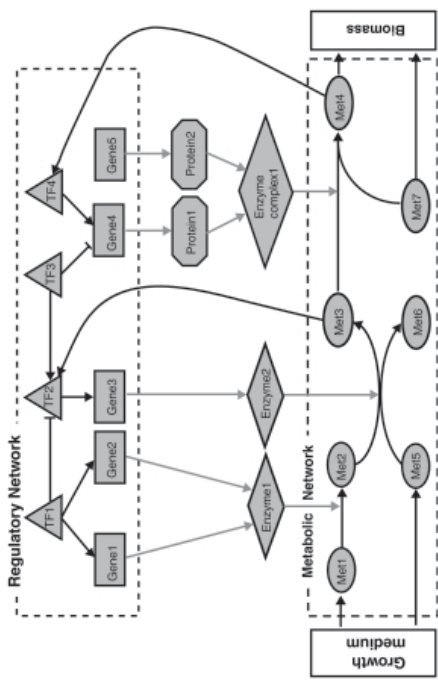




# Metabolism and gene regulation



Shlomi et al. 2007

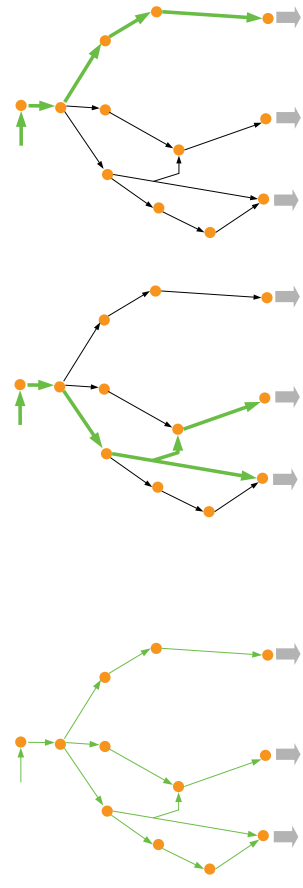
- ▷ Gene products/enzymes catalyse reactions.
- ▷ Genes are regulated by gene and reaction products.



# Working hypothesis

Palinkas/Builk/Bockmayr/Holzhtüter 14

Switching between pathways may improve overall efficiency:

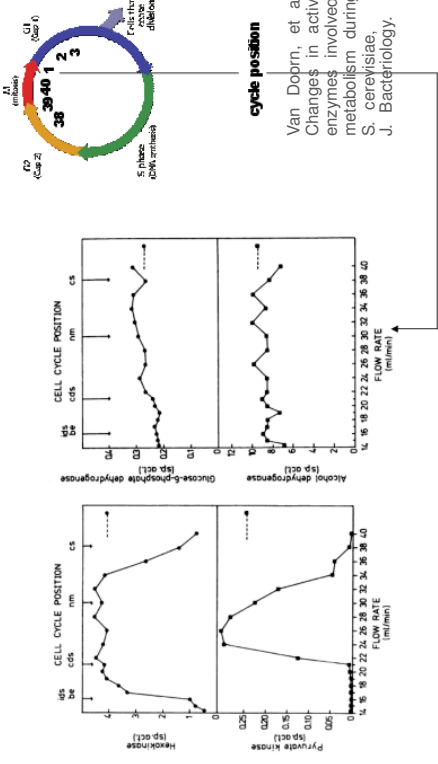


The output is produced by a single flux mode produce the output with higher flux rates.



# 9. Alterations in metabolism

- ▷ Metabolism adapts to changing environments.
- ▷ Even in constant environments, metabolism exhibits changes in enzyme activity.
- ▷ Significant metabolic alterations during cell cycle.



Van Dohrn, et al. (1988) Changes in activities of several enzymes involved in carbohydrate metabolism during the cell cycle of S. cerevisiae, J. Bacteriology. 170, 4808-15.



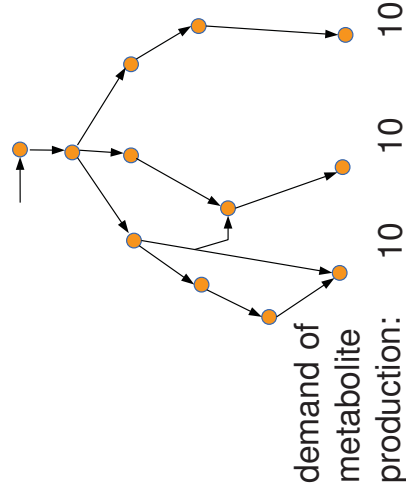
# When is this possible ?

- ▷ Assume metabolic network with internal metabolites  $M^\#$  and output metabolites  $M^*$ , for which there is a demand  $\Gamma$ .
- ▷ A flux mode  $v$  which is executed for some time  $\tau \geq 0$  satisfies the demand if  $\tau \cdot S^* v \geq \Gamma$ .
- ▷ Two flux modes  $v^1, v^2$  which are executed consecutively for time  $\tau_1$  resp.  $\tau_2$  satisfy the demand if  $\tau_1 \cdot S^* v^1 + \tau_2 \cdot S^* v^2 \geq \Gamma$ .
- ▷ Can we be more efficient with two flux modes  $v^1, v^2$  than with one flux mode  $v$  ?
- ▷ In an FBA context, this is not possible, since we may always choose  $v = \frac{\tau_1}{\tau_1 + \tau_2} v^1 + \frac{\tau_2}{\tau_1 + \tau_2} v^2$ , which has the same efficiency  $\tau = \tau_1 + \tau_2$ .



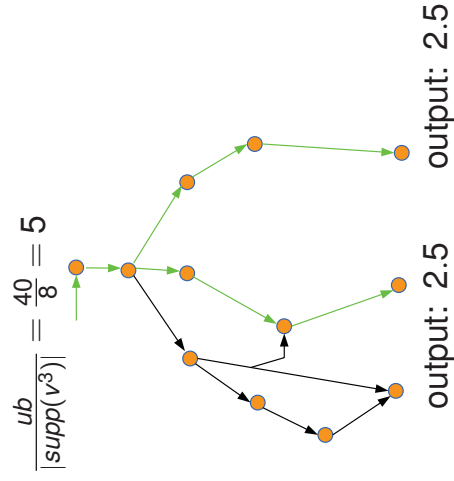
# Illustrating the principle

Assume flux bounds  $0 \leq v \leq ub/|supp(v)|$ , here  $ub = 40$ .



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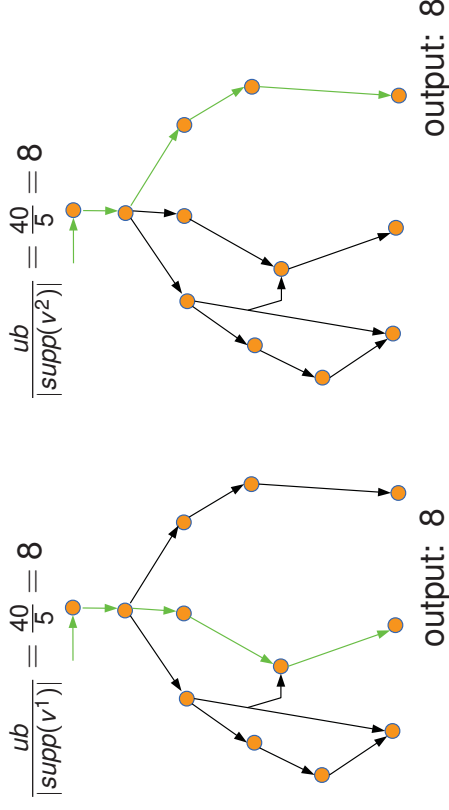


To satisfy demand, need  $4 \cdot v^3$ , i.e.,  $\tau = 4$ .



# Illustrating the principle

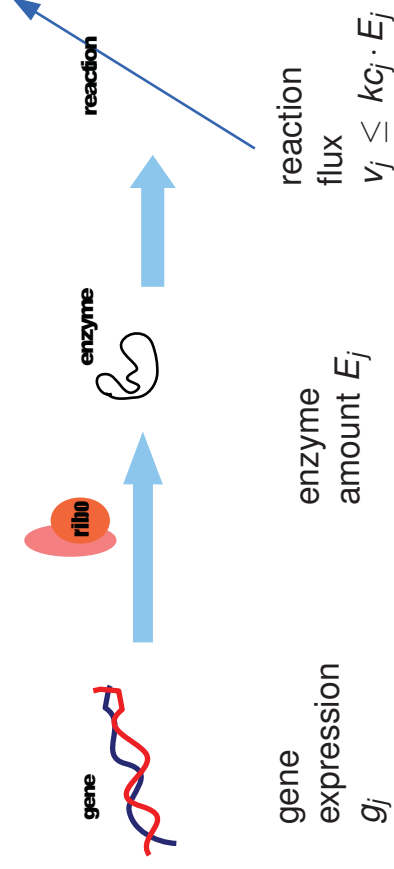
Assume flux bounds  $0 \leq v \leq ub/|supp(v)|$ , here  $ub = 40$ .



To satisfy demand, need  $1.25 \cdot v^1 + 1.25 \cdot v^2$ , i.e.,  $\tau = 2.5$ .



# Modeling approach



**Basic assumption:** Total amount of protein in the cell is limited.



## Sharing available enzymes

- ▷ Synthesis and degradation of  $i$ -th enzyme:

$$dE_j/dt = g_j k_s A - kd_j E_j,$$

where  $A$  is the total mass of free amino acids.

- ▷ Steady-state condition:
 
$$E_j = g_j A \eta_j, \text{ with } \eta_j = ks_j / kd_j.$$
- ▷ Assume **fixed total mass of amino acids**

$$A_{tot} = A + \sum E_i \gamma_i \left[ = A + \sum (g_i A \eta_i) \gamma_i = A(1 + \sum g_i \gamma_i \eta_i) \right],$$
 where  $\gamma_i$  is the molecular mass of the  $i$ -th enzyme.
- ▷ Resulting **upper bound**:

$$v_j \leq kc_j \cdot E_j = kc_j \cdot A_{tot} \frac{g_j \eta_j}{1 + \sum_i g_i \gamma_i \eta_i}$$



## Optimizing cellular output

- ▷ Internal metabolites  $M^\#$ , output metabolites  $M^*$ , all reactions irreversible.
- ▷ Assume cell has to produce a certain amount  $\Gamma$  of output metabolites  $M^*$ .
- ▷ Allow using up to  $l$  flux modes  $v^1, \dots, v^l$  in  $l$  consecutive time intervals of length  $\tau_1, \dots, \tau_l$ .
- ▷ Output in  $k$ -th time interval:  $\tau_k \cdot S^* v^k$
- ▷ **Goal**: Minimize the total time  $\tau_1 + \dots + \tau_l$  needed to produce  $\Gamma$ .
- ▷ Lower bounds  $lb \geq 0$  (minimum activity of certain reactions).



## Non-linear mixed 0-1 optimisation problem

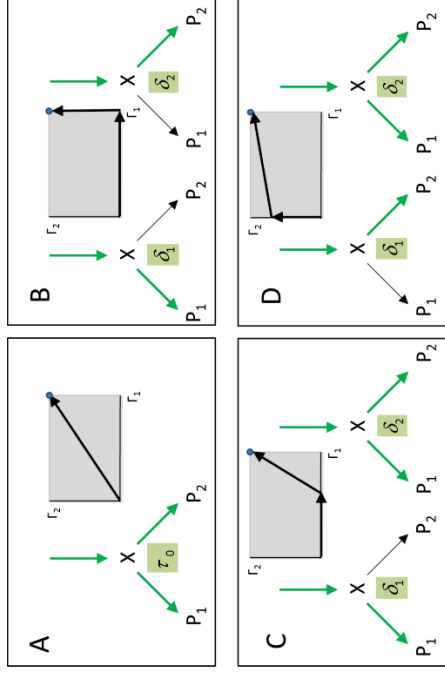
$$\begin{aligned} \min \sum_{k=1}^l \tau_k & \\ S^\# v^k = 0, & \quad \sum_{k=1}^l \tau_k S^* v^k \geq \Gamma, \\ lb_j \leq v_j^k \leq kc_j \cdot A_{tot} \frac{g_j \eta_j}{1 + \sum_i g_i \gamma_i \eta_i}, & \\ l \in \mathbb{N}, k = 1, \dots, l, j = 1, \dots, n, & \\ \tau_k \in \mathbb{R}_{\geq 0}, v^k \in \mathbb{R}^n, g^k \in \{0, 1\}^n. & \end{aligned}$$

↪ can be reformulated as mixed 0-1 quadratic program (MIQP).

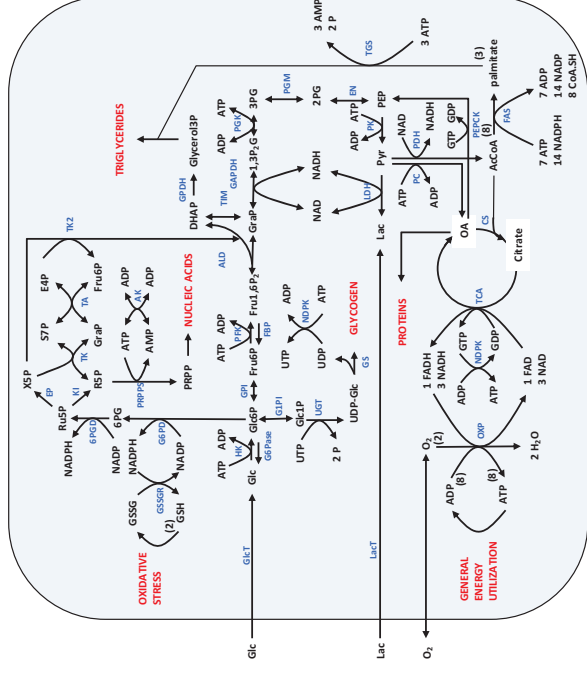


## Modeling gene expression levels

- ▷  $g \in [0, 1]^n$ : fine tuning of genes  
(similar to FBA with Molecular Crowding, cf. Beg et al. 2007)
  - ↪ feasible region is convex
  - ↪ no improvement possible through switching
- ▷  $g \in \{0, 1\}^n$ : genes switched on or off individually.
- ▷  $g \in U \subset \{0, 1\}^n$ : genes switched on or off in functional groups,
  - ↪ biologically more meaningful  
(e.g. common transcription factors)
  - ↪ may use **MinModes** (Hoffmann et al. 2006)



- ▷ Improvement by switching depends on parameter values.
- ▷ Random sampling gives improvement in 83% of the cases.
- ▷ Higher improvement if more protein is spent downstream.



Switching MinModes On and Off

Sub	/	$\Sigma$	$\tau_1$	$\tau_2$	$\tau_3$	$\tau_4$	# reaction switches	# active reactions
glc, lac	1	7.405h	2.302h	3.242h			0	41
	2	5.544h	2.429h	0.176h	2.201h		14	29,43
	3	4.805h	<b>2.214h</b>	<b>0.098h</b>	<b>0.118h</b>	<b>2.362h</b>	26 (14/12)	35,41,29
	4	<b>4.792h</b>					<b>26 (8/10)</b>	<b>29,37,41,35</b>
glc	1	10.700h	0.203h	7.764h			0	41
	2	7.967h	0.239h	5.832h	1.559h		9	38,35
	3	7.631h	0.071h	1.386h	6.029h	0.121h	11 (8/3)	39,35,32
	4	7.607h					14 (4/3/7)	32,32,35,36
lac	1	7.405h	0.728h	5.214h			0	41
	2	5.942h	2.688h	2.429h	0.728h		7	40,35
	3	5.845h	0.210h	2.688h	2.429h	0.437h	9 (2/7)	33,35,40
	4	5.764h					10 (3/2/5)	36,33,35,38