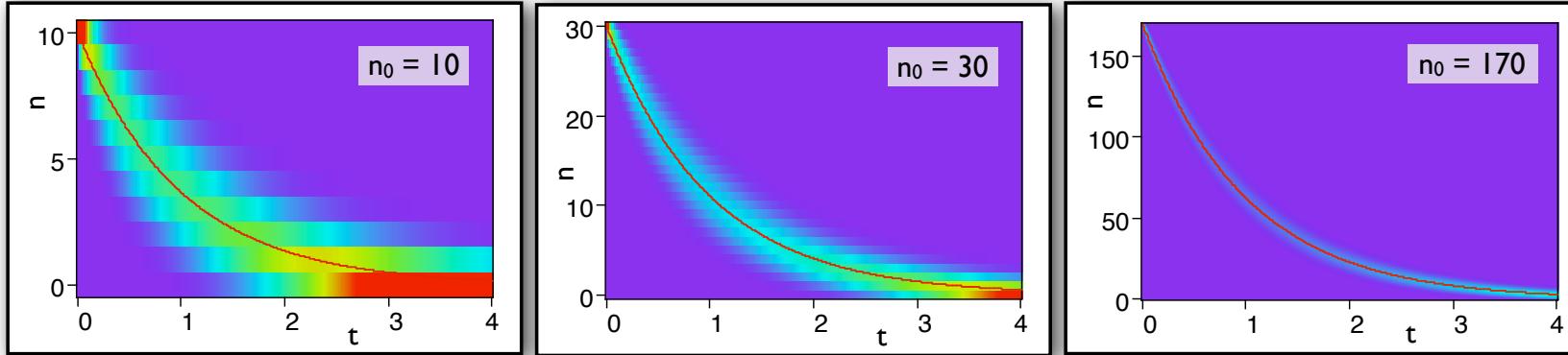


Bioinformatics 3

V24 – Molecular Stochastic Simulations & a Systems Biology Intro

Fri, Jan 27, 2012

Stochastic or Not?



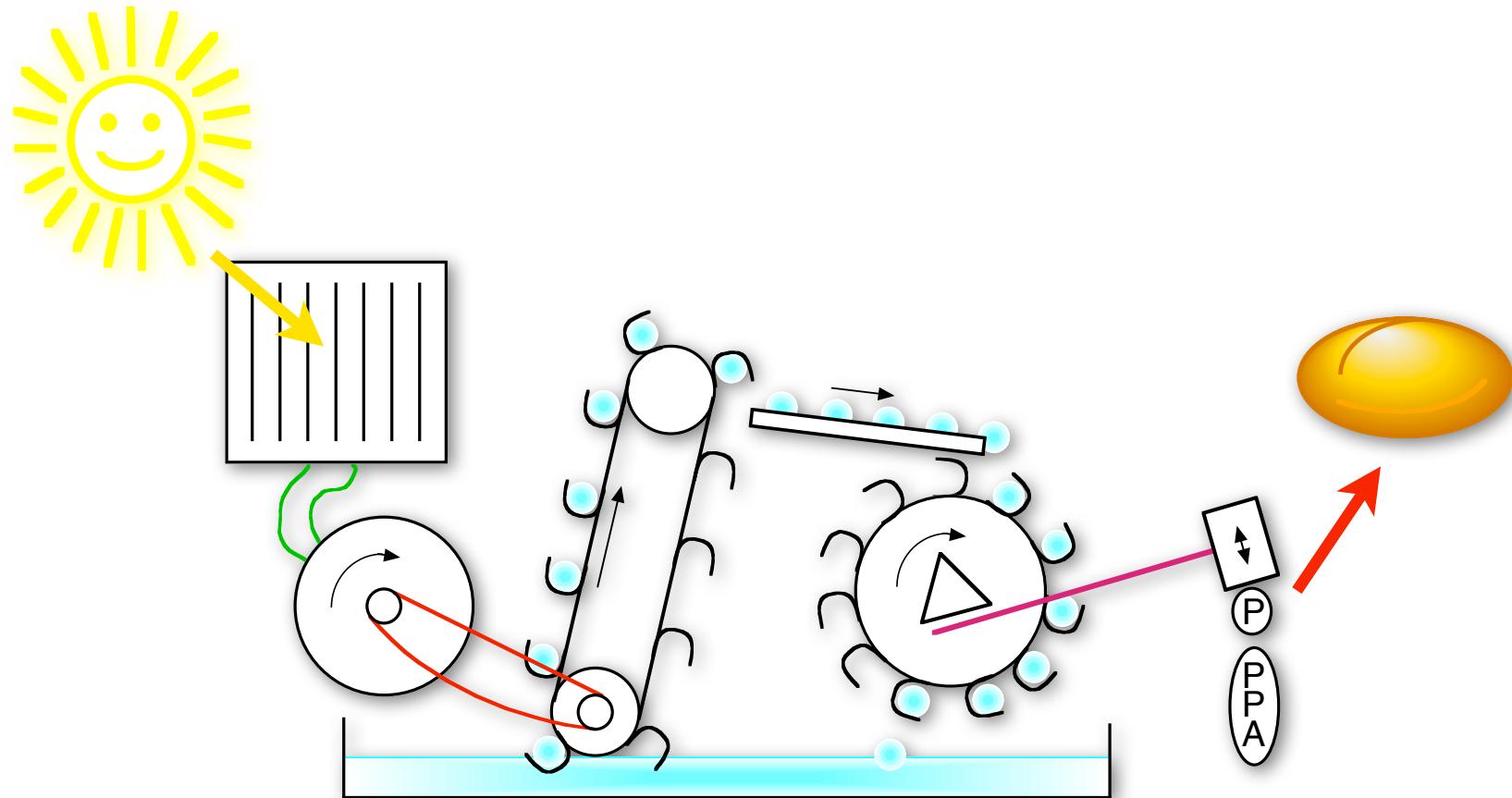
For **well-stirred chemical** systems

=> continuous is okay when the particle number variance is negligible
=> what is "negligible"?????

... noise ... different averages ... different dynamics ...

For **biological** systems with a more complicated reaction **network** topology
=> ???

Bacterial Photosynthesis



Light energy

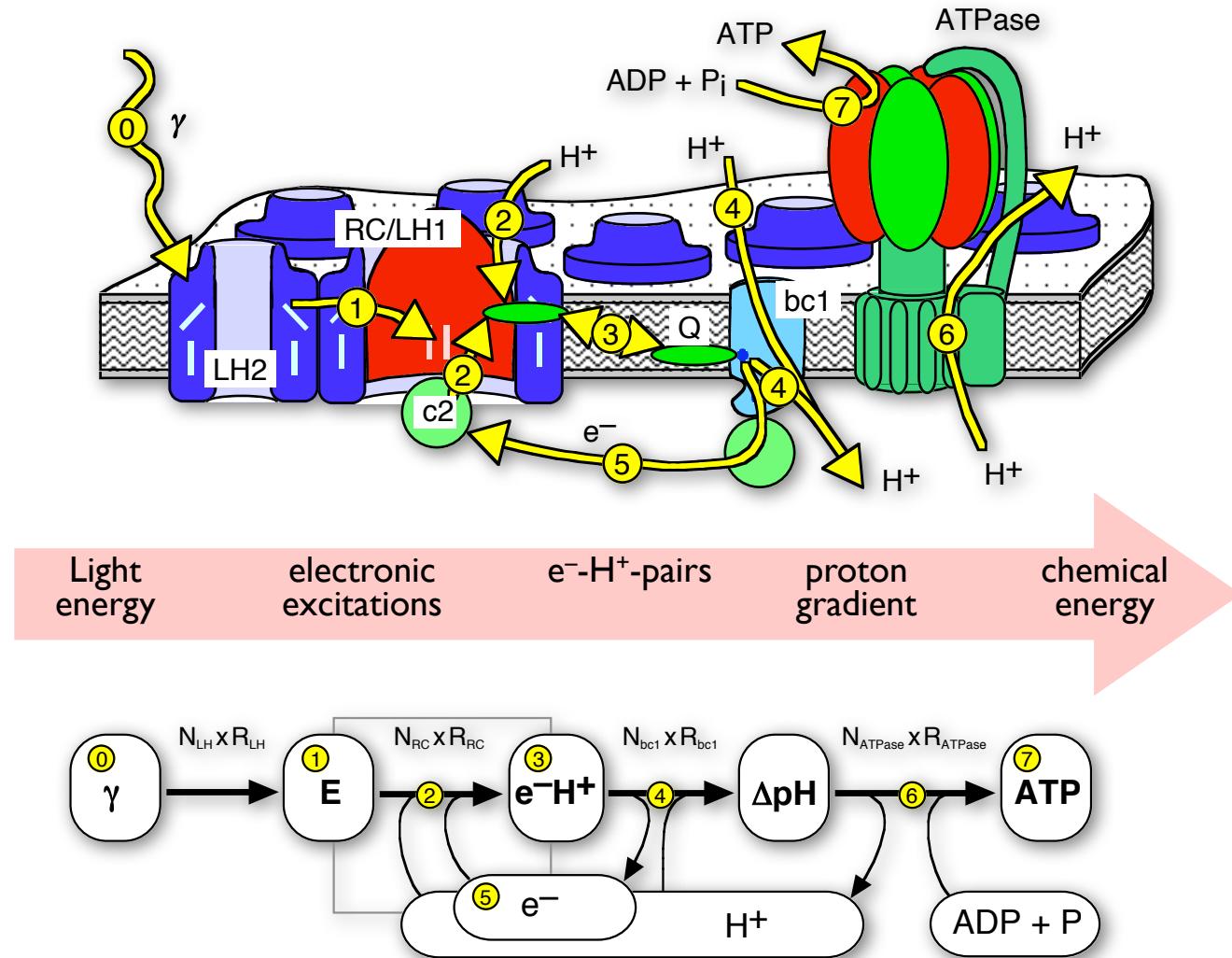
=>

(intermediates)

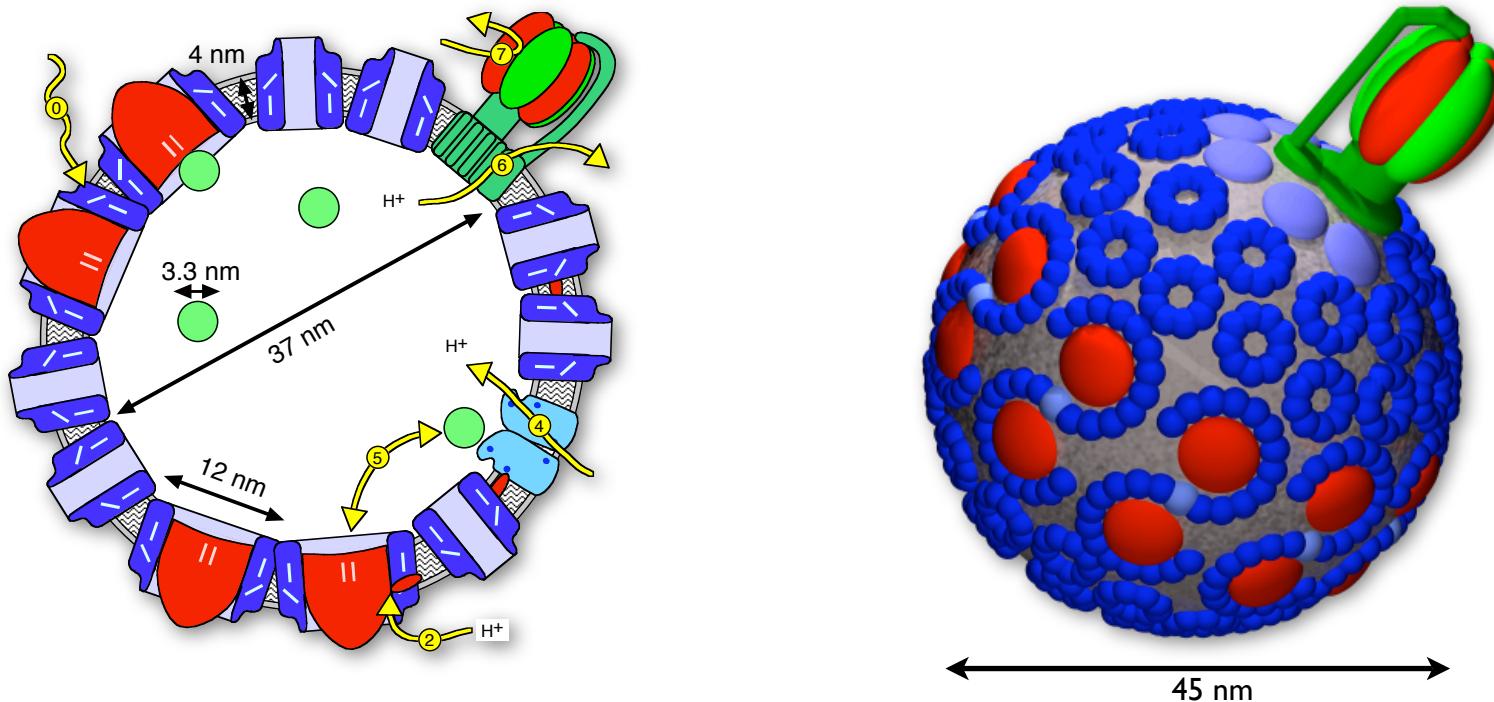
=>

Food

Bacterial Photosynthesis

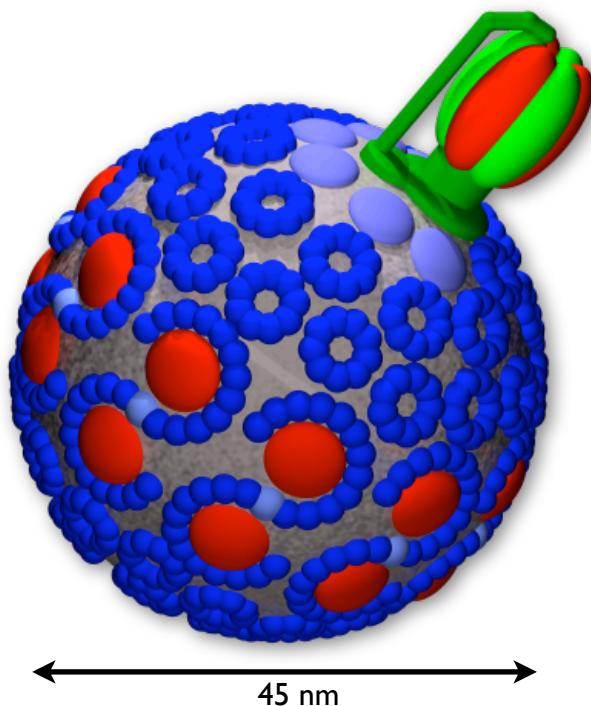


Chromatophore Vesicles



- => Simple: 4 proteins + 2 transporters + H^+ ; crystal structures & reactions
- => Small: <30 proteins + LHCs; all processes inside the vesicle
- => Closed: well defined boundary conditions for a simulation
- => Convenient: probe with light, measure spectroscopically

Densities in Chromatophores?



45 nm outer diameter
=> 1/20 H⁺ inside at pH 7
=> 1 H⁺ ≈ pH 4.1

"Density" is not an applicable concept anymore...

20 RCs per vesicle
=> 1 e⁻ transfer = 5% change

No continuous averages...

=> continuous rate equation model too macroscopic
(but, how important are the differences?)

Molecular Stochastic Model

=> Linking molecular details and macroscopic experiments

bottom-up ansatz:

start from (well defined) elementary reactions in the proteins
=> make use of extensive molecular biology knowledge

One-metabolite reactions: conditions/probabilities

=> Proteins = **building blocks** (plug-and-play)

Standardized **connectors** to metabolite pools

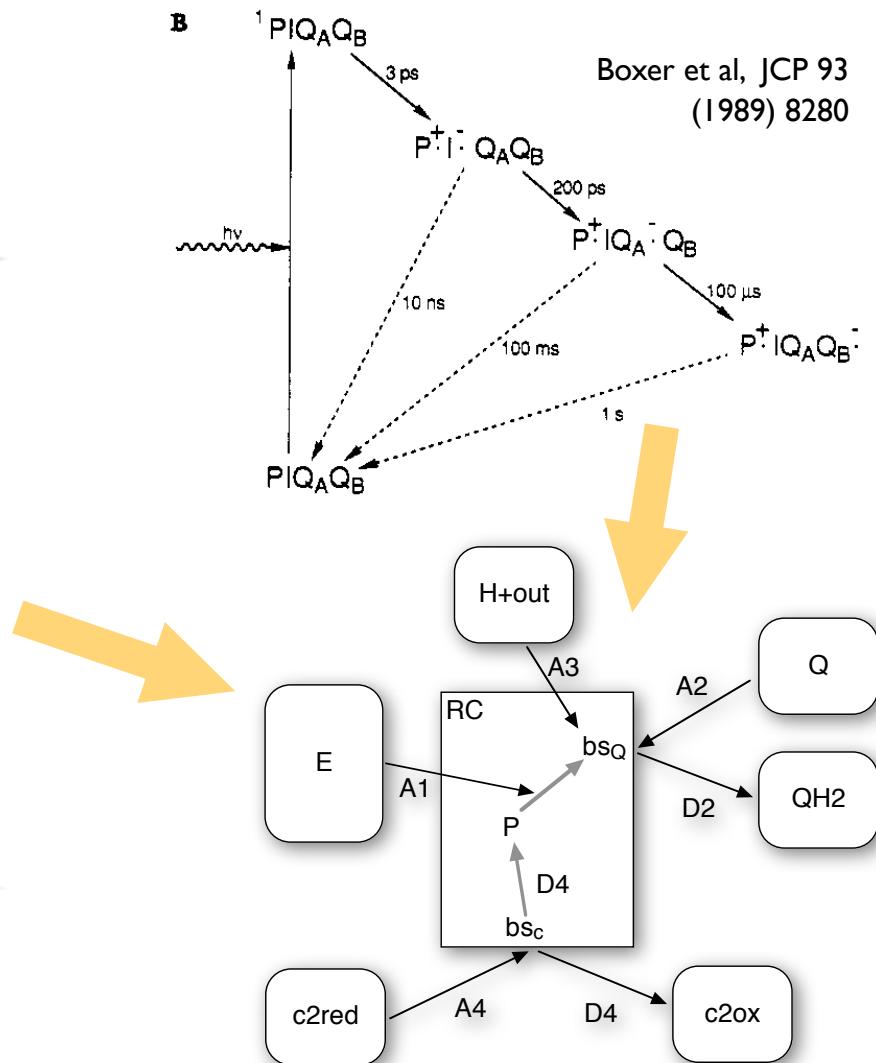
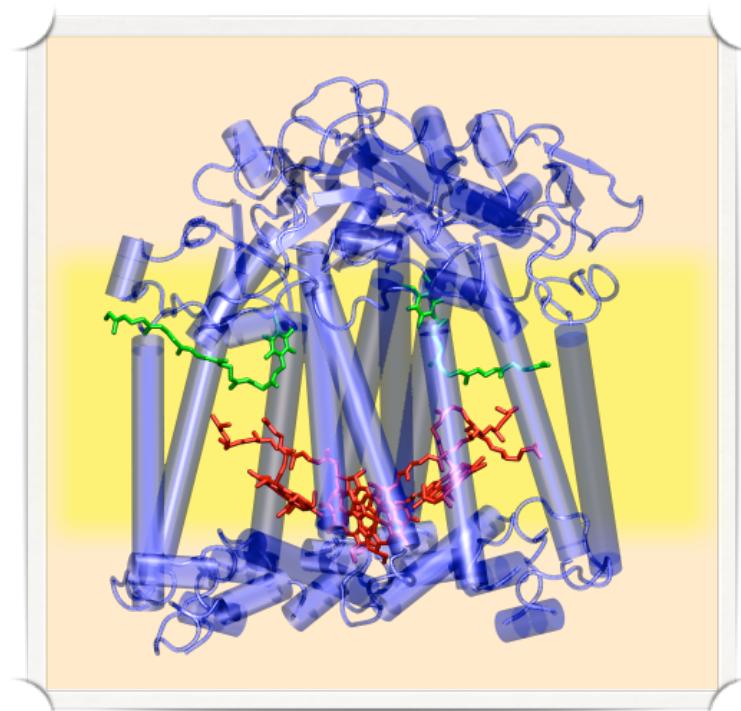
=> Modularity a la nature

=> No predefined pathways

=> Pools-and-Proteins model

Building the Reaction Center (RC)

RC: electronic excitation
=> charge transfer



Stochastic Reactions: Substrate Binding

When BS is empty => Association is possible: BS + X => BS:X

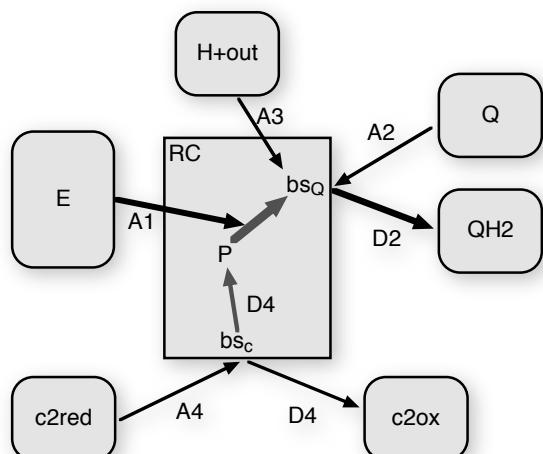
- 1) all conditions fulfilled?
- 2) chemical reaction dynamics:

Reaction rate:

$$\frac{d[\text{BS:X}]}{dt} = k_{on} [\text{BS}] [\text{X}]$$

Association-prob. per BS:

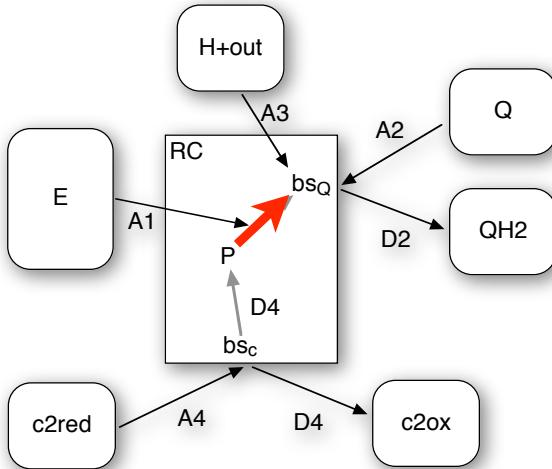
$$P_{on} = k_{on} [\text{X}] \Delta t$$



```
for each timestep t:  
  for each reaction:  
    conditions fulfilled?  
    determine probability:  
    perform reaction
```

Implementation

"...Upon arrival of an exciton an electron is translocated from the reduced special pair (P) on the periplasmic side of the RC to the bound Q_b at the cytoplasmic side. When the Q_b is loaded with two electron-proton-pairs..."



```
if (bs_Q &&
    (reg_SP == 1) &&
    (reg_Qe == 0) &&
    ((reg_QHe == 0) || (reg_QHe == 1)))
{
    if (LHPoolp->take_out(LH_kon))
    {
        reg_SP = 0;
        reg_Qe = 1;
        HInternalPoolp->put_back();
        writeInternals();
    }
}
```

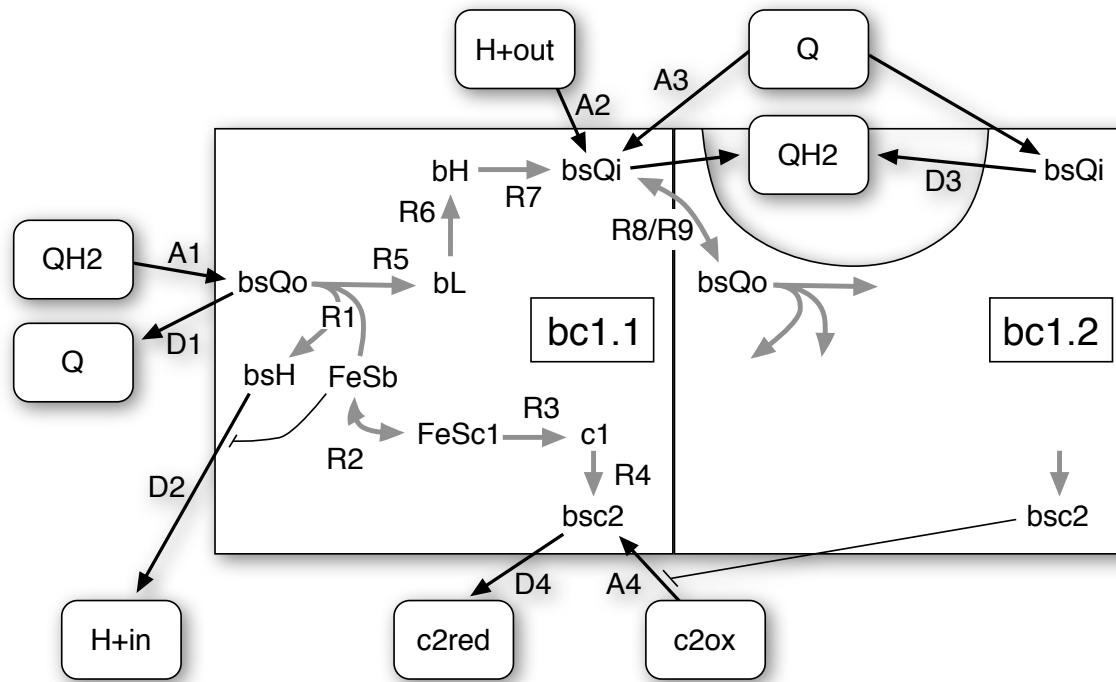
Conditions

probability

reaction

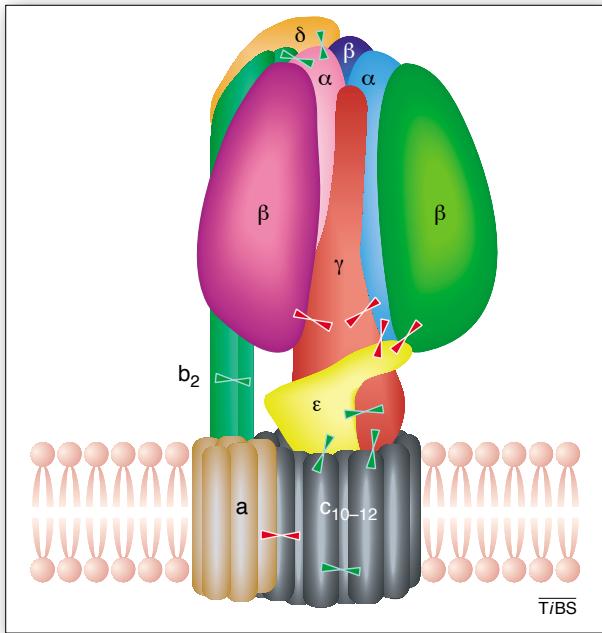
Propagate: **loop** over all **reactions** of all **proteins**
=> **complex behavior** from simple kinetics

Slightly More Complex...

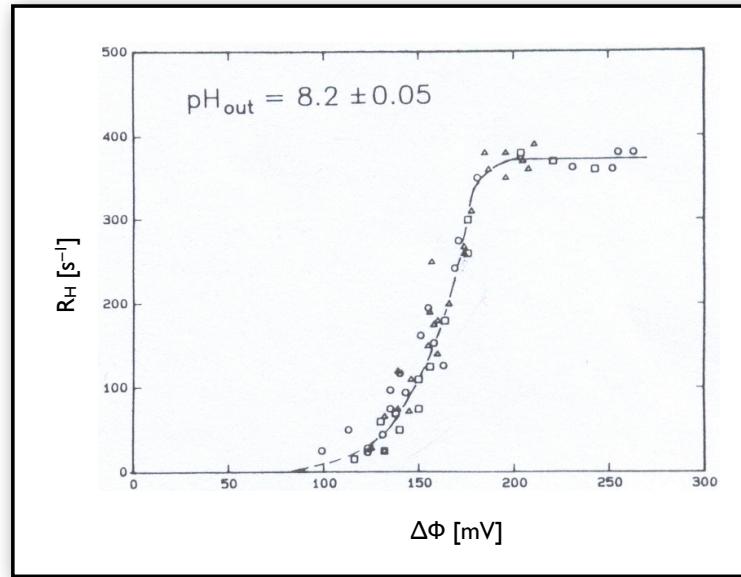


Cytochrome bc_1 dimer:
20 reactions
 2×4 binding sites
 2×11 internal variables } 28 parameters

... Or Crudely Simplified

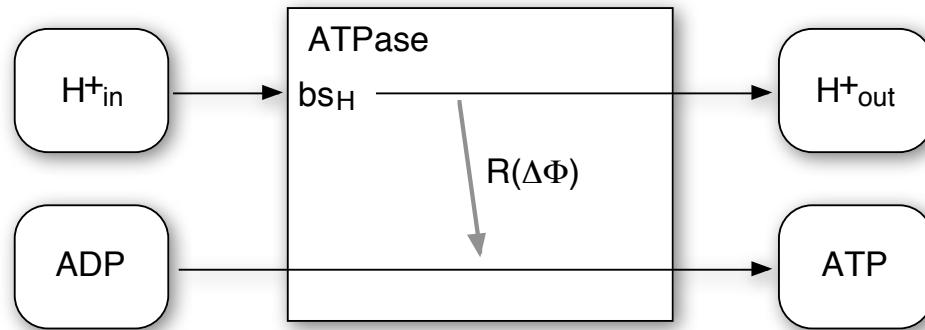


Capaldi, Aggeler, TiBS 27 (2002) 154



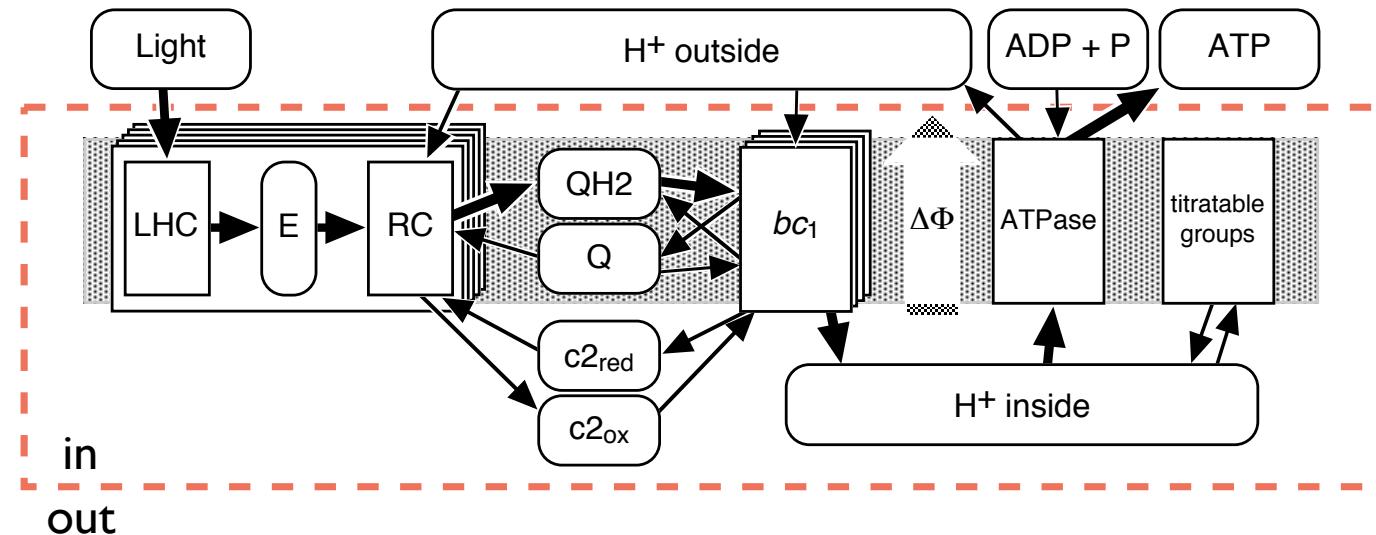
Junesch, Gräber, FEBS Lett 294 (1991) 275

I ATP every fourth H+,
characteristic fitted



Hook 'em Up: The Circuit diagram

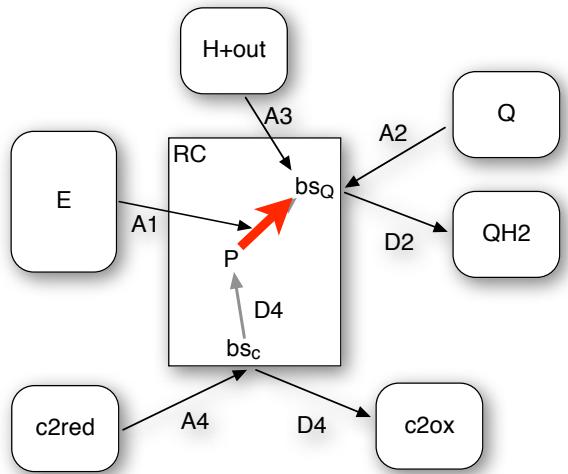
(without the internal circuitry)



holds a certain metabolite
(volume, #particles)

where the work is done
(binding sites, reactions, rates)

Combinatorial Explosion



For **one RC**:

- oxidation state of P => reduced/oxidized
- c₂ binding site => empty/occupied
- Q binding site => empty/occupied
- #(e-H-pairs) @ Qb => 0/1/2
- #(e⁻) @ Qb => 0/1

$$\Rightarrow 2 \times 2 \times 2 \times 3 \times 2 = 48 \text{ states}$$

One vesicle: 10 core complexes of 2 RCs + 1 LHC (3-4 states)

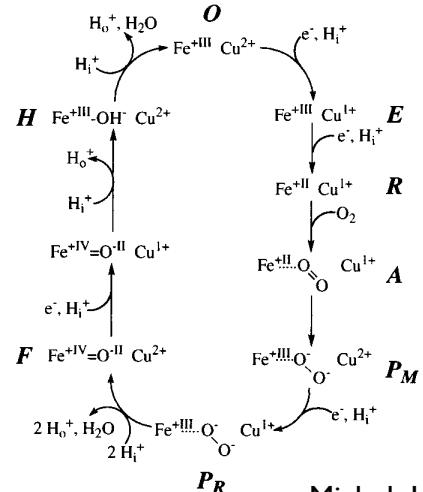
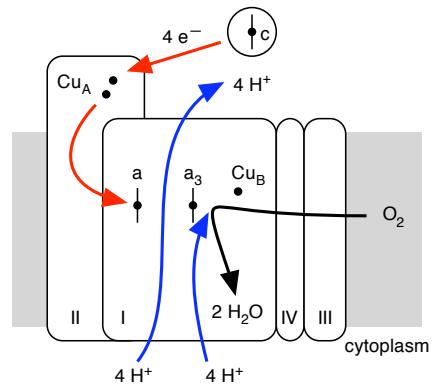
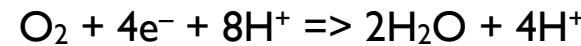
$$\Rightarrow (48 \times 48 \times 4)^{10} = 9216^{10} \approx 10^{40} \text{ states for the core complexes alone}$$

Plus 10 bcl dimers with ≈ 200 states each...

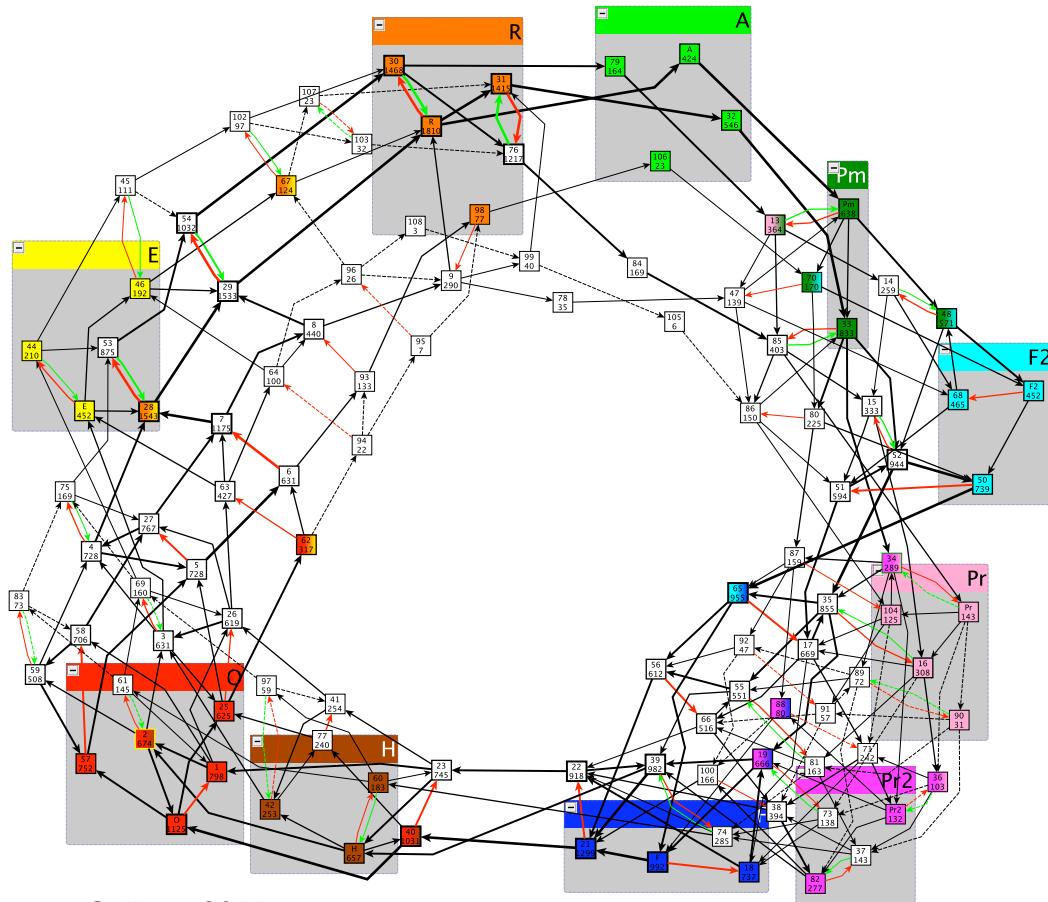
=> state selective representation of multiple protein copies impossible in state-based approach (rate equations, Gillespie)

Do What You Want...?

Cytochrome c oxidase:



Michel, 1998



Gollmer, 2011

The "Pools-and-Proteins" Model

Start from molecular biological knowledge

=> encapsulated, **independent** protein **building blocks**

=> **connected** via their metabolites

=> direct implementation (it's not Gillespie!)

- no combinatorial **explosion** (complexity contained locally)
- **complex behavior** from simple kinetics (dynamics!)
- **no network** prescribed
- different **levels of detail** inside the proteins
- **recycle proteins** in many projects

Vesimulus: Why not Gillespie?

Gillespie:

Based on states
=> complexity!

Based on (pre-averaged) rate equations

One reaction at a time

Efficient, exact

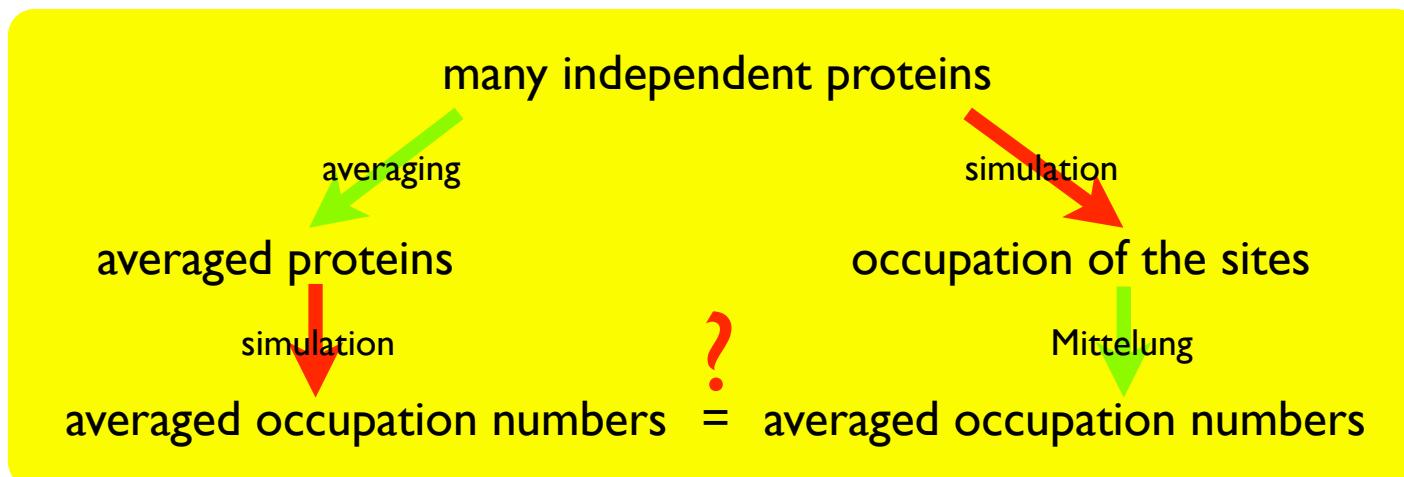
Pools-and-Proteins:

Occupation of independent sites
=> use "states" as filter for analysis

Averaging only during analysis

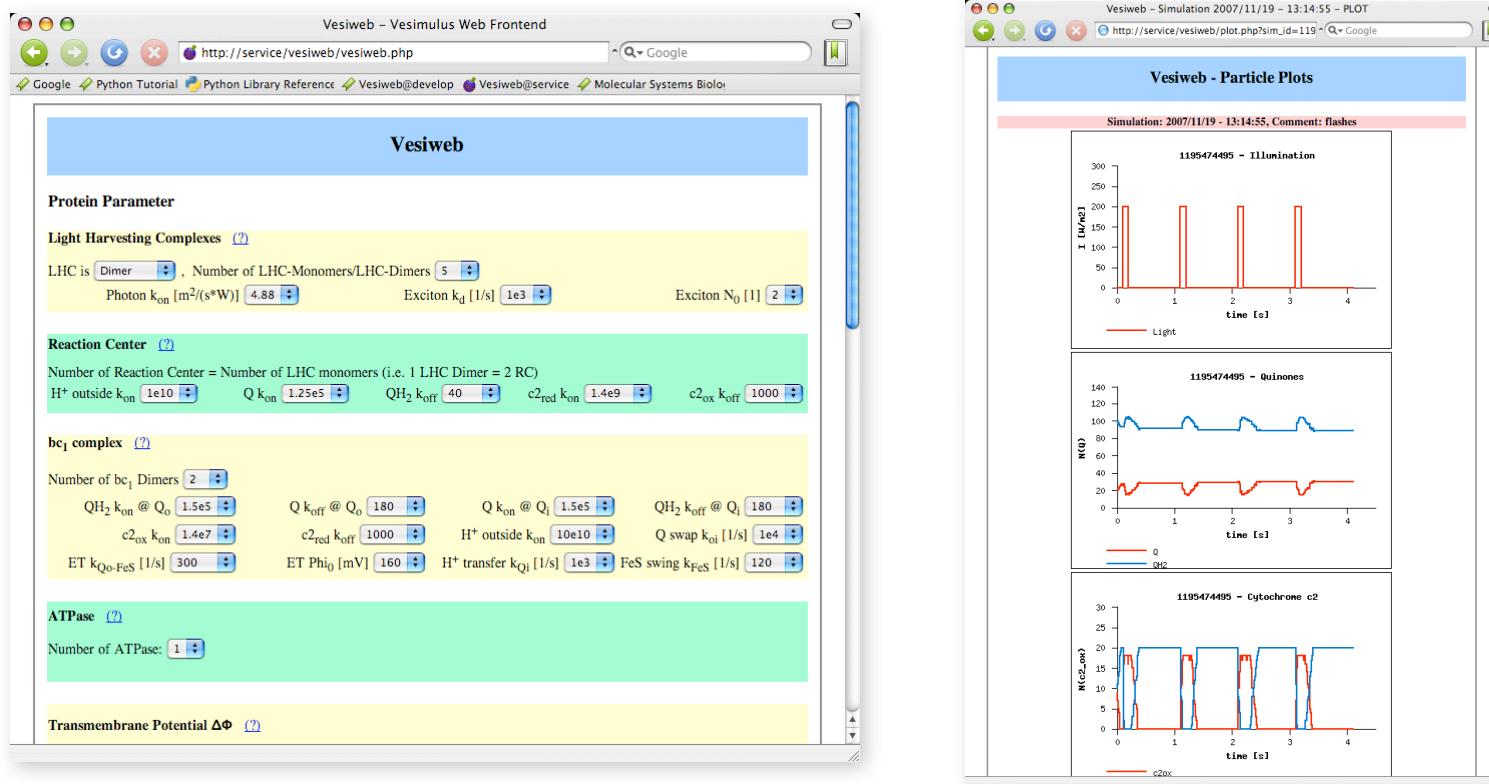
Multiple reactions per timestep

natural modelling



Web Interface

Play with photosynthesis: service.bioinformatik.uni-saarland.de/vesiweb



Used in classroom:
=> **stochastic effects** in a (small) biological system

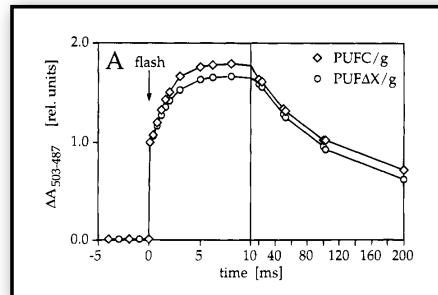
Systemic Parametrization

15248

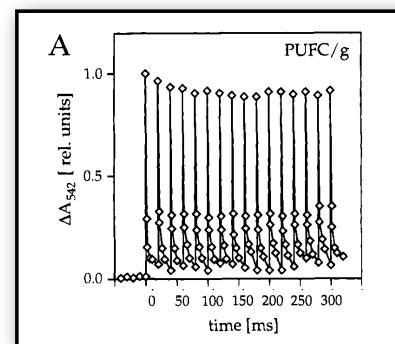
Role of the PufX Protein in 2. PufX Is Required for Reaction Center

Wolfgang P. Barz,^{‡,§} Francesco Francia,^{||} Giovanni Venturoli,^{||} B. Andrea Melandri,^{||} André Vermélio,[†] and
Dieter Oesterhelt^{*,‡}

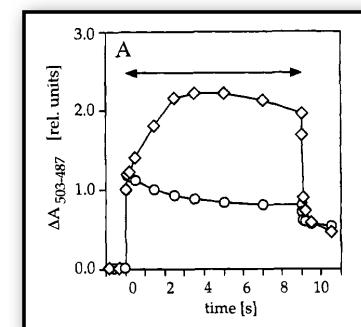
Max-Planck-Institute for Biophysical
Chemistry, Göttingen, Germany



•••

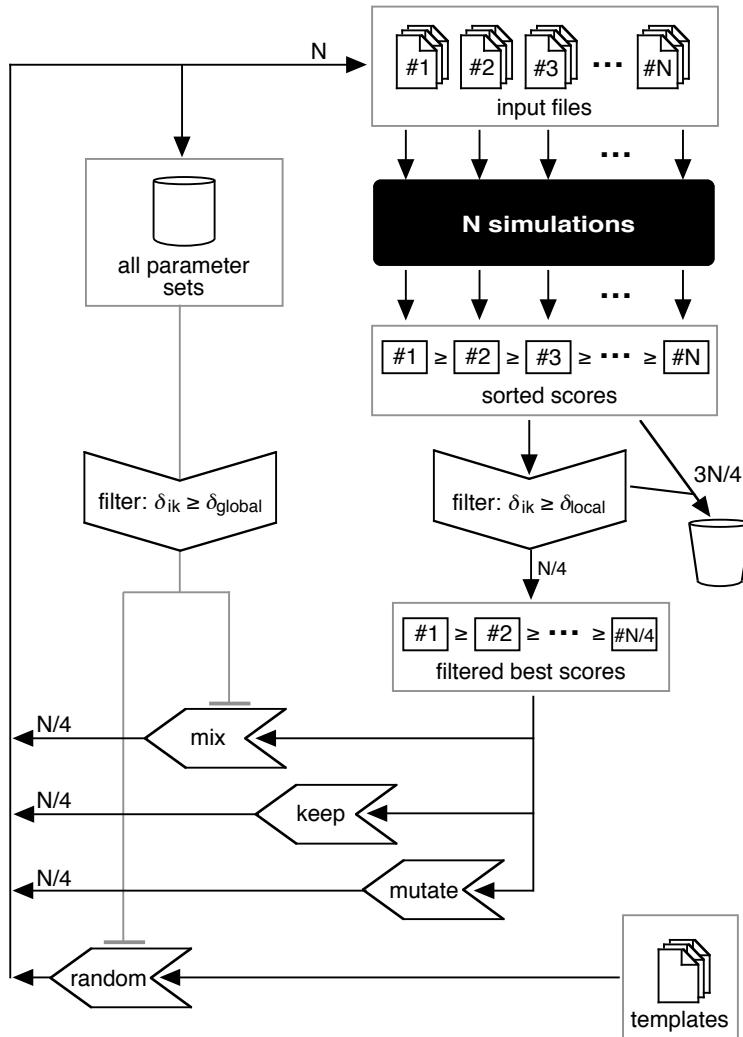


•••



$\Delta\Phi_{el}$ – cytochrome c oxidation – RC special pair oxidation – #QH

Evolutionary Parameter Optimization



Scoring:

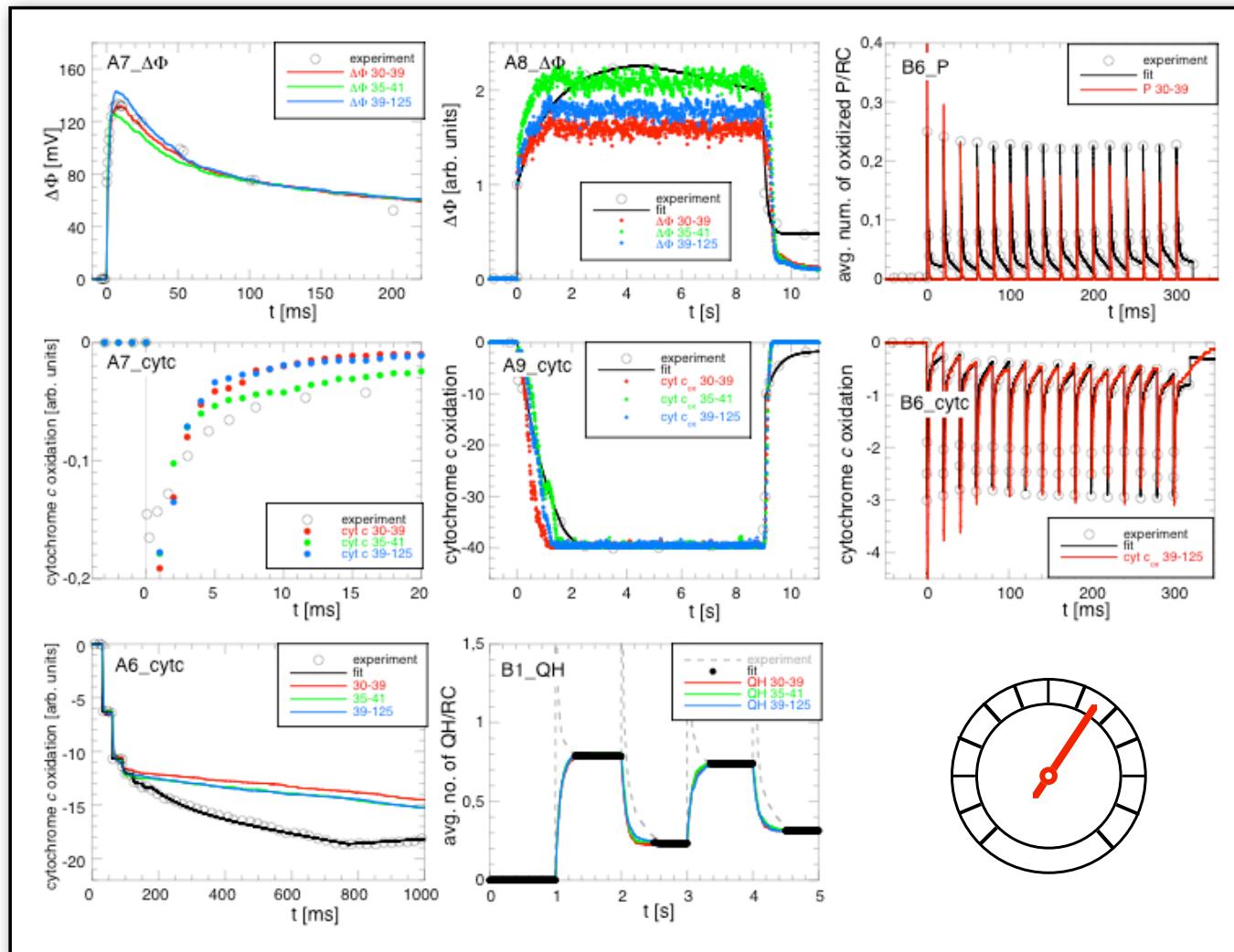
- 9 dynamic experiments
- squared distance d_i^2 to exp. scores $s_i = 1 / d_i^2$
- masterscore $S = \prod s_i$

Optimization:

- 27 parameters of the 45
- two runs with 17 and 12 parms
- 41 generations of 800 individuals
=> 32800 parameter sets
- 3500 CPU-h

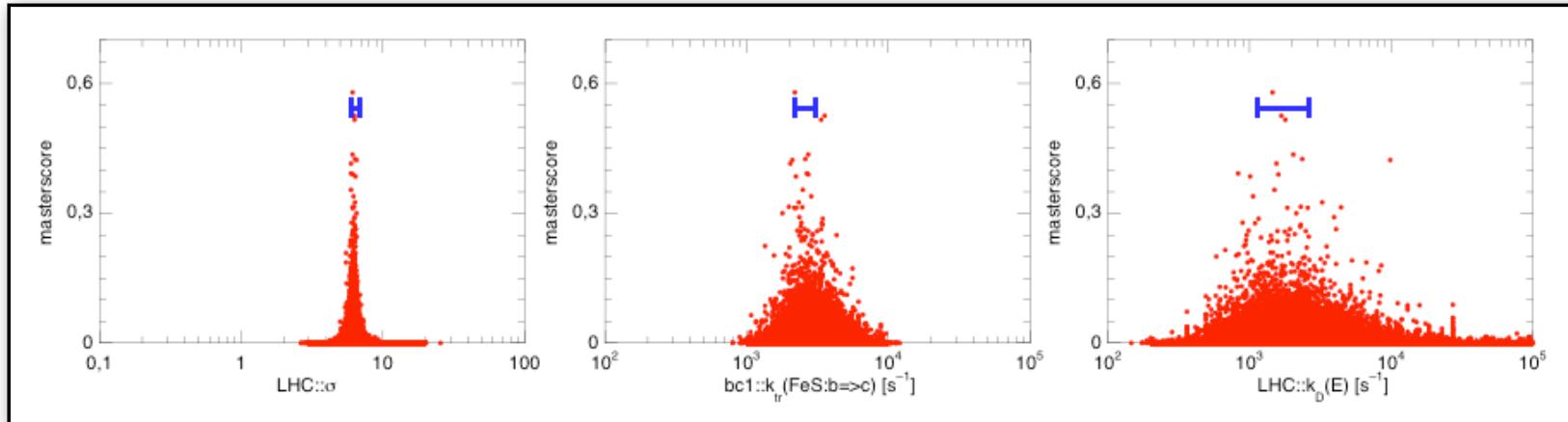
On a grid: $32800^{1/17} = 1.84$

Yes, It Works.



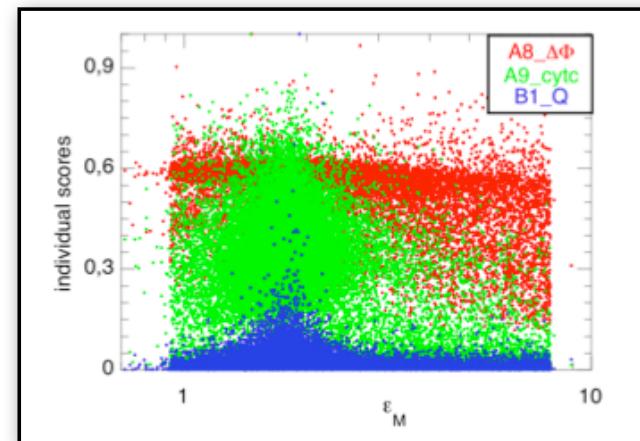
Data Analysis

Master score vs. parameter values => optimal **values** and **sensitivities**

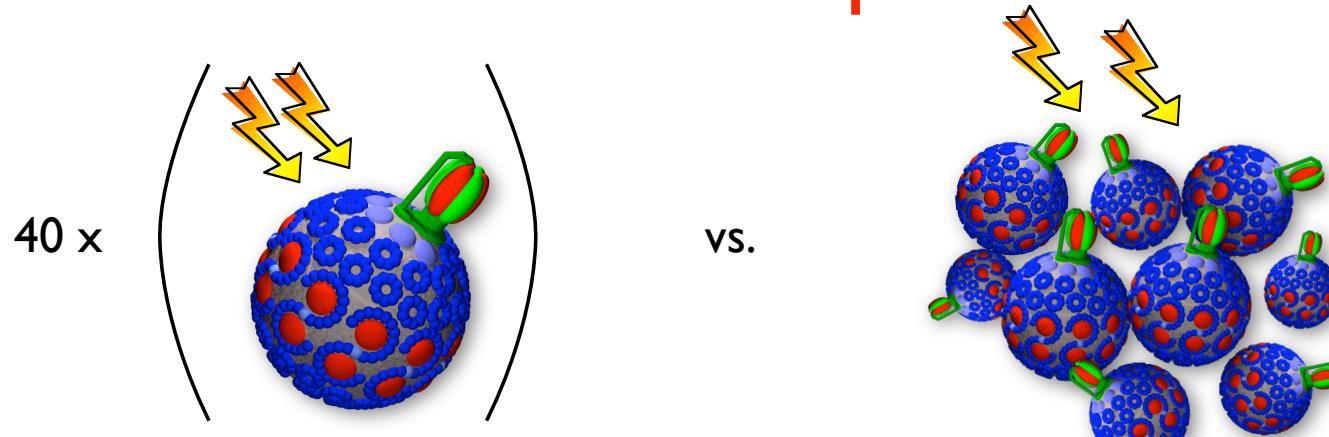


Individual scores vs. parameter values
=> relative **importance** of each
of the experiments

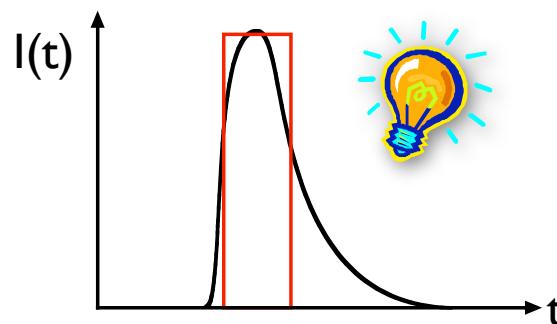
=> **Consistent** set of kinetic **parameters**
for the chosen model and scenarios



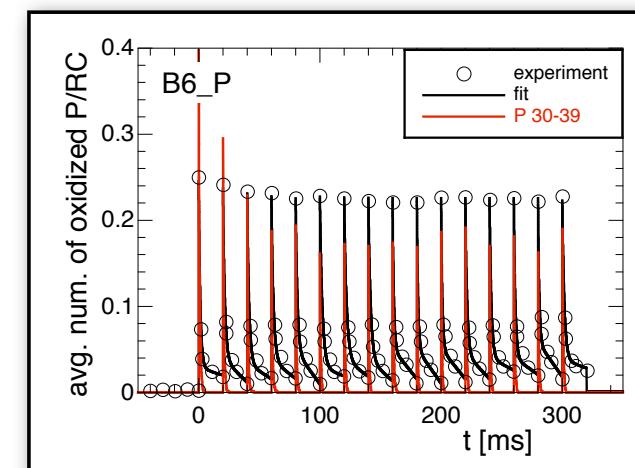
Simulation vs. Experiment



=> Effects of **different sizes** or stoichiometries?



=> Time course of the **flashes**?

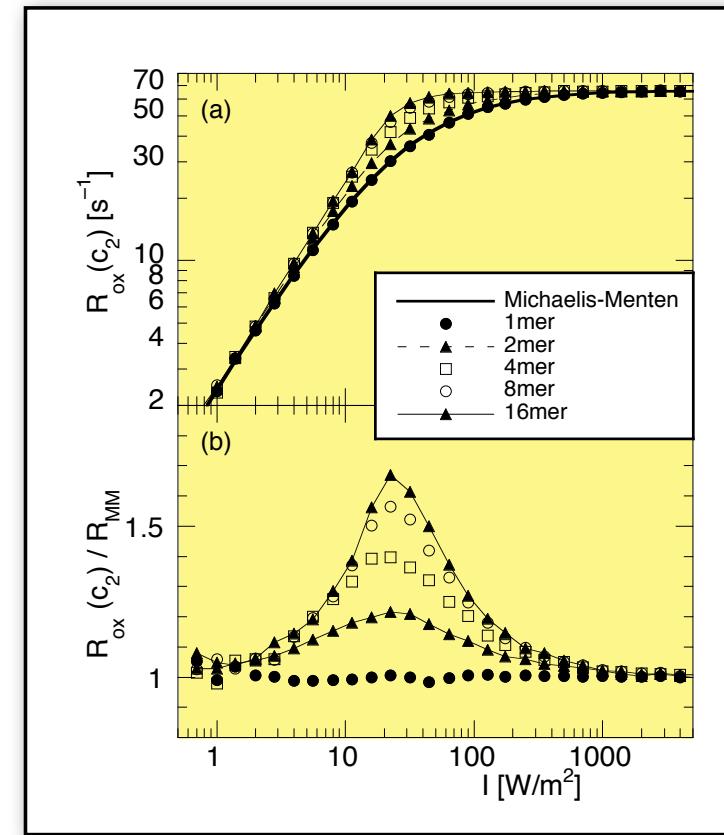
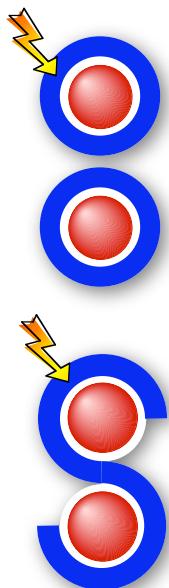


Example I: Connectivity Matters

Monomeric vs. dimeric LHI

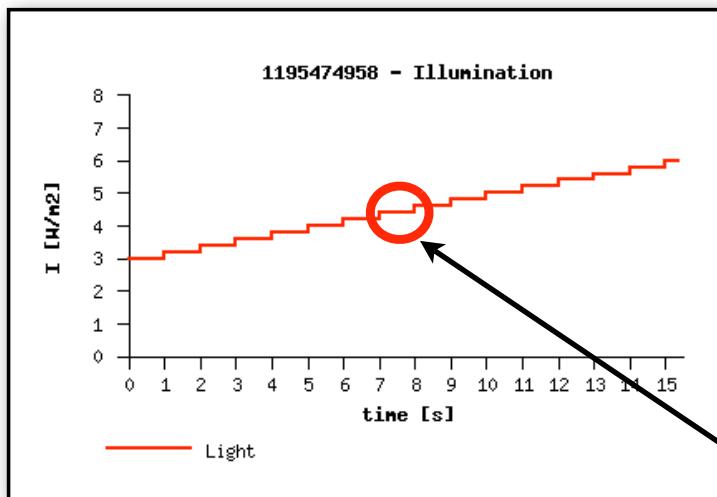
model connectivity in N -mer by common exciton pool for N LHCs and RCs

=> stochastic effects ???



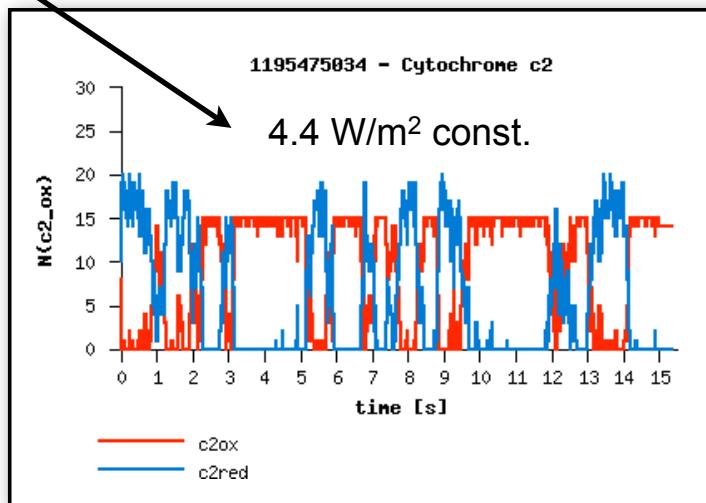
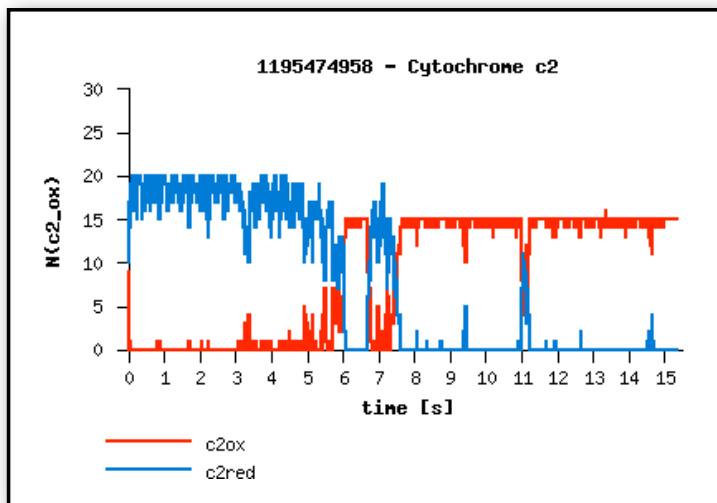
efficiency increased through more continuous exciton supply

Example 2: c_2 Oxidation State



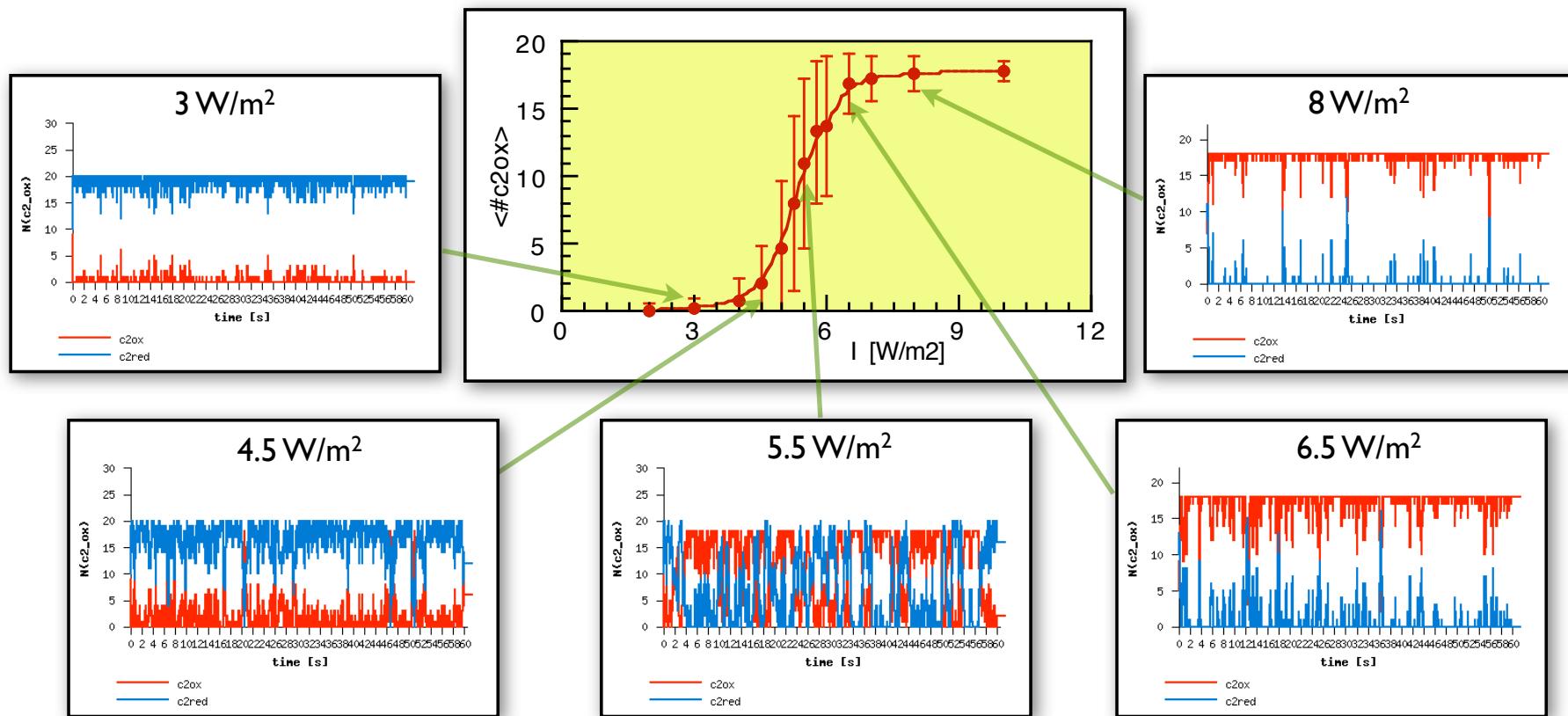
slowly increase light intensity
=> change of the c_2 oxidation state

No sharp transition
=> fluctuations in the proteins' turnover



Averaged Response Curve

Run simulation with 5 RC/LHC dimers and 2 bcl dimers for 60 sec. at const light



=> Softened response with large fluctuations in the intermediate regime

Omicomics??

In biology: **trend** to have well **separated areas** of research

Modern fields encountered in this lecture:

Protein complexes => proteomics

Genes and their regulation => genomics

Protein transcription => transcriptomics

Metabolic networks => metabolomics

regulomics, "buzzwordomics..."

Overheard on a conference: "This is not proteomics what *they* are doing..."

"Fields" of biology <=> *omics = "the science of *"

Once Upon a Time...

Do Not Miss:

Prof. Dr. Matthias REUSS
Institut für Bioverfahrenstechnik
(Biochemical Engineering),
Universität Stuttgart

Tomorrow in the ZBI-Kolloquium
E2.I SRI, 17:00



**"Dynamic modeling of the central metabolism of *E.coli* –
Linking metabolite and regulatory networks"**

=> Combining the various -omics of systems biology to recover the whole

=> what is "Systems Biology"???

Systems Biology — What's That?

Notes from a conference:

9th Joint EMBO/EMBL Conference:

"Systems and Synthetic Biology: Scientific and Social Implications"

7.-8. Nov. 2008, EMBL HD

http://www.embl.de/aboutus/science_society/conferences/conference_2008/programme/index.html

Marvin Cassman:

"SB = modeling dynamic networks coupled to experiments"

Adriano Henney (AstraZeneca):

**"Systems biology and drug discovery":
Reductionist approach to drug development
=> poor rate of success
information != knowledge
=> from reductionist to integrated approach**



Biology vs. Science?

Evelyn Fox Keller (MIT)

Theor. Physics => Bio+Physics => Philosophy of science



"Systems biology: new paradigm or just fashion?

To some, the recent enthusiasm around Systems Biology might seem to reflect merely a passing fad; to others, the opportunity to apply familiar techniques to a new arena; and to still others, the occasion for deep reflection about what disciplines that have been historically isolated from the life sciences might have to offer to the study of biology. In this paper, I focus on the last of these options, looking in particular at the tension between different cultural traditions regarding the place of simplicity and complexity in scientific analysis."

Systems Biology: Definitions

Prof. Mark W. Kirschner
Prof. of Systems Biology
Harvard Medical School



Indeed, I am a biologist. One or two is probably among us now. However, if forced to provide some kind of label for systems biology, I would simply say that systems biology is the study of the behavior of complex biological organization and processes in terms of the molecular constituents. It is built on molecular biology in its special concern for information transfer, on physiology for its special concern with adaptive states of the cell and organism, on developmental biology for the importance of defining a succession of physiological states in that process, and on evolutionary biology and ecology for the appreciation that all aspects of the organism are products of selection, a selection we rarely understand on a molecular level. Systems biology attempts all of this through quantitative measurement, modeling, reconstruction, and theory. Systems biology is not a branch of physics but differs from physics in that the primary task is to understand how biology generates variation. No such imperative to create variation exists in the physical world. It is a new principle that Darwin understood and upon which all of life hinges. That sounds different enough for me to justify a new field and a new name. Furthermore, the success of systems biology is essential if we are to understand life; its success is far from assured—a good field for those seeking risk and adventure.

Cell 121 (2005) 503

V 24 – 31

SB — An "Official" Definition (2005)



Complete report @ <http://www.wtec.org/sysbio/>

- Contents:**
1. Executive Summary and Introduction
 2. Data and Databases
 3. Network Inference
 4. Modeling and Network Organization
 5. Systems Biology in Plant Research
 6. Education, National Programs, and Infrastructure in Systems Biology

From the "Executive Summary"

Marvin Cassman (2005: Institute for Quantitative Biomedical Research):



BACKGROUND

Systems biology has become a major force in the past five to seven years. As with all new developments in science, the emergence of new approaches is a result of limitations in the existing model, in this case the limitations of molecular biology. For the past 40 years the paradigm for predicting phenotype has focused on single gene defects. This extraordinarily powerful approach has been the major contributor to an understanding of the function of individual genes and proteins. It seems less likely that it will yield an understanding of complex biological behavior, from individual cellular activities such as motility to the operation and integration of organ systems.

=> global view of the cell instead of focus on isolated proteins

All this interest has emerged despite the inability to arrive at a consensus definition of systems biology. Elements that appear in virtually all definitions are “networks,” “computation,” “modeling” and often, “dynamic properties.” For the purposes of this study the objective of systems biology has been defined as the understanding of network behavior, and in particular their dynamic aspects, which requires the utilization of mathematical modeling tightly linked to experiment. This involves a variety of approaches, such as the identification and validation of networks, the creation of appropriate datasets, the development of tools for data acquisition and software development, and the use of modeling and simulation software in close linkage with experiment, often done to understand dynamic processes. Of course, the definition becomes ambiguous

=> dynamic networks of all kinds

SB @ D

2006 founded by the BMBF:

FORSYS = Forschungseinheiten der Systembiologie

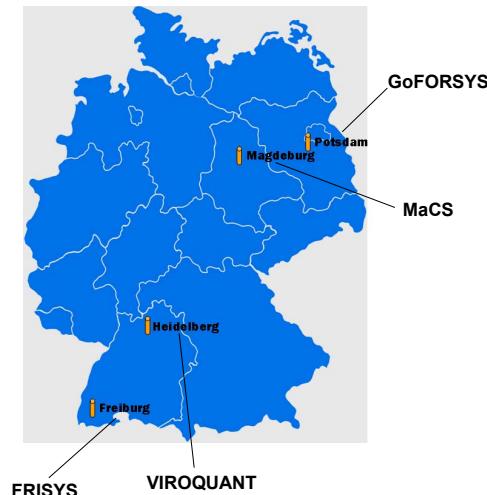
- 4 "FORSYS-Zentren" + 12 "FORSYS-Partner":



=> network methods



=> viruses



FRISYS
Freiburg Initiative for Systems Biology

=> regulation

GoFORSYS

=> plant physiology

- 2007 – 2011: 45 Mio € for FORSYS-Zentren
35 Mio € for FORSYS-Partner

Yet Another Definition(?)

From <http://www.forsys.net/background.html>:

tremendously emerged to a novel by far more powerful level than ever.

Interestingly, the systems biology community still hasn't agreed on a distinct and generally accepted definition of the term systems biology. Some scientists consider systems biology to be a field of study on the interaction between the components of a biological system and how these components generate form and function of that particular system, organ or entire organism. Others think of systems biology as a novel paradigm in life sciences, which strives to put things together rather than tearing them apart (Noble, 2006). In other words, systems biology represents the integration of data and facts rather than a process of simplifying and reducing them to a minimal consensus model. However, there are even more opinions on how systems biology should be referred to. Some people refer to systems biology simply as a number of operational protocols used to carry out life science research. Some just define it as an application of systems theory to molecular biology, and others consider it to represent a socioscientific phenomenon focusing on the integration of selected interaction data of components of biological systems with the help of interdisciplinary tools and personnel.

Despite the controversy on a unique definition of systems biology, it is undoubtful

Home: Systembiologie

<http://www.systembiologie.de/de>

systembiologie.de

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[SBMC 2012] Conference on Systems Biology of Mammalian Cells

4th SBMC · 2012 July 9th - 11th
Gewandhaus Leipzig | Germany

Januar

Mo	Di	Mi	Do	Fr	Sa	So
26	27	28	29	30	31	01
02	03	04	05	06	07	08
09	10	11	12	13	14	15
16	17	18	19	20	21	22
23	24	25	26	27	28	29
30	31	01	02	03	04	05

Neue Veranstaltung
Keine Termine gefunden

Veranstaltungen
Name der Veranstaltung
Stadt
suchen

systembiologie in deutschland

Willkommen bei systembiologie.de, dem Portal für systembiologische Forschung in Deutschland.

Systembiologie widmet sich der Erforschung biologischer Prozesse auf der Systemebene. Sie will ein Gesamtbild schaffen von den dynamischen Vorgängen des Lebens unter Einbeziehung sämtlicher Ebenen – vom Genom über das Proteom bis hin zur kompletten Zelle oder gar einem vollständigen Organismus. Dazu verknüpft sie quantitative Methoden aus der Molekulärbiologie mit dem Wissen aus Mathematik, Informatik und Systemwissenschaften. In einem iterativen Prozess zwischen Laborexperiment und Modellierung im Computer werden mathematische Konzepte auf biologische Systeme angewandt.

Das BMBF hat das große Innovationspotential der Systembiologie frühzeitig erkannt und der Förderung dieses jungen Wissenschaftszweiges als bedeutenden Bestandteil der Hightech-Initiative der Bundesregierung einen hohen Stellenwert eingeräumt.

Kostenlos - lesen oder bestellen Sie unser Magazin

systembiologie.de

spezial:
systemmedizin



Bewerbung MTZ Award
2012

MTZ® stiftung
– for a better future –

Weitere Informationen [hier](#).

BMBF-Initiativen

Weitere Informationen zu den verschiedenen Systembiologie-Initiativen des BMBF finden Sie [hier](#).

Sie suchen Informationen?

M. Cassman, Again

7.11.08 in Heidelberg, EMBL:



"Integrative approaches to biology in the 21st century"

In the past 8-10 years systems biology has progressed from a fad to something resembling a discipline, even if it is not quite there. The fad part is easy to see. Many new programs and centers have been established calling themselves systems biology - and some of them actually are. Turning it into a discipline, however, requires more than a label. The essence of systems biology, and in distinction from systematic biology, is a focus on networks, computational modeling, and dynamics. In order to permit progress in such an area a set of conceptual and material capabilities ("infrastructure") must be put in place, together with research training programs that have a significant emphasis in mathematics."

Systems Biology: Promises



Leroy Hood, founder of the "Institute for Systems Biology" (Seattle) together with Alan Aderem and Ruedi Aebersold

Image and text from
<http://www.systemsbiology.org/>

"Studying the interactions and interplay of many levels of biological information, systems biology will enable us not only to cure complex diseases but also to predict an individual's health and extend the human body's natural lifespan by preventing diseases. The new era of predictive, preventive, and personalized medicine—made possible by systems biology—represents a profound shift in the practice of medicine and will reach into many corners of our lives."

*Leroy Hood, Ph.D, M.D.
President
Institue for Systems Biology*

Hype and Challenge

Adriano Henney, AstraZeneca, UK, 8.11.08 in HD:

Challenges and opportunities for systems biology and drug discovery: a perspective

A number of initiatives, reports and symposia have also covered the topic, and we are beginning to witness an increasing and unwelcome tendency to hype what Systems Biology might be able to offer. This is likely to damage how Systems Biology is perceived by the wider community, through a combination of misunderstanding, misinterpretation and, potentially, misrepresentation of the discipline, which many regard as the natural successor to the Human Genome Project.

As a result, policy makers, pharma executives, venture capitalists and many other stakeholders are unclear whether it can have any impact on human health, or as some sceptics believe, it is likely to fall significantly short of expectations and deliver nothing but disappointment.

Systems Biology is...

...a **new**, but not yet well defined **field**

=> there is still a lot to discover/define/understand

...a buzzword (still) helping to acquire a lot of **money**

...the **ansatz** to explicitly consider and make use of the **complexity** of biological processes (= life)

=> what is the best way to do that?

...a field that **unites** many other fields: molecular biology, genetics, physiology, ..., chemistry, physics, mathematics, informatics, ...

=> need for (at least) basic knowledge on the other fields

=> interdisciplinary collaborations

...**interesting** and unavoidable :-)

Approaching Systems Biology



- Inhalt:**
1. Executive Summary and Introduction
 2. Data and Databases
 3. Network Inference
 4. Modeling and Network Organization
 5. Systems Biology in Plant Research
 6. Education, National Programs, and Infrastructure in Systems Biology

Lots of Data



Choose the right (biological) subject:
hepatocytes, viruses, *E. coli*, *S. cerevisiae*, *A. thaliana*, red blood cells, ...

The Most Simple Thing



Peer Bork
EMBL HD



Luis Serrano
Barcelona

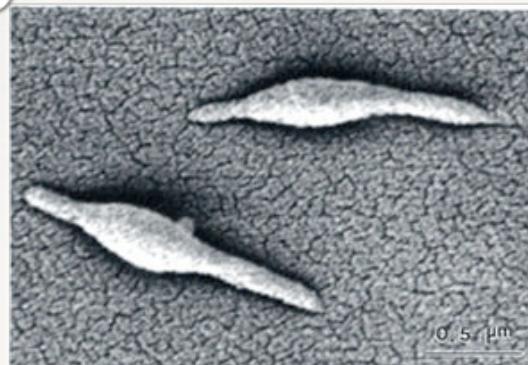


Bettina Böttcher
Edinburgh

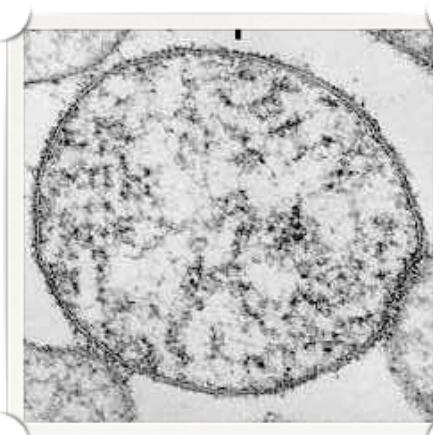


Anne-Claude Gavin
EMBL

Mycoplasma pneumoniae: self-replicating organism with one of the smallest genomes



Bioinformatics 3 – WS 11/12 – Tihamer Geyer



689 protein
encoding genes

Systems Biology of *M. pneumonia*

Proteome Organization in a Genome-Reduced Bacterium

Sebastian Kühner,^{1*} Vera van Noort,^{1*} Matthew J. Betts,¹ Alejandra Leo-Macias,¹ Claire Batisse,¹ Michaela Rode,¹ Takuji Yamada,¹ Tobias Maier,² Samuel Bader,¹ Pedro Beltran-Alvarez,¹ Daniel Castaño-Diez,¹ Wei-Hua Chen,¹ Damien Devos,¹ Marc Güell,² Tomas Norambuena,³ Ines Racke,¹ Vladimir Rybin,¹ Alexander Schmidt,⁴ Eva Yus,¹ Ruedi Aebersold,⁴ Richard Herrmann,⁵ Bettina Böttcher,^{1†} Achilleas S. Frangakis,¹ Robert B. Russell,¹ Luis Serrano,^{2,6} Peer Bork,^{1‡} Anne-Claude Gavin^{1‡}

Science **326** (2009) 1235

+104 pages supplementary material

First task:
extensive data collection
(proteome, metabolome,
transcriptome, spatial data)

Impact of Genome Reduction on Bacterial Metabolism and Its Regulation

Eva Yus,¹ Tobias Maier,¹ Konstantinos Michalodimitrakis,¹ Vera van Noort,² Takuji Yamada,² Wei-Hua Chen,² Judith A. H. Wodke,¹ Marc Güell,¹ Sira Martínez,¹ Ronan Bourgeois,¹ Sebastian Kühner,² Emanuele Raineri,¹ Ivica Letunic,² Olga V. Kalinina,^{2,3} Michaela Rode,² Richard Herrmann,³ Ricardo Gutiérrez-Gallego,⁴ Robert B. Russell,² Anne-Claude Gavin,² Peer Bork,^{2*} Luis Serrano^{1,6}

Science **326** (2009) 1263

+126 pages supplementary material

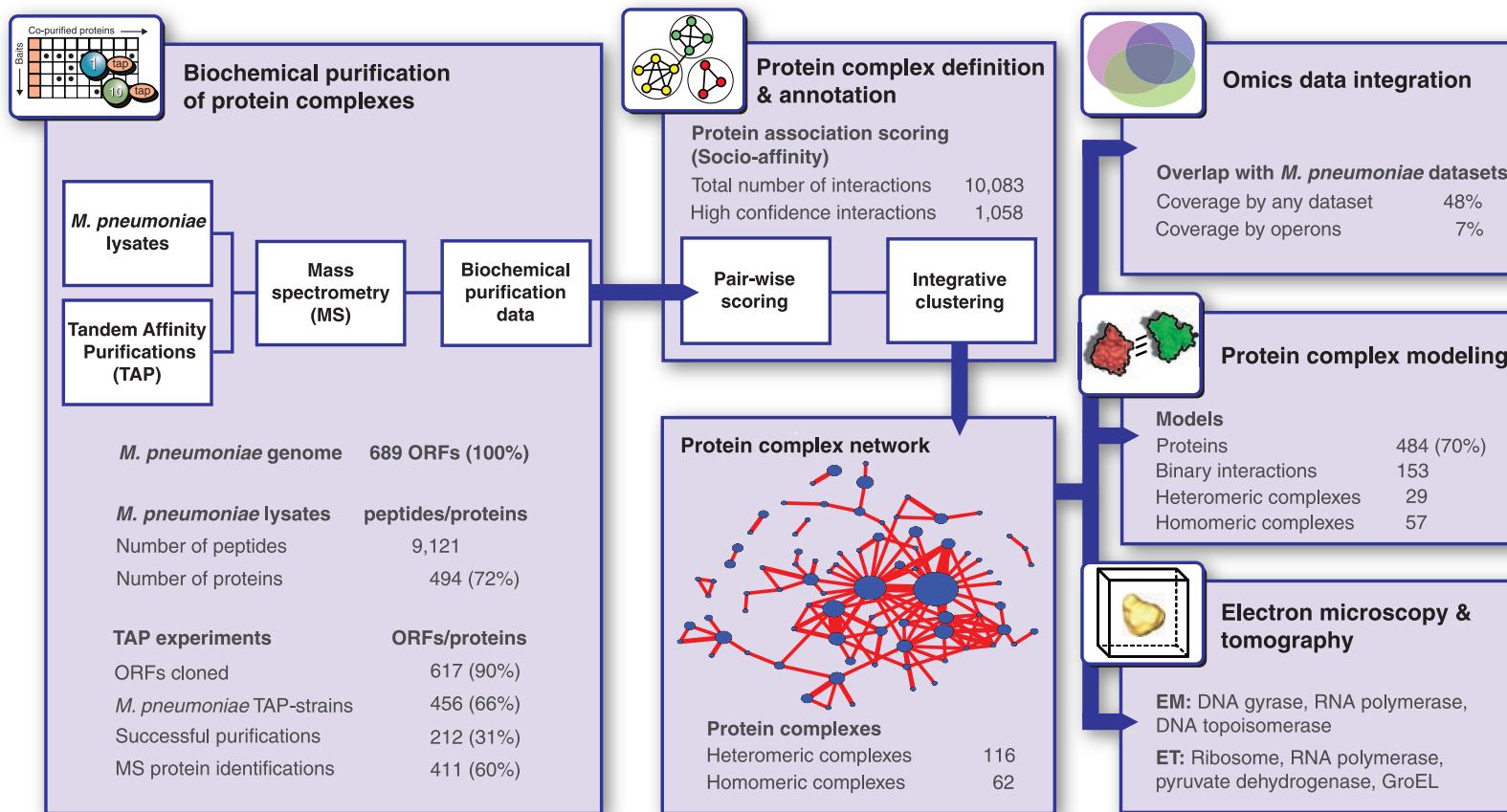
Transcriptome Complexity in a Genome-Reduced Bacterium

Marc Güell,¹ Vera van Noort,² Eva Yus,¹ Wei-Hua Chen,² Justine Leigh-Bell,¹ Konstantinos Michalodimitrakis,¹ Takuji Yamada,² Manimozhiyan Arumugam,² Tobias Doerks,² Sebastian Kühner,² Michaela Rode,² Mikita Suyama,^{2*} Sabine Schmidt,² Anne-Claude Gavin,² Peer Bork,^{2†} Luis Serrano^{1,3†}

Science **326** (2009) 1268

+94 pages supplementary material

Scan for Protein Complexes



E. coli: ~6000 proteins

TAP-MS

689 protein encoding genes

617 successfully cloned

456 strains with exogenic tagged
copies of one protein/gene

352 strains with soluble TAP fusions

212 successful TAP purifications
electrophoresis, MS

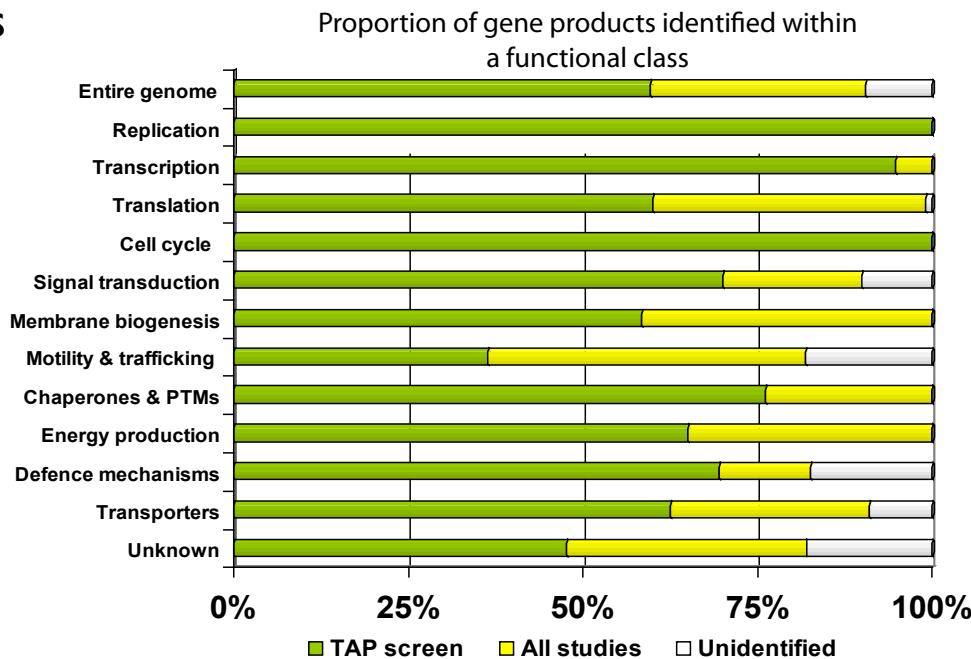
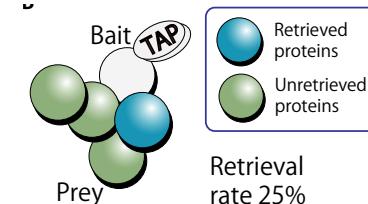
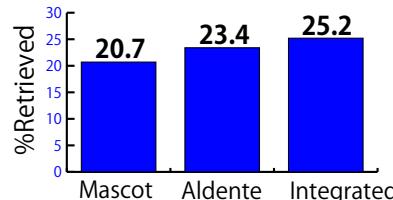
10447 MS samples

5899 identifications

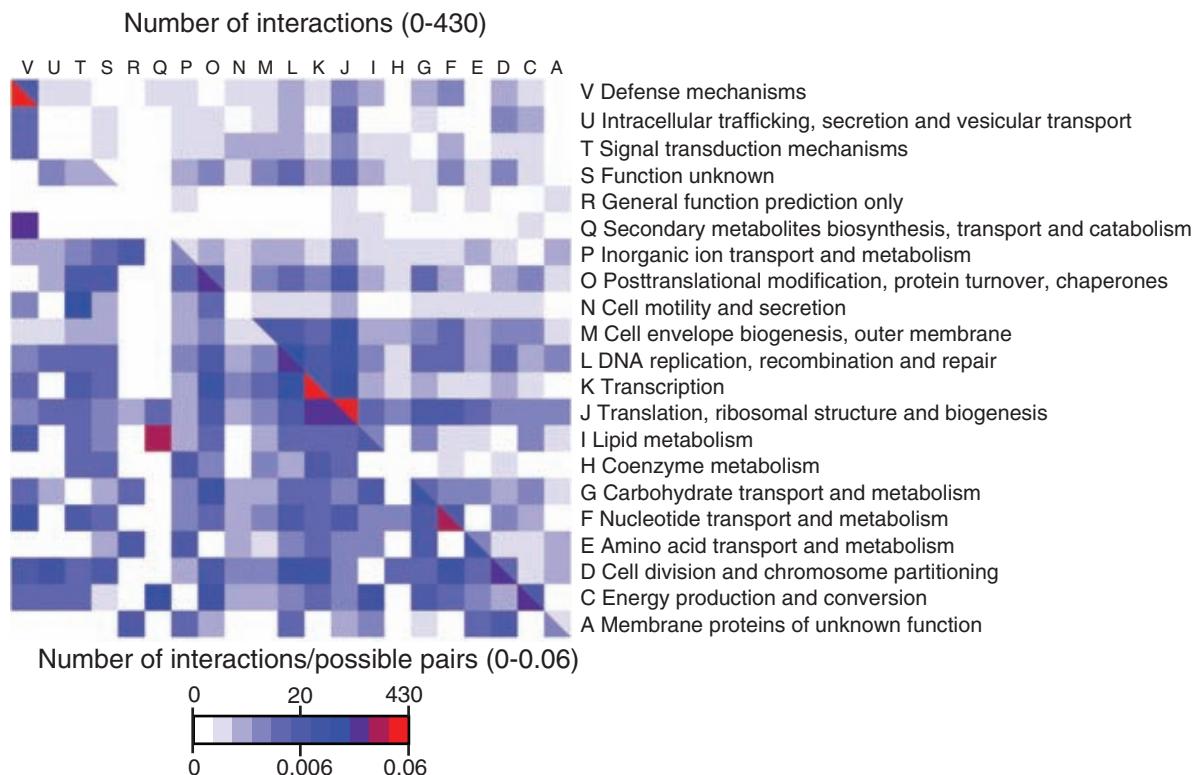
=> 411 distinct proteins

= 60% of the
annotated ORFs

= 85% of the (predicted)
soluble proteome



Interactions between Protein Classes



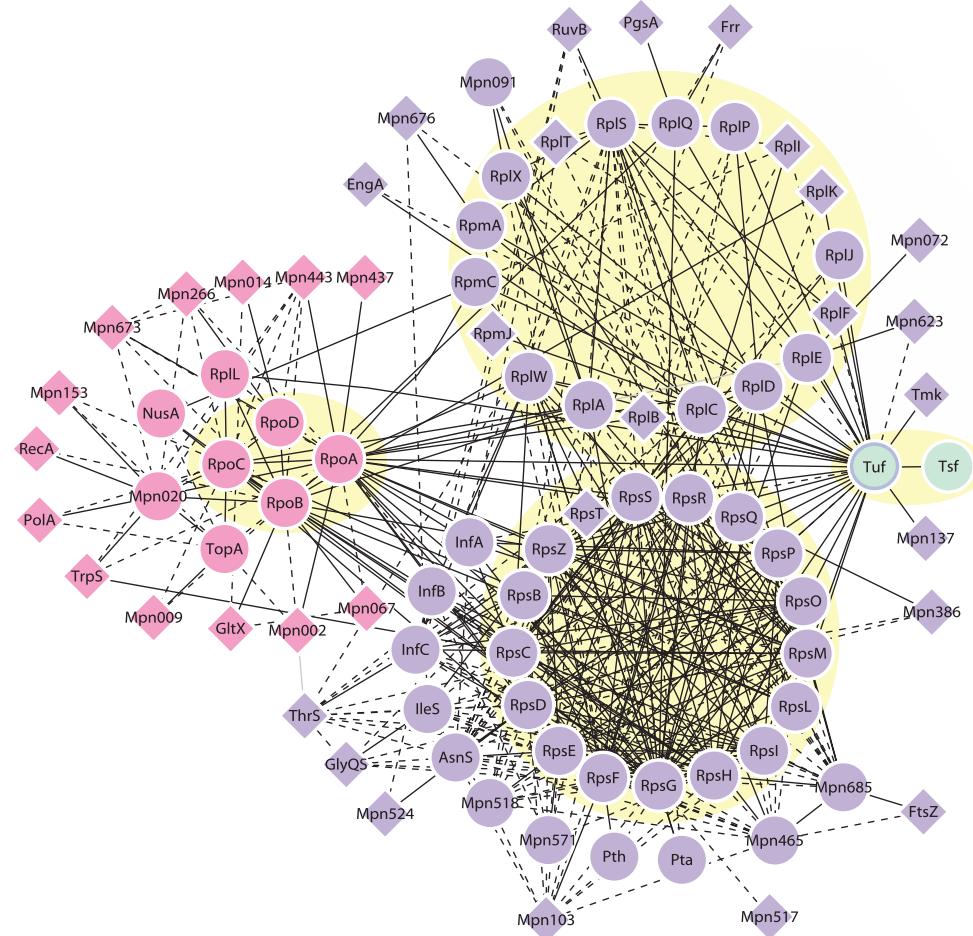
Most linked: J (Translation) and K (Transcription)

Complex Details

Assembly of
RNA polymerase,
ribosome,
translation elongation factor

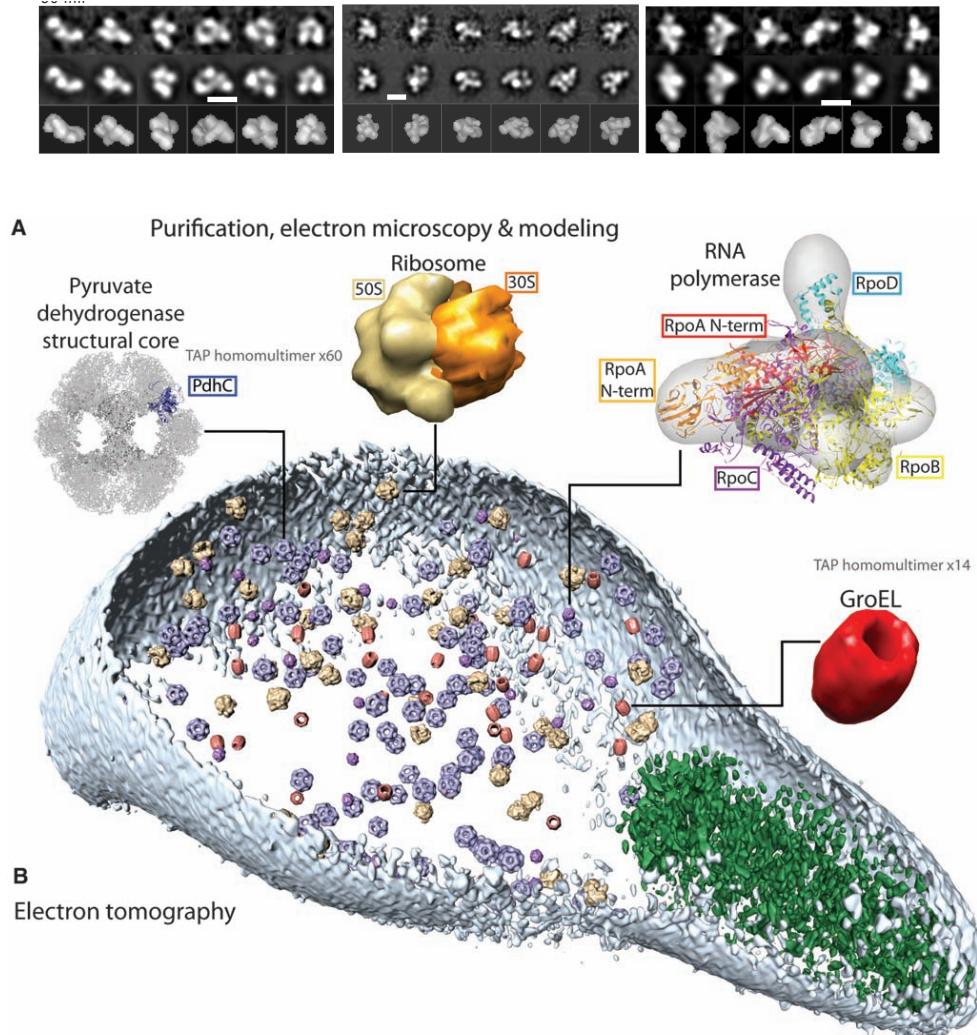
Core complexes
(multiple links):
circles

attachments (1 link):
diamonds

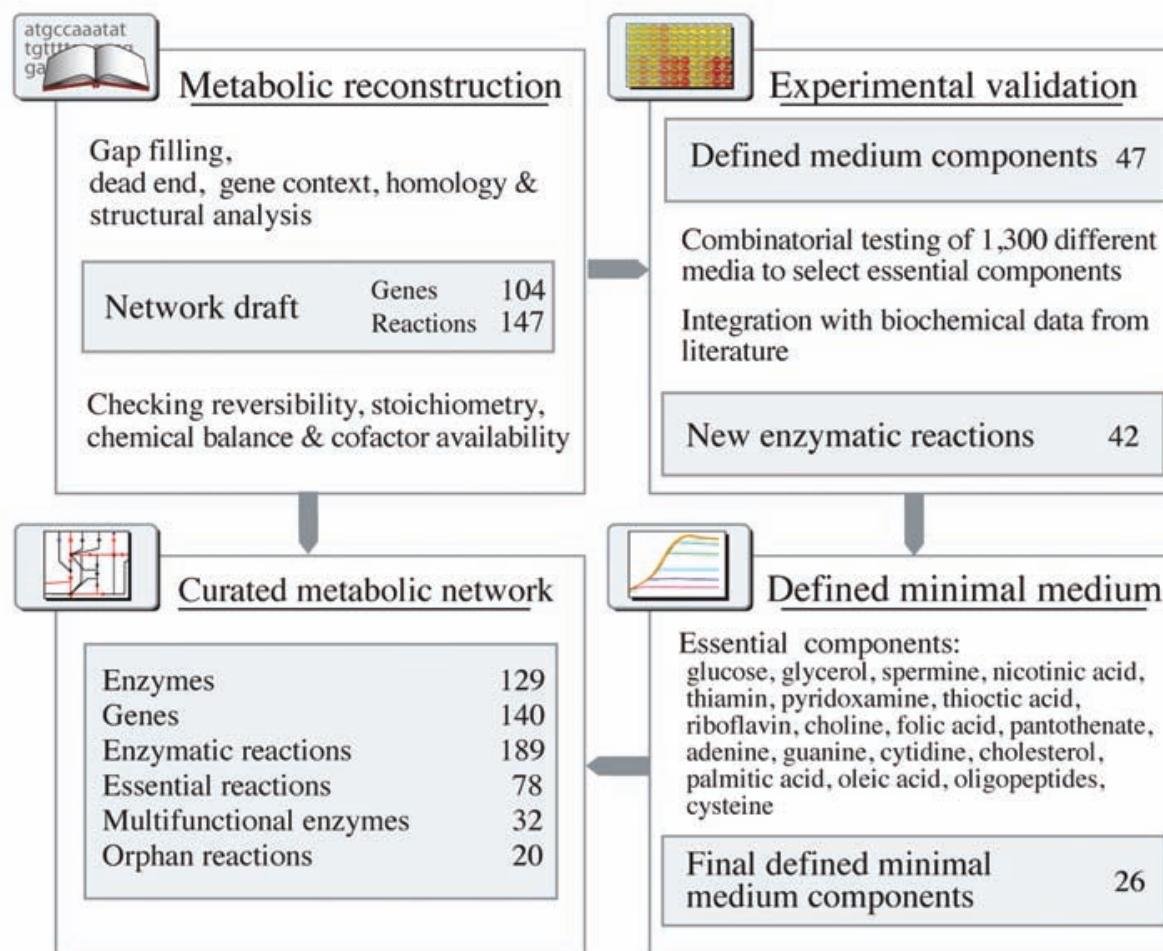


EM-Imaging

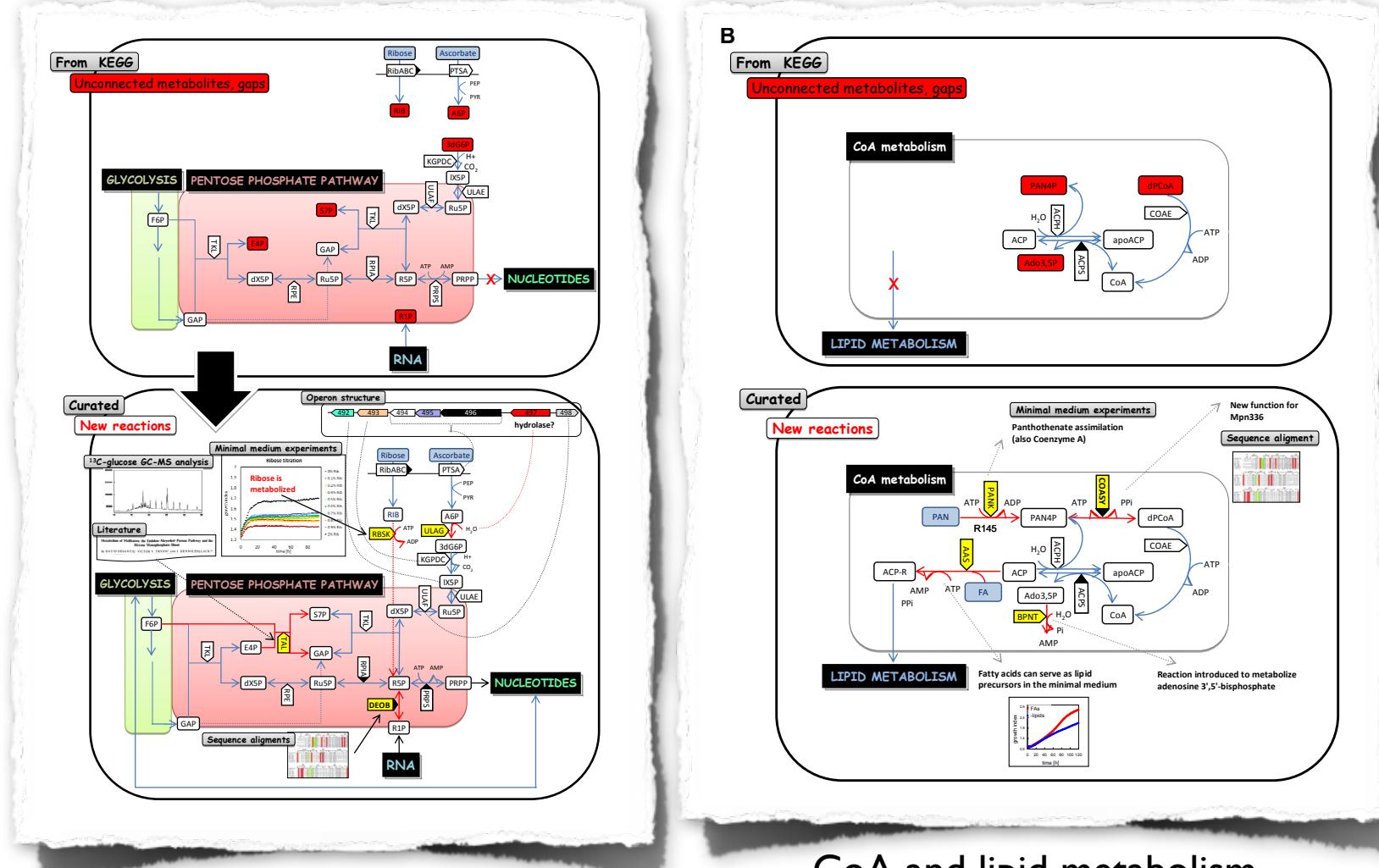
- 1) image and reconstruct some of the larger complexes (DNA gyrase, DNA topoisomerase, RNA polymerase)
- 2) image and reconstruct whole cells
=> identify complexes in the bacterium



All About Metabolism



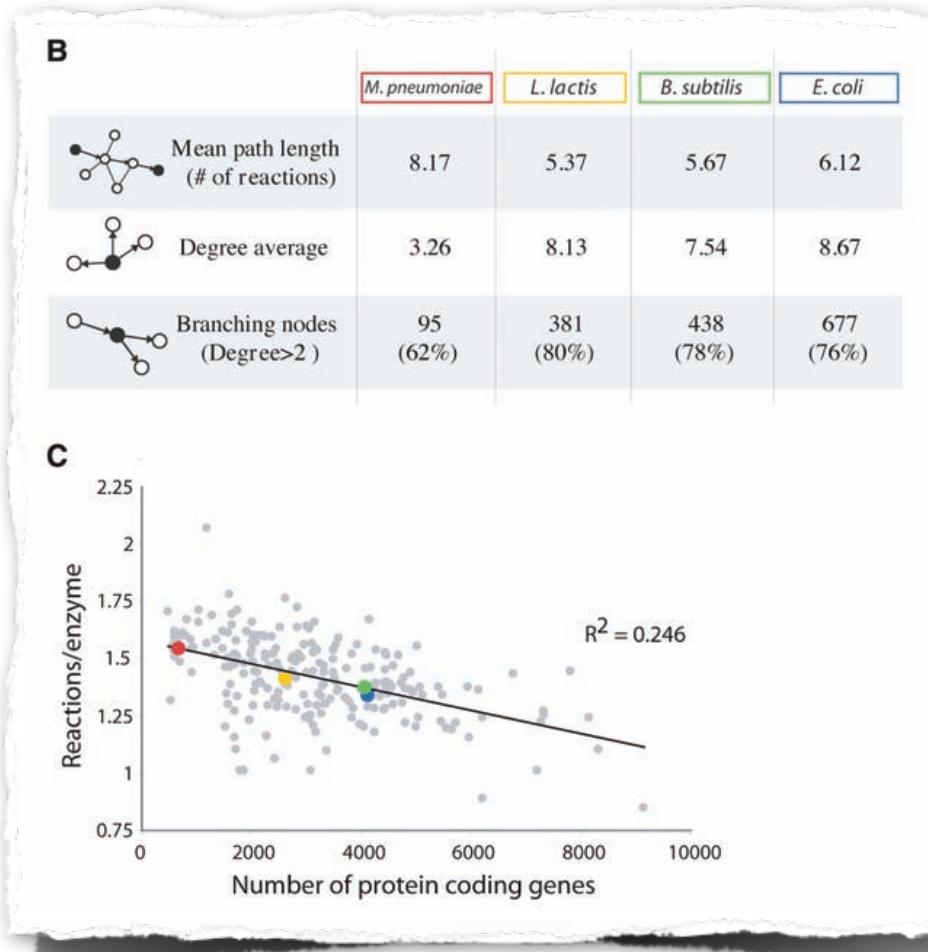
Network Improvements



Pentose-phosphate pathway

CoA and lipid metabolism

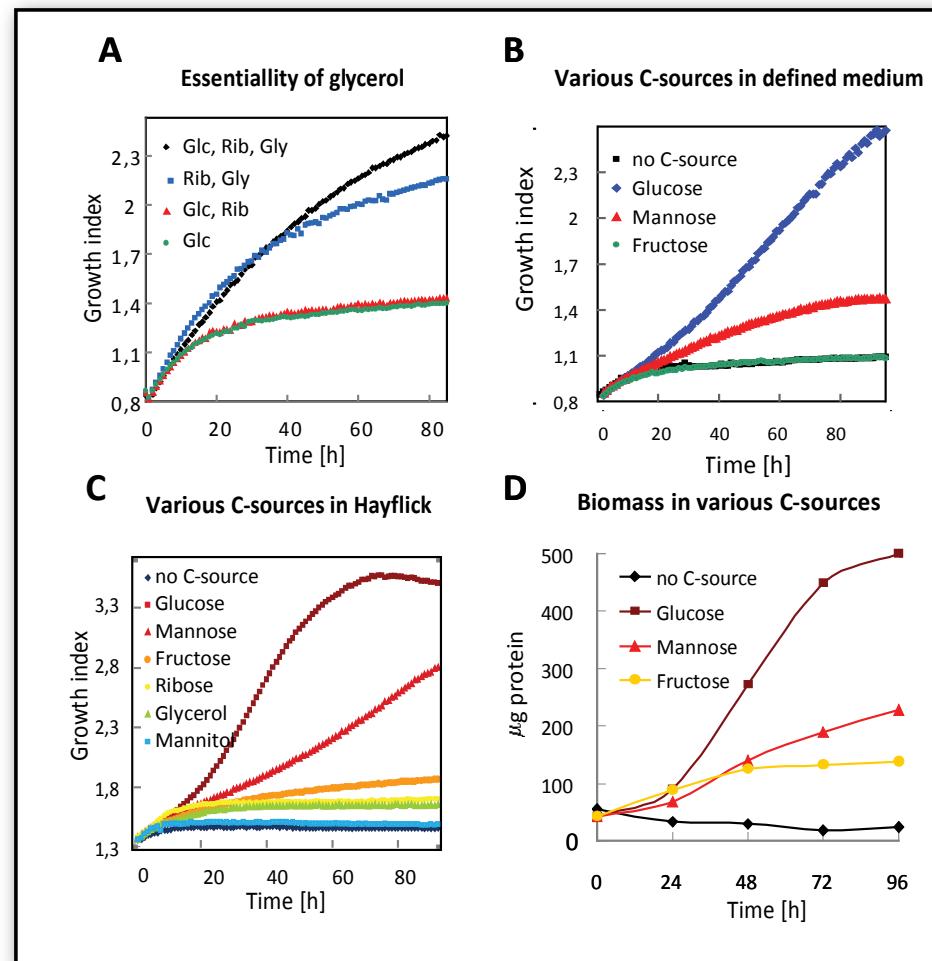
Local Graph Measures



Small genome (few proteins)
in *M. pneumonia*
=> metabolic network
contains more linear
pathways,
less interconnections
=> more multifunctional
enzymes (required?)

The Minimal Medium

Observe growth in different media
=> find minimal medium for full growth speed



The Complete Map

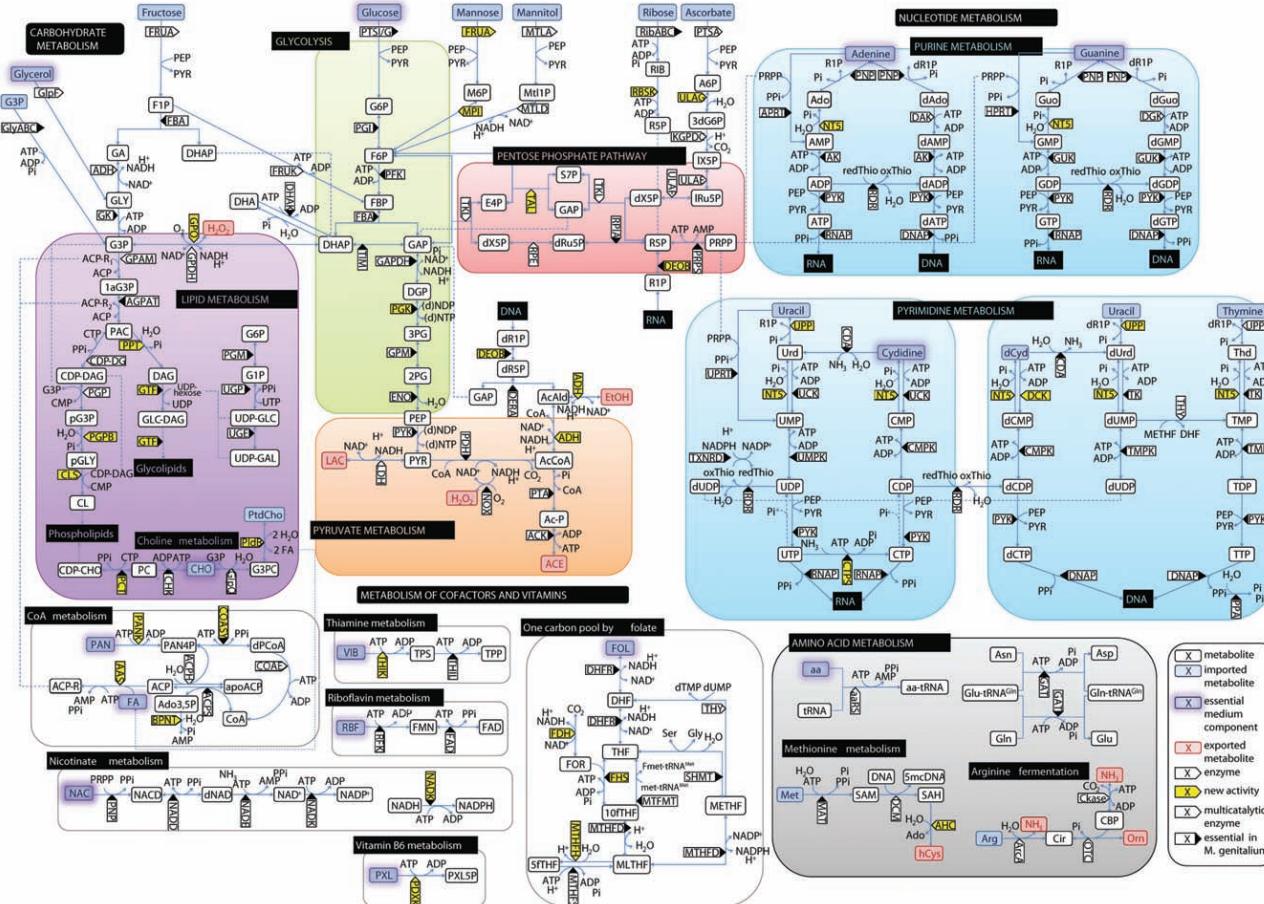
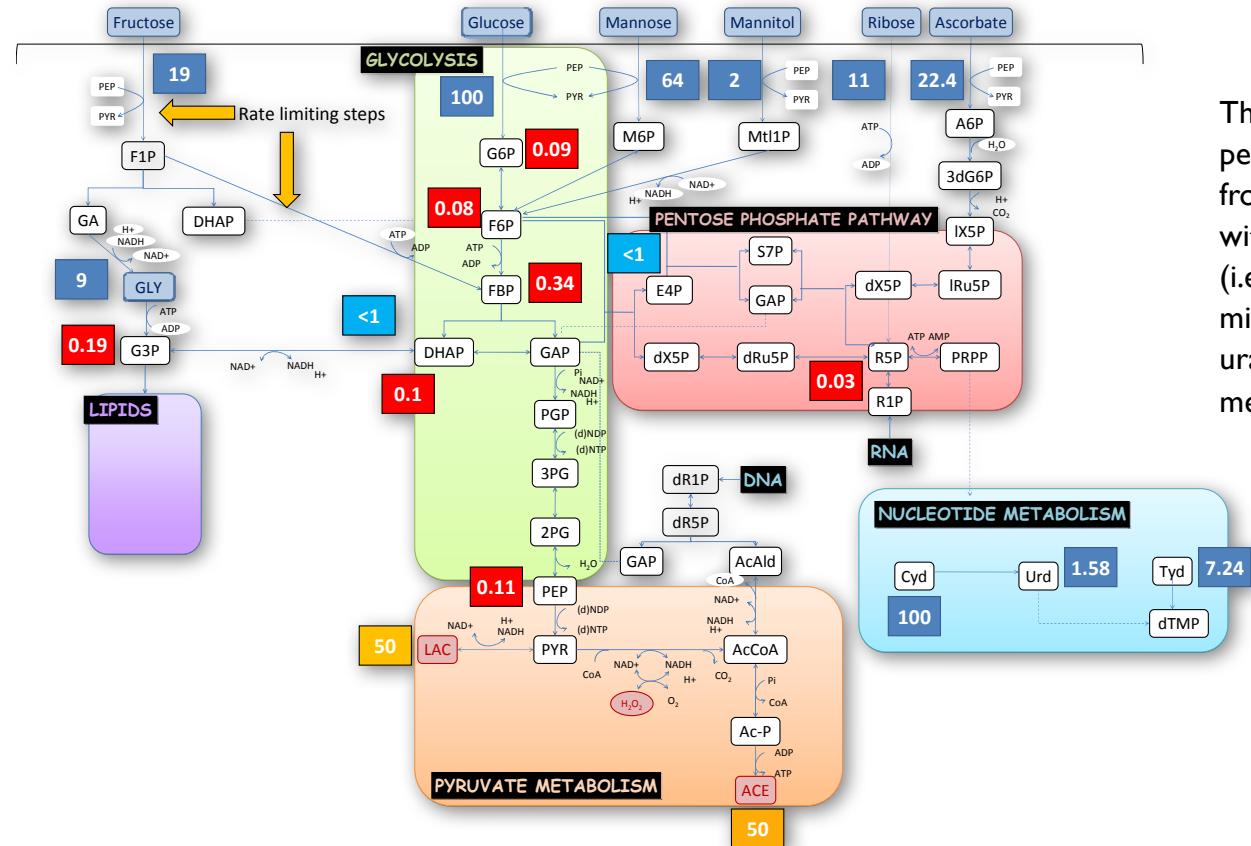


Fig. 2. Metabolic map of *M. pneumoniae*. Main metabolites are shown as boxes, and enzymes are shown as pentagons. Input metabolites are indicated in blue, and output products are indicated in red. New enzymatic activities determined in this study are displayed in yellow, and enzymes catalyzing multiple reactions are bold. Essential enzymes (according to the

mutagenesis study in *M. genitalium*) are indicated with a black triangle. Minimal medium components have been shadowed in blue. See the bottom-right legend for details, fig. S12 and table S2 for description of the enzymatic reactions and enzymes, and table S25 for metabolite abbreviations. aaRS, aminoacyl-tRNA synthase.

Metabolic Fluxes

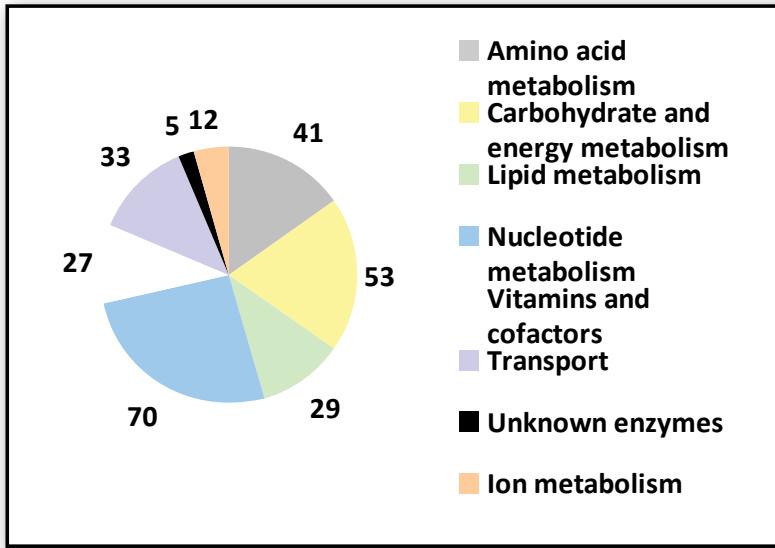


The numbers in blue represent the percentage of growth as determined from analysis of the growth curves with respect to the best nutrient (i.e. glucose in glycolysis or a mixture of cytidine, thymidine and uracil in pyrimidine nucleotide metabolism).

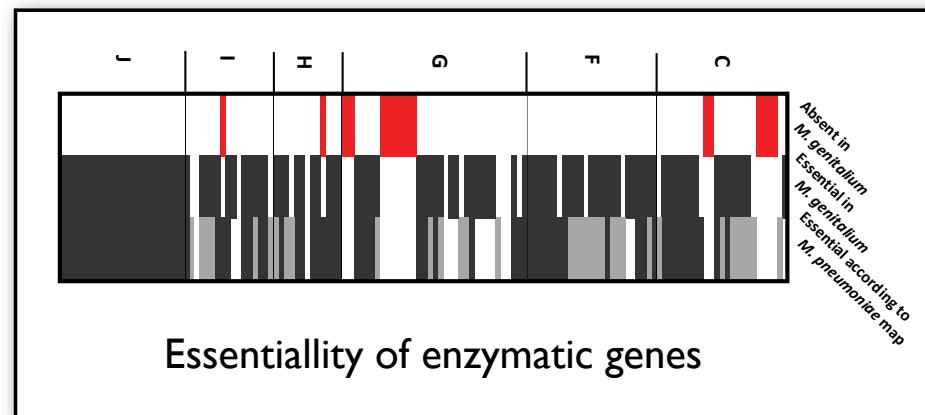
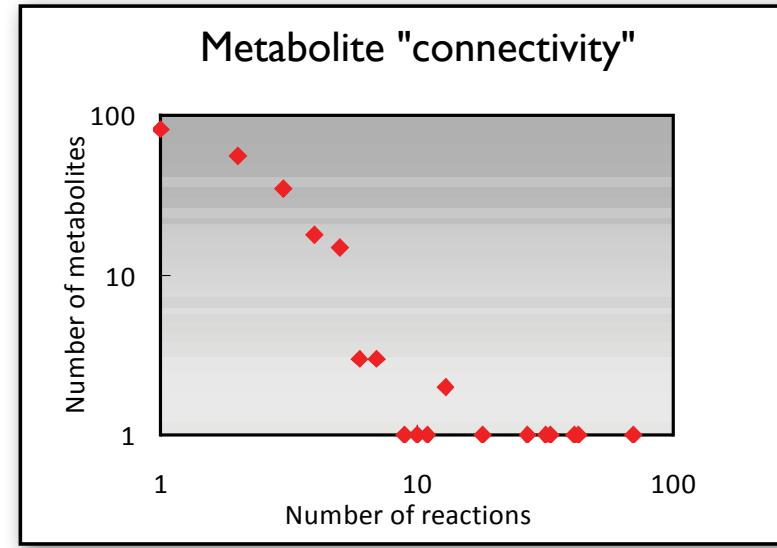
Fluxes determined from

- growth curves
- mass spectrometry determination of glycolysis intermediate metabolites.

Other Metabolic Properties



Distribution of enzymes and transporters in functional categories



Summary

Today:

Stochastics and molecular modelling

=> pools-and-proteins approach

=> bacterial photosynthesis as an example

"Systems Biology"???

=> What it is — fad or fashion?

=> little *M. pneumonia* — the first completely covered species

Next lecture:

Short Test #4

Exam: Feb. 7, 2012