - graph search
- graph layout engine
- visual modeling:
 - simulation engine supports (ODE, DAE, hybrid, stochastic, 1D PDE);
 - composite models;
 - agent based modeling, rule based modelling;
 - parameters fitting;
- genome browser (supports DAS protocol, tracks import/export);
- data analyses and workflows – specialized plug-ins for microarray analysis, integration with R/Bioconductor, JavaScript support, interactive script console.

Building virtual cell

Challenges:

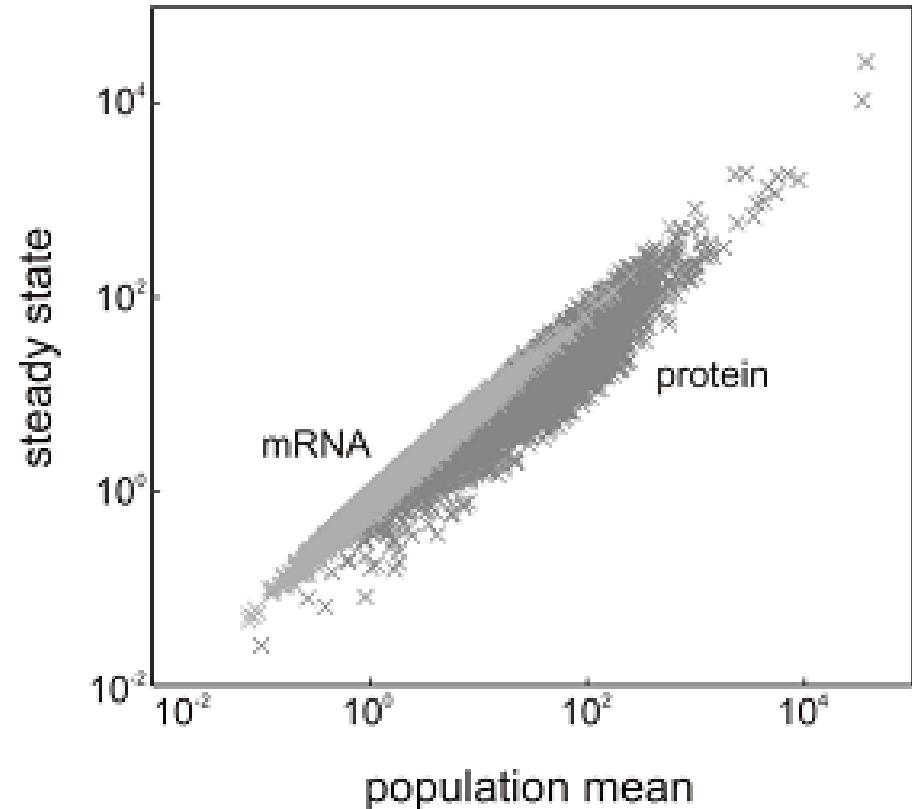
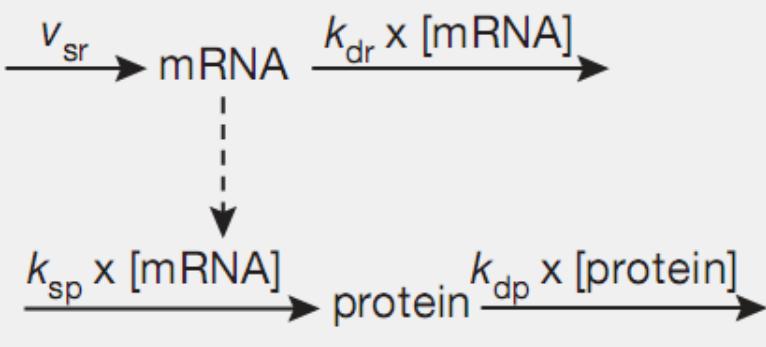
- **methodology** - how can we build, modify, verify and apply complex mathematical models for practical purposes;
- **organization** - how we can split main tasks into smaller, manageable parts and organize collaboration between researchers;
- **software** - we need a software platform that will provide necessary infrastructure for collaborative work of many researchers and will support needed methodology.

Story 1: genome-scale model for prediction of synthesis rates of mRNAs and proteins

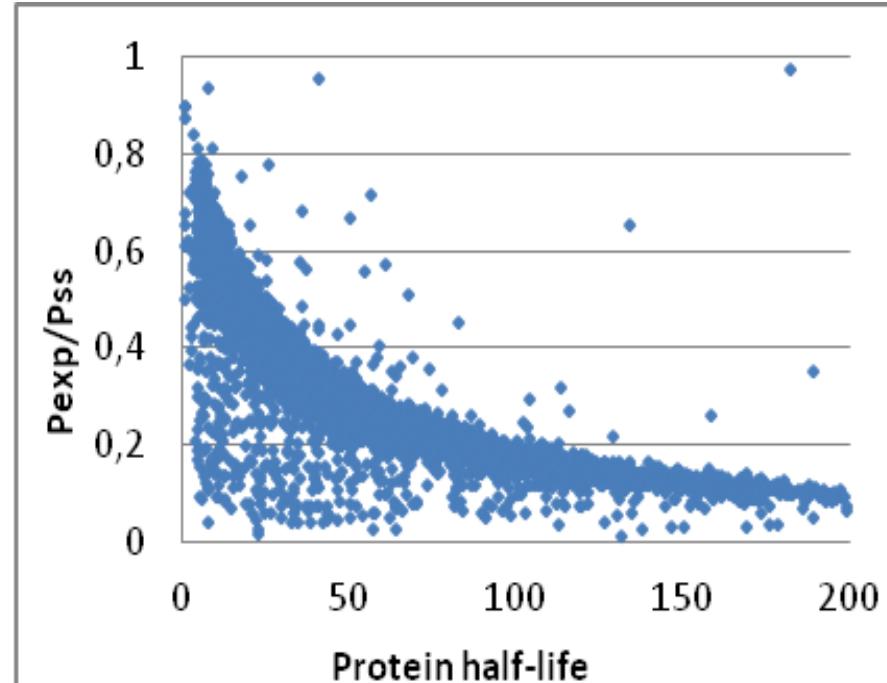
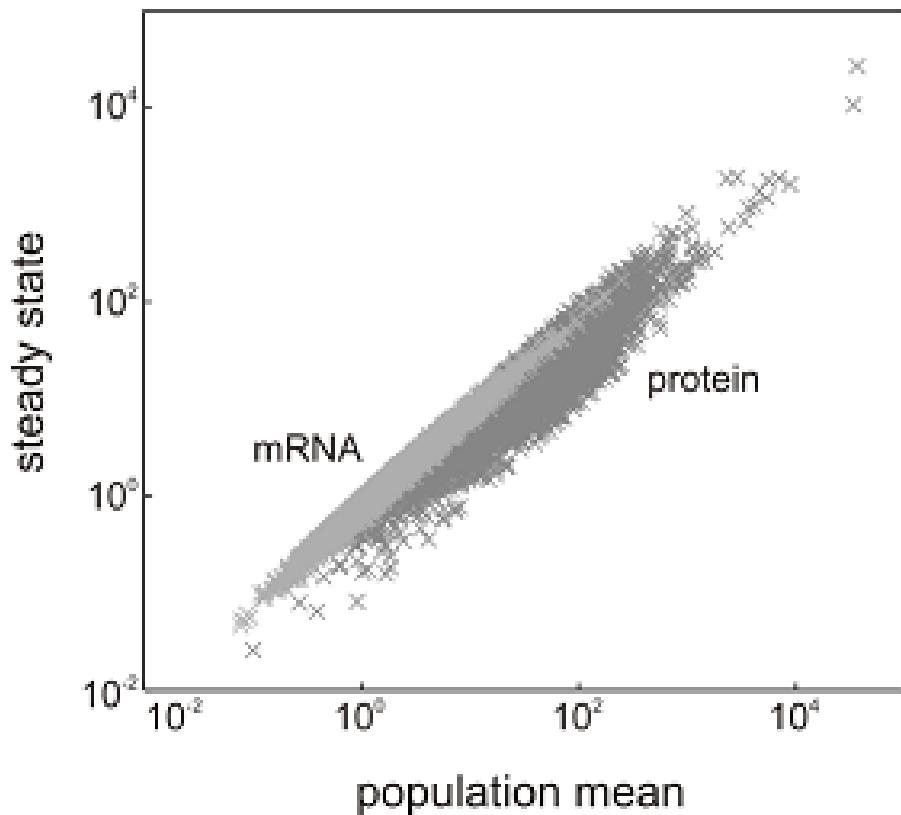
Initial data:

Schwanhäusser B, Busse D, Li N, Dittmar G, Schuchhardt J, Wolf J, Chen W, Selbach M. **Global quantification of mammalian gene expression control.** Nature, 2011, 473(7347):337-342.

- mouse fibroblasts, parallel metabolic pulse labelling
- simultaneously measured absolute mRNA and protein **abundance** and **turnover** for 5000+ genes
- first genome-scale quantitative model for prediction of synthesis rates of mRNAs and proteins



Schwanhäusser B., et al., 2011 - Fig. 6:b Comparison of synthesis rates of mRNA and proteins assuming the measured levels reflect averages over one cell cycle or steady-state values.
 For the synthesis rates of mRNA (light gray), the deviation between the two approaches is small, because mRNA half lives are mostly smaller than the cell cycle time. For protein synthesis (dark gray), the differences are substantial; **they can differ for more than one order of magnitude.**



P – protein, exp – population mean,
ss – steady state;

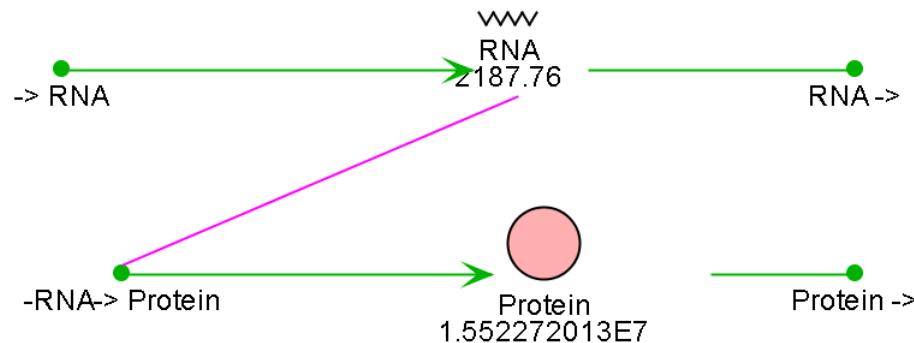
Schwanhäusser B., et al., 2011 - Fig. 6:b Comparison of synthesis rates of mRNA and proteins assuming the measured levels reflect averages over one cell cycle or steady-state values.

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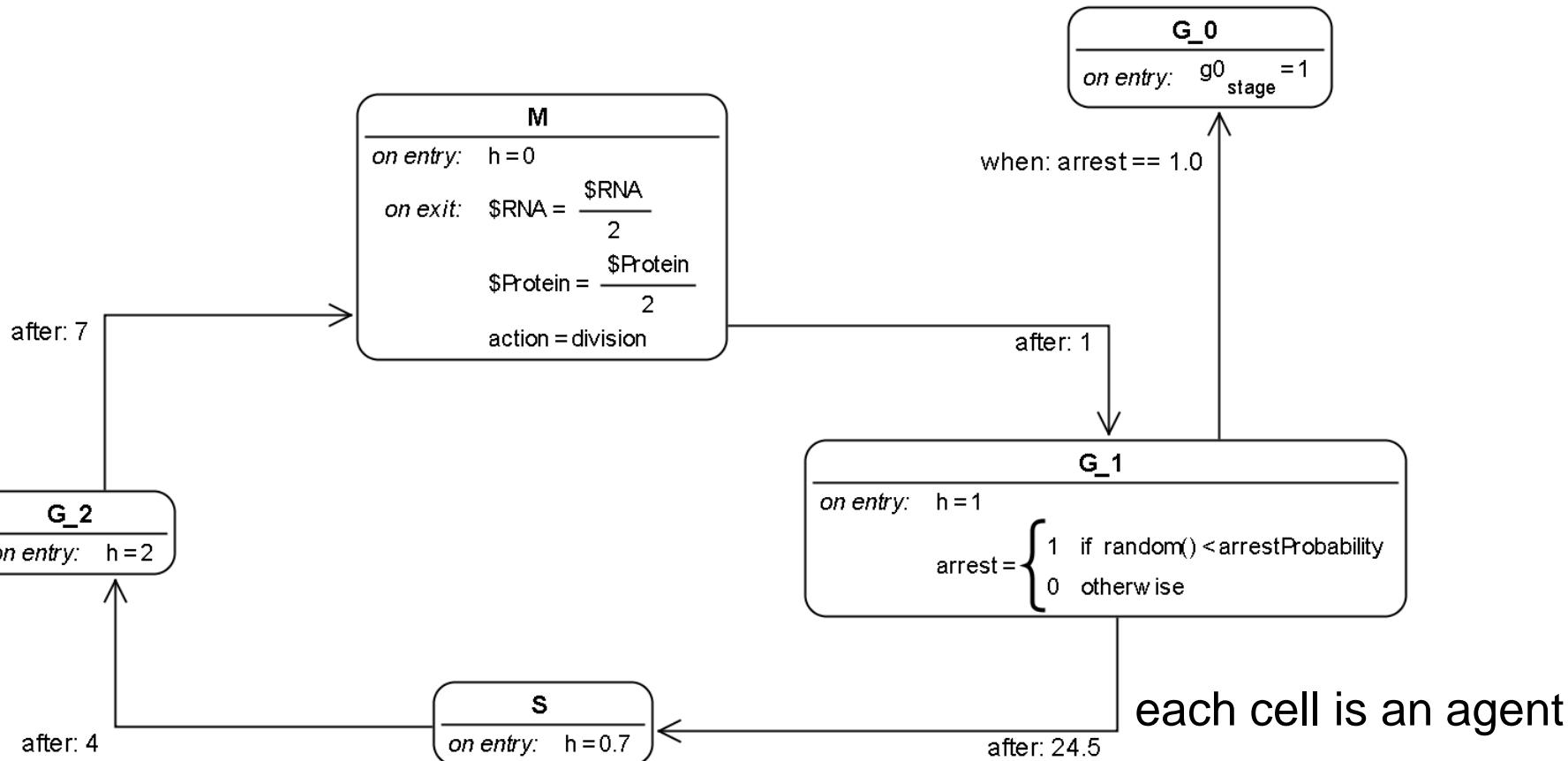
“They (formulas) do not take into account that gene expression in mammalian cells is non-continuous. In addition, the non-uniform age distribution of cells in culture as described in 19, 23 is neglected, since this effect is expected to be small compared to the deviation obtained by neglecting the cell cycle.“

Schwanhäusser B., et al., 2011,
supplementary materials

Agent based model



4247 blocks for protein synthesis

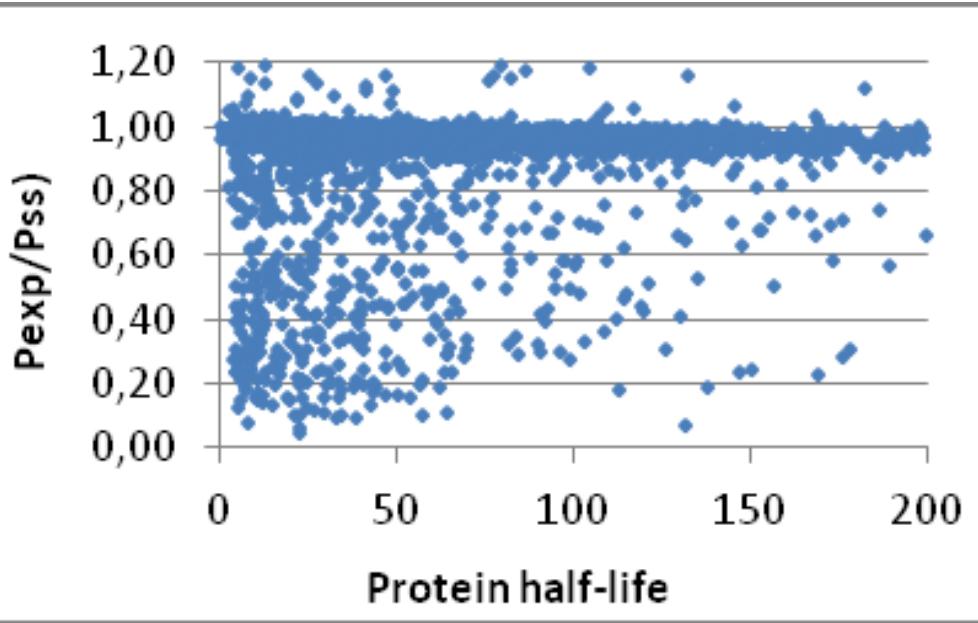


Numerical experiment.

The initial size of population is 200 cells which divide within 108 hours. Average quantity of protein molecules were calculated. This experiment was repeated for 4247 proteins.

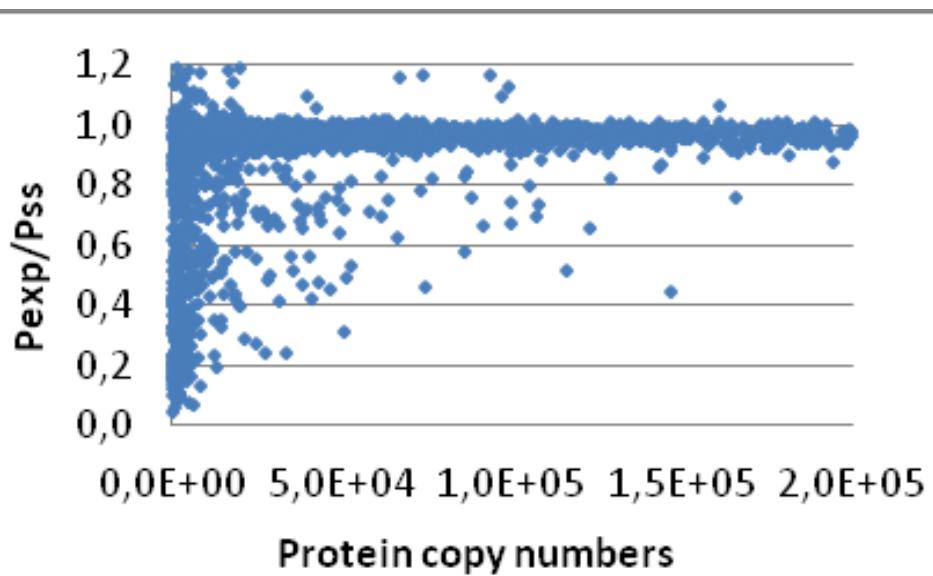
Phase of a cellular cycle	Percent of cells in phase	Rate of transcription
G1	50.8%	V_{sr}
S	22.9%	$0.7*V_{sr}$
G2	13%	$2*V_{sr}$
M	3.3%	0
G0	10%	V_{sr}

Tab.1. Parameters of a cellular cycle



Correlation of experiment and numerical modeling is equal to $R=0.99$

Absolute values also were coordinated (so for 81,6% of proteins absolute values differ by less than 7%)



Main deviations from experimental values are observed for proteins with extremely low copy numbers, where experimental error can be significant.

Used features of BioUML platform

- tables support (import, calculated columns);
- JavaScript API for model generation (from tabular data)
- visual modeling – diagram visualization
- agent based modeling
- ODE solver

BioUML workbench

File Database Diagram Data Help

Tables : schwannhausser

First Previous Page 1 of 101 Next Last Show 50 entries

	ID	Protein Names	Gene Names	Protein Descriptions	Uniprot IDs	RefSeq protein IDs	Refseq mRNA ID
1	IPI00229543...	Histone H2A type ...	Hist1h2af;Hist3h2...	Histone H2A type 1-F;Histo...	Q8CGP5;Q61668;Q8BF...	NP_783592;NP_835736;...	ENSMUST0000007326...
2	IPI00624840...	Histone H4	Hist1h4a;Hist1h4...	12 kDa protein;similar to his...	P62806;B2RTM0;Q6166...	XP_981474;NP_291074;N...	ENSMUST0000007300...
3	IPI00110850...	Actin, cytoplasmic...	Actb	Actin, cytoplasmic 1;Putativ...	P60710;B2RRX1;Q3TJ9;...	NP_031419	NM_007393
4	IPI00348270...	Histone H2B type ...	Hist2h2bb	Histone H2B type 2-B	Q64525	NP_783597	ENSMUST0000001824...
5	IPI00282848...	Histone H3.2	Hist1h3b;H3-53;...	histone cluster 2, H3c1;Hist...	P84228;A1L0U3;B9E1B5	NP_835734;NP_038576;...	ENSMUST0000007555...
6	IPI00470152...	40S ribosomal pro...	Rps27a;Uba80;Ub...	ribosomal protein S27a;simi...	P62983;Q642L7;Q3TWD1	NP_001029037;NP_0772...	NM_001033865
7	IPI00307837...	Elongation factor ...	Eef1a1;Eef1a	Elongation factor 1-alpha 1;...	P10126;Q3TIB;Q3UA81;...	NP_034236	NM_010106

Parameter Table:

id	name	value	description	status
22	mRNA half-life replic...	Text	mRNA half-life replic...	
23	mRNA half-life avera...	Text	mRNA half-life avera...	<input checked="" type="checkbox"/>
24	transcription rate (vsr)...	Text	transcription rate (vsr...)	<input checked="" type="checkbox"/>
25	transcription rate (vsr)...	Text	transcription rate (vsr...)	<input checked="" type="checkbox"/>
26	transcription rate (vsr)...	Text	transcription rate (vsr...	<input checked="" type="checkbox"/>
27	translation rate const...	Text	translation rate const...	<input checked="" type="checkbox"/>
28	translation rate const...	Text	translation rate const...	<input checked="" type="checkbox"/>
29	translation rate const...	Text	translation rate const...	<input checked="" type="checkbox"/>
30	mRNA degradation	Text	mRNA degradation	<input checked="" type="checkbox"/>

Columns Samples Groups Filters Application Log Search results Clipboard JavaScript Search linked Tasks SQL editor

- table with initial data (Schwannhauser B.et al., 2011);
- calculated columns (k degradation)

BioUML workbench

File Database Diagram Data Help

Tables : schwannhausser

First Previous Page 1 of 101 Next Last

	ID	Protein ...	Gene N...	Protein ...	Uniprot ...	RefSeq ...	Refseq ...	ENSEM... BOM	MGI ID	Protein I...	Prot
1	IPI00229543...	Histone H2...	Hist1h2af;H...	Histone H2...	Q8CG5P;Q6...	NP_783592;...	ENSMUST0...	MGI:244830...	130		1317
2	IPI00624840...	Histone H4	Hist1h4a;Hi...	12 kDa prot...	P62806;B2R...	XP_981474;...	ENSMUST0...	MGI:244841...	105		1037
3	IPI00110850...	Actin, cyto...	Actb	Actin, cyto...	P60710;B2R...	NP_031419	NM_007393	ENSMUST0...	MGI:87904;...	375	41,74
4	IPI00348270...	Histone H2...	Hist2h2bb	Histone H2...	Q64525	NP_783597	ENSMUST0...	MGI:2448413	126		9427
5	IPI00282848...	Histone H3.2	Hist1h3b;H...	histone clu...	P84228;A1L...	NP_835734;...	ENSMUST0...	MGI:244831...	181		6948
6	IPI00470152...	40S riboso...	Rps27a;Uba...	ribosomal ...	P62983;Q64...	NP_001029...	NM_001033...	ENSMUST0...	MGI:192554...	156	17,95
7	IPI00307837...	Elongation ...	Eef1a1;Eef1a	Elongation ...	P10126;Q3T...	NP_034236	NM_010106	ENSMUST0...	MGI:1096881	462	50,11

JavaScript

```

var diagram = data.get("data/Collaboration/Schwannhausser/Data/Diagrams/Schwannhausser model"); //result diagram
var table = data.get("data/Collaboration/Schwannhausser/Data/Tables/Schwannhausser"); //input table
for (var i=0; i<table.getSize(); i++) //iterating through table data
{
    var tableRow = table.getValueAt(i).getValues();
    var proteinName = tableRow[0];
    var proteinCopies = tableRow[14];
    model.addSpecies(diagram, proteinName, proteinCopies);

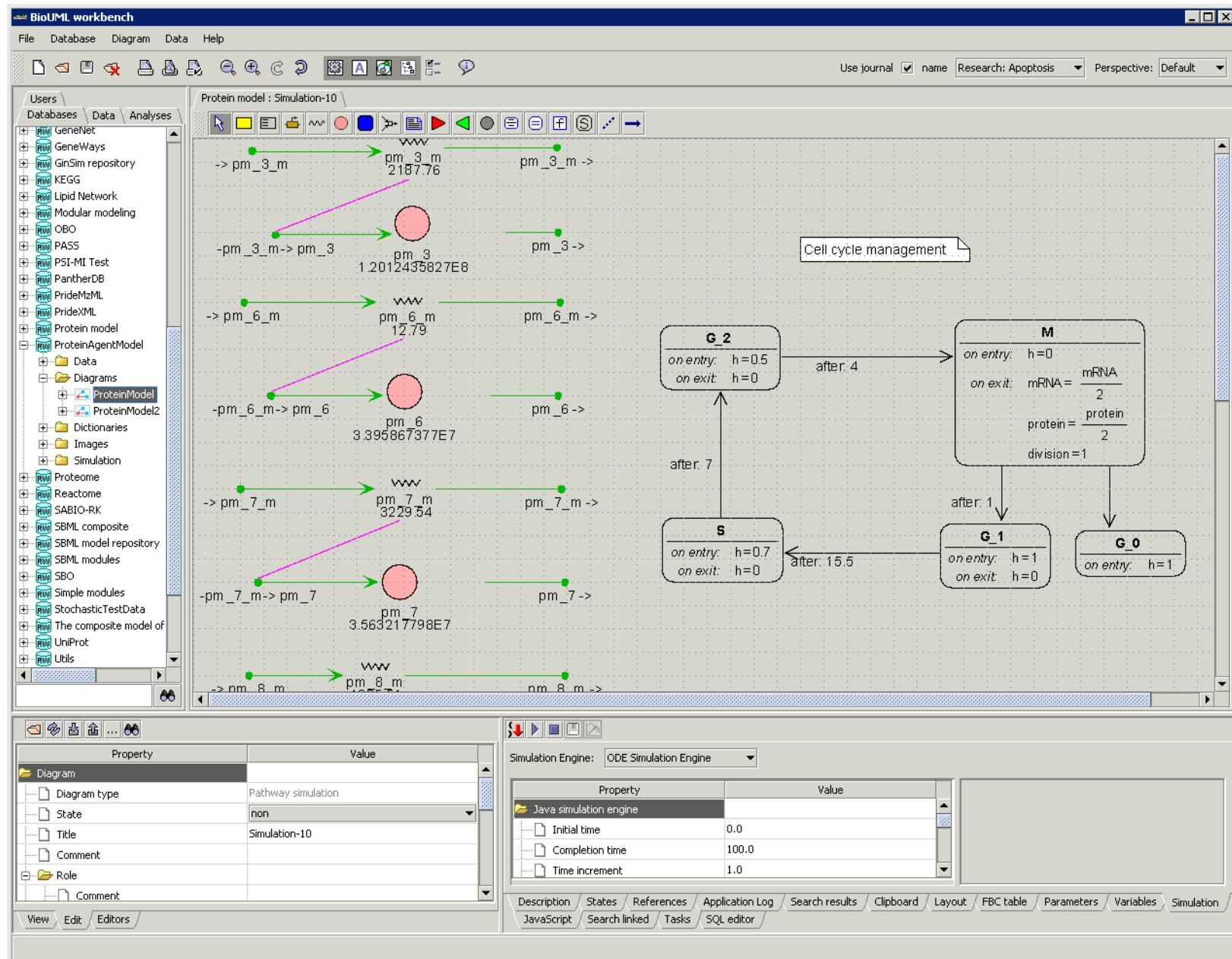
    var rnaName = proteinName + "_m";
    var rnaCopies = tableRow[17];
    model.addSpecies(diagram, proteinName, rnaCopies);

    var proteinDegradationRate = "Math.log(2) /" + tableRow[20];
    var rnaDegradationRate = "Math.log(2) / " + tableRow[23];
}

```

Columns Samples Groups Filters Application Log Search results Clipboard JavaScript Search linked Tasks SQL editor

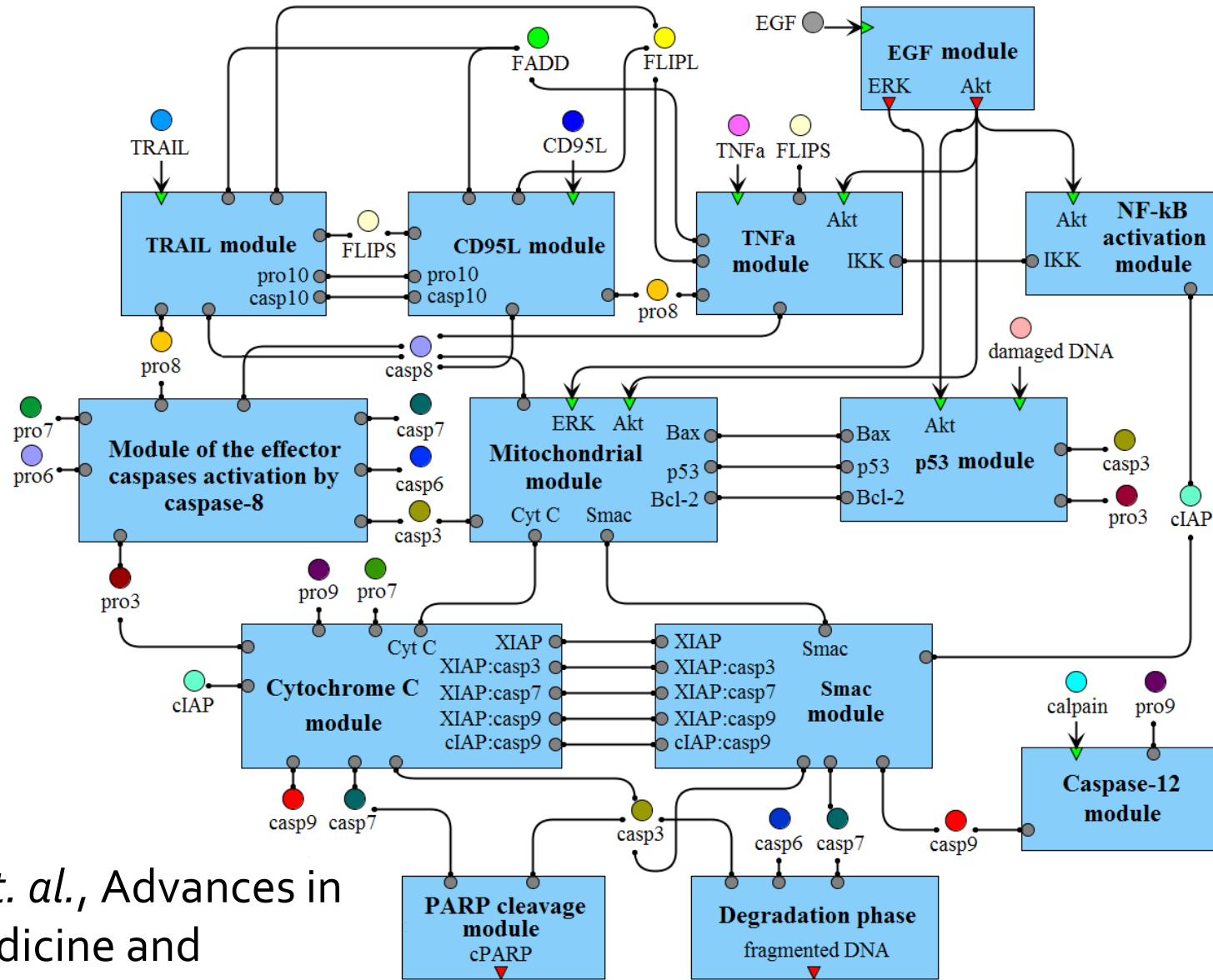
Java script for diagram generation



Agent-based model

Story 2: the modular model of apoptosis

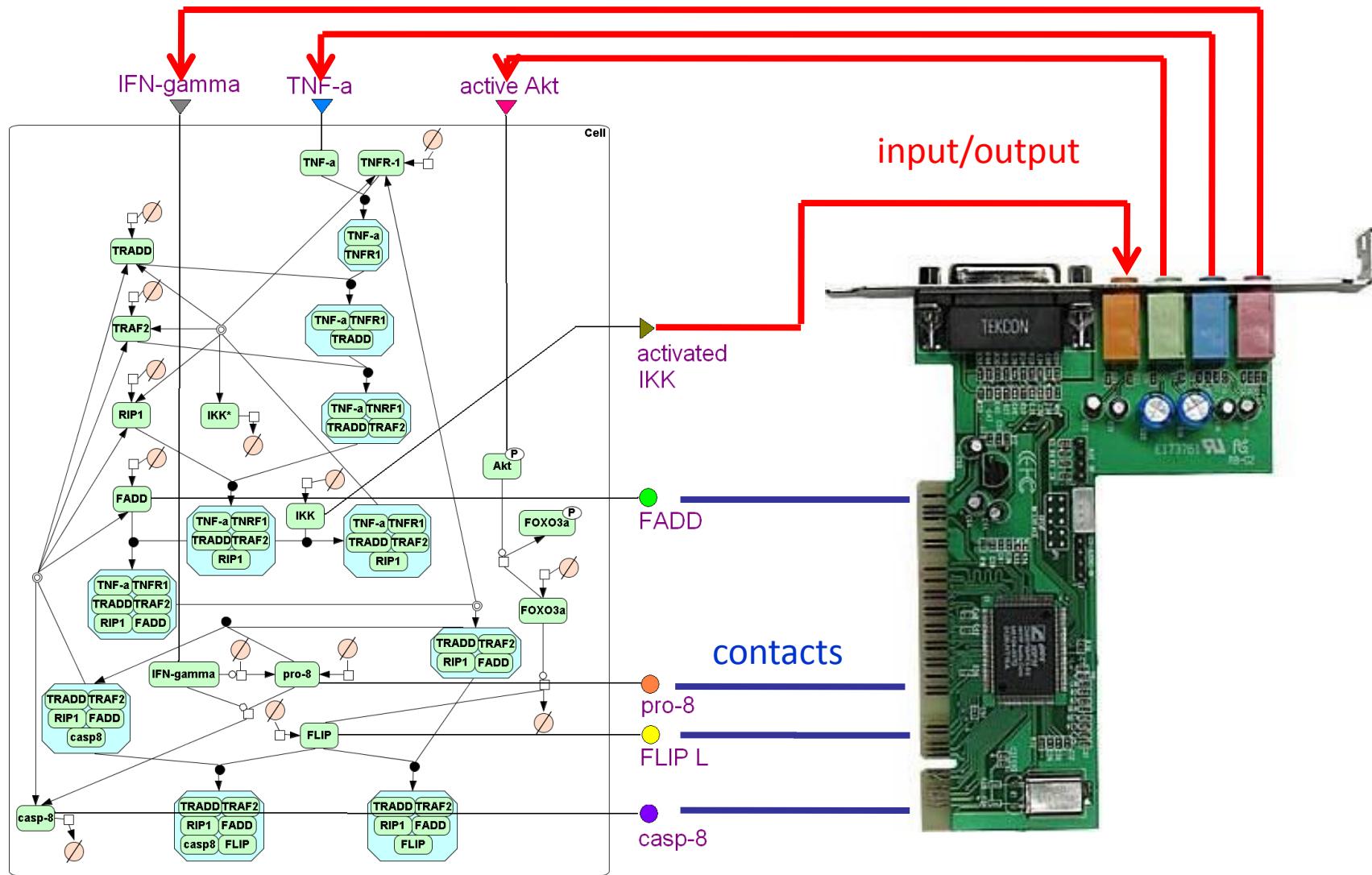
- 13 modules
 - 279 species
 - 372 reactions
 - 459 parameters



Kutumova E.O. et. al., Advances in Experimental Medicine and Biology, 2012, 736(2):235-245

Modules:

clear specification of interfaces



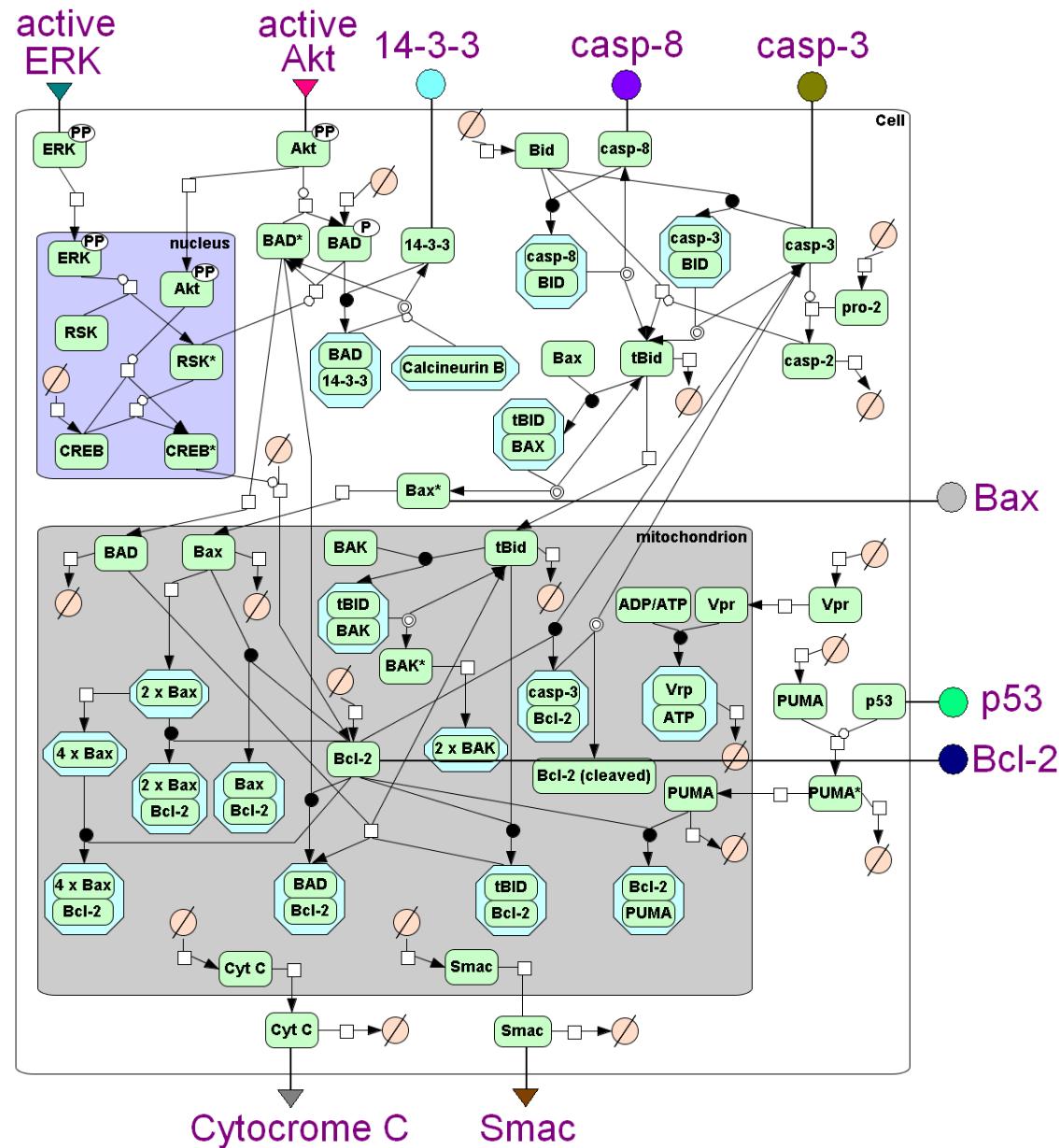
Mitochondron module

(BMOND ID: Int_Mitoch_module)

Bagci EZ, et al,
Biophysical J 2006
Albeck JG, et al,
PLoS Biol 2008

Additions:

- ✓ Activation of CREB and deactivation of BAD by Akt-PP and ERK-PP
- ✓ Upregulation of Bcl-2 by CREB
- ✓ Bcl-2 suppression by p53



EGF module

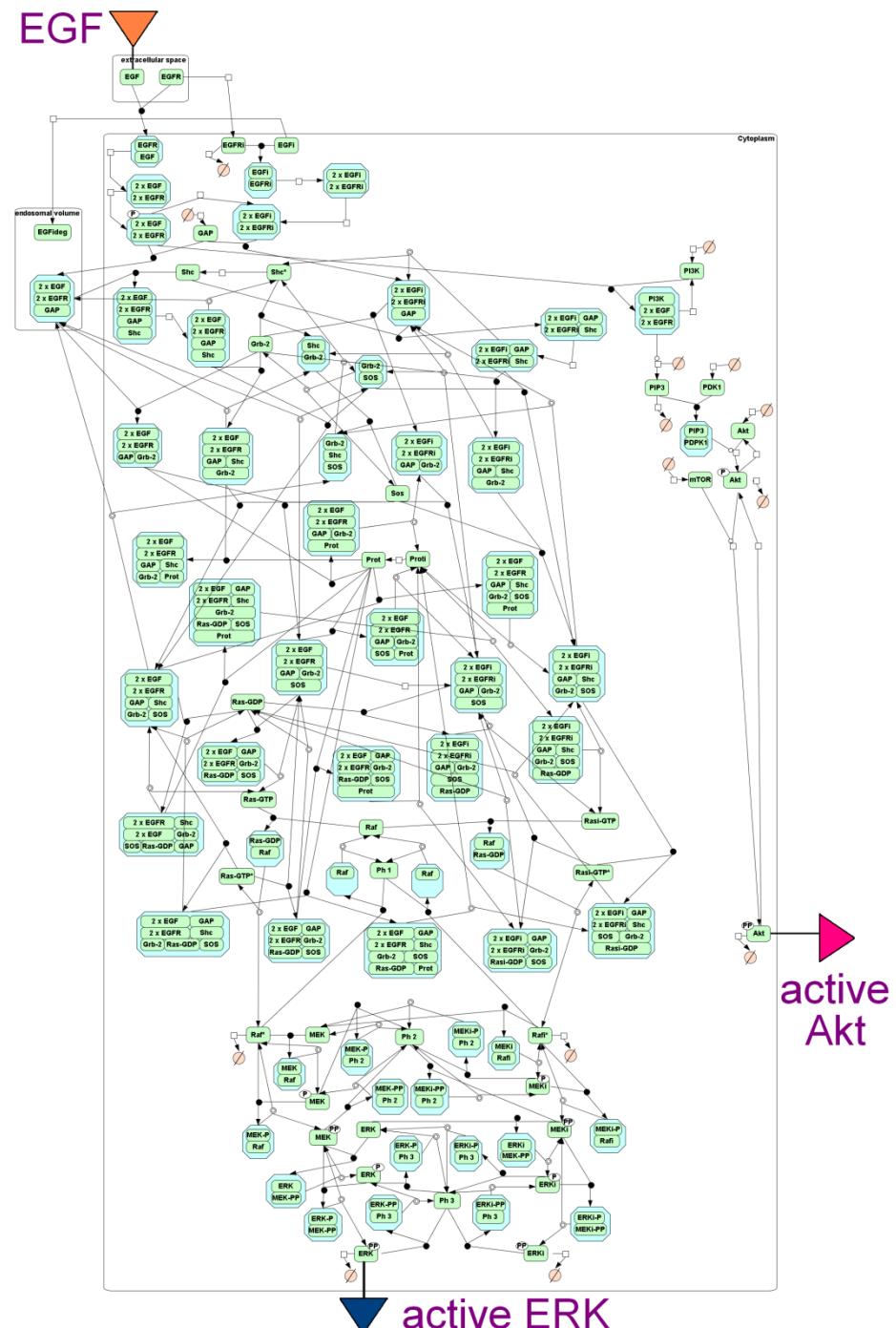
(BMOND ID: Int_EGF_module)

Schoeberl B, et al: *Nature Biotechnology* 2002

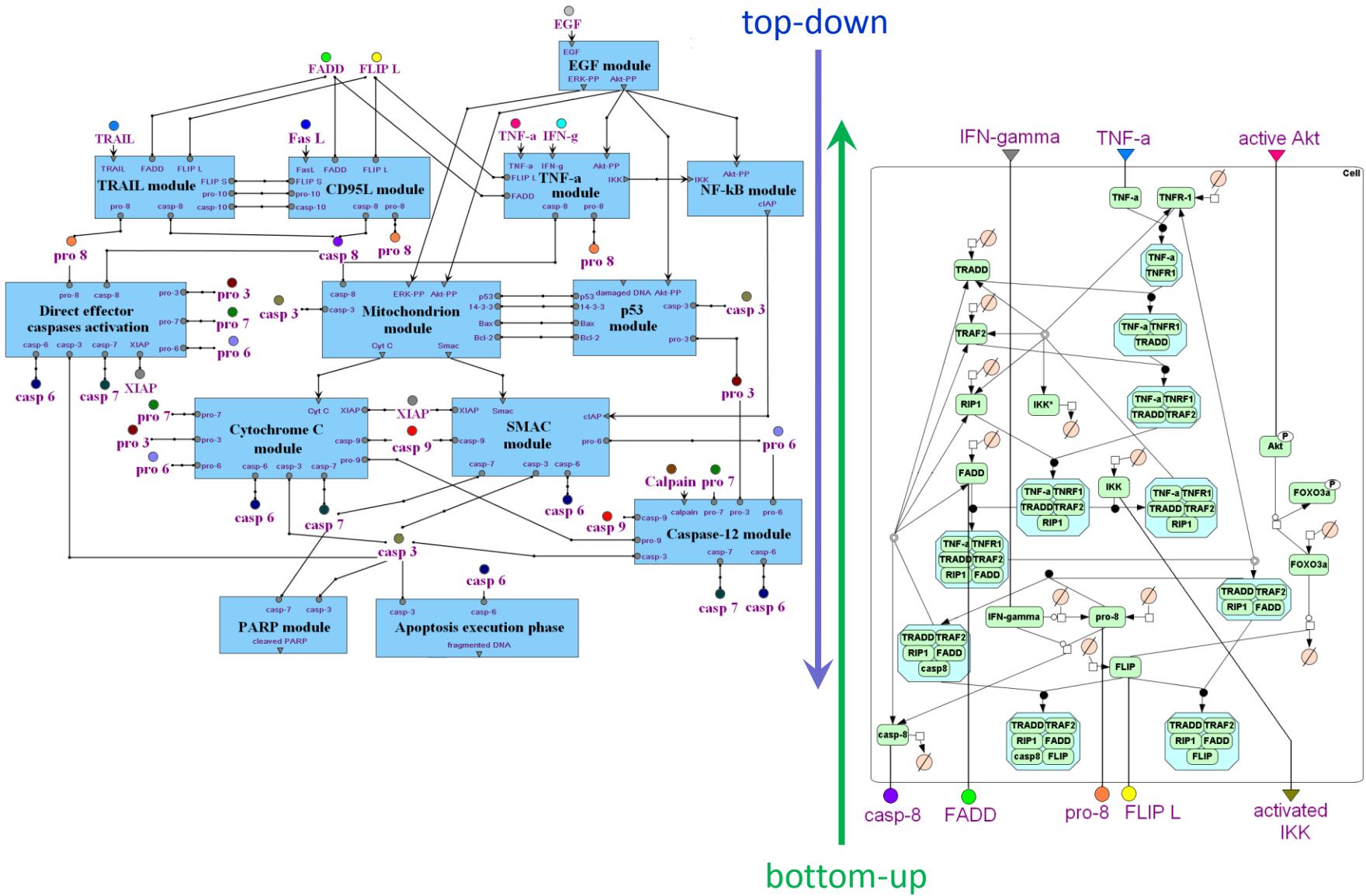
Borisov N, et al: *Molecular Systems Biology* 2009

Additions:

- ✓ Reactions of protein syntheses and degradations



Modular model allows us to combine both up-down and bottom-up approaches



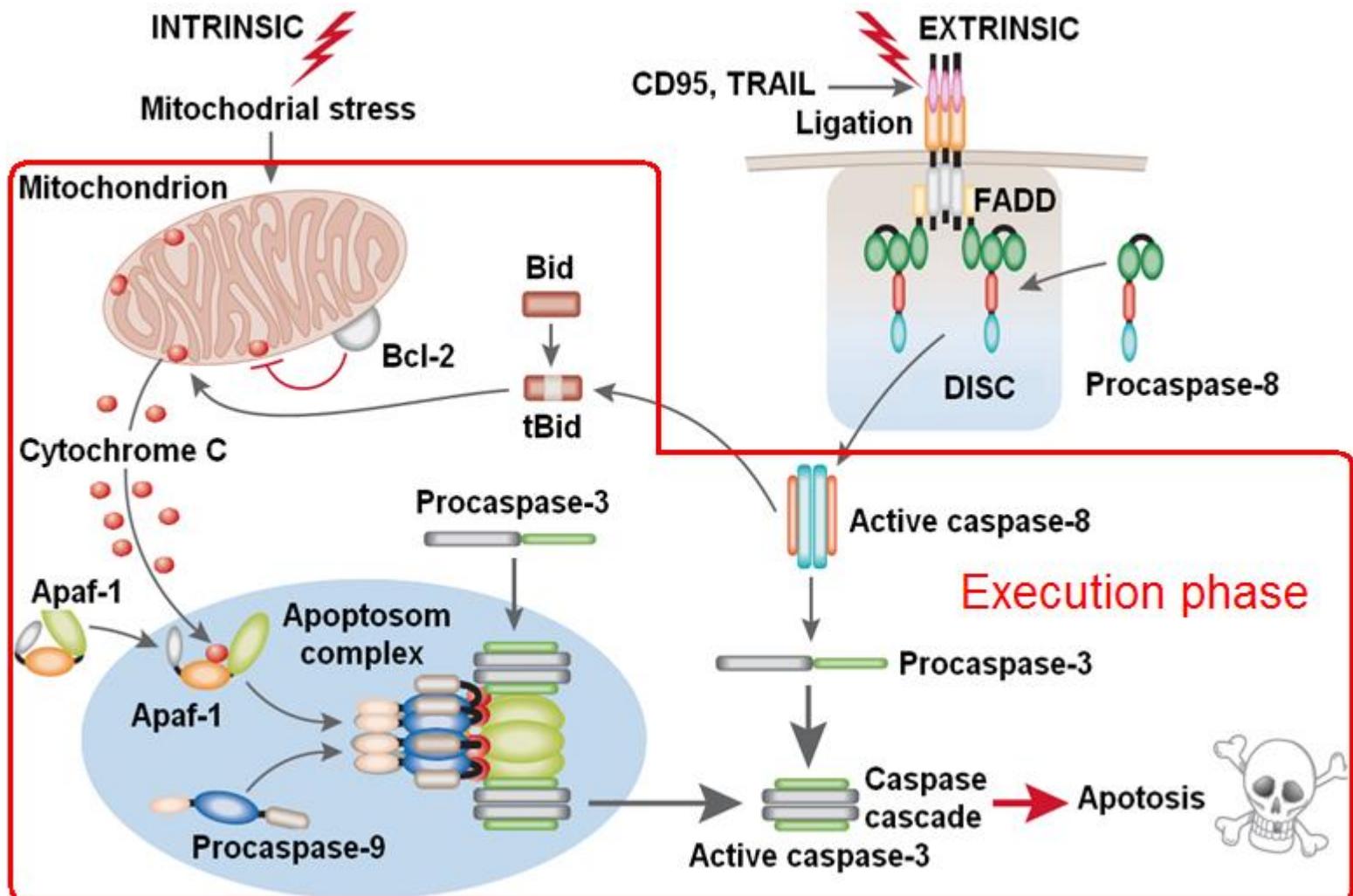
Extreme programming (XP) methodology

- Planning
 - User stories
 - Make frequent small releases
 - The project is divided into iterations
- Coding
 - Code must be written to agreed standards
 - Unit test first
 - Integrate often
 - Collective ownership
- Testing
 - Unit/acceptance tests

XP adaptation to modeling

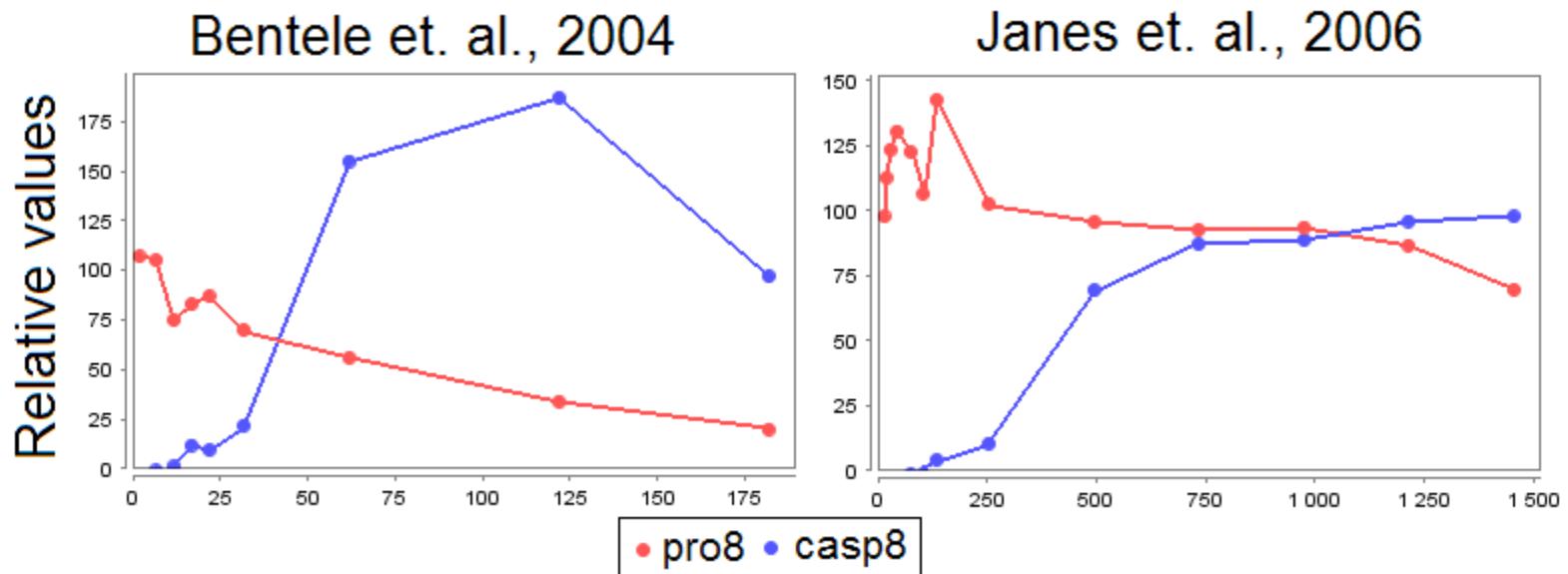
- Planning
 - **User stories:** requirements for the model based on the experimental data
 - **Make frequent small releases**
 - **Iterations:** after each iteration a new set of experimental data should be reproduced
- Coding
 - **Standards:** SBGN, SBML, comp extension
 - **Unit test first**
 - **Integrate often:** model is saved into public database
 - **Collective ownership:** collaborative editing and chat
- Testing
 - **Unit/acceptance tests:** BioUML provides the facilities for testing the models.

Execution phase of apoptosis



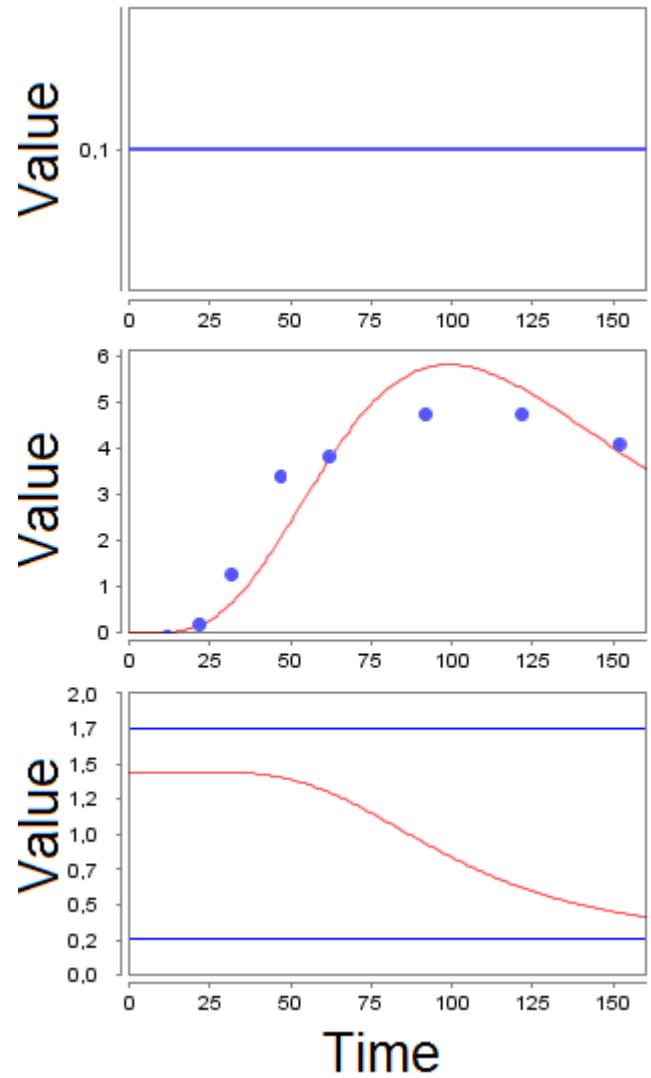
User stories: requirements for the model

- No external signals → concentration of the cleaved PARP is zero. **Iteration 1**
- CD95L signaling → dynamics of pro-8 and casp-8 according to Bentele et. al. **Iteration 2**
- TNF-a signaling → dynamics of pro-8 and casp-8 according to Janes et. al. **Iteration 3**



Types of the acceptance tests

- Steady-state
- Time course
- Control of the variable values



Iterations and acceptance tests

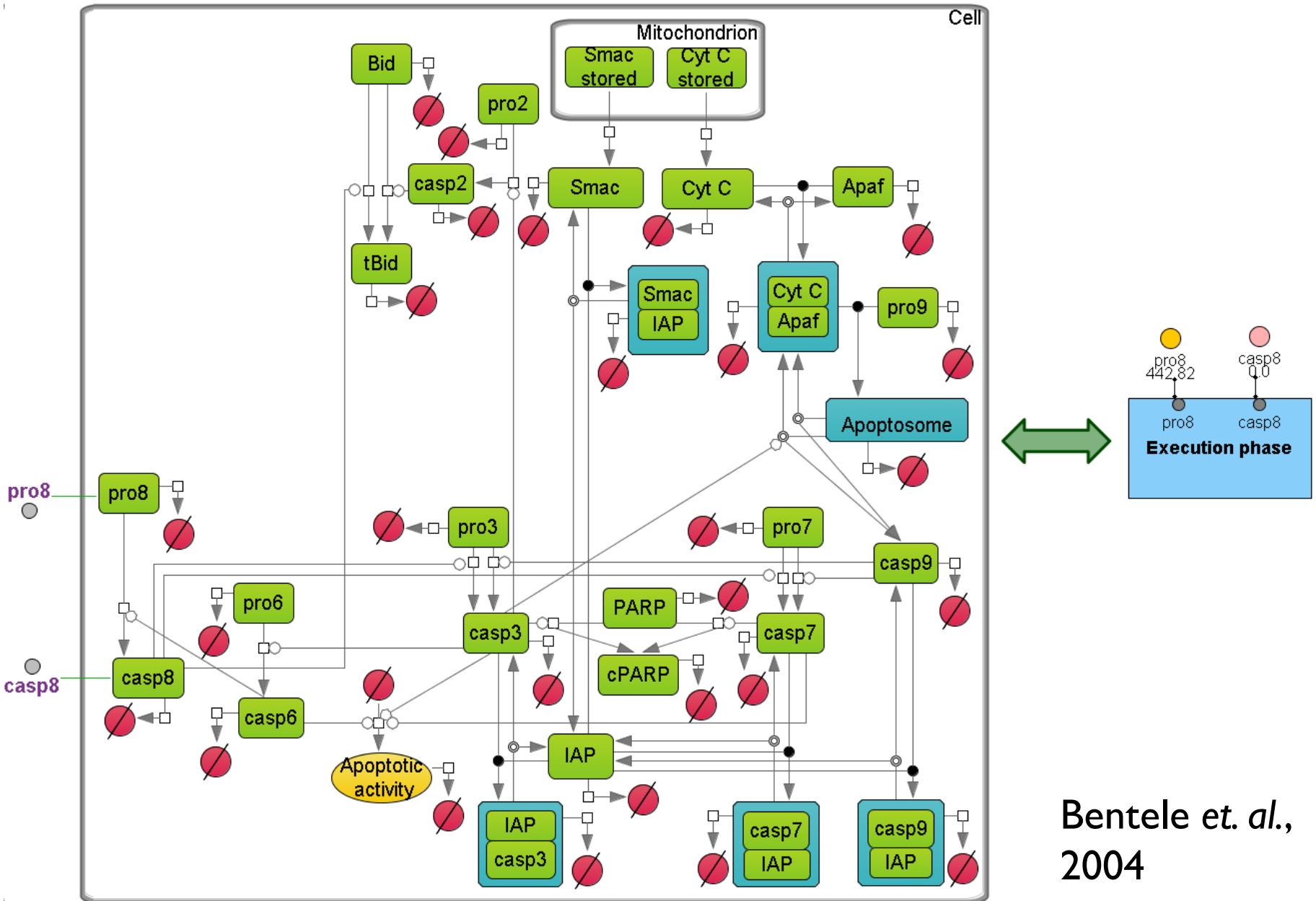
Unit test				
	Name	State	Info	Time limit
1	Steady-state case			10.0
2			Steady state: cleaved PARP	10.0
3	CD95L signaling	CD95L signaling		50.0
4		CD95L signaling	Experiment: Bentle et. al., procaspase-8	20.0
5		CD95L signaling	Experiment: Bentle et. al., caspase-8	30.0
6	TNF α signaling	TNF α signaling		40.0
7		TNF α signaling	Experiment: Janes et. al., procaspase-8	10.0
8		TNF α signaling	Experiment: Janes et. al., caspase-8	30.0

Iteration 1

Iteration 2

Iteration 3

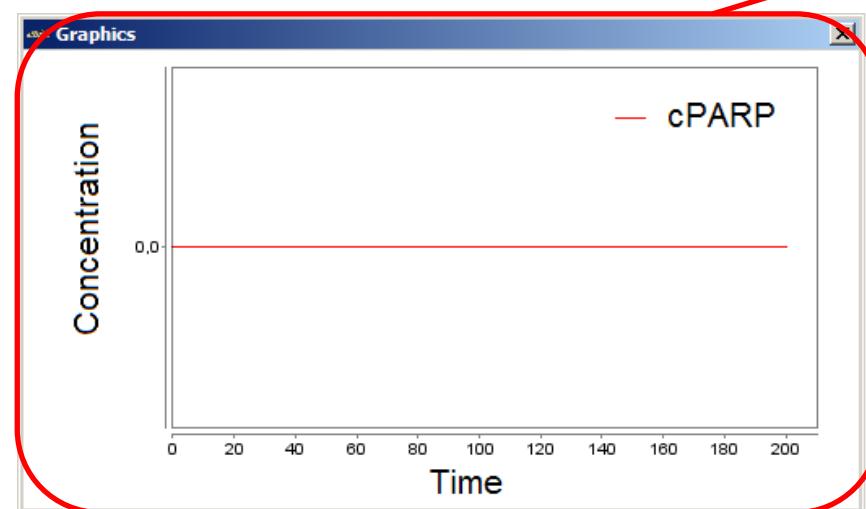
Modeling of the execution phase of apoptosis



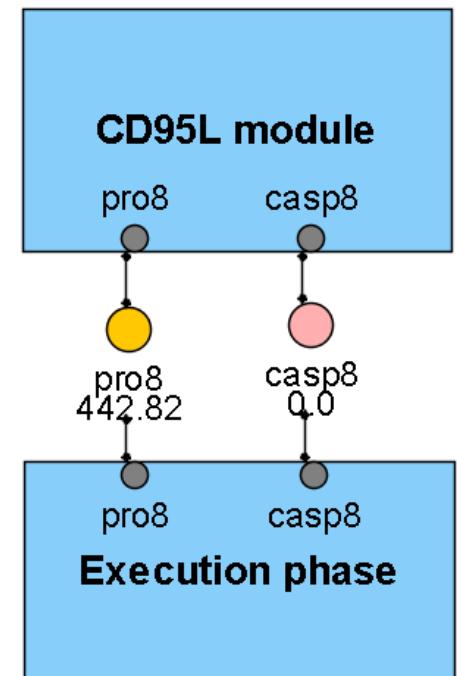
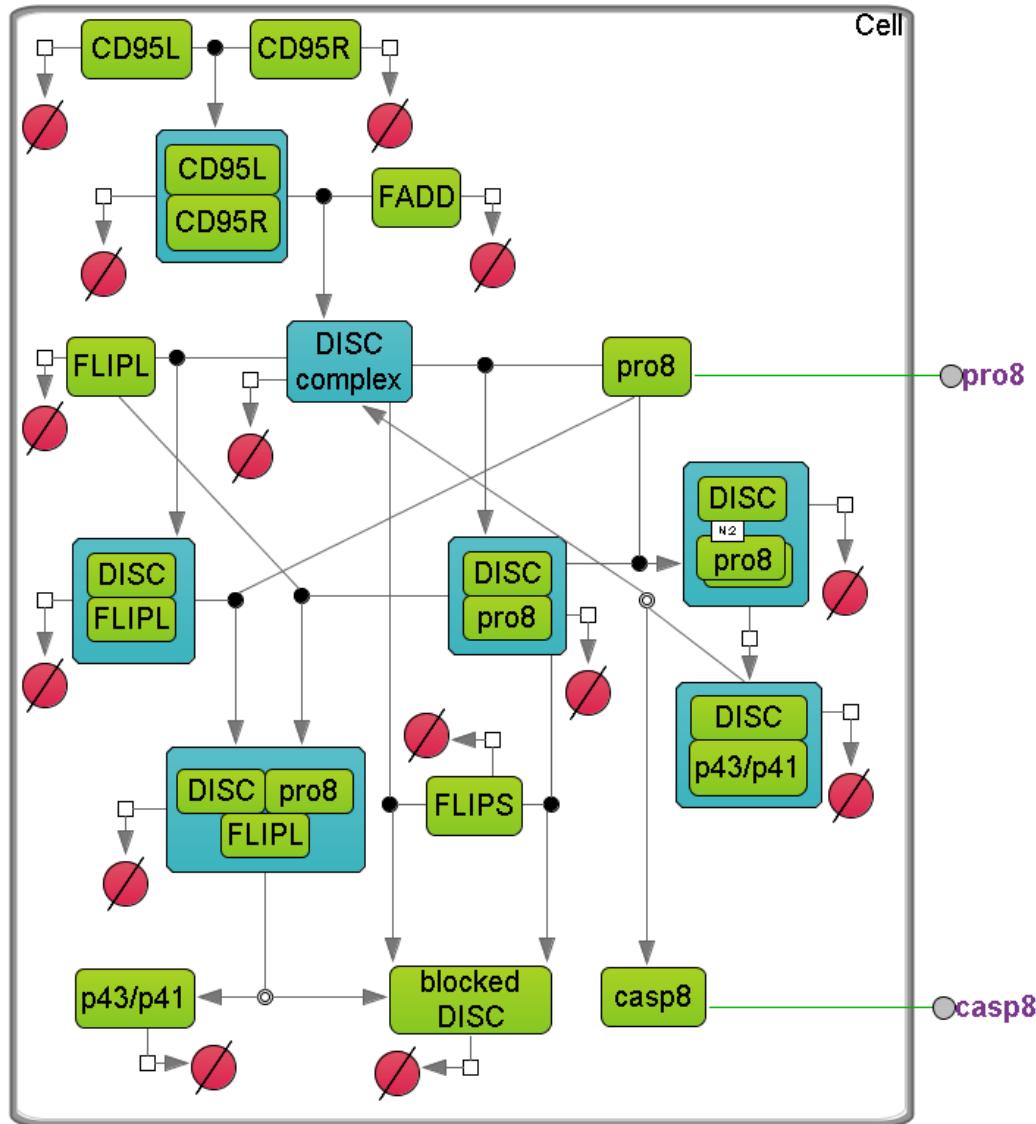
Iteration I: execution phase

Steady-state acceptance test

	Name	State	Info	Time limit	Test duration	Error	Status	Plot
1	Steady-state case			0	4,500		SUCCESS	
2		Steady-state	Steady state: cleaved PARP	0	4,500		SUCCESS	View



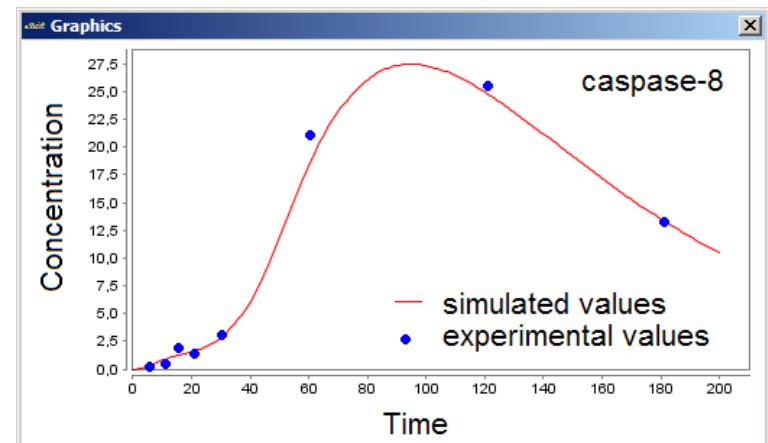
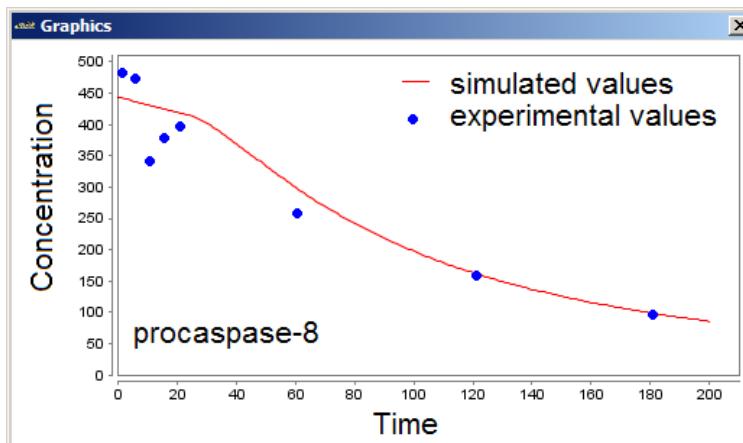
Iteration 2: CD95-signaling



Iteration 2: CD95-signaling

Experiment time courses for pro-8
and casp-8 according to the data by
Bentelle, et. al., 2004

Unit test \									
	Name	State	Info	Time limit	Test duration	Error	Status	Plot	
1	Steady-state case			0	4,500		SUCCESS		
2			Steady state: cleaved PARP	0	4,500		SUCCESS	<button>View</button>	
3	CD95L signaling	CD95L signaling		0	2,657		SUCCESS		
4		CD95L signaling	Experiment: Bentelle et. al., procaspase-8	0	2,657		SUCCESS	<button>View</button>	
5		CD95L signaling	Experiment: Bentelle et. al., caspase-8	0	2,657		SUCCESS	<button>View</button>	



Used features of BioUML platform

- visual modeling (SBGN notation)
- modular modelling
- parameters fitting
- acceptance tests
- ODE solver

Parameters fitting – user interface

BioUML workbench

File Database Diagram Help

Databases Data Analyses

opt_1.xml

	Name	Lower bound	Value	Upper bound	Local	Units	Comment
0	k2_1	0.0	0.1	0.5	<input type="checkbox"/>		
1	k2_10	0.0	0.1	0.5	<input type="checkbox"/>		
2	k2_11	0.0	0.01	0.05	<input type="checkbox"/>		
3	k2_12	0.0	0.1	0.5	<input type="checkbox"/>		
4	k2_13	0.0	0.01	0.05	<input type="checkbox"/>		
5	\$"CMP0219....	10.0	50.0	150.0	<input checked="" type="checkbox"/>		
6	\$"CMP0219....	10.0	50.0	150.0	<input checked="" type="checkbox"/>		

ID: Evolution strategy (SRES)
Description:
Stochastic ranking evolution strategy (SRES)¹
In the (μ, λ) -ES algorithm, the individual i is a set of real-vectors $(x_i, \sigma_i) \forall i \in \{1, \dots, \lambda\}$. The initial population generated according to a uniform n -dimensional prob distribution over the search space S . Let δx be an approx measure of the expected distance to the global optimum the initial setting for the "mean step sizes" should be

Method: Evolution strategy (SRES)

Property	Value
Method parameters	
Diagram	databases/Biopath/Diagra...
Number of iterations	50
Population size	2

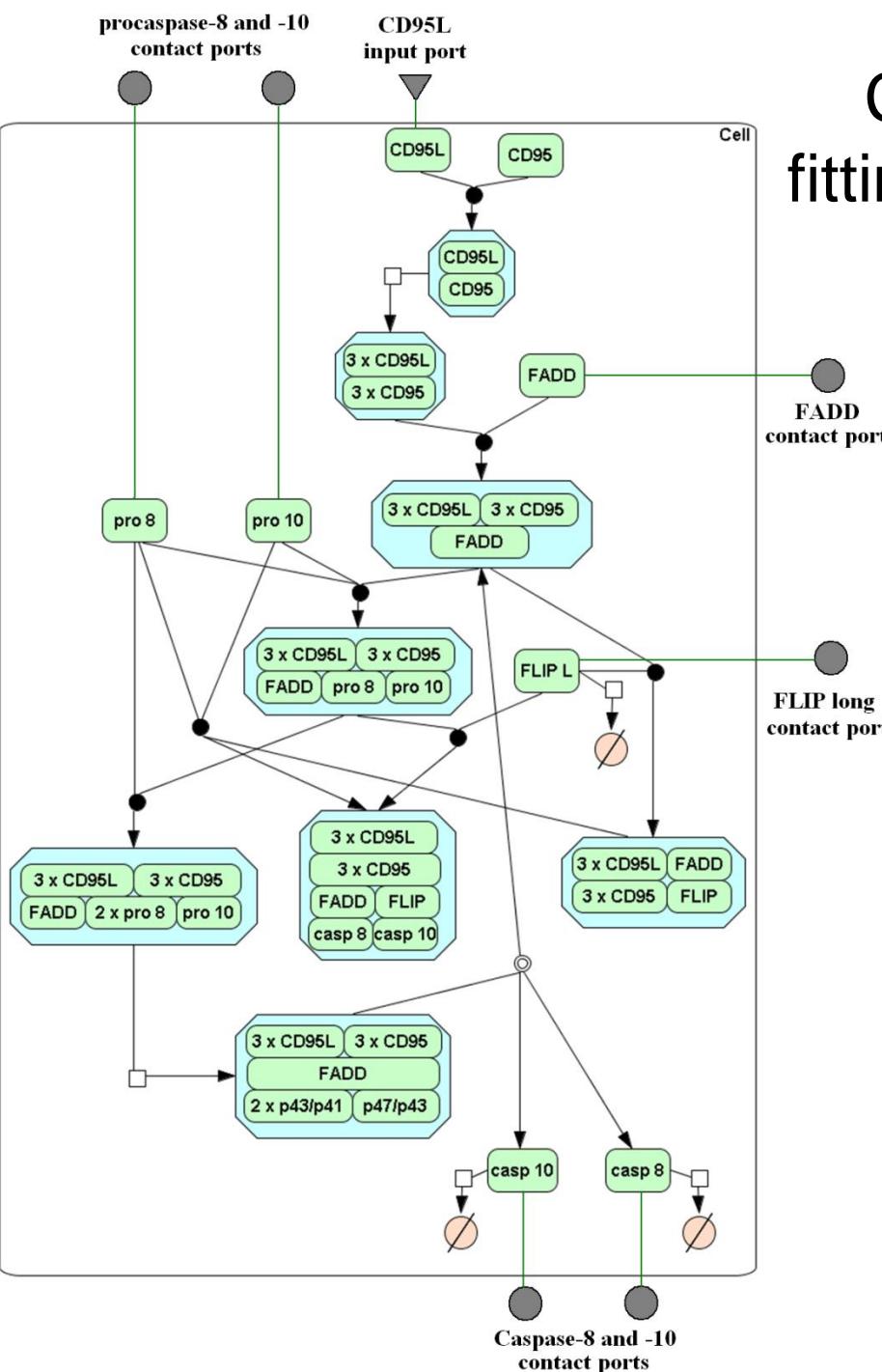
Objective function: _____
Penalty function: _____
Evaluations: _____

Optimization Experiments Simulation Parameters Variables Constraints
Application Log Search results Clipboard JavaScript Search linked SQL editor

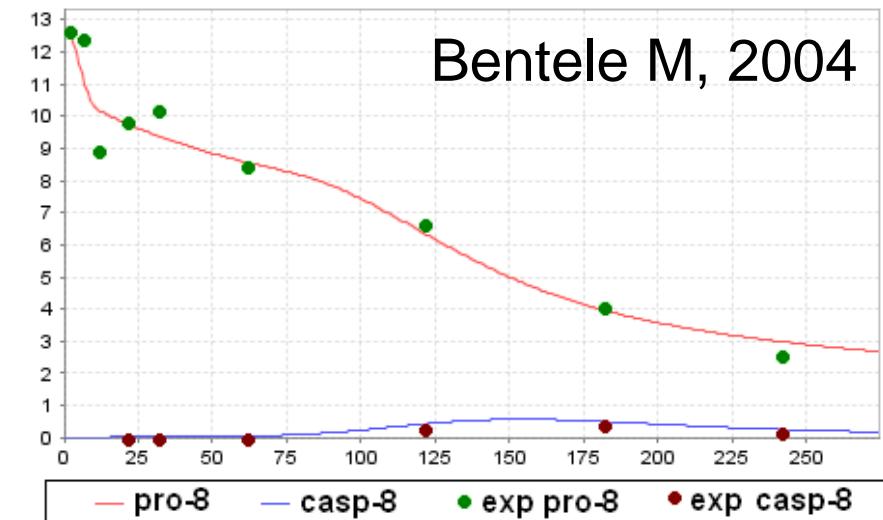
Parameters fitting - main features

- Experimental data – time courses or steady states expressed as exact or relative values of substance concentrations
- Different optimization methods for analysis
- Multi-experiments fitting
- Constraint optimization
- Local/global parameters
- Parameters optimization using java script

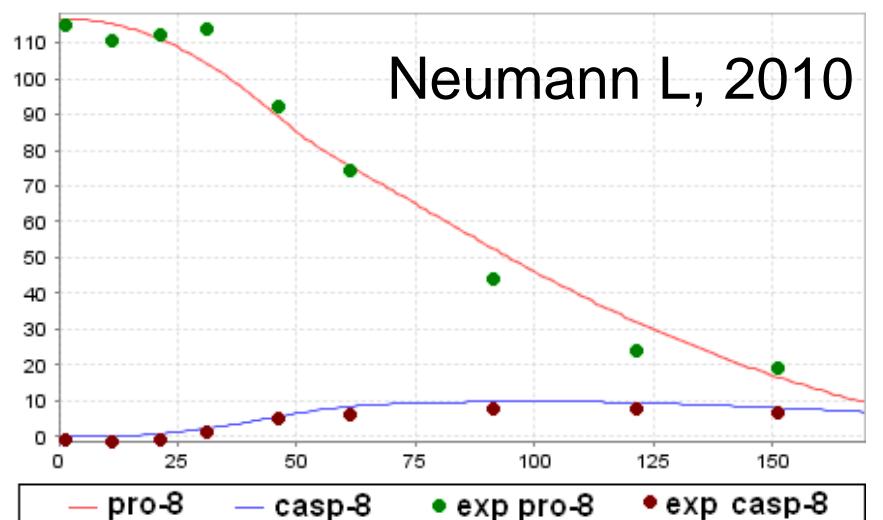
CD95L module and results of fitting its dynamics to experimental data



Bentle M, 2004



Neumann L, 2010



Story 3

Glicomics – rule based modeling

Rule-based modeling involves the representation of molecules as structured objects and molecular interactions as rules for transforming the attributes of these objects.

Data and approach:

Bennun SV, Yarema KJ, Betenbaugh MJ, Krambeck FJ. **Integration of the transcriptome and glycome for identification of glycan cell signatures.**

PLoS Comput Biol. 2013;9(1):e1002813. doi:
10.1371/journal.pcbi.1002813.

BioNetGen – language and approach for rule based modeling

<http://bionetgen.org>

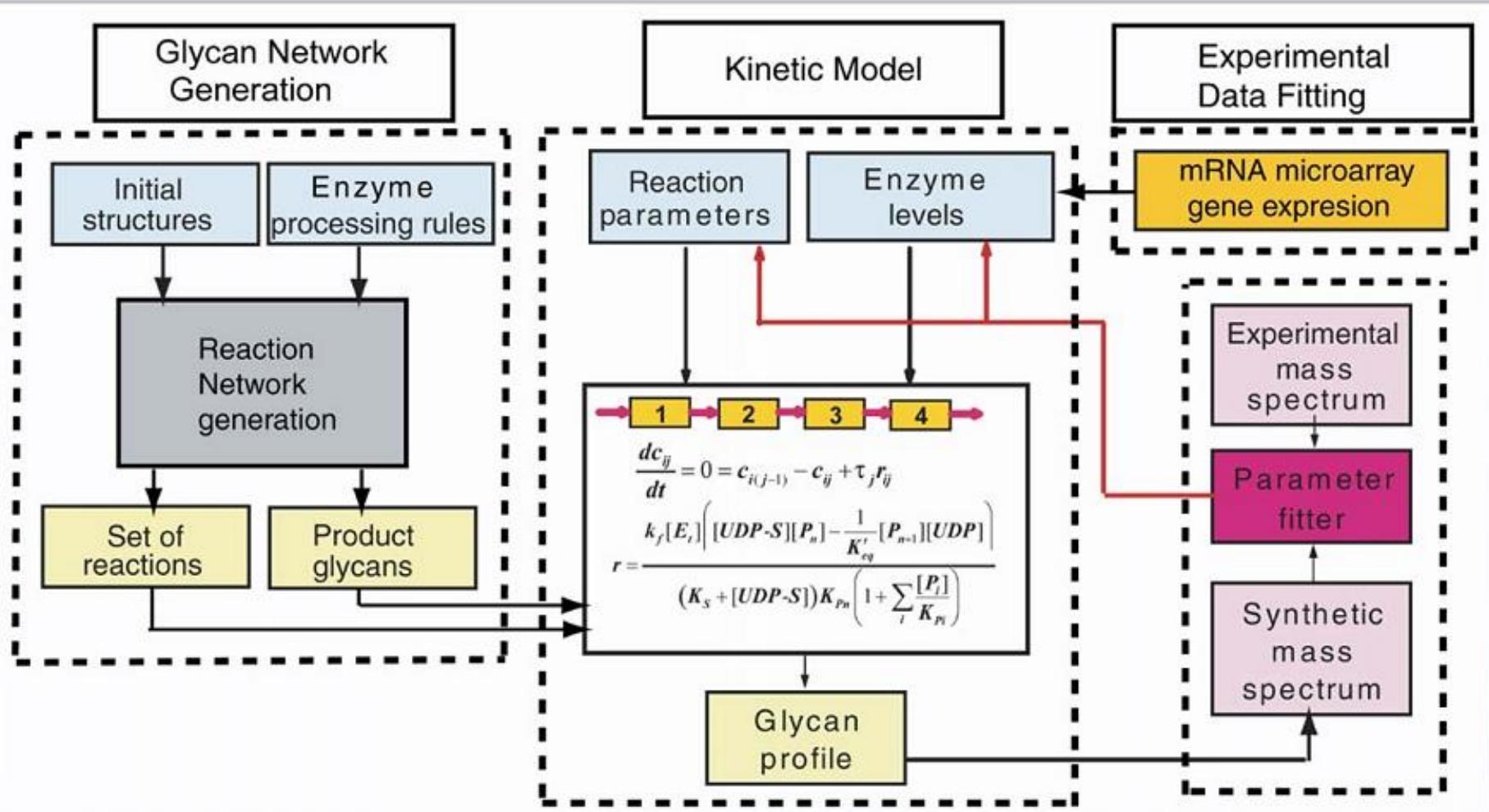
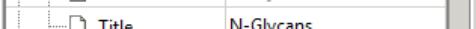
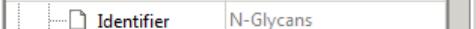
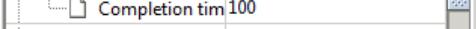
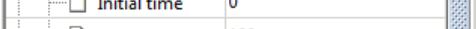
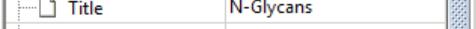
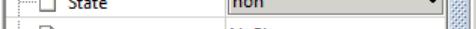
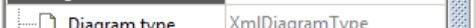
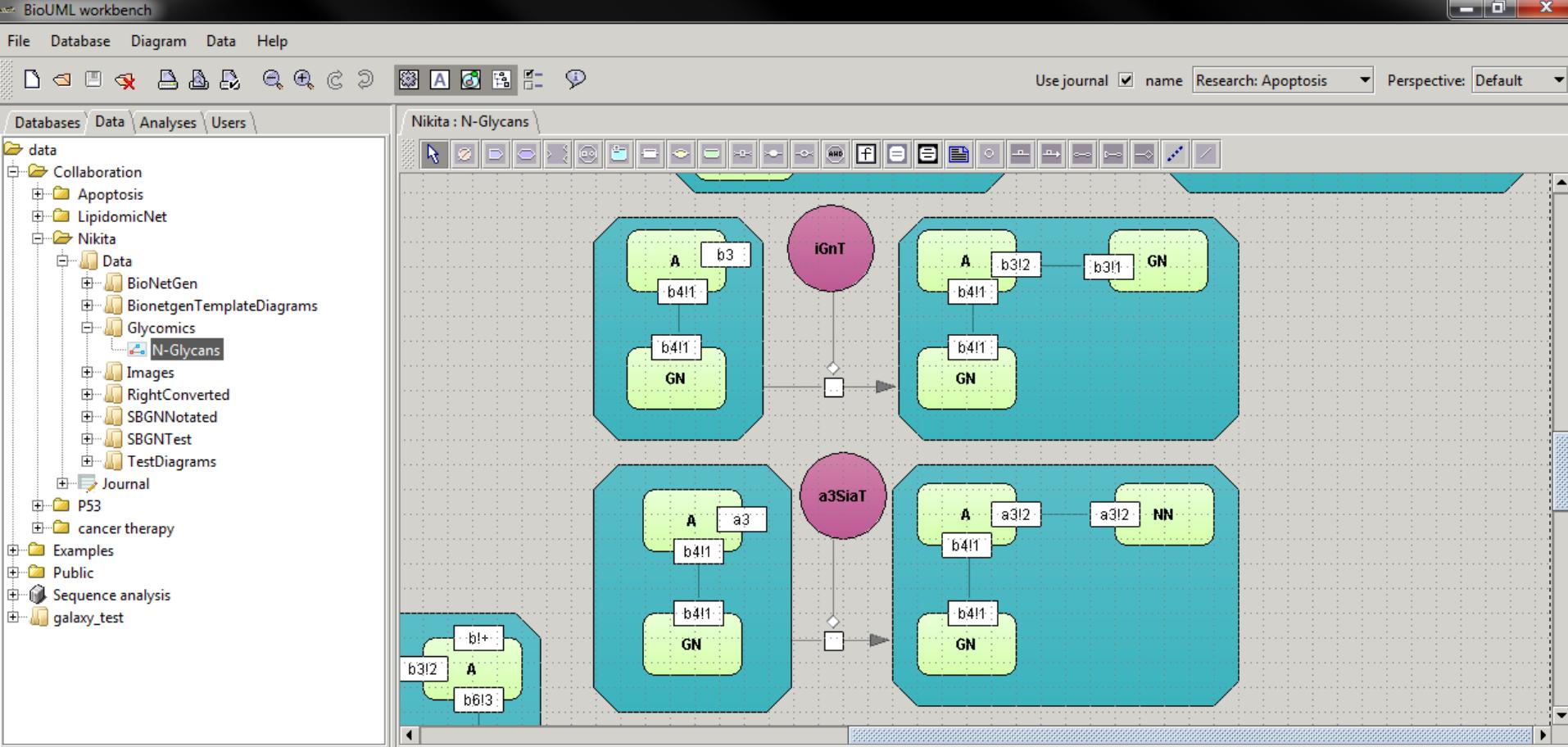


Table 2. Current reaction rules.

Index	Enzyme	Substrate	Product	Constraint
1	ManI	(Ma2Ma	(Ma	~*2Ma3(...Ma6)Ma6 & ~Ga3
2	ManI	(Ma3(Ma2Ma3(Ma6)Ma6)	(Ma3(Ma3(Ma6)Ma6)	~Ga3
5	ManII	(Ma3(Ma6)Ma6	(Ma6Ma6	(GNb2 Ma3 & ~Gnbis
6	ManII	(Ma6Ma6	(Ma6	(GNb2 Ma3 & ~Gnbis
7	a6FucT	GNb4GN	GNb4(Fa6)GN	GNb2 Ma3 & #A=0 & ~Gnbis
8	GnT I	(Ma3(Ma3(Ma6)Ma6)Mb4	(GNb2Ma3(Ma3(Ma6)Ma6)Mb4	
9	GnT II	(GNb2 Ma3(Ma6)Mb4	(GNb2 Ma3(GNb2Ma6)Mb4	
10	GnT III	GNb2 Ma3	GNb2 Ma3(GNb4)	~Ab & ~Gnbis
11	GnT IV	(GNb2Ma3	(GNb2(GNb4)Ma3	~Gnbis
12	GnT V	(GNb2Ma6	(GNb2(GNb6)Ma6	~Gnbis
13	iGnT	(Ab4GN	(GNb3Ab4GN	~*_Ma3 Mb4
14	b4GalT	(GN	(Ab4GN	~*GNb4)(...Ma6)Mb4
15	a3SiaT	(Ab4GN	NNa3Ab4GN	
16	lGnT	(Ab4GNb3Ab	(Ab4GNb3(GNb6)Ab	
17	a6SiaT	(Ab4GN	NNa6Ab4GN	
18	b3GalT	(GN	(Ab3GN	~*GNb4)(...Ma6)Mb4
20	FucTLe	Ab3GNb	Ab3(Fa4)GNb	
21	FucTLe	(...Ab4GNb	(Fa3(...Ab4)GNb	
22	FucTH	(Ab3GNb	(Fa2Ab3GNb	
23	FucTH	(Ab4GNb	(Fa2Ab4GNb	
24	a3FucT	(...Ab4GNb	(Fa3(...Ab4)GNb	
25	GalNAcT-A	(Fa2Ab	(Fa2(ANa3)Ab	
26	GalT-B	(Fa2Ab	(Fa2(Aa3)Ab	



Property

Value

Diagram	
Diagram type	XmlDiagramType

Diagram

Value

Diagram type	XmlDiagramType
State	non
Title	N-Glycans
Comment	
Role	
Comment	
Initial time	0
Completion time	100
Data	
Identifier	N-Glycans
Title	N-Glycans

```
#11
```

```
#need constraints
```

```
GnTIV + GN(a3,a4,a6,b2!1,b3,b4,b4,b6).M(a2,a2,a3!+,a3,a6,a6,b2!1,b4,b6) -> GnTIV +
GN(a3,a4,a6,b2!1,b3,b4,b4,b6).GN(a3,a4,a6,b2,b3,b4,b6!2).M(a2,a2,a3!+,a3,a6,a6,b2!1,b4,b6) MM(kf11, Km11)
```

```
#12
```

```
#need constraints
```

```
GnTV + GN(a3,a4,a6,b2!1,b3,b4,b4,b6).M(a2,a2,a3,a3,a6!+,a6,b2!1,b4,b6) -> GnTV +
GN(a3,a4,a6,b2!1,b3,b4,b4,b6).GN(a3,a4,a6,b2,b3,b4,b6!2).M(a2,a2,a3,a3,a6!+,a6,b2!1,b4,b6!2) MM(kf12, Km12)
```

```
#13
```

```
#need constraints
```

```
iGnT + A(a2,a3,a6,b3,b4!1,b6).GN(b4!1) -> iGnT + GN(a3,a4,a6,b2,b3!1,b4,b4,b6).A(a2,a3,a6,b3!1,b4!2,b6).GN(b4!2)\MM(kf13, Km13) include_reactants(2,M(a3!1).M(a3!1,b4!+)) include_products(2,M(a3!1).M(a3!1,b4!+))
```

Used features of BioUML platform

- visual modeling
- BioNetGen support (passed 8 available tests)
- synchronisation between model code and diagram
- parameters fitting

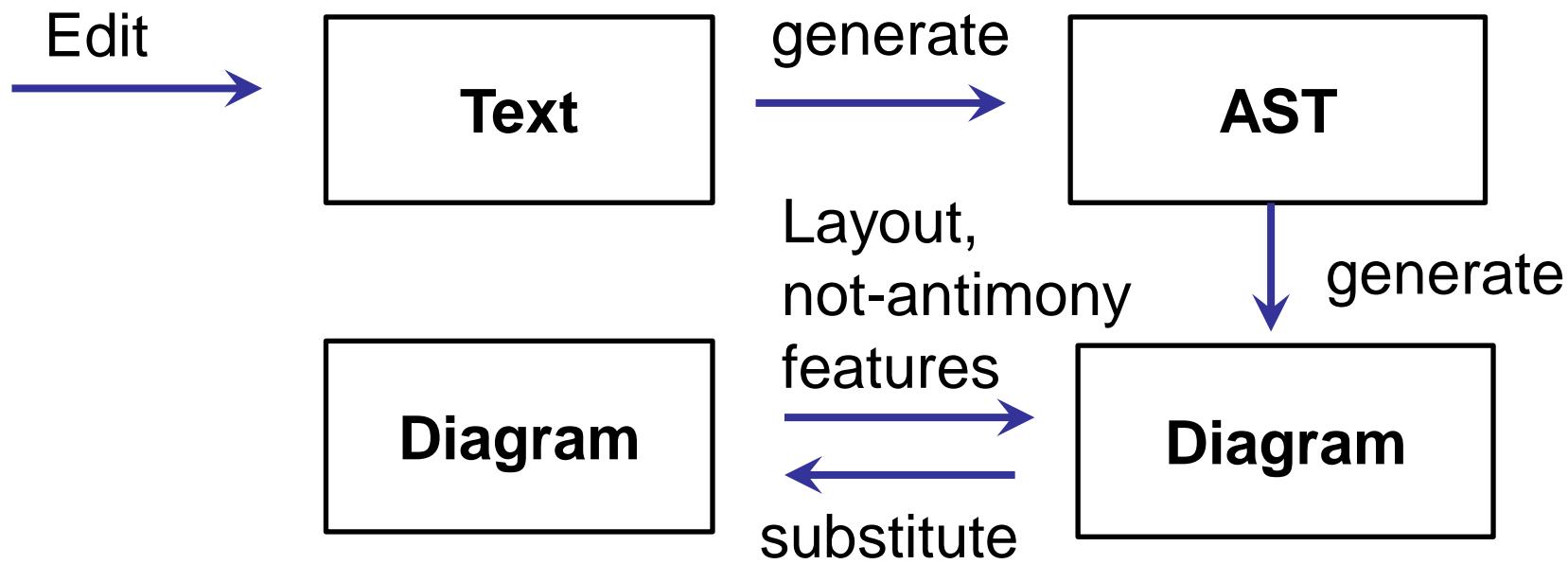
Antimony plug-in

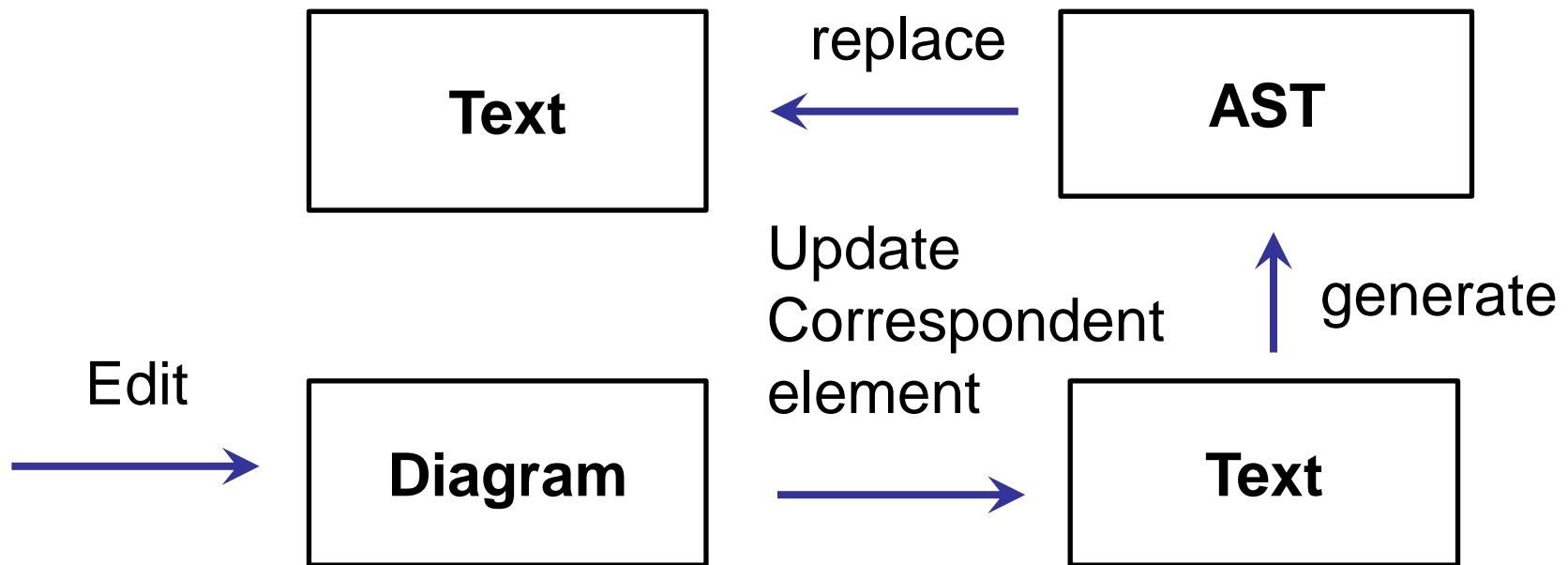
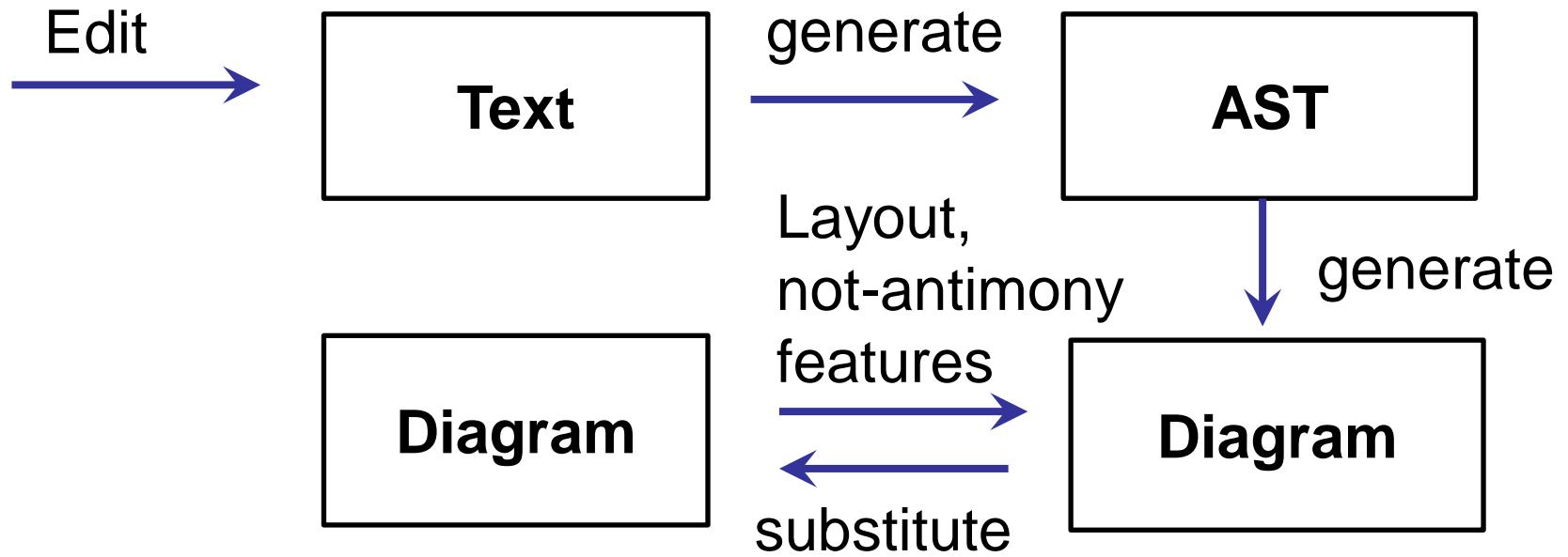
Alexandr Bukharov, Ilya Kiselev

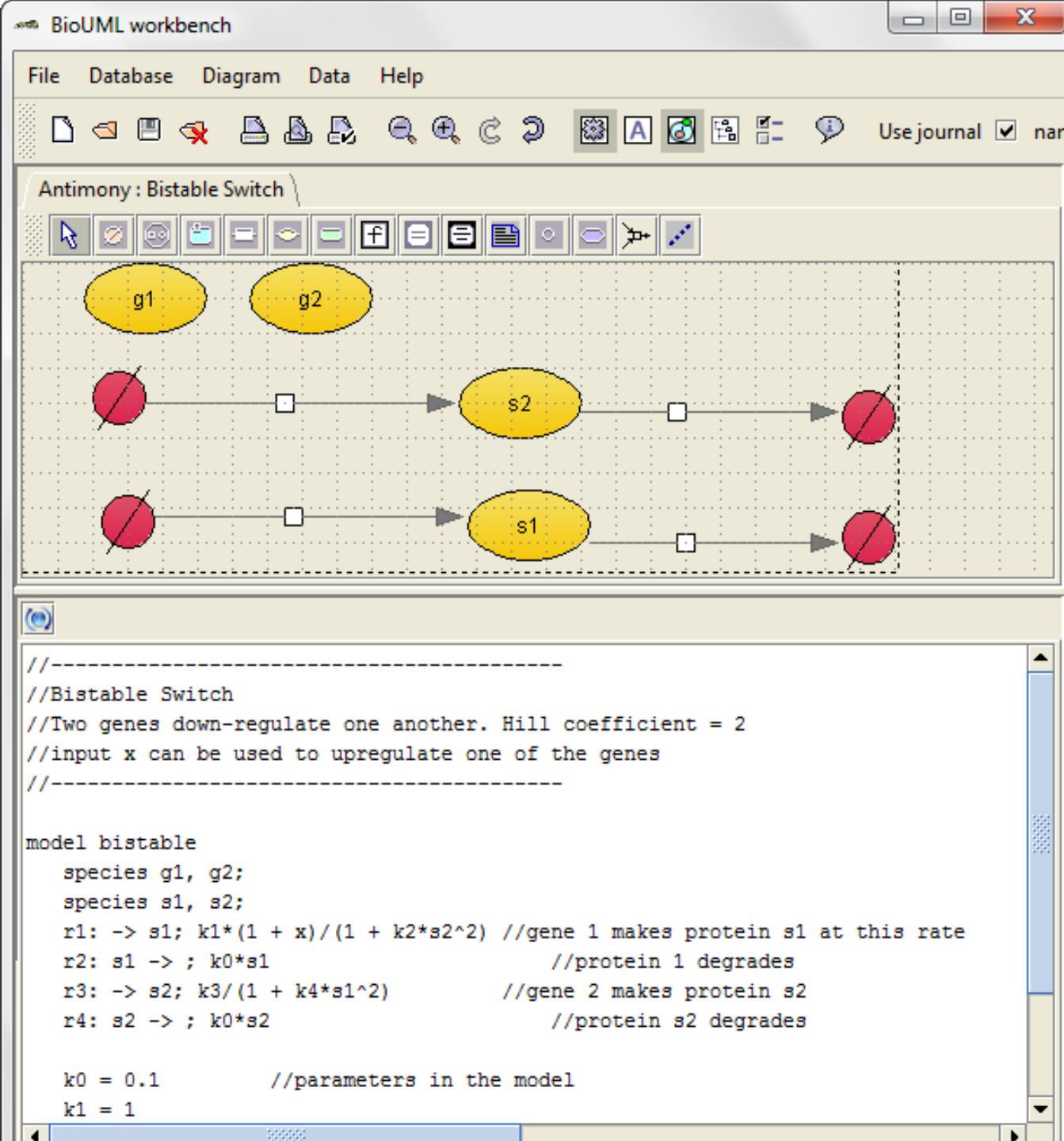
Live synchronization between code and model view

- Import/Export of Antimony text
- Visual representation using SBGN notation
- Live synchronization between text and visual representation.
- Import/Export to SBML
- Antimony as SBML annotation

Yet to implement Antimony modular support







Collaborative research goals

- Allow scientists to effectively work together even if they are separated far away from each other
- Help experimentalists and theorists to work together
- Engage third-party experts



Collaborative research

1. Share
 - Project data can be shared between several people
 - Changes are immediately visible by other participants
 - No need to ask administrator or somebody else to share the project
2. Communicate
 - Talk to each other in messenger
 - Conference chat
3. Collaborate
 - Edit together
 - Edit and chat
 - Review the changes of other participants
4. History
 - Monitor changes performed on the document
 - Rollback to older versions of the document
 - Compare different versions of the document
 - Project journal
5. Organize work (planned)
 - Create tasks (“works”) for other participants
 - Call for collaborators to solve particular problem
 - Review the results
6. Privacy
 - Your activity and data is invisible for people not belonging to your projects

BioStore

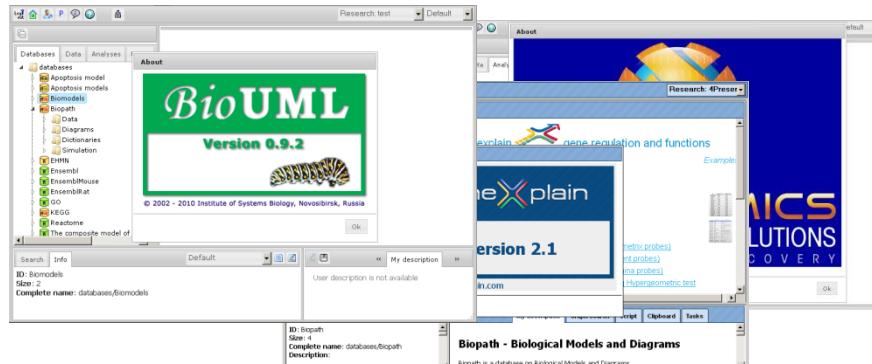
<http://bio-store.org/>

- BioStore is aimed to be the single place where researchers can register and obtain various products and services (either free or commercial).
- Having single BioStore account you may have an access to many BioUML servers, projects, downloads, etc.



BioStore

Servers

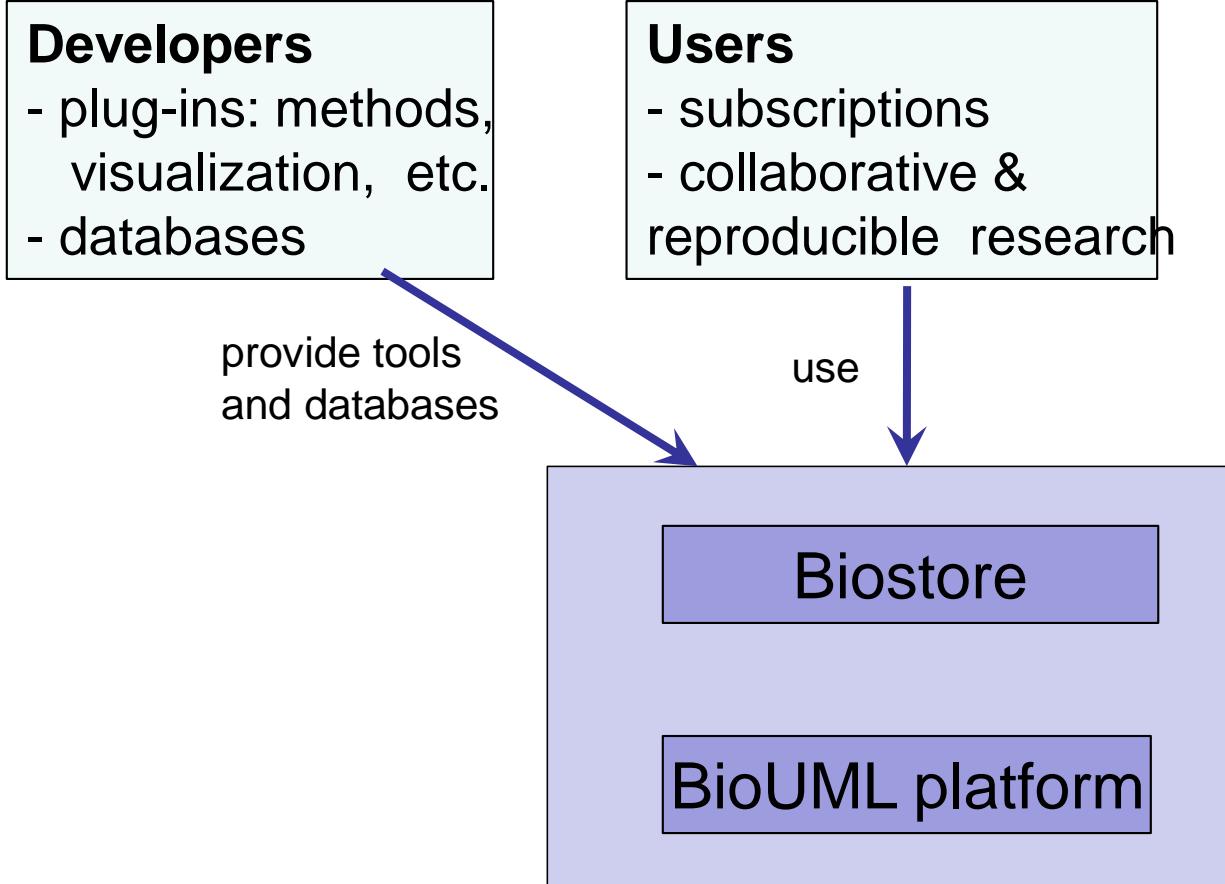


Downloads

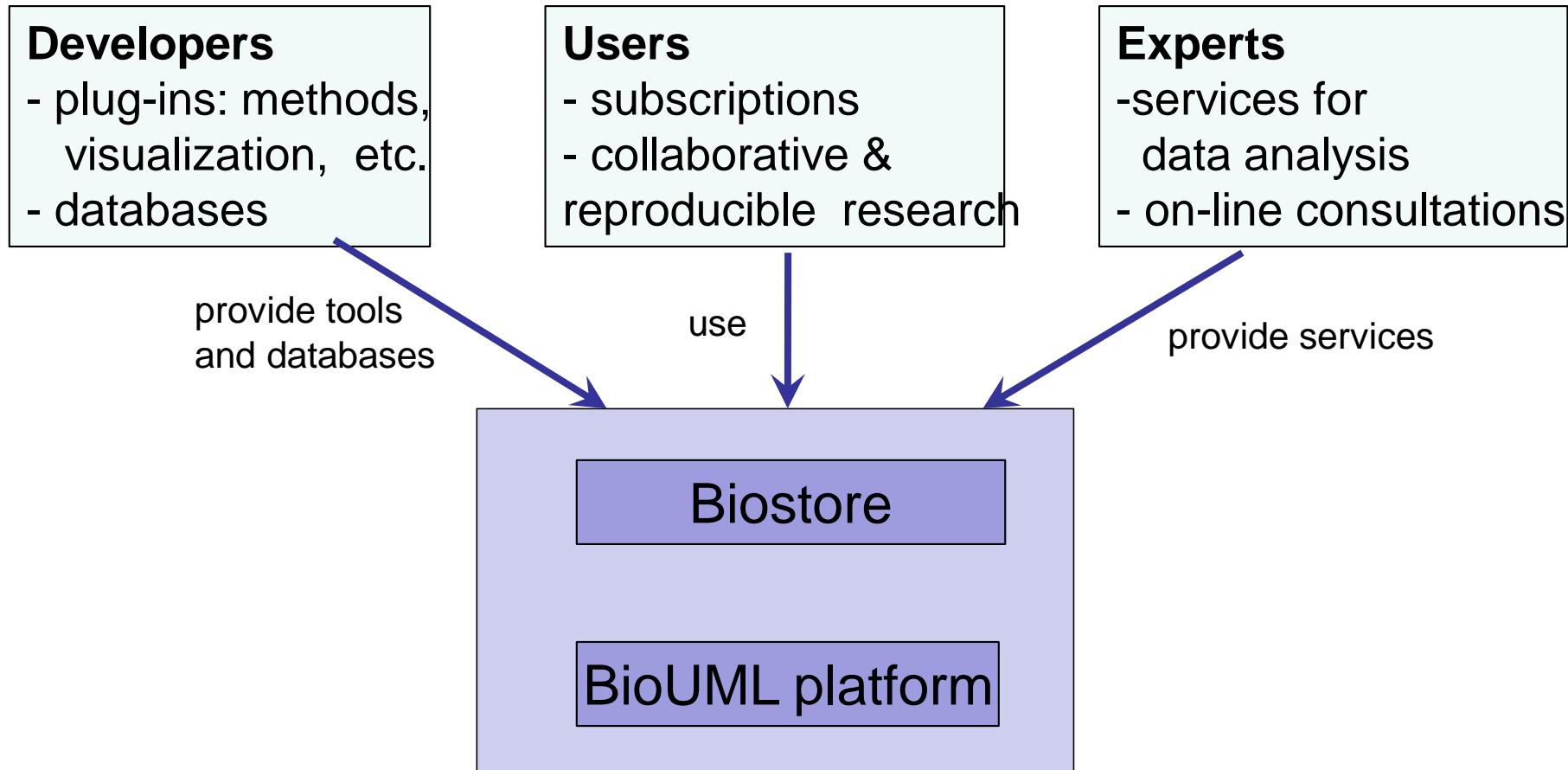
Services

Software

BioUML ecosystem



BioUML ecosystem



Building virtual cell

Answers:

- **methodology**
 - modular modeling;
 - application of some practices from XP (eXtreme Programming):
 - user stories,
 - iterative development,
 - acceptance tests;
- **organization** – [Biostore](#) - portal for collaborative research and crowd sourcing;
- **software** - [BioUML platform](#) - integrated open source platform for collaborative research in systems biology.

BioUML

open platform
for biomedical research

BioUML platform

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BioUML wiki

Welcome to BioUML wiki! Now it is the main web site for BioUML platform.

BioUML is an open source integrated Java platform for building virtual cell and virtual physiological human. It spans a 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, simulation, parameters fitting and analyses. Due to scripts (R, JavaScript) and workflow support it provides powerful possibilities for analyses of high-throughput data. The plug-in based architecture (Eclipse run time from IBM is used) allows to add new functionality using plug-ins.

Currently we have **549 articles**.

For BioUML users

- [BioUML overview](#)
 - [BioUML workbench](#)
 - [BioUML web edition](#)
- [Main features](#)
- [Download](#)
- [BioUML user interface](#)
- [Databases](#)
- [Modelling](#)
 - [Simulation](#)
 - [Modular modeling](#)
- [Analyses & workflows](#)
 - [Projects](#)
 - [Analyses](#)

For administrators/developers

- [BioUML installation](#)
- [BioUML Development Kit](#)
- [Plugins](#)
- [Extension points](#)
- [Creating Galaxy tool](#)
- [Roadmap](#)
- [History](#)

Community

- [News](#)
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- [Contributors](#)
 - [BioUML team](#)
 - [geneXplain](#)

Editing this wiki

To edit this wiki you have to register in [BioStore](#).

Consult the [User's Guide](#) for information on using the wiki software.

Try BioUML web edition

- <http://ie.biouml.org/bioumlweb> (free)
- <http://platform.genexplain.com> (trial, commercial)

Virtual Biology

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Home > **No 1 (2013)**

Virtual Biology

Virtual Biology: from virtual cell to virtual human

DOI: 10.12704/vb

No 1 (2013)

First issue

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Elena Kutumova, Anna Ryabova, Tagir Valeev, Fedor Kolpakov

Modular Modeling of Biological Systems

[PDF](#) [HTML](#)

Ilya Kiselev, Fedor Kolpakov

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Institute of Systems Biology

"From virtual cell to virtual human and virtual patient"

International workshop, Novosibirsk, Russia, June 24, 2012

BioUML - open source Java platform for systems biology

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Scientific program

Sunday, June 24

Time	Topic	Speaker/Leader	Report	Questions	Slides
10:00 - 10:30	<i>Registration, coffee</i>				
10:30 - 10:45	Welcome, introduction to workshop "From virtual cell to virtual human and virtual patient"	Fedor Kolpakov Alexander Kel			
10:45 - 11:00	General concept of the project	Fedor Kolpakov			
11:00 - 11:15	Discussion				
11:15 - 11:30	<i>Short coffee break</i>				
11:30 - 13:30	Methodology	chair: Alexander Kel			
11:30 - 12:00	BioUML - platform for building virtual cell and virtual human - an overview	Fedor Kolpakov			
12:00 - 12:15	Biostore and collaborative research	Tagir Valeev			
12:15 - 12:30	Modular modeling	Ilya Kiselev			
	Applying XP methodology for model development				

Next workshop – June 20-22, 2014, Novosibirsk, Russia
You are welcome!

BioUML team

Tagir Valeev

Ilya Kiselev

Elena Kutumova

Alexandr Bukharov

Nikita Mandrik

Ivan Yevshin
Yuriy Kondrakhin
Dmitriy Levanov

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