

Parallelised Monte-Carlo simulation of large biological networks using the EGEE grid

Christoph Wierling

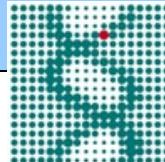
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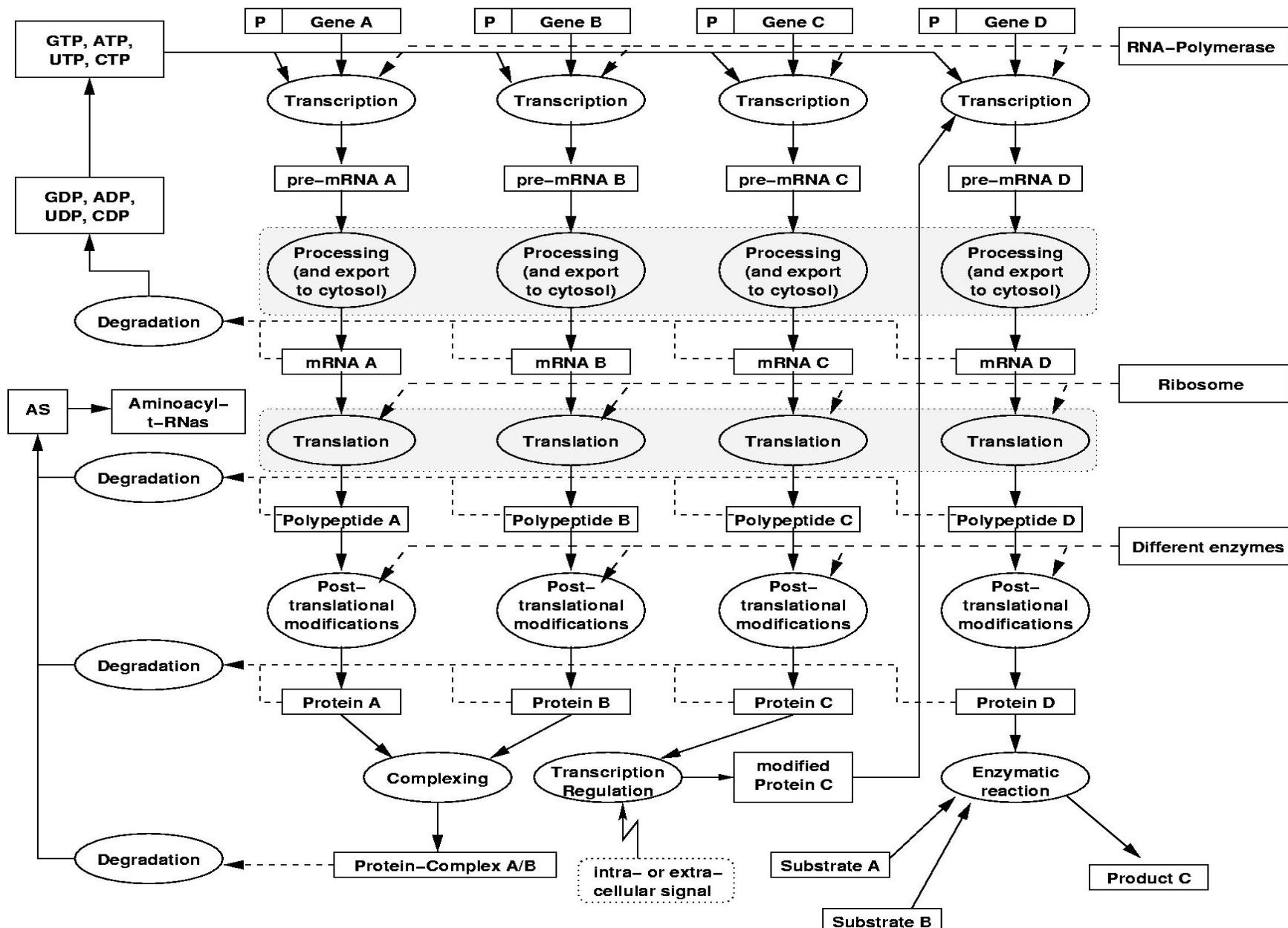
Max-Planck-Institut
für molekulare Genetik

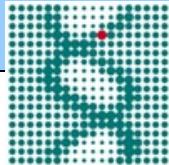


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Cellular Processes





Modelling and Data Resources

Data required for modelling:

- Information about the *substrates* and *products* of a reaction and its *stoichiometry*
- Information about the catalyzing *enzyme* and its *kinetics*
- Information about the reactants and enzyme *concentrations*

Databases:

- KEGG (Kyoto Encyclopedia of Genes and Genomes)
- Reactome
- Transpath (Database of signal transduction pathways)
- SRS (Sequence Retrieval System)
- BioCyc
- Kinetikon (Kinetics database)
- Database of experimental data (Expression data, Protein/Protein interaction, ...)

PyBioS

(<http://pybios.molgen.mpg.de>)

Detailed
hierarchical
model

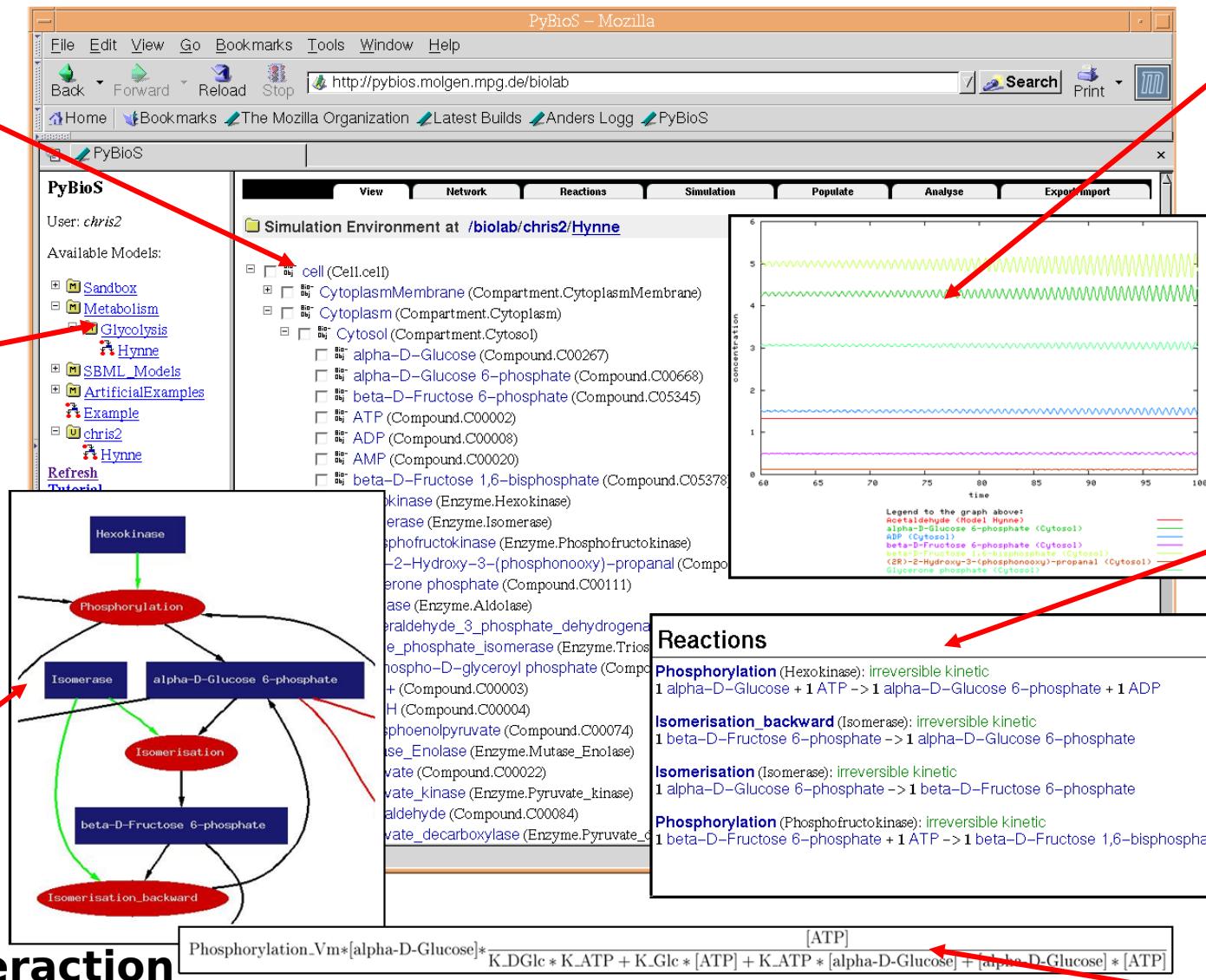
Model
repository

Auto-
matically
generated interaction
diagram of the model

Diagram of
simulation
results

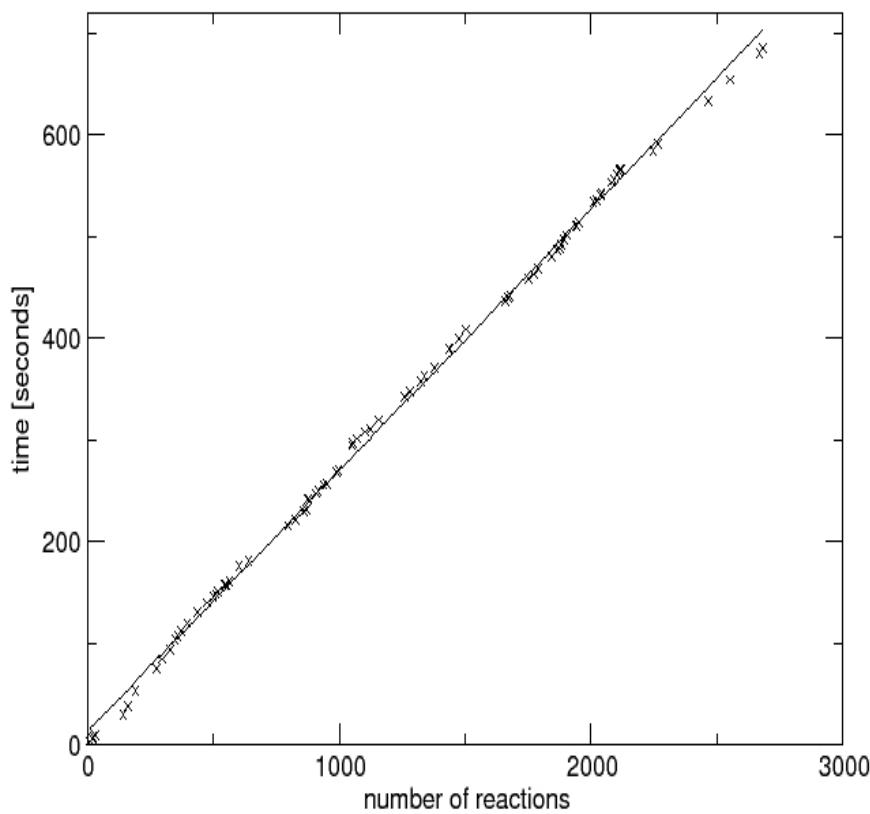
List of
reactions

Details of
the kinetics

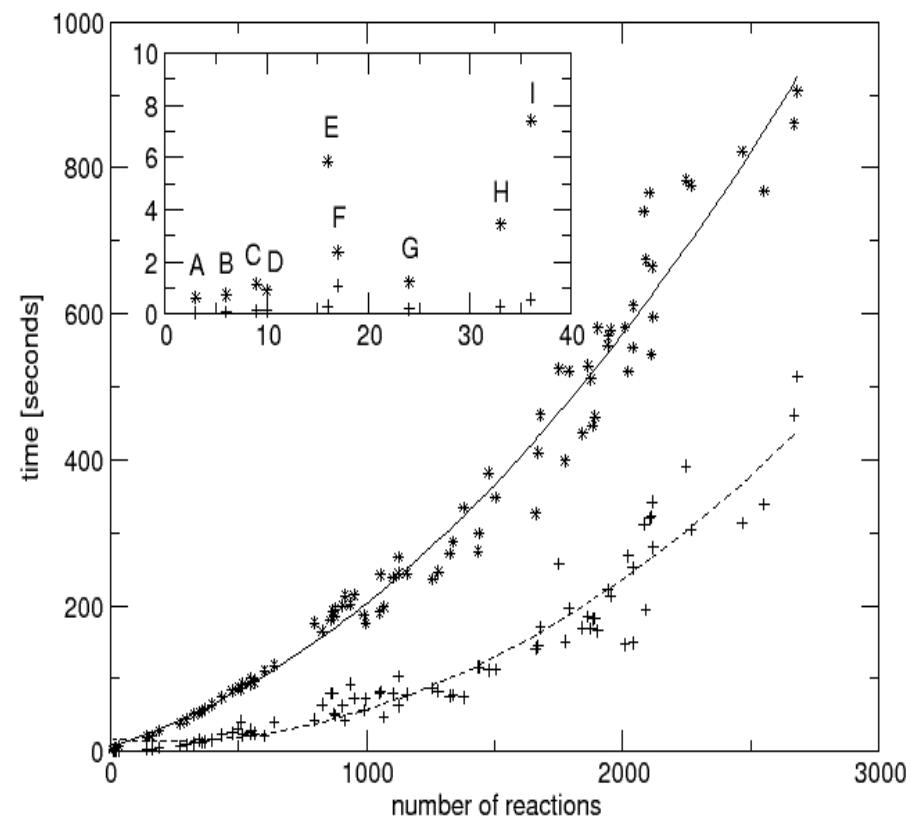


Scaling of Model Population and Simulation

Population

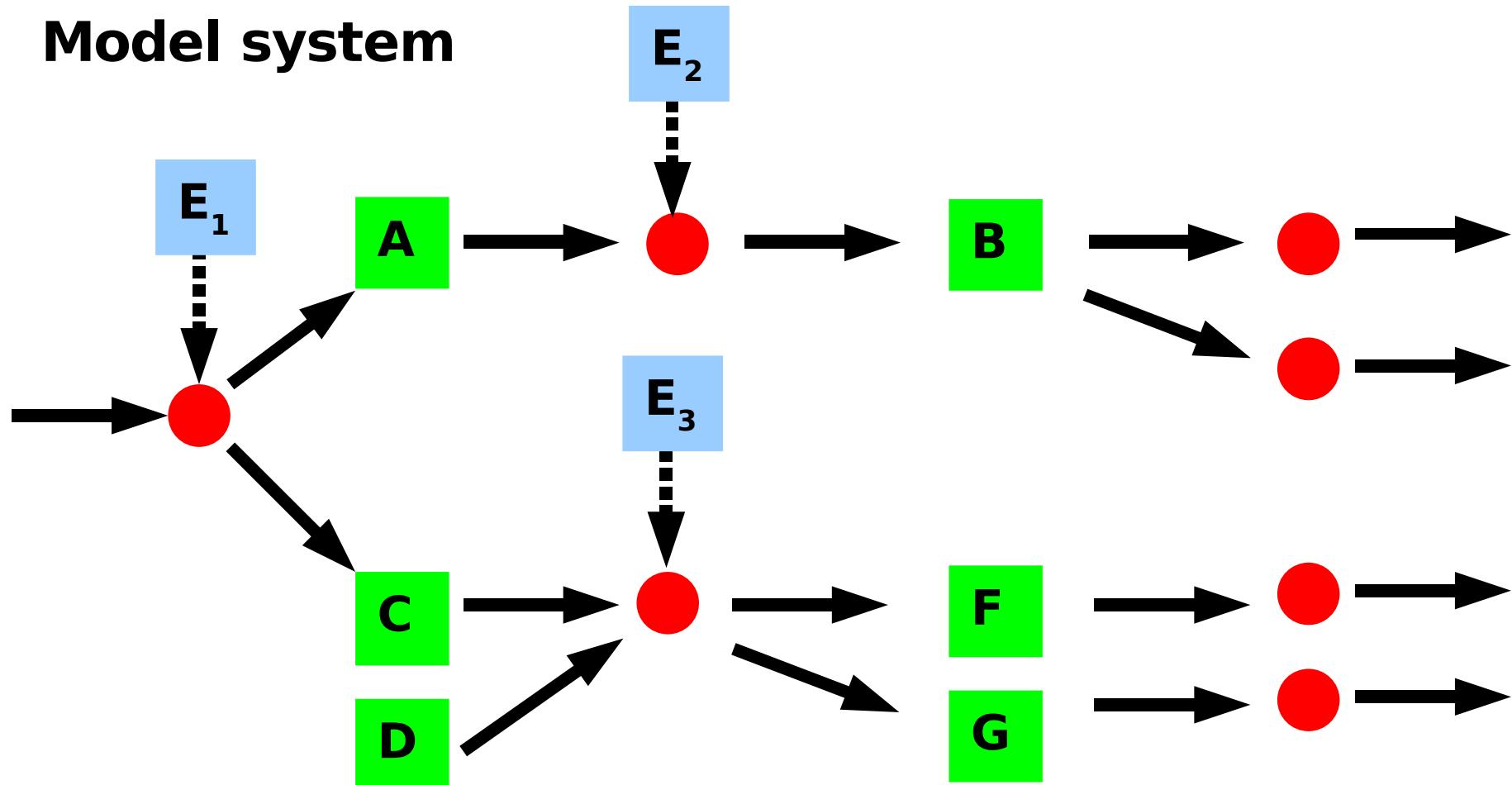


Simulation

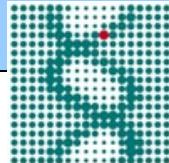


Simulation studies in EGEE grid (I)

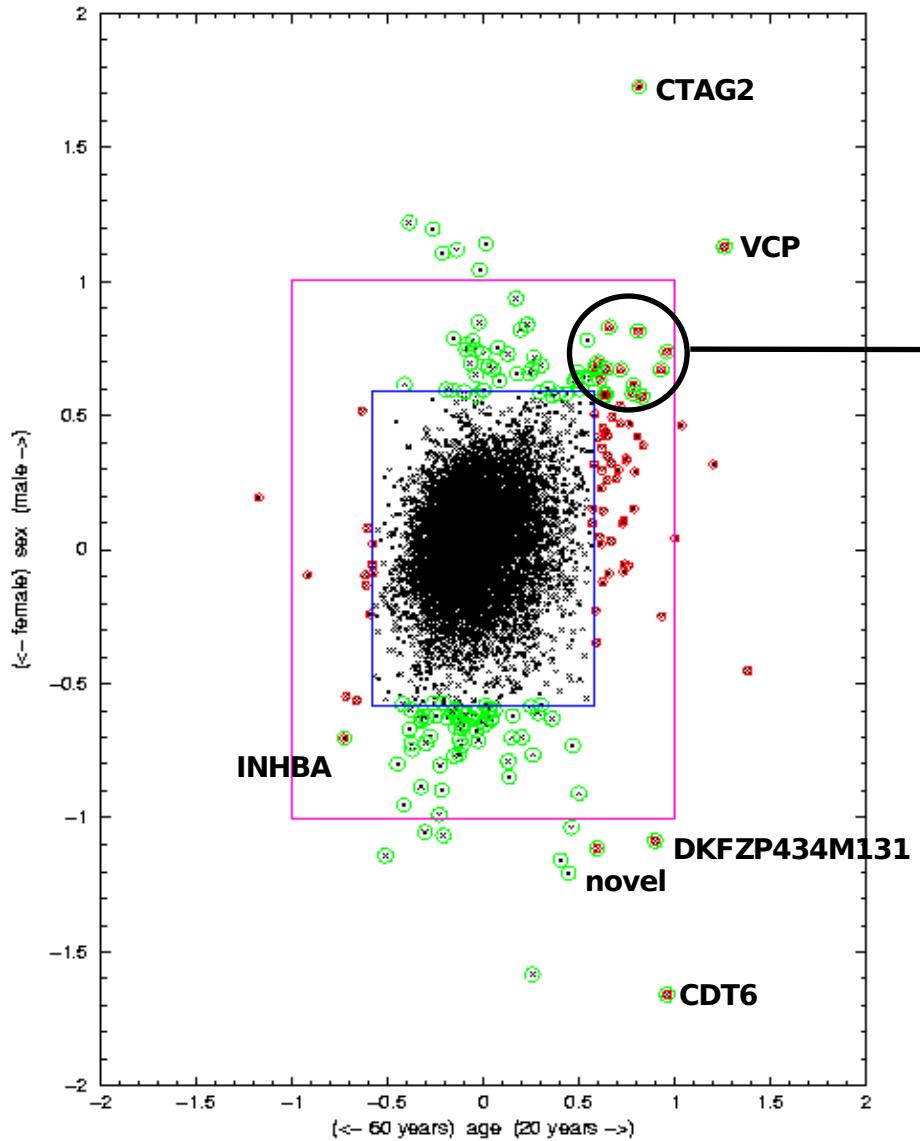
Model system



- Pure Metabolic Model: e.g. from KEGG (>1400 reactions)
- Metabolic & Signal-Transduction pathways: e.g. from Reactome (>1500)



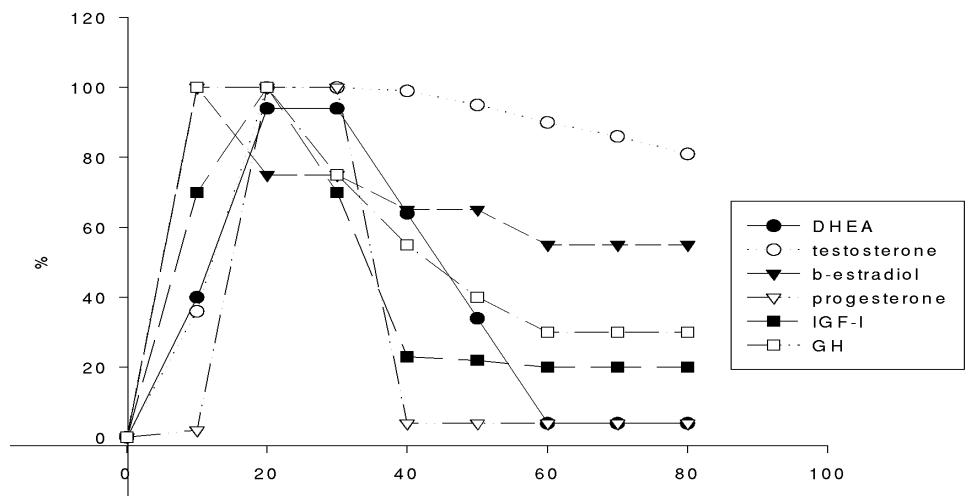
Gene expression – modelling and simulation (I)



HNRPU
novel
novel
ACTN1
HLA-C
KIAAO090
BRUNOL5
novel
EEF2
FLJ12592
MAP3K3
NXN
DHRC7
C20orf172

Skin ageing project:
MPIMG (James Adjaye)
Charite CBF
Dermatology
(Prof. Christos Zouboulis)

Serum levels of hormones decline with age in human individuals:

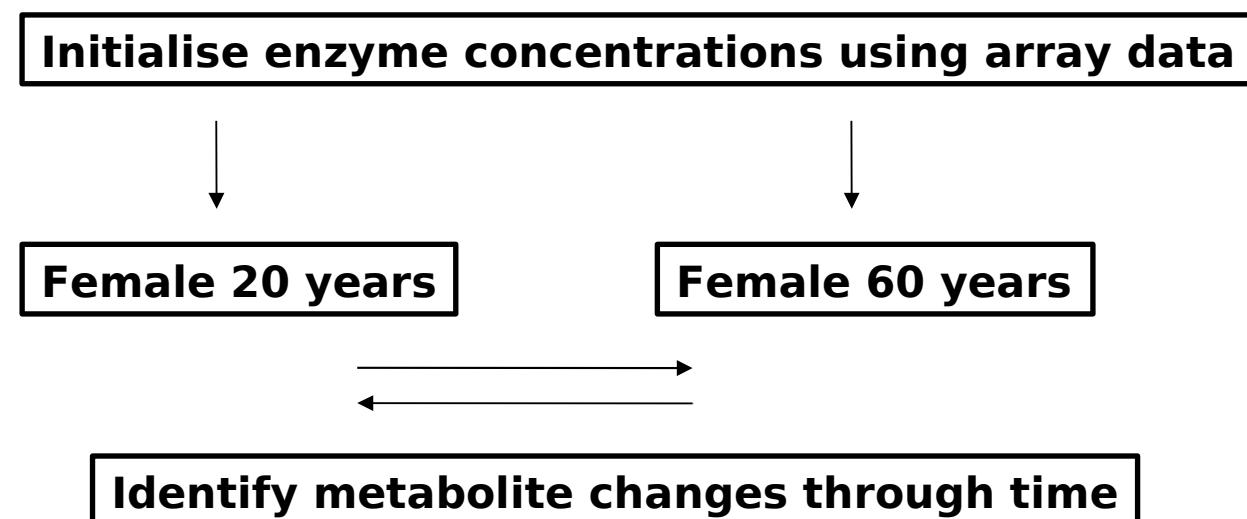


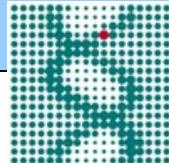


Gene expression – modelling and simulation (II)

KEGG database (<http://www.genome.ad.jp/kegg/kegg2.html>): 1,104 enzymes

- Ensembl chip: 745 (67%)
- Metabolic profiling of conditions (Example: Skin ageing project)
 - Condition 1: hormone-induced cell lines mimicking female 20 years old
 - Condition 2: hormone-induced cell lines mimicking female 60 years old





Gene expression – modelling and simulation (III)

1. Populate the metabolic reactions from KEGG (~1,600 objects and ~2,300 reactions)
(for example Carbohydrate Met., Energy Met., Lipid Met.); determines network topology

2. Fit a probability density for the initial concentrations (derived from array data):

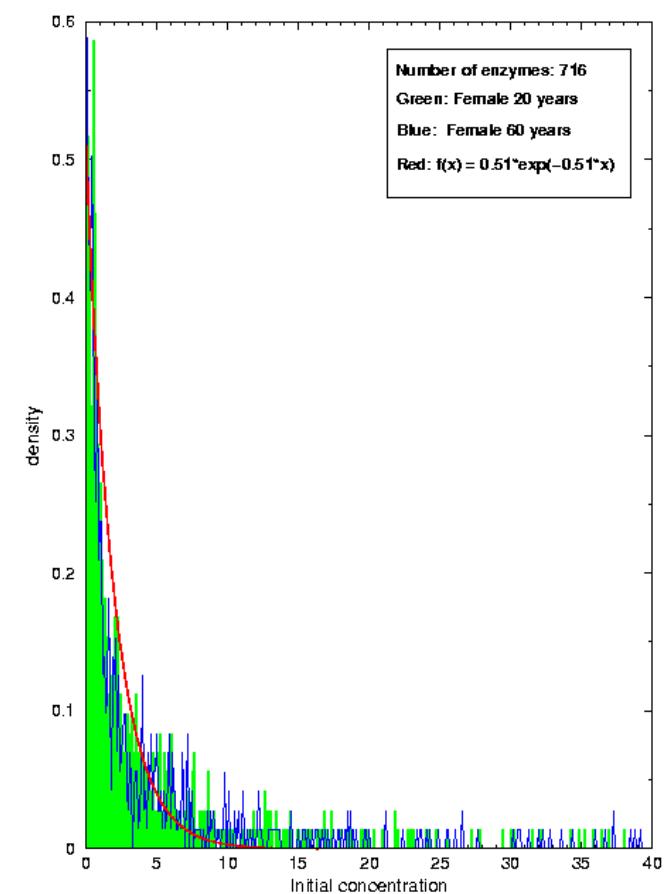
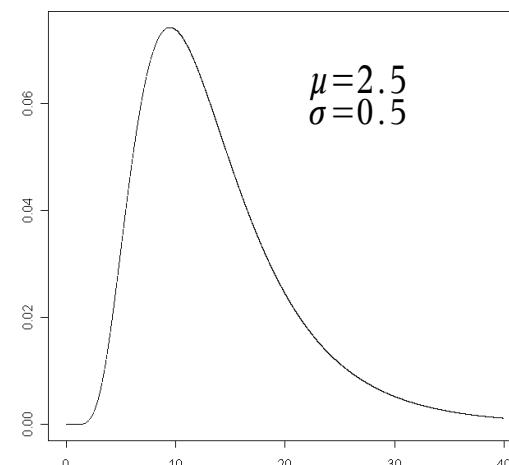
$$f(x) = 0.51 e^{-0.51x}$$

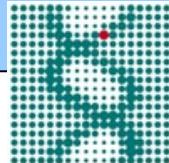
3. Assume a probability density for the kinetic constants

4. Run time series for the two conditions

5. Repeat step 3. and 4. twenty times

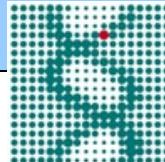
6. Identify changes in metabolite concentrations



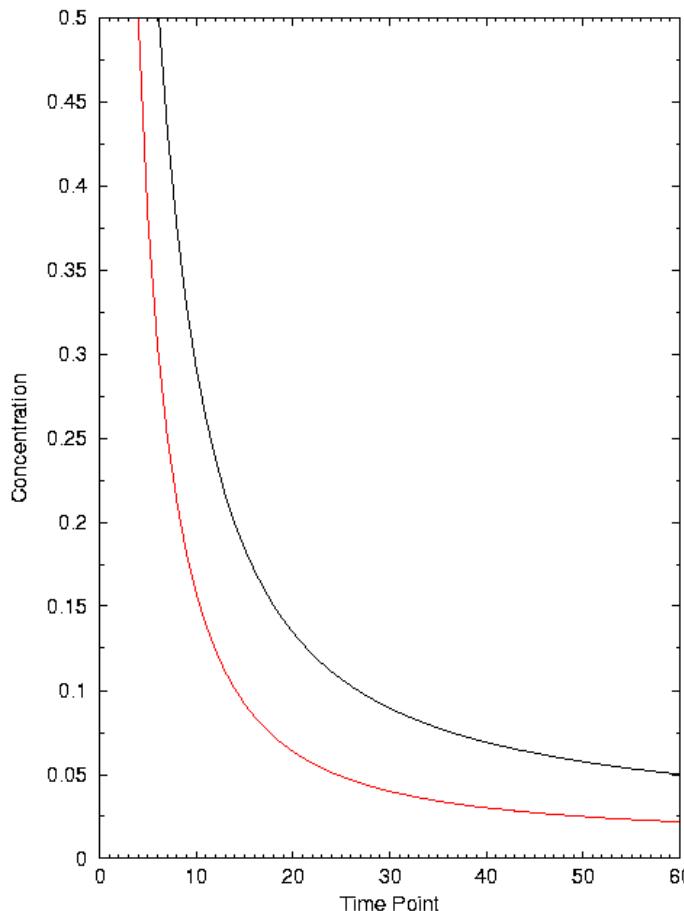


Gene expression – modelling and simulation (IV)

| | | | |
|------------------------------------|------|-----------|---|
| 1. Squalene | 2.16 | decreased | Passi, S. et al. (2003) <i>Biofactors</i> 18:289-297, Andersson, M. et al. (1995) <i>Mech Ageing Dev</i> 85:1-14. |
| 2. Leukotriene B4 | 1.60 | decreased | Viggiano, D. et al. (1994) <i>Pediatr Res</i> 36:60-63. |
| 3. Carnosine | 0.51 | increased | Hyland, P. et al. (2000) <i>Mech Ageing Dev</i> 121:203-215. |
| 4. 3-hydroxy-3-methyl-glutaryl-CoA | 0.64 | increased | Pallottini, V. et al. (2003) <i>Biogerontology</i> 4:371-378. |
| 5. Ubiquinone | 1.00 | unchanged | Andersson, M. et al. (1995) <i>Mech Ageing Dev</i> 85:1-14. |
| 6. 4-hydroxybenzoate | 1.06 | unchanged | Andersson, M. et al. (1995) <i>Mech Ageing Dev</i> 85:1-14. |



Gene expression – modelling and simulation (V)



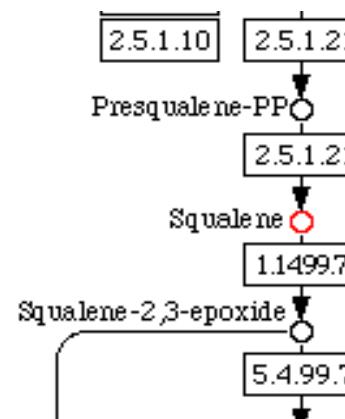
Problems:

- no steady-state analysis
- many substrates approach zero concentration

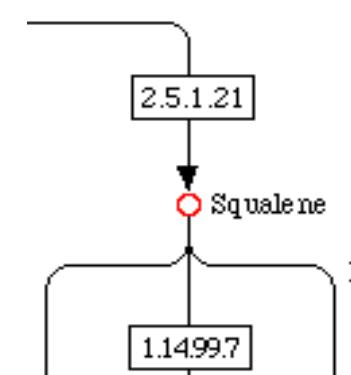
Example: *Squalene*

Metabolic Processes:

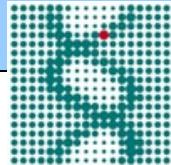
sterols, vitamin K,E biosynthesis



terpenoid biosynthesis



| | F20 | F60 | Ratio | BG-Tags | P-Value |
|--|------|-------|-------|-----------------|-----------------------|
| 2.5.1.21 FDFT1 <i>squalene synthase</i> | 8.12 | 5.58 | 1.46 | (>0.99 in both) | 4.3*10 ⁻² |
| 1.1499.7 SQLE <i>squalene epoxidase</i> | 8.30 | 11.49 | 0.72 | (>0.99 in both) | 1.28*10 ⁻¹ |



Simulation studies in EGEE grid (II)

Applications

Cancer application

Melanoma celllines:

[primary tumor vs. metastases (tumor progression) vs. control]

Homepage of ESBIC-D (EU project):

<http://pybios.molgen.mpg.de/ESBIC-D>

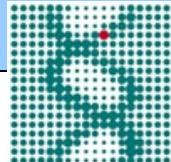
Type-2 diabetes

Mouse model (NZO):

[standard diet vs. high fat diet]

Nutrigenomik (BioProfile – BMBF – Germany):

http://www.molgen.mpg.de/~lh_bioinf/projects/Nutrigenomik/



Acknowledgement



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Remi Mollon



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