Computational Environments for Modeling Biochemical Networks

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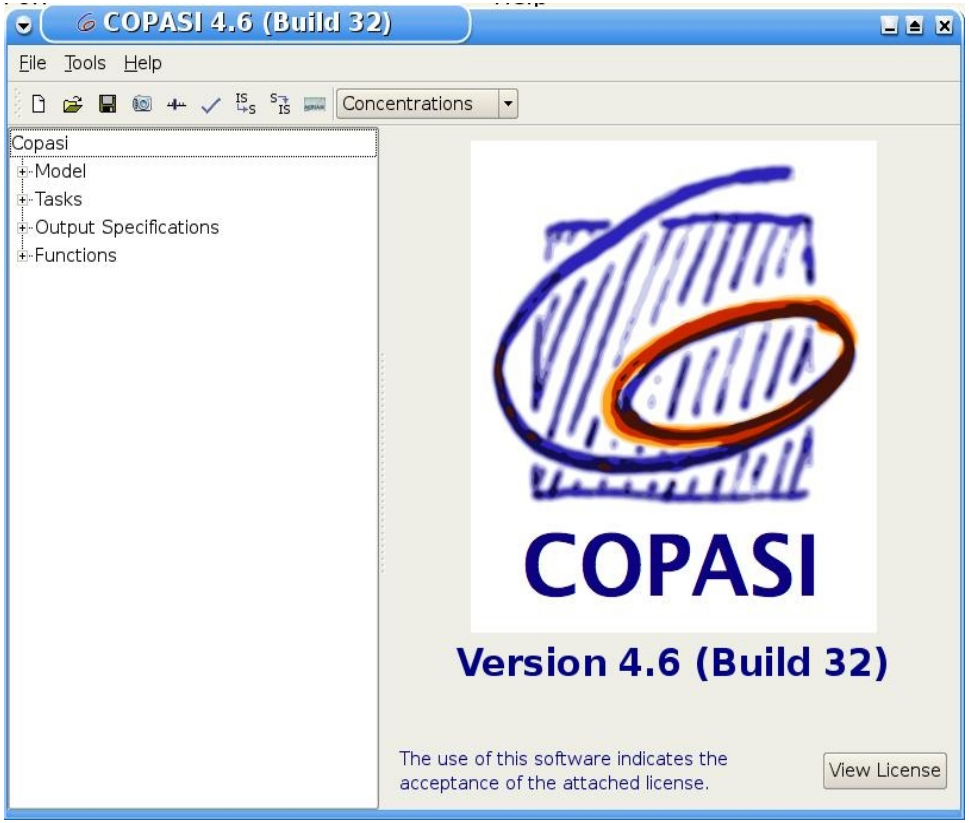
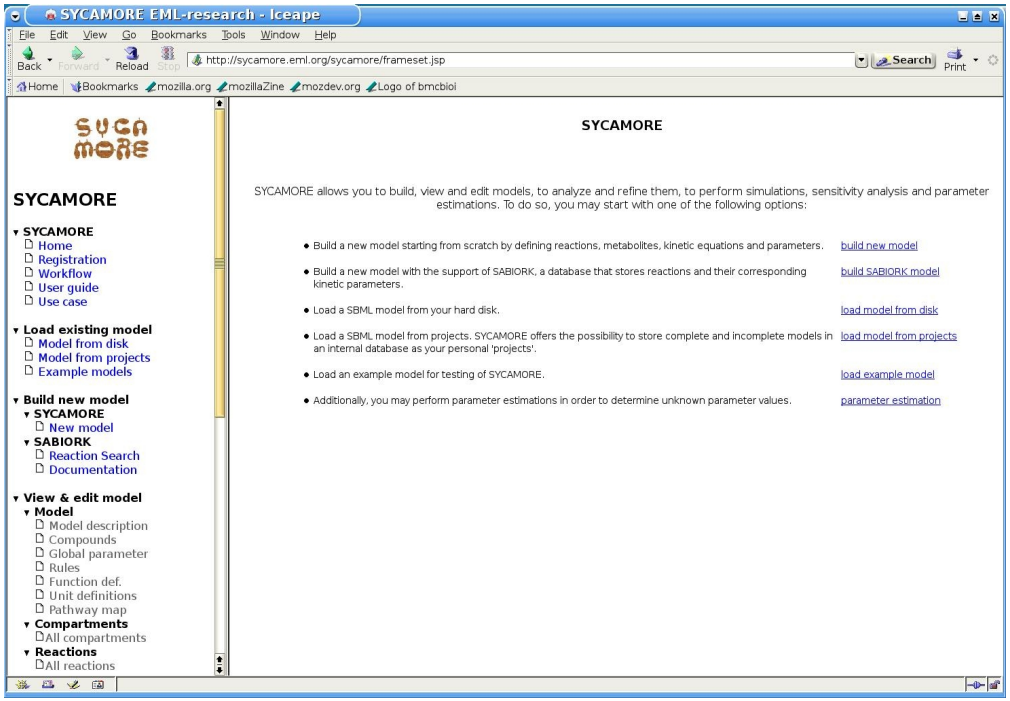
Germany



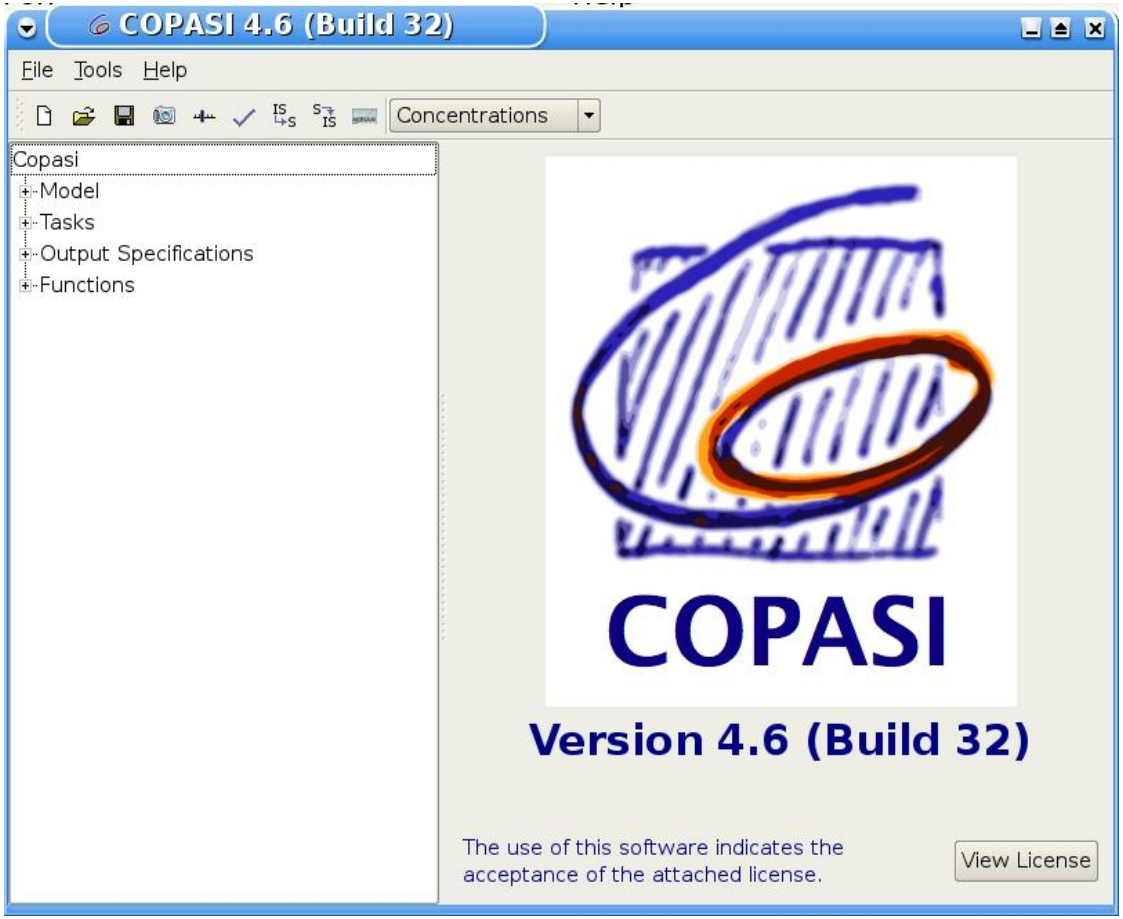
Copasi:

with Pedro Mendes (USA, UK)



Sycamore:

with Rebecca Wade, Wolfgang Müller, HITS, Germany



Hoops, Sahle et al., Bioinformatics, 2006

-> open source

-> free

-> platform independent

-> stand-alone

-> C++/QT

-> GUI and command line versions

ca. 5000 downloads per release

Model formalisms

-> Copasi models are reaction/process centered

(except if you define all equations as assignments)

-> reaction networks are translated into ODE systems

-> can be deterministically or stochastically simulated

-> diverse analysis methods

-> SBML compliant

lambeth_biomodels - COPASI 4.6 (Build 32) /home/.../optcontrolana

File Tools Help

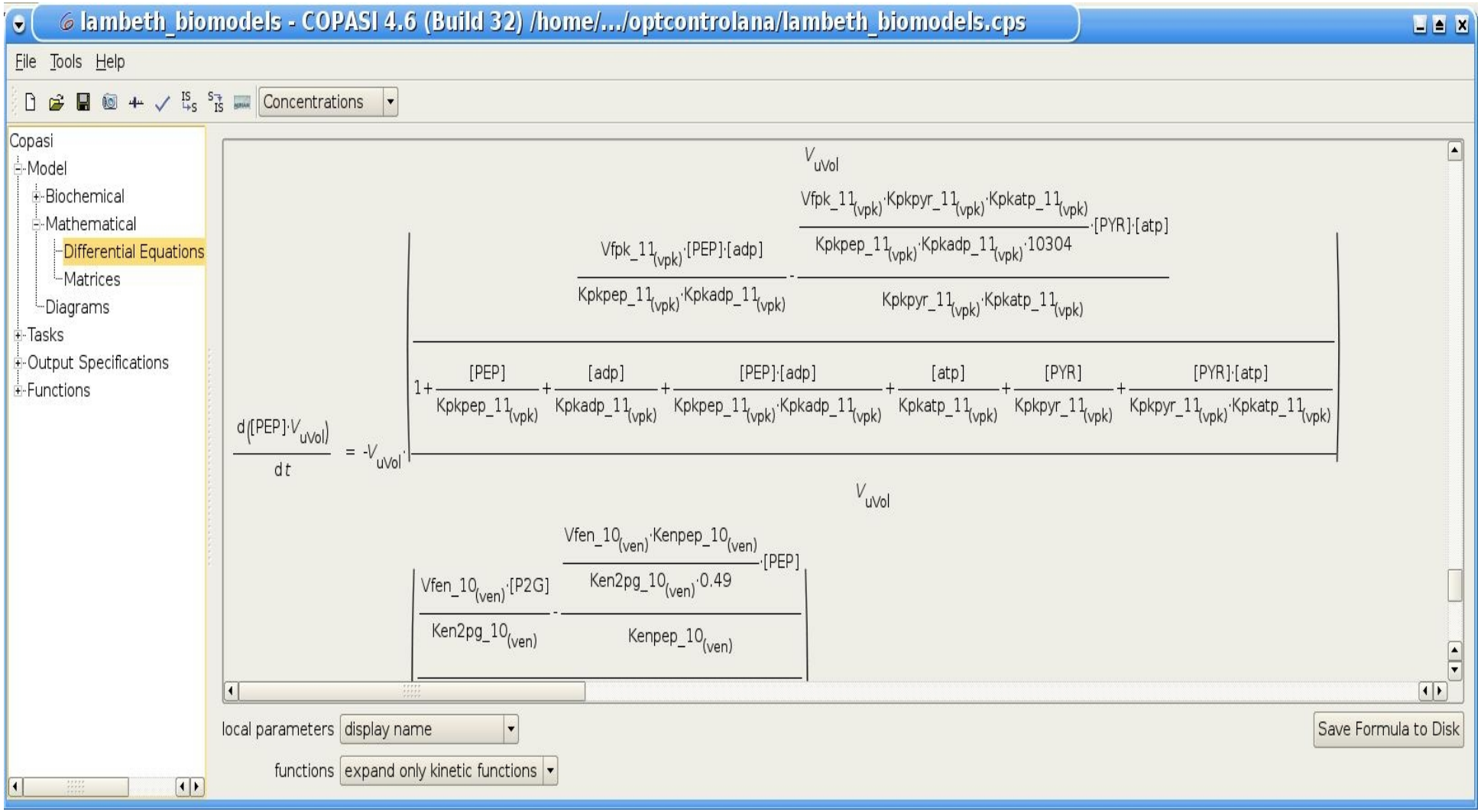
Concentrations

- Copasi
  - Model
    - Biochemical
      - Compartments
      - Species
      - Reactions
      - Global Quantities
      - Events
      - Parameter Overview
    - Mathematical
    - Diagrams
  - Tasks
    - Steady-State
    - Stoichiometric Analysis
    - Time Course
    - Metabolic Control Analysis
    - Lyapunov Exponents
    - Time Scale Separation Analysis
    - Parameter Scan
    - Optimization
    - Parameter Estimation
    - Sensitivities
  - Output Specifications
  - Functions

Search:

#	Name	Equation	Rate Law
1	vgp	P + Gly = G1P; amp	function_4_vgp
2	vpglm	G1P = G6P	function_4_vpglm
3	vpgi	G6P = F6P	function_4_vpgi
4	vpfk	atp + F6P = adp + FDP; amp	function_4_vpfk
5	vald	FDP = DHAP + GAP	function_4_vald
6	vtpi	GAP = DHAP	function_4_vtpi
7	vgapdh	P + GAP + NAD = NADH + DPG	function_4_vgapdh
8	vpgk	adp + DPG = atp + P3G	function_4_vpgk
9	vpgm	P3G = P2G	function_4_vpgm
10	ven	P2G = PEP	function_4_ven
11	vpk	adp + PEP = atp + PYR	function_4_vpk
12	vldh	NADH + PYR = LAC + NAD	function_4_vldh
13	vck	atp + Cr = adp + PCr	function_4_vck
14	vadk	atp + amp = 2 * adp	function_4_vadk

New Delete Delete All



$$\frac{d([PEP]\cdot V_{uVol})}{dt} = -V_{uVol}\cdot\frac{\left|\dfrac{\dfrac{Vfpk\_11_{(vpk)}\cdot[PEP]\cdot[adp]}{Kpkpep\_11_{(vpk)}\cdot Kpkadp\_11_{(vpk)}} - \dfrac{\dfrac{Vfpk\_11_{(vpk)}\cdot Kpkpyr\_11_{(vpk)}\cdot Kpkatp\_11_{(vpk)}}{Kpkpep\_11_{(vpk)}\cdot Kpkadp\_11_{(vpk)}\cdot 10304}\cdot[PYR]\cdot[atp]}{Kpkpyr\_11_{(vpk)}\cdot Kpkatp\_11_{(vpk)}}}{1+\dfrac{[PEP]}{Kpkpep\_11_{(vpk)}}+\dfrac{[adp]}{Kpkadp\_11_{(vpk)}}+\dfrac{[PEP]\cdot[adp]}{Kpkpep\_11_{(vpk)}\cdot Kpkadp\_11_{(vpk)}}+\dfrac{[atp]}{Kpkatp\_11_{(vpk)}}+\dfrac{[PYR]}{Kpkpyr\_11_{(vpk)}}+\dfrac{[PYR]\cdot[atp]}{Kpkpyr\_11_{(vpk)}\cdot Kpkatp\_11_{(vpk)}}}\right|}{V_{uVol}}$$

$$\left|\frac{Vfen\_10_{(ven)}\cdot[P2G]}{Ken2pg\_10_{(ven)}} - \frac{\dfrac{Vfen\_10_{(ven)}\cdot Kenpep\_10_{(ven)}}{Ken2pg\_10_{(ven)}\cdot 0.49}\cdot[PEP]}{Kenpep\_10_{(ven)}}\right|$$

Automatic translation into differential equations

YeastGlycolysis - COPASI 4.6 (Build 32) /home/ursula/copasi/YeastGlycolysis.gps

File Tools Help

Concentrations

- Copasi
  - Model
    - Biochemical
      - Compartments
      - Species
      - Reactions
        - ADH
        - AK
        - ALD
        - ATPase
        - ENO
        - G3PDH
        - GAPDH
        - Glycogen Branch
        - HK
        - HXT
        - PDC
        - PFK
        - PGI
        - PGK
        - PGM
        - PYK
        - Succinate Branch
        - TPI
        - Trehalose Branch
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Reaction | Annotation | RDF Browser

Name: ENO

Chemical Equation: P2G = PEP

☒ Reversible ☐ Multi Compartment

Rate Law: ENO kinetics [New Rate Law]

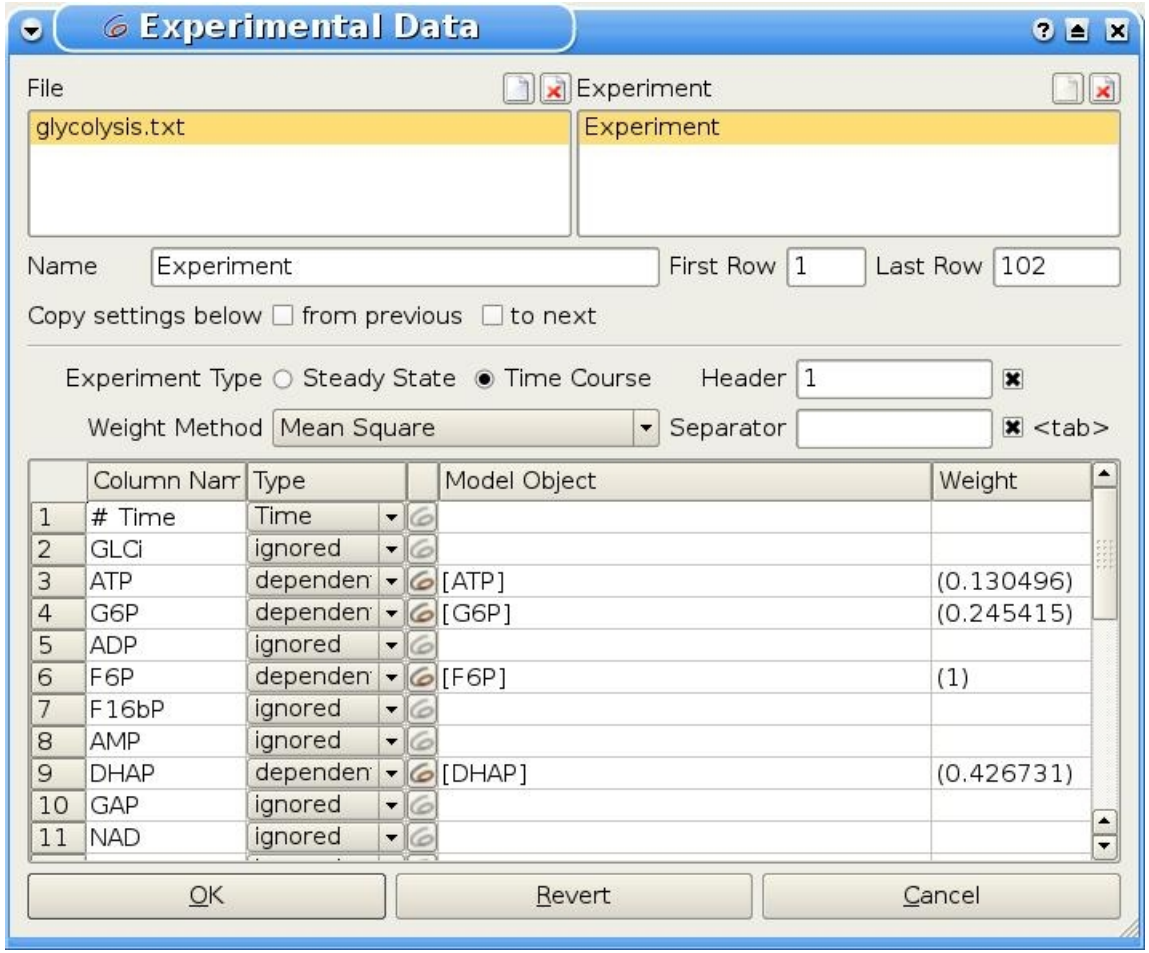
Flux (mmol/min): 0 Vmax*(A/Kp2g-P/(Kp2g*Keq))/(1+A/Kp2g+P/Kpep)

Symbol Definition

Description	Name		Value	Unit
Substrate	A		P2G	mmol/ml
Product	P		PEP	mmol/ml
Parameter	Vmax	global	201.6	mmol/(ml*min)
Parameter	Kp2g	global	0.04	mmol/ml
Parameter	Keq	global	6.7	1
Parameter	Kpep	global	0.5	mmol/ml

Commit | Revert | New | Delete

Parameter estimation



- single or multiple experiment
- steady state or time course data
- individualized weights

YeastGlycolysis - COPASI 4.6 (Build 32) /home/ursula/copasi/YeastGlycolysis.gps

File Tools Help

Concentrations

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  - Optimization
  - Parameter Estimation
    - Result
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Parameter Estimation

☐ update model ☐ executable

Experimental Data

Parameters (13) | Constraints (0)

1	0.0111 ≤ (ADH).Kacald ≤ 12.21; Start Value = 0.178293
2	6.9e-07 ≤ (ADH).Keq ≤ 0.000759; Start Value = 5.67327e-06
3	0.17 ≤ (ADH).Ketoh ≤ 187; Start Value = 1.10087
4	0.011 ≤ (ADH).Kiacald ≤ 12.1; Start Value = 3.08827
5	0.9 ≤ (ADH).Kietoh ≤ 990; Start Value = 1.57793
6	0.0092 ≤ (ADH).Kipad ≤ 10.12; Start Value = 3.28573

Object		(ALD).Kdhap
Lower Bound	☐ - Infinity	0.02
Upper Bound	☐ + Infinity	22
Start Value		1.71094
Affected Experiments	☒ all	

Duplicate for each Experiment

Method: Evolutionary Programming

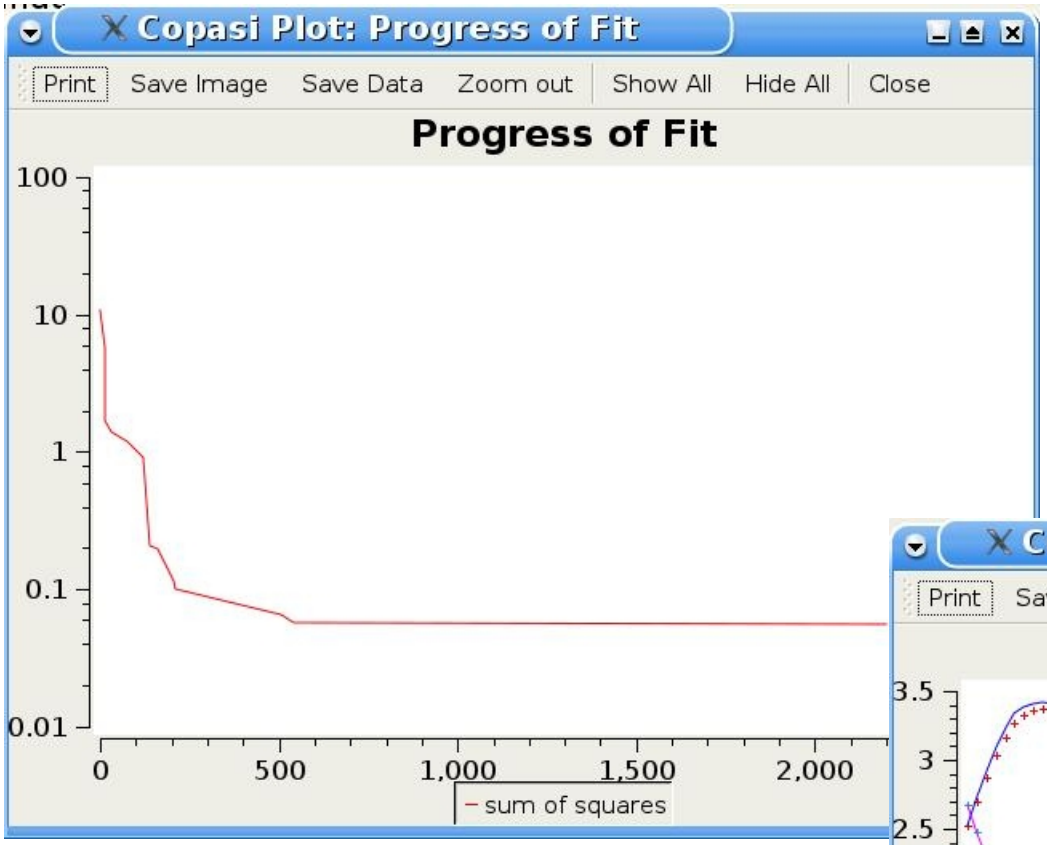
Parameter

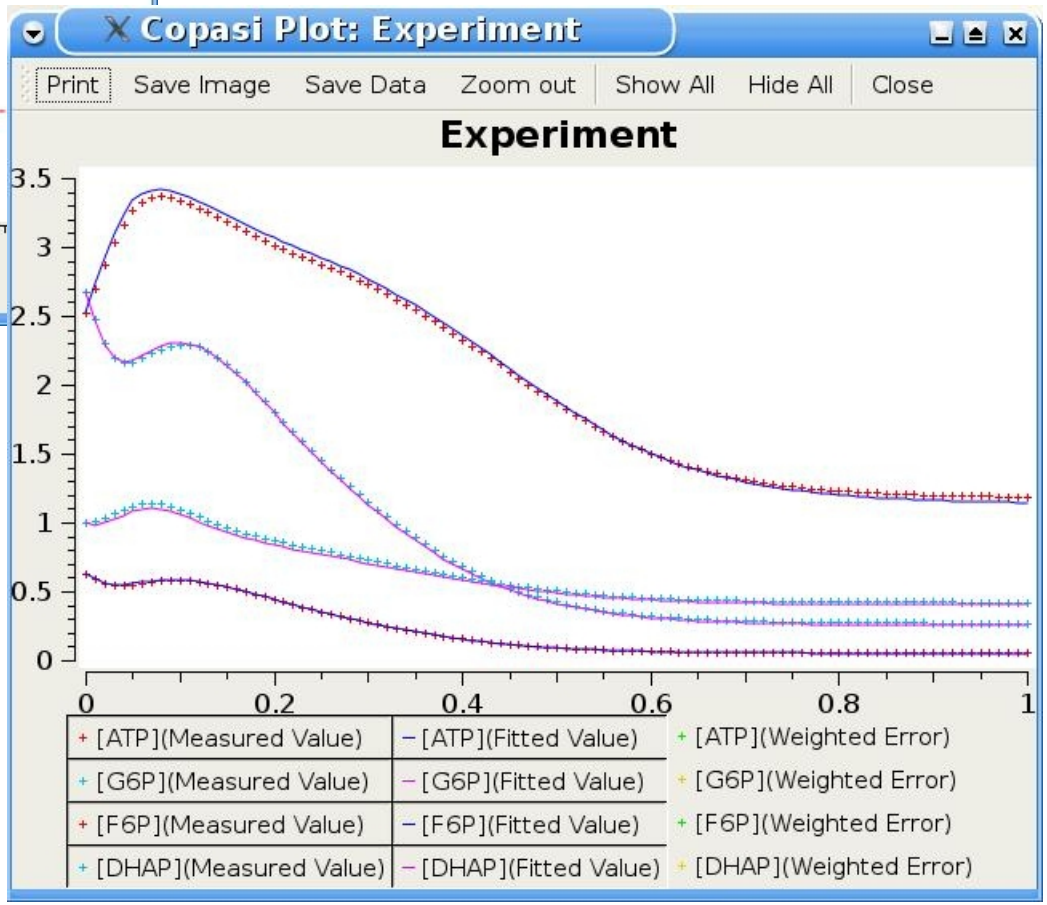
- Current Solution Statistics
- Genetic Algorithm
- Genetic Algorithm SR
- Hooke & Jeeves
- Levenberg - Marquardt
- Evolutionary Programming
- Random Search
- Nelder - Mead
- Particle Swarm

	200
	20
	1
	0

Run

Report | Output Assistant


Copasi Plot: Progress of Fit
Print
Save Image
Save Data
Zoom out
Show All
Hide All
Close
Progress of Fit
100
10
1
0.1
0.01
0
500
1,000
1,500
2,000
sum of squares


Copasi Plot: Experiment
Print
Save Image
Save Data
Zoom out
Show All
Hide All
Close
Experiment
3.5
3
2.5
2
1.5
1
0.5
0
0
0.2
0.4
0.6
0.8
1
[ATP](Measured Value)
[ATP](Fitted Value)
[ATP](Weighted Error)
[G6P](Measured Value)
[G6P](Fitted Value)
[G6P](Weighted Error)
[F6P](Measured Value)
[F6P](Fitted Value)
[F6P](Weighted Error)
[DHAP](Measured Value)
[DHAP](Fitted Value)
[DHAP](Weighted Error)

YeastGlycolysis - COPASI 4.6 (Build 32) /home/ursula/copasi/YeastGlycolysis.gps

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Parameter Estimation Result

Save to File

Main | Parameters | Experiments | Fitted Values | Correlation | Fisher Information

Bars

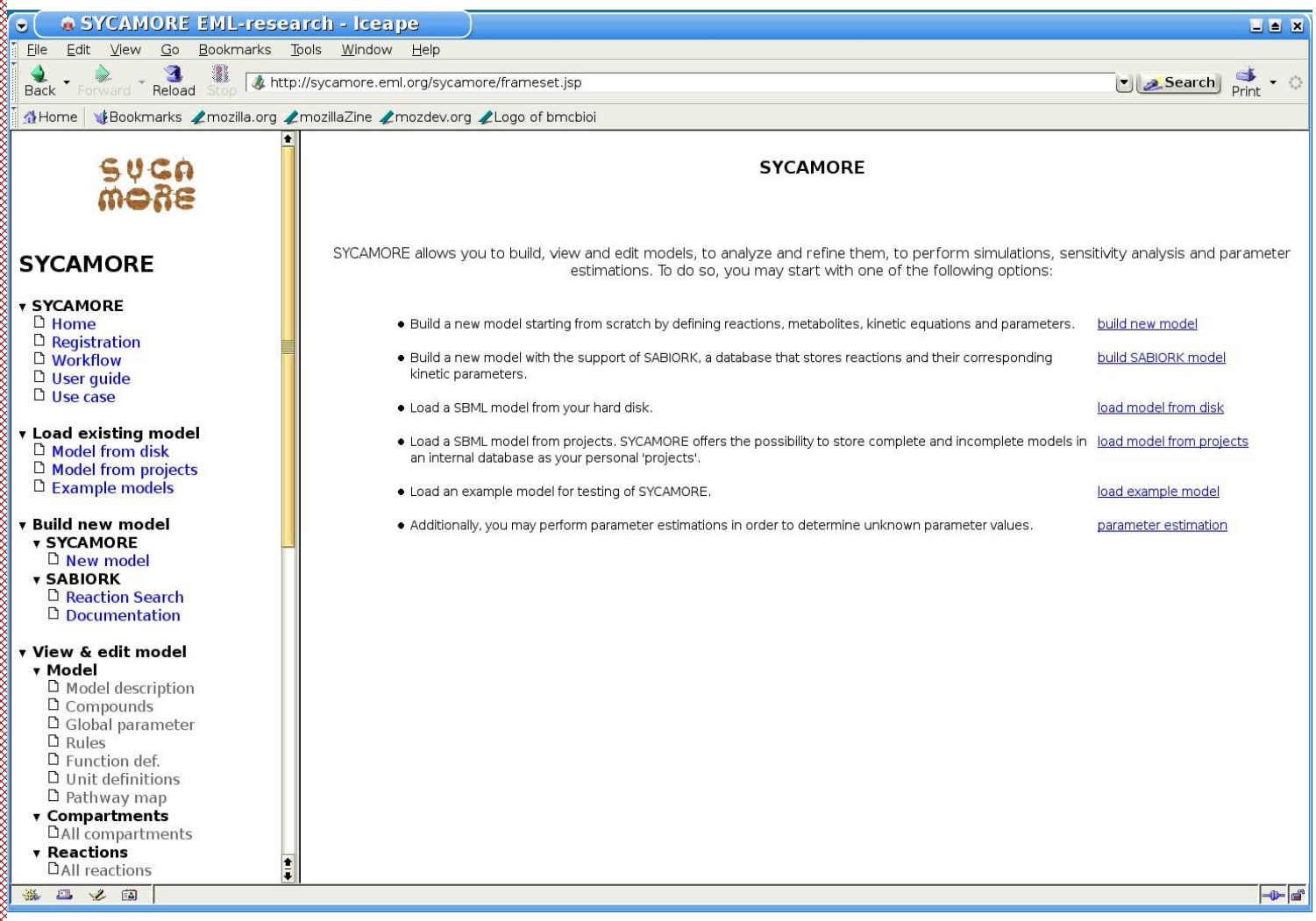
	(ADH).Kacal	(ADH).Keq	(ADH).Ketoh	(ADH).Kiacal	(ADH).Kietoh	(ADH).Kinad	(ADH).Kinadh	(ADH).Knad	(ADH).Knadh	(ADH).Vmax	(AK).k1
(ADH).Kacald	1	0.468439	0.173617	-0.83425	0.0644338	-0.18858	-0.0657232	-0.070638	0.0394785	0.349875	-0.104379
(ADH).Keq	0.468439	1	-0.0303357	-0.457856	-0.0607665	0.0173694	0.281993	-0.294225	0.400887	0.170667	-0.124746
(ADH).Ketoh	0.173617	-0.0303357	1	-0.0587027	0.0937214	-0.595202	-0.225064	-0.165223	-0.607436	0.809825	0.0788902
(ADH).Kiacald	-0.83425	-0.457856	-0.0587027	1	0.0709501	0.0258424	-0.239824	0.0123004	-0.0792957	-0.258577	0.15221
(ADH).Kietoh	0.0644338	-0.0607665	0.0937214	0.0709501	1	-0.74283	-0.494981	0.281462	-0.0654644	0.244197	0.0884566
(ADH).Kinad	-0.18858	0.0173694	-0.595202	0.0258424	-0.74283	1	0.47416	-0.19426	0.353581	-0.655298	-0.0770208
(ADH).Kinadh	-0.0657232	0.281993	-0.225064	-0.239824	-0.494981	0.47416	1	-0.0841744	-0.109002	-0.296946	-0.179414
(ADH).Knad	-0.070638	-0.294225	-0.165223	0.0123004	0.281462	-0.19426	-0.0841744	1	-0.396333	0.293891	0.131221
(ADH).Knadh	0.0394785	0.400887	-0.607436	-0.0792957	-0.0654644	0.353581	-0.109002	-0.396333	1	-0.548747	-0.147319
(ADH).Vmax	0.349875	0.170667	0.809825	-0.258577	0.244197	-0.655298	-0.296946	0.293891	-0.548747	1	0.119541
(AK).k1	-0.104379	-0.124746	0.0788902	0.15221	0.0884566	-0.0770208	-0.179414	0.131221	-0.147319	0.119541	1
(AK).k2	-0.11289	-0.147445	0.0750887	0.159746	0.0899464	-0.0771846	-0.184122	0.136889	-0.150571	0.110588	0.999305
(ALD).Kdhap	-0.221806	-0.608844	0.190561	0.184608	0.259288	-0.222068	-0.18072	0.0790533	-0.26968	-0.0148938	0.0240411

Parameter – sources and estimations

- experiments as basis for parameter estimation
- literature
- estimations from sequence and structural data

-> Development of Sycamore

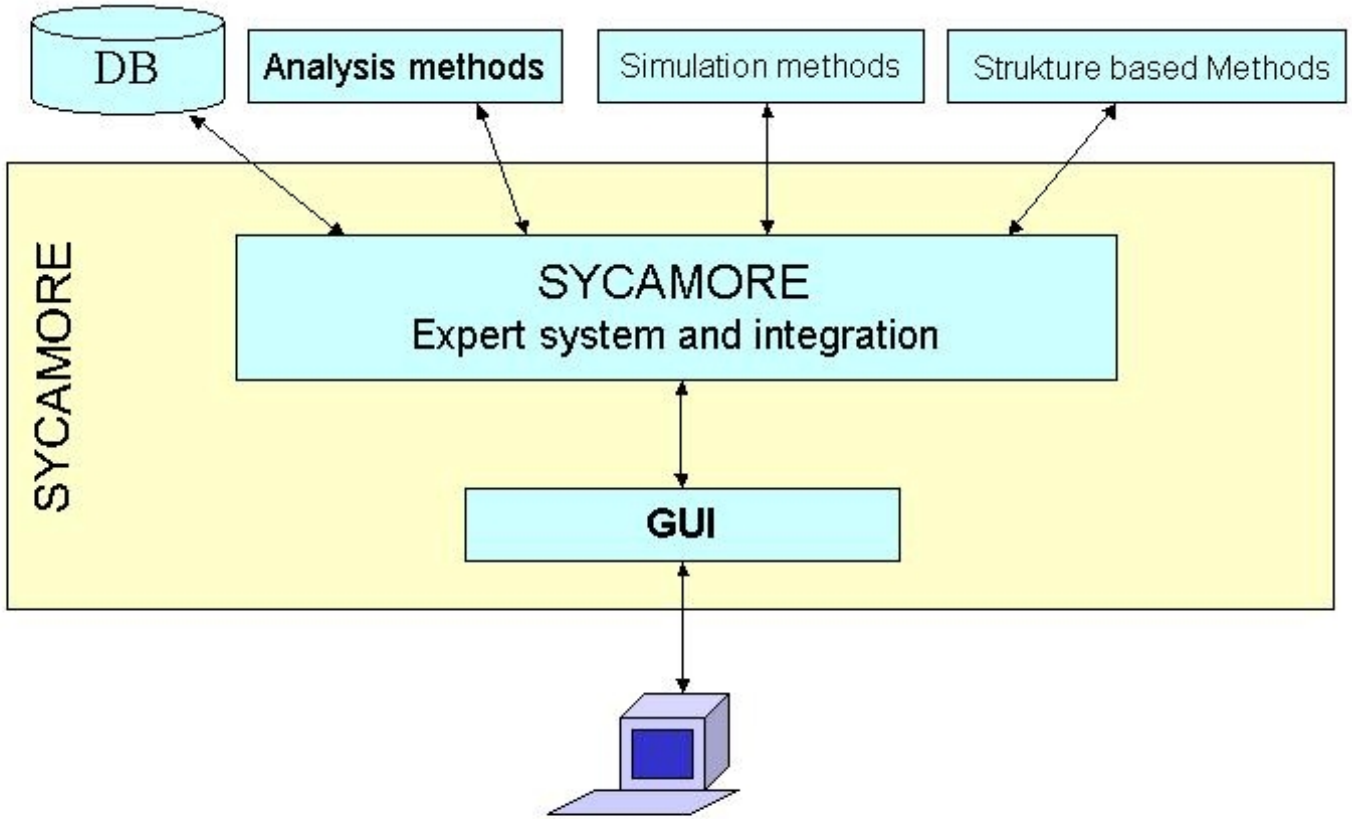
Sycamore



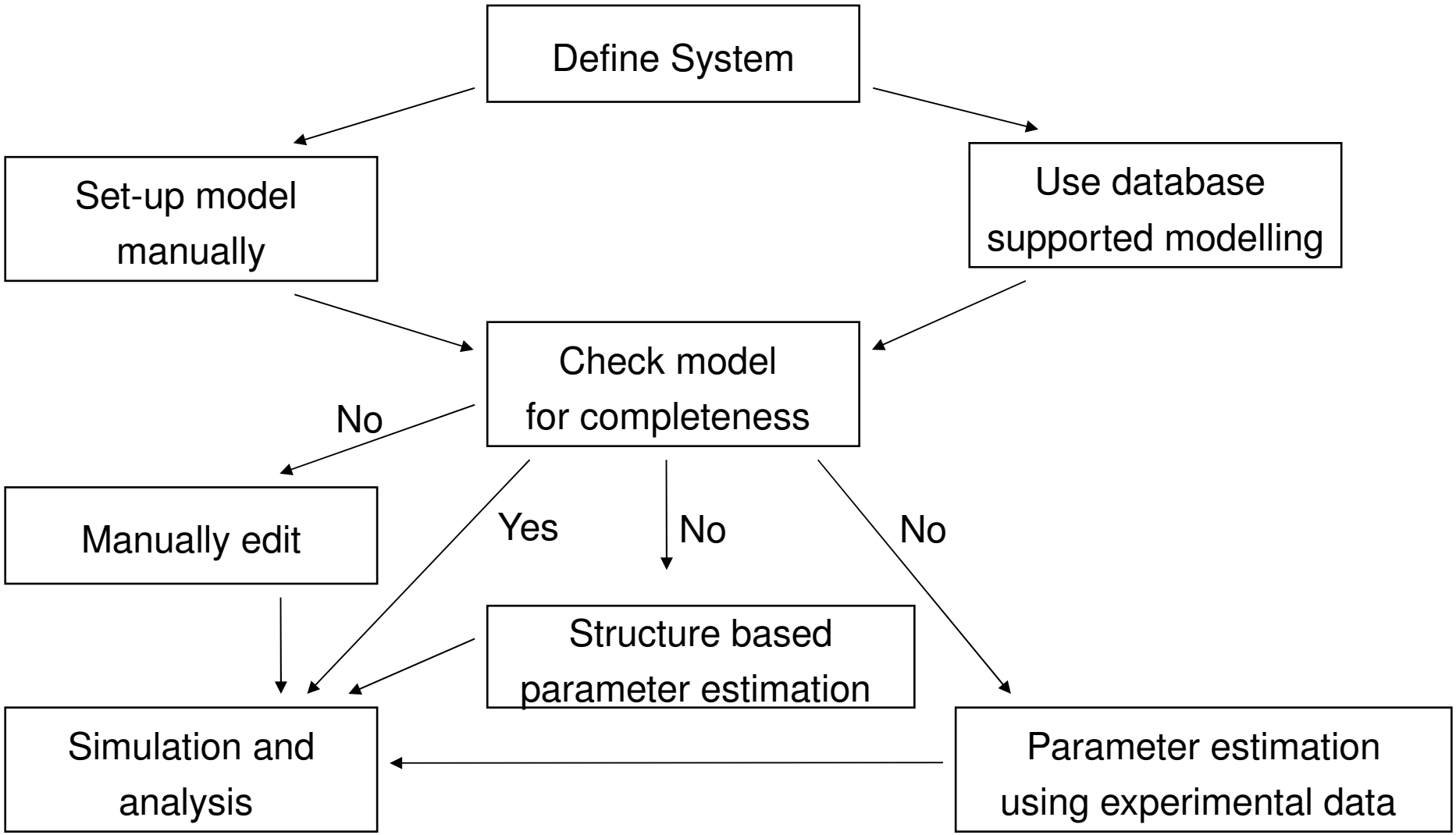
- web based
- interfaces to databases
- simple workflow
- simple analysis
- personal work space
- SBML compliant
- simplified export to e.g. COPASI
- few hundred requests per month on average

Weidemann et al., Bioinformatics, 2009

Architecture:



Workflow


Define System
Set-up model manually
Use database supported modelling
Check model for completeness
No
Manually edit
Yes
No
No
Structure based parameter estimation
Simulation and analysis
Parameter estimation using experimental data

SYCAMORE EML-research - Iceape

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EML Research

SYCAMORE

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  - Workflow
  - User guide
  - Use case
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  - Model from disk
  - Model from projects
  - Example models
- **Build new model**
  - **SYCAMORE**
    - New model
  - **SABIORK**
    - Reaction Search
    - Documentation
- **View & edit model**
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    - Model description
    - Compounds
    - Global parameter
    - Rules
    - Function def.
    - Unit definitions
    - Pathway map
  - **Compartments**
    - All compartments
  - **Reactions**
    - All reactions
- **Refine & analyze model**

SYCAMORE

SYCAMORE allows you to build, view and edit models, to analyze and refine them, to perform simulations, sensitivity analysis and parameter estimations. To do so, you may start with one of the following options:

- Build a new model starting from scratch by defining reactions, metabolites, kinetic equations and parameters. — build new model
- Build a new model with the support of SABIORK, a database that stores reactions and their corresponding kinetic parameters. — build SABIORK model
- Load a SBML model from your hard disk. — load model from disk
- Load a SBML model from projects. SYCAMORE offers the possibility to store complete and incomplete models in an internal database as your personal 'projects'. — load model from projects
- Load an example model for testing of SYCAMORE. — load example model
- Additionally, you may perform parameter estimations in order to determine unknown parameter values. — parameter estimation

SYCAMORE EML-research - Iceape

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  - Completeness
  - Sensitivity analysis
  - Model simulation
    - Copasi
    - JWS online
    - Software launcher

SABIO REACTION KINETICS DATABASE

Search criteria in blue are used to define the search conditions for reactions, independently if there is or not kinetic data for these reactions.

Specify Search Criteria: Submit Search Reset Form

with **Reactants(s)** [ ][ ]

in **Pathway(s)** [ ][ ]

Glycolysis classical

Join entries with AND or OR

having **Enzyme(s)** [ ][ ]

in **Publication** [ ][ ]

related to **Protein** (UniProtID) [ ][ ]

in **Organism(s)** [ ][ ]

Lactococcus lactis

Join entries with AND or OR

in **Tissue(s)/Cell Type(s)** [ ][ ]

Search for reactions, select kinetic data (use green squares), than click button 'send data to SYCAMORE' and finally add the data to the model by clicking this button:

add data to model

Find stopped.

Adresse http://emlsv21/SABIORK/writeSBML.jsp?concvalue=1&unitvalue=mM&compartment=Intracellular&spc=0&concvalue=1&unitvalue=mM&compartment=Intracellular&spc=1&concvalue=1&unitvalue=mM&compart Links


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      </unitDefinition>
    - <unitDefinition id="time">
      - <listOfUnits>
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      </unitDefinition>
    - <unitDefinition id="substance">
      - <listOfUnits>
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        </listOfUnits>
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    </listOfUnitDefinitions>
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    </listOfCompartments>
  - <listOfSpecies>
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      <specie id="spc_1" name="Glycerone phosphate" compartment="Intracellular" initialConcentration="1" />
      <specie id="spc_2" name="alpha-D-Glucose 6-phosphate" compartment="Intracellular" initialConcentration="1" />
      <specie id="spc_3" name="NADH" compartment="Intracellular" initialConcentration="1" />
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      <specie id="spc_5" name="Phosphate" compartment="Intracellular" initialConcentration="1" />
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      <specie id="spc_9" name="ATP" compartment="Intracellular" initialConcentration="1" />
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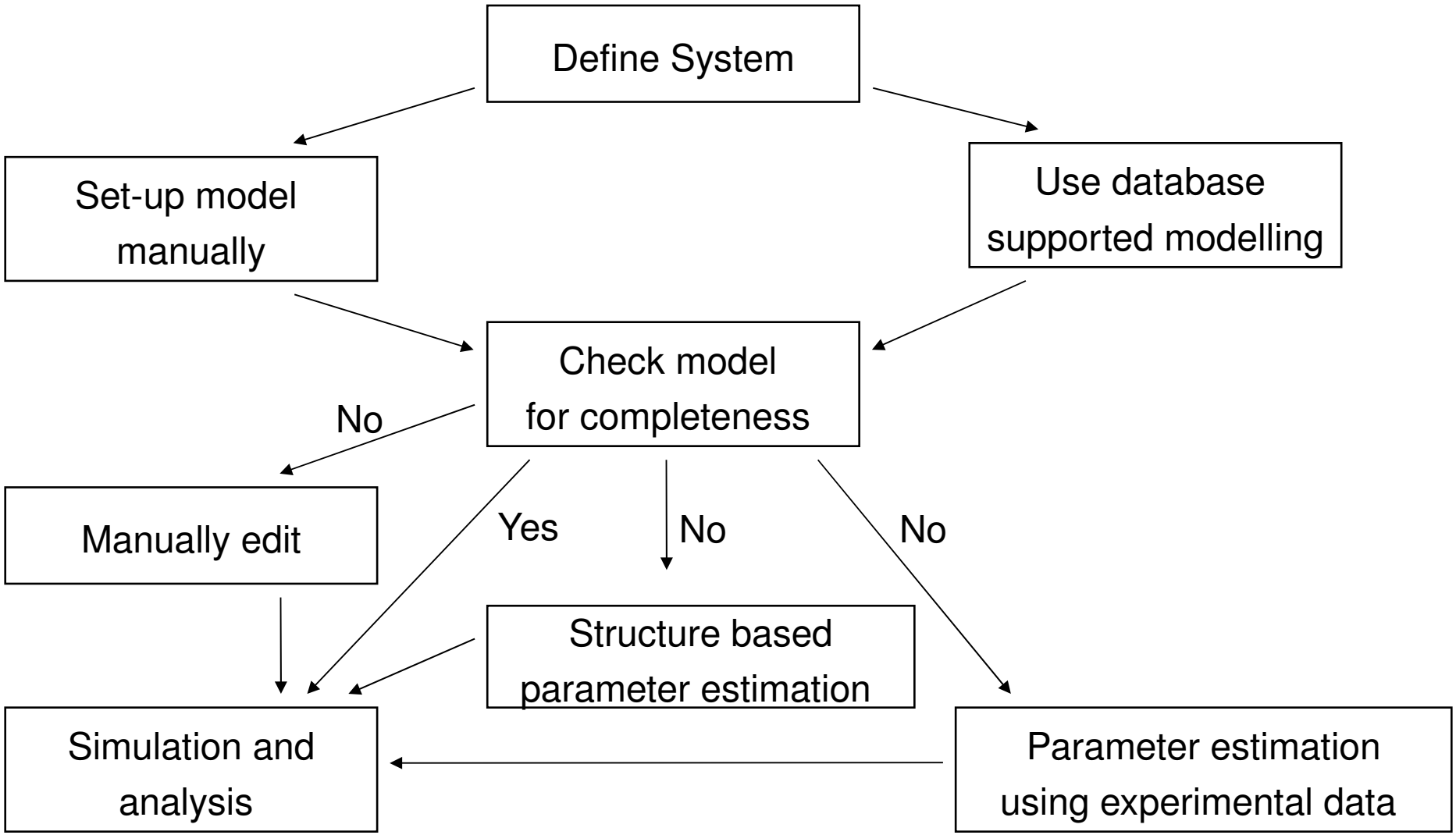
```

Workflow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    - All compartments
    - compartment
  - **Reactions**
    - All reactions
    - HXT
    - HK

Model Yeast glycolysis model of Pritchard and Kell

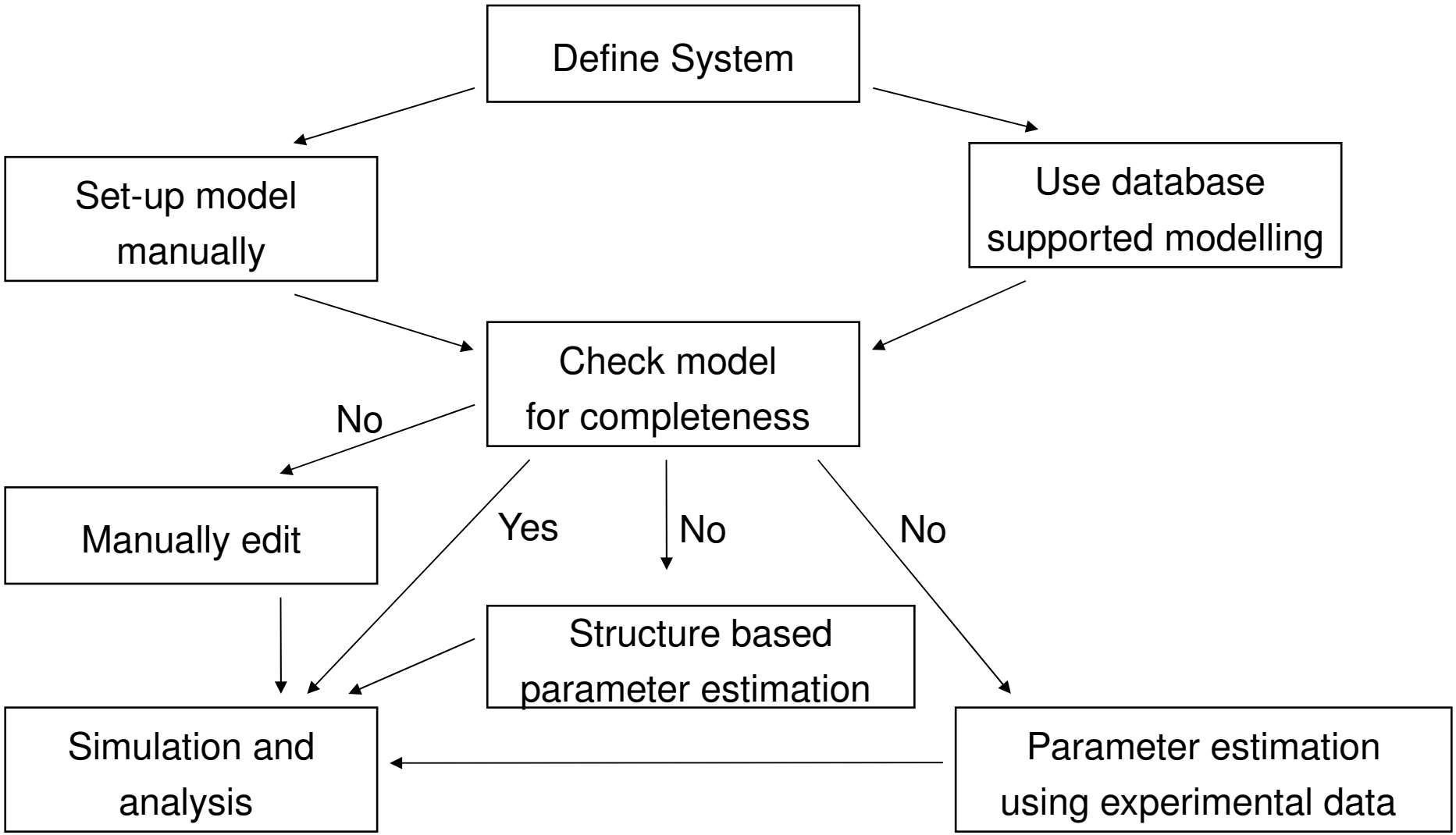
Reactions

#	Name	Reaction	Reversible	Edit
0	HXT	GLCo <=> GLCi	true	edit
1	HK	GLCi + ATP <=> G6P + ADP	true	edit
2	PGI	G6P <=> F6P	true	edit
3	PFK	F6P + ATP => F16bP + ADP ; AMP , F26bP	false	edit
4	ALD	F16bP <=> DHAP + GAP	true	edit
5	TPI	DHAP <=> GAP	true	edit
6	GAPDH	GAP + NAD <=> BPG + NADH	true	edit
7	PGK	BPG + ADP <=> P3G + ATP	true	edit
8	PGM	P3G <=> P2G	true	edit
9	ENO	P2G <=> PEP	true	edit
10	PYK	PEP + ADP <=> PYR + ATP	true	edit
11	PDC	PYR => AcAld + CO2	false	edit
12	ADH	EtOH + NAD <=> AcAld + NADH	true	edit
13	ATPase	ATP => ADP	false	edit
14	AK	2 ADP <=> ATP + AMP	true	edit
15	G3PDH	DHAP + NADH => Glycerol + NAD	false	edit
16	Glycogen Branch	G6P + ATP => ADP + Glycogen	false	edit
17	Trehalose Branch	2 G6P + ATP => ADP + Trehalose	false	edit
18	Succinate Branch	2 AcAld + 3 NAD => Succinate + 3 NADH	false	edit

Compounds

Name	Initial amount	Intitial Concentration	Unit	Compartment	Boundary Condition	Edit
GLCo	2.0	.	default	compartment	true	edit
GLCi	0.097652231064563	.	default	compartment	false	edit

Workflow


Define System
Set-up model manually
Use database supported modelling
Check model for completeness
No
Manually edit
Yes
No
No
Structure based parameter estimation
Simulation and analysis
Parameter estimation using experimental data

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- Reactions
  - All reactions
  - HXT
  - HK
  - PGI
  - PFK
  - ALD
  - TPI
  - GAPDH
  - PGK
  - PGM
  - ENO
  - PYK
  - PDC
  - ADH
  - ATPase
  - AK
  - G3PDH
  - Glycogen Branch
  - Trehalose Branch
  - Succinate Branch
- Refine & analyze model
  - Completeness
  - Sensitivity analysis
  - Model simulation
    - Copasi
    - JWS online
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  - Parameter estimation
    - Start
    - Software launcher
    - User guide
- Save model
  - View XML code
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- Resources

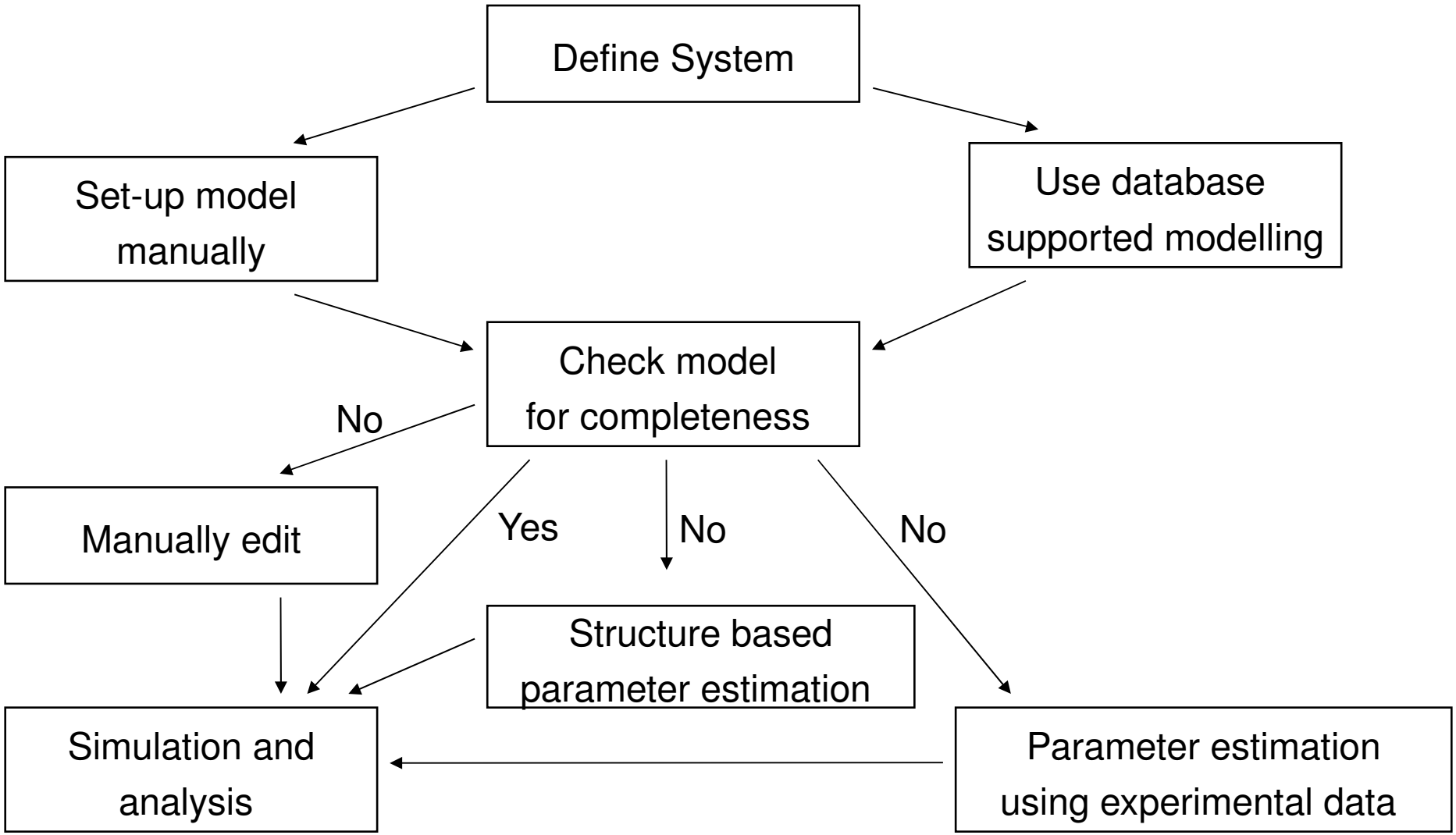
Registration

Model completeness

Compartments
compartment_0
No errors detected.

Reactions
HXT
The kinetic law formula is missing.
HK
No errors detected.
PGI
No errors detected.
PFK
No errors detected.
ALD
No errors detected.
TPI
No errors detected.
GAPDH
No errors detected.
PGK
No errors detected.
PGM
No errors detected.
ENO
No errors detected.
PYK
No errors detected.
PDC
No errors detected.
ADH

Workflow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    - Rules
    - Function def.
    - Unit definitions
    - Pathway map
  - **Compartments**
    - All compartments
    - compartment
  - **Reactions**
    - All reactions
    - HXT
    - HK

Model Yeast glycolysis model of Pritchard and Kell

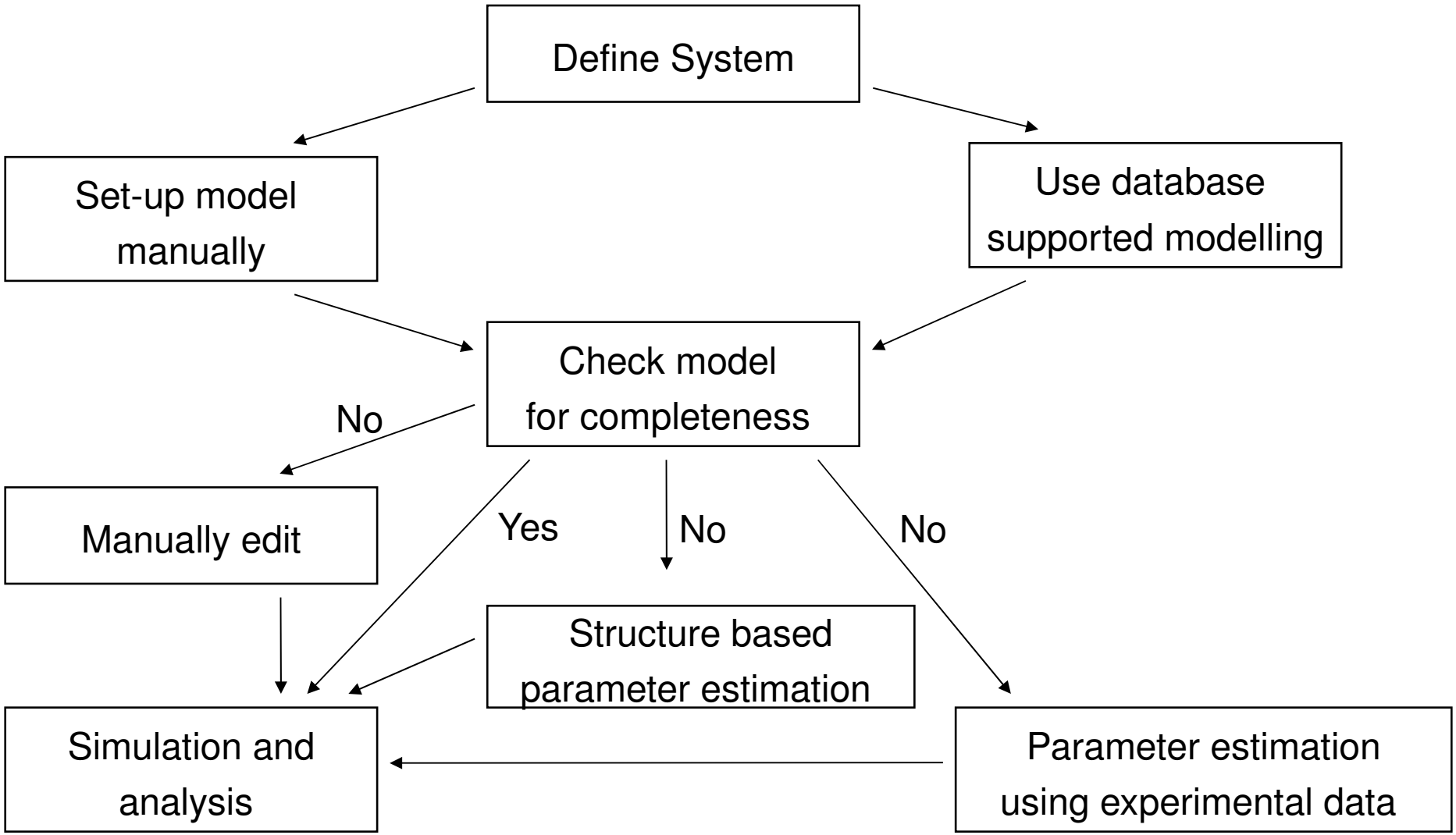
Reactions

#	Name	Reaction	Reversible	Edit
0	HXT	GLCo <=> GLCi	true	edit
1	HK	GLCi + ATP <=> G6P + ADP	true	edit
2	PGI	G6P <=> F6P	true	edit
3	PFK	F6P + ATP => F16bP + ADP ; AMP , F26bP	false	edit
4	ALD	F16bP <=> DHAP + GAP	true	edit
5	TPI	DHAP <=> GAP	true	edit
6	GAPDH	GAP + NAD <=> BPG + NADH	true	edit
7	PGK	BPG + ADP <=> P3G + ATP	true	edit
8	PGM	P3G <=> P2G	true	edit
9	ENO	P2G <=> PEP	true	edit
10	PYK	PEP + ADP <=> PYR + ATP	true	edit
11	PDC	PYR => AcAld + CO2	false	edit
12	ADH	EtOH + NAD <=> AcAld + NADH	true	edit
13	ATPase	ATP => ADP	false	edit
14	AK	2 ADP <=> ATP + AMP	true	edit
15	G3PDH	DHAP + NADH => Glycerol + NAD	false	edit
16	Glycogen Branch	G6P + ATP => ADP + Glycogen	false	edit
17	Trehalose Branch	2 G6P + ATP => ADP + Trehalose	false	edit
18	Succinate Branch	2 AcAld + 3 NAD => Succinate + 3 NADH	false	edit

Compounds

Name	Initial amount	Intitial Concentration	Unit	Compartment	Boundary Condition	Edit
GLCo	2.0	.	default	compartment	true	edit
GLCi	0.097652231064563	.	default	compartment	false	edit

Workflow


Define System
Set-up model manually
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Check model for completeness
No
Manually edit
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No
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Structure based parameter estimation
Simulation and analysis
Parameter estimation using experimental data

Structure based parameter estimation

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Registration

qPIPSA Parameter Retrieval and Estimation Module

What this module does?

1. Retrieval of relevant parameters and associated information from BRENDA and SABIO-RK, as well as protein sequences from Swiss-Prot and protein structures from PDB, MODBASE and SWISSMODEL
2. Parameter estimation using available protein structure information. Currently the PIPSA method is used to do this. PIPSA analysis can be used to aid the estimation of kinetic parameters from a similarity analysis of the electrostatic potentials of the enzyme for which the parameter is needed and the enzymes for which parameters are already known.

For more information on the use of this module click here.

Retrieval of parameters and related information

This is based on insertion of a unique protein identifier. Currently a Swiss-Prot accession code must be given. The workflow depends on an EC annotation in the description line of your Swiss-Prot entry. This EC link is used to search in BRENDA and SABIO-RK entries.

Please enter :	
	Swiss-Prot accession code (eg. P35557 or P35520:4.2.1.22) [?]
	a valid email address [?]
	Start search

In case of unknown or only vaguely known protein functionality ProFAT may assist in detecting protein function and structural homology.

http://cluster-1.mpi-cbg.de/profat/profat.html

ProFAT is a tool for the functional annotation of proteins via the detection of weak homologies. Sequence homology is detected with NCBI's PSI-BLAST system. Structural homology is detected with UCL's Threader software. These results are then combined by the use of GenBank annotation and basic text mining.

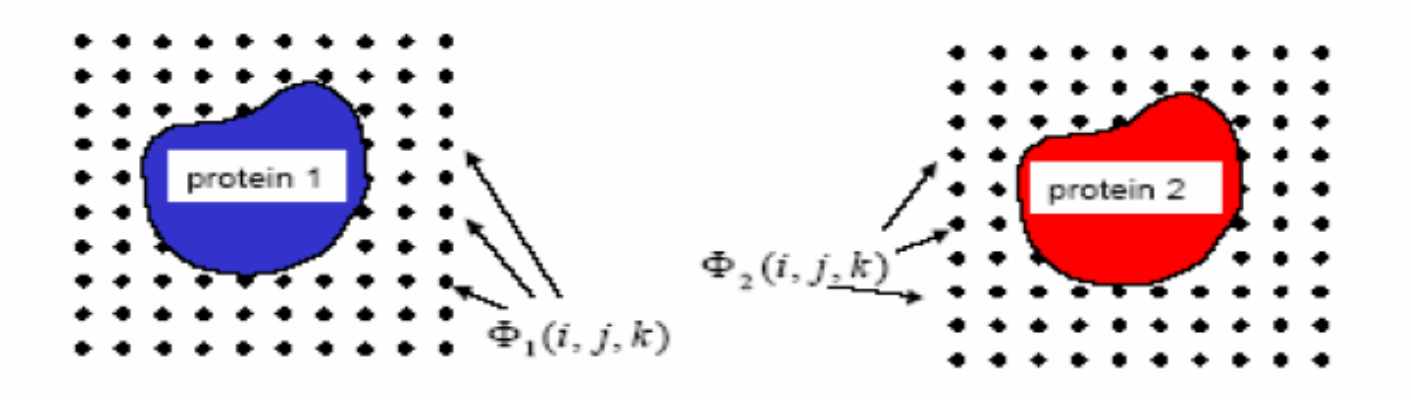
ProFAT requires the user to submit a keyword list along with the protein sequence. Several pre-made keyword lists are available, however, the system is used optimally with a user defined keyword list consisting of suspected or experimentally determined information.

Bradshaw C. R., Surendranath V., and Habermann B. BMC Bioinformatics 2006, 7:466

New features (Spring 2009)

The following new features are now available:

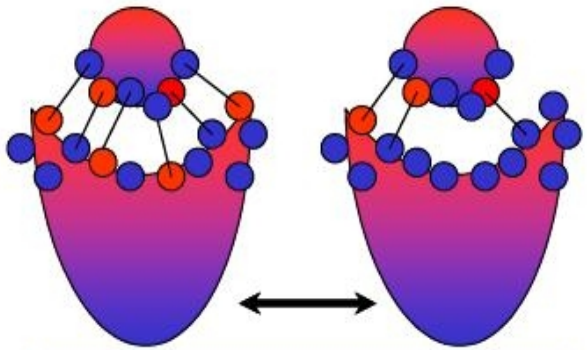
PIPSA
(Protein Interaction Property Similarity Analysis)



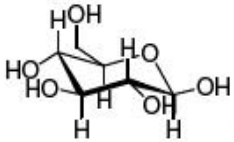
- Interaction fields are calculated on a set of points
- Field values on corresponding points are compared
- Φ = electrostatic potential, shape, probe interaction field, ...

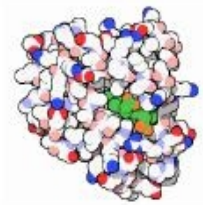
Slide kindly provided by Matthias Stein

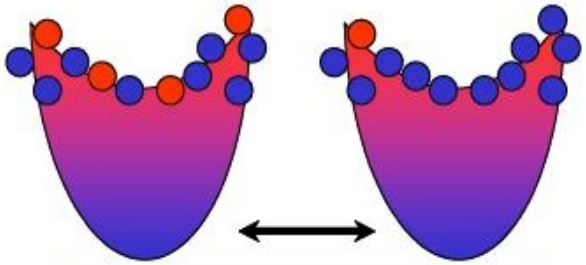
quantitative
Protein **I**nteraction **P**roperty **S**imilarity **A**nalysis (qPIPSA)



comparing interactions

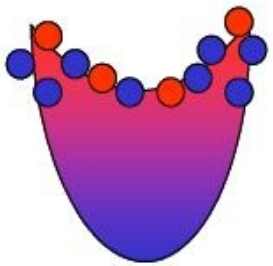






comparing interaction fields:

- Charge distribution
- Potential
- Shape
- ...



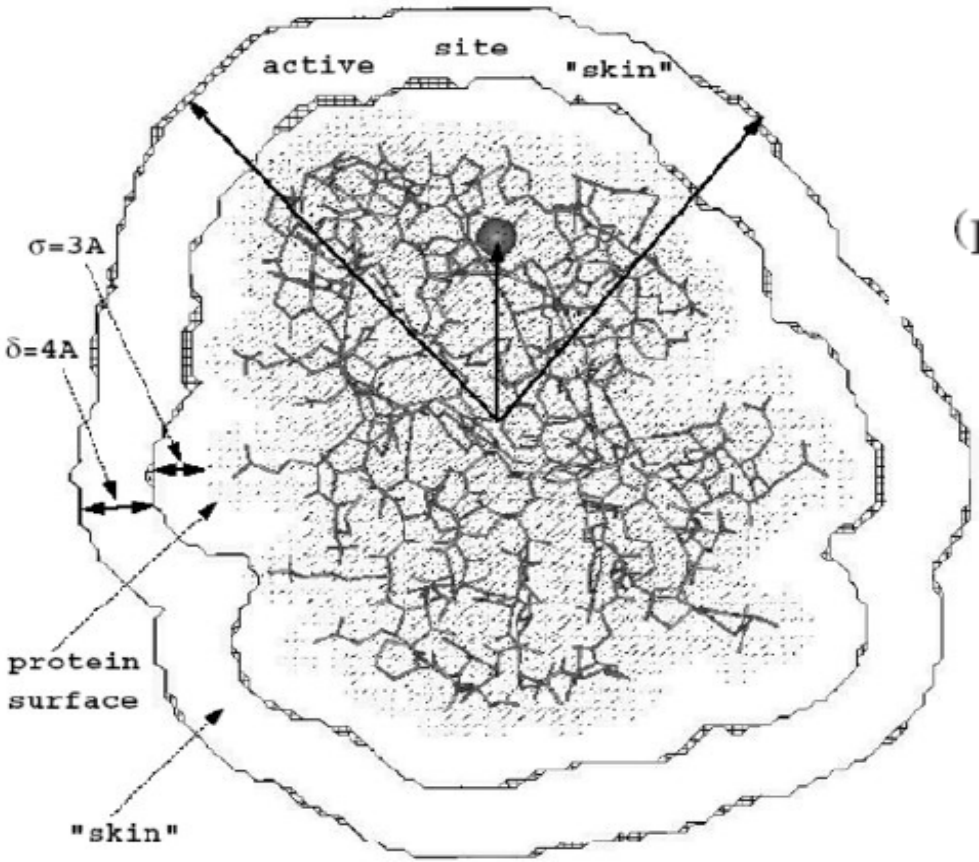
Protein-ligand

Protein-protein

Estimate Kinetic Parameters from a Comparison of Molecular Interaction Fields

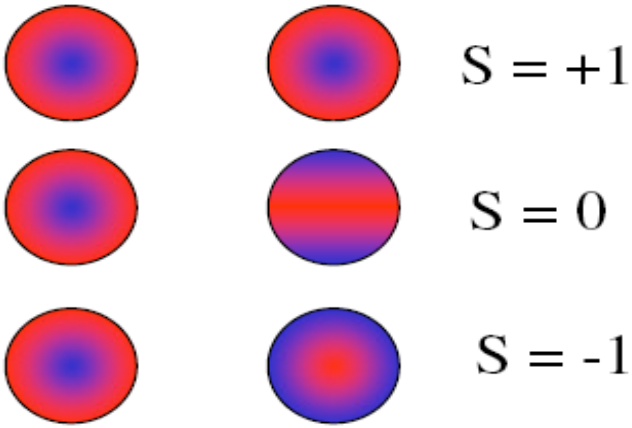
Slide kindly provided by Matthias Stein

PIPSA
(Protein Interaction Property Similarity Analysis)



$$SI_{12} = \frac{2(\mathbf{p}_1, \mathbf{p}_2)}{(\mathbf{p}_1, \mathbf{p}_1) + (\mathbf{p}_2, \mathbf{p}_2)}$$

$$(\mathbf{p}_1, \mathbf{p}_2) = \sum_{i,j,k} \phi_1(i, j, k)\phi_2(i, j, k)$$



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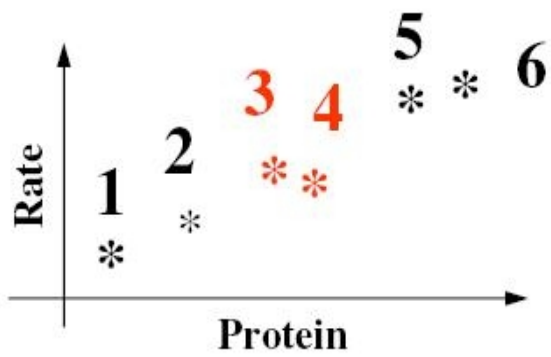
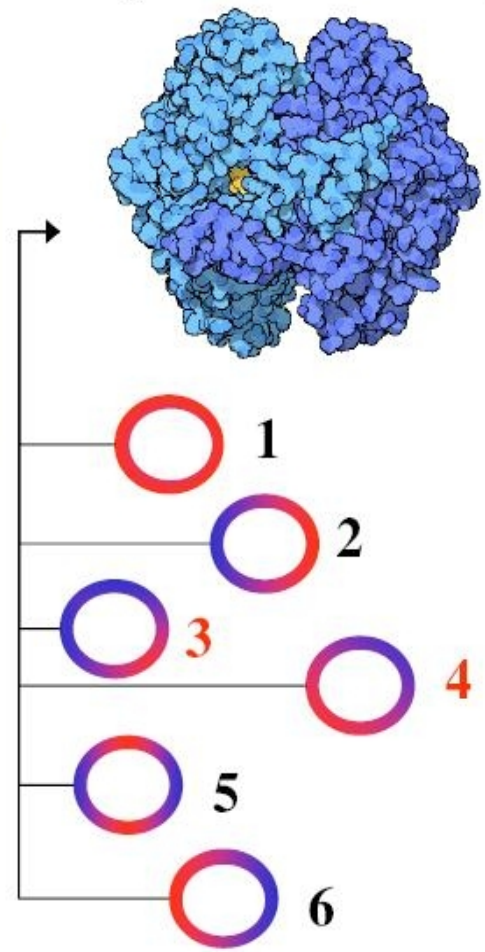
quantitative PIPSA (qPIPSA)

- Comparing Molecular Interaction Fields
- Quantify Similarities and Differences
- Training Set Required with Experimental Information
- Predict Relative Ordering and Trends

d





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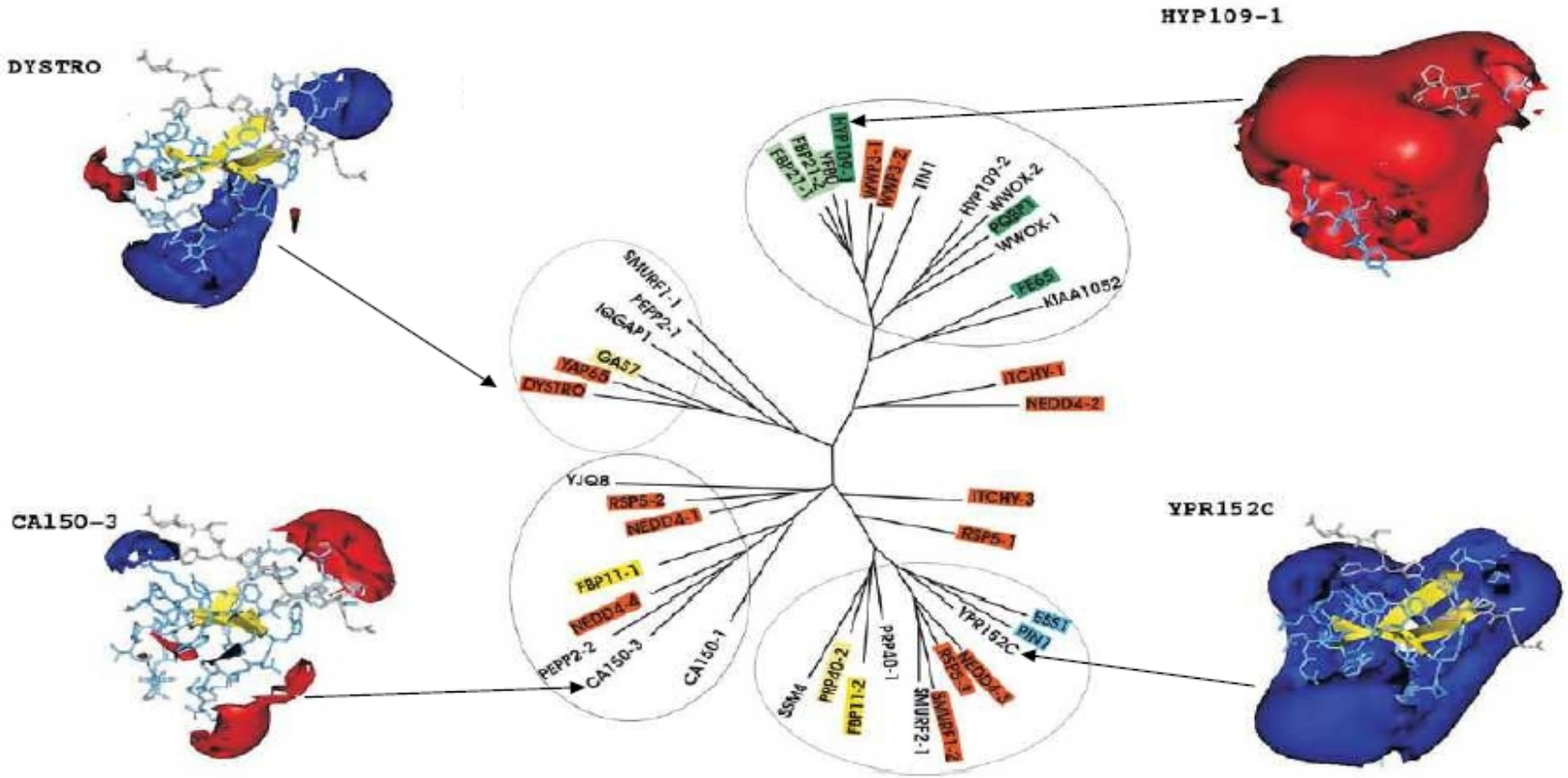
PIPSA (Protein Interaction Property Similarity Analysis)



42 WW domains, Schleinkofer etal, 2004

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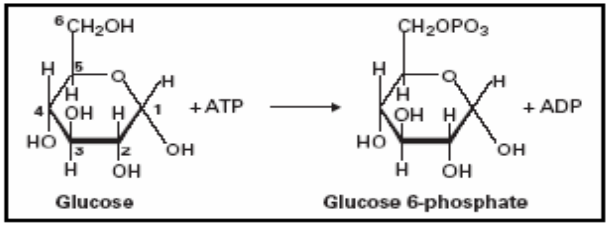
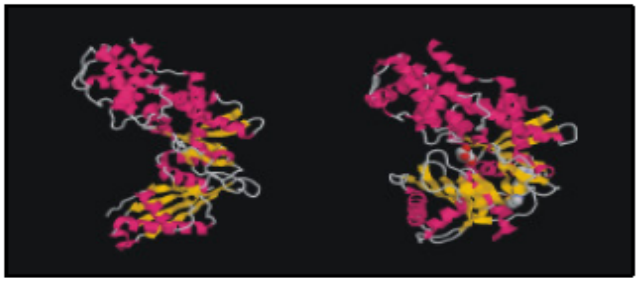
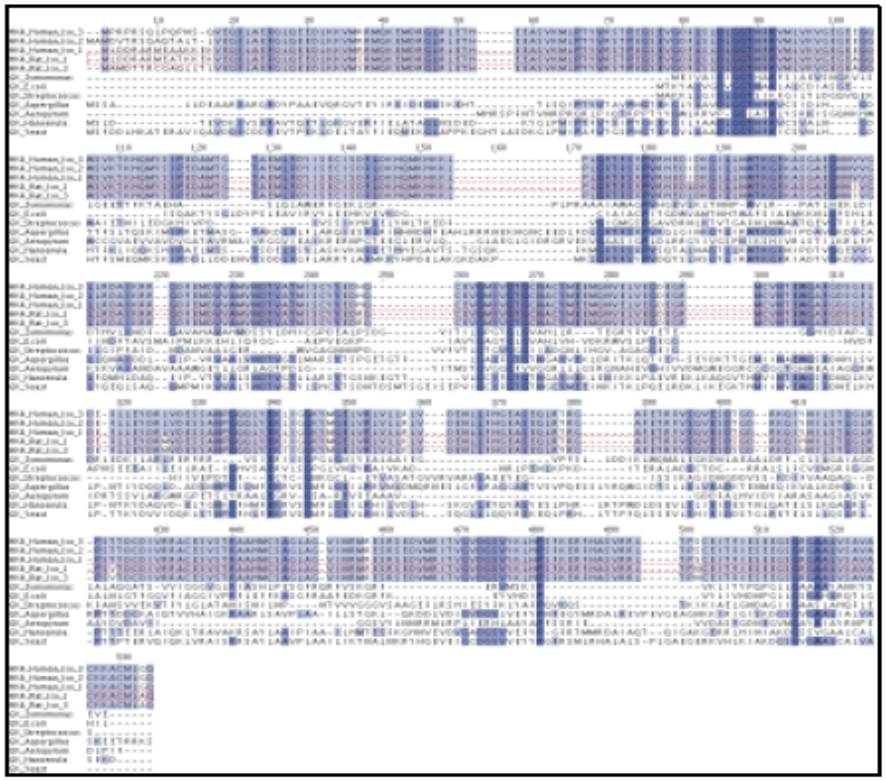
Example PIPSA: Glucokinases



1. Identify Chemical Reaction of Interest



3. Choice of Appropiate Template



2. Multiple Sequence Alignment

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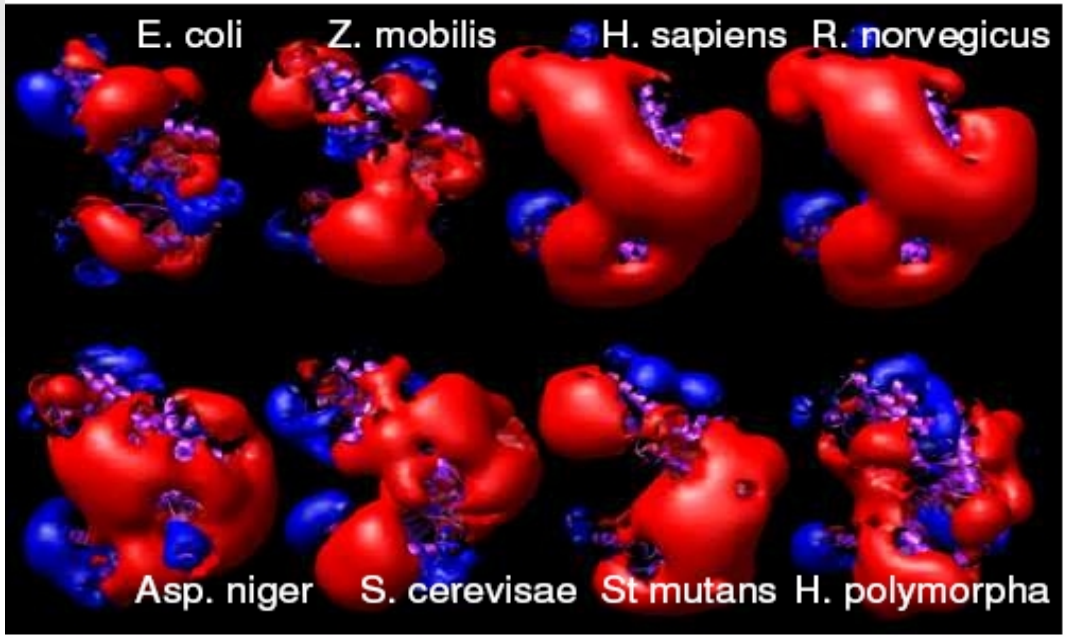
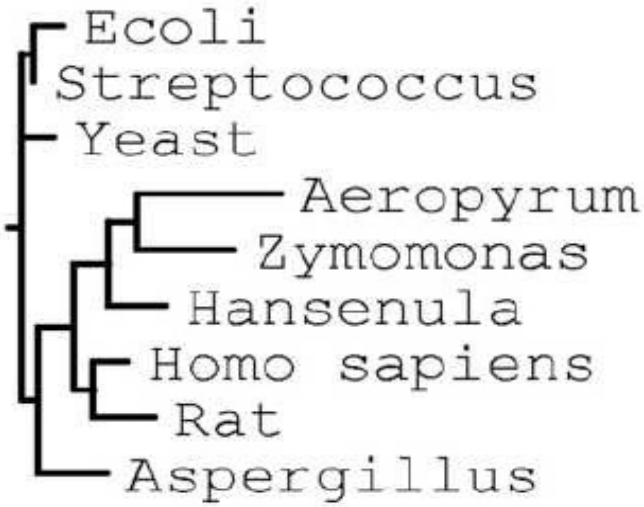
Example PIPSA: Glucokinases





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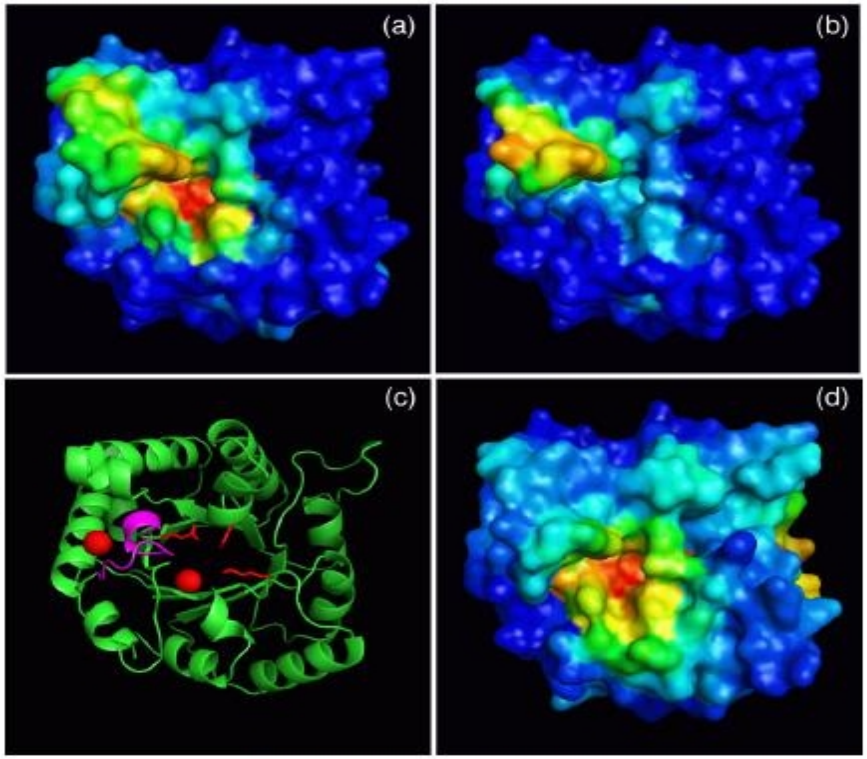
TPI: Different Spots of Protein Correlate with Different Kinetic Parameters

k_{cat} / K_m

K_m



Flexible Loop

Active Site

Conservation of Electrostatic Potential

blue → red
better predictions

Gabdoulline, Stein, Wade
BMC Bioinformatics 2007

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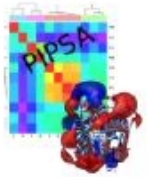
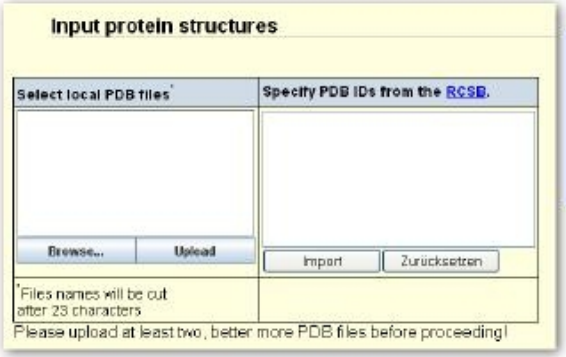
webPIPSA: An automated PIPSA workflow

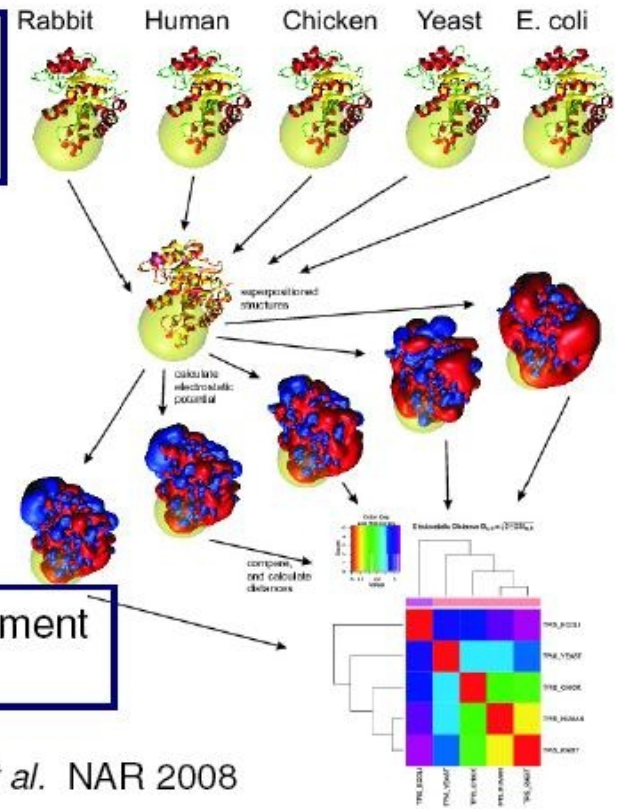


webPIPSA

Protein Interaction Property Similarity Analysis



Superpositioning
Calculation of Epot
Comparison



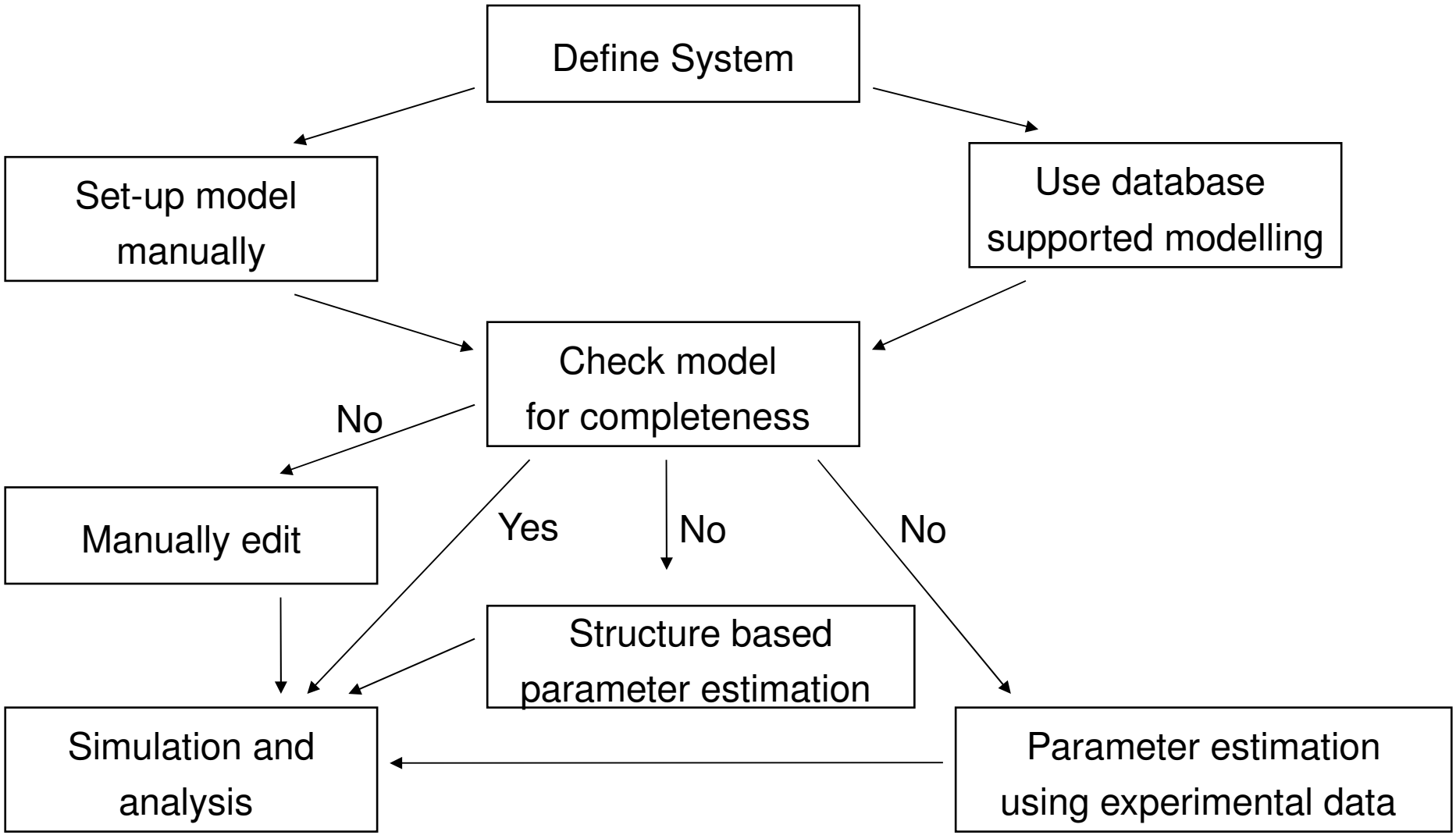
Multiple Sequence Alignment
Comparative Modeling

http://pipsa.eml.org

Richter, Wenzel, Stein *et al.* NAR 2008

Slide kindly provided by Matthias Stein

Workflow

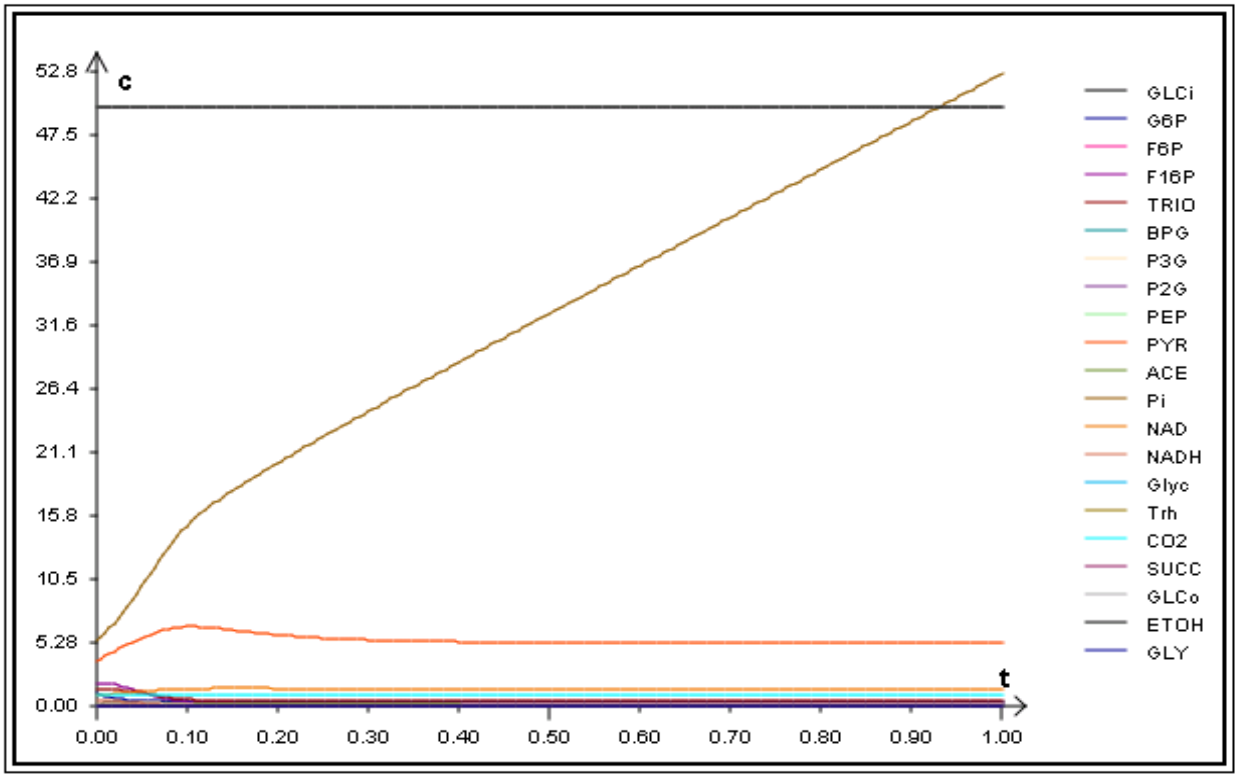

Define System
Set-up model manually
Use database supported modelling
Check model for completeness
No
Manually edit
Yes
No
No
Structure based parameter estimation
Simulation and analysis
Parameter estimation using experimental data

Sycamore – basic model analysis

- All reactions
  - vGLK
  - vPGI
  - vGLYCO
  - vTreha
  - vPFK
  - vALD
  - vGAPDH
  - vPGK
  - vPGM
  - vENO
  - vPYK
  - vPDC
  - vSUC
  - vGLT
  - vADH
  - vG3PDH
  - vATP
- **Refine & analyze model**
  - Completeness
  - Sensitivity analysis
  - **Model simulation**
    - Copasi
    - Software launcher
    - General
  - **Parameter estimation**
    - Start
    - User guide
- **Save model**
  - View XML code

Deterministic simulation

Result:



Sycamore – basic model analysis

- Global parameter
- Rules
- Function def.
- Unit definitions
- Pathway map

▼ **Compartments**
- All compartments
- cell

▼ **Reactions**
- All reactions
- reac_0
- reac_1
- influx
- eff

▼ **Refine & analyze model**
- Completeness
- Sensitivity analysis

▼ **Model simulation**
- Copasi
- General

▼ **Parameter estimation**
- Start
- User guide

▼ **Save model**
- View XML code
- Save on disk
- Save as project

► **Resources**

Registration

User guide

Sensitivity analysis

Function(s) to be derived:
Non-Constant Concentrations of Metabolites
Calculation to perform: Steady State
Variable(s) for 1. derivation:
All Parameter Values
Method: Sensitivities Method
Delta factor: 1e-06
Delta minimum: 1e-12
Sensitivities Result:
Sensitivities array

Rows: Target functions, Non-Constant Concentrations of Metabolites
Columns: Variables 1, All Parameter Values

Sensitivity analysis

Variable	(reac_0).Keq	(reac_0).V	(reac_0).Kp	(reac_0).Ks	(reac_1).V	(reac_1).Kp	(reac_1).Keq	(reac_1).Ks	(influx).k_influx	(e
D-Glucose 6-phosphate	0.334	-0.593	-0.608	0.170	-0.264	0.151	-9.263e-09	-0.001	0.000	
D-Fructose 6-phosphate	-0.093	0.166	0.169	-0.047	0.008	-0.013	3.341e-10	0.000	0.000	
D-Glucose	-0.243	0.431	0.442	-0.124	0.256	-0.138	8.931e-09	0.001	-0.160	
ATP	-0.243	0.431	0.442	-0.124	0.256	-0.138	8.931e-09	0.001	0.000	
ADP	nan.000	nan.000	nan.000	nan.000	nan.000	nan.000	nan.000	nan.000	nan.000	

Negative values	Positive values
-0.795 - -0.662	0.662 - 0.795
-0.662 - -0.530	0.530 - 0.662

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- ENO
- PYK
- PDC
- ADH
- ATPase
- AK
- G3PDH
- Glycogen Branch
- Trehalose Branch
- Succinate Branch

Refine & analyze model

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JWS online model simulation

$Failed

For further information visit JWS online.

Loading Java Applet Failed...

JWS Online: queralt model - Iceape

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Search | Upload | About | Help

JWS Online

Para...	Value
ksclb2	0.03
kdclb2	0.03
kadcl...	0.2
kaad...	2
kscd...	0.015
kdcd...	0.05
kadc...	2
kdcdh	0.01
kadcdh	1
kapcdh	1
Jcdh	0.002
Cdh1T	1
ksse...	0.03
kdse...	0.05
kads...	2
ksse...	0.001
kdse...	0.004
lasec...	500
ldsec...	1

Param Reset

Evaluate Model

Sim State

Start value 0

End value 50

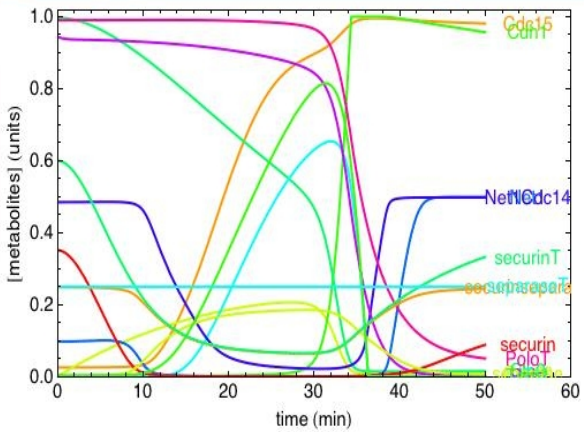
Rates

Metabolites

Select values

Cdc15
Cdc20
Cdh1
Clb2
MEN
Net1
Net1Cdc14
Polo

http://jjj.biochem.sun.ac.za - JWS On line - Iceape



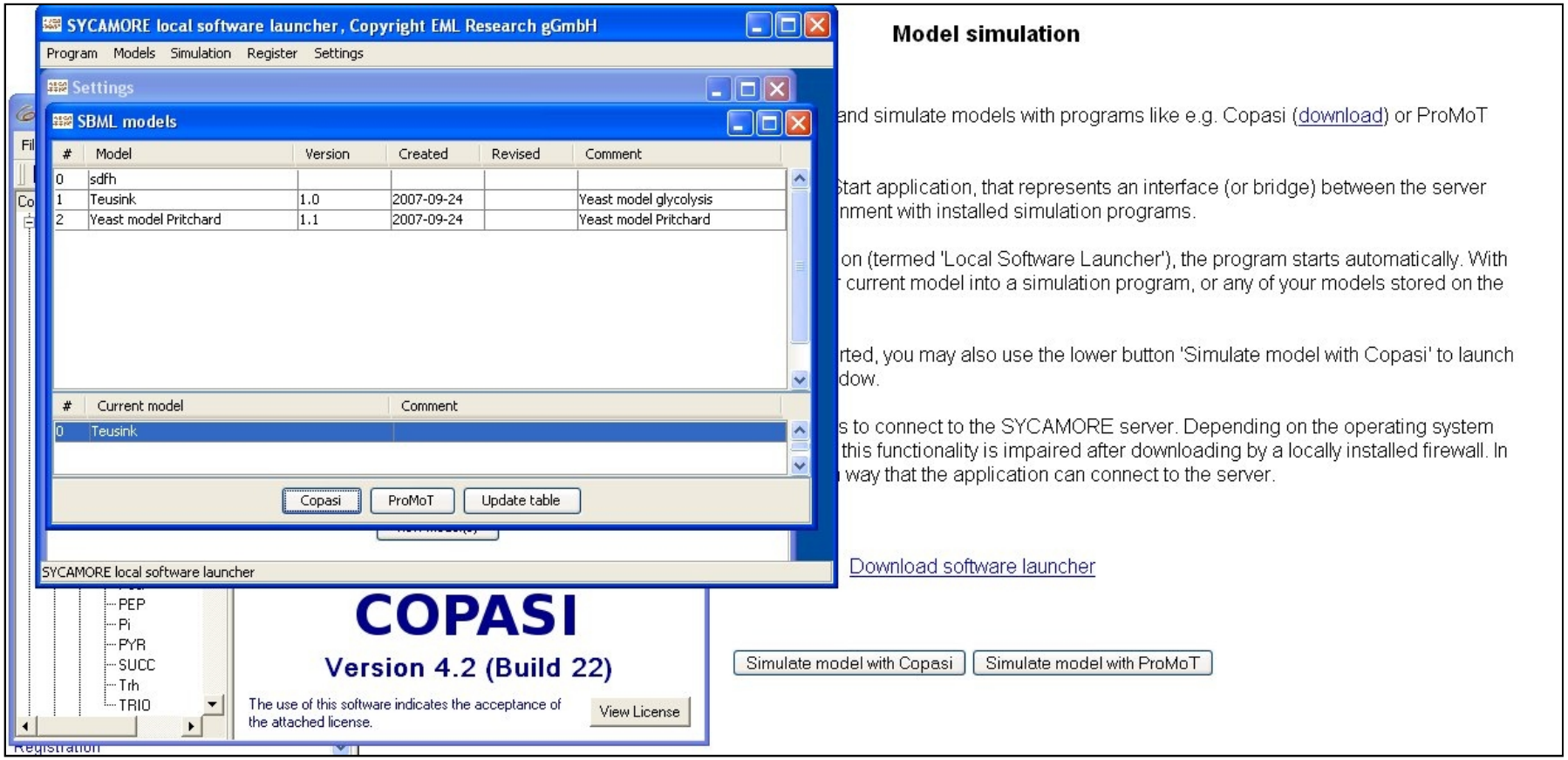
Download the results in text or comma separated value format (e.g. for Excel import):

Text CSV

POWERED BY Wolfram webMathematica

Done

Launching of locally installed software tools



FEBSX-SysBio 2011

We cordially invite you to the

Joint FEBS/Systems X Advanced Lecture Course **on**

Systems Biology – From Molecules to Function

26 February 2011 – 3 March 2011: Innsbruck, Austria, EU

http://cdl.univie.ac.at/sysbio2011/

Acknowledgements

University of Heidelberg, Germany:

Sven Sahle, Ralph Gauges, Paul Willy, Natalia Simus, Irina Surovtsova, Katrin Hübner, Ulla Rost, Tim Maiwald, Jennifer Levering, Tim Johann, Deepa Damodaran, Andreas Weidemann, Nadine Veith, Jan-Ulrich Schad, Duygu Kesten

VBI, USA:

Pedro Mendes, Stefan Hoops, Aejaaz Kamal

University of Manchester, UK:

Pedro Mendes, Joseph Dada, Jürgen Pahle, Robert Platt, Natalie Stanford, Ed Kent, Olusegun Oshota

HITS, Heidelberg, Germany:

Isabel Rojas, Wolfgang Müller

Rebecca Wade, Stefan Richter, Matthias Stein, Razif Gabdoulline

SBML-team and libSMBL-team

Financing:

BMBF

NIH

Klaus Tschira Foundation

VBI

BBSRC and EPSRC