# Optimal switching behavior, Just-in-time production

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- Theory Unbranched reaction chain
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#### 3 Michaelis-Menten kinetics

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#### Temporal Optimality

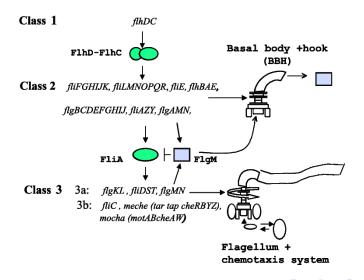
Maximizing a functional of a time-dependent function while respecting a given set of constraints.

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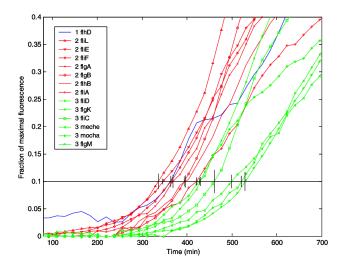
# **Observing temporal optimality**

 Kalir, S., McClure, J., Pabbaraju, K., Southward, C., Ronen, M., Leibler, S., Surette, M. G., and Alon, U. (2001).
 Ordering genes in a flagella pathway by analysis of expression kinetics from living bacteria. *Science*, 292(5524):2080–3.

#### Temporal optimality - can it be observed?

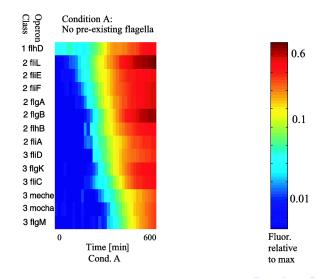


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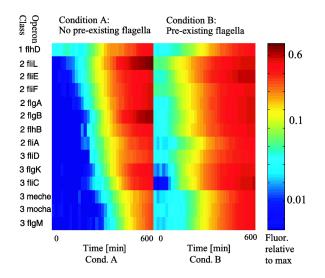
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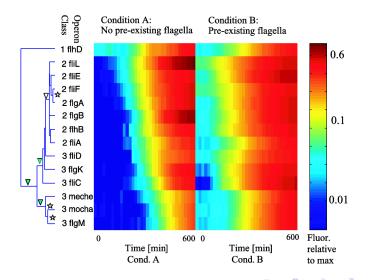
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#### Temporal optimality - can it be observed?



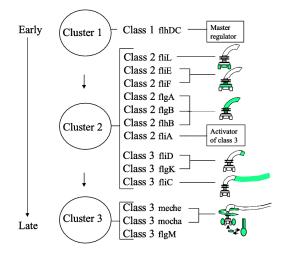
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#### Temporal optimality - can it be observed?



Jonas Maaskola, Kawe Yoocef Optimal switching behavior, Just-in-time production

### Temporal optimality - can it be observed?



# Linear kinetics

#### Theoretical foundation and application

 Klipp, E., Heinrich, R., and Holzhütter, H.-G. (2002).
 Prediction of temporal gene expression: Metabolic optimization by re-distribution of enzyme activities.
 *Eur J Biochem*, 269(22):5406–5413.

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### Unbranched reaction chain, linear kinetics

$$S \xrightarrow{E_1} X_1 \xrightarrow{E_2} X_2 \cdots X_{j-1} \xrightarrow{E_j} \cdots X_{n-1} \xrightarrow{E_n} P$$

System equations

$$\frac{dS}{dt} = -k_1 \cdot E_1 \cdot S \tag{1}$$

$$\frac{dX_i}{dt} = k_i \cdot E_i \cdot X_{i-1} - k_{i+1} \cdot E_{i+1} \cdot X_i$$
(2)

$$\frac{dP}{dt} = k_n \cdot E_n \cdot X_{i-1} \tag{3}$$

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Theory - Unbranched reaction chain Application - Central metabolism of yeast

### Unbranched reaction chain, linear kinetics

$$S \xrightarrow{E_1} X_1 \xrightarrow{E_2} X_2 \cdots X_{j-1} \xrightarrow{E_j} \cdots X_{n-1} \xrightarrow{E_n} P$$

#### Constraint

$$\sum_{i=1}^{n} E_i(t) = E_{\text{tot}}$$
(4)

#### Performance

$$\tau = \frac{1}{C} \int_0^\infty \left( C - P(t) \right) dt \tag{5}$$

$$C = S|_{t=0} \tag{6}$$

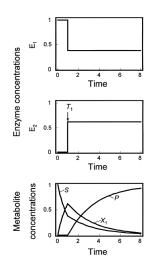
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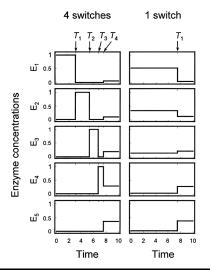
#### Unbranched reaction chain



- Optimize over the Banach-space of piecewise-constant functions
- One intermediary metabolite
- Solution for the optimization problem found explicitely

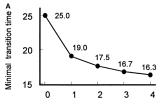
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# Unbranched reaction chain



- Four intermediary metabolites
- Numerical optimization of  $T_i$  and  $E_i(j)$ 
  - Explicit solution of system equations for P(t) depending on T<sub>i</sub> and E<sub>i</sub>(j)
  - 3 Explicit calculation of the transition time  $\tau$
  - Minimization of \(\tau\) by a steepest descent method

### Unbranched reaction chain



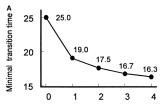
Number of allowed switches (m)

Figure A 4 intermediary metabolites Figure B 0 to 9 intermediary metabolites

- Minimal transition time decreases with number of switches but only until # of switches reaches # of metabolites
- With increasing pathway length the payoff of time-dependent optimality increases

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### Unbranched reaction chain



Number of allowed switches (m)

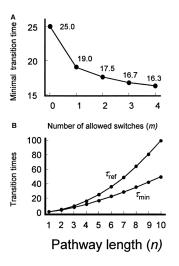
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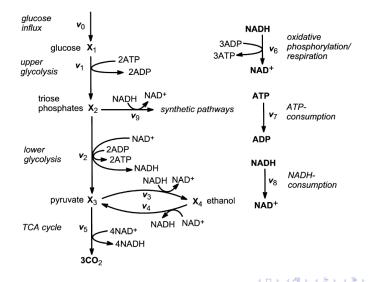
### Unbranched reaction chain



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Theory - Unbranched reaction chain Application - Central metabolism of yeast

### Central metabolism of yeast



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Theory - Unbranched reaction chain Application - Central metabolism of yeast

# Central metabolism of yeast - Mathematical formulation

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System equations

Constraint

$$NADH + NAD^+ = const.$$
 (8)

$$ATP + ADP = const.$$
(9)

$$\sum_{i=1}^{6} E_i(t) \leq E_{tot}$$
(10)

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#### Performance

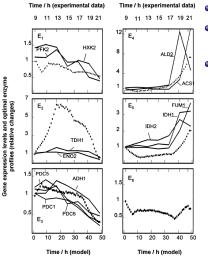
$$\vartheta = t \Theta (ATP - ATP_c) \Theta (NADH - NADH_c)$$
(11)

$$\Theta(x) = \begin{cases} 1 & \text{if } x \ge 0 \\ 0 & \text{if } x < 0 \end{cases}$$
(12)

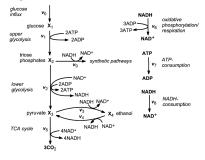
$$\vartheta \rightarrow MAXIMUM$$
 (13)

# Central metabolism of yeast - Optimal enzyme profiles

curves



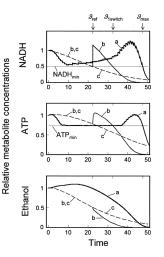
- Optimal enzyme profiles: dotted curvesRelated gene expression profiles: solid
- Optimization performed with a genetic algorithm



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Theory - Unbranched reaction chain Application - Central metabolism of yeast

### Central metabolism of yeast - Time-courses of metabolites



- Curves A optimal enzyme profiles
- Curves B one optimal single switch of enzyme acitvities
- Curves C time-independent enzyme concentrations

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# Towards a Michaelis-Menten kinetics modelling

 R. Heinrich and E. Klipp, J. Theor. Biol. (1996), 182, 243-352 Control Analysis of Unbranched Enzymatic Chains in States of Maximal Activity. *Nat. Genet.*, 36(5):486–91.

# Metabolic Control Analysis

#### MCA results for linear kinetics

- distributions of control coefficients and of enzyme concentrations correspond with eachother
- maximization of the steady-state flux leads to a decrease in enzyme concentrations and control coefficients along the pathway when equilibrium constants > 1

#### Extension to Michaelis Menten kinetics (Heinrich & Klipp, 1996)

- optimization performed also with respect to intrinsic kinetic parameters
- optimal results depend on external substrate concentrations

# Metabolic Control Analysis

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# **Optimization in a Michaelis-Menten Pathway**

 Zaslaver, A., Mayo, A. E., Rosenberg, R., Bashkin, P., Sberro, H., Tsalyuk, M., Surette, M. G., and Alon, U. (2004).
 Just-in-time transcription program in metabolic pathways. *Nat Genet*, 36(5):486–91.

### Unbranched reaction chain, Michaelis-Menten kinetics

$$S_0 \ \stackrel{E_1}{\longrightarrow} \ S_1 \ \stackrel{E_2}{\longrightarrow} \ S_2 \ \stackrel{E_3}{\longrightarrow} \ P$$

metabolites: 
$$\frac{dS_i}{dt} = V$$

$$\frac{dS_i}{dt} = V_i E_i \frac{S_{i-1}}{S_{i-1} + Km_i} - V_{i+1} E_{i+1} \frac{S_i}{S_i + Km_{i+1}} - \alpha S_i$$

enzymes:

$$\frac{dE_i}{dt} = \beta_i \frac{1}{1 + R(t)/k_i} - \alpha E_i$$

 $\alpha$  cell division rate

R(t) active repressor level k; repression coefficient イロトイロトイミト ミーラ マヘベ

### Unbranched reaction chain, Michaelis-Menten kinetics

$$\label{eq:solution} S_0 \ \stackrel{E_1}{\longrightarrow} \ S_1 \ \stackrel{E_2}{\longrightarrow} \ S_2 \ \stackrel{E_3}{\longrightarrow} \ P$$

metabolites: 
$$\frac{dS_i}{dt} = V_i E_i \frac{S_{i-1}}{S_{i-1} + Km_i} - V_{i+1} E_{i+1} \frac{S_i}{S_i + Km_{i+1}} - \alpha S_i$$

$$\frac{dE_i}{dt} = \beta_i \frac{1}{1 + R(t)/k_i} - \alpha E$$

- $\alpha$  cell division rate
- eta maximal promoter activity

### Unbranched reaction chain, Michaelis-Menten kinetics

$$\label{eq:solution} S_0 \ \stackrel{E_1}{\longrightarrow} \ S_1 \ \stackrel{E_2}{\longrightarrow} \ S_2 \ \stackrel{E_3}{\longrightarrow} \ P$$

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R(t) active repressor level  $k_i$  repression coefficient

-2

# Unbranched reaction chain, Michaelis-Menten kinetics

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enzymes:

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- $\alpha$  cell division rate
- $\beta$  maximal promoter activity

R(t) active repressor level  $k_i$  repression coefficient

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### Unbranched reaction chain, Michaelis-Menten kinetics

$$S_0 \ \stackrel{E_1}{\longrightarrow} \ S_1 \ \stackrel{E_2}{\longrightarrow} \ S_2 \ \stackrel{E_3}{\longrightarrow} \ P$$

Optimality with respect to a cost function to be minimized:

$$C = a \sum_{i} \int_{0}^{T} \beta_{i} \frac{1}{1 + R(t)/k_{i}} dt + \int_{0}^{T} \left| \frac{dP}{dt} - \frac{dP}{dt}_{goal} \right| dt$$

#### Goals:

- minimize the total enzyme concentration used
- as fast as possible substrate-product turnover

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### Unbranched reaction chain, Michaelis-Menten kinetics

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$$S_0 \ \xrightarrow{E_1} \ S_1 \ \xrightarrow{E_2} \ S_2 \ \xrightarrow{E_3} \ P$$

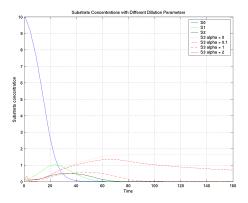
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#### Goals:

- minimize the total enzyme concentration used
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#### Results: Substrates in Time at Different Cell Division Rates

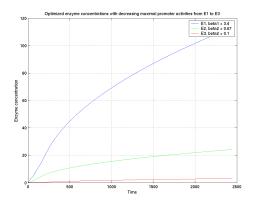


 dilution effects due to cell division determine the slope of the product concentration (red curves)

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#### Results: Optimal Enzyme Concentrations

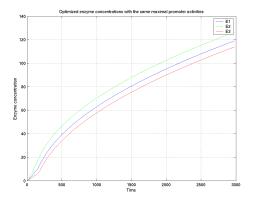


• optimal promoter activity levels are distributed through time in a hierarchical manner  $\beta_1 > \beta_2 > \beta_3$  just as the respective enzyme concentrations

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#### Results: Enzyme Concentrations at a Uniform Promoter Activity

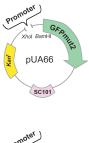


• reference enzyme concentrations levels with the same promoter activity levels  $\beta_1 = \beta_2 = \beta_3$ 

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Theoretical Results Just-in-time Transcription Program in Aminoacid Biosynthesis Pathways

### Aminonacid Biosynthesis Pathways

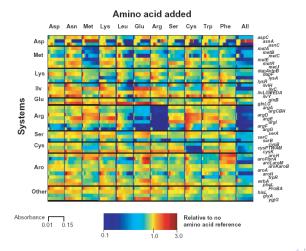




- time measurements of promoter activity of genes involved in aminoacid biosynthesis (AAB) using GFP and Lux Reporter genes (resolution: 8 minutes)
- activity of AAB-Promoters in a medium lacking all amino-acids vs. a medium with one aminoacid and all aminoacids

Theoretical Results Just-in-time Transcription Program in Aminoacid Biosynthesis Pathways

### Aminonacid Biosynthesis Pathways



- decrease of AAB promoter activity of involved genes when adding the respective aminoacid to the medium
- decrease of activity of all promoters when adding all aminoacids

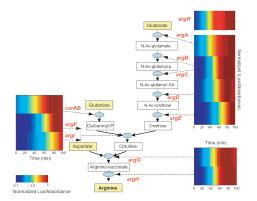
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Theoretical Results Just-in-time Transcription Program in Aminoacid Biosynthesis Pathways

문제 문

### Temporal Order: Arginine Biosynthesis

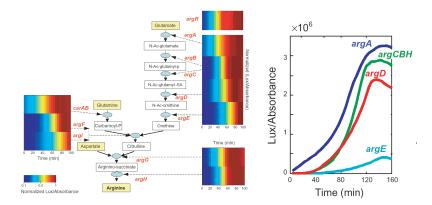


# • Observing temporal ordering in promoter activity profiles and in unnormalized expression kinetics

Theoretical Results Just-in-time Transcription Program in Aminoacid Biosynthesis Pathways

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### Temporal Order: Arginine Biosynthesis

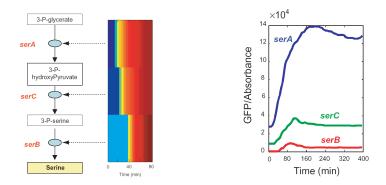


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Theoretical Results Just-in-time Transcription Program in Aminoacid Biosynthesis Pathways

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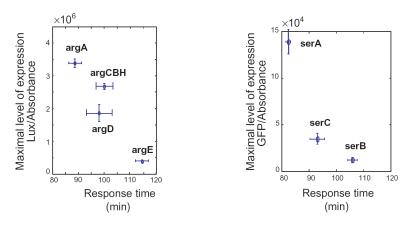
#### Temporal Order: Serine Biosynthesis



 Observing temporal ordering in promoter activity profiles and in unnormalized expression kinetics

Theoretical Results Just-in-time Transcription Program in Aminoacid Biosynthesis Pathways

#### Early Pathway Appearence, a Higher Promoter Activity



• The maximal promotor activity level is higher and it is reached faster for enzymes appearing earlier in the pathway (left: arginine, right: serine)

- evolutionary development of biological systems implies a non-random distribution of parameters within pathways
- optimization is performed with respect to certain goal functions
- introduced optimality principles in unbranched linear and Michaelis-Menten kinetic pathways
  - temporal optimality
  - switching behaviour
  - just-in-time production

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#### Take-home messages

#### Principle of temporal optimality

Maximizing a functional of time dependent functions while respecting a given set of constraints

#### Just-in-time production

Producing enzymes right when they are needed is often optimal

# Bibliography I

Kalir, S., McClure, J., Pabbaraju, K., Southward, C., Ronen, M., Leibler, S., Surette, M. G., and Alon, U. (2001). Ordering genes in a flagella pathway by analysis of expression kinetics from living bacteria. Science, 292(5524):2080-3.

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