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Biological Systems**

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**Functional Dynamics Modelling of Biological Systems**

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# Modelling Biological Function

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# *examples of biological function*

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- Reproduction



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- Energy utilization  
glycolytic flux



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## *examples of biological function*

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- Reproduction
- Energy utilization  
glycolytic flux
- Physiological rhythms  
(oscillations)
- Mimicry (patterns)
- Biological function is a possible process in an intact biological system at a certain timescale and under biological meaningful conditions.





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- Fast muscle contraction is a function which is obviously of importance for survival.





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- It requires a substantial change of ATP consumption within seconds.



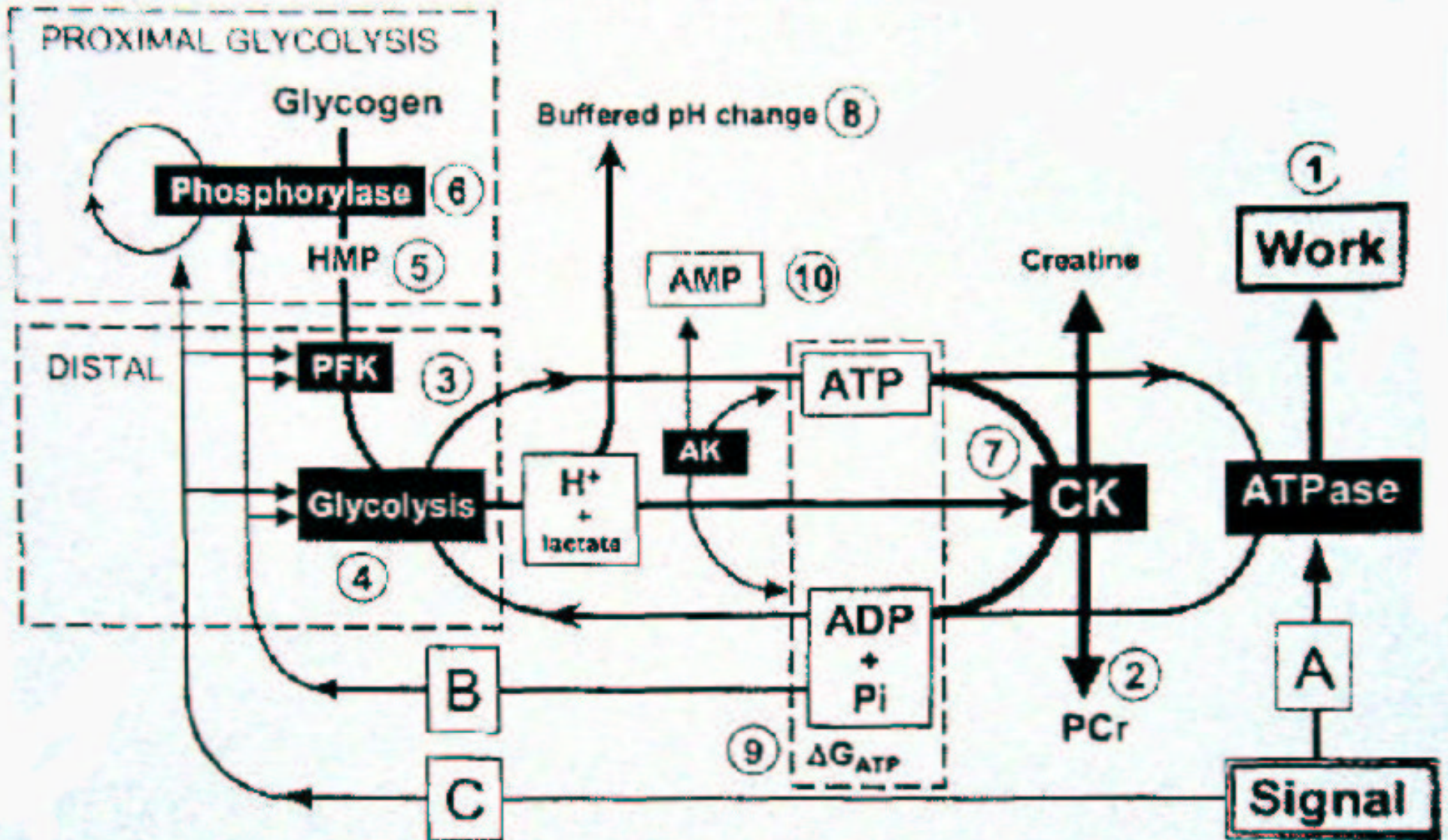
# *skeletal muscle contraction*

- Fast muscle contraction is a function which is obviously of importance for survival.
- It requires a substantial change of ATP consumption within seconds.
- Can the associated changes of flux be understood by current knowledge of the influence of metabolites on flux.





# metabolome of muscle power plant



# experimental results on muscle work in humans

NMR measurements of  
pCr (phosphocreatine)  
P (phosphate) and pH at  
(a) 70% MVC  
(maximal voluntary contraction)  
(b) 90% MVC.

- 1<sup>st</sup> ↓ Contraction
- 2<sup>st</sup> ↓ Anaerobic "recovery"
- 3<sup>st</sup> ↓ Aerobic recovery

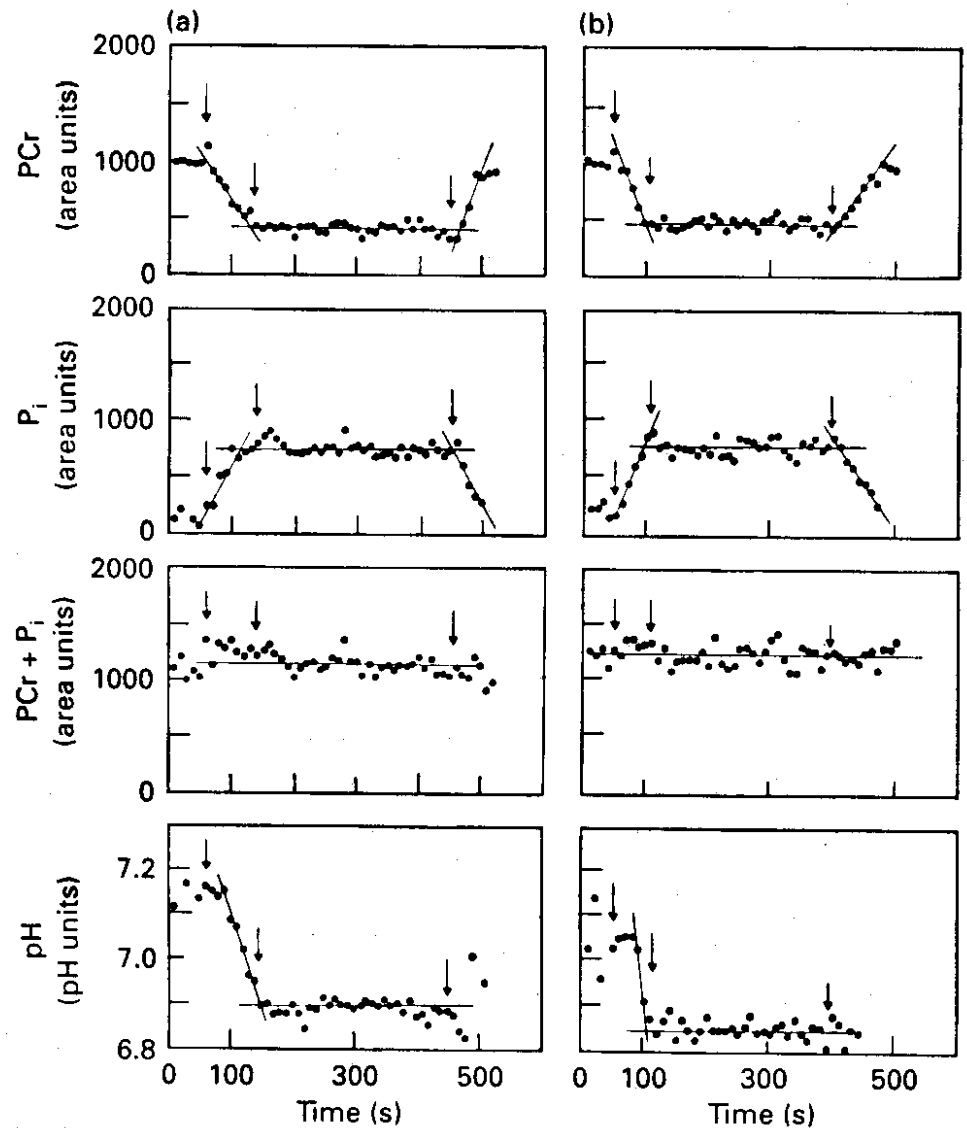


Figure 3 Effect on PCr,  $P_i$  and pH of isometric contraction and recovery during ischaemia followed by aerobic recovery

# *structural hierachy at cellular level*

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Genome



Proteome



Metabolome



Cellular structure and function

# *timescales for cell processes*

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- Gene interactions (secs - hours)



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- Protein function (enzymatic reactions) (millisecs - hours)

# *Modelling of metabolic networks*

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- Systematic methods for quantitative modelling of steady states in metabolic networks.

# *Modelling of metabolic networks*

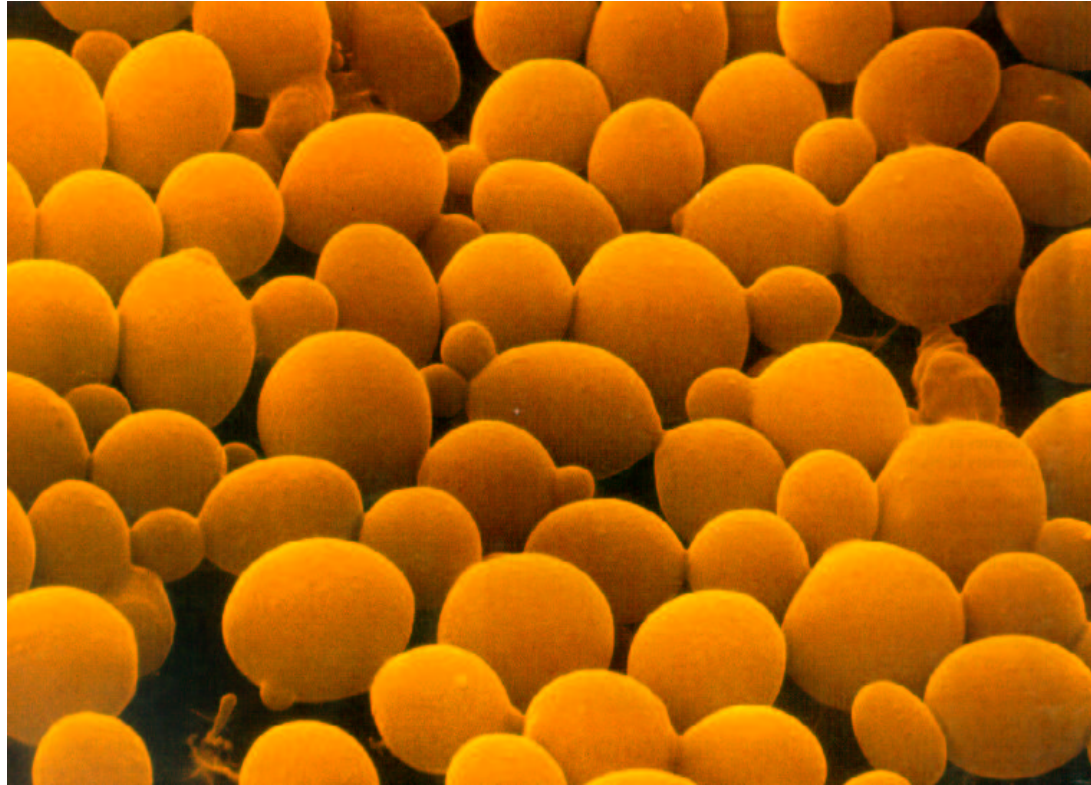
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- Systematic methods for quantitative modelling of steady states in metabolic networks.
- Example on modelling glycolysis in yeast cells which in many respects is similar to glycolysis in muscle cells.



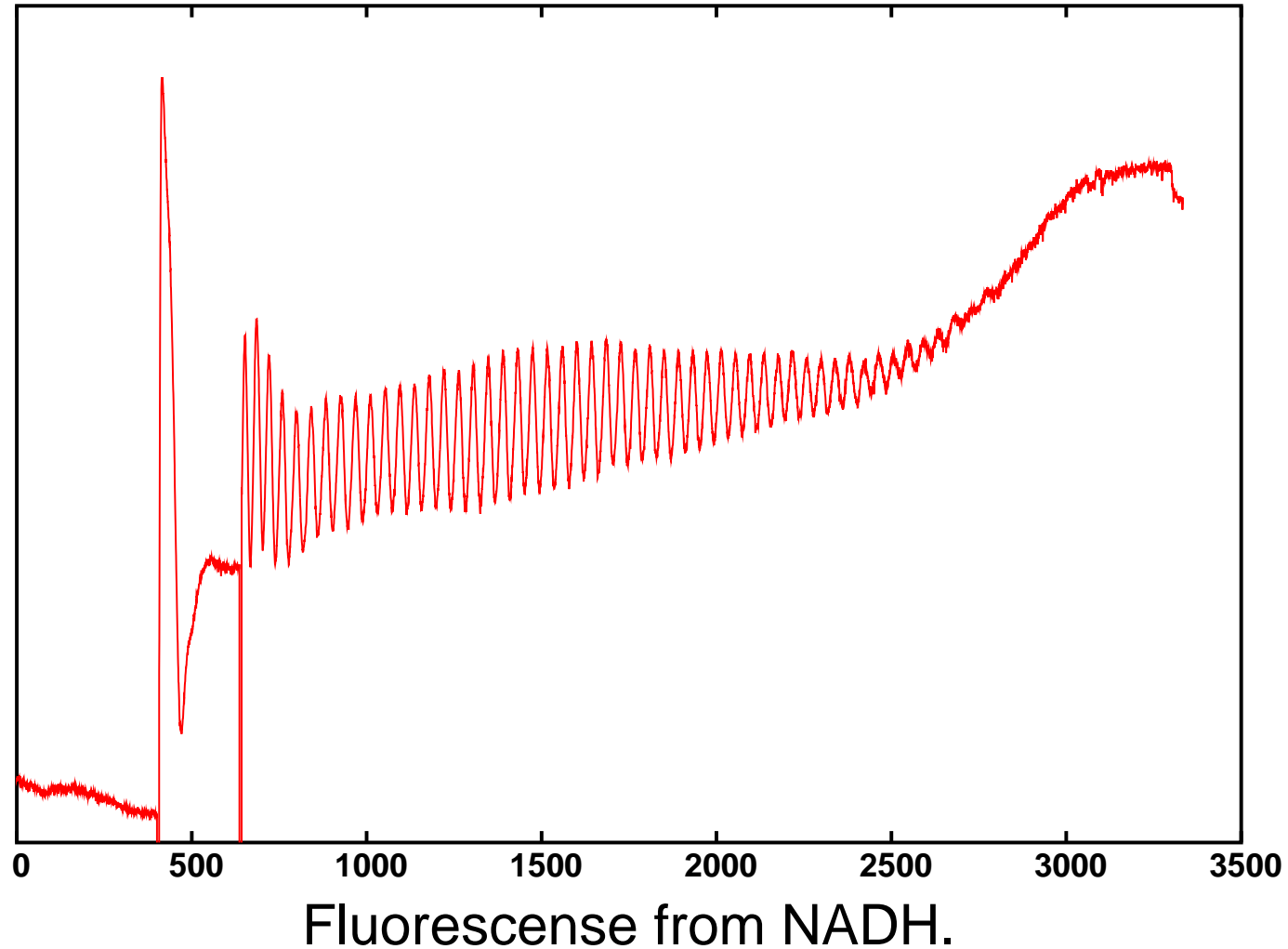
# *the quest for the oscillophore of yeast cells*

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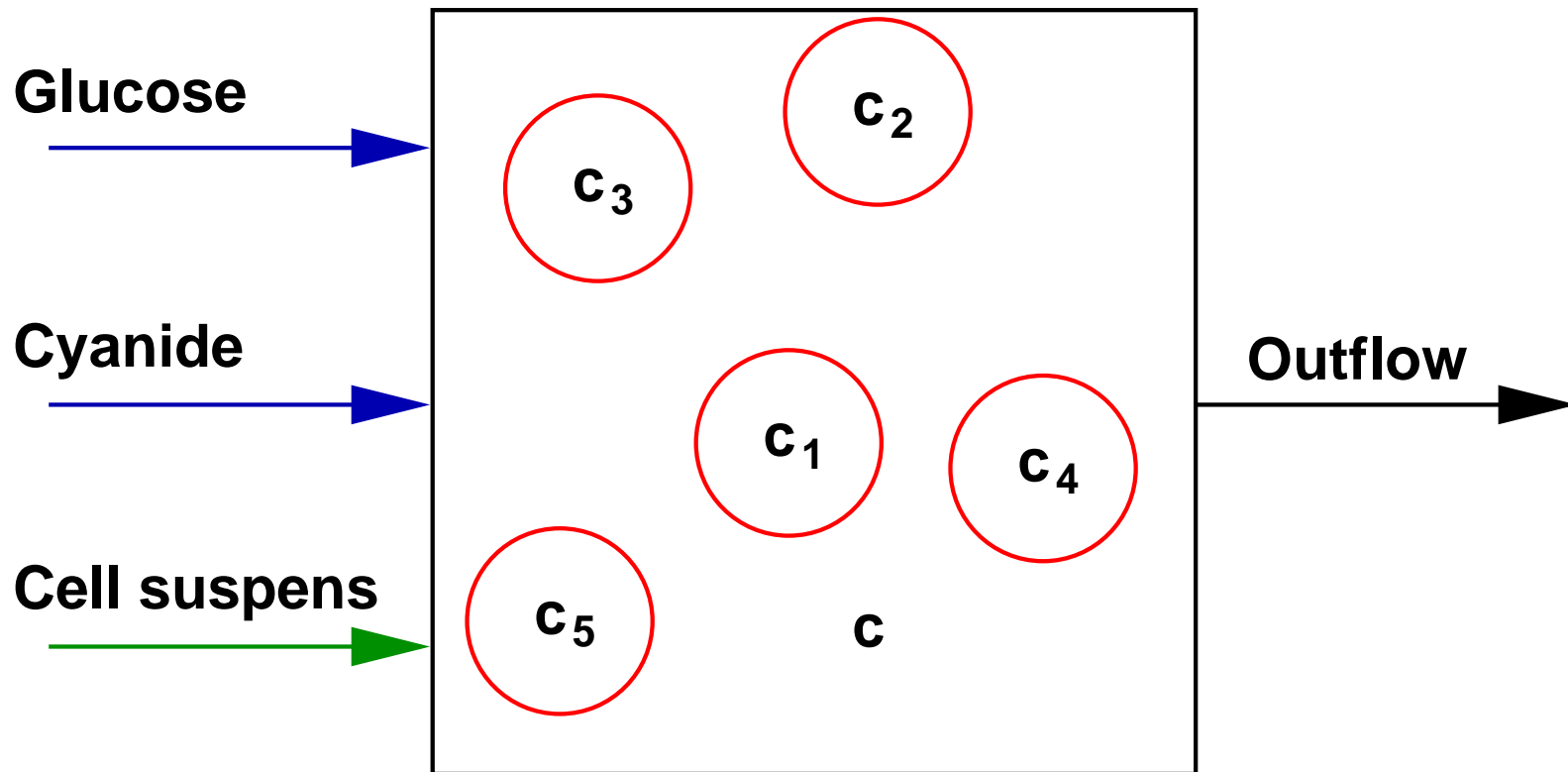
Cells of *Saccharomyces cerevisiae* are grown aerobically in batch. They are harvested at glucose depletion (diauxic shift) and then starved for some hours in a buffer. At 5°C the cells can be stored for several days.

# Oscillations in a closed system

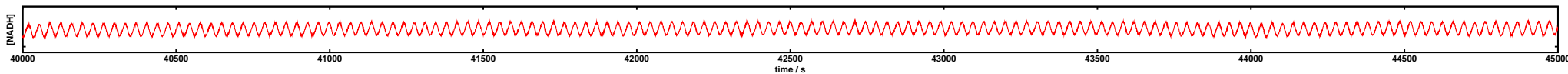


Addition of glucose at  $t=400s$ . Addition of cyanide at  $t = 650$ .

# Continuous oscillations using a flow reactor



The reactor is fed with constant flow of cell suspension together with glucose and cyanide. Oscillations are observed if the cells oscillate in phase. Amplitude depends on glucose concentration.



# ***stationary experimental data for the cell suspension***

- Measurements of stationary concentrations

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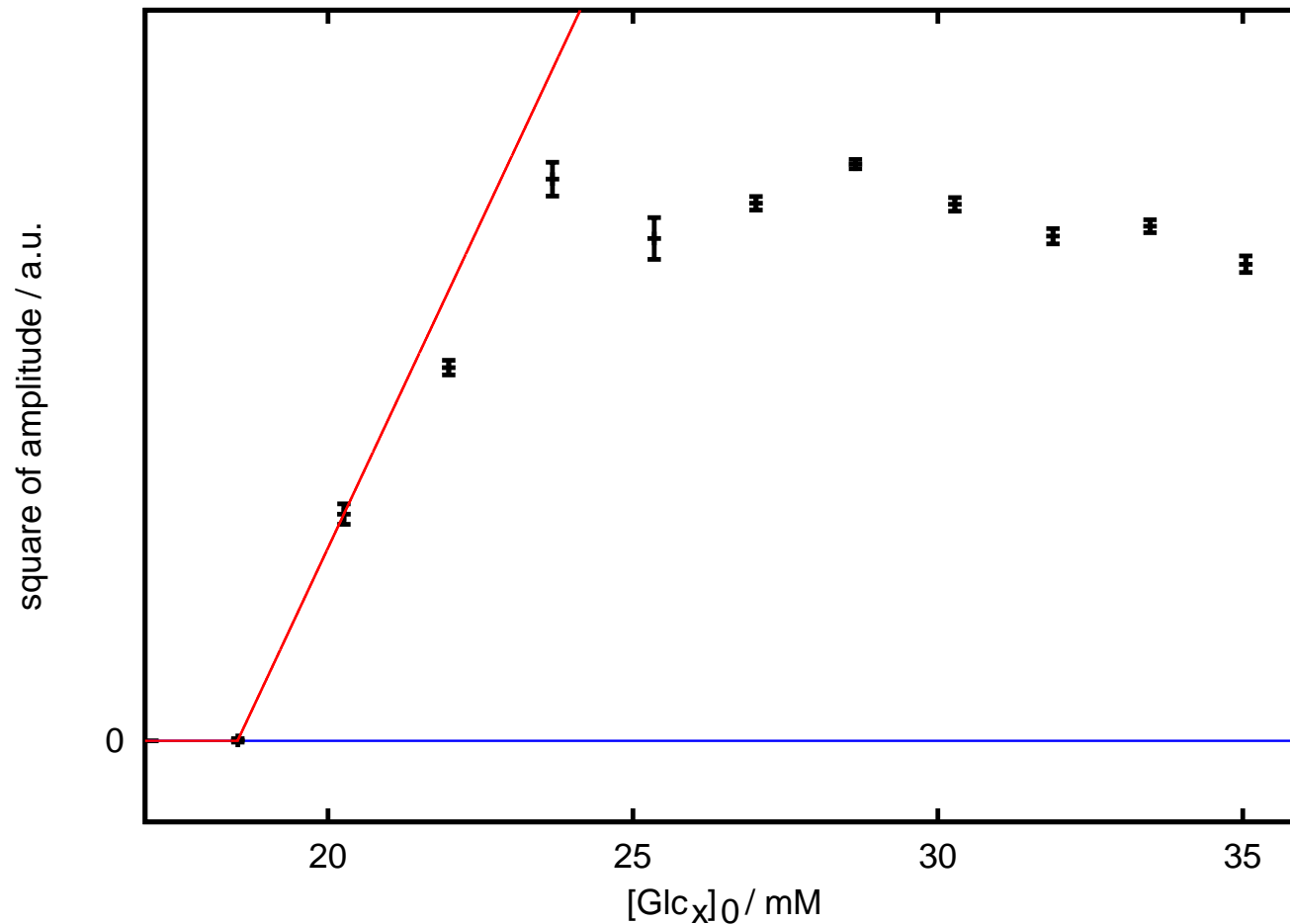
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- Can a complete model using *in vitro* determined parameters explain the experimental data

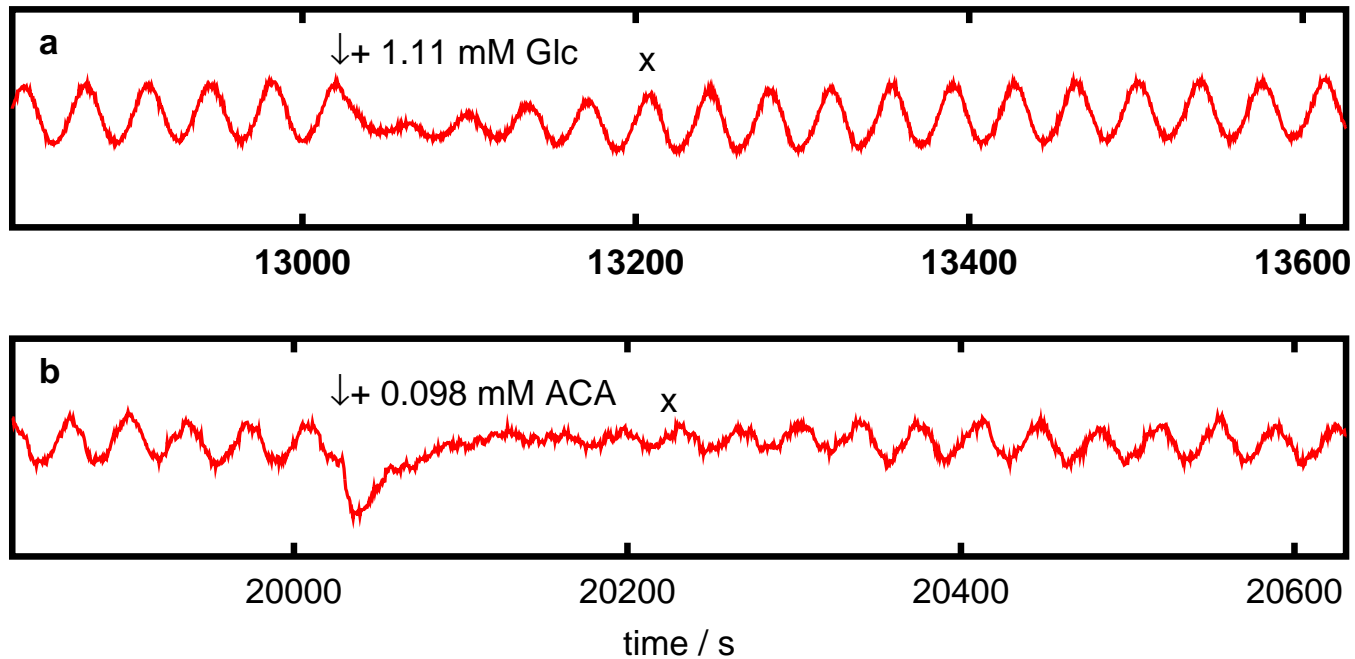
# stationary experimental data for the cell suspension

- Measurements of stationary concentrations
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- Measurements of *in vitro* enzymatic parameters
- Measurements of amplitude and phases for metabolite oscillations
- Can a complete model using *in vitro* determined parameters explain the experimental data
- **NO**

Dependence of amplitude on glucose concentrations.

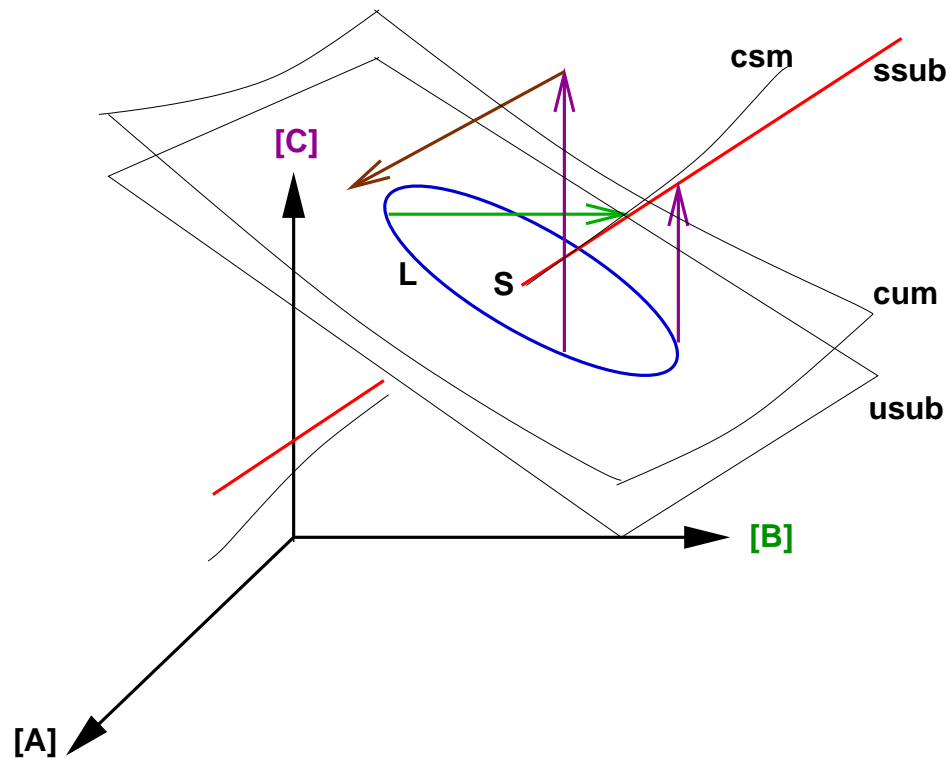


Quenchings of the oscillations.



The reactor is perturbed with instantaneous additions of  
a: glucose and b: acetaldehyde.

# Geometry of quenching



Hopf bifurcation in 3 dimensional concentration space. **ssub** and **usub** are the stable and unstable subspace of the unstable stationary state **S**. **L** is the stable limit cycle embedded in the center-unstable manifold **cum** tangent to **usub** at **S**. **csm** is the center-stable manifold of **S** tangent to **ssub** at **S**.



# network for reactions in flow reactor

Intracellular reactions

Extracellular reactions

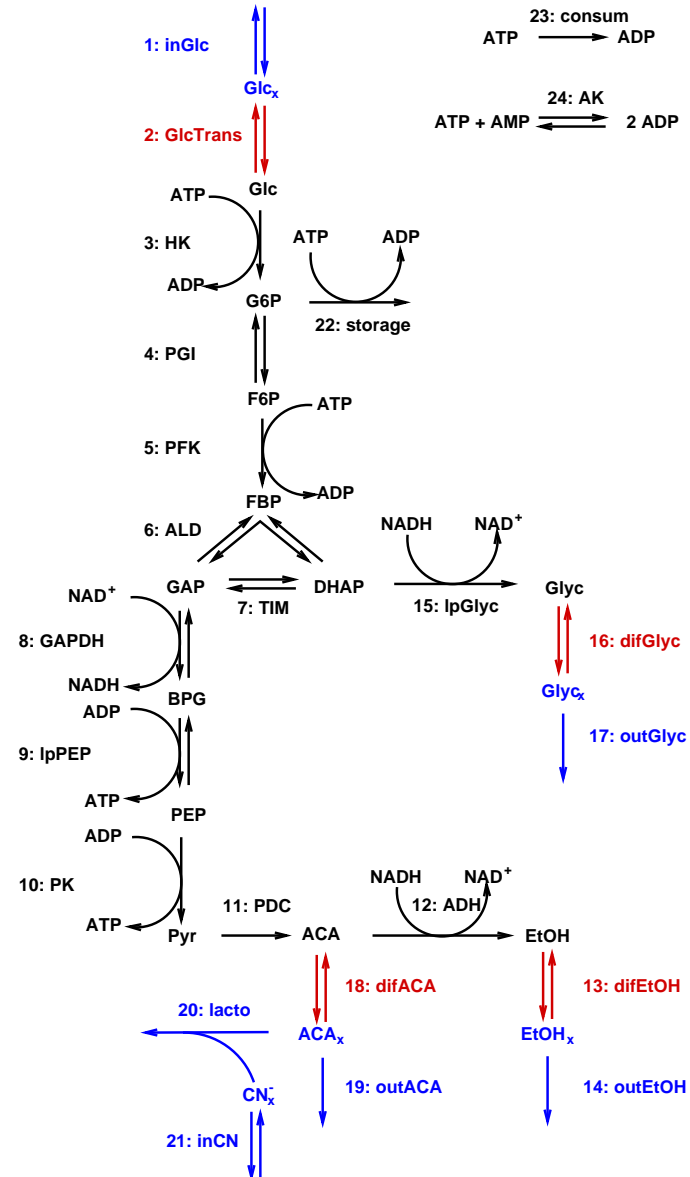
Transport across cellular membrane

ODE model at metabolome level

20 variables

24 reactions

60 parameters



# *direct optimization method*

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- Kinetic equations:  $\frac{dc_s}{dt} = \sum_r \nu_{s,r} v_r$

$c_s$  is concentration of species  $s$

$\nu$  is the stoichiometric matrix

$v_r$  is the rate of reaction  $r$

# Selected reaction rates $v_r$

$$2: v_{\rightarrow} = \frac{V_{2m} \frac{[\text{Glc}_x]}{K_{2\text{Glc}}}}{1 + \frac{[\text{Glc}_x]}{K_{2\text{Glc}}} + \frac{P_2}{P_2} \frac{[\text{Glc}_x]}{K_{2\text{Glc}}} + 1 \left( 1 + \frac{[\text{Glc}]}{K_{2\text{Glc}}} + \frac{[\text{G6P}]}{K_{2\text{IG6P}}} + \frac{[\text{Glc}][\text{G6P}]}{K_{2\text{Glc}}K_{2\text{IG6P}}} \right)}$$

$$v_{\leftarrow} = \frac{V_{2m} \frac{[\text{Glc}]}{K_{2\text{Glc}}}}{1 + \frac{[\text{Glc}]}{K_{2\text{Glc}}} + \frac{P_2}{P_2} \frac{[\text{Glc}]}{K_{2\text{Glc}}} + 1 \left( 1 + \frac{[\text{Glc}_x]}{K_{2\text{Glc}}} \right) + \frac{[\text{G6P}]}{K_{2\text{IG6P}}} + \frac{[\text{Glc}][\text{G6P}]}{K_{2\text{Glc}}K_{2\text{IG6P}}}$$

$$5: v_{\rightarrow} = \frac{V_{5m} [\text{F6P}]^2}{K_5 \left( 1 + \kappa_5 \frac{[\text{ATP}]^2}{[\text{AMP}]^2} \right) + [\text{F6P}]^2}$$

$$6: v_{\rightarrow} = \frac{V_{6f} [\text{FBP}]}{K_{6\text{FBP}} + [\text{FBP}] + \frac{[\text{GAP}]K_{6\text{DHAP}}V_{6f}}{K_{6\text{eq}}V_{6r}} + \frac{[\text{DHAP}]K_{6\text{GAP}}V_{6f}}{K_{6\text{eq}}V_{6r}} + \frac{[\text{FBP}][\text{GAP}]}{K_{6\text{IGAP}}} + \frac{[\text{GAP}][\text{DHAP}]V_{6f}}{K_{6\text{eq}}V_{6r}}$$

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$$8: v_{\rightarrow} = \frac{V_{8m} [\text{GAP}][\text{NAD}^+]}{K_{8\text{GAP}}K_{8\text{NAD}} \left( 1 + \frac{[\text{GAP}]}{K_{8\text{GAP}}} + \frac{[\text{BPG}]}{K_{8\text{BPG}}} \right) \left( 1 + \frac{[\text{NAD}^+]}{K_{8\text{NAD}}} + \frac{[\text{NADH}]}{K_{8\text{NADH}}} \right)}$$

$$v_{\leftarrow} = \frac{V_{8m} \frac{[\text{BPG}][\text{NADH}]}{K_{8\text{eq}}}}{K_{8\text{GAP}}K_{8\text{NAD}} \left( 1 + \frac{[\text{GAP}]}{K_{8\text{GAP}}} + \frac{[\text{BPG}]}{K_{8\text{BPG}}} \right) \left( 1 + \frac{[\text{NAD}^+]}{K_{8\text{NAD}}} + \frac{[\text{NADH}]}{K_{8\text{NADH}}} \right)}$$

$$15: v_{\rightarrow} = \frac{V_{15m} [\text{DHAP}]}{K_{15\text{DHAP}} \left( 1 + \frac{K_{15\text{NADH}}}{[\text{NADH}]} \left( 1 + \frac{[\text{NAD}^+]}{K_{15\text{INAD}}} \right) \right) + [\text{DHAP}] \left( 1 + \frac{K_{15\text{NADH}}}{[\text{NADH}]} \left( 1 + \frac{[\text{NAD}^+]}{K_{15\text{INAD}}} \right) \right)}$$

Other reaction rates are Michaelis-Menten or mass action.

## *direct optimization method*

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The rate has the form:  $v_r = V_r g_r(c, K_r)$

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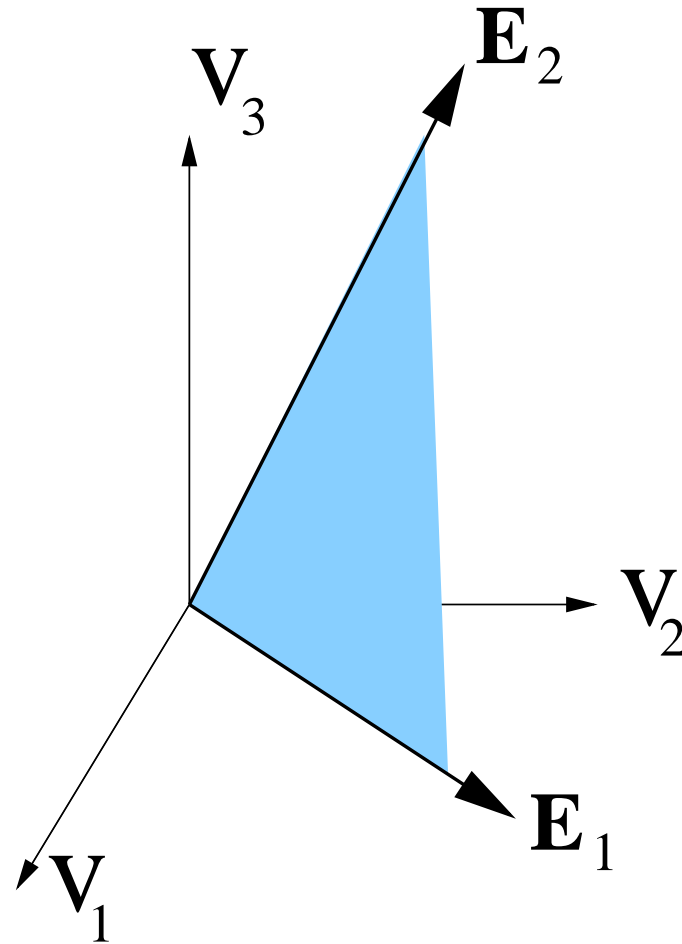
rate parameter  
↓  
↑  
intrinsic parameters

- Null space:  $\sum_r \nu_{s,r} v_r^{ss} = 0$

# *direct optimization method*

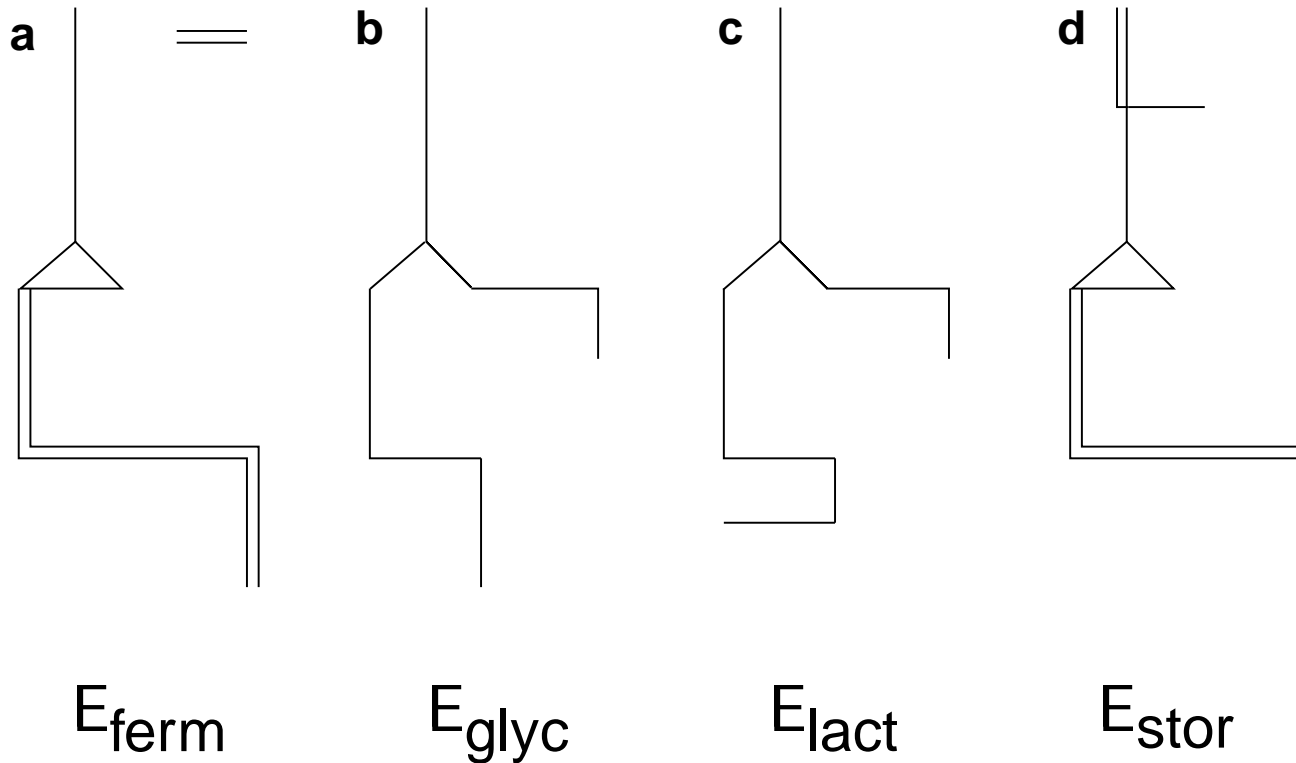
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Extreme currents in a 3 dimensional reaction space



# *direct optimization method*

Extreme currents for glycolysis at Hopf point.



$$E^{ss} = a_1 E_{\text{ferm}} + a_2 E_{\text{glyc}} + a_3 E_{\text{lact}} + a_4 E_{\text{stor}}$$



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- g: select new parameters and goto a

# Parameter optimization

	$c_s/\text{mM}$	$a_s/a$	$\theta_s/\text{deg}$	$q_s/q_{\text{ACA}_x}$	$\phi_s/\text{deg}$
Glc <sub>x</sub>	1.55 (1.6)	0.013	135	5.3 (11)	355 (4)
Glc	0.57	1.83	12	19	81
G6P	4.2 (4.1)	15.8 (21)	190 (260)	1.7	67
F6P	0.49 (0.5)	2.16 (2.7)	178 (250)	1.7	72
FBP	4.64 (5.1)	22.2 (26)	32 (70)	4.4	218
GAP	0.115 (0.12)	0.295 (0.04)	30	7.0	255
DHAP	2.95 (2.5)	6.97 (0.5)	38	7.9	195
BPG	0.0003 (n.d)	0.002	136	0.53	287
PEP	0.04 (0.04)	0.023 (0.07)	18	1.1	286
Pyr	8.7 (8.7)	4.06 (7)	79	125	180
ACA	1.48	0.894	196	2.5	268
EtOH <sub>x</sub>	16.5	0.035	114	$\infty$ (n.p)	undef
EtOH	19.2	1.22	26	$\infty$	undef
Glyc	4.2	1.68	98	$\infty$	undef
Glyc <sub>x</sub>	1.68	0.005	188	$\infty$ (n.p)	undef
ACA <sub>x</sub>	1.29	0.037 (0.3)	284 (200)	1 (1)	181 (172)
CN <sub>x</sub> <sup>-</sup>	5.2	$5 \times 10^{-5}$	193	2400 (n.p)	271
ATP	2.1 (2.1)	10.8 (8)	139 (180)	0.50	289
ADP	1.5 (1.5)	6.32 (9.4)	319 (0)	1.0	290
AMP	0.33 (0.33)	4.5 (3.6)	319 (0)		
NADH	0.33 (0.33)	1 (1)	0 (0)	0.68	106
NAD <sup>+</sup>	0.65 (0.65)	1 (0.6)	180 (180)		

Comparison of optimized model with experimental results (in paranthesis).

$c_s$  : concentrations of the stationary state.  $a_s$  : relative amplitudes of oscillations.  $\theta_s$  : angles of oscillations.  $q_s$  : relative quenching amplitudes.  $\phi_s$  : quenching phases.



# ***Control coefficients for amplitude and frequency***

---

The quest for the oscillophore can be closed by calculating control coefficients for the oscillations from the comprehensive model.

- Control coefficient for square amplitude and frequency

$$\Gamma_E^{a^2} = E \frac{\partial a^2}{\partial E} \quad C_E^{\omega_{lc}} = \frac{E}{\omega_{lc}} \frac{\partial \omega_{lc}}{\partial E}$$

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- The control coefficients satisfy summation rules which can be obtained from the timescale invariance of trajectories by differentiating  $a^2$  with a scale factor  $h$  for time

$$\frac{\partial a^2}{\partial h} = \sum_r \frac{\partial a^2}{\partial (hE_r)} \frac{\partial (hE_r)}{\partial h} \stackrel{h \equiv 1}{=} \sum_r \frac{\partial a^2}{\partial E_r} E_r = \sum_r \Gamma_{E_r}^{a^2} = 0$$

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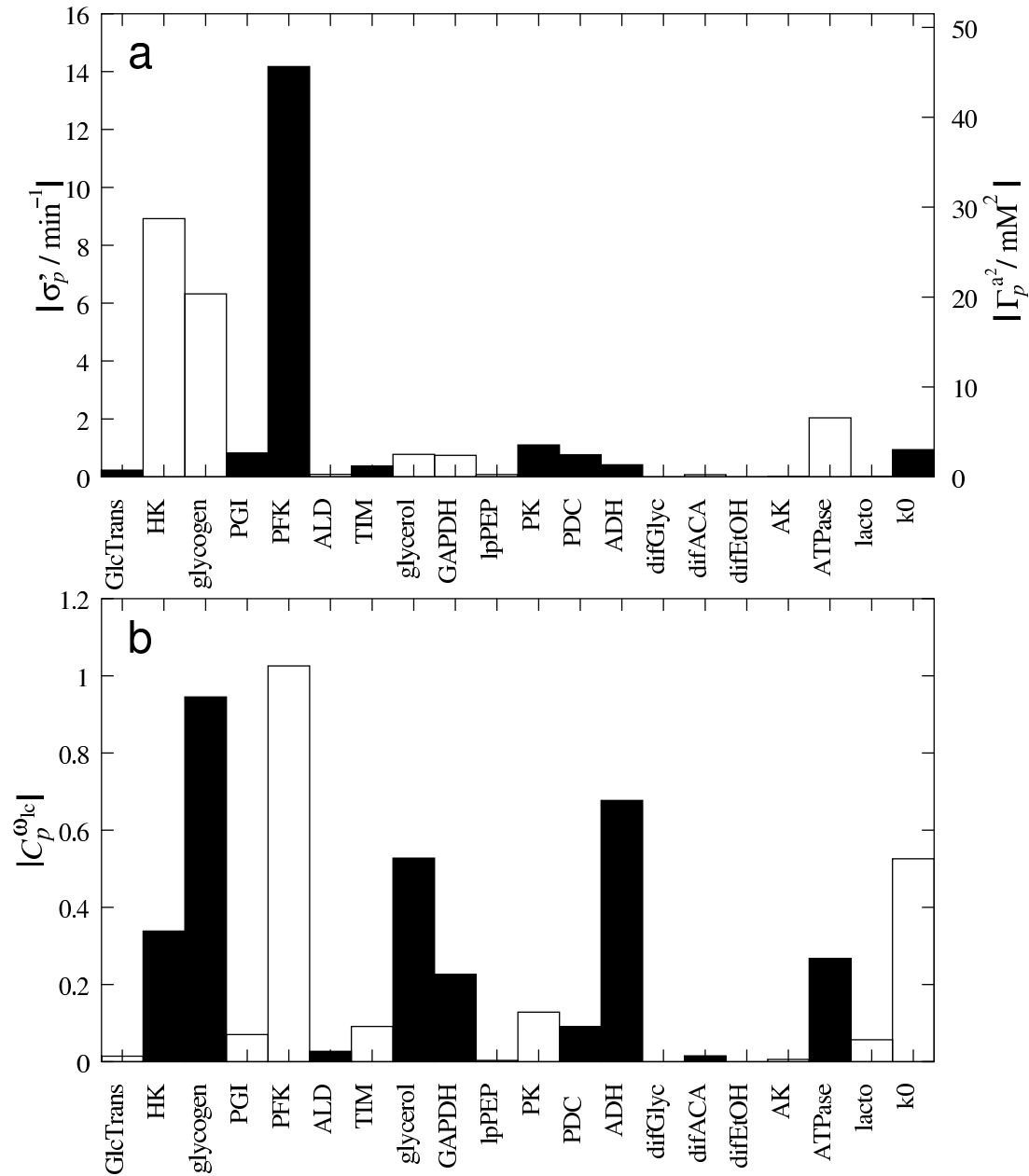
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- Similarly

$$\frac{\partial \omega_{lc}}{\partial h} = \sum_r \frac{\partial \omega_{lc}}{\partial (hE_r)} \frac{\partial (hE_r)}{\partial h} \stackrel{h \equiv 1}{=} \sum_r \frac{\partial \omega_{lc}}{\partial E_r} E_r = \omega_{lc} \sum_r C_{E_r}^{\omega_{lc}} = \omega_{lc}$$

$$\text{such that } \sum_r C_{E_r}^{\omega_{lc}} = 1$$

# Control of amplitude and frequency



# *Hopf interpretation of control coefficients*

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- Stuart-Landau equation:  $\dot{z} = (i\omega_0 + \sigma\mu)z + gz|z|^2$
- Control coefficients for Hopf:

$$\frac{d\text{Re}(\lambda)}{dp/p_0} = \frac{d\text{Re}(\lambda)}{d\mu} = \sigma'_p$$

$$C_p^{\omega_{1c}} = \frac{d\ln(\omega)}{d\ln(p)} = \frac{1}{\omega} \frac{d(\omega)}{d(\mu)} = \frac{1}{\omega_0} \left( \sigma''_p - \sigma'_p \frac{g''}{g'} \right)$$

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- One enzyme usually control several functions.
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- Control coefficients of a metabolic network depends on the stationary state.

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- A model is satisfactory if it describes all available experimental data.
- Measurements of stationary concentrations are usually not sufficient to discriminate between different sets of model parameters.
- The simplest dynamic information is obtained from small instantaneous perturbations of the state of biological systems.
- From a timeseries of responses to random perturbations with all metabolites you can determine the Jacobian.

Sune Danø

Finn Hynne

Mads Ipsen

Mads Madsen

Bjørn Quistorff

Henrik Skødt