



# Resource allocation in microorganisms: Some control-theoretical problems

Hidde de Jong  
IBIS  
INRIA Grenoble – Rhône-Alpes  
Hidde.de-Jong@inria.fr

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# IBIS: bacterial systems biology

- **IBIS**: systems biology group at INRIA/Université Grenoble Alpes/CNRS in Grenoble  
Microbiologists, computer scientists, mathematicians, physicists, ...



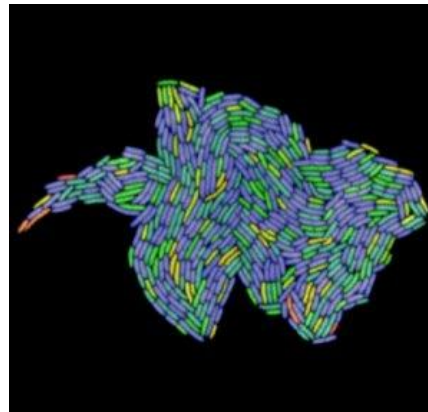
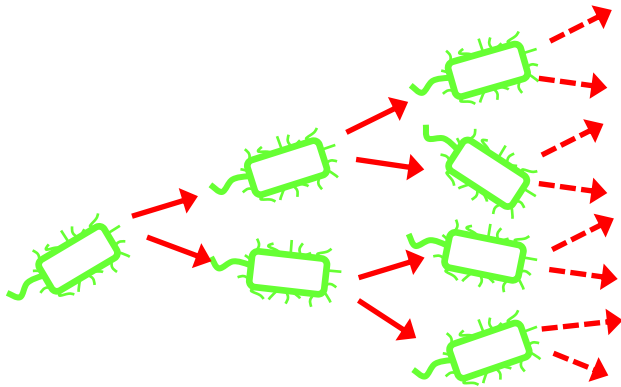
<https://team.inria.fr/ibis/>



- **Objective:** understanding, predicting, and controlling the dynamics of regulatory networks in bacteria
  - Specific research problems shaped by **biological questions**
  - Problems often addressed by combination of **models and experiments**

# Bacterial growth

- Bacteria are unicellular organisms geared towards **growth**  
*E. coli* cells have doubling times up to 20 min



Stewart *et al.* (2005), *PLoS Biol.*, 3(2): e45

- Changes in environment cause **adaptation** of growth rate, and more generally, change functioning of bacterial cell

# Bacterial growth and gene expression

- Growth transitions involve changes in gene expression
  - Macromolecular composition of the cell

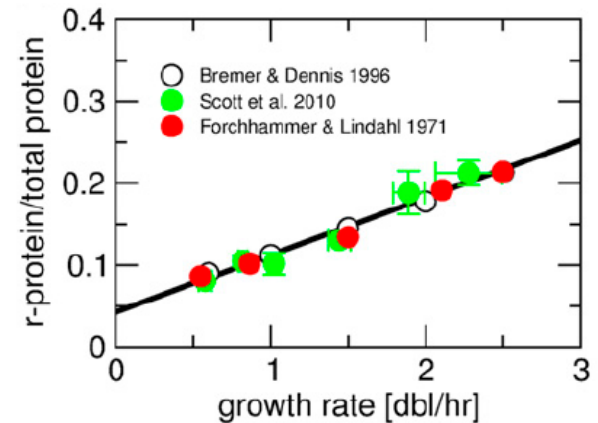
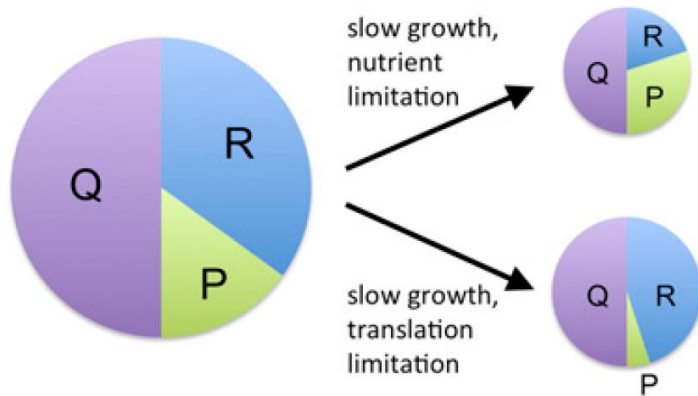
TABLE 2 Macromolecular composition of exponentially growing *E. coli* B/r as a function of growth rate at 37°C<sup>a</sup>

Parameter	Symbol	Units	At $\tau$ (min) and $\mu$ (doublings per h):					Observed parameter(s)
			$\tau$ , 100 $\mu$ , 0.6	$\tau$ , 60 $\mu$ , 1.0	$\tau$ , 40 $\mu$ , 1.5	$\tau$ , 30 $\mu$ , 2.0	$\tau$ , 24 $\mu$ , 2.5	
Protein/mass	$P_M$	$10^{17}$ aa/OD <sub>460</sub>	6.5	5.8	5.2	5.1	5.0	$P, M$
RNA/mass	$R_M$	$10^{16}$ nucl./OD <sub>460</sub>	4.3	4.9	5.7	6.6	7.8	$R, M$
DNA/mass	$G_M$	$10^8$ genomes/OD <sub>460</sub>	18.3	12.4	9.3	8.0	7.6	$G, M$
Cell no./mass	$C_M$	$10^8$ cells/OD <sub>460</sub>	11.7	9.7	9.0	2.7	2.0	$C$
(P + R + G)/M	$PRD_M$	$\mu\text{g}/\text{OD}_{460}$	149	137	129	131	136	
Protein/genome	$P_G$	$10^8$ aa residues	3.5	4.7	5.6	6.3	6.6	$P_M, G_M$
RNA/genome	$R_G$	$10^7$ nucl. residues	2.3	4.0	6.1	8.2	10.3	$R_M, G_M$
Origins/genome	$O_G$	Dimensionless	1.25	1.32	1.44	1.58	1.73	$C$
Protein/origin	$P_O$	$10^8$ aa residues	2.8	3.6	3.9	4.0	3.8	$P_G, O_G$
Protein/cell	$P_C$	$10^8$ aa residues	5.6	8.7	13.0	18.9	25.0	$P_M, C_M$
	$P_C$ ( $\mu\text{g}$ )	$\mu\text{g}/10^9$ cells	100	156	234	340	450	
RNA/cell	$R_C$	$10^7$ nucl. residues	3.7	7.3	14.3	24.4	39.0	$R_M, C_M$
	$R_C$ ( $\mu\text{g}$ )	$\mu\text{g}/10^9$ cells	20	39	77	132	211	
DNA/cell	$G_C$	genome equiv./cell	1.6	1.8	2.3	3.0	3.8	$C, D$
	$G_C$ ( $\mu\text{g}$ )	$\mu\text{g}/10^9$ cells	7.6	9.0	11.3	14.4	18.3	
Mass/cell	$M_C$	OD <sub>460</sub> units/ $10^9$ cells	0.85	1.49	2.5	3.7	5.0	$C_M$
	$M_C$ ( $\mu\text{g}$ )	$\mu\text{g}$ dry weight/ $10^9$ cells	148	258	433	641	865	$\mu\text{g}/\text{OD}_{460}$
Sum P + R + G	$PRD_C$	$\mu\text{g}/10^9$ cells	127	204	322	486	679	$P_C, R_C, G_C$ (in $\mu\text{g}$ )
Origins/cell	$O_C$	no./cell	1.96	2.43	3.36	4.70	6.54	$C, D$
Termini/cell	$T_C$	no./cell	1.23	1.37	1.54	1.74	1.94	$D$
Replication forks/cell	$F_C$	no./cell	1.46	2.14	3.64	5.92	9.19	$C, D$

Bremer and Dennis (1996), *Escherichia Coli and Salmonella*, ASM Press, 1553-69

# Bacterial growth and gene expression

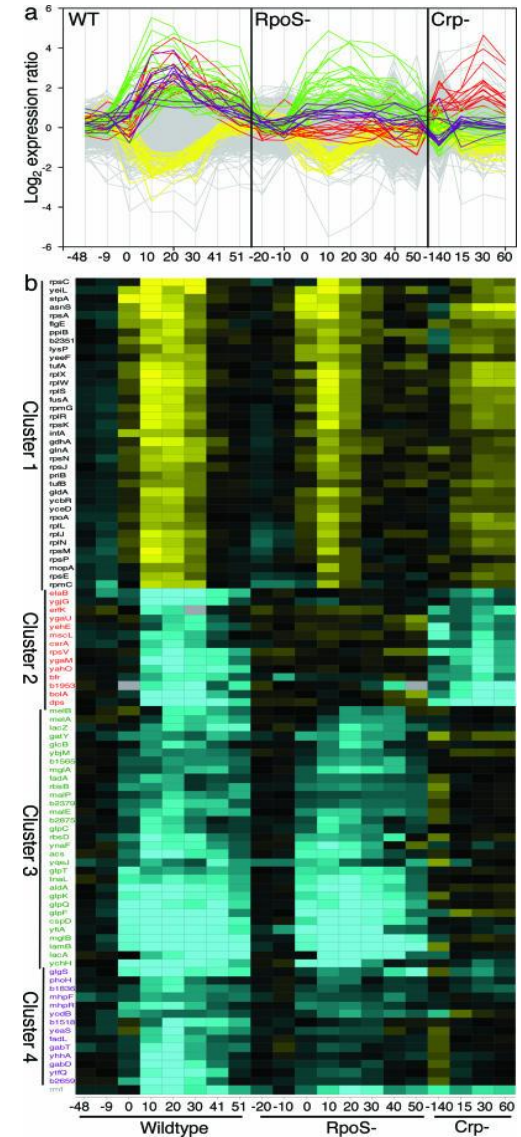
- Growth transitions involve changes in **gene expression**
  - Macromolecular composition of the cell
  - Distribution of proteins over different categories



Klump *et al.* (2013), *Proc. Natl Acad. Sci. USA*, 110(42):16754-9

# Bacterial growth and gene expression

- Growth transitions involve changes in **gene expression**
  - Macromolecular composition of the cell
  - Distribution of proteins over different categories
  - Expression of genes required for specific cellular functions



Traxler *et al.* (2006), *Proc. Natl. Acad. Sci. USA*, 103(7):2374–9

# Overview

- **Adaptation of gene expression and growth as a dynamical resource allocation problem**

Giordano *et al.* (2016), *PLoS Comput. Biol.*, 12(3): e1004802

- **Control of growth rate by reengineering of transcriptional control of RNA polymerase**

Izard, Gomez Balderas *et al.* (2015), *Mol. Syst. Biol.*, 11:840

# Self-replicator model of bacterial growth

- Reorganization of gene expression in response to changes in environment is **resource allocation problem**
  - How does cell optimally distribute available resources over cellular functions?
  - For microorganisms, “optimal” often interpreted as “enabling maximum growth”
- Resource allocation in bacteria can be studied using simplified **self-replicator models**

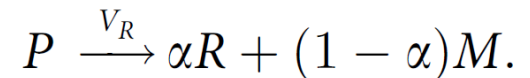
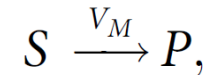
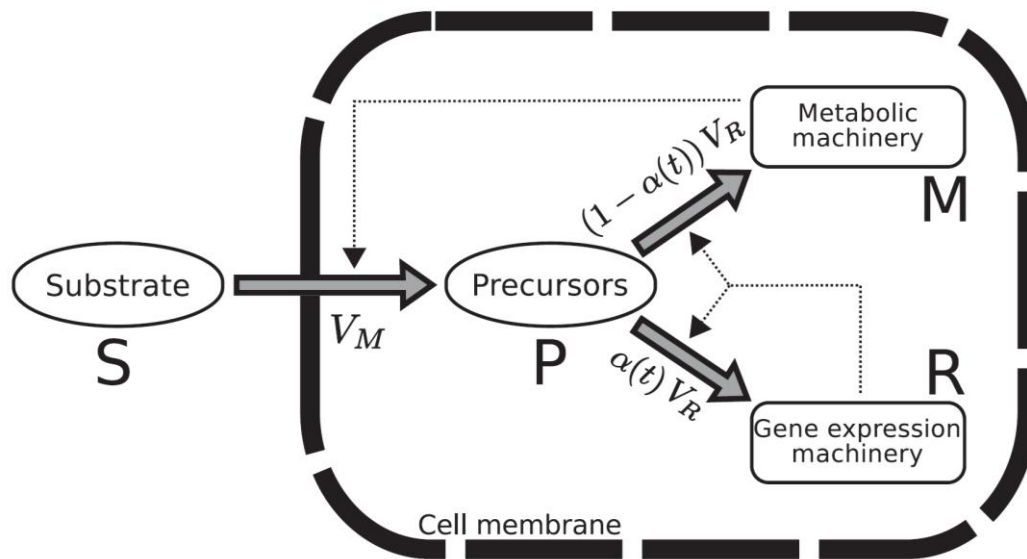
Molenaar *et al.* (2009), *Mol. Syst. Biol.*, 5:323

Hinshelwood (1952), *J. Chem Soc. (Res.)*, 745-55



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- Resource allocation in bacteria can be studied using simplified **self-replicator models**



$$V \circ l = \beta (M + R),$$

$$\mu = \frac{1}{V \circ l} \frac{dV \circ l}{dt}$$

Giordano et al. (2016), *PLoS Comput. Biol.*, 12(3): e1004802

# Self-replicator model of bacterial growth

- Model of self-replicator

$$\frac{dp}{dt} = v_M(s, r) - v_R(p, r) (1 + \beta p),$$

$$\frac{dr}{dt} = v_R(p, r) (\alpha(t) - \beta r),$$

$$r + m = 1/\beta$$

with

$$v_M(s, r) = k_M m \frac{s}{K_M + s} = k_M (1/\beta - r) \frac{s}{K_M + s},$$

$$v_R(p, r) = k_R r \frac{p}{K_R + p},$$

$$\mu = \frac{1}{\text{Vol}} \frac{d\text{Vol}}{dt} = \frac{1}{M + R} \frac{d(M + R)}{dt} = \beta v_R(p, r).$$

Giordano et al. (2016), *PLoS Comput. Biol.*, 12(3): e1004802

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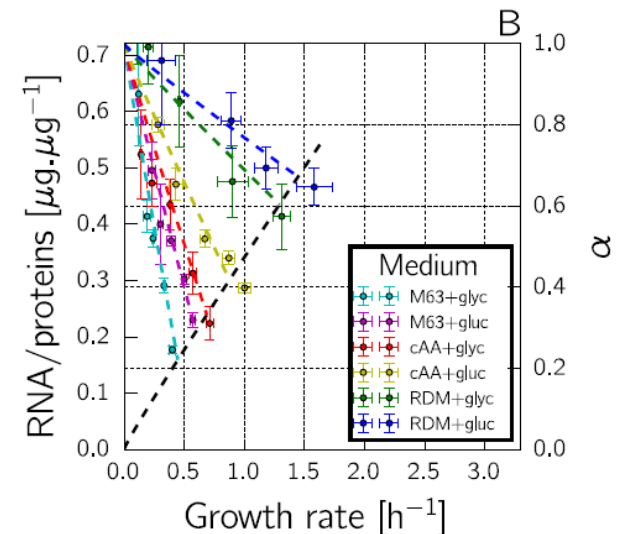
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# Self-replicator model and growth laws

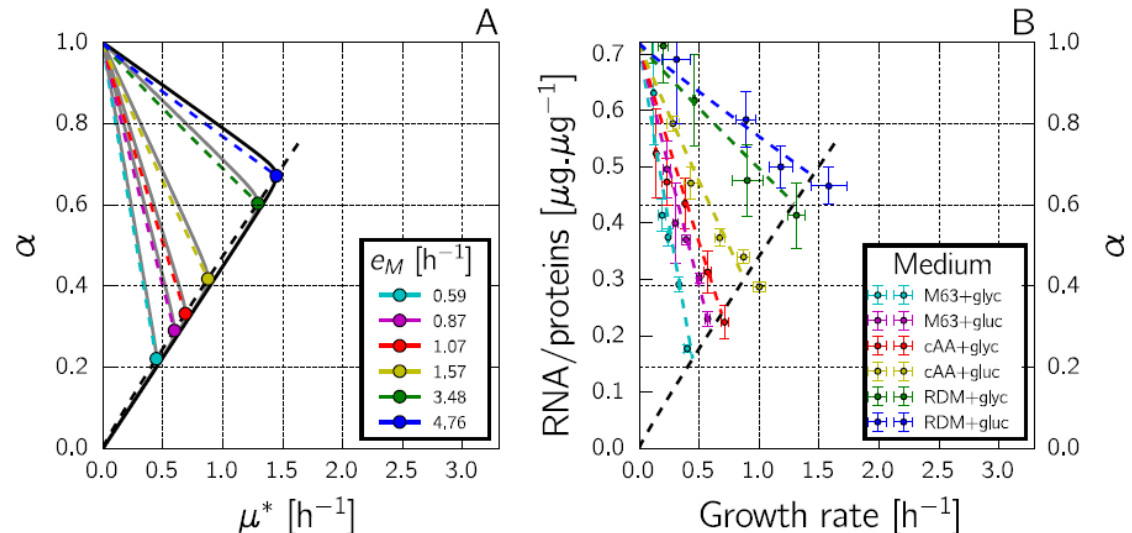
- Empirical **growth laws** show linear relation between growth rate and RNA/protein fraction at steady state  
RNA/protein fraction proxy for resource allocation parameter  $\alpha$



Scott *et al.* (2010), *Science*,  
330(6007):1099-102

# Self-replicator model and growth laws

- Empirical **growth laws** show linear relation between growth rate and RNA/protein fraction at steady state
  - RNA/protein fraction proxy for resource allocation parameter  $\alpha$
- Self-replicator model reproduces steady-state growth laws under assumption of growth-rate maximization
  - Reasonable parameter values from literature



Scott *et al.* (2010), *Science*,  
330(6007):1099-102

# Dynamical adaptation of bacterial growth

- Bacteria rarely in steady state (constant environment) outside laboratory
- **Question:** what would be optimal resource allocation scheme in changing environment?
  - Prototypical change in environment: nutrient upshift or downshift
- In framework of self-replicator, question can be formulated as **optimal control problem**

$$J(\alpha) = \int_0^\tau \mu(t) dt = \int_0^\tau \beta v_R(p, r) dt,$$

where  $\alpha$  is a time-dependent function

Find  $\alpha_{opt} = \arg \max_{\alpha \in \mathcal{U}} J(\alpha)$ .

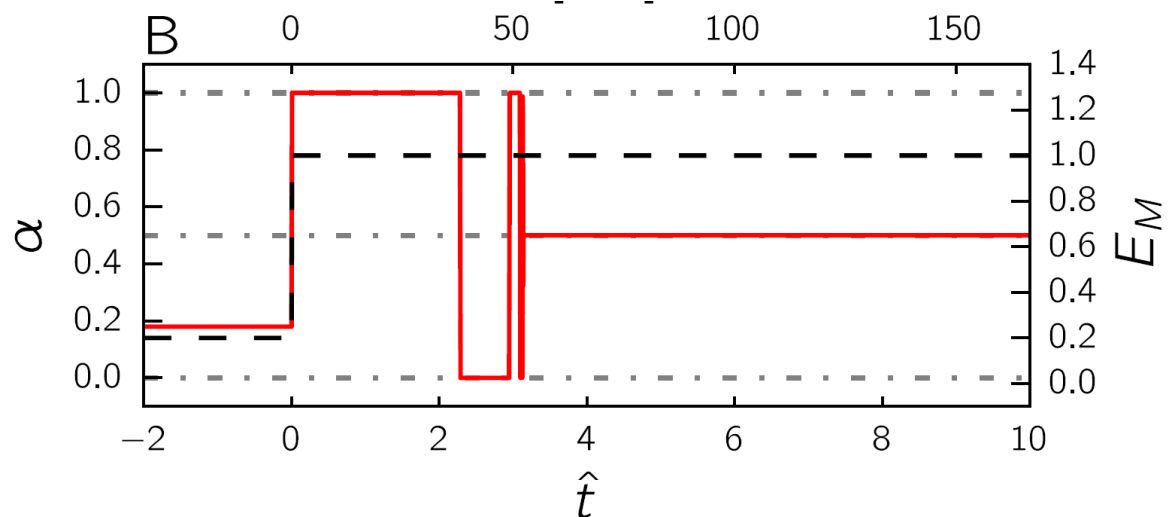
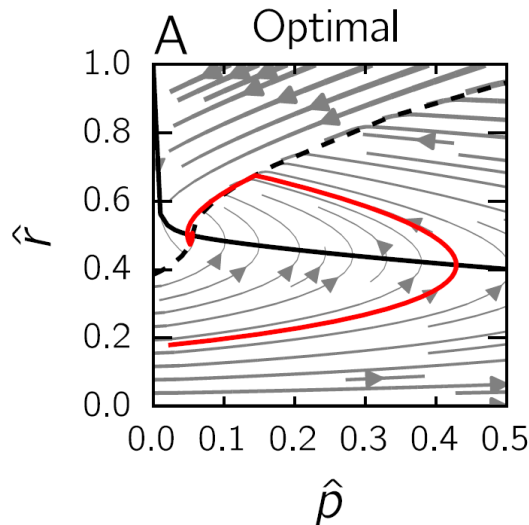
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- Optimal control problem can be solved using version of Pontryagin Maximum Principle
  - Nondimensionalized system, Infinite Horizon Maximum Principle, Kelley condition, chattering arc, switching curve, turnpike property

Giordano et al. (2016), *PLoS Comput. Biol.*, 12(3): e1004802

# Dynamical adaptation of bacterial growth

- Optimal resource allocation scheme is **bang-bang singular**
  - Sequence of switches between  $\alpha = 1$  (maximal synthesis of gene expression machinery) and  $\alpha = 0$  (maximal synthesis of metabolic machinery)
  - $\alpha$  is then set to  $\alpha_{opt}^*$ , value leading to maximal growth rate in new medium
  - Numerical solution using BOCOP





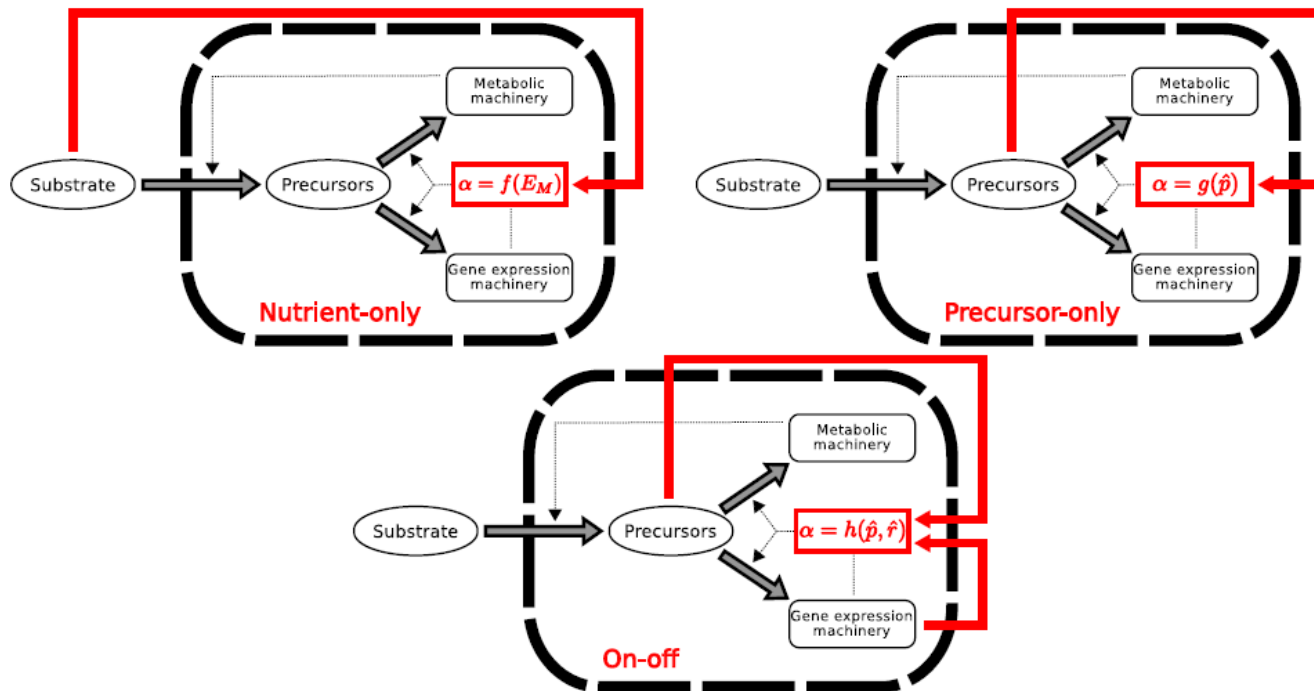
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  - Numerical solution using BOCOP
- Optimal resource allocation scheme provides gold standard against which actual strategies can be compared

# Feedback control strategies for growth-rate adaptation

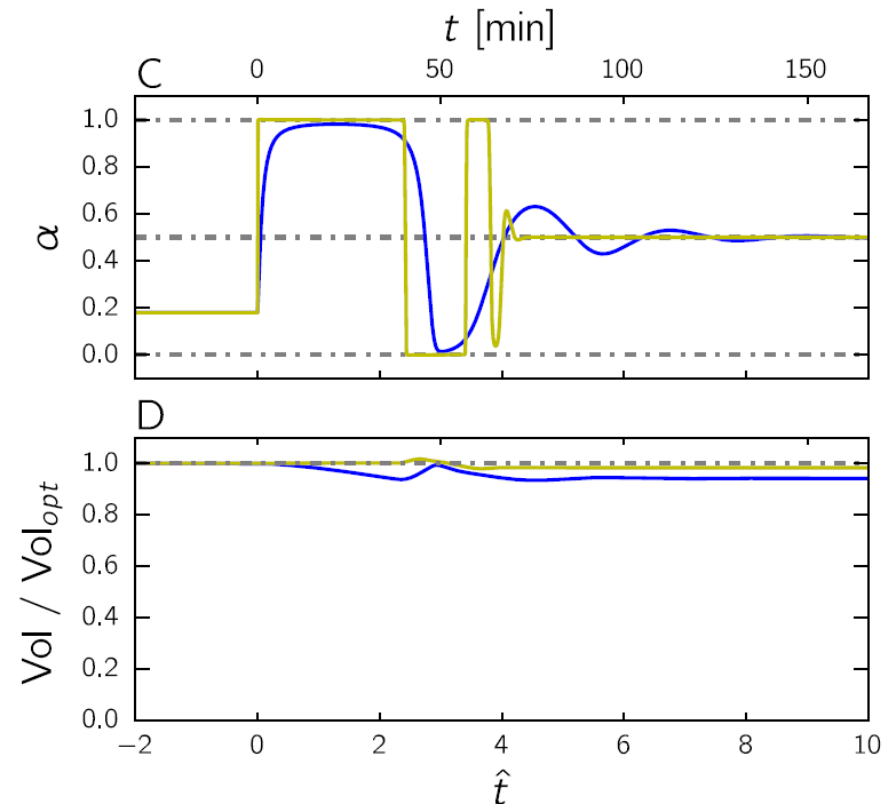
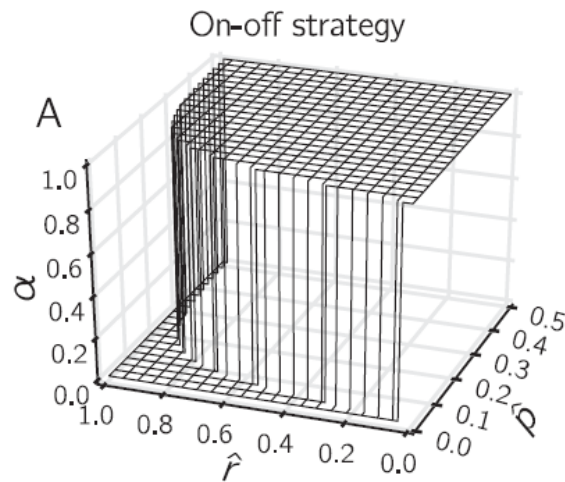
- Different strategies can implement **feedback growth control** for adapting resource allocation in response to changes in environment

Exploit information on system variables and/or environment



# Feedback control strategies for growth-rate adaptation

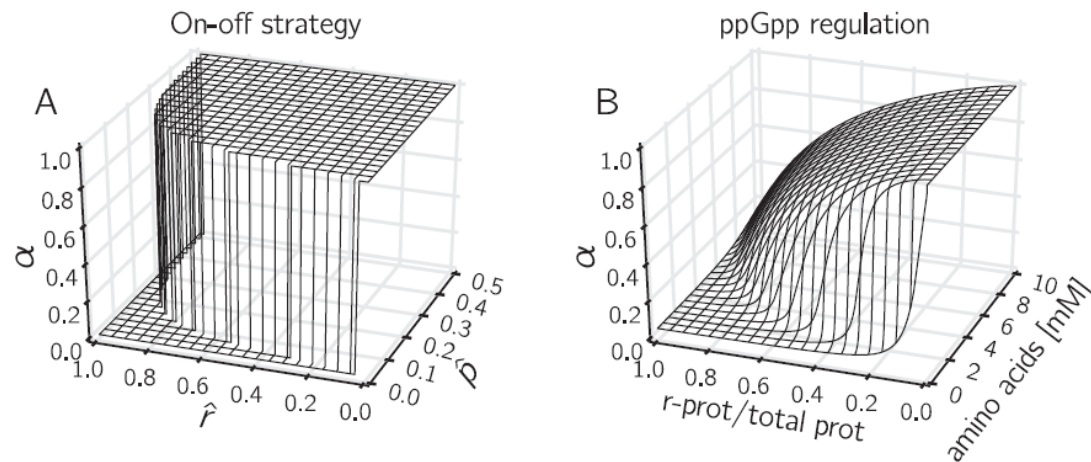
- **On-off control strategy** leads to near-optimal behavior
  - Drive self-replicator to optimal balance between precursors and gene expression machinery at all times



# Feedback control strategies for growth-rate adaptation

- **On-off control strategy** leads to near-optimal behavior
  - Drive self-replicator to optimal balance between precursors and gene expression machinery at all times
- On-off strategy resembles effect of ppGpp regulation in bacteria
  - Effect of ppGpp regulation derived from kinetic model of ppGpp system

Bosdriesz *et al.* (2015), *FEBS J.*, 282:209-



# Experimental test of growth-rate adaptation

- Bang-bang schemes have been identified before in biology  
Development of intestinal crypts: minimize time to attain mature crypt  
*Iitzkovitz et al. (2012), Cell, 148(3):608-19*
- Some old data available in the literature consistent with bang-bang profiles after nutrient upshift in bacteria  
Oscillatory patterns in ppGpp concentrations and ribosome synthesis rates
- However, low resolution and population-level measurements

# Conclusions

- Bacterial growth can be profitably modeled by means of **self-replicators**
- Dynamic growth-rate adaptation in bacteria can be framed as **optimal control problem**
  - Predicted optimal scheme for growth-rate adaptation has bang-bang singular profile
- Ubiquitous ppGpp system has structural similarities with feedback control strategy approaching theoretical maximum
  - Sensing discrepancy between precursor/ribosome concentrations, adjust ribosome synthesis in on-off fashion
- Is predicted optimal resource allocation strategy observed experimentally?
  - Extension of self-replicators: cost of regulation, energy metabolism, ...

# Overview

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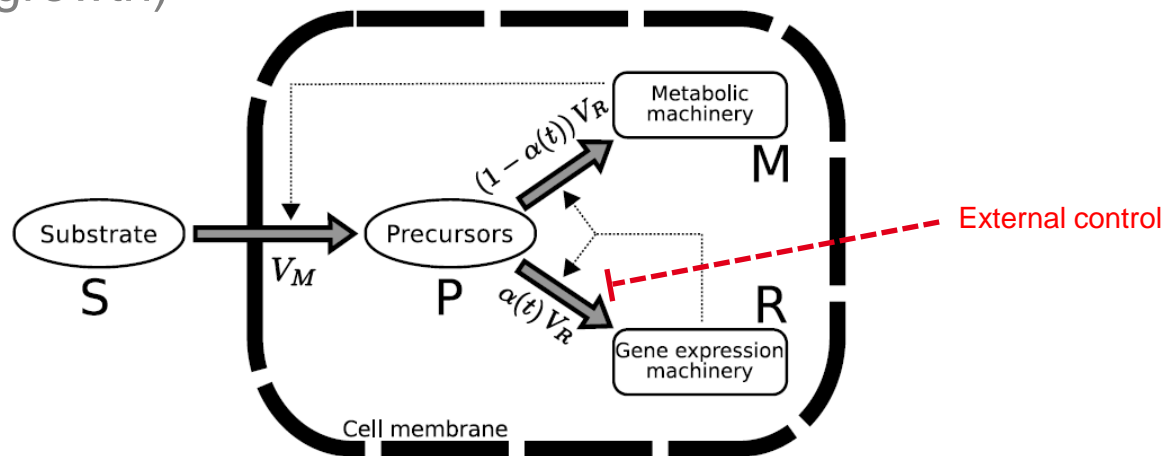
Izard, Gomez Balderas *et al.* (2015), *Mol. Syst. Biol.*, 11:840

# Control of gene expression machinery

- For biotechnological applications, one would like to **change** the natural resource allocation strategies of the cell

de Jong *et al.* (2017), *Trends Microbiol.*, 25(6):480-93

- Can **control of gene expression machinery** be harnessed for this purpose?
  - Global reallocation of resources through arrest of gene expression machinery (and thus growth)



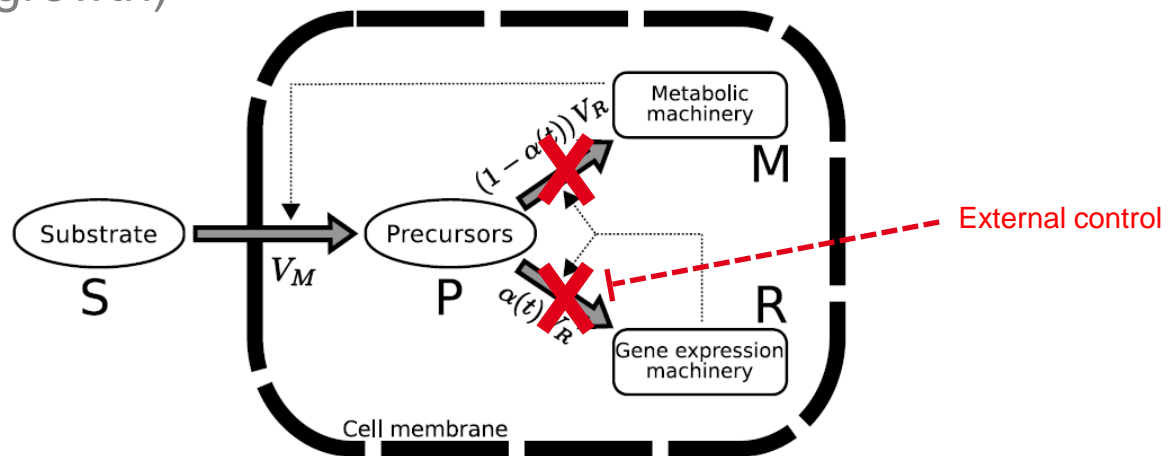


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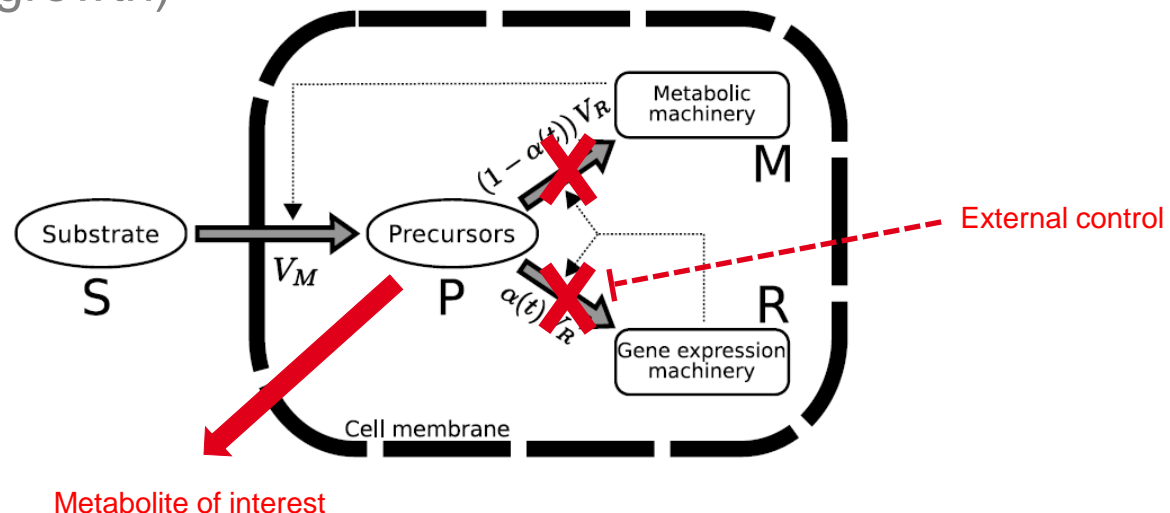


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# Control of gene expression machinery

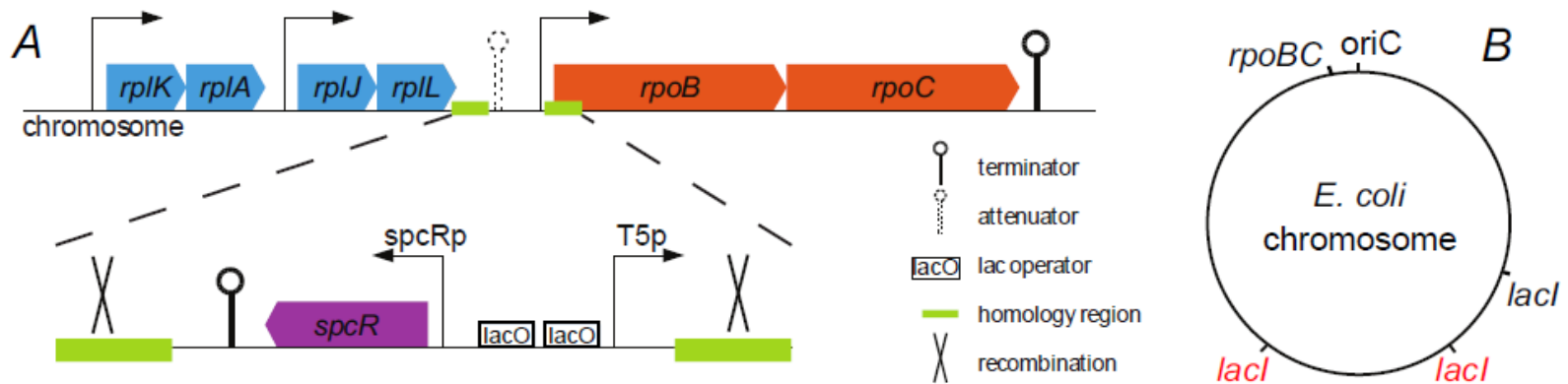
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- Can **control of gene expression machinery** be harnessed for this purpose?
  - Global reallocation of resources through arrest of gene expression machinery (and thus growth)
  - Restart gene expression machinery when enzymes have been degraded
- Does this approach work?

# Reengineering of gene expression machinery

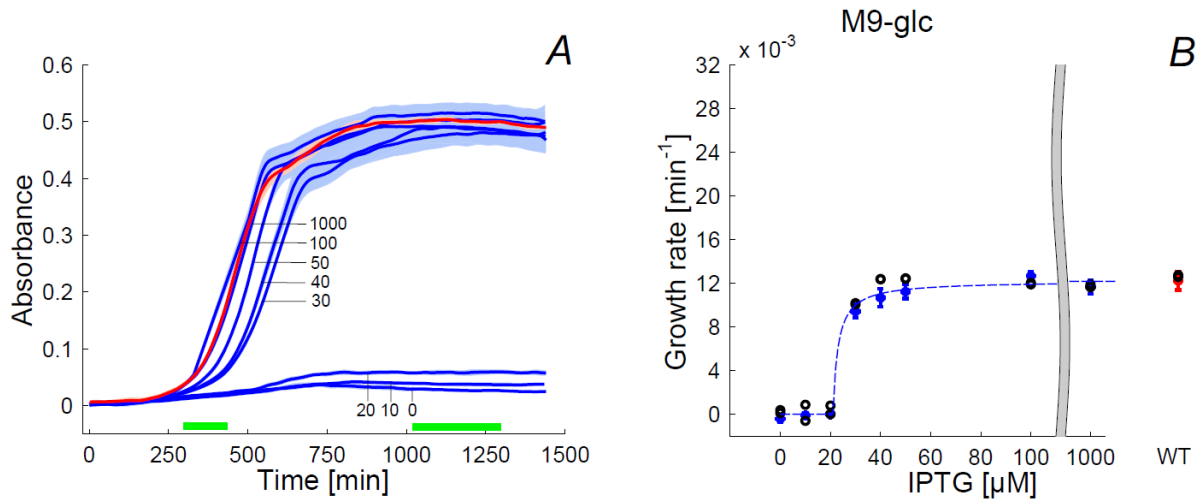
- External control of expression of **RNA polymerase**
  - Transcription of *rpoBC* operon (encoding  $\beta\beta'$  subunits) controlled by IPTG-inducible promoter



- Several copies of *lacI* on chromosome

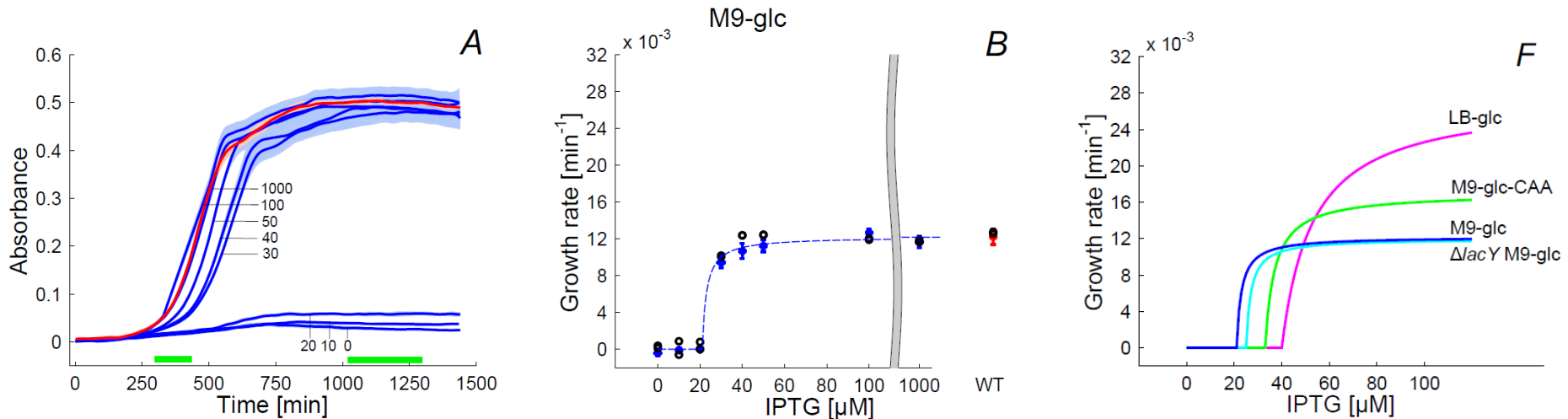
# Synthetic growth switch

- Reengineering of GEM results in **growth switch**



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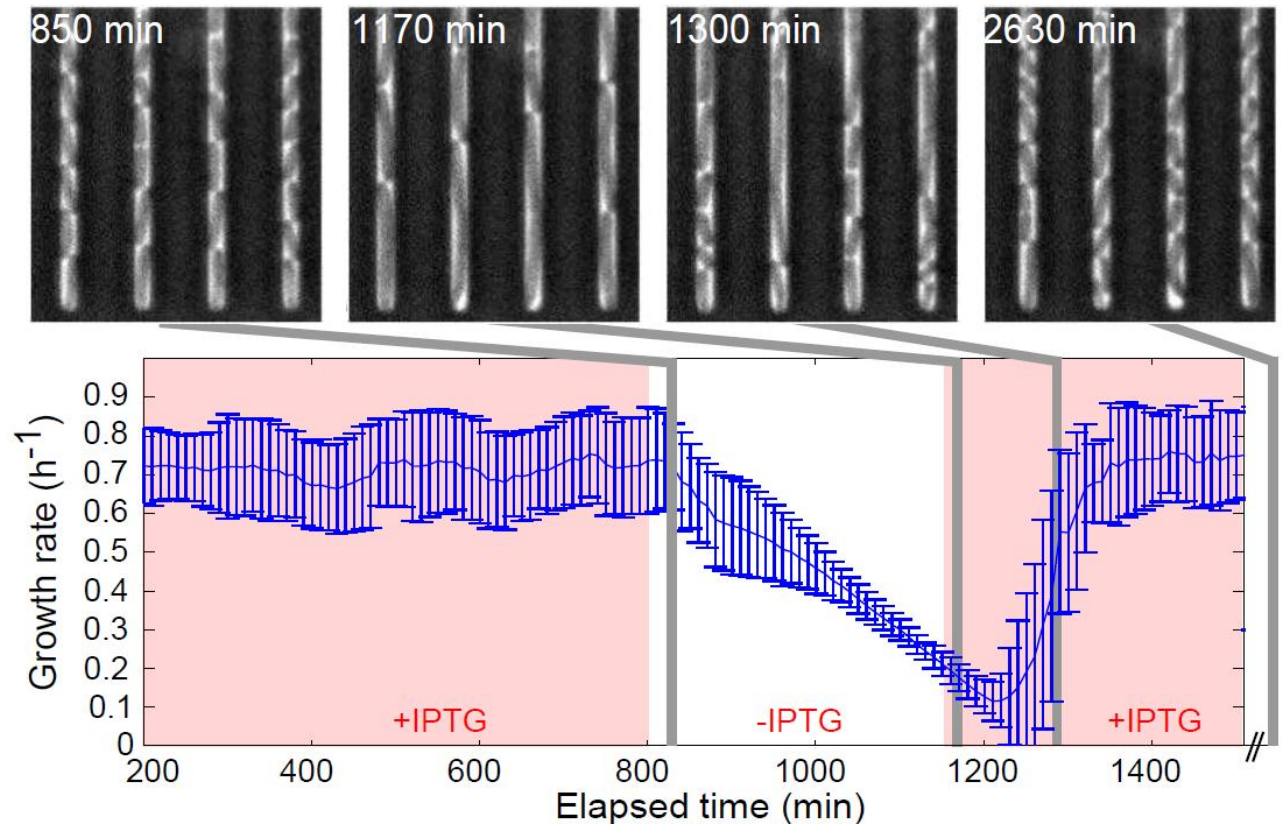


- Growth switch is **medium-independent**: works in different media supporting different maximum growth rates

# Synthetic growth switch

- Growth switch is **reversible**

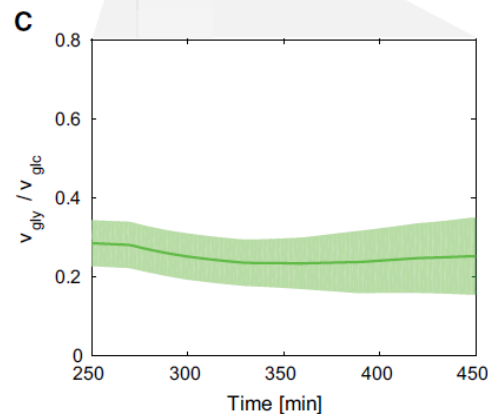
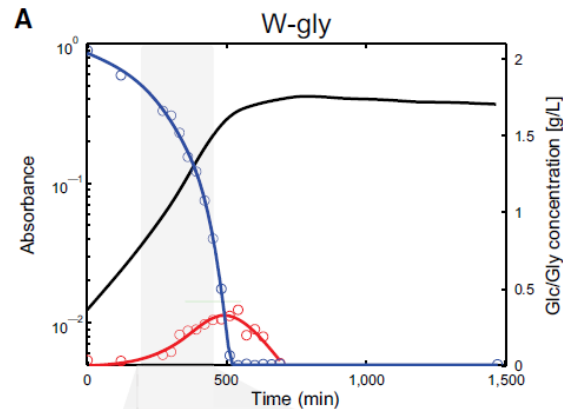
Microfluidics/time-lapse microscopy experiment, followed by quantification of growth rate of individual cells



# Growth switch improves product yields

- Production of glycerol from glucose by adding plasmid carrying genes that code for glycerol pathway in yeast

Liang *et al.* (2011), *Appl. Microbial. Biotechnol.*, 89:57-62

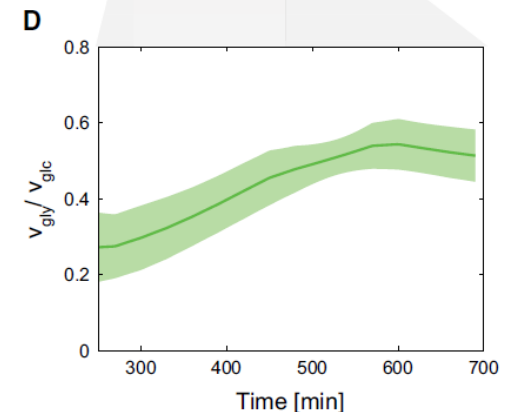
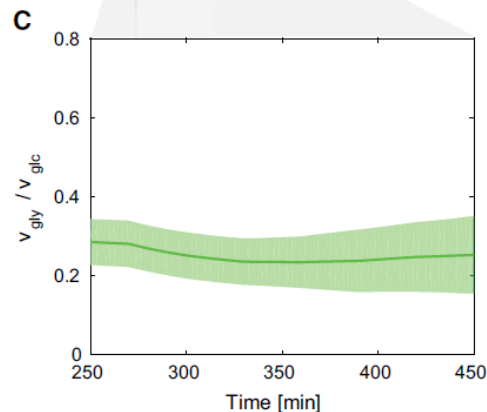
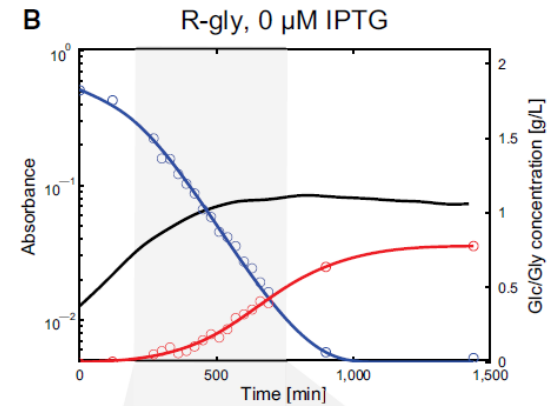
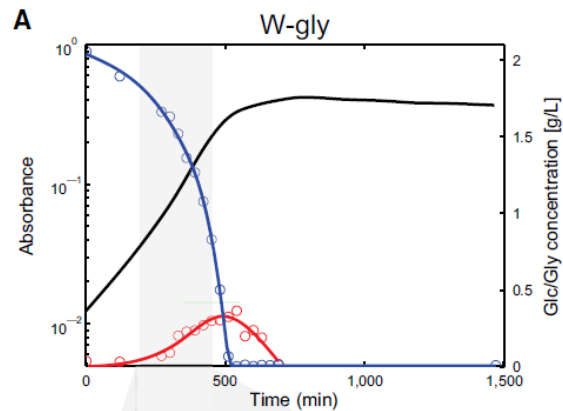




# Growth switch improves product yields

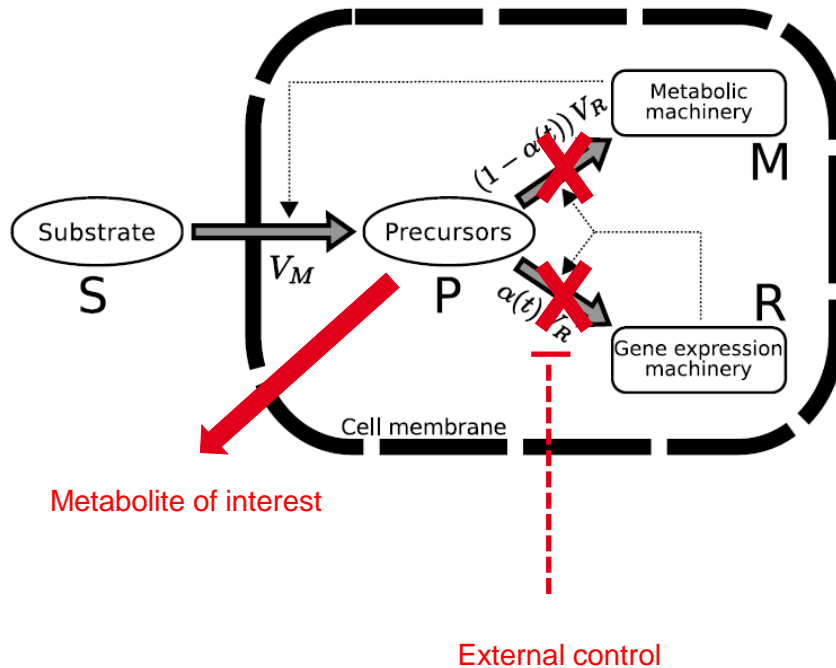
- Production of glycerol from glucose by adding plasmid carrying genes that code for glycerol pathway in yeast
- External reduction of growth rate **increases production yield**

Yield close to predicted theoretical maximum



# Optimization of growth switch

- Model of self-replicators with metabolite production and growth switch



$$\frac{ds(t)}{dt} = v_S(t) - v_M(t) \frac{\mathcal{V}(t)}{\mathcal{V}_{\text{ext}}},$$

$$\frac{dp(t)}{dt} = v_M(t) - v_R(t) - v_X(t) - \mu(t) p(t),$$

$$\frac{dr(t)}{dt} = u(t) v_R(t) - \mu(t) r(t),$$

$$\frac{dx(t)}{dt} = v_X(t) - \mu(t) x(t),$$

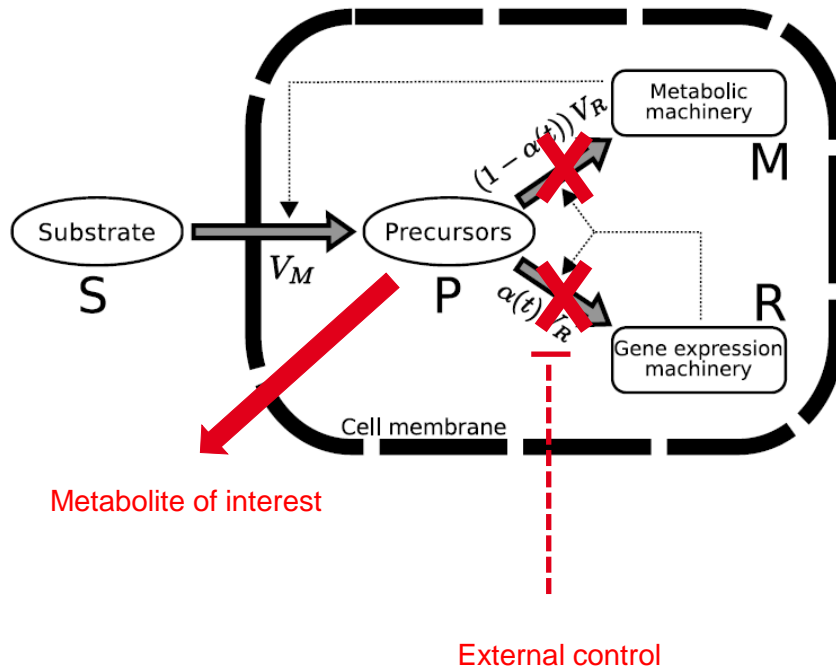
$$\frac{d\mathcal{V}(t)}{dt} = \mu(t) \mathcal{V}(t),$$

$$m(t) = \frac{1}{\beta} - r(t), \quad X(t) = x(t) \mathcal{V}(t),$$

Yegorov et al. (2017), in preparation

# Optimization of growth switch

- Model of self-replicators with metabolite production and growth switch



$$\frac{d\hat{s}(t)}{dt} = \hat{v}_S(t) - k_2 \frac{\hat{s}(t)(1 - \hat{r}(t))}{K_2 + \hat{s}(t)} \frac{\mathcal{V}(t)}{\mathcal{V}_{\text{ext}}},$$

$$\frac{d\hat{p}(t)}{dt} = k_2 \frac{\hat{s}(t)(1 - \hat{r}(t))}{K_2 + \hat{s}(t)} - (1 + \hat{p}(t)) \frac{\hat{p}(t)\hat{r}(t)}{K + \hat{p}(t)} - k_1 \frac{\hat{p}(t)(1 - \hat{r}(t))}{K_1 + \hat{p}(t)},$$

$$\frac{d\hat{r}(t)}{dt} = (u(t) - \hat{r}(t)) \frac{\hat{p}(t)\hat{r}(t)}{K + \hat{p}(t)},$$

$$\frac{d\hat{x}(t)}{dt} = k_1 \frac{\hat{p}(t)(1 - \hat{r}(t))}{K_1 + \hat{p}(t)} - \frac{\hat{p}(t)\hat{r}(t)}{K + \hat{p}(t)} \hat{x}(t),$$

$$\frac{d\mathcal{V}(t)}{dt} = \frac{\hat{p}(t)\hat{r}(t)}{K + \hat{p}(t)} \mathcal{V}(t),$$

$$\hat{m}(t) = 1 - \hat{r}(t), \quad \hat{X}(t) = \hat{x}(t) \mathcal{V}(t),$$

$$\hat{t} \in [0, \hat{T}].$$

Yegorov et al. (2017), in preparation

# Optimization of growth switch

- Model of self-replicators with metabolite production and growth switch
- Optimization of metabolite production

$$\hat{X}(\hat{T}) \longrightarrow \max_{u(\cdot) \in \mathcal{U}}$$

- Preliminary results of optimal control analysis: growth phase followed by production phase

In agreement with dynamical control schemes in biotechnology

Yegorov *et al.* (2017), in preparation

# Conclusions

- Reengineering gene expression machinery leads to **reversible and medium-independent growth switch**
- Growth-arrested cells capable of **reorienting nutrient fluxes** towards increased production of metabolite of interest
  - Test on other heterologous pathways in pre-industrial setting
- Proof-of-principle shows that growth switch may be useful **extension of toolbox of biotechnological engineers**
  - But: cofactor imbalances or toxic intermediates may occur in other applications
- How can production of metabolites of interest be **dynamically optimized?**
  - Timing of arrest and restart of gene expression machinery

# Contributors

- Joint work with

- Jérôme Izard (INRIA Grenoble - Rhône-Alpes/Université Grenoble Alpes)
- Cindy Gomez Balderas (Université Grenoble Alpes)
- Delphine Ropers (INRIA Grenoble - Rhône-Alpes)
- Stephan Lacour (Université Grenoble Alpes)
- Ariel Lindner (INSERM, Paris)
- Johannes Geiselmann (Université Grenoble Alpes)
- Irina Mihalcescu (Université Grenoble Alpes)
- Nils Giordano (INRIA Grenoble - Rhône-Alpes/Université Grenoble Alpes)
- Jean-Luc Gouzé (INRIA Sophia-Antipolis - Méditerranée)
- Francis Mairet (INRIA Sophia-Antipolis - Méditerranée)
- Ivan Yegorov (INRIA Sophia-Antipolis - Méditerranée)

- Funding



Action d'envergure Colage



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# Contributors

- Joint work with
  - Jérôme Izard (INRIA Grenoble - Rhône-Alpes/Université Grenoble Alpes)
  - Cindy Gomez Balderas (Université Grenoble Alpes)
  - Delphine Ropers (INRIA Grenoble - Rhône-Alpes)
  - Stephan Lacour (Université Grenoble Alpes)
  - Ariel Lindner (INSERM, Paris)
  - Johannes Geiselmann (Université Grenoble Alpes)
  - Nils Giordano (INRIA Grenoble - Rhône-Alpes/Université Grenoble Alpes)
  - Jean-Luc Gouzé (INRIA Sophia-Antipolis - Méditerranée)
  - Francis Mairé (INRIA Sophia-Antipolis - Méditerranée)
- **Open PhD position!**



ANR Maximic

**Merci !**



[team.inria.fr/ibis](http://team.inria.fr/ibis)

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