Programmable Bacterial Catalysts

Vítor Martins dos Santos

Division of Microbiology
Helmholtz Centre for Infection Research
Braunschweig, Germany

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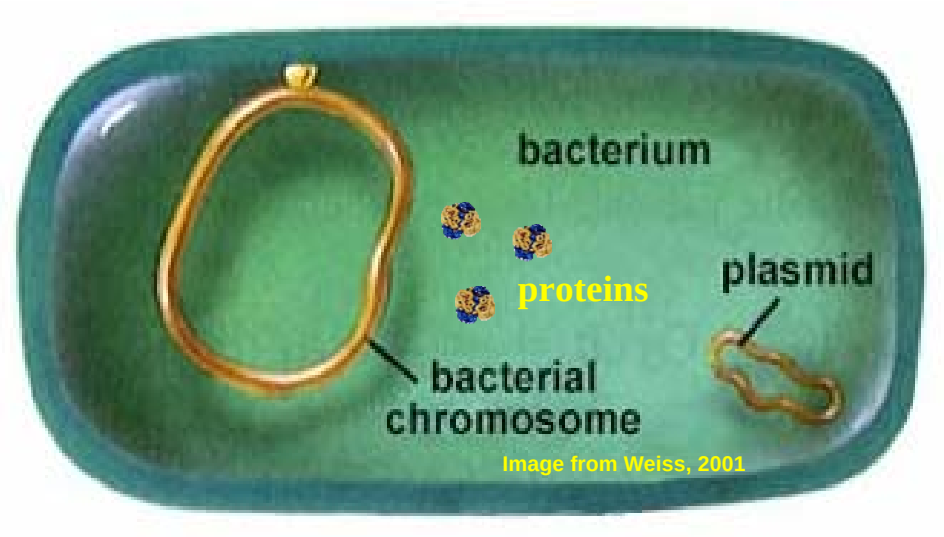
MISSION OF METABOLIC ENGINEERING

To understand microbial cellular behaviour [from a Systems Biology perspective] and to translate this insights into relevant biotechnological applications



Ideal biocatalyst: design from scratch?

Engineering framework: Interplay circuits of interest and genome

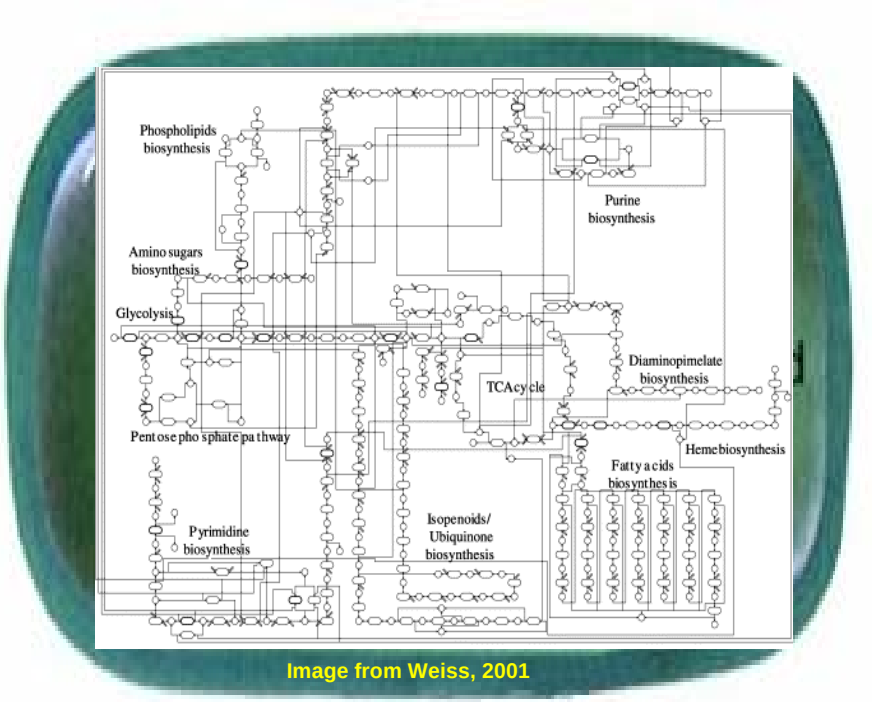
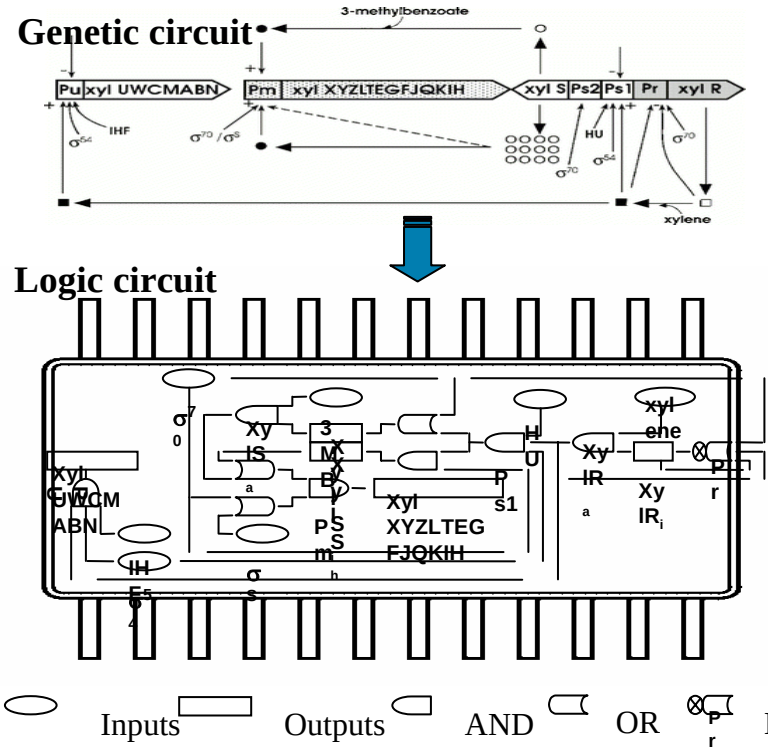


Image from Weiss, 2001



Aim is to have an integrated bacterial blueprint to enable (re-)programming

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GOALS: PROBACTYS

To construct of a functioning, **streamlined bacterial cell** devoid of much of its genome and endowed with a series of coordinated, newly **assembled genetic circuits** for the **production of aromatic derivatives** that would include synchronized behaviour,**low-temperature biocatalysis**.

By achieving such constructs as a **proof-of-principle**, it is aimed at establishing a solid, rational framework for the engineering of cells **performing effectively biocatalytic processes, in this case production of aromatic derivatives**

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The global work strategy

1) develop a basic interrogation **scaffold** (blue print);

2) genome **minimization (**random ; directed**)**

3) **engineering** the different **genetic circuits** of choice (Biotransformation parts list etc.);

5) assessment of the **interplay of constructed circuits** with the template genome

6) **re-programme** for specific biocatalytic conditions : cold shock

7) **use of the model framework** and **constructed** cells for the **production of high-added value products** from halogenated aromatics

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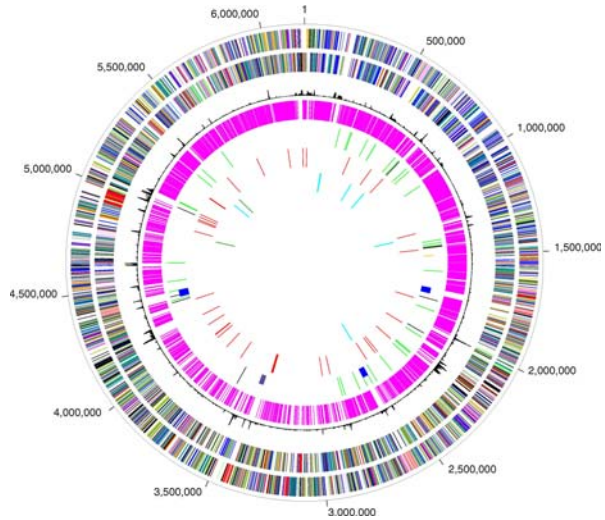
Pseudomonas putida as cell factory

***Pseudomonas putida* KT2440**

- **Paradigm of ubiquitous copiotrophic soil bacteria**
- **Great metabolic diversity**
- **Certified biosafety strain**
- **Preferred host for the design of novel degradation/biocatalytic processes**
- **Large range of applications:**

Agricultural, environmental, industrial



- **Biotransformation of a wealth of chemicals, in particular aromatic and aliphatic derivatives**
- **Resistance to many stresses (eg. solvents)**
- **Genetically amenable for engineering**
- **Excellent host for heterologous expression**

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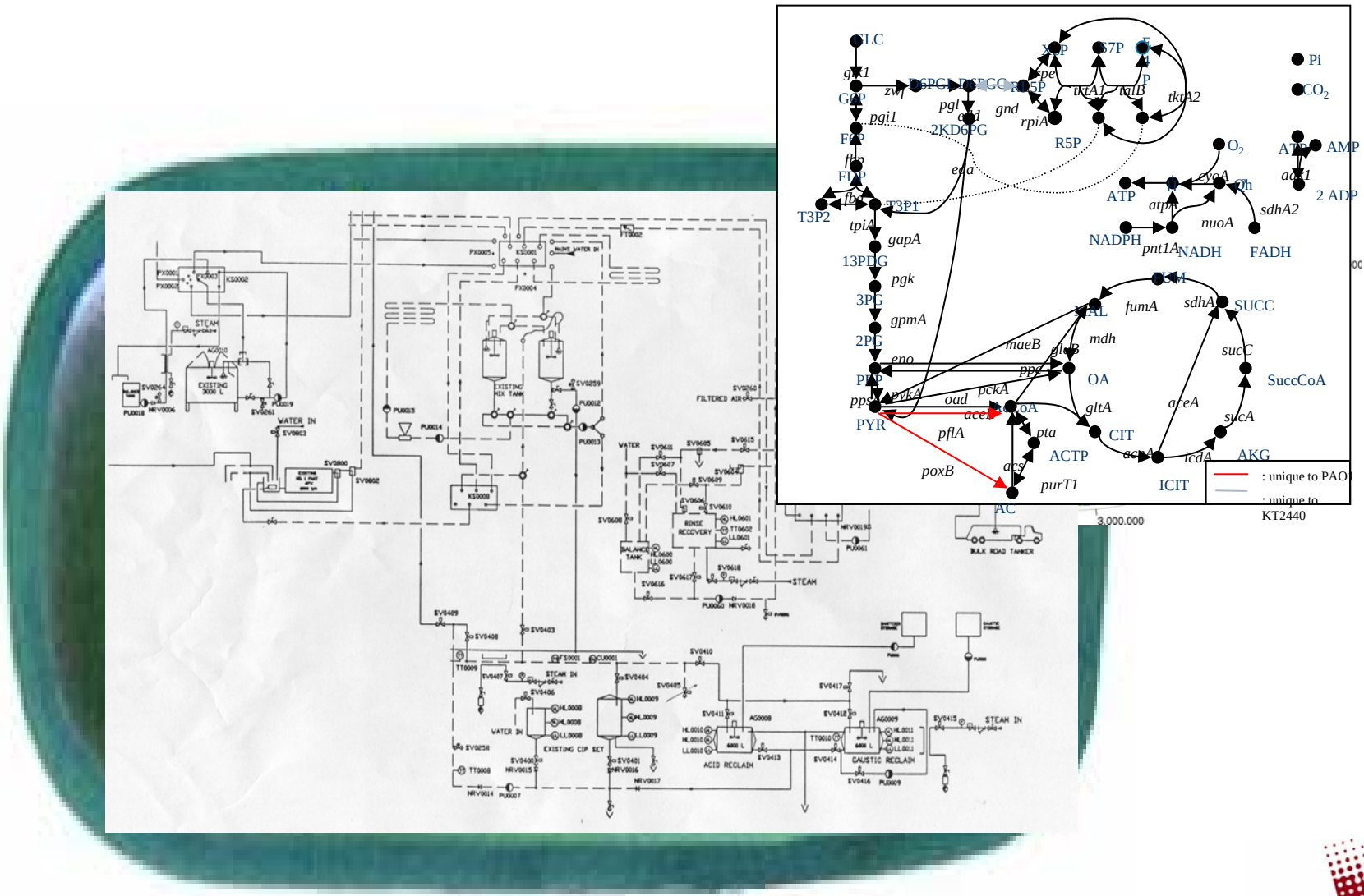
Towards a microbial blueprint:



What we get from the genome sequence

Central Metabolism (EMP, PPP, TCA cycle, Electron transport)

aceA, aceB, aceE, aceF, ackA, acnA, acnB, acs, adhE, agp, appB, appC, atpA, atpB, atpC, atpD, atpE, atpF, atpG, atpH, atpI, cydA, cydB, cydC, cydD, cyoA, cyoB,
cyoC, cyoD, dld, eda, edd, eno, fba, fbp, fdhF, fdnG, fdnH, fdnI, fdoG, fdoH, fdoI, frdA, frdB, frdC, frdD, fumA, fumB, fumC, galM, gapA, gapC_1, gapC_2, glcB, glgA
glgC, glgP, glk, glpA, glpB, glpC, glpD, gltA, gnd, gpmA, gpmB, hyaA, hyaB, hyaC, hybA, hybC, hycB, hycE, hycF, hycG, icdA, lctD, ldhA, lpdA, malP, mdh, ndh,
nuoA, nuoB, nuoE, nuoF, nuoG, nuoH, nuoI, nuoJ, nuoK, nuoL, nuoM, nuoN, pckA, pfkA, pfkB, pflA, pflB, pflC, pflD, pgi, pgk, pntA, pntB, poxB, ppc, ppsA, pta, pur
pykA, pykF, rpe, rpiA, rpiB, sdhA, sdhB, sdhC, sdhD, sfcA, sucA, sucB, sucC, sucD, talB, tktA, tktB, tpiA, trxB, zwf, pgl(Fraenkel, 1996*), mae*B(Fraenkel, 1996)

Alternative Carbon Source *adhC, adhE, agaY, agaZ, aldA, aldB, aldH, araA, araB, araD, bglX, cpsG, deoB, deoC, fruK, fucA, fucI, fucK, fucO, galE, galK, galT, galU, gatD, gatY, glk, glpK,gntK, gntV, gpsA, lacZ, manA, melA, mtlD, nagA, nagB, nanA, pfkB, pgi, pgm, rbsK, rhaA, rhaB, rhaD, srlD, treC, xylA, xylB*

Amino Acid Metabolism ***adi, aldH, alr, ansA, ansB, argA, argB, argC, argD, argE, argF, argG, argH, argI, aroA, aroB, aroC, aroD, aroE, aroF, aroG, aroH, aroK, aroL, asd, asnA, asnB,aspA, aspC, avtA, cadA, carA, carB, cysC, cysD, cysE, cysH, cysI, cysJ, cysK, cysM, cysN, dadA, dadX, dapA, dapB, dapD, dapE, dapF, dsdA, gabD, gabT, gadA,gadB, gdhA, glk, glnA, gltB, gltD, glyA, goaG, hisA, hisB, hisC, hisD, hisF, hisG, hisH, hisI, ilvA, ilvB, ilvC, ilvD, ilvE, ilvG_1, ilvG_2, ilvH, ilvI, ilvM, ilvN, kbl, ldc***

leuA, leuB, leuC, leuD, lysA, lysC, metA, metB, metC, metE, metH, metK, metL, pheA, proA, proB, proC, prsA, putA, sdaA, sdaB, serA, serB, serC, speA, speB, speC,
***speD, speE, speF, tdcB, tdh, thrA, thrB, thrC, tnaA, trpA, trpB, trpC, trpD, trpE, tynA, tyrA, tyrB, ygjG, ygjH, ala*B**(Reitzer, 1996*), dap*C(Greene, 1996*), pat*(McFall an
Newman, 1996*), prr*(McFall and Newman, 1996*), sad*(Berlyn et al., 1996*), Methylthioadenosine nucleosidase*(Glansdorff, 1996*), 5-Methylthioribose kinase*(Glansdorf 1996*), 5-Methylthioribose-1-phosphate isomerase*(Glansdorff, 1996*), Adenosyl homocysteinase*(Matthews, 1996*), L-Cysteine desulfhydrase*(McFall and Newman, 1996*), Glutaminase* A(McFall and Newman, 1996*), Glutaminase* B(McFall and Newman, 1996)

Purine & Pyrimidine Metabolism *add, adk, amn, apt, cdd, cmk, codA, dcd, deoA, deoD, dgt, dut, gmk, gpt, gsk, guaA, guaB, guaC, hpt, mutT, ndk, nrdA, nrdB, nrdD, nrdE, nrdF, purA, purB, purC,purD, purE, purF, purH, purK, purL, purM, purN, purT, pyrB, pyrC, pyrD, pyrE, pyrF, pyrG, pyrH, pyrI, tdk, thyA, tmk, udk, udp, upp, ushA, xapA,* *yicP, CMPglycosyla*se(Neuhard and Kelln, 1996)

Vitamin & Cofactor Metabolism *acpS, bioA, bioB, bioD, bioF, coaA, cyoE, cysG, entA, entB, entC, entD, entE, entF, epd, folA, folC, folD, folE, folK, folP, gcvH, gcvP, gcvT, gltX, glyA, gor, gshA,gshB, hemA, hemB, hemC, hemD, hemE, hemF, hemH, hemK, hemL, hemM, hemX, hemY, ilvC, lig, lpdA, menA, menB, menC, menD, menE, menF, menG, metF, mutnadA, nadB, nadC, nadE, ntpA, pabA, pabB, pabC, panB, panC, panD, pdxA, pdxB, pdxH, pdxJ, pdxK, pncB, purU, ribA,*
ribB, ribD, ribE, ribH, serC, thiC, thiE, ththiG, thiH, thrC, ubiA, ubiB, ubiC, ubiG, ubiH, ubiX, yaaC, ygiG, nadD(Penfound and Foster, 1996*), nad*F(Penfound and Foster, 1996*), nad*G(Penfound and Foster,1996*), pan*E(Jackowski, 1996*), pnc*A(Penfound and Foster, 1996*), pnc*C(Penfound and Foster, 1996*), thi*B(White and Spenser, 1996*), thi*D(White and Spenser, 1996) *thi*K(White and Spenser, 1996*), thi*L(White and Spenser, 1996*), thi*M(White and Spenser, 1996*), thi*N(White and Spenser, 1996*),*
*ubi*E(Meganathan, 1996*),*
*ubi*F(Meganathan, 1996*), Arabinose-5-phosphate isomerase*(Karp et al., 1998*), Phosphopantothenate-cysteine ligase*(Jackowski, 1996*), Phosphopantothenate-cystein decarboxylase*(Jackowski, 1996*), Phospho-pantetheine adenylyltransferase*(Jackowski, 1996*), DephosphoCoA kinase*(Jackowski, 1996*), NMN glycohydrolase*(Penfound and Foster, 1996)

Lipid Metabolism *accA, accB, accD, atoB, cdh, cdsA, cls, dgkA, fabD, fabH, fadB, gpsA, ispA, ispB, pgpB, pgsA, psd, pssA, pgp*A(Funk et al., 1992)

Cell Wall Metabolism *ddlA, ddlB, galF, galU, glmS, glmU, htrB, kdsA, kdsB, kdtA, lpxA, lpxB, lpxC, lpxD, mraY, msbB, murA, murB, murC, murD, murE, murF, murG, murI, rfaC, rfaD,rfaF, rfaG, rfaI, rfaJ, rfaL, ushA, glm*M(Mengin-Lecreulx and van Heijenoort, 1996*), lpc*A(Raetz, 1996*), rfa*E(Raetz, 1996*), Tetraacyldisaccharide 4' kinase*(Raetz,1996*), 3-Deoxy-D-manno-octulosonic-acid 8-phosphate phosphatase*(Raetz, 1996)

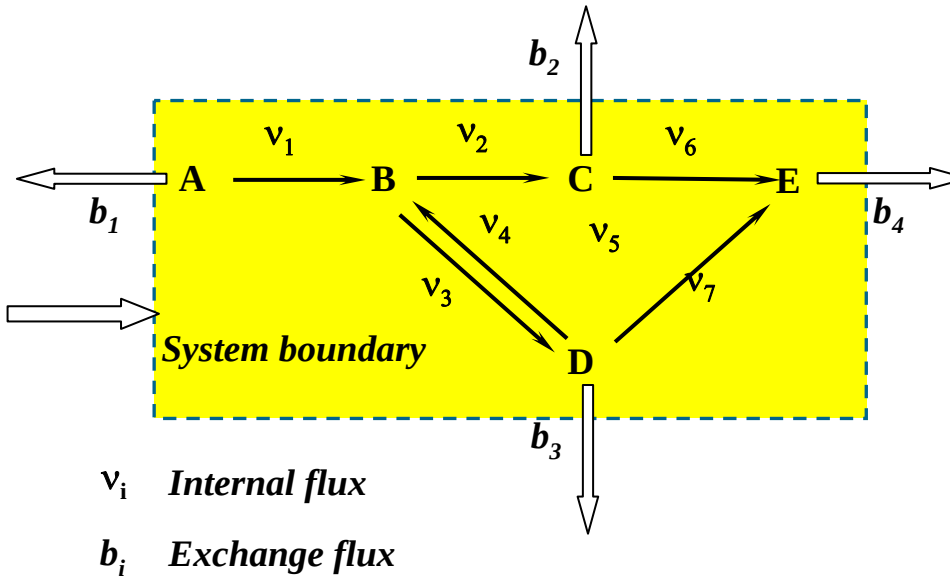
Transport Processes *araE, araF, araG, araH, argT, aroP, artI, artJ, artM, artP, artQ, brnQ, cadB, chaA, chaB, chaC, cmtA, cmtB, codB, crr, cycA, cysA, cysP,*

The stoichiometric matrix as a metabolic map

Genetic content

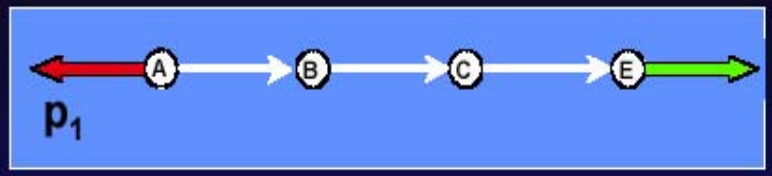
gene	enzyme	flux	rxn
mglA, maglB	galactose transporter	v_1	A ⇌ B
galT	uridyl transferase	v_2	B ⇌ C
galK	galactokinase	v_3	B ⇌ D

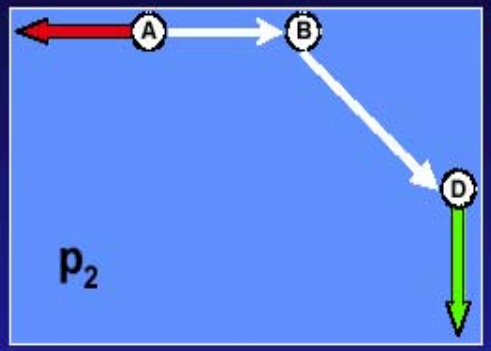
Biochemical reaction network

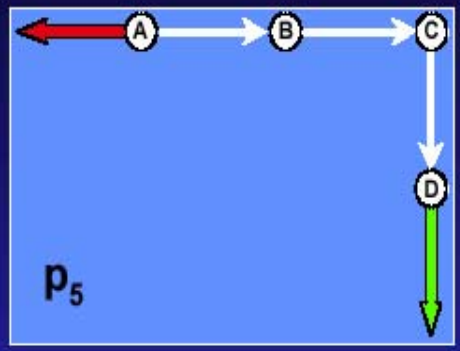


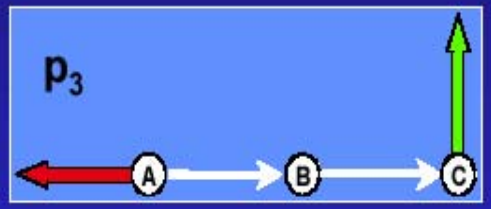
After Palsson, 2000

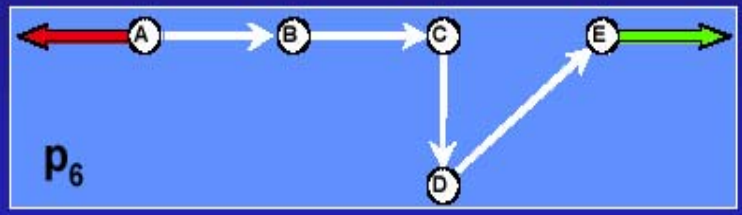
Extreme Pathways

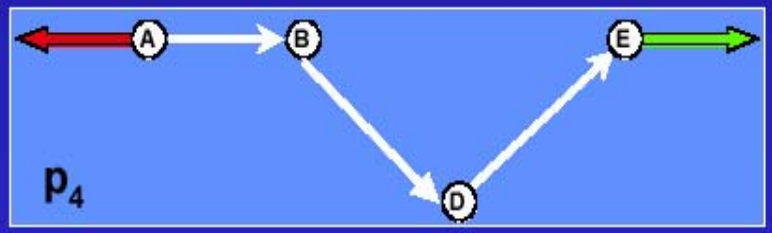


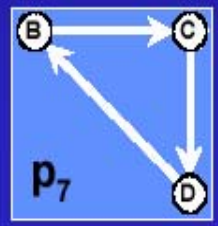


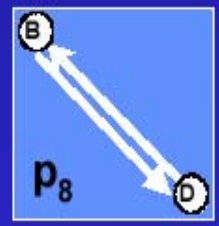


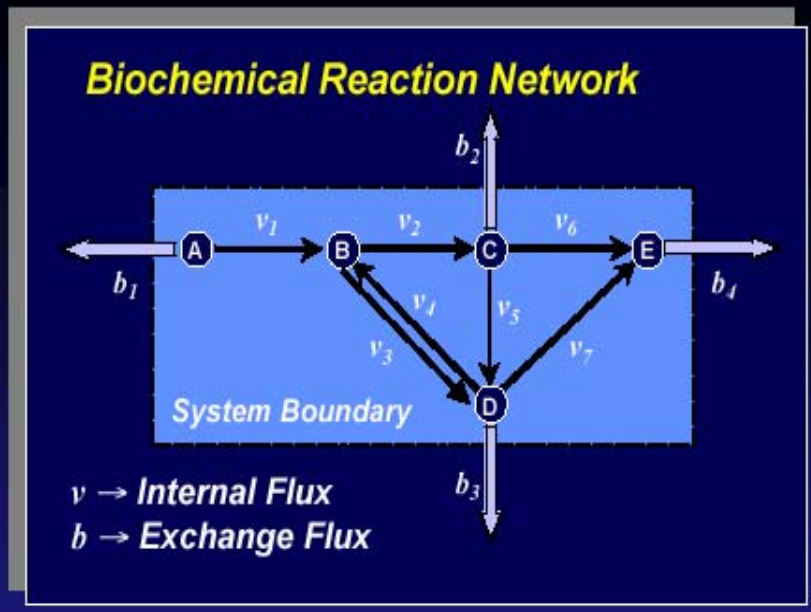










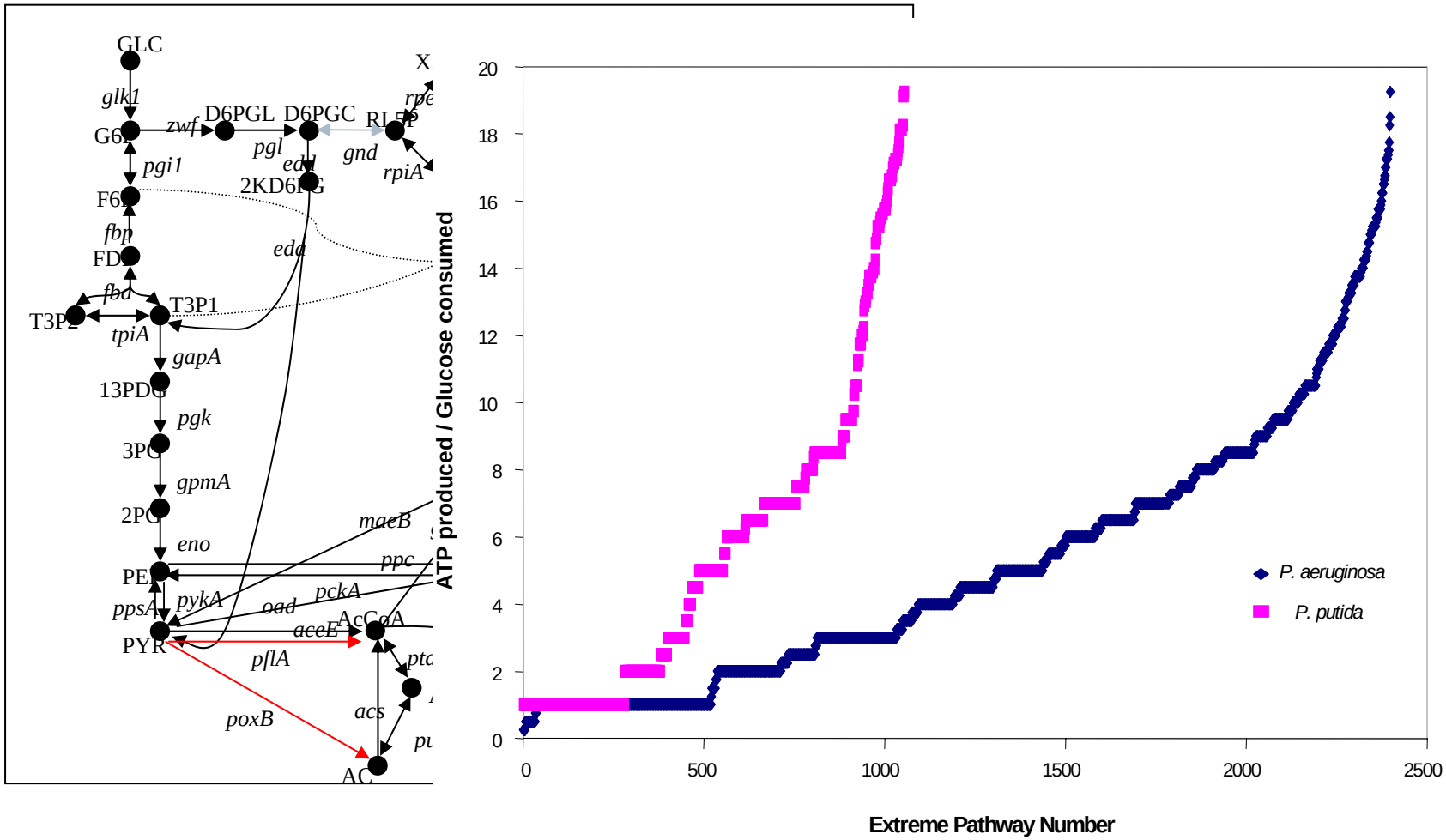


7 internal fluxes
+ 4 exchange fluxes
n = 11 fluxes
m = 5 metabolites

- stoichiometric matrix (5 x 11)
- dimension of null space = 6
- # of extreme pathways = 8

Palsson´s

In silico genotype-phenotype relationship of *P. putida* KT2440 and *P. aeruginosa* PAO1



Emergent property of the system, not predictable from linear comparison of gene lists

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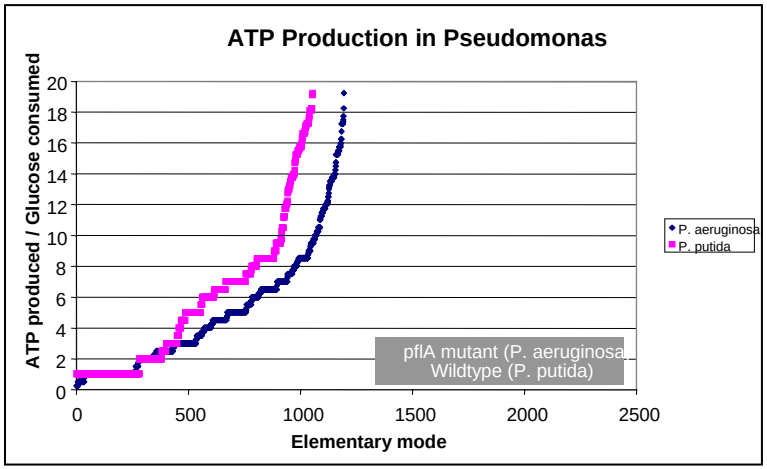
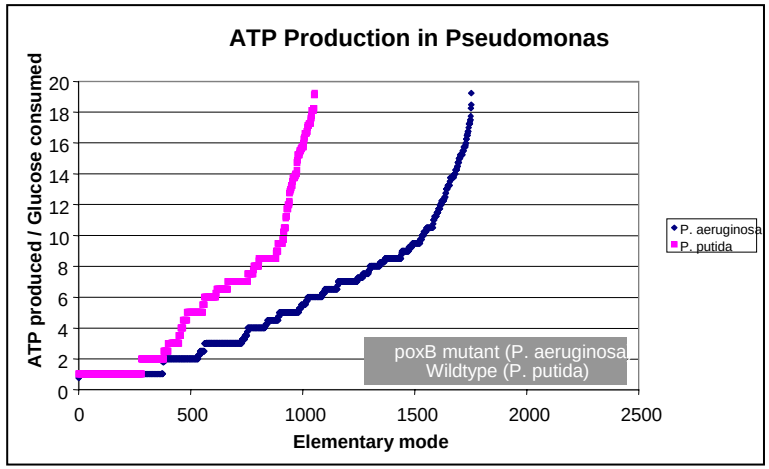
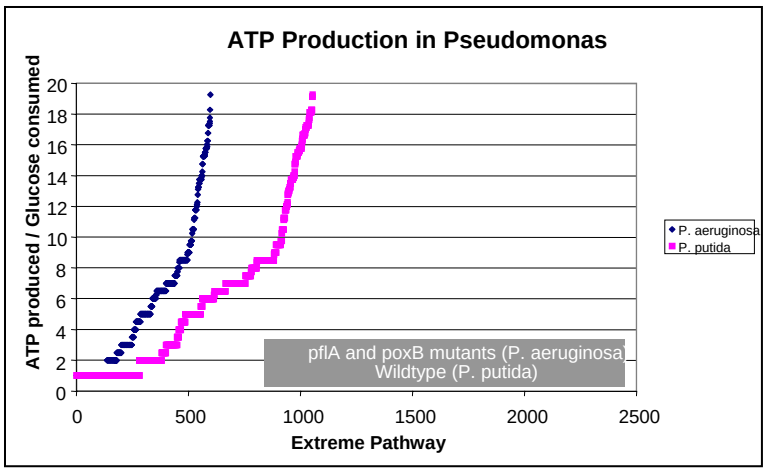
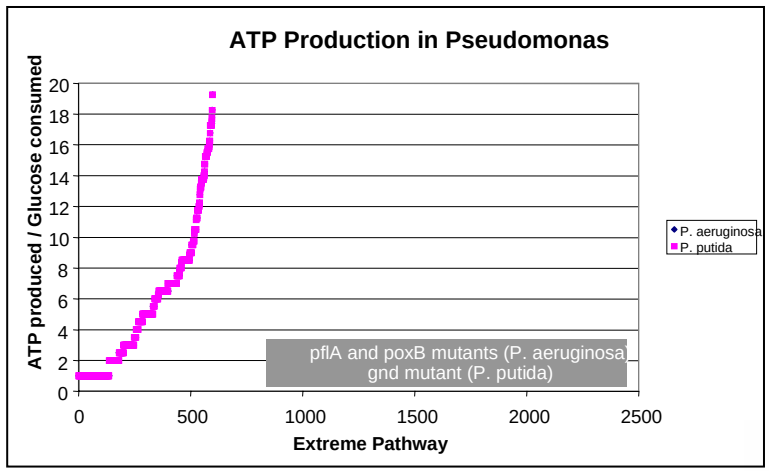
In silico mutants assist rational experimental design









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Emergent properties

An apparent small genetic difference can be strongly amplified

Emergent properties not evident from gene list only

Ps. aeruginosa* shows more redundancy than *Ps. Putida

But,

Is this real?

What is true biological meaning?

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Experimental testing with tranposon mutants

		Comparison to annotated *P. aeruginosa* PA01		
Sample	**Transposon flanking region in KT2440 genome**	**flanking region found in gene list**	**PA No.**	**E.C. No.**
AUX28	3-methyl-2-oxobutanoate hydroxymethyltransferase	ORF		2.1.2.11
AUX29	lipoate synthase	ORF	3996	
AUX46	catabolite repression control protein	ORF	5332	3.1.11.2
AUX14	Tryptophan synthase beta chain	ORF 00127	OO36	4.2.1.20
AUX108	phosphoribosylaminoimidazole carboxylase, catalytic subunit	ORF 00363	5426	4.1.1.21
AUX30	orotate phosphoribosyltransferase	ORF 00434	5331	2.4.2.10
AUX73	acetylglutamate kinase	ORF 00438	5323	2.7.2.8
AUX13	Phosphomannomutase AlgC	ORF 00439	5322	5.4.2.8
AUX25	N-acetylglutamate synthase	ORF 00607	5204	2.3.1.1
AUX27	FAD binding domain	ORF 00650		
AUX59	dihydroxy-acid dehydratase	ORF 00694	353	4.2.1.9
AUX125	dihydroxy-acid dehydratase	ORF 00694	353	4.2.1.9
AUX126	dehydroxyaciddehydratase	ORF 00694	353	4.2.1.9
AUX3	Homoserine-O-Acetyl-Aminotransferase	ORF 00743	O390	2.3.1.31
AUX90	homoserine O-acetyltransferase	ORF 00743		2.3.1.46
AUX113	Aspartate carbamyltransferase	ORF 00911		
AUX78	adenosylhomocysteinase	ORF 00943		3.3.1.1
AUX4	S-adenosyl-L-homocysteine hydrolase	ORF 00948	O432	3.3.1.1
AUX76	adenosylhomocysteinase	ORF 00948		
AUX84	adenosylhomocysteinase	ORF 00948		3.3.1.1
AUX12	(Probable) phosphoserine phosphatase	ORF 01053	4960	3.1.3.3
AUX64	histidyl-tRNA synthetase	ORF 01085	3802	6.1.1.21
AUX23	phosphoribosylamine--glycine ligase	ORF 01203	4855	6.3.4.13
AUX95	phosphoribosylamine--glycine ligase	ORF 01203	4855	6.3.4.13
AUX122	lipoate-protein ligase B	ORF 01238		
AUX119	Mutation zwischen 2 ORFs	kein ORF vorhanden (vorher ORF 01239)		
AUX41	dihydrodipicolinate reductase	ORF 01370	4759	1.3.1.26
AUX50	dihydrodipicolinate reductase	ORF 01370	4759	1.3.1.26

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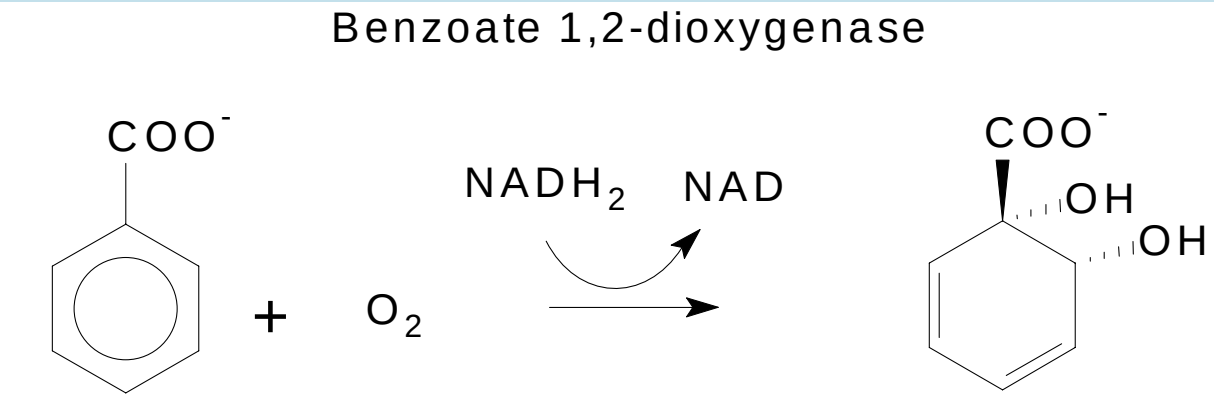
Production of high-added value chemicals



Benzoate

1-carboxy-1,2-cis-dihydroxy-cyclohexa-3,5-diene

(CDCD)

- precursor for many industrially relevant enantiopure derivatives
- difficult to synthesize chemically

Attractive alternative: cofactor dependent biotransformation

Metabolic engineering.

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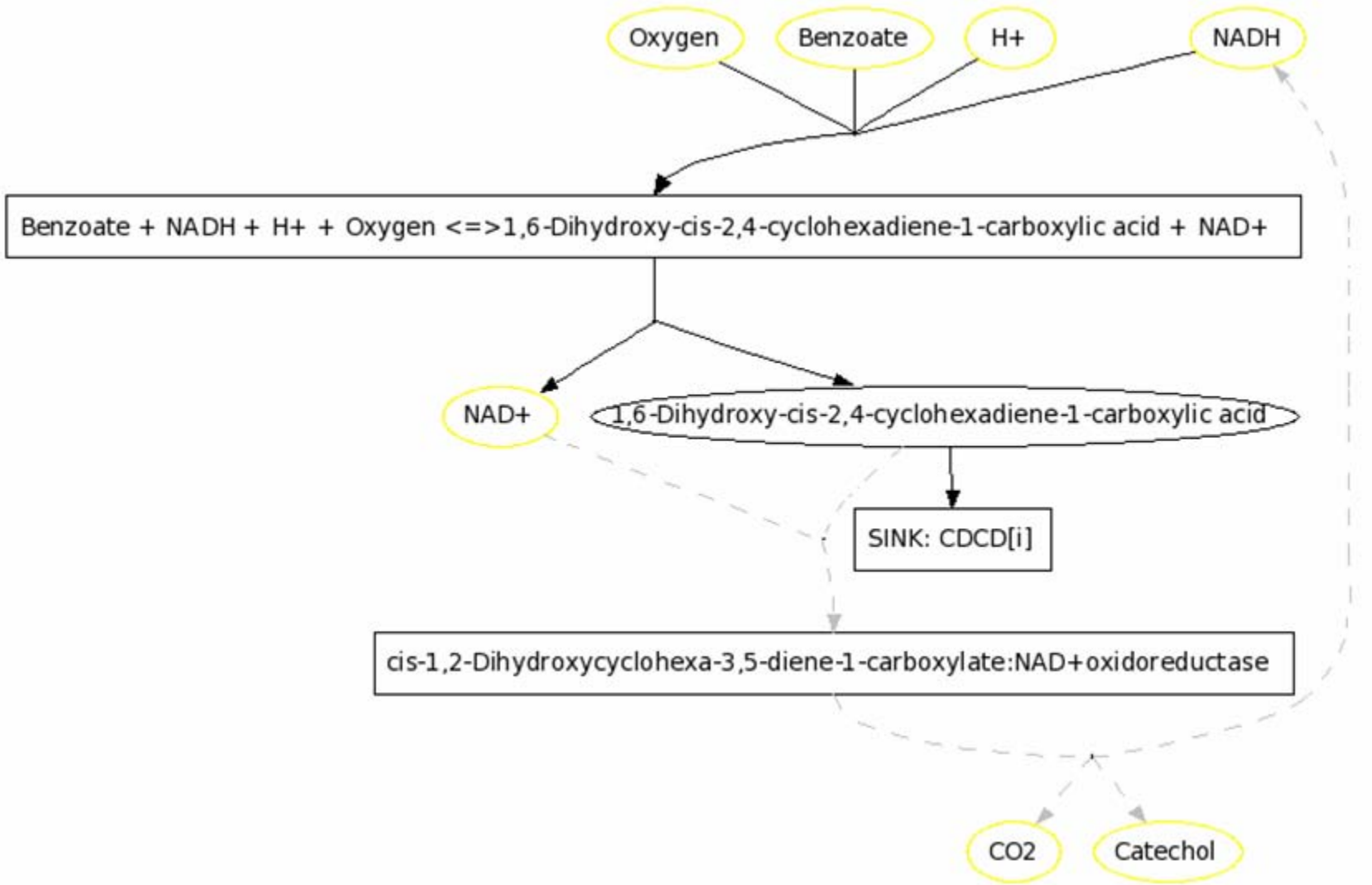
Navigation example : Preliminary model of CDCD



Engineering framework: Interplay circuits of interest and genome

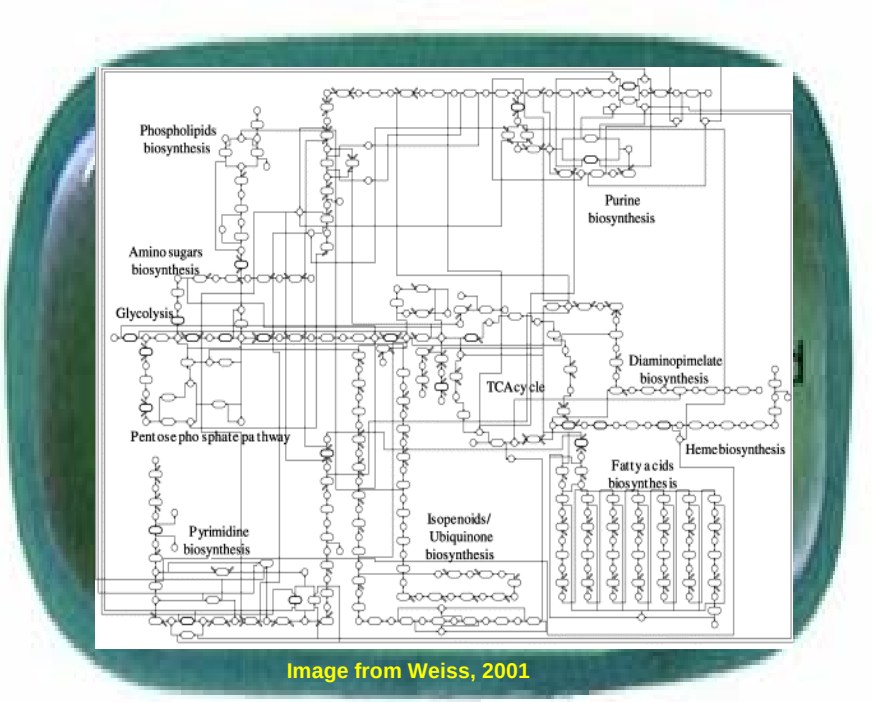
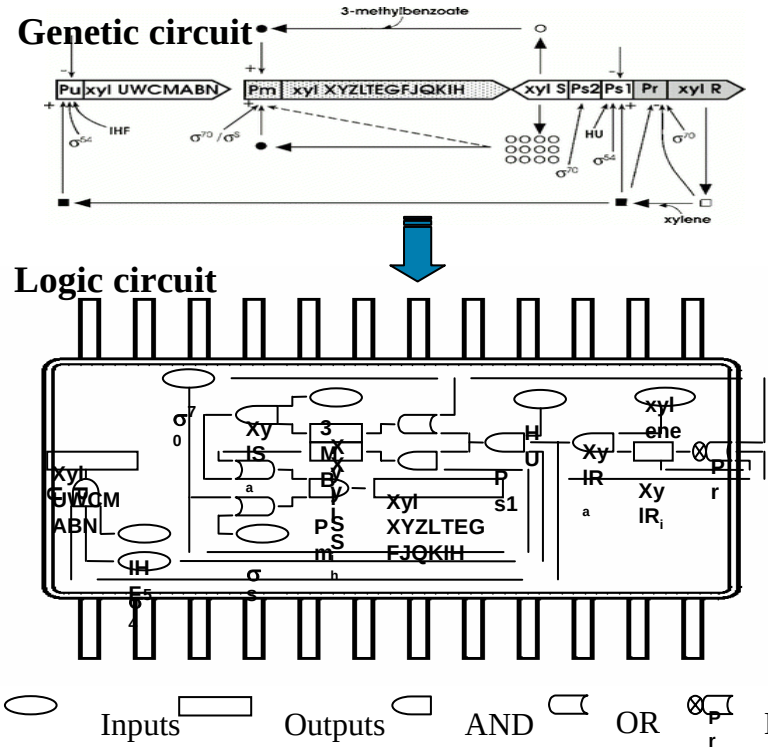


Image from Weiss, 2001



Aim is to have an integrated bacterial blueprint to enable (re-)programming

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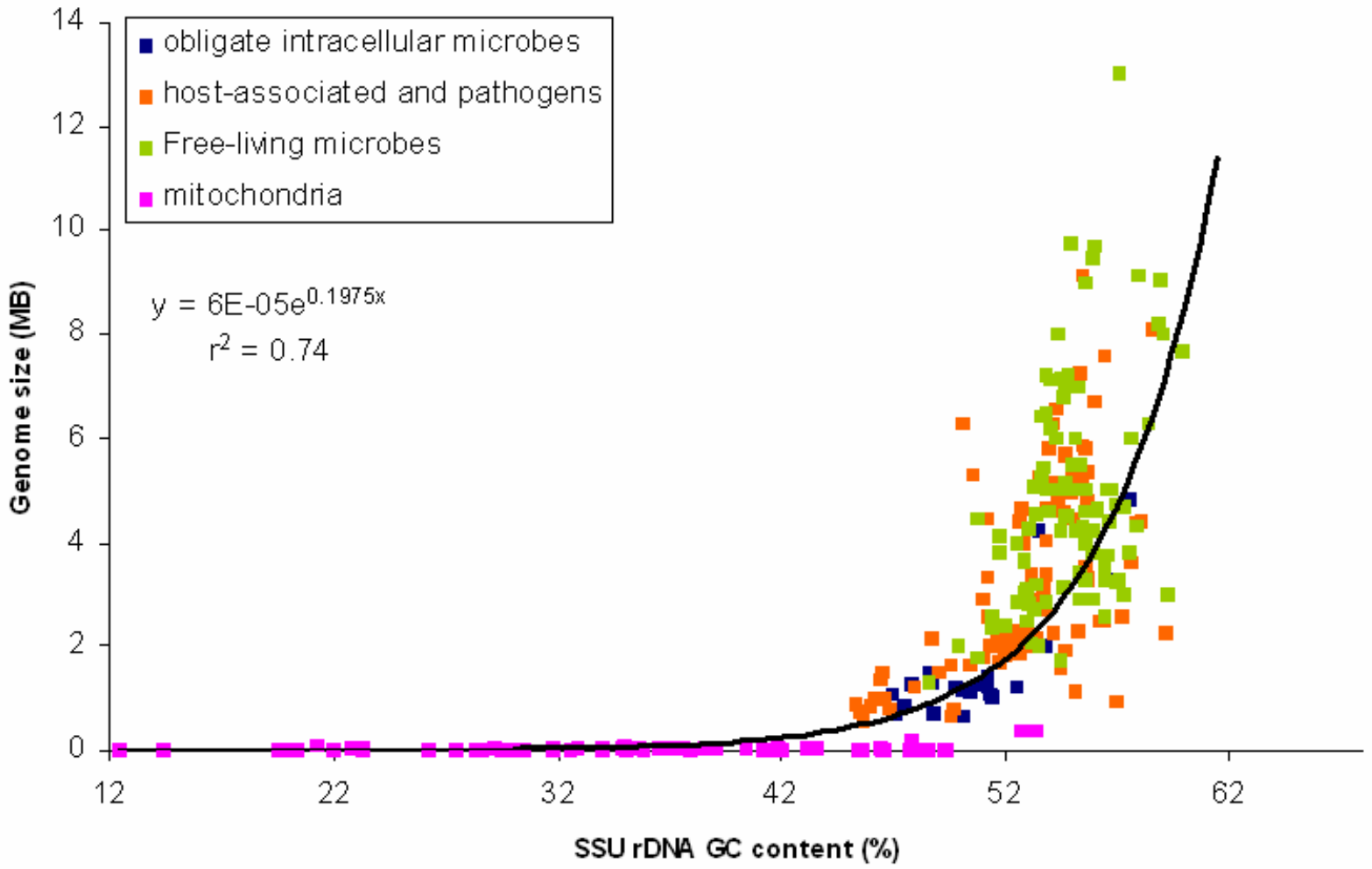
Minimisation: Genome size vs SSU rDNA GC content



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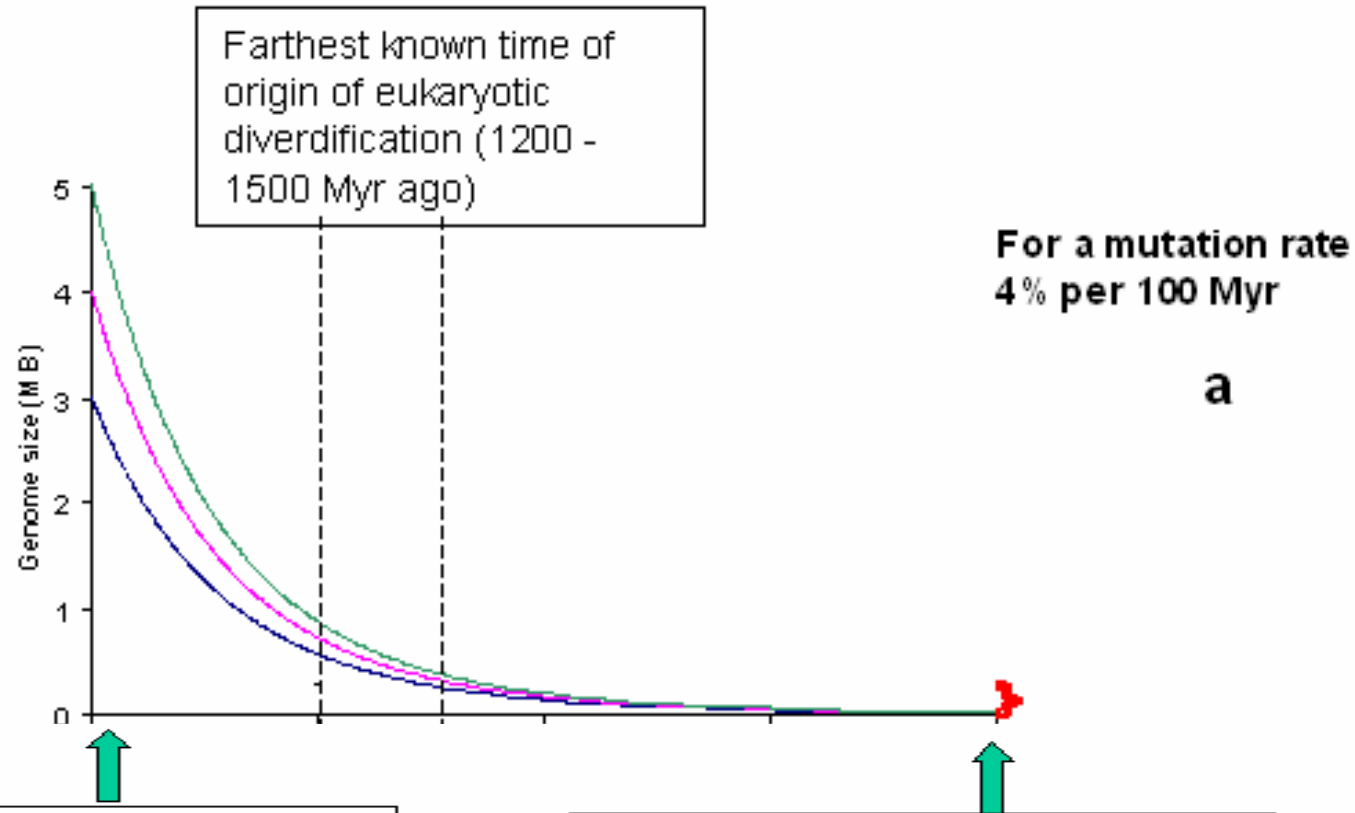
Bootstrapping to a timeline

Khachane et al., Mol. Biol. Evol, in press

$$\Delta GC \text{ per unit time} = m \times \frac{(IV \text{ ratio} + \frac{1}{2})}{(IV \text{ ratio} + 1)} \times (GCf - GCc)$$

$$size(t) = [0.00006m*k] * size(t-1) (1 - m*k) * e^{0.1975*m*k*GCf}$$



Implications and outlook

Most genome loss occur at early stages of evolution, possibly in chunks

Rational dissection of functional networks (evolutionary patterns, constraint-based analysis) will provide candidate modules for directed deletion / expansion

Experimentally:

Global, transposon mutagenesis, random saturation with site-specific recombination sites and expression under strong selection processes, etc.

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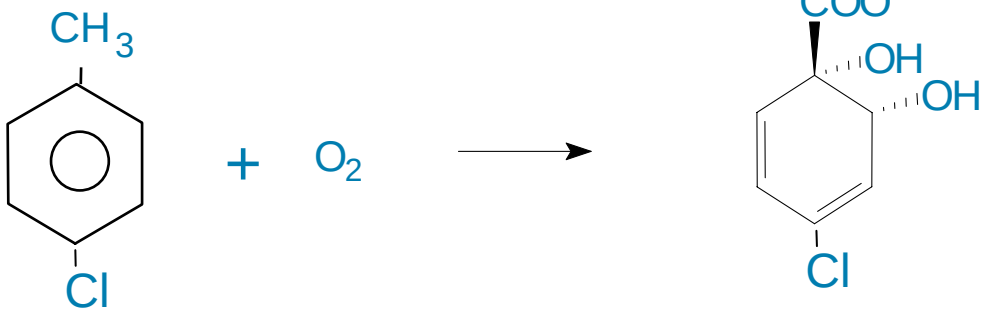
Circuit design for the production of fine chemicals



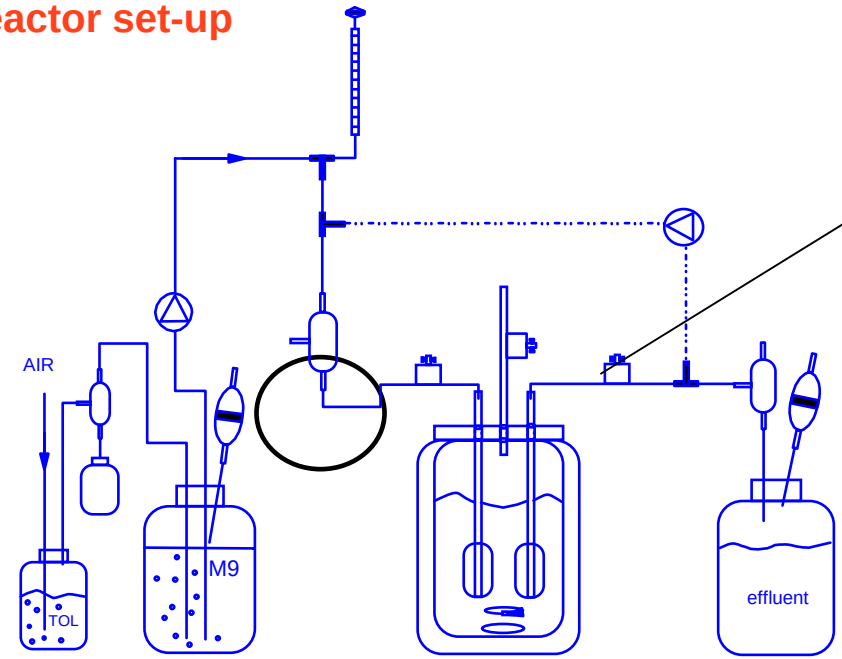
4-Cl toluene

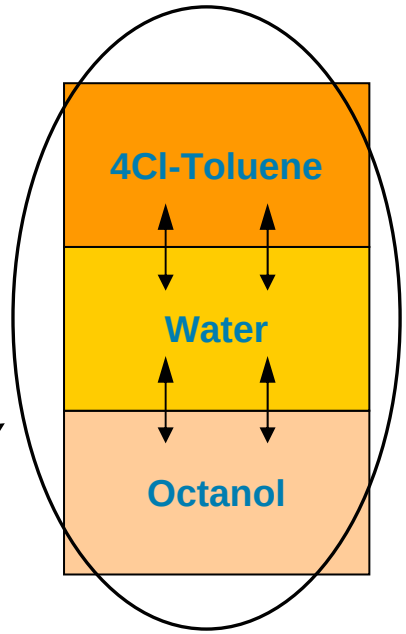
cis-4-chlorodyhydrodiol

Attractive alternative: cofactor dependent biotransformation in two-phase systems

- precursor for many industrially relevant enantiopure derivatives
- difficult to synthesize chemically

Reactor set-up





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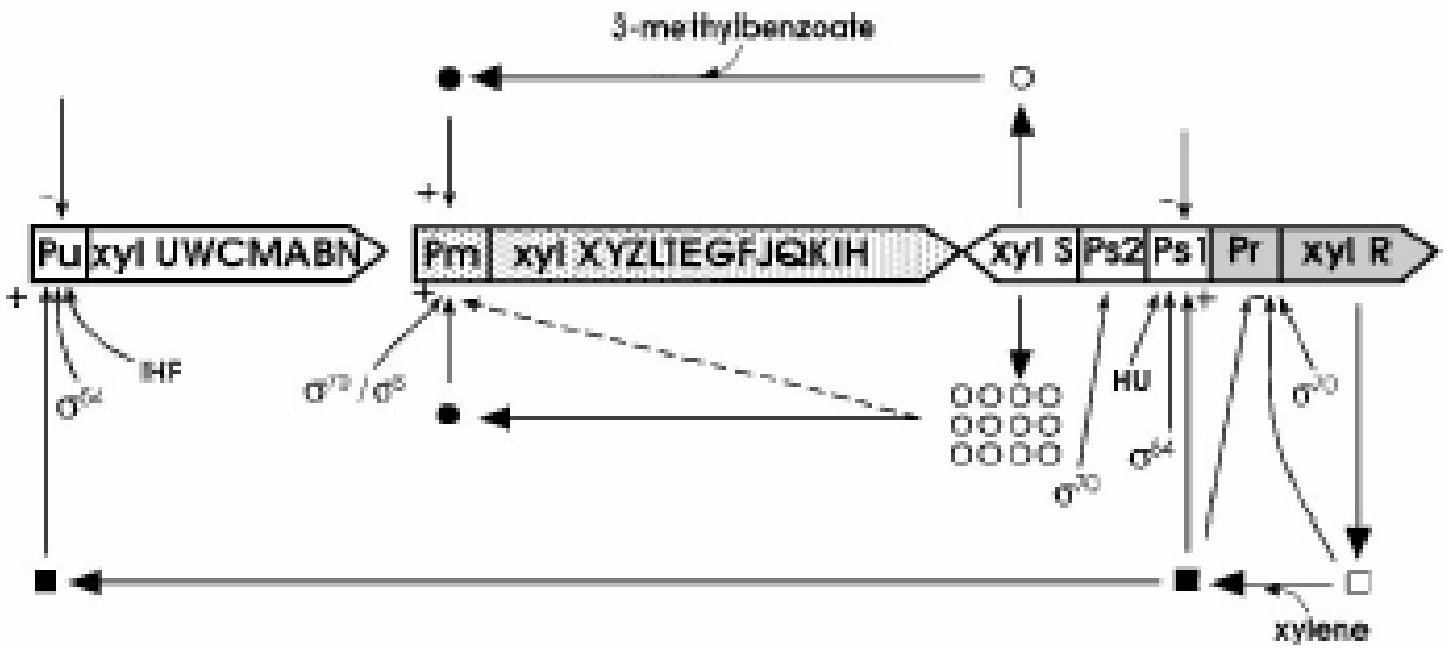
But,

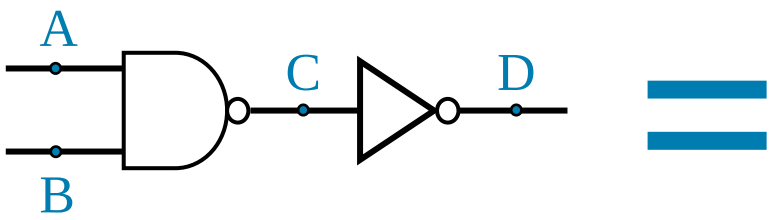
this reaction is part of a complex metabolic network and

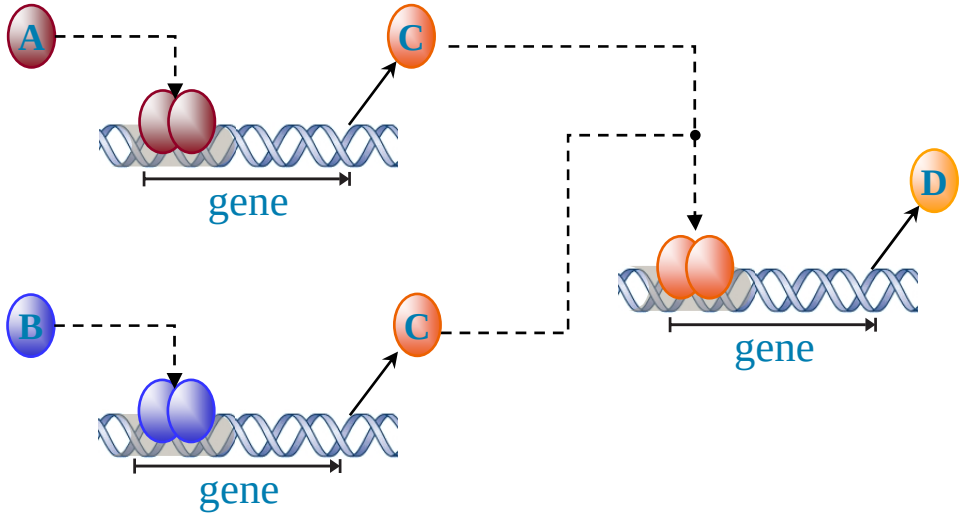
is under control of various interconnected regulatory loops



Logic genetic circuits based on inverters

With properly designed inverters, any (finite) digital circuit can be built





proteins are the wires, genes are the gates

NAND gate = “wire-OR” of two genes

- Need a genetic circuit to combine *promoter* inputs
- Modular, interchangeable inputs and outputs
- Integrating more signals provides more environmental

AND

IN 1	IN 2	OUT
0	0	0
1	0	0
0	1	0
1	1	1

OR

IN 1	IN 2	OUT
0	0	0
1	0	1
0	1	1
1	1	1

After Weiss, 2002

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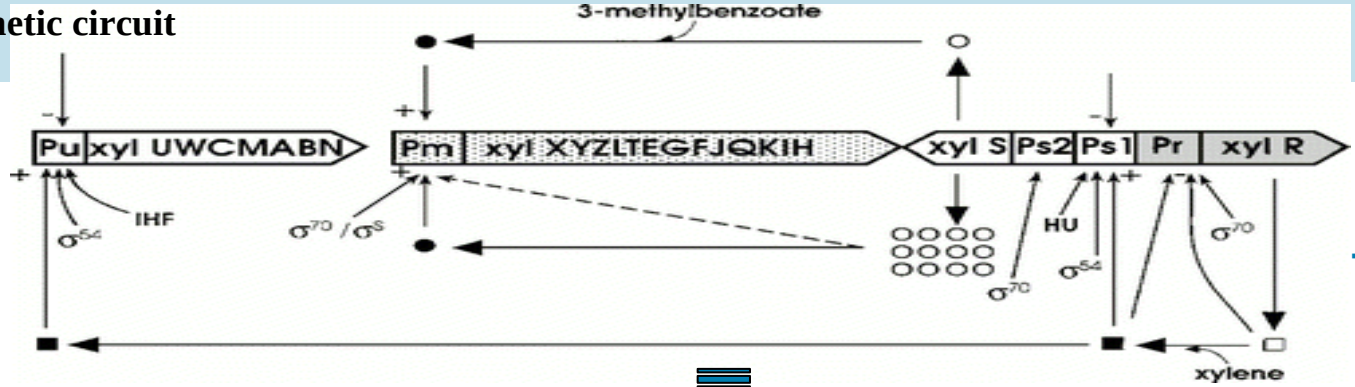
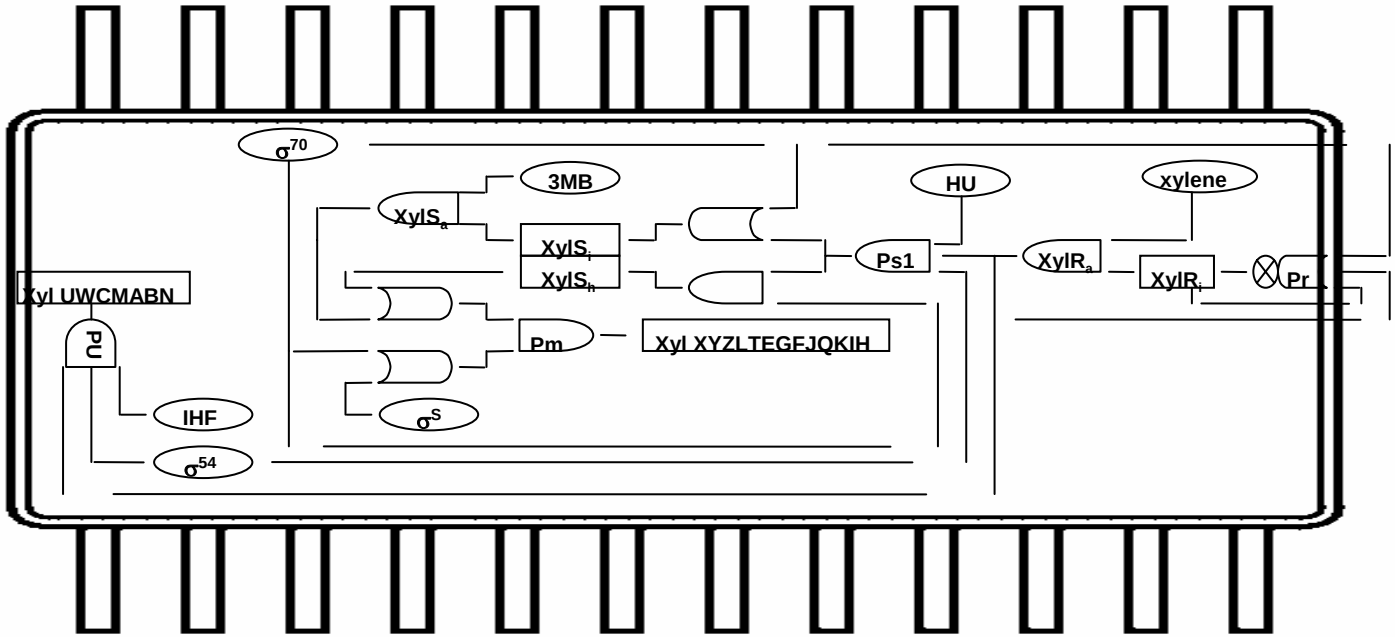
Genetic circuit



TOL-on-a-CHIP

Logic circuit



Inputs Outputs AND OR Pr NOR

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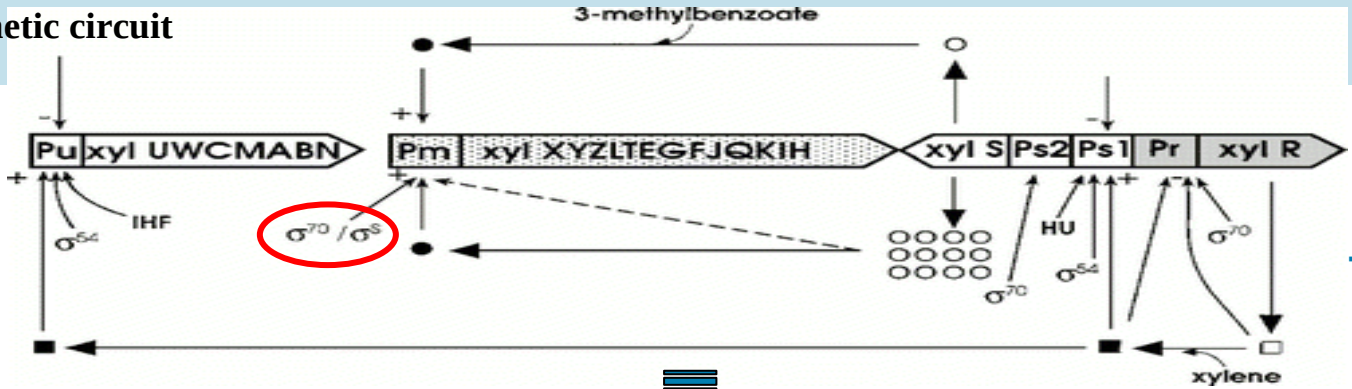
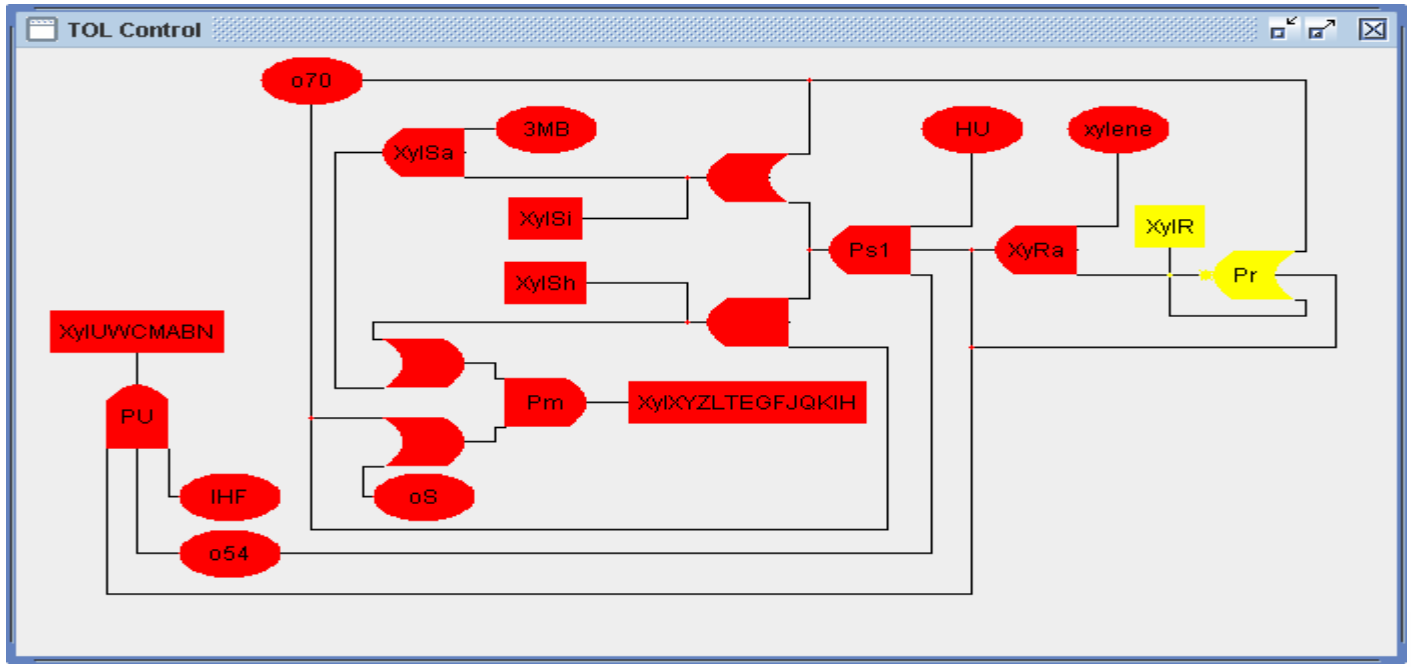
Genetic circuit



TOL-on-a-CHIP

Logic circuit



Inputs Outputs AND OR NOR

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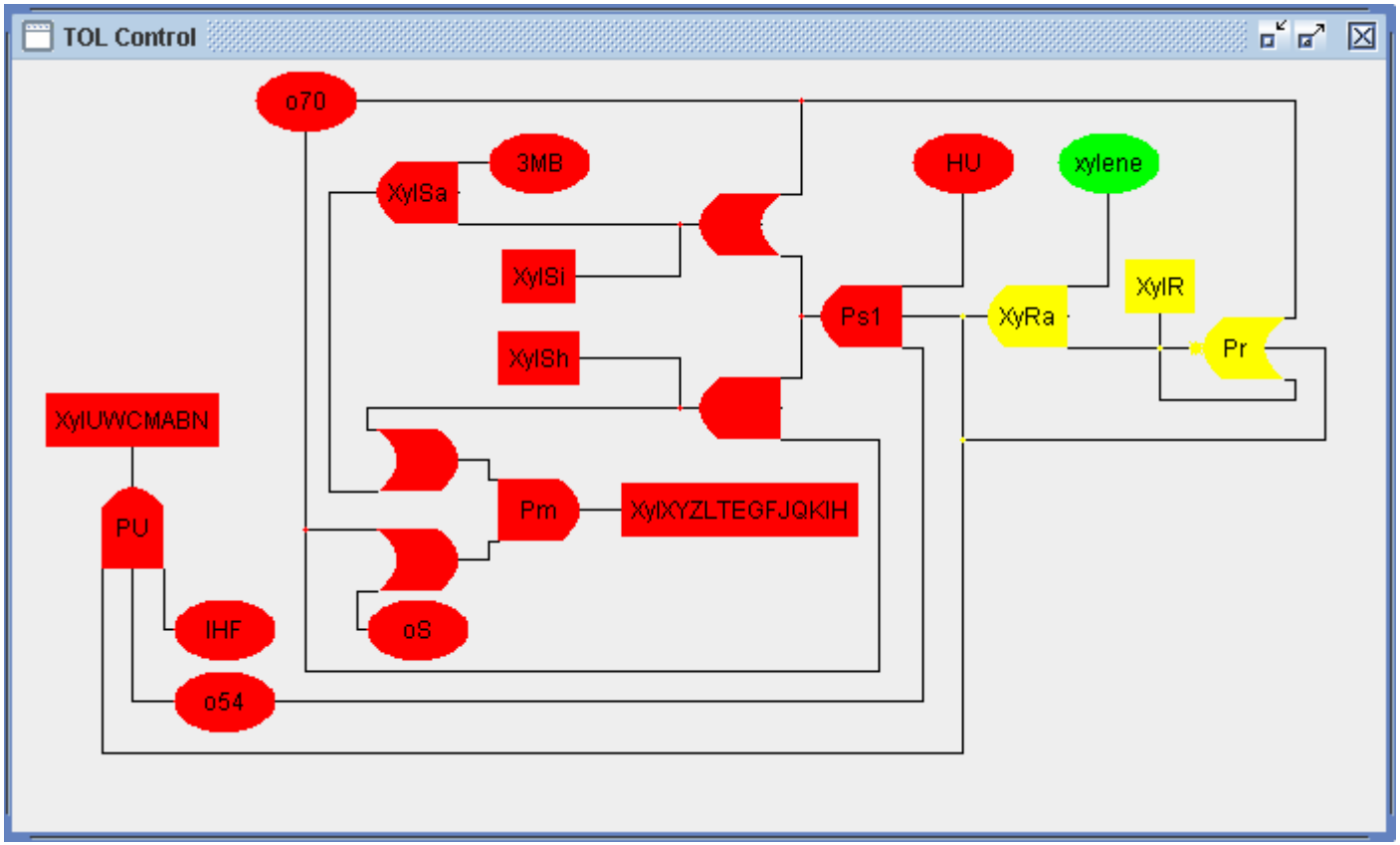

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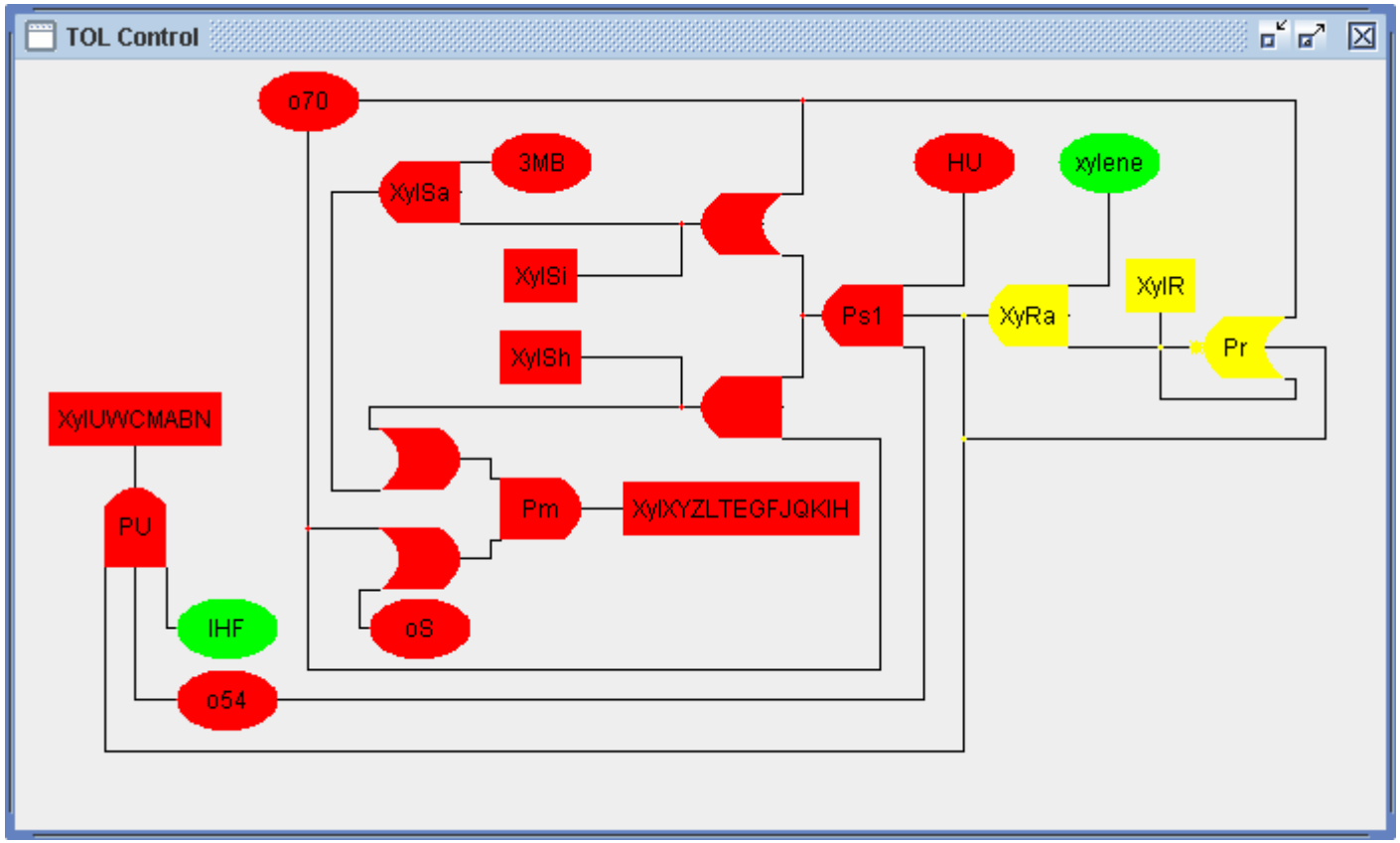

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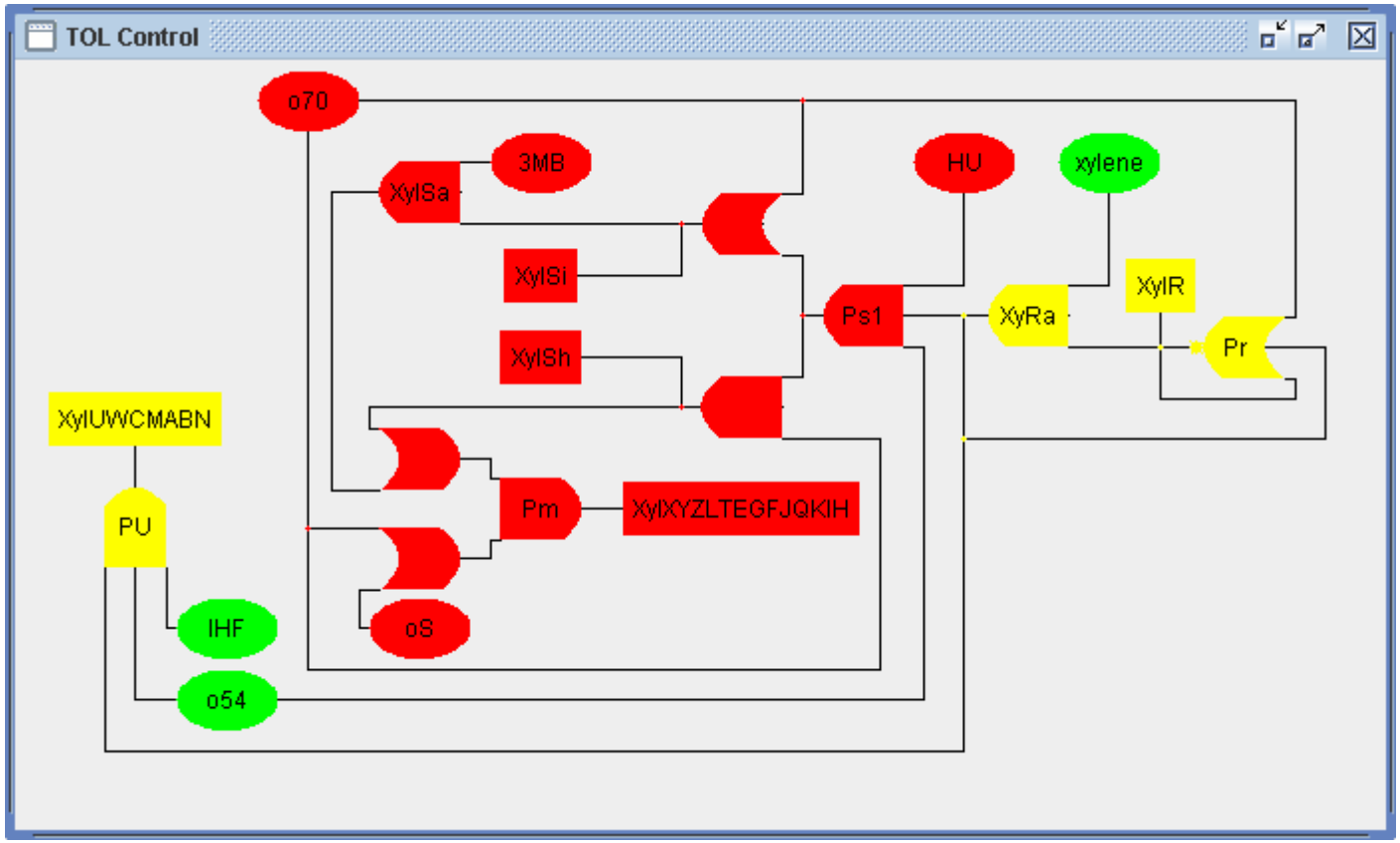

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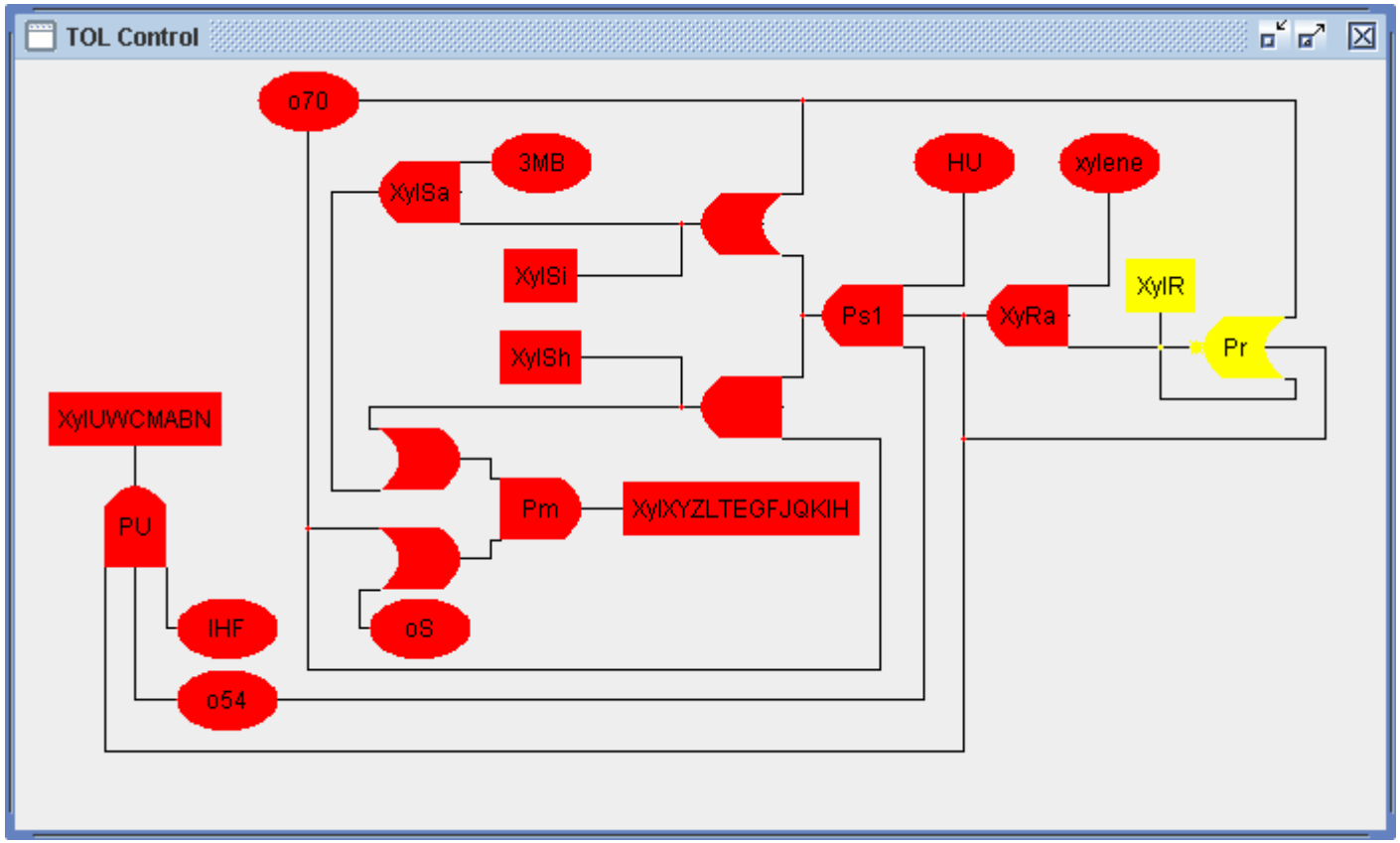

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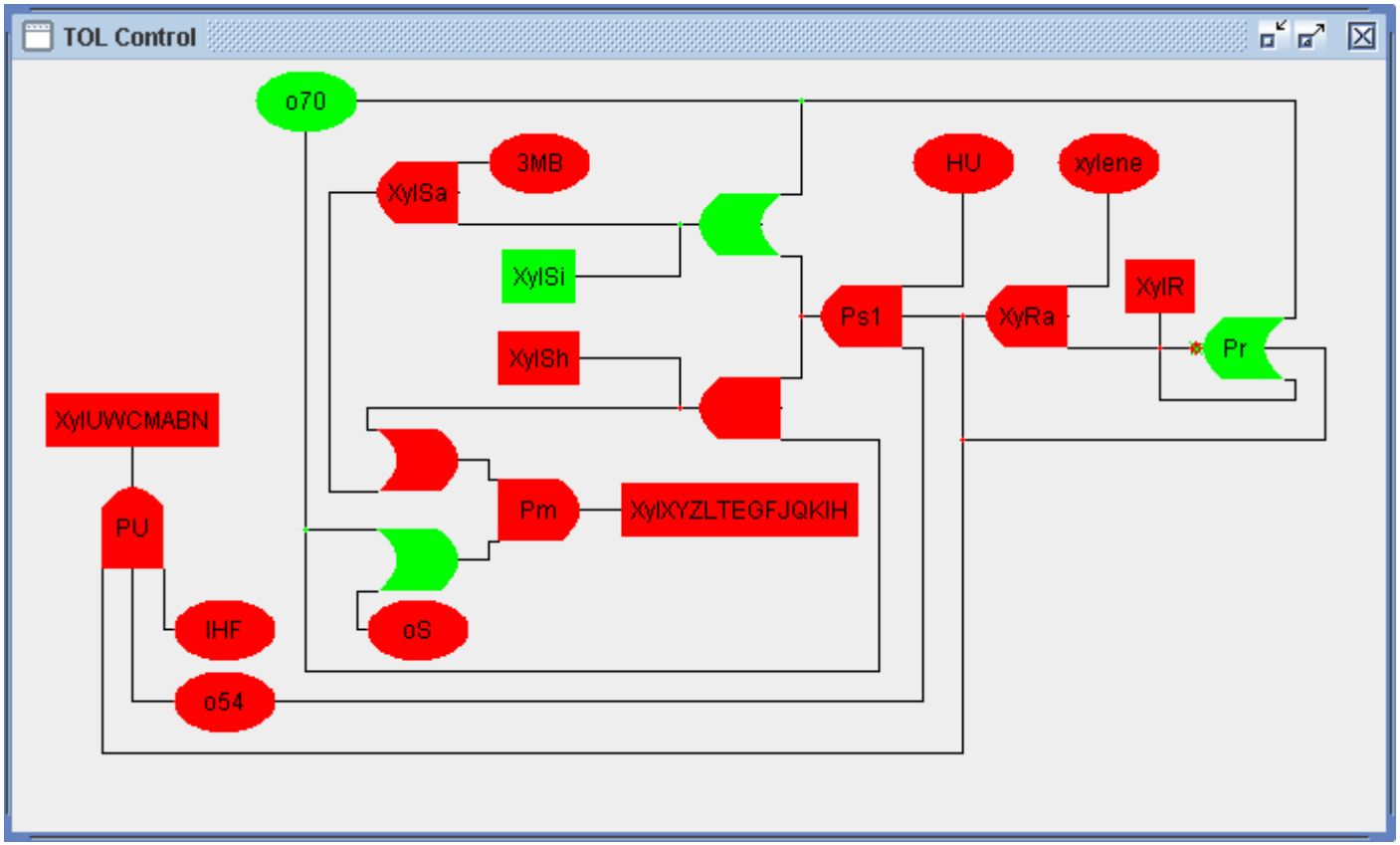

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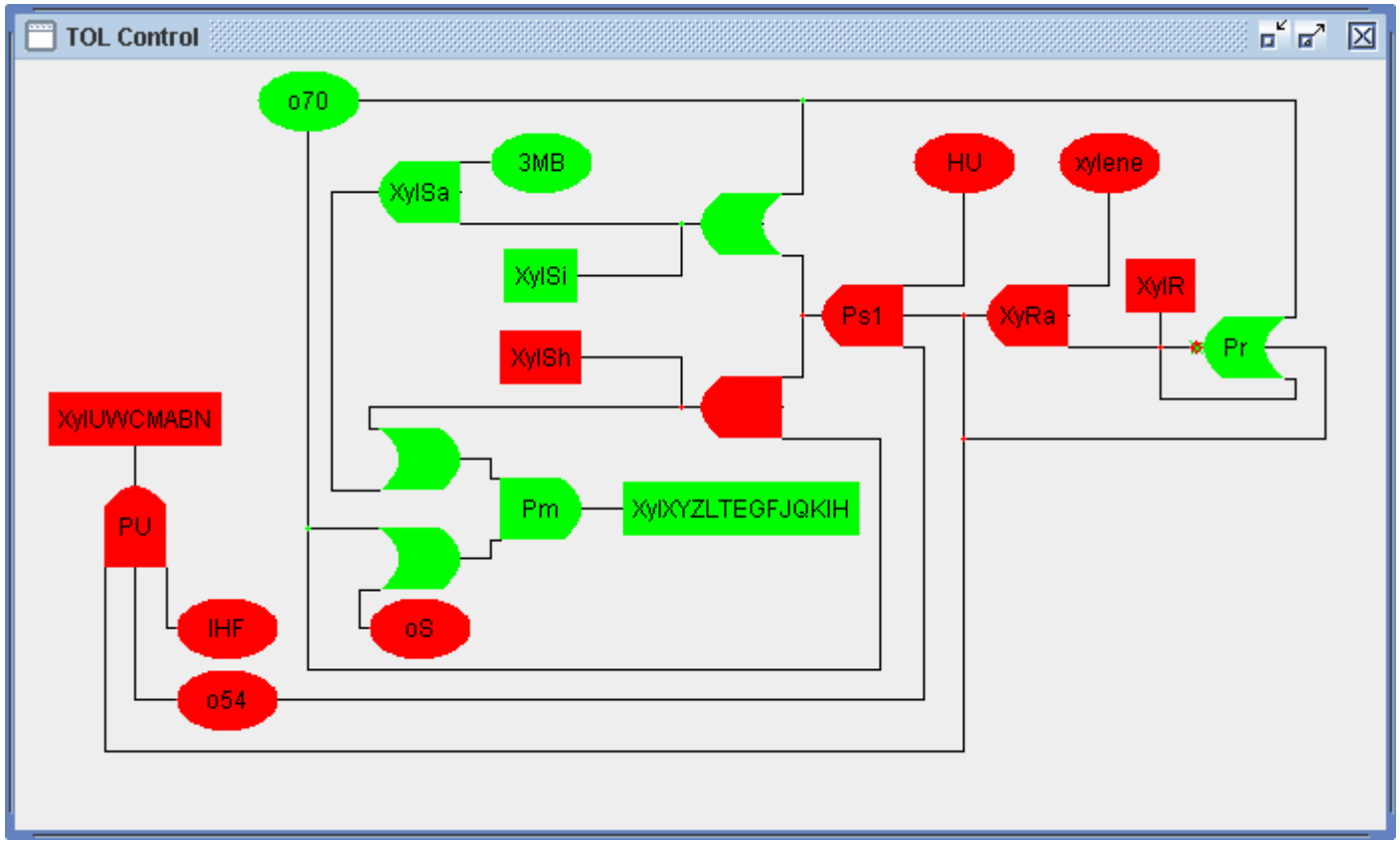

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Model prediction of expression levels

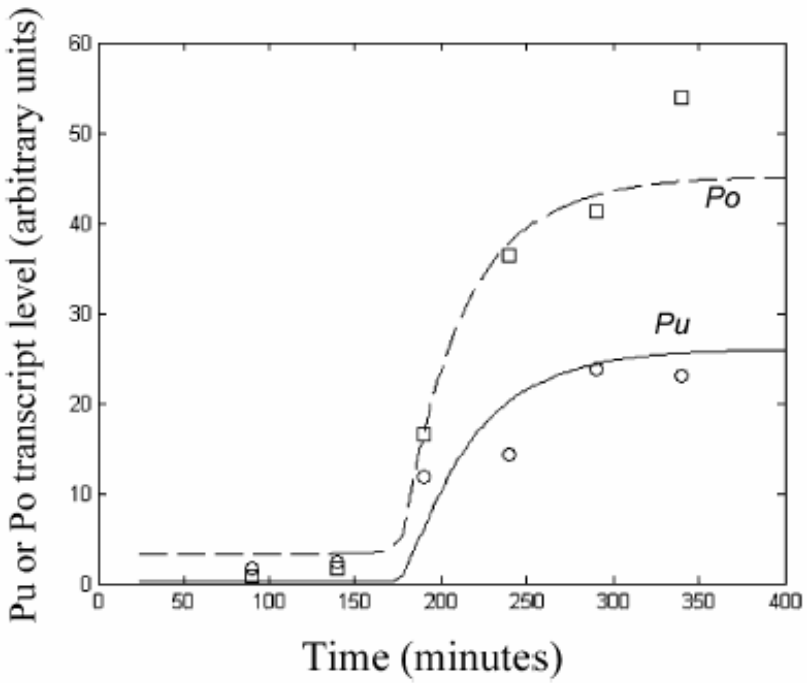

Fig. 1. Model simulation of transcription from σ^{54}-dependent promoters in wild-type cells.

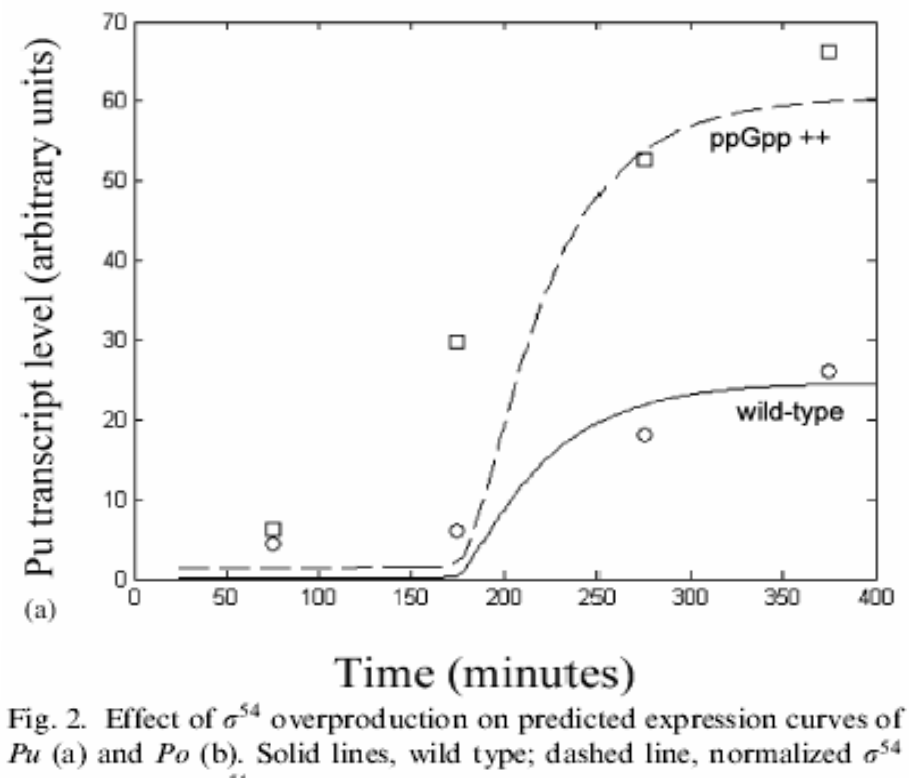

Fig. 2. Effect of σ^{54} overproduction on predicted expression curves of *Pu* (a) and *Po* (b). Solid lines, wild type; dashed line, normalized σ^{54}

Sze et al., 2002, Cases et al., 2001, van Dien et al., 2003

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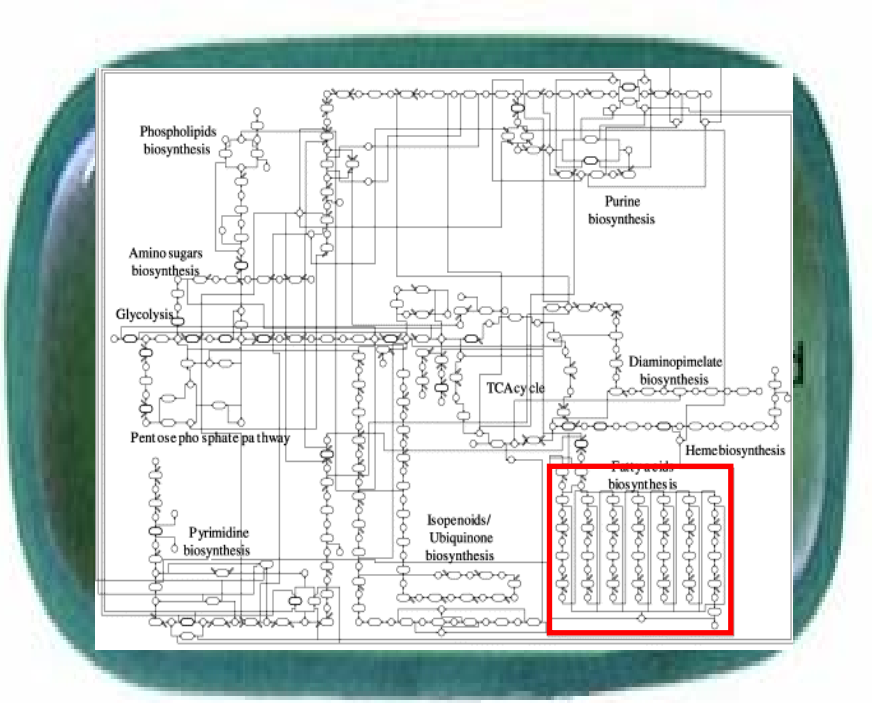
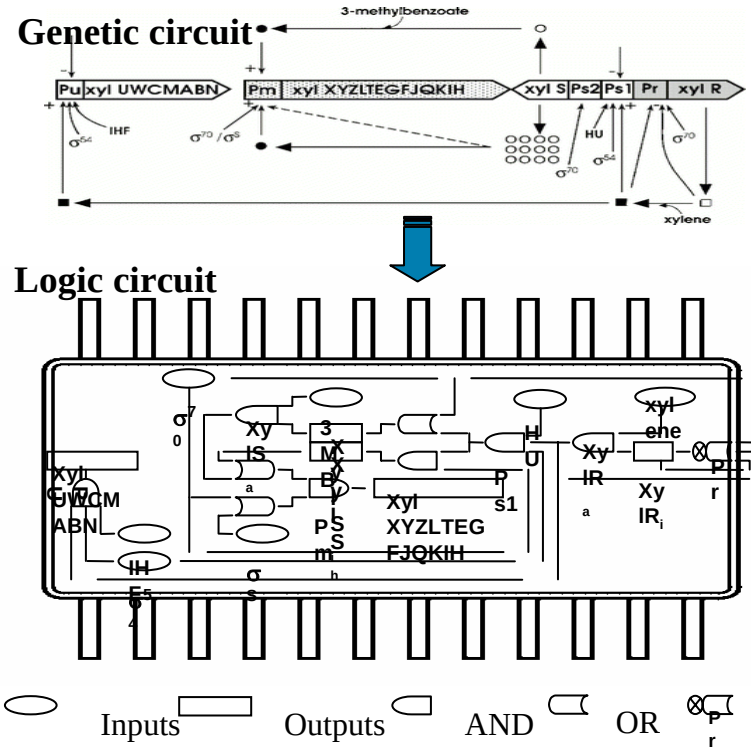
Interplay circuits of interest and genome





Aim is to have an integrated bacterial blueprint to enable (re-)programming

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Niche advantages: importance of cold-adapted enzymes

- Biocatalysis at lower temperatures
- Higher enantioselectivities at low temperatures
- Lower energy consumption
- Bioremediation in cold environments

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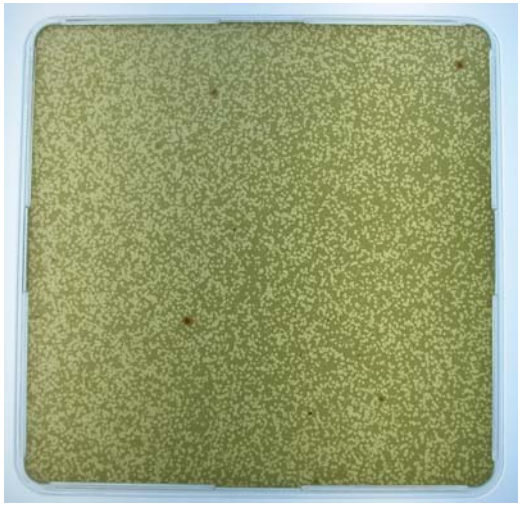
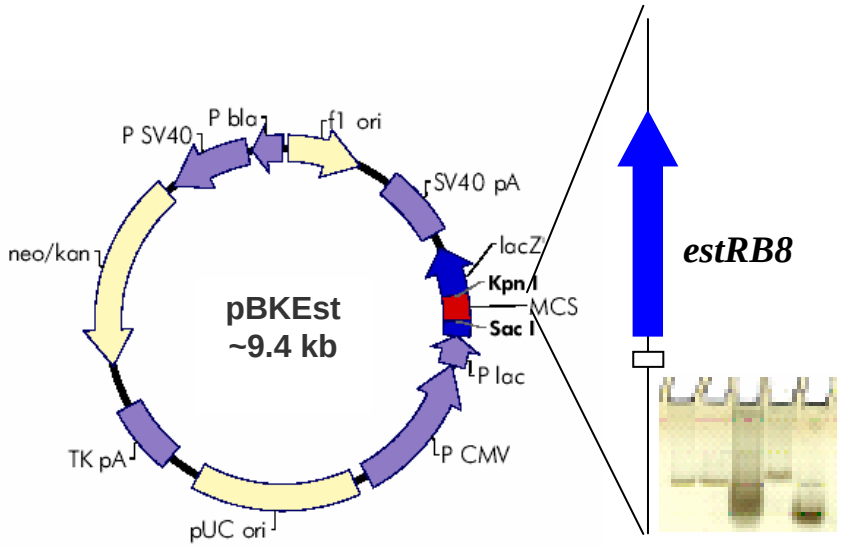
An esterase from an expression library of the *O. antarctica* genome



Screening of ca. 10,000 phage clones with chromogenic substrates

Subcloning,

hyperexpression



- Esterase EstRB8 obtained from an expression library of *O. antarctica*
- Exhibited low activity when expressed in *E. coli* at 30-37° C
- Reason? Misfolding? Problem with chaperones?
- Why? Chaperones are responsible for the folding and refolding of more than 20-30% of the proteins of the cell

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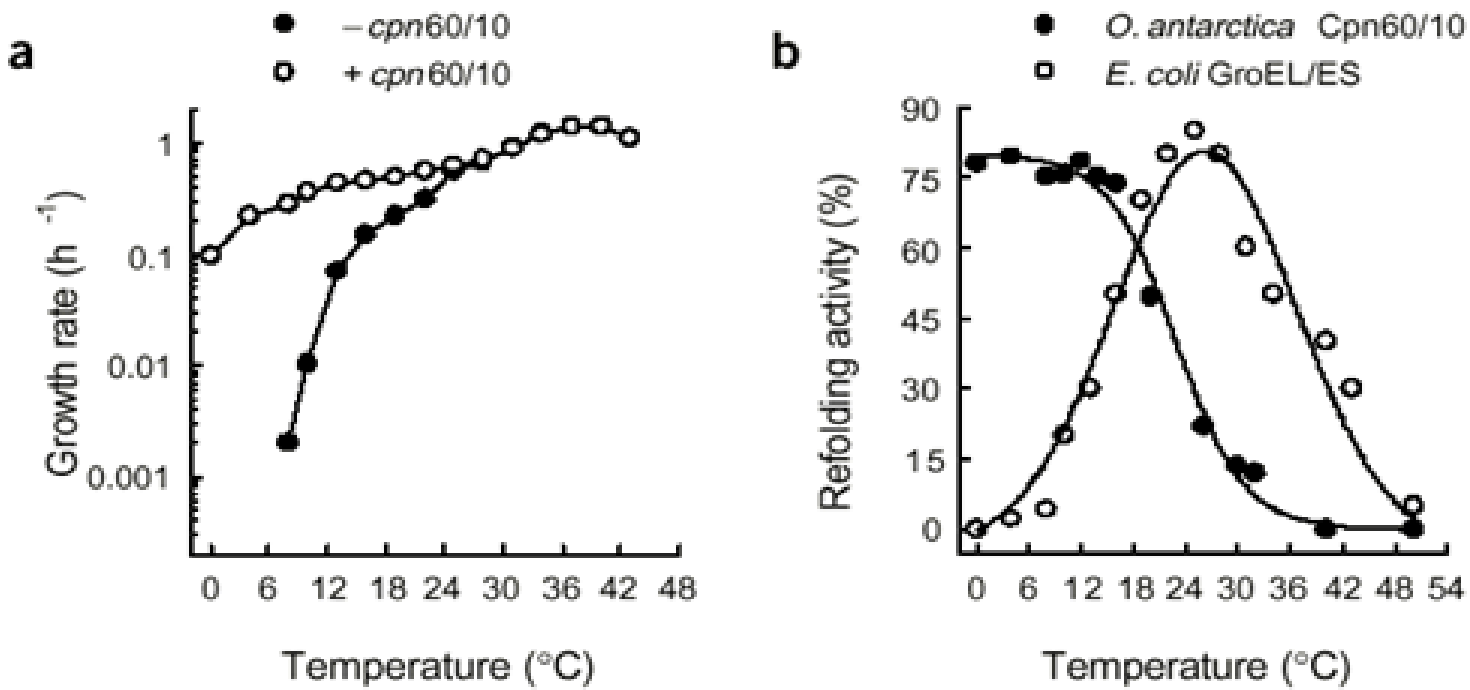
Psychrophilic chaperonin provides advantage to e.coli



Expression of Cpn in *E. coli* lowers its minimum growth temperature from 7.5° C to below 0° C (theoretical minimum -13.5° C!) and substantively improves its growth at temperatures below 20° C, which correlates with the low temperature optimum of *in vitro* refolding activity of Cpn

Nature Biotechnol (2003)21: 1266-1267

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Questions:

Why does systems failure take place in *e. Coli* at low temperatures?

How does cpn protect *e. Coli* at low temperatures?

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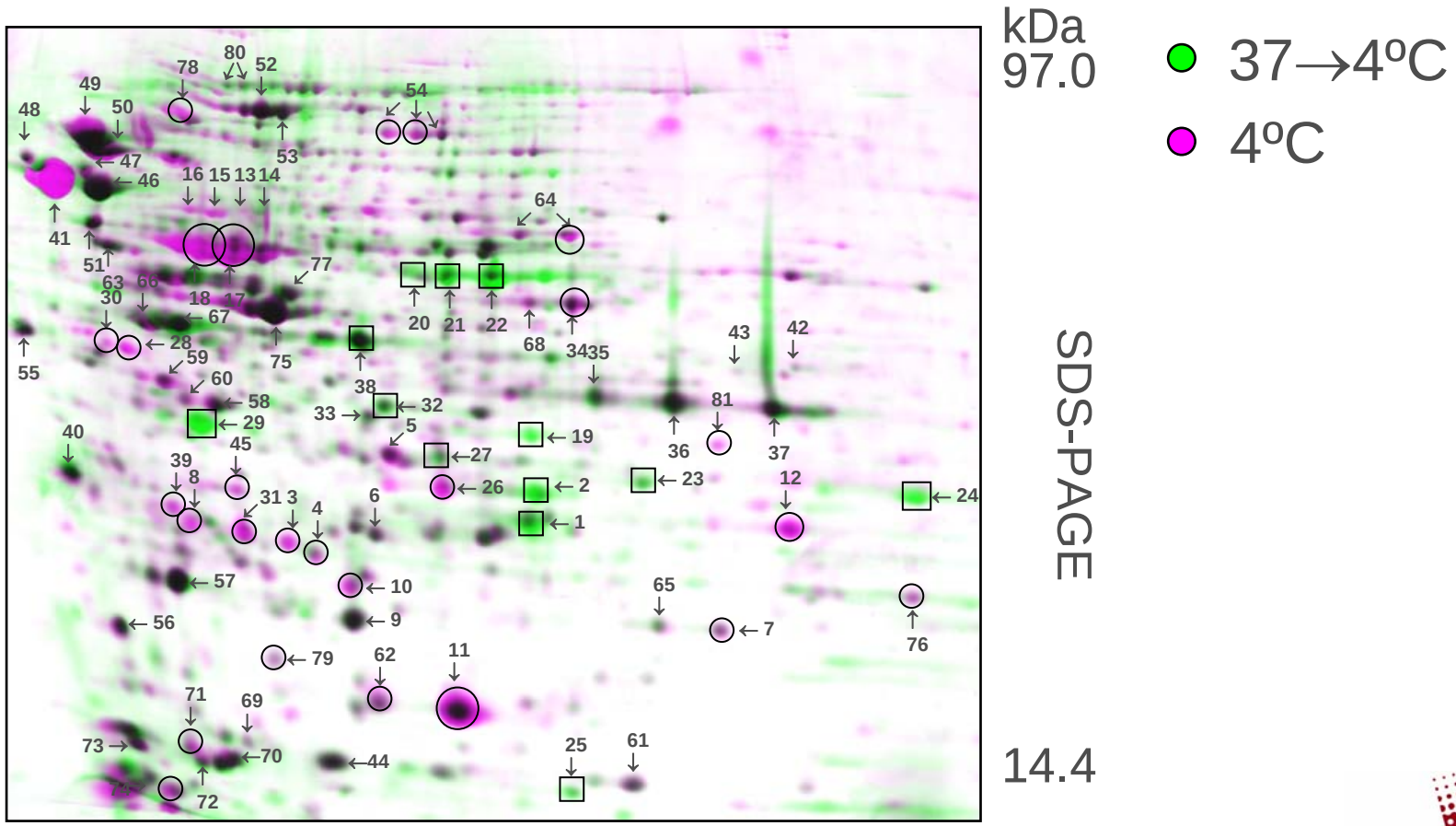
Testing *E. coli* to (cold) destruction: proteomics of systems failure in *E. coli* cells at 4° C and rescue by Cpn



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Why system's breakdwon at low temperatures

- A range of housekeeping proteins, in particular nucleic acid metabolism and chaperone functions, are found at higher levels in Cpn$^+$ *E. coli* cells at 4°C.

- Systems failure in Cpn$^-$ *E. coli* cells at 4°C presumably results from cold inactivation of one or more of these

- Prevention of systems failure probably results from increased interactions of the key protein(s) with the Cpn chaperonins

- Can these interactions be captured by co-precipitation with Cpn?

- anti-Cpn60 antibody raised (anti-GroE antibody used as a control) and used to precipitate Cpn in cells grown at different temperatures

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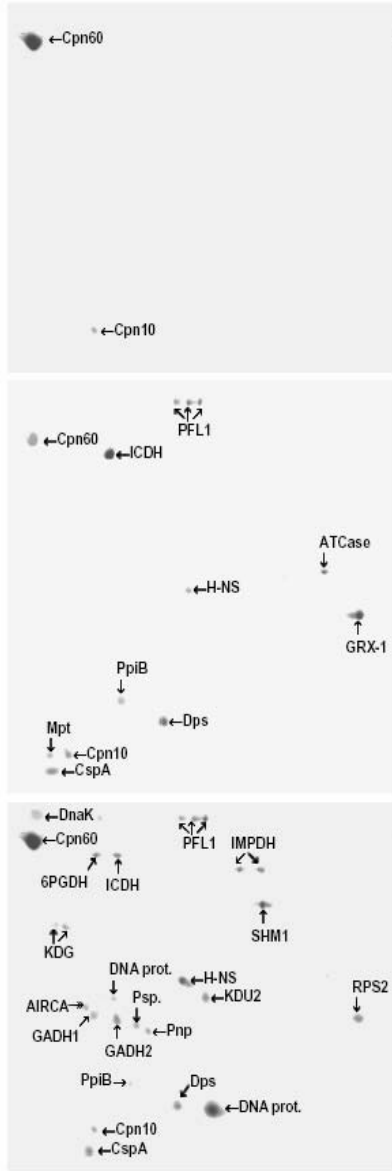
Co-precipitation with Cpn

Key housekeeping *E. coli* proteins up-regulated at low temperatures co-precipitate with Cpn but not GroEL/ES

- DNA-binding proteins (Dps, H-NS, Rps2, Rps6, RbfA and Psp),
- Molecular chaperones (CspA, ClpB, PpiB and Grx),
- Proteins involved in energy metabolism (GADH, ICDH and 6-PGDH),
- Nucleic acid metabolism (Pnp)
- Polysaccharide degradation (KDU and KDG),
- *de novo* purine biosynthesis pathway (AIRCA),
- Amino acid biosynthesis (ATCase),
- Pyruvate metabolism (PFL1) and acid resistance (GAD)

all present at significantly higher levels (up to 114-fold)



Strocchi et al., Proteomics 2005

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HOW DOES cpn PROTECT *E. Coli* AT LOW TEMPERATURES?

- Cpn exhibits temperature-dependent double ring to single ring transitions of its barrel structure

- The single ring form dominating at low temperatures exhibits a greater hydrophobic patch surface

- The single ring form forms more stable associations with proteins fulfilling key cold sensitive functions whose inactivation leads to cellular systems failure

- This association protects these key functions and thereby prevents systems breakdown

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Improved expression of important activities

- **EstRB8 esterase activities expressed in *E. coli* grown at 4° C were orders of magnitude higher than those in *E. coli* grown at 37° C**
- ***In vitro*, the *O. antarctica* chaperonins did not promote re-folding of denatured EstRB8, so denatured EstRB8 seems not to be a substrate of Cpn**
- **the role of Cpn in obtaining high yields of active EstRB8 esterase is to allow growth of the host strain at 4° C, a temperature optimal for production and stability of the esterase**

Applications of the cpn^{+} *e.Coli* system

Functional expression/obtaining high yields of heterologous proteins, esp. thermosensitive proteins

Functional expression of hydrophobic proteins

Re-folding of some denatured proteins and prevention of aggregation

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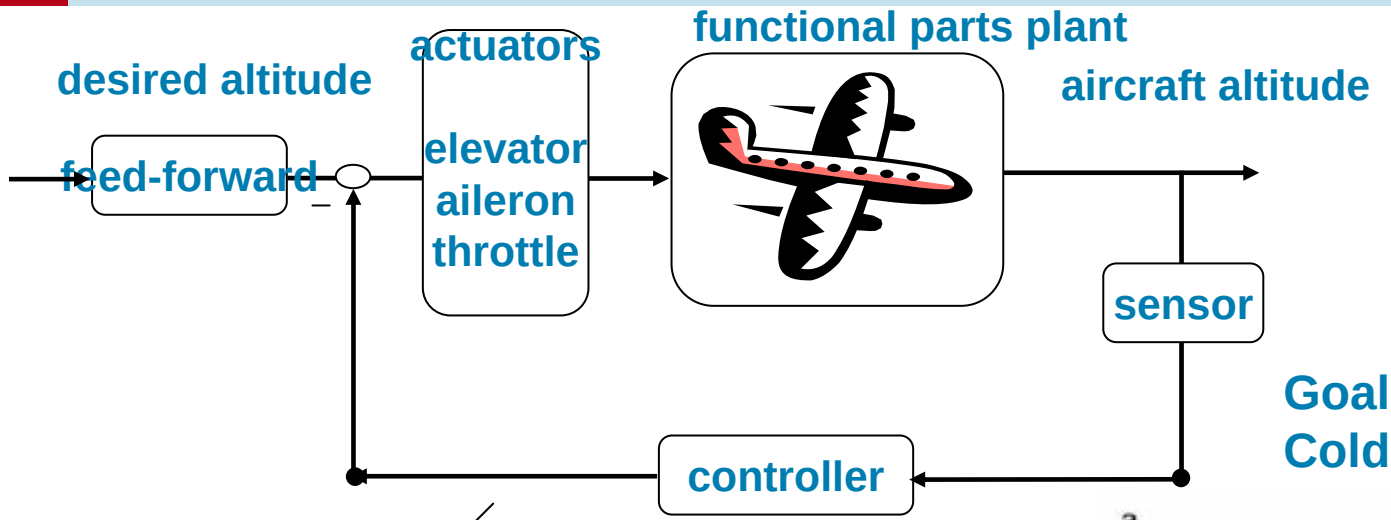
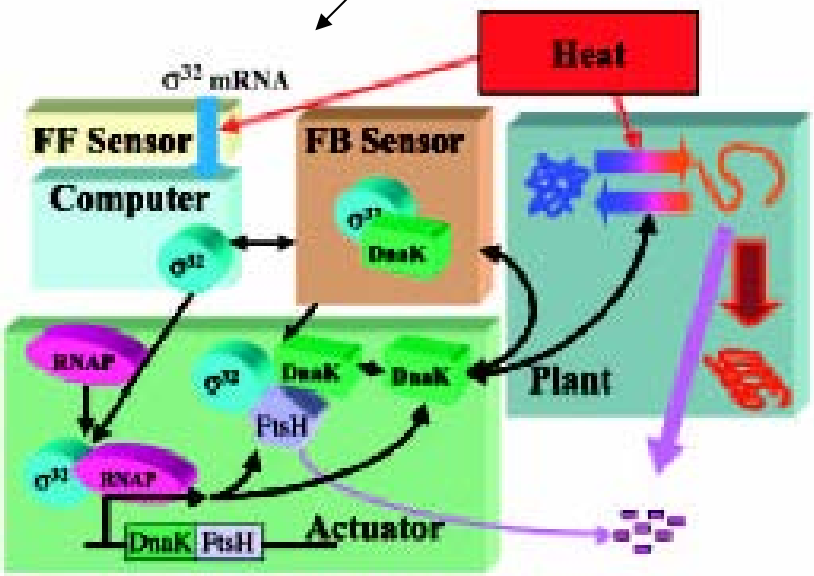
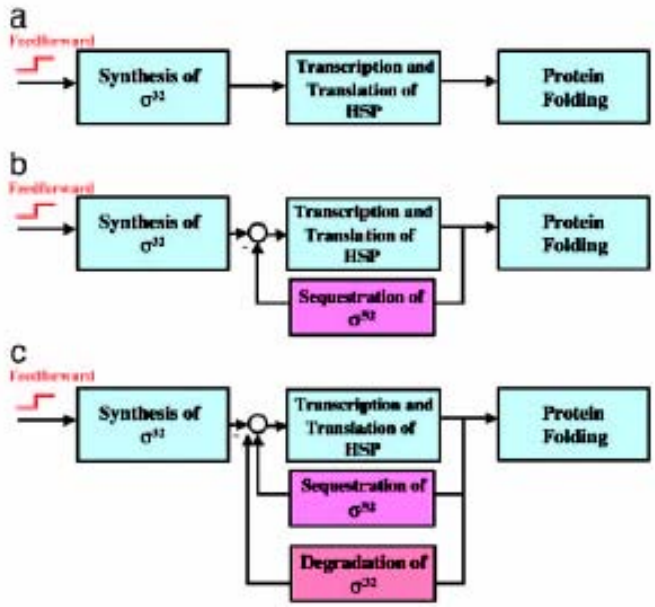
Reverse engineering of the cold network module



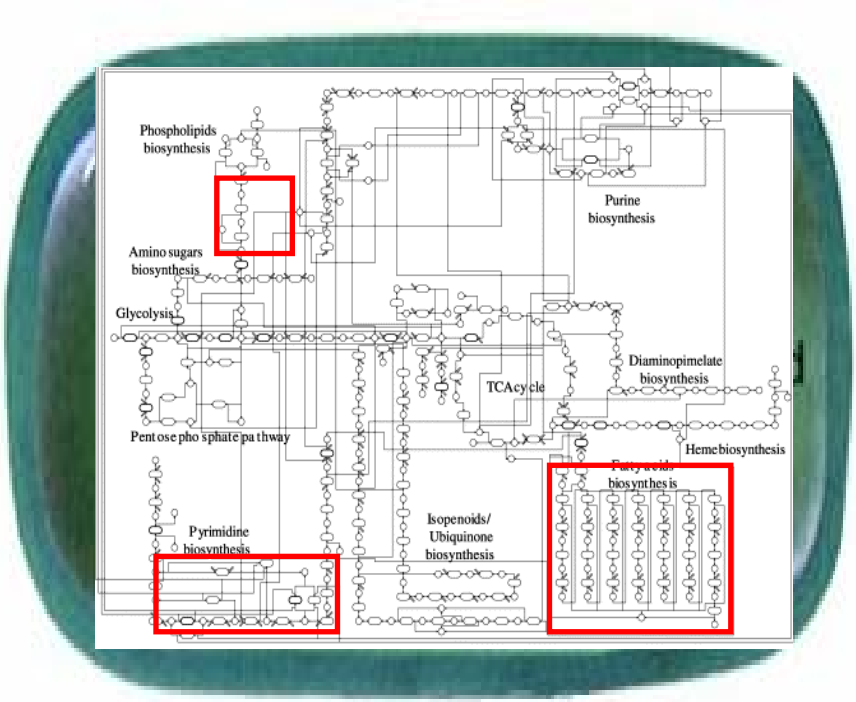
Goal: Obtain blueprint of Cold shock network

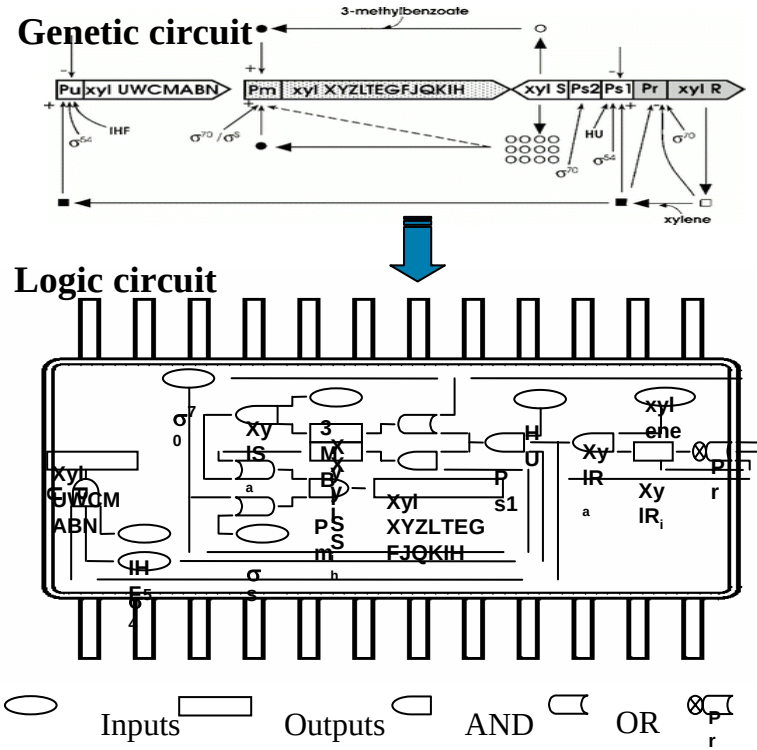




After Axelrod PNAS 2005, El-Samad et al., PNAS 2005

Interplay circuits of interest and genome





Aim is to have an integrated bacterial blueprint to enable (re-)programming

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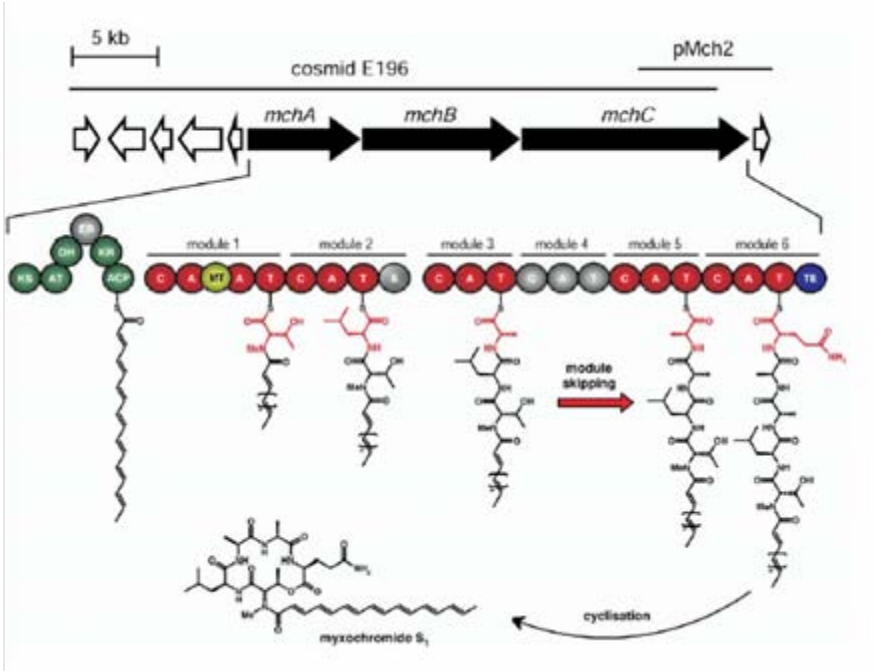
Outlook

- Modular description, design and construction of circuits for biocatalysis

- Explore the Pseudomonas „Chassis“ for heterologous expession of
- genes poorly expressed in traditional hosts and gene clusters
- from metagenomes



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Ken Timmis

PROBACTYS partners:

Victor de Lorenzo, CNB, ES
E. Pistikopoulos, Imperial College London, UK
Antoine Danchin, Institute Pasteur, FR
Jan de Bont, TNO, NL
Huanming Yang, Beijing Genome Centre, CHina
Angel Cebolla, Biomedal, SP

External Collaborations:
J. Papin/M. Oberhardt Univ. Virginia, USA
J. Edwards Univ. Delaware, USA
B. Tümmler, MHH, DE

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