

Dynamics of post-translational genetic regulation in enteric bacteria

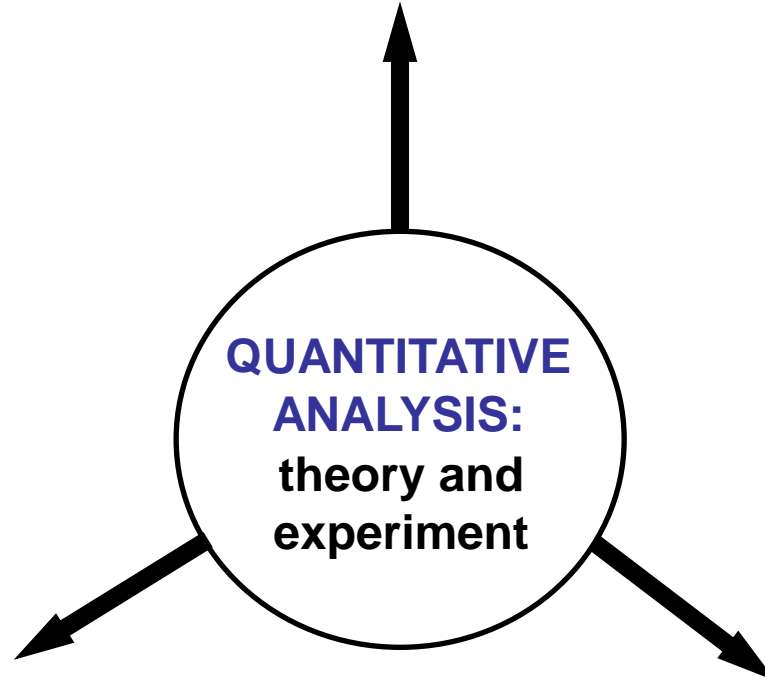
Alexander Y. Mitrophanov

Howard Hughes Medical Institute

Department of Molecular Microbiology, Washington University School of Medicine



**Basic molecular biology:
understanding life**



**QUANTITATIVE
ANALYSIS:
theory and
experiment**

**Synthetic biology: making
regulatory circuits with
useful properties**

**Molecular medicine: drug
development**

This talk

Mathematical modeling



Genotype → phenotype

This talk

Mathematical modeling



Genotype → phenotype



Signal integration systems: structure → function

This talk

Mathematical modeling



Genotype → phenotype



Signal integration systems: structure → function



Bacterial antibiotic resistance mechanisms

Main questions

Main questions

1. What are the rules that govern the dynamics of **genetic circuits** involving **protein–protein interactions**?

Main questions

1. What are the rules that govern the dynamics of **genetic circuits** involving **protein–protein interactions**?
2. What are the **functional** consequences of **structural** diversity in genetic circuits of closely related bacterial species?

Extracellular signals modulate gene expression

Signal

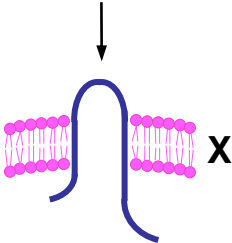
Metal ions, small molecules, pH, etc.

Extracellular signals modulate gene expression

Signal

Metal ions, small molecules, pH, etc.

Sensor

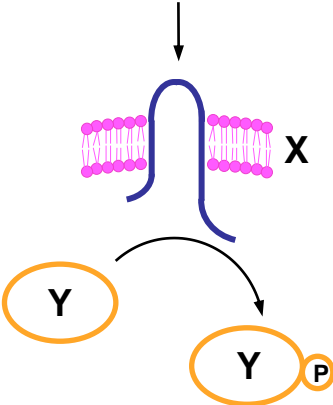


Extracellular signals modulate gene expression

Signal

Metal ions, small molecules, pH, etc.

Sensor



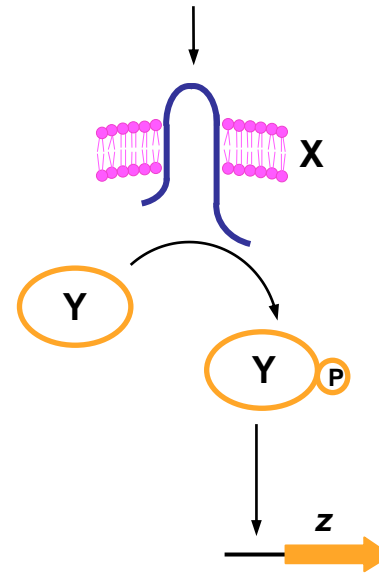
Regulatory circuit

Extracellular signals modulate gene expression

Signal

Metal ions, small molecules, pH, etc.

Sensor



Regulatory circuit

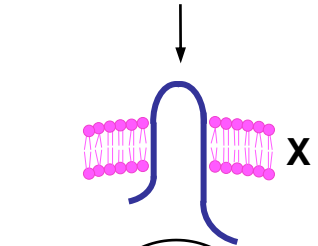
Effectors

Extracellular signals modulate gene expression

Signal

Metal ions, small molecules, pH, etc.

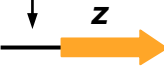
Sensor



Regulatory circuit



Effectors

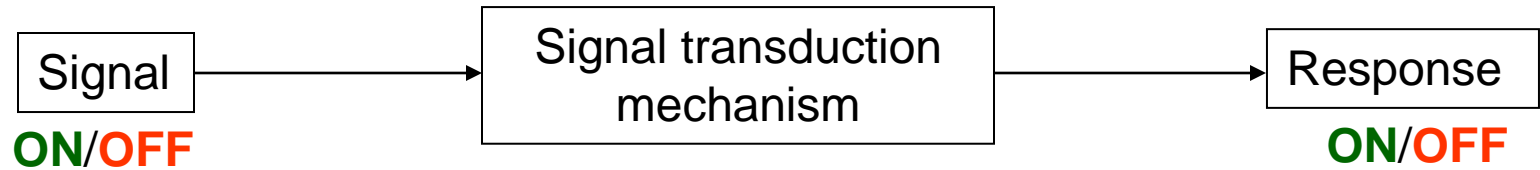


Response

Physiological reaction

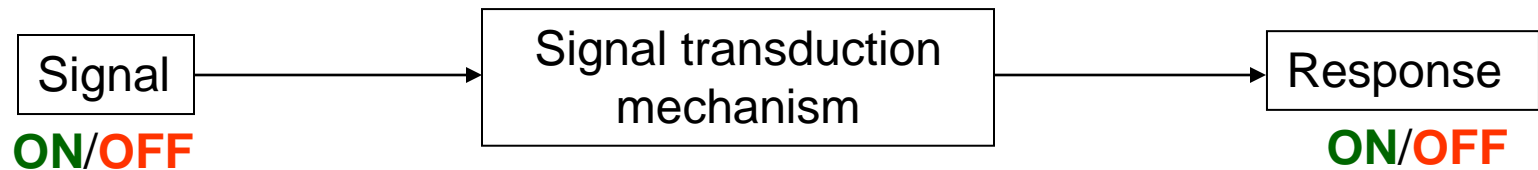
Qualitative vs. quantitative analysis of signal transduction

1. Qualitative analysis

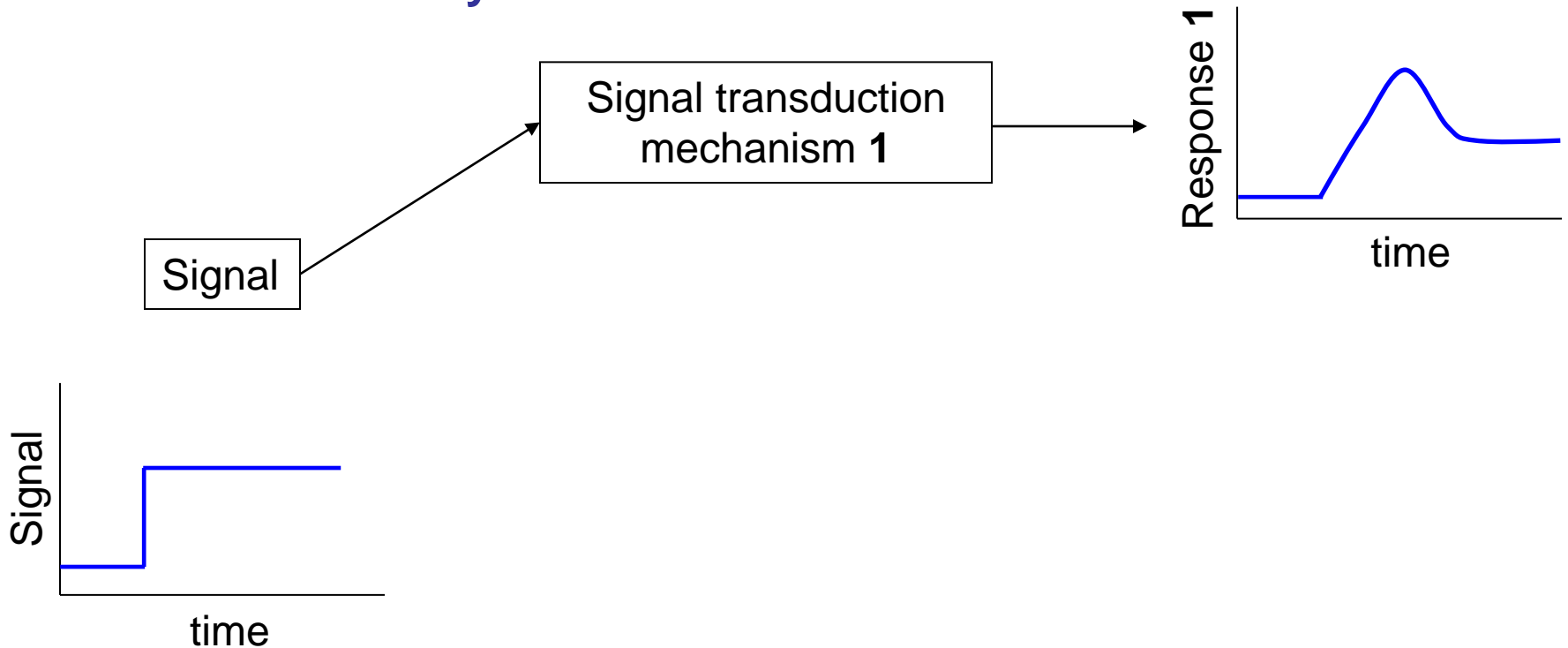


Qualitative vs. quantitative analysis of signal transduction

1. Qualitative analysis

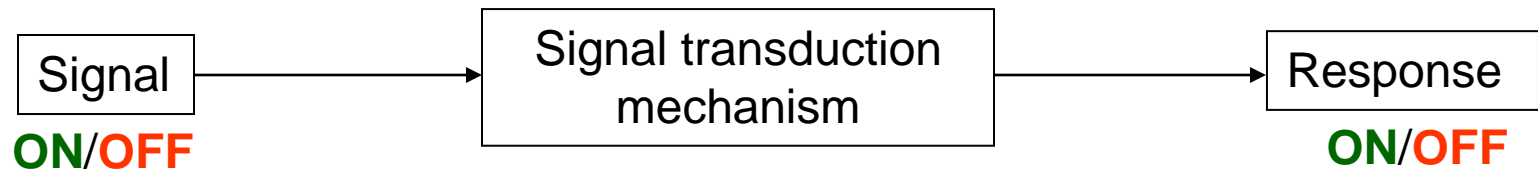


2. Quantitative analysis

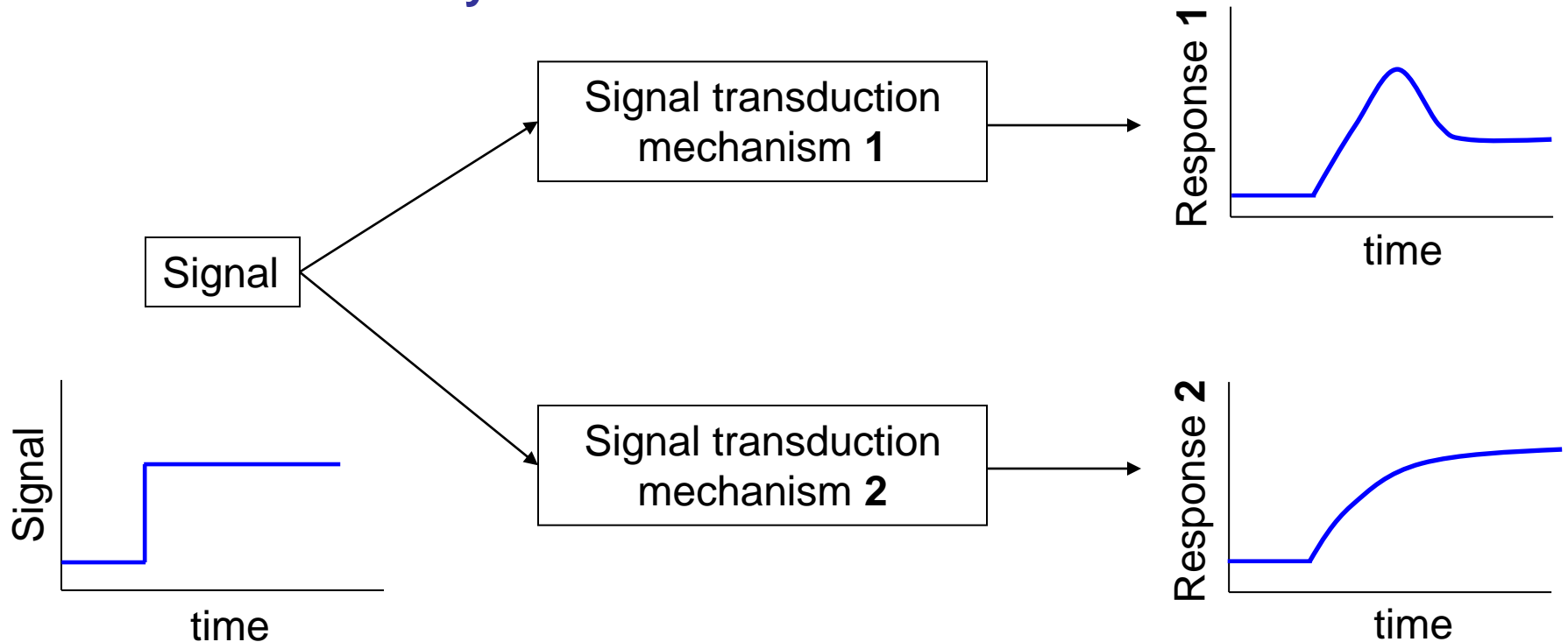


Qualitative vs. quantitative analysis of signal transduction

1. Qualitative analysis



2. Quantitative analysis

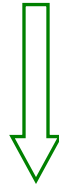
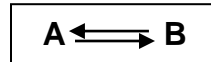


Mathematical modeling of signal transduction mechanisms

Experiment



Conceptual model

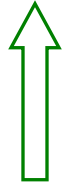
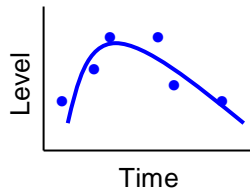


Mathematical model

$$\frac{dX}{dt} = Sv(X(t))$$



Model verification

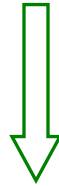
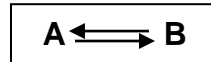


Mathematical modeling of signal transduction mechanisms

Experiment



Conceptual model

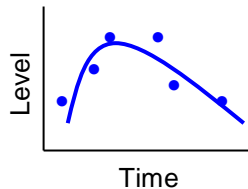


Mathematical model

$$\frac{dX}{dt} = Sv(X(t))$$



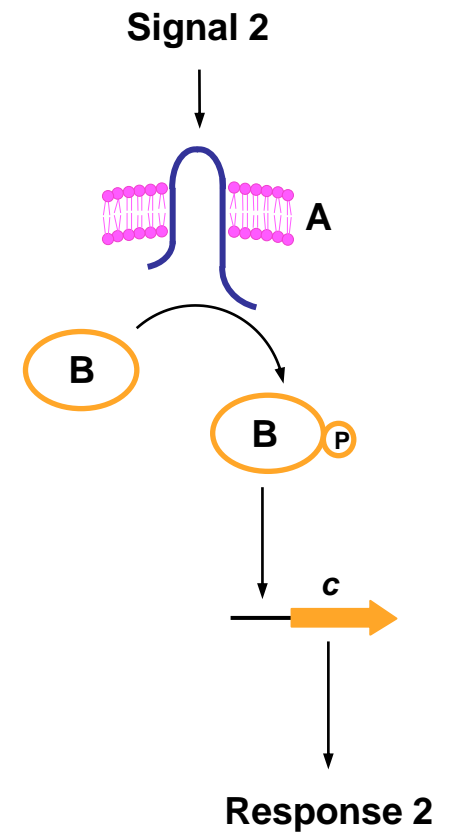
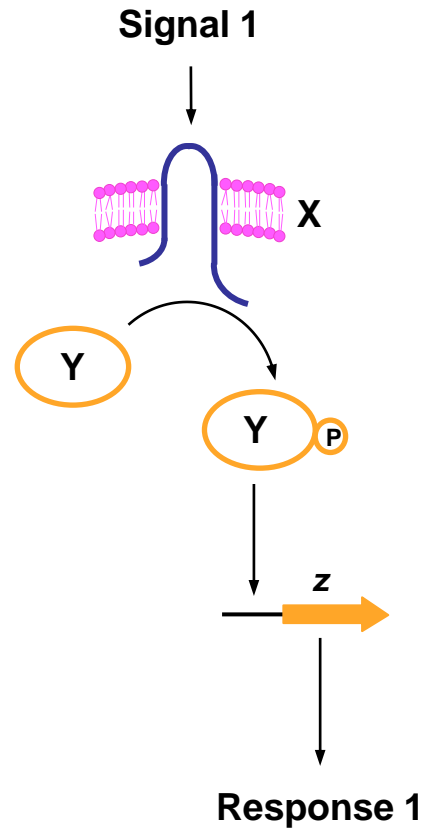
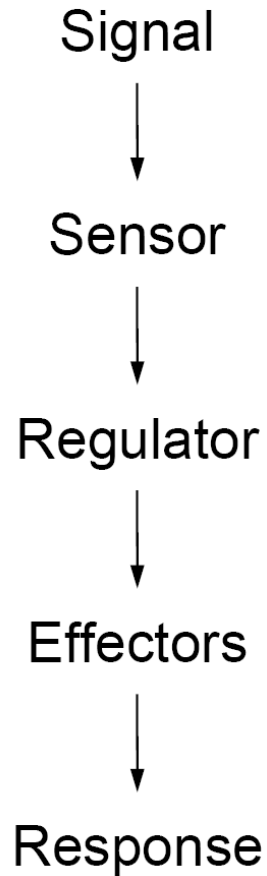
Model verification



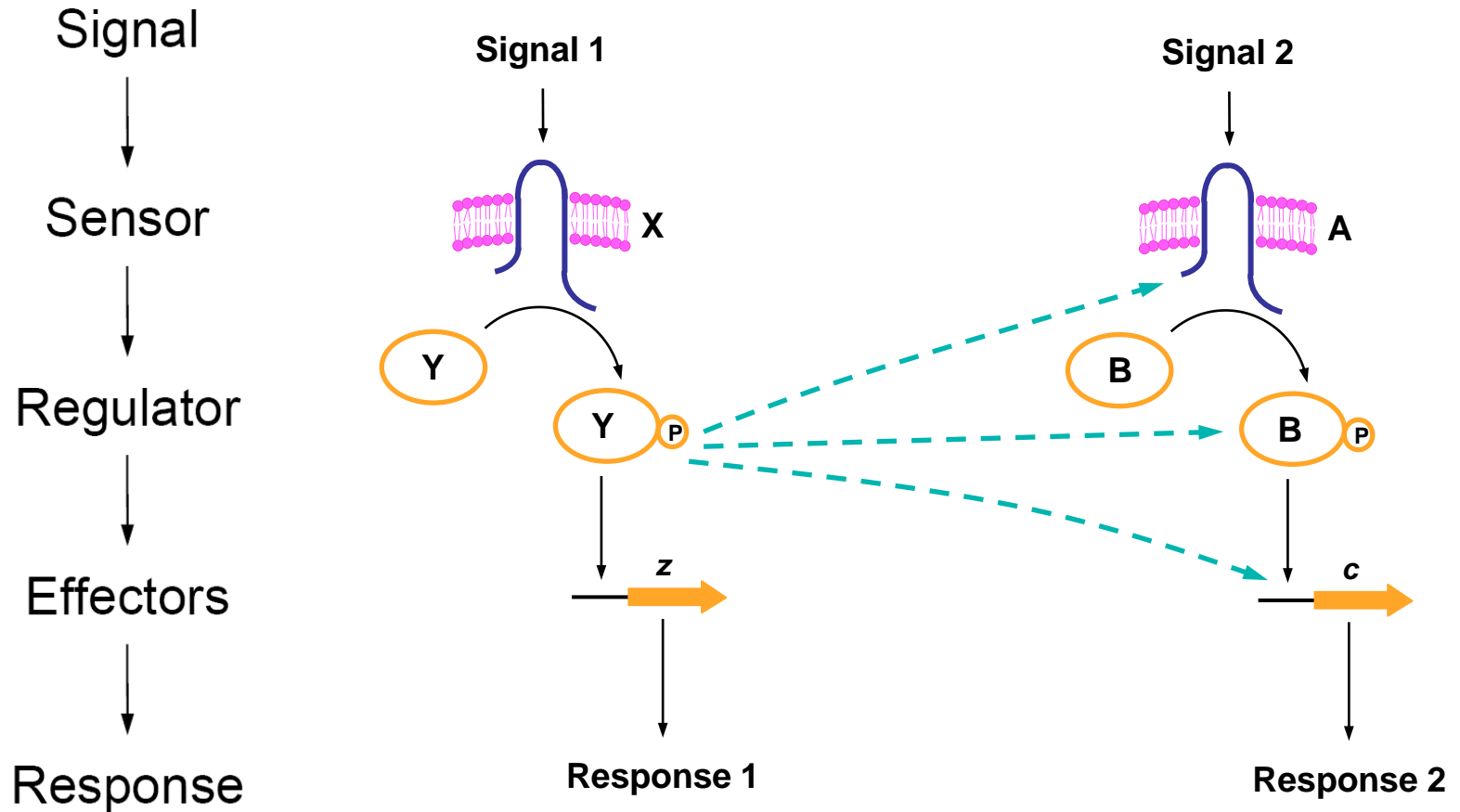
Advantages of modeling

- Explanation and prediction of quantitative effects
- General results difficult to obtain experimentally
- Means to modify system behavior in desirable ways

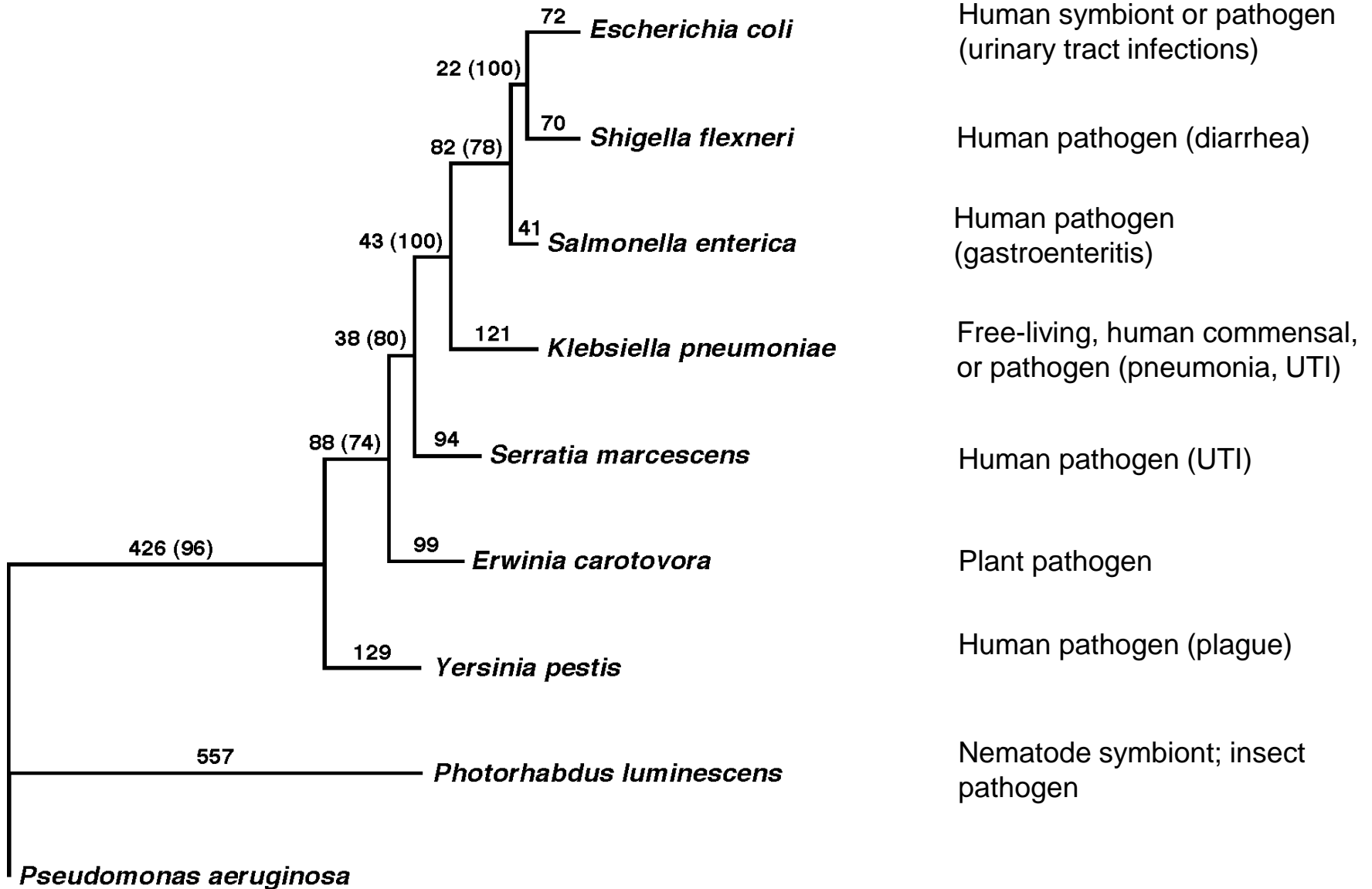
Different signals activate distinct response networks



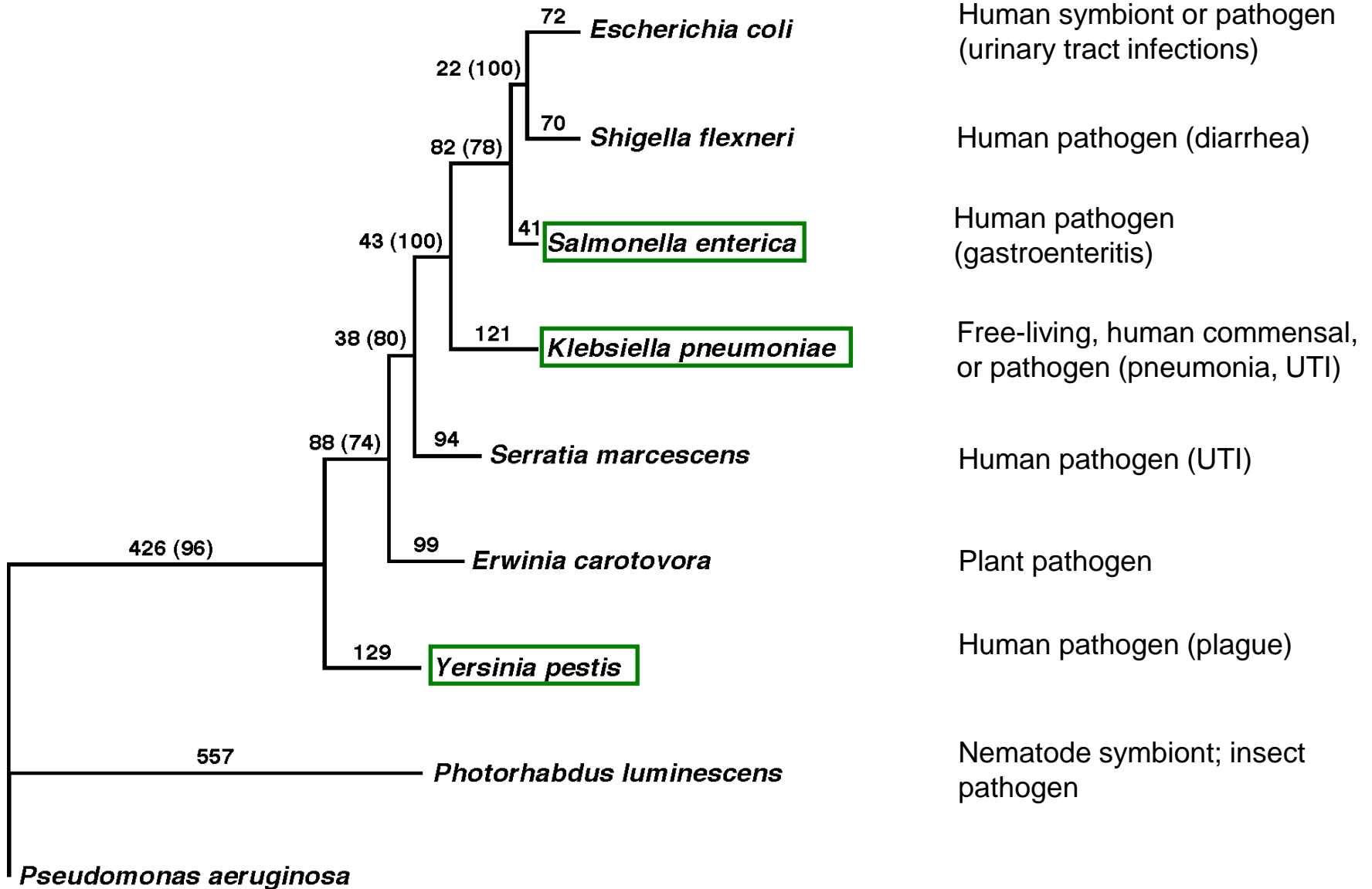
What are the functional implications of different modes of signal integration?



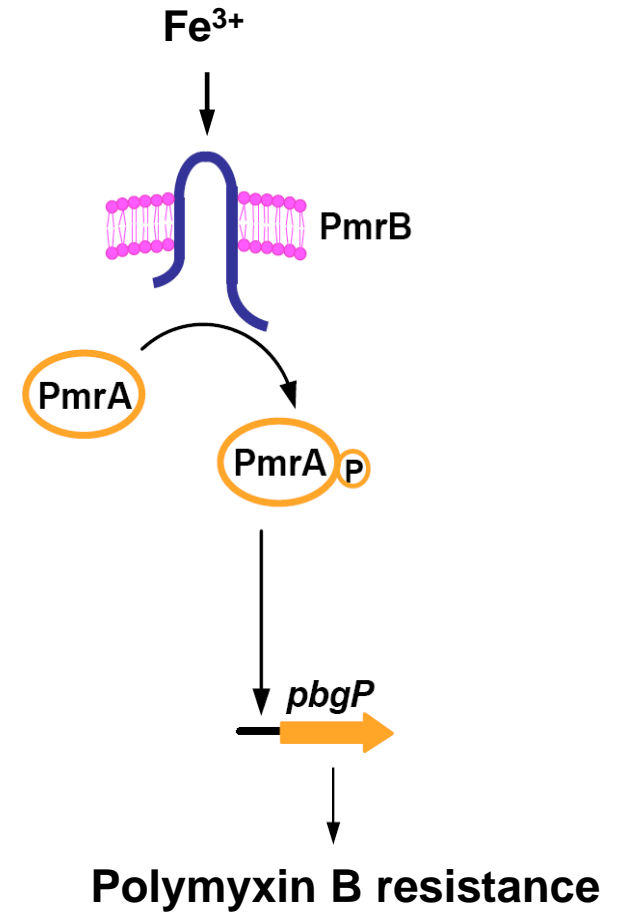
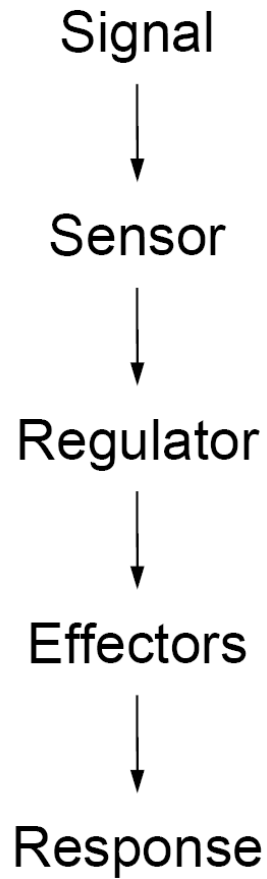
Enteric bacteria as model organisms



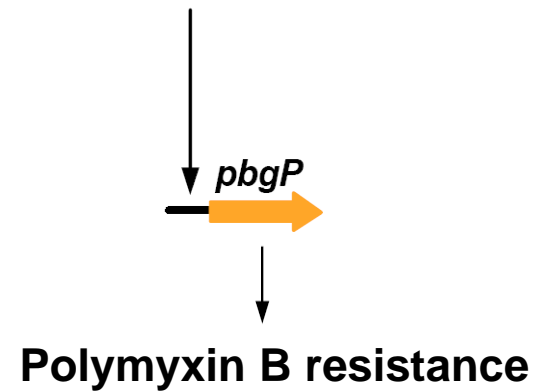
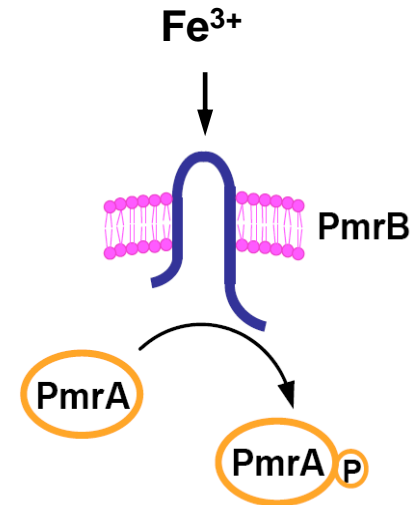
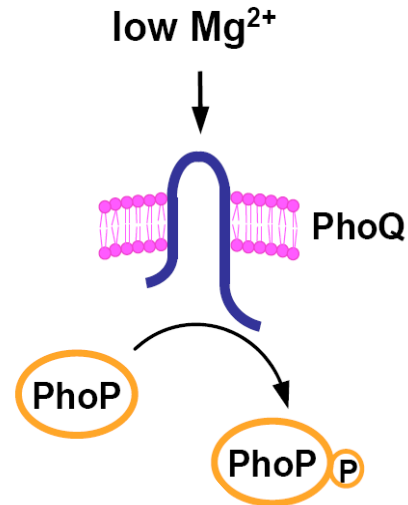
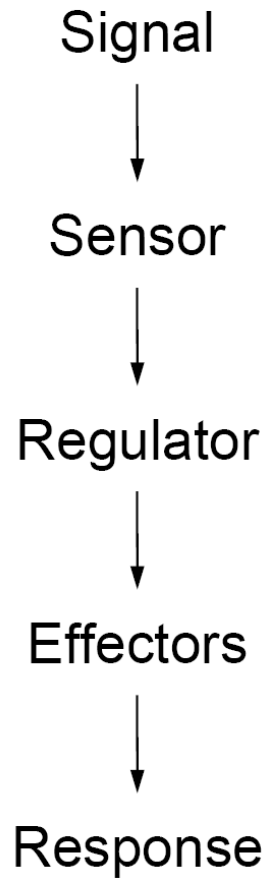
Enteric bacteria as model organisms



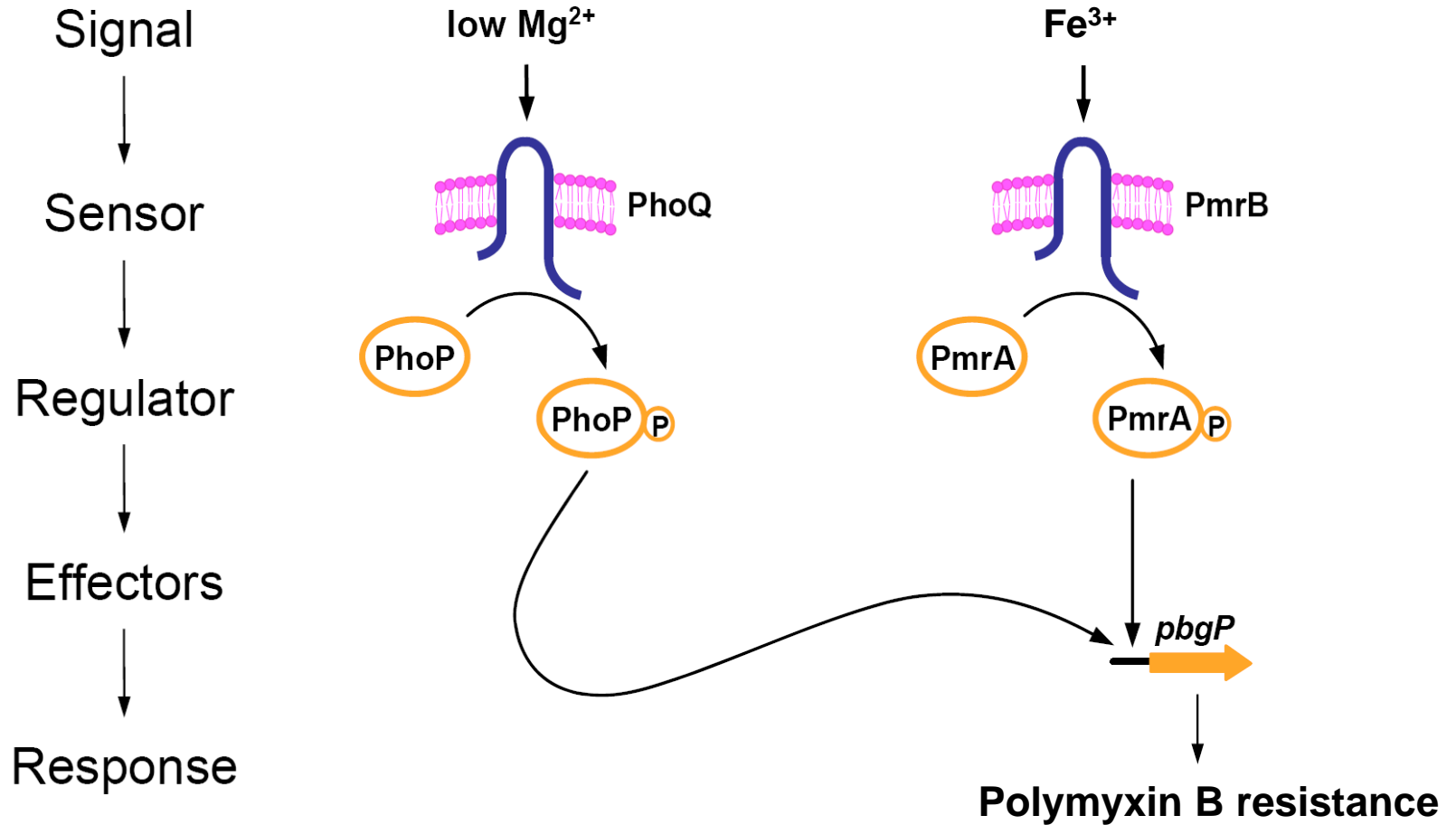
Two-component systems regulating polymyxin B resistance



Two-component systems regulating polymyxin B resistance



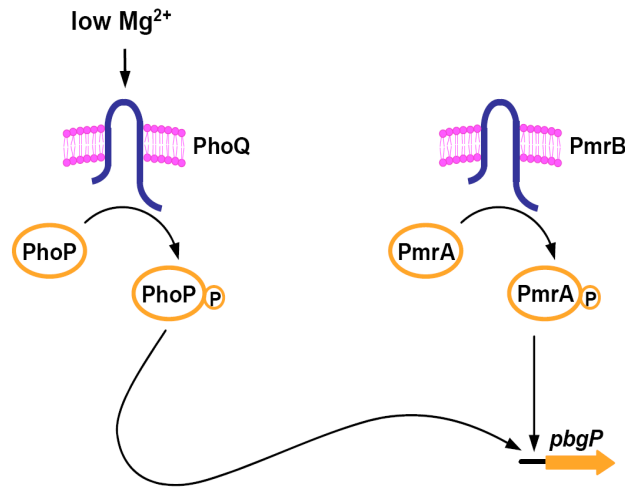
Two-component systems regulating polymyxin B resistance



Direct regulation circuit

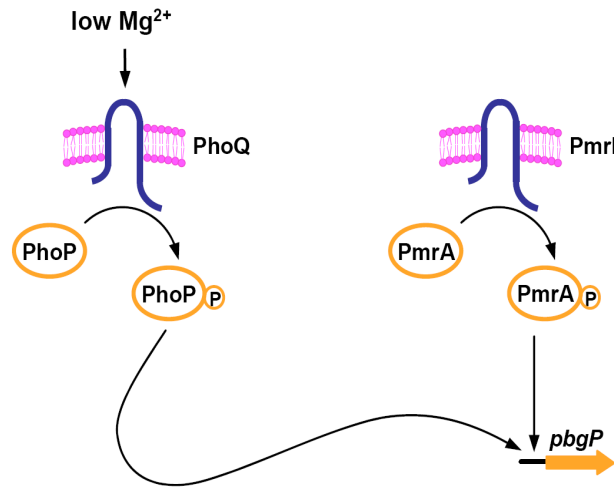
Yersinia pestis

Different species of enterics use distinct architectures to activate *pbgP* by low Mg^{2+}

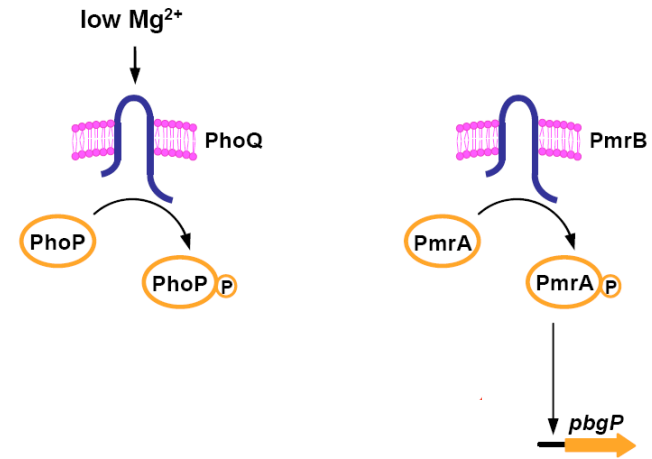


Direct regulation circuit
Yersinia pestis

Different species of enterics use distinct architectures to activate *pbgP* by low Mg^{2+}

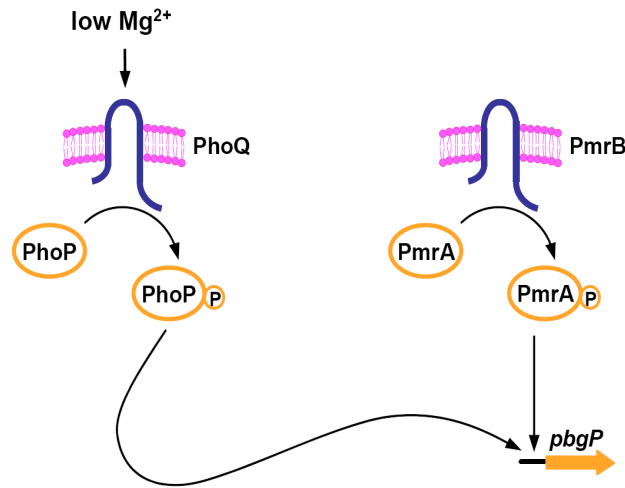


Direct regulation circuit
Yersinia pestis

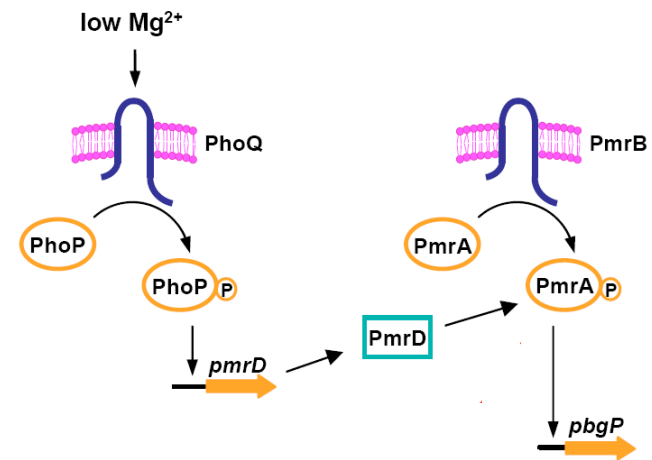


Salmonella enterica

Different species of enterics use distinct architectures to activate *pbgP* by low Mg^{2+}

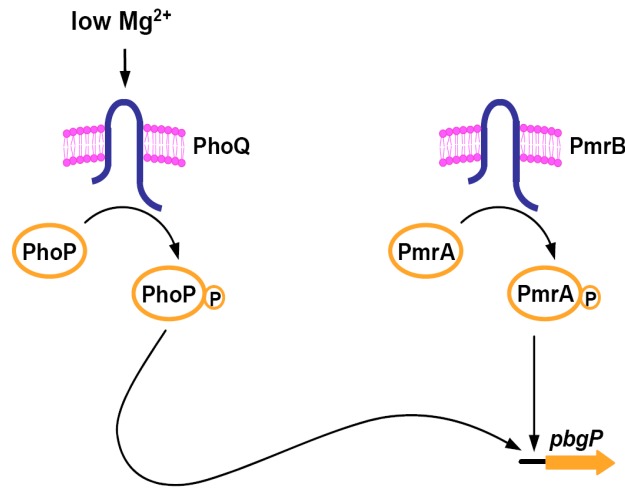


Direct regulation circuit
Yersinia pestis

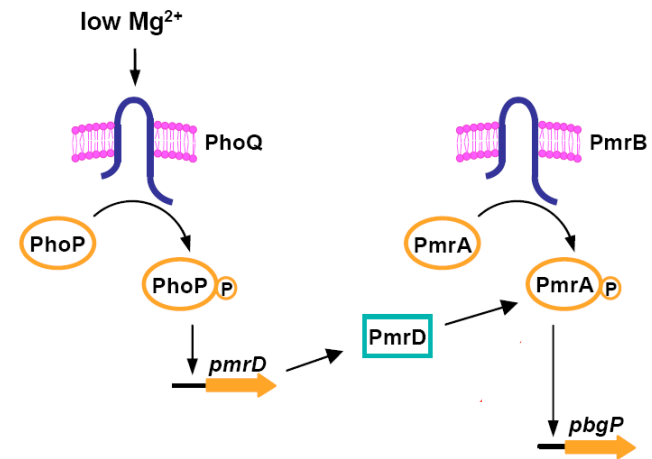


Connector-mediated pathway
Salmonella enterica

Different species of enterics use distinct architectures to activate *pbgP* by low Mg^{2+}



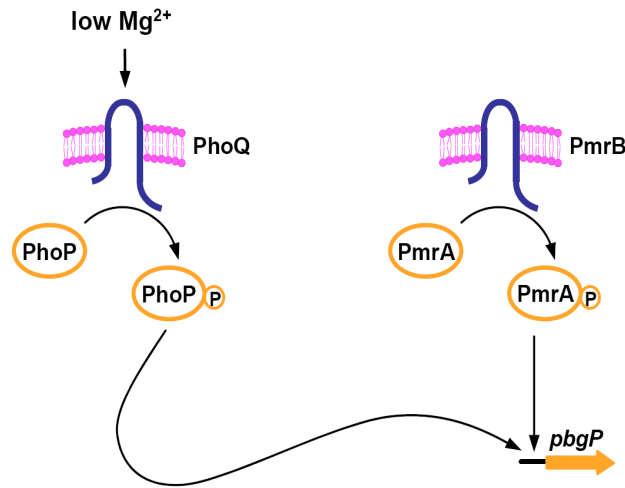
Direct regulation circuit
Yersinia pestis



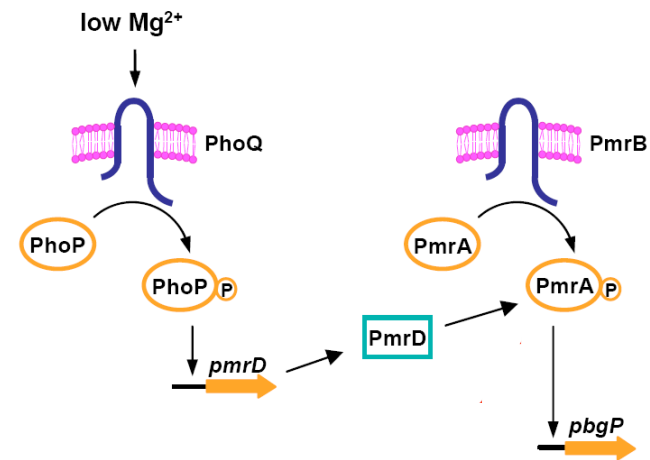
Connector-mediated pathway
Salmonella enterica

- How does the circuit architecture affect the **induction ratios**?

Different species of enterics use distinct architectures to activate *pbgP* by low Mg^{2+}



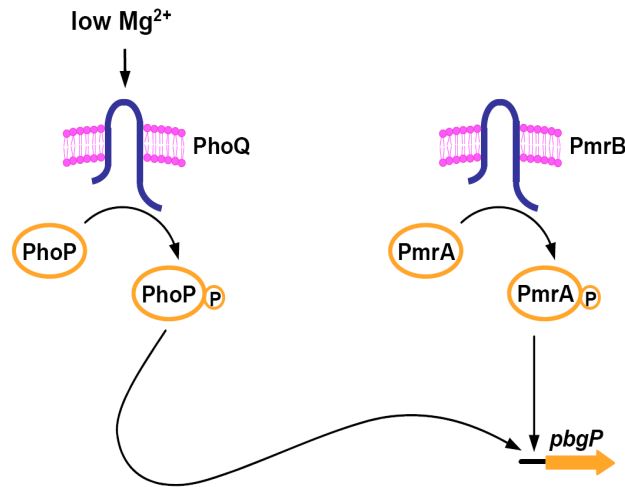
Direct regulation circuit
Yersinia pestis



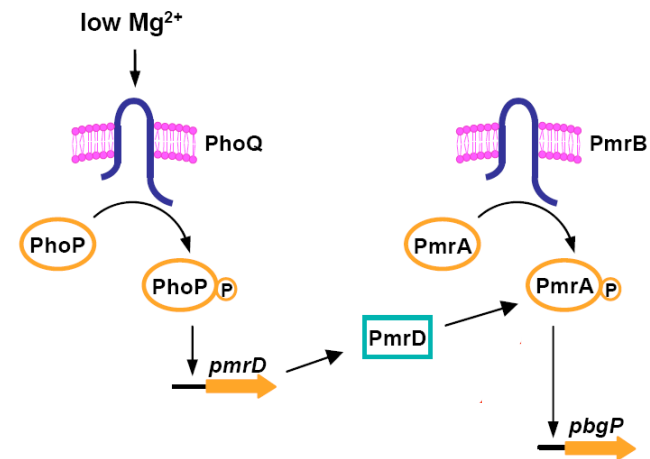
Connector-mediated pathway
Salmonella enterica

- How does the circuit architecture affect the **induction ratios**?
- What is the connection between the circuit architecture and **response timing**?

Different species of enterics use distinct architectures to activate *pbgP* by low Mg^{2+}



Direct regulation circuit
Yersinia pestis



Connector-mediated pathway
Salmonella enterica

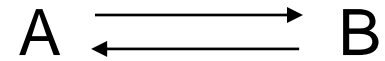
- How does the circuit architecture affect the **induction ratios**?
- What is the connection between the circuit architecture and **response timing**?
- How does the circuit architecture influence the **response levels**?

Foundation of mathematical modeling: chemical kinetics



Foundation of mathematical modeling: chemical kinetics

Chemical reaction



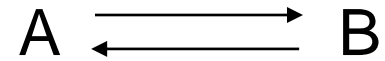
Mass action law

A is depleted with rate $k_1[A]$

B is depleted with rate $k_2[B]$

Foundation of mathematical modeling: chemical kinetics

Chemical reaction



Mass action law

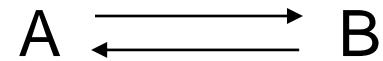
A is depleted with rate $k_1[A]$
B is depleted with rate $k_2[B]$

Mathematical formulation

$$\begin{cases} d[A]/dt = k_2[B] - k_1[A]; & [A](0) = A_0 \\ d[B]/dt = k_1[A] - k_2[B]; & [B](0) = B_0 \end{cases}$$

Foundation of mathematical modeling: chemical kinetics

Chemical reaction



Mass action law

A is depleted with rate $k_1[A]$
B is depleted with rate $k_2[B]$

Mathematical formulation

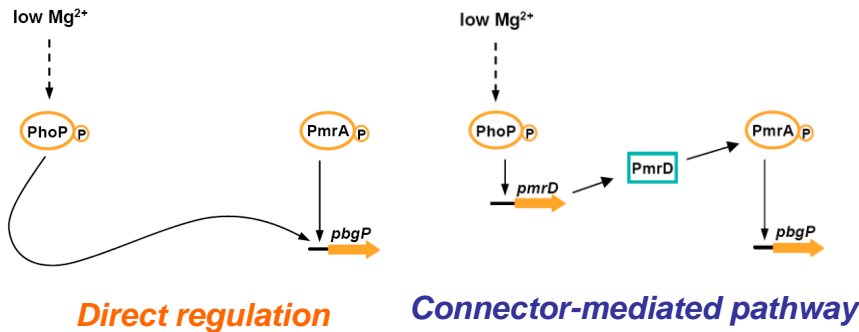
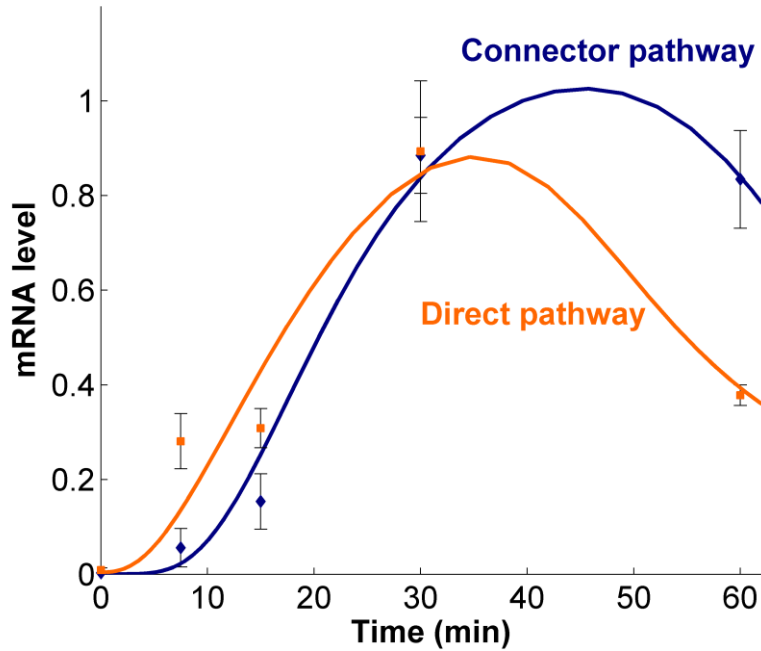
$$\begin{cases} d[A]/dt = k_2[B] - k_1[A]; & [A](0) = A_0 \\ d[B]/dt = k_1[A] - k_2[B]; & [B](0) = B_0 \end{cases}$$



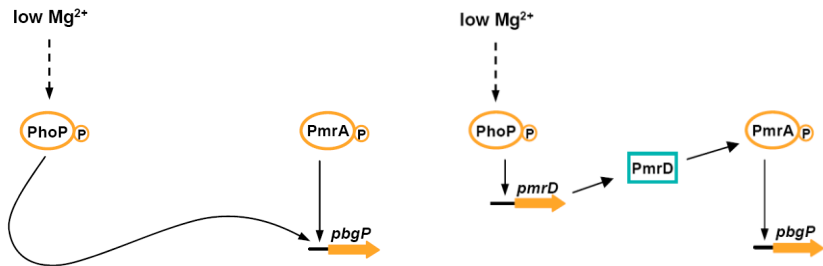
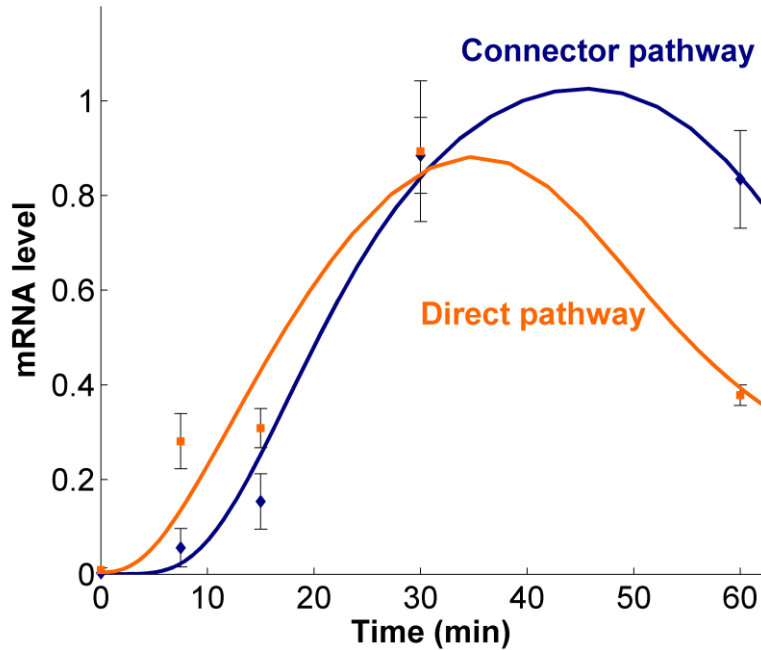
Solution

$[A]$, $[B]$ as functions of time

Pathway activation data can be used to fit and test the pathway mathematical models



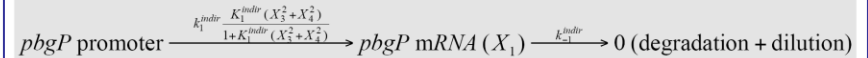
Pathway activation data can be used to fit and test the pathway mathematical models



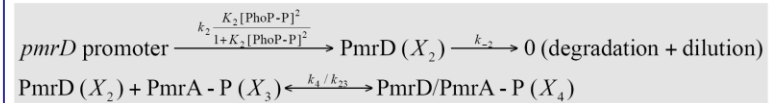
Direct regulation

Connector-mediated pathway

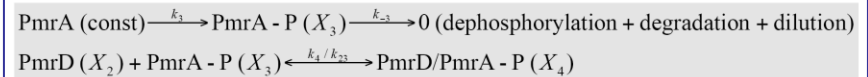
$$\frac{dX_1}{dt} = k_1^{indir} \frac{K_1^{indir} (X_3^2 + X_4^2)}{1 + K_1^{indir} (X_3^2 + X_4^2)} - k_{-1}^{indir} X_1 ; \quad [1]$$



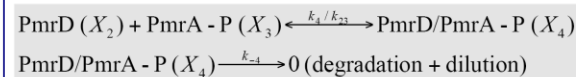
$$\frac{dX_2}{dt} = k_2 \frac{K_2 [\text{PhoP} - P]^2}{1 + K_2 [\text{PhoP} - P]^2} + k_{23} X_4 - k_{-2} X_2 - k_4 X_2 X_3 ; \quad [2]$$



$$\frac{dX_3}{dt} = k_3 + k_{23} X_4 - k_{-3} X_3 - k_4 X_2 X_3 ; \quad [3]$$

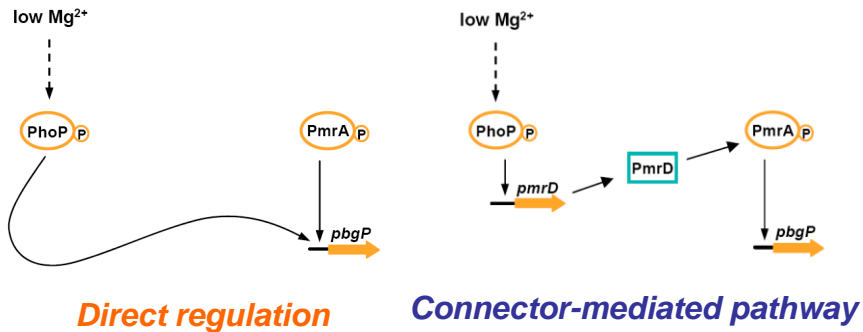


$$\frac{dX_4}{dt} = k_4 X_2 X_3 - (k_{23} + k_{-4}) X_4 . \quad [4]$$

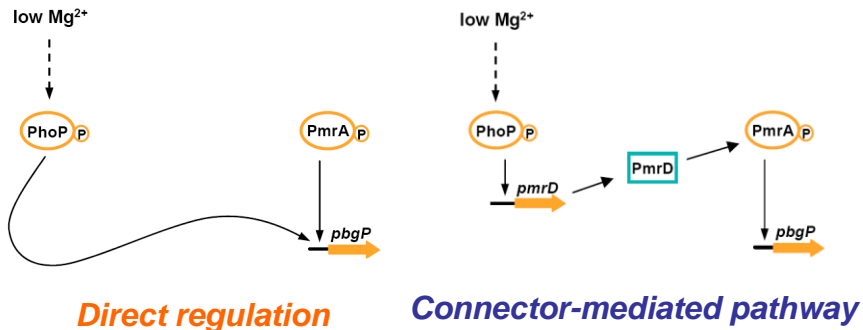
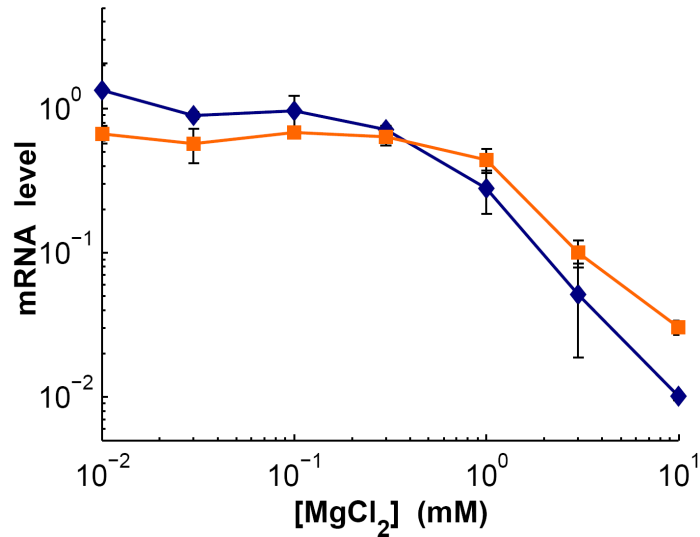


$$\frac{dX_1}{dt} = k_1^{dir} \frac{K_1^{dir} [\text{PhoP} - P]^2}{1 + K_1^{dir} [\text{PhoP} - P]^2} - k_{-1}^{dir} X_1 . \quad [6]$$

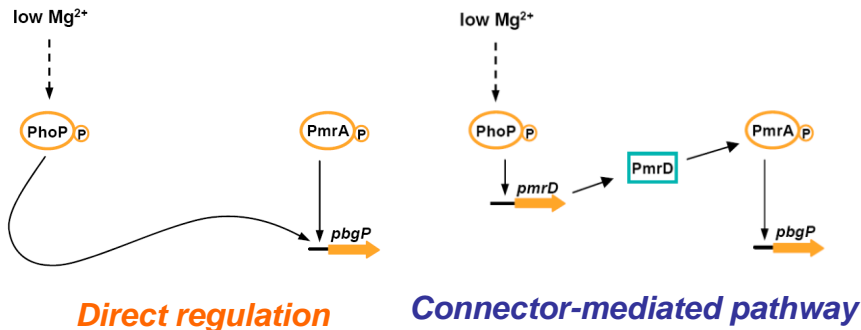
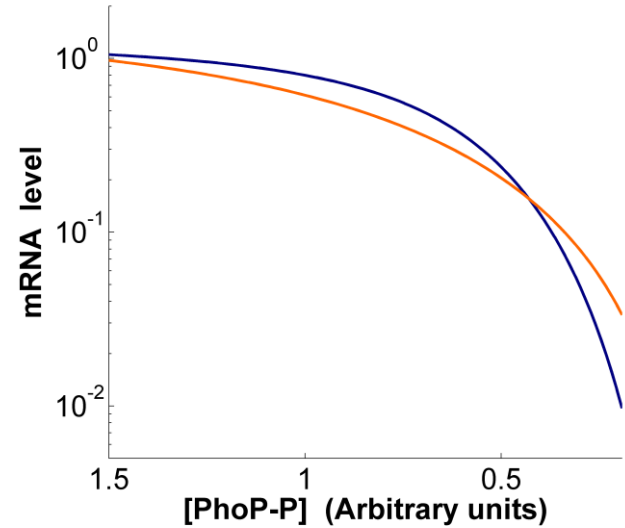
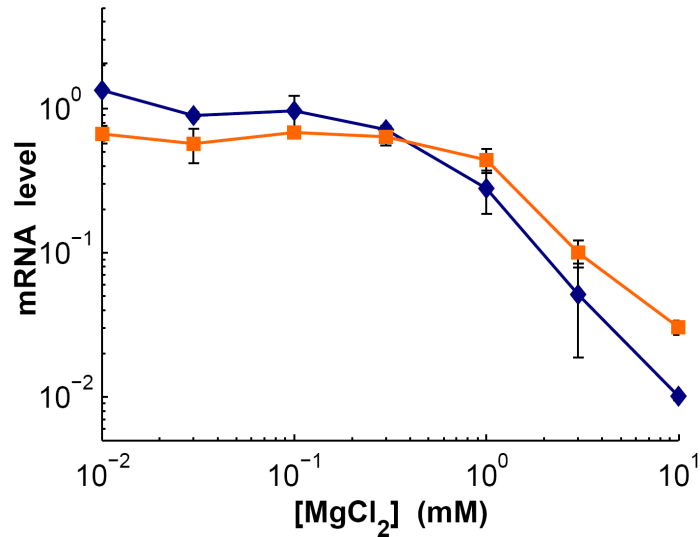
Fitted mathematical models predict steady-state output levels as functions of PhoP-P concentration



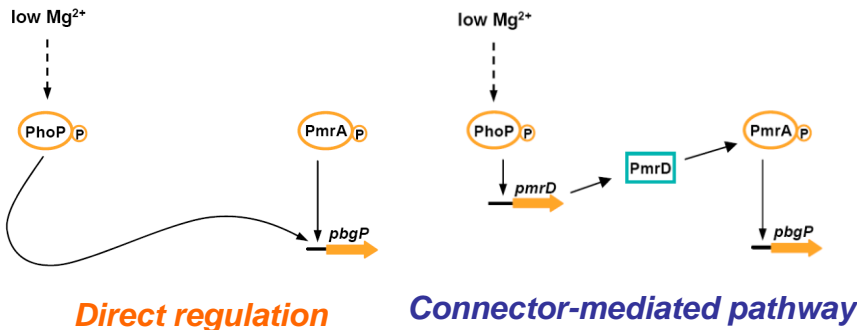
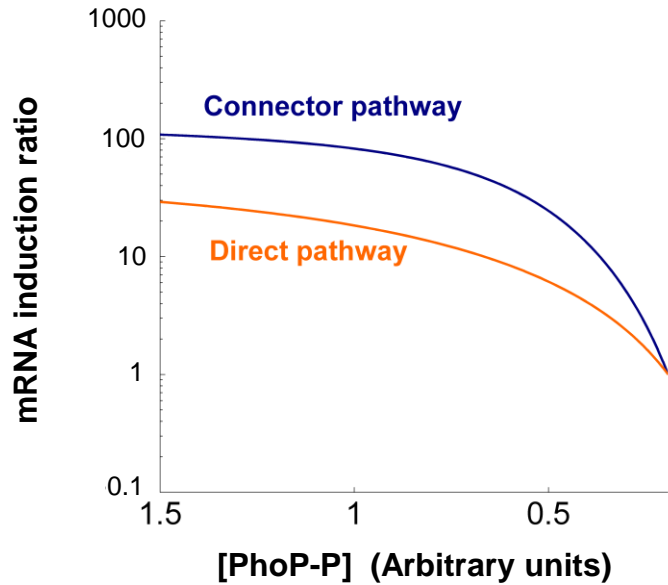
Fitted mathematical models predict steady-state output levels as functions of PhoP-P concentration



Fitted mathematical models predict steady-state output levels as functions of PhoP-P concentration



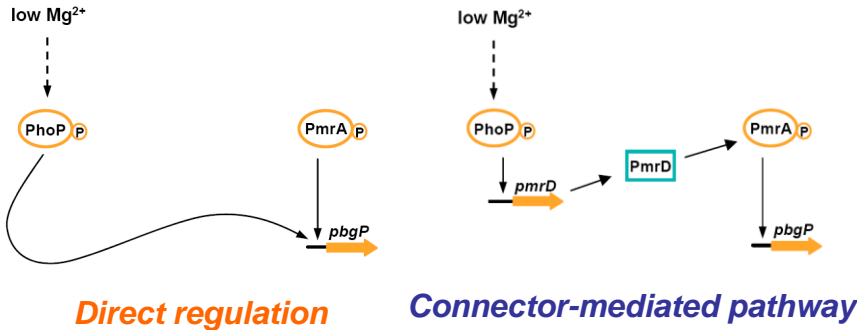
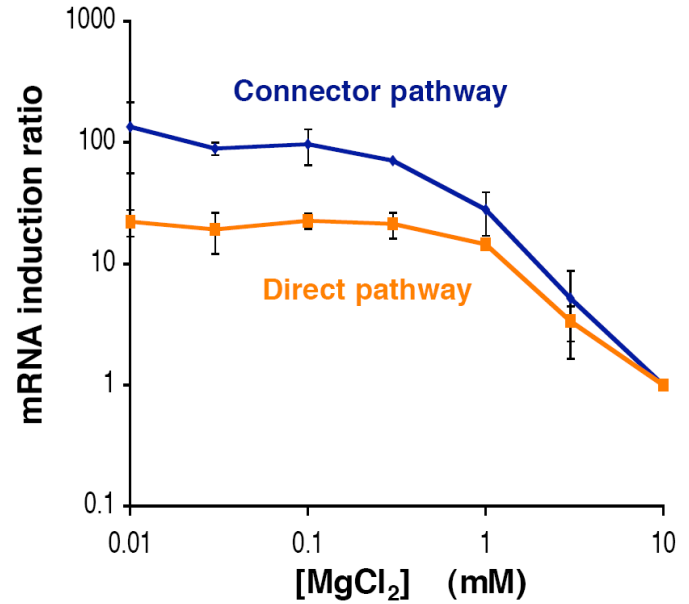
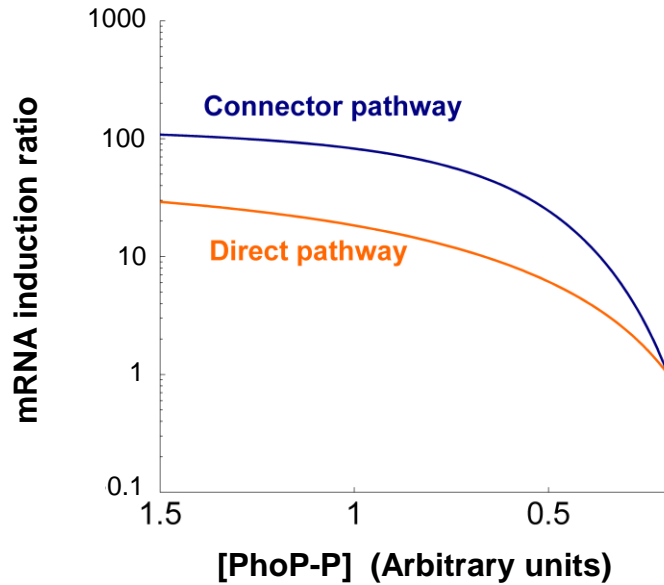
Connector-mediated pathway promotes signal amplification



Induction ratio =

$$\frac{\text{mRNA level (inducing conditions)}}{\text{mRNA level (repressing conditions)}}$$

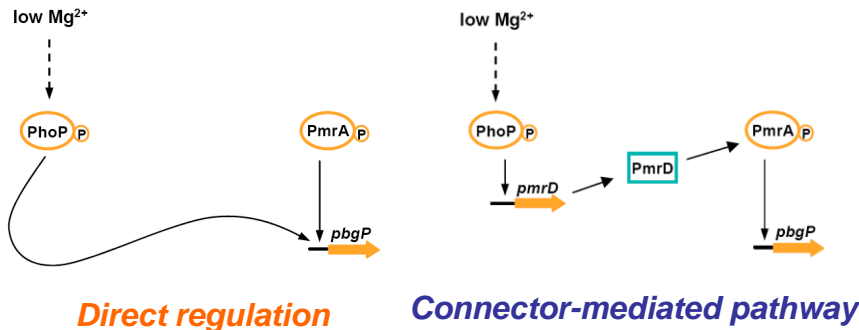
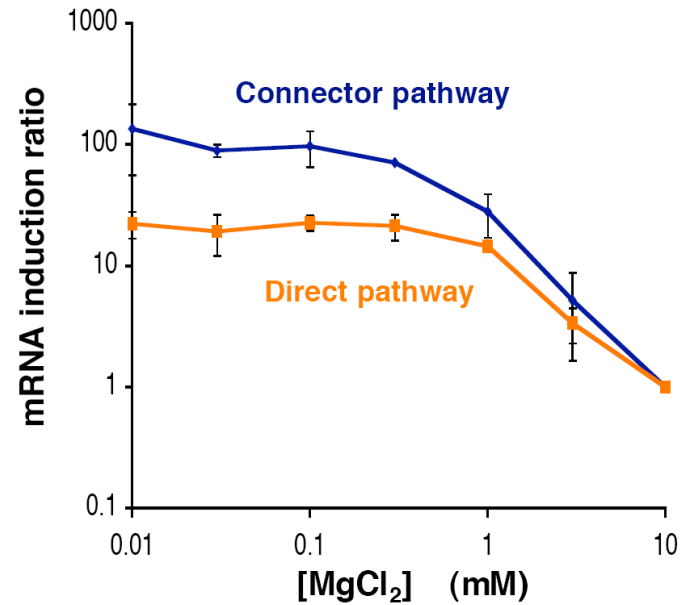
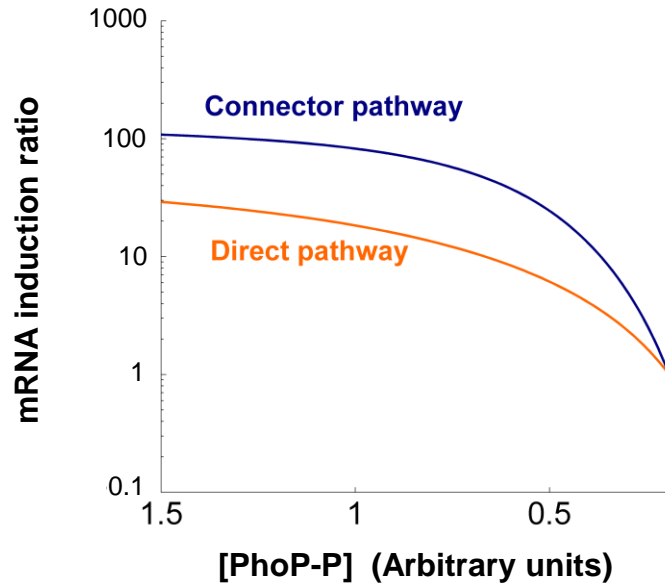
Connector-mediated pathway promotes signal amplification



Induction ratio =

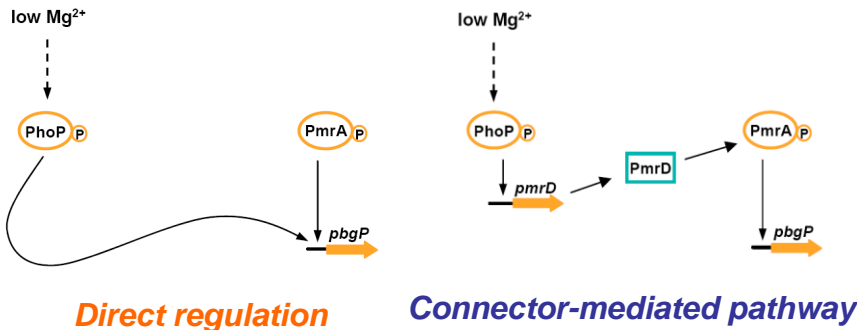
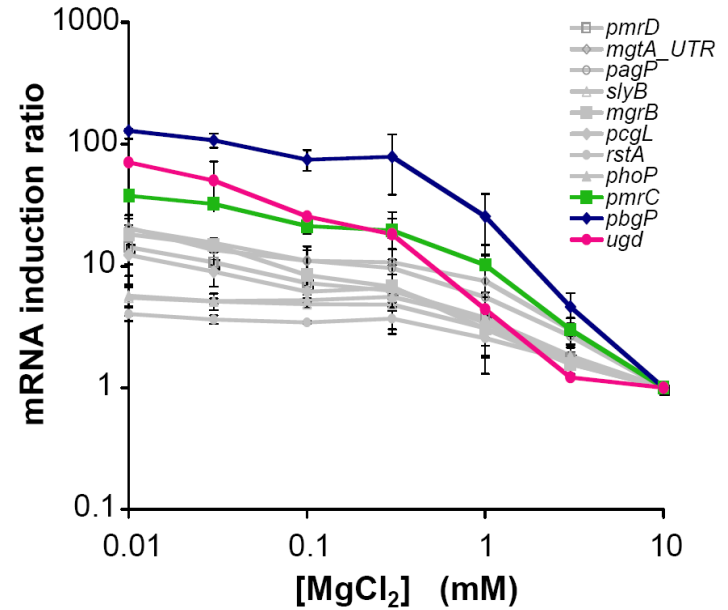
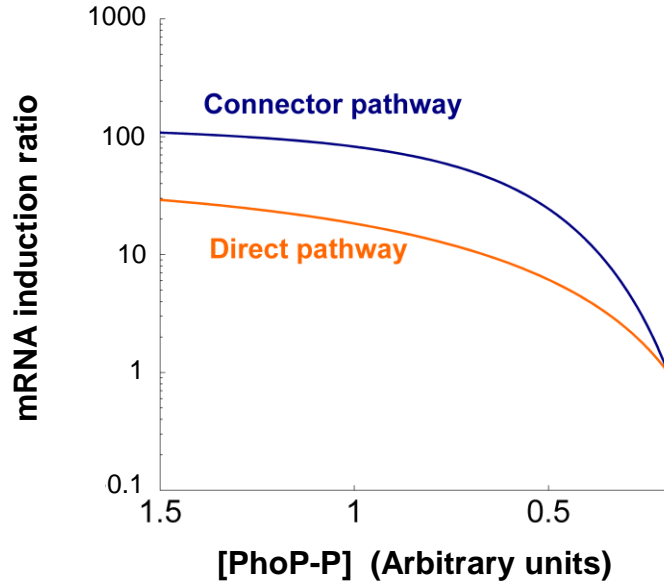
$$\frac{\text{mRNA level (inducing conditions)}}{\text{mRNA level (repressing conditions)}}$$

Connector-mediated pathway promotes signal amplification



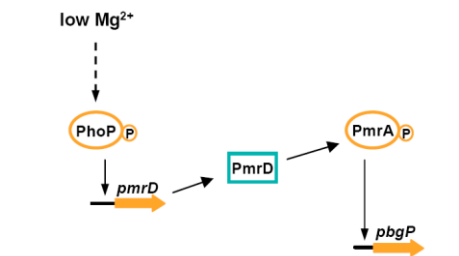
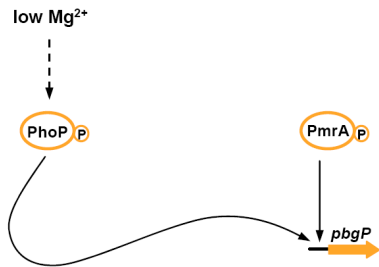
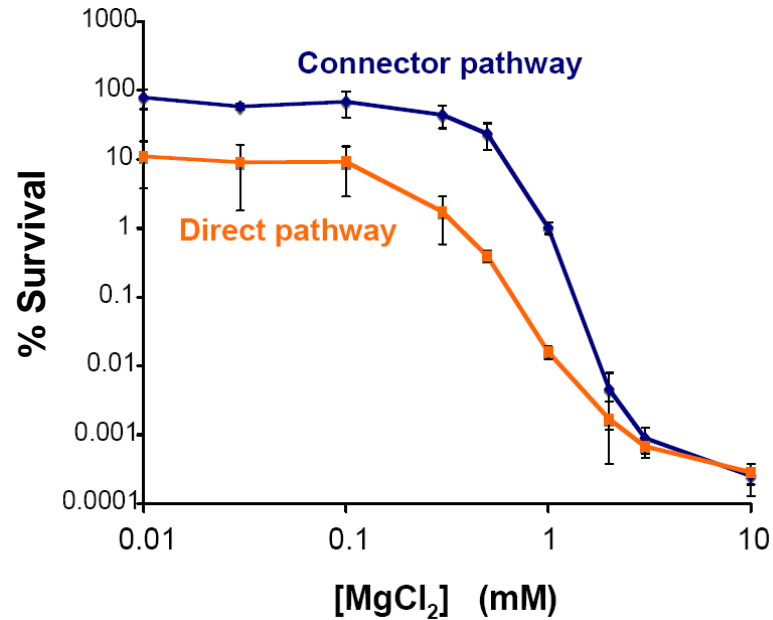
Mathematical result: signal amplification occurs in the *connector-mediated pathway* for sufficiently high signal levels

Connector-mediated pathway promotes signal amplification



Mathematical result: signal amplification occurs in the *connector-mediated pathway* for sufficiently high signal levels

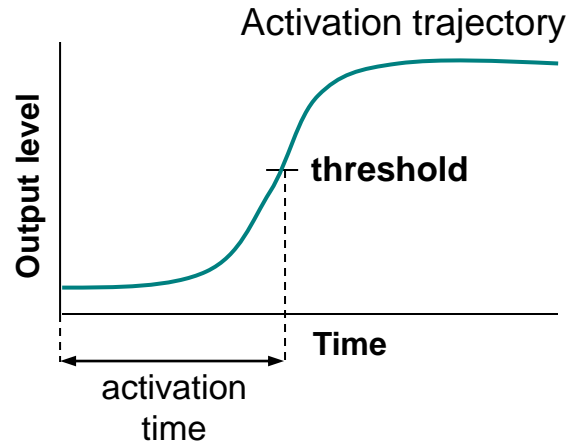
Connector-mediated pathway promotes heightened polymyxin B resistance



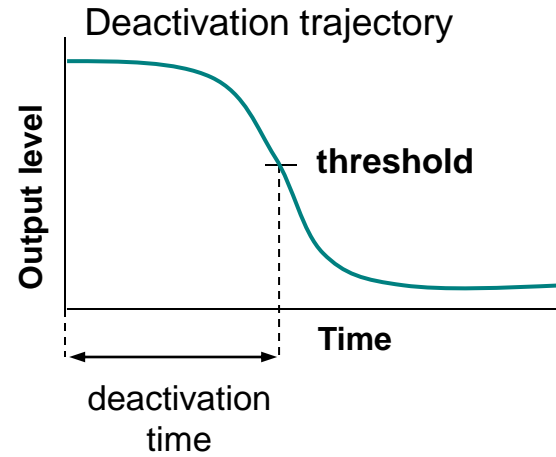
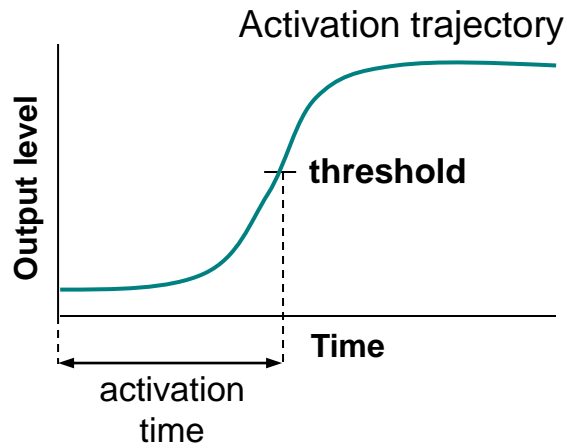
Direct regulation

Connector-mediated pathway

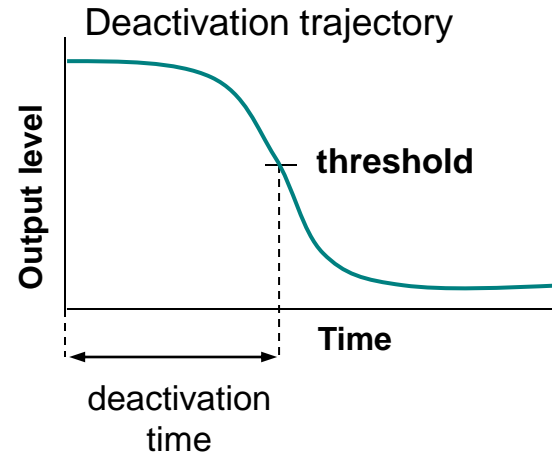
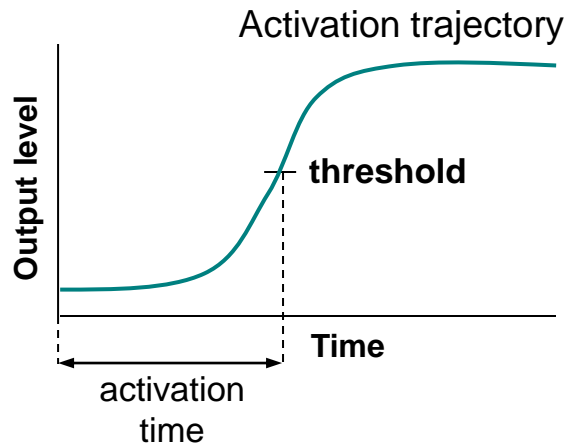
Analysis of response timing



Analysis of response timing

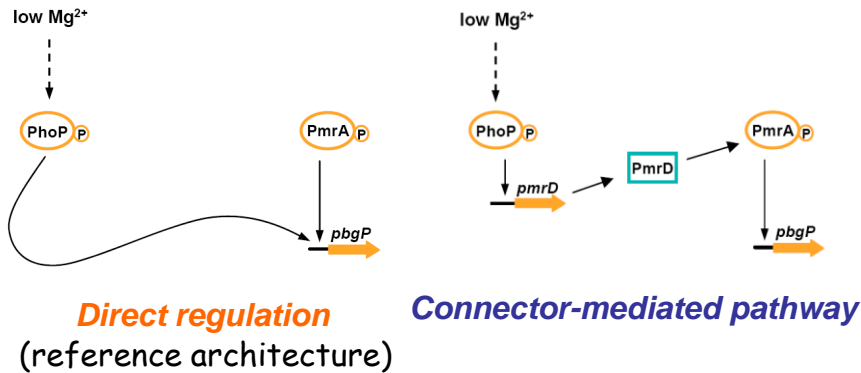
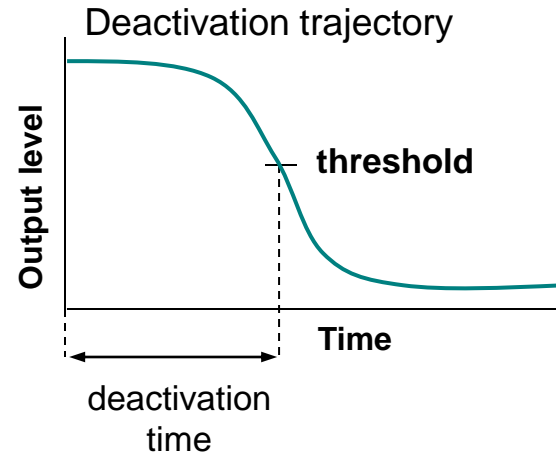
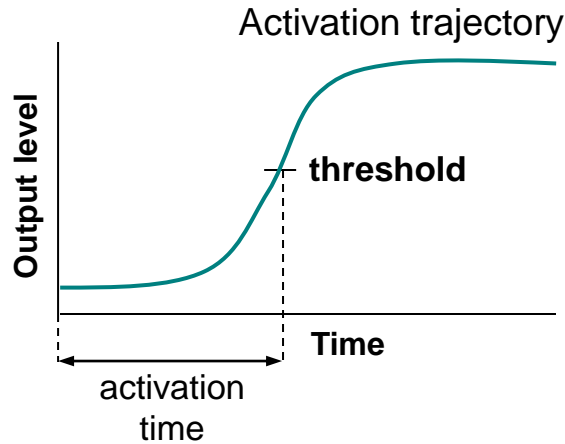


Analysis of response timing



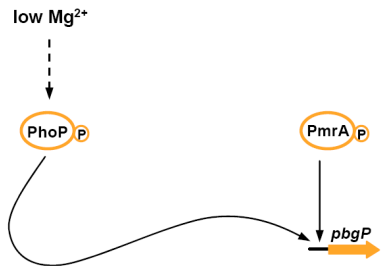
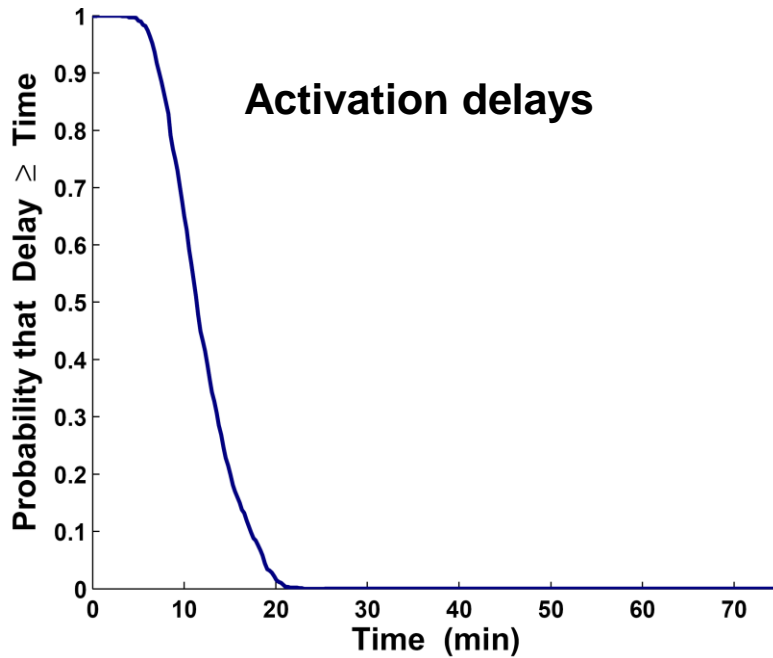
Activation (deactivation) delay: the difference in activation (deactivation) times between the **architecture of interest** and a **reference architecture**

Analysis of response timing

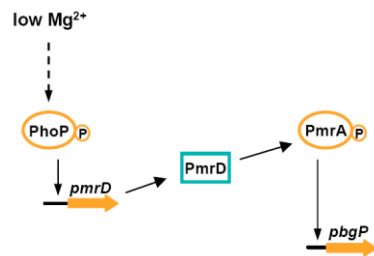


Activation (deactivation) delay: the difference in activation (deactivation) times between the **architecture of interest** and a **reference architecture**

Connector-mediated pathway exhibits expression delays

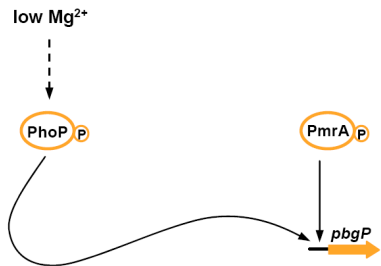
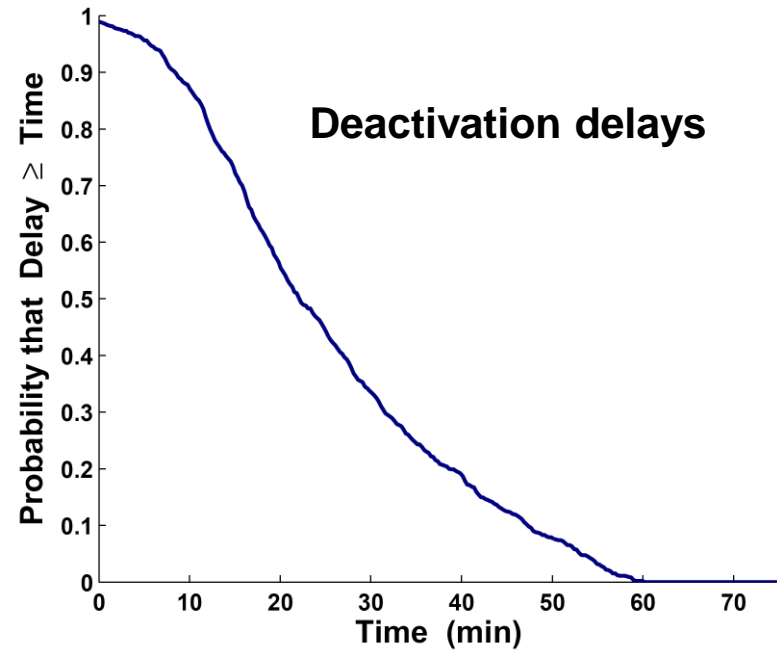
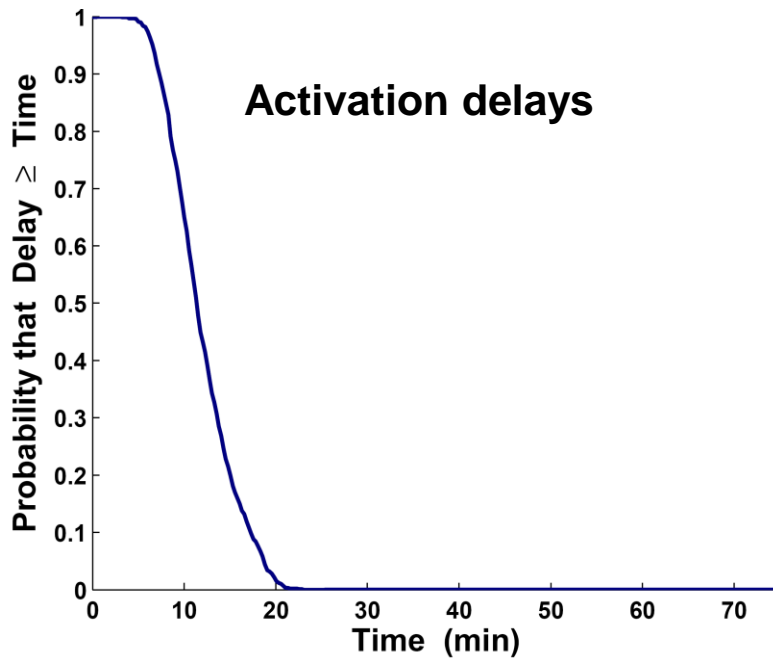


Direct regulation
(reference architecture)

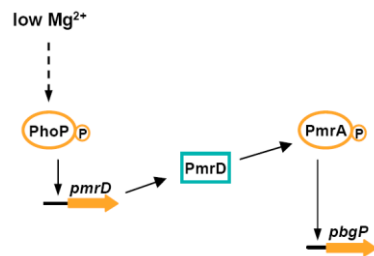


Connector-mediated pathway

Connector-mediated pathway exhibits expression delays

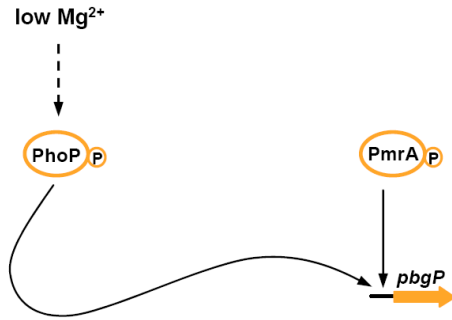


Direct regulation
(reference architecture)



Connector-mediated pathway

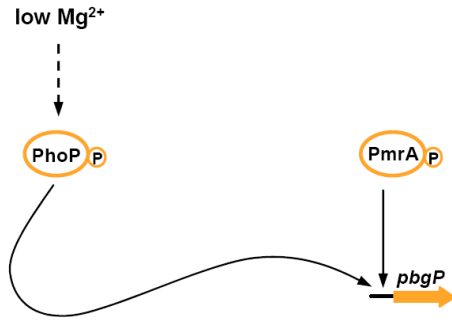
Feedforward connector loop is an intermediate stage between direct and connector-mediated regulation



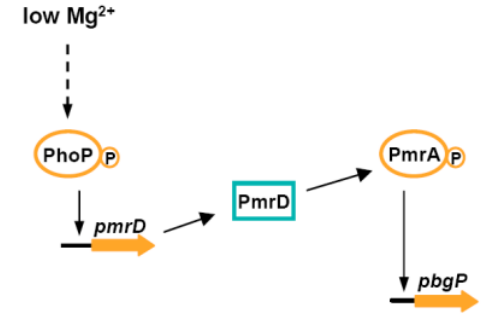
Direct pathway

Yersinia pestis

Feedforward connector loop is an intermediate stage between direct and connector-mediated regulation

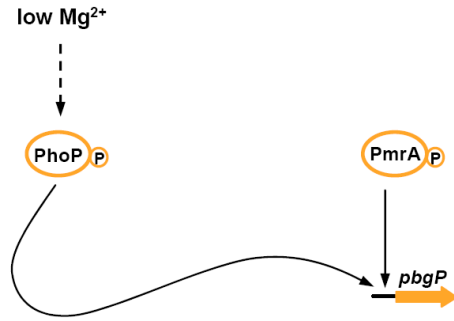


Direct pathway
Yersinia pestis

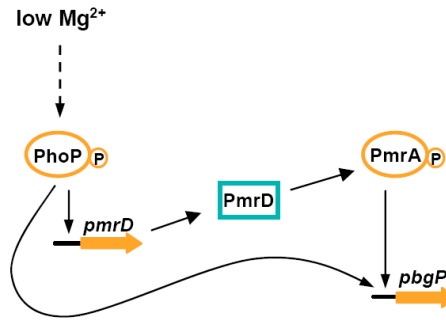


Connector-mediated pathway
Salmonella enterica

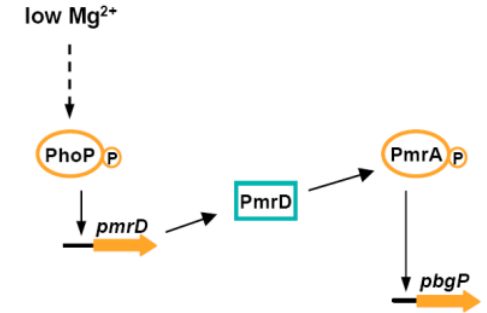
Feedforward connector loop is an intermediate stage between direct and connector-mediated regulation



Direct pathway
Yersinia pestis

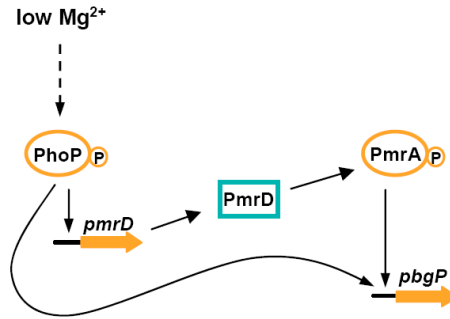


Feedforward connector loop (FCL)
Klebsiella pneumoniae

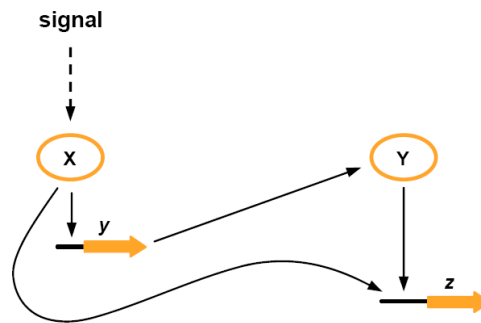


Connector-mediated pathway
Salmonella enterica

Feedforward connector loop resembles the ubiquitous feedforward loop

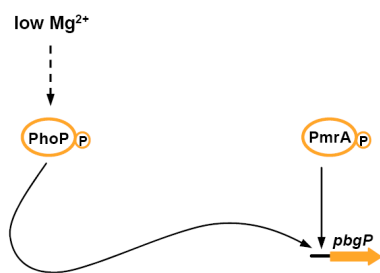
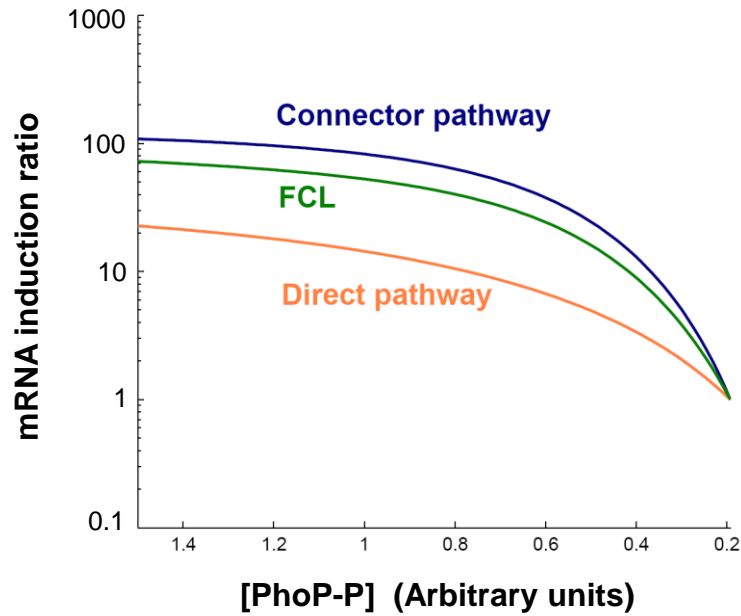


Feedforward connector loop (FCL)
Klebsiella pneumoniae

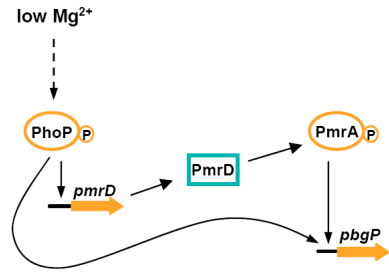


Feedforward loop (FFL)

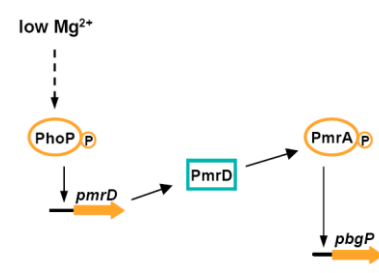
Feedforward connector loop promotes signal amplification



Direct regulation

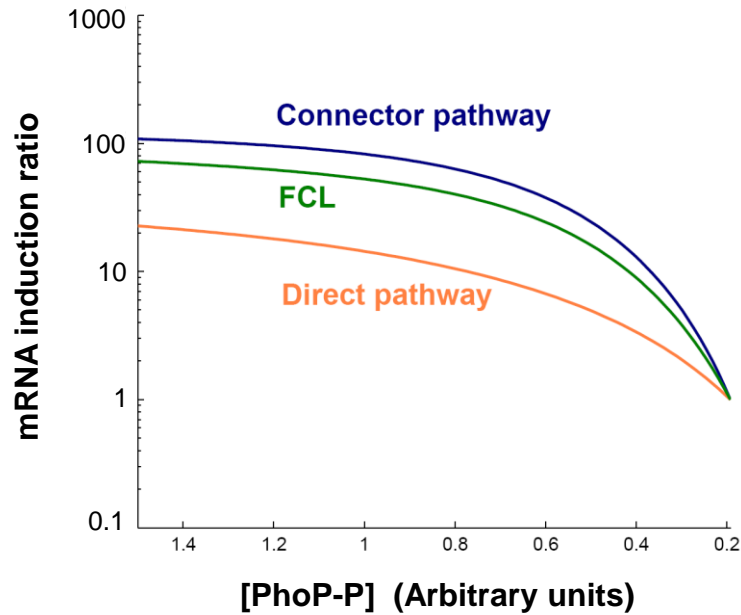


Feedforward connector loop (FCL)



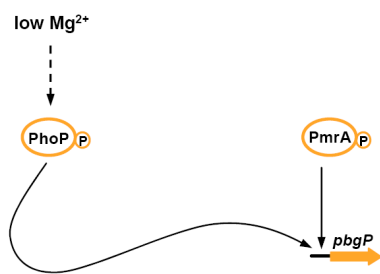
Connector-mediated pathway

Feedforward connector loop promotes signal amplification

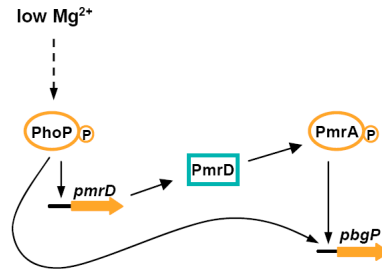


Mathematical results:

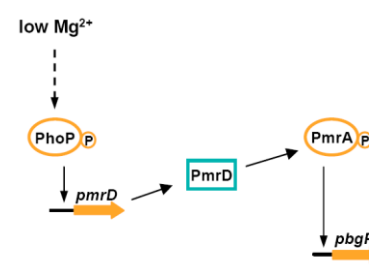
- (a) Signal amplification occurs for the **FCL** for sufficiently high signal levels
- (b) Signal amplification for the **FCL** is less pronounced than for the **connector-mediated pathway**



Direct regulation

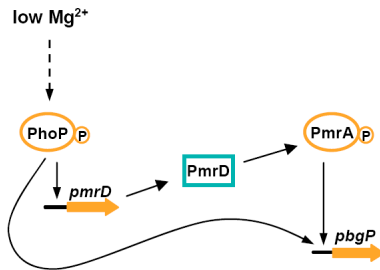
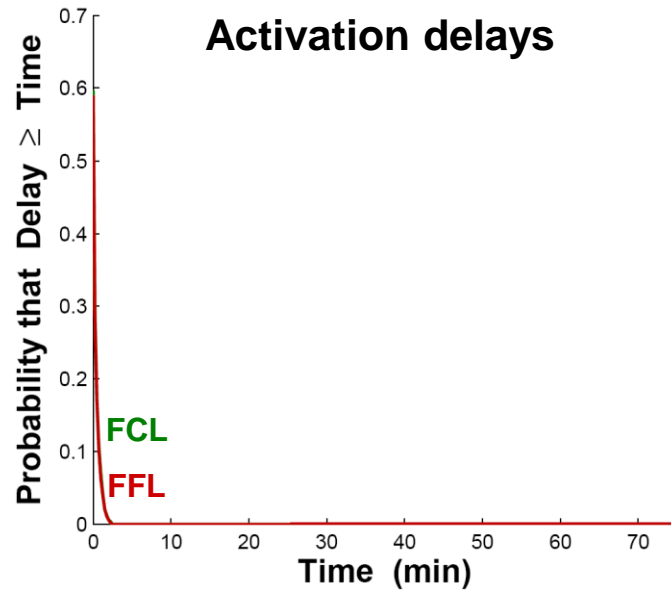


Feedforward connector loop (FCL)

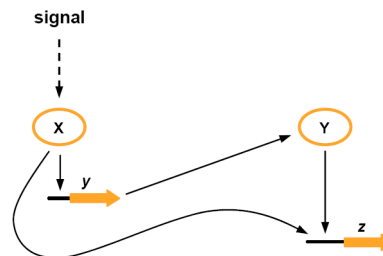


Connector-mediated pathway

FCL and FFL demonstrate fast activation

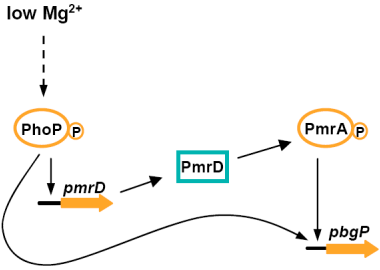
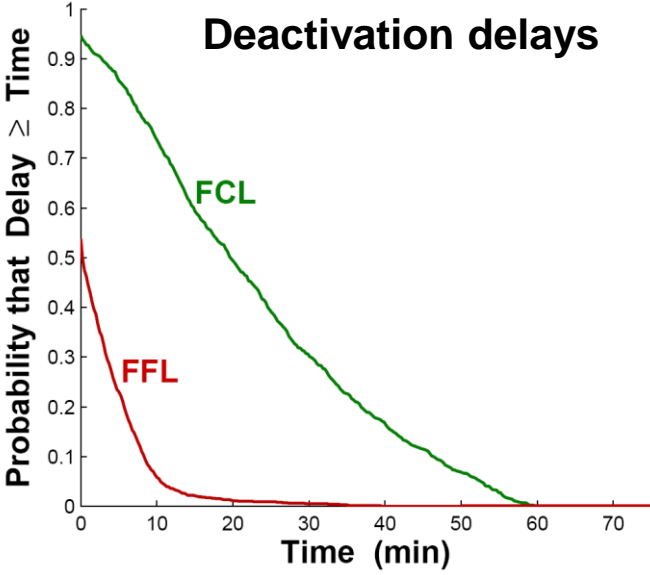
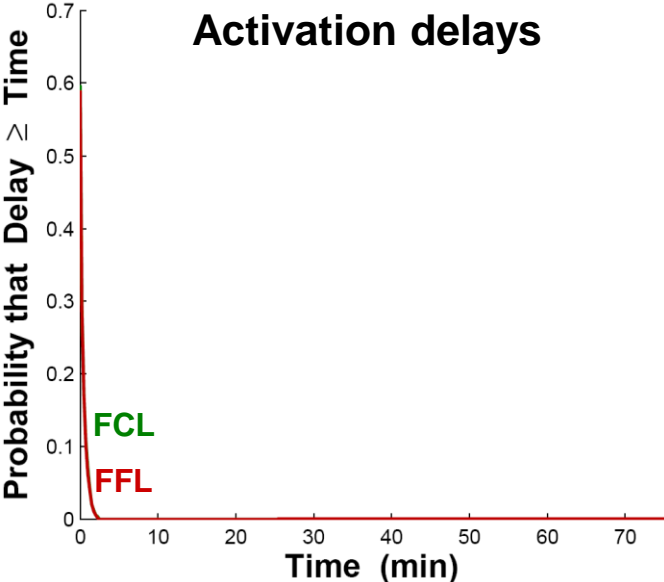


Feedforward connector loop (FCL)

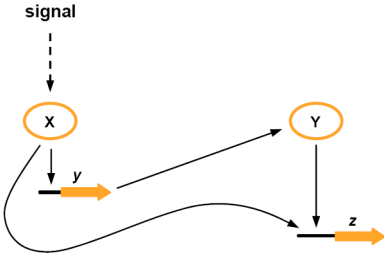


Feedforward loop (FFL)

FCL exhibits larger deactivation delays than FFL

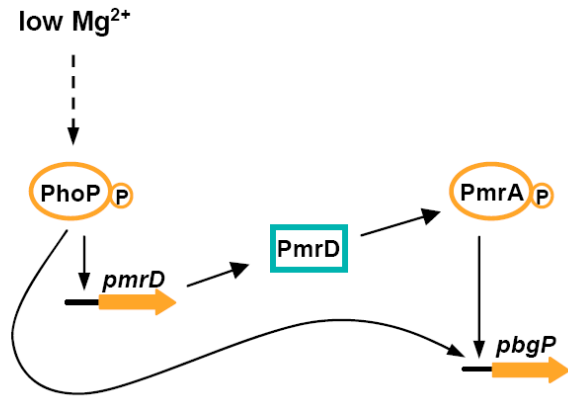


Feedforward connector loop (FCL)

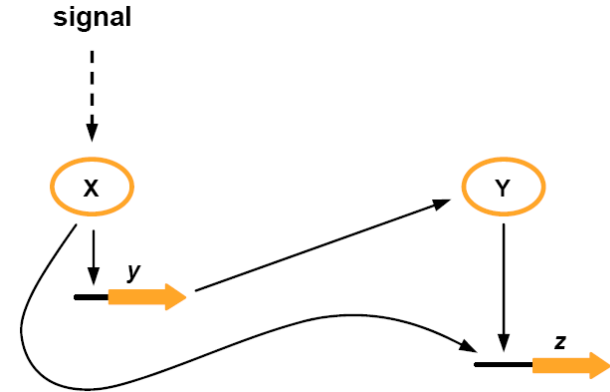


Feedforward loop (FFL)

What is the role of the direct branch of regulation in FCL and FFL?

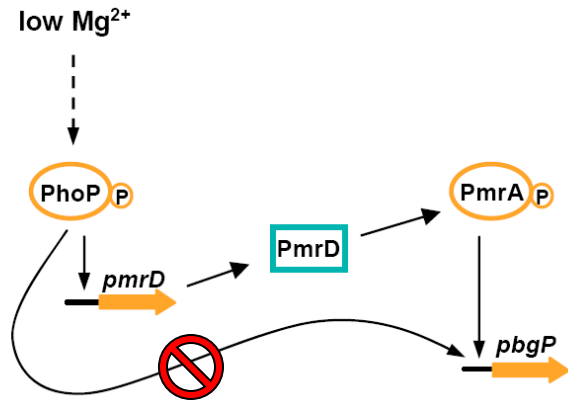


Feedforward connector loop (FCL)

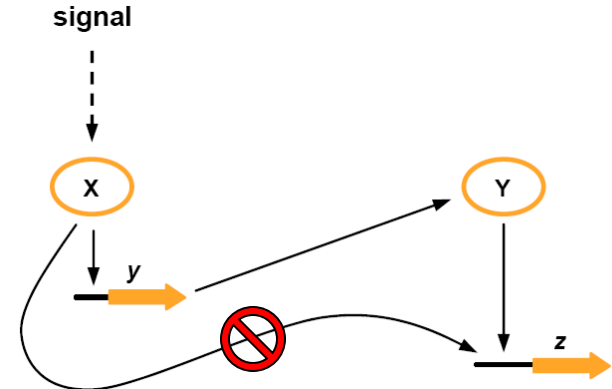


Feedforward loop (FFL)

What is the role of the direct branch of regulation in FCL and FFL?

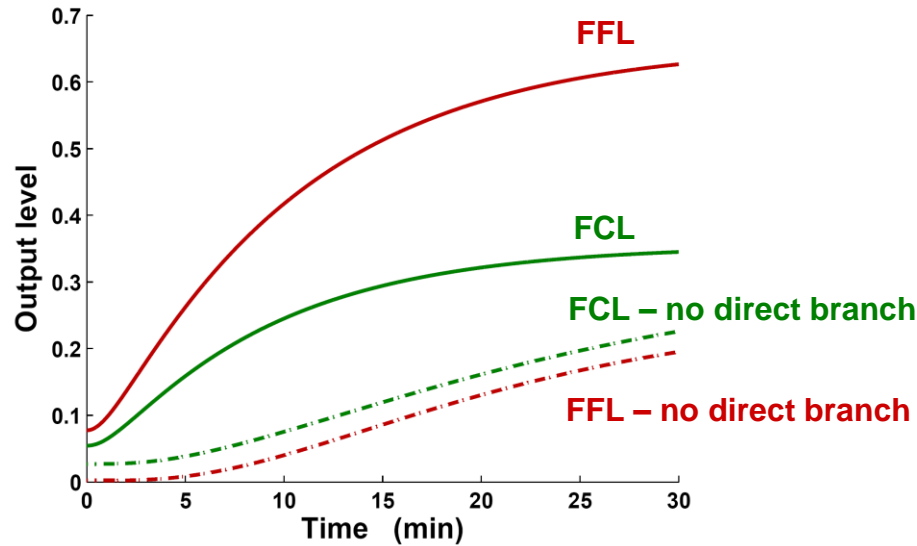


Feedforward connector loop (FCL)

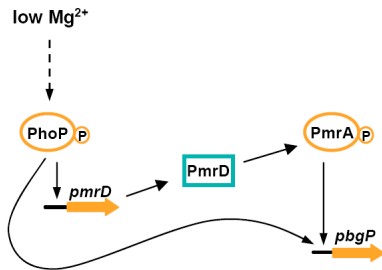


Feedforward loop (FFL)

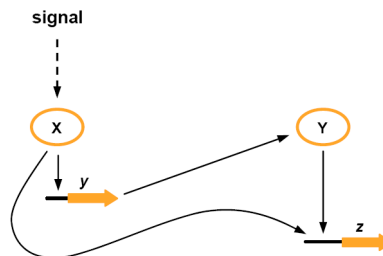
FCL and FFL display higher output levels than their cascade counterparts



Mathematical result:
having two regulation branches leads to higher output levels

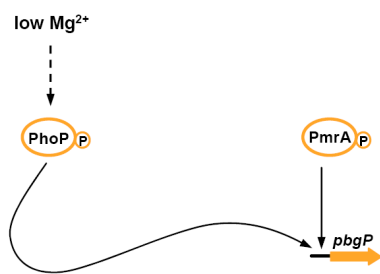
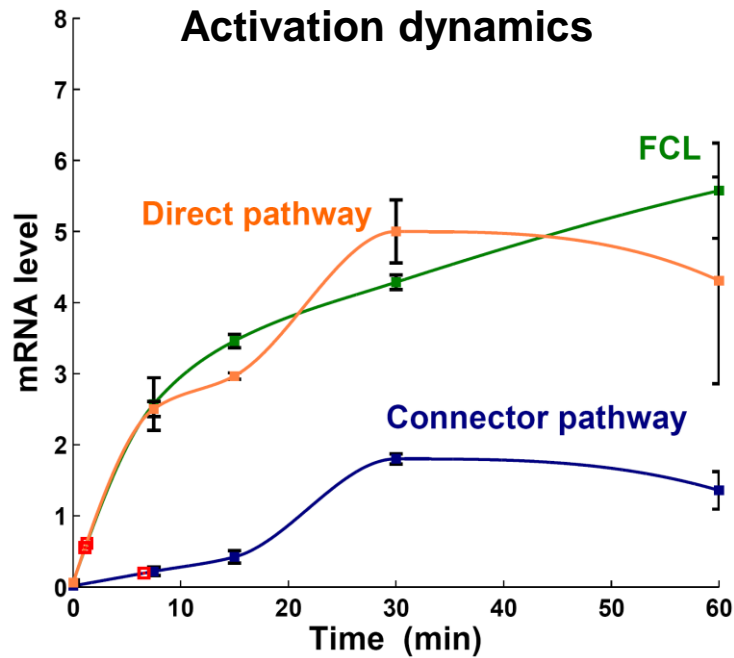


Feedforward connector loop (FCL)

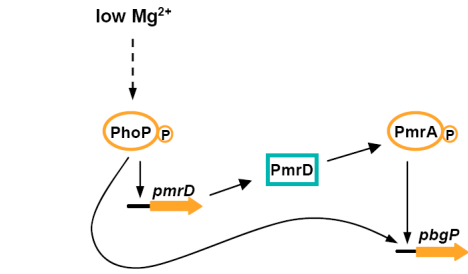


Feedforward loop (FFL)

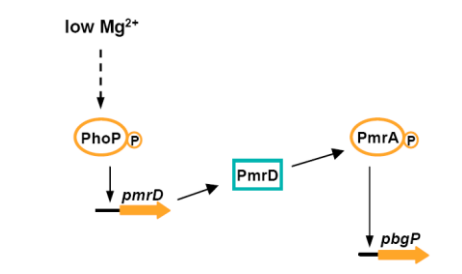
In vivo dynamics of regulatory architectures



Direct regulation

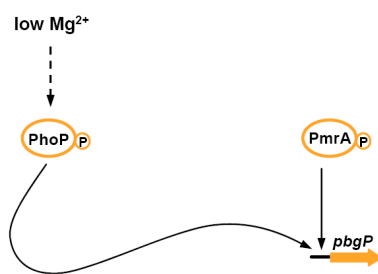
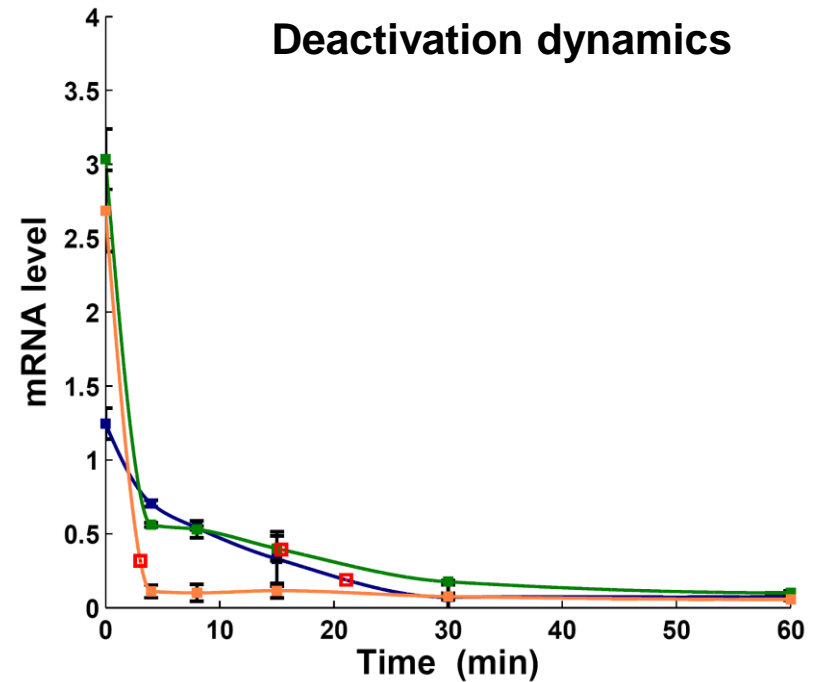
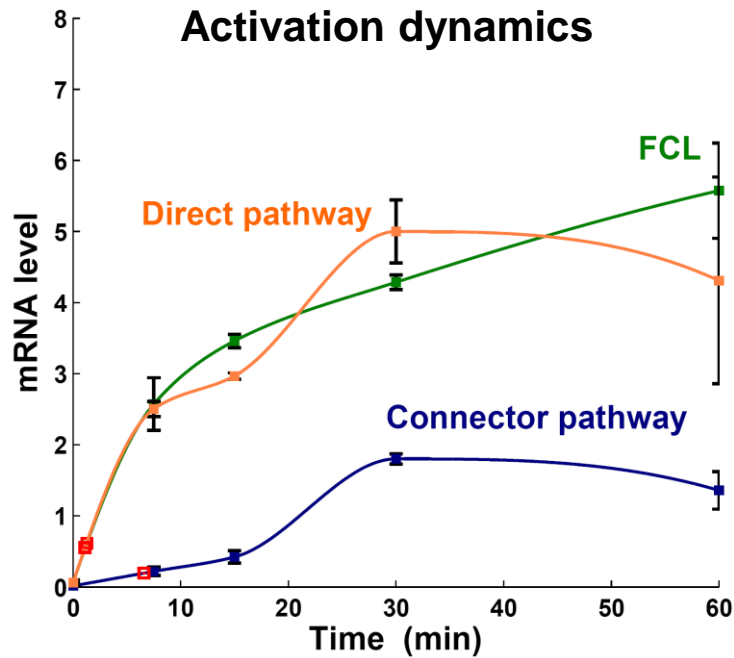


Feedforward connector loop (FCL)

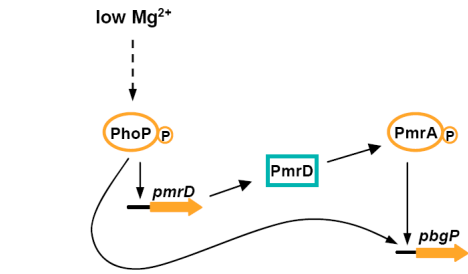


Connector-mediated pathway

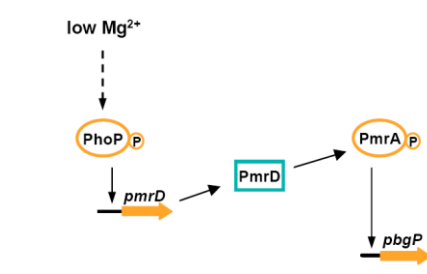
In vivo dynamics of regulatory architectures



Direct regulation



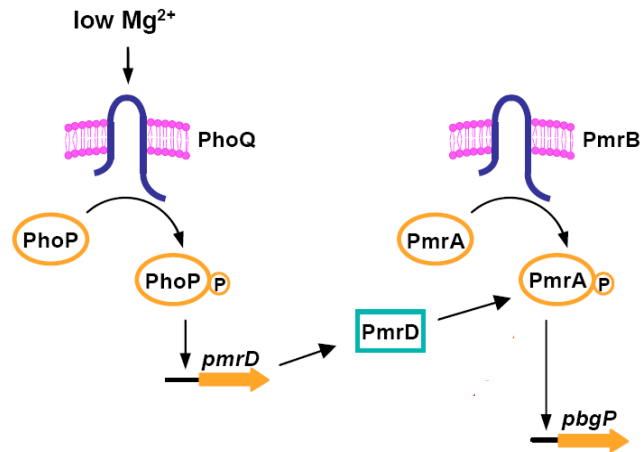
Feedforward connector loop (FCL)



Connector-mediated pathway

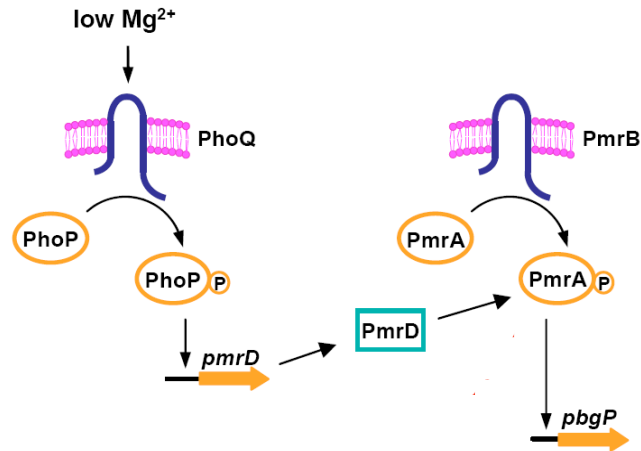
Connector-mediated regulation is an emerging paradigm in bacterial gene expression control

Salmonella enterica

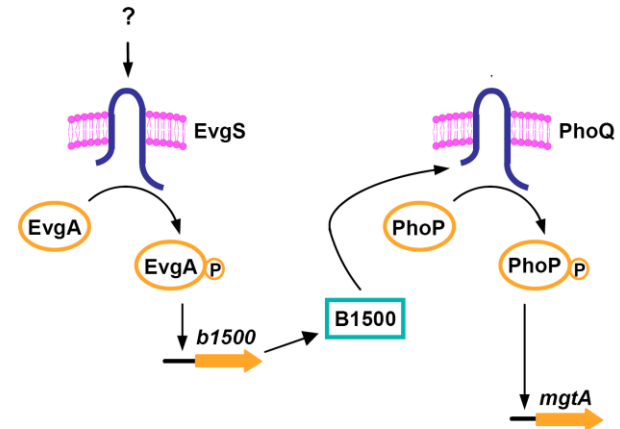


Connector-mediated regulation is an emerging paradigm in bacterial gene expression control

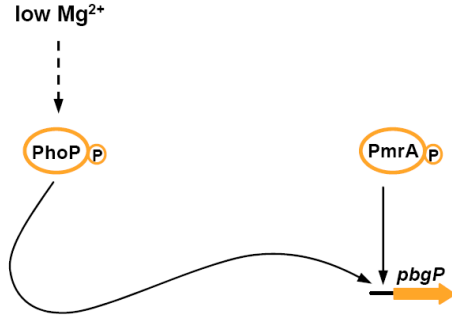
Salmonella enterica



Escherichia coli

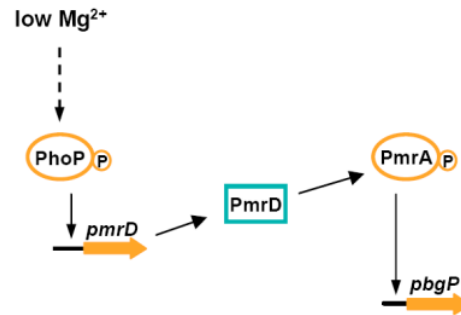


Conclusions



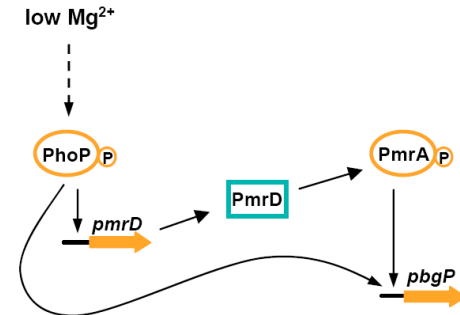
Direct pathway

Yersinia pestis



Connector-mediated pathway

Salmonella enterica

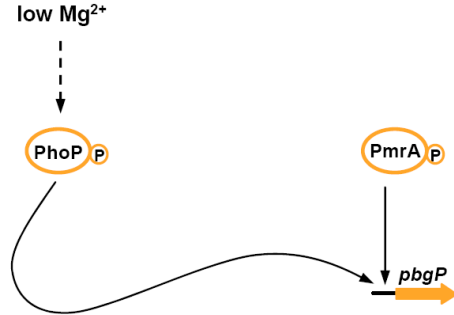


Feedforward connector loop (FCL)

Klebsiella pneumoniae

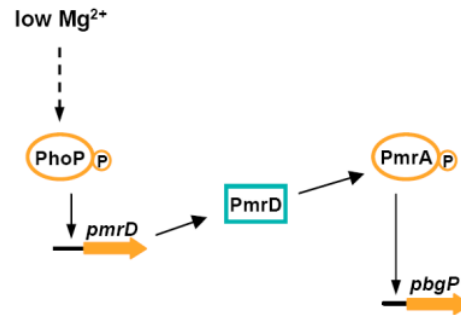
- **Properties of induction ratios, activation/deactivation timing, and response levels are determined by the structure of regulatory circuits**

Conclusions



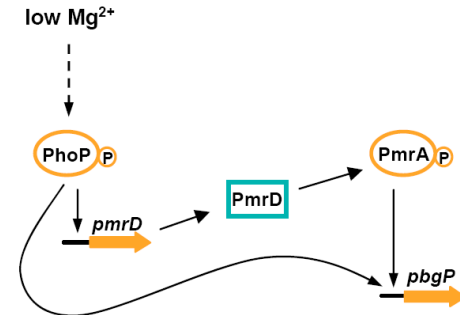
Direct pathway

Yersinia pestis



Connector-mediated pathway

Salmonella enterica

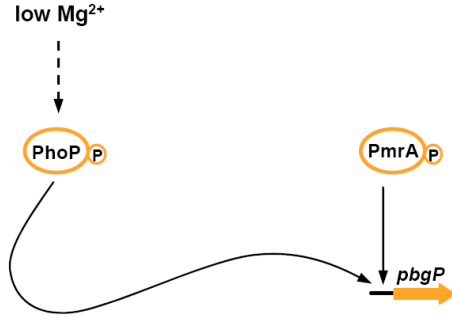


Feedforward connector loop (FCL)

Klebsiella pneumoniae

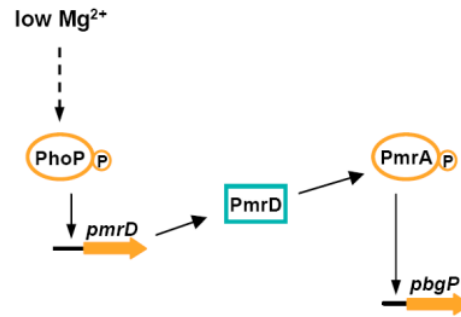
- Properties of induction ratios, activation/deactivation timing, and response levels are determined by the structure of regulatory circuits
- Connector-mediated regulatory mechanisms confer special functional features on the regulatory circuits

Conclusions



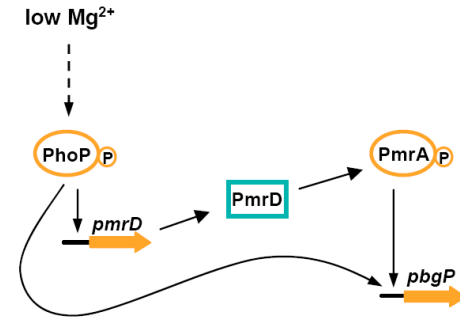
Direct pathway

Yersinia pestis



Connector-mediated pathway

Salmonella enterica



Feedforward connector loop (FCL)

Klebsiella pneumoniae

- Properties of induction ratios, activation/deactivation timing, and response levels are determined by the structure of regulatory circuits
- Connector-mediated regulatory mechanisms confer special functional features on the regulatory circuits
- Different regulatory architectures may contribute to different lifestyles of bacterial species

Acknowledgements



Akinori Kato

Eduardo Groisman (Washington U)

Groisman Lab

Henry Huang (Washington U)



Mollie Jewett

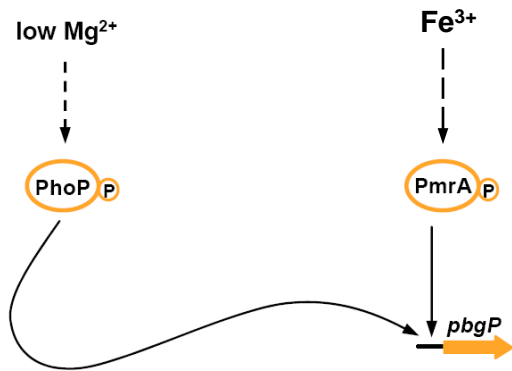
Howard Hughes Medical Institute

National Institutes of Health

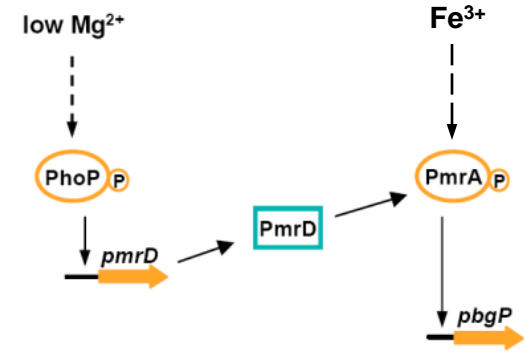


Tricia Hadley

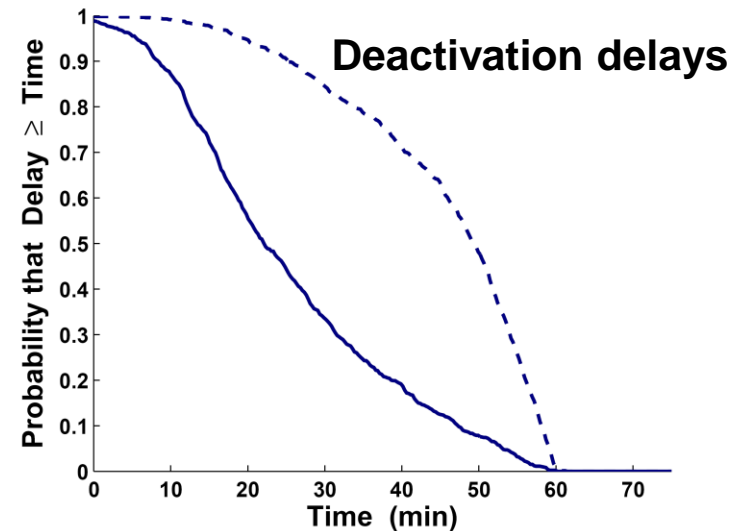
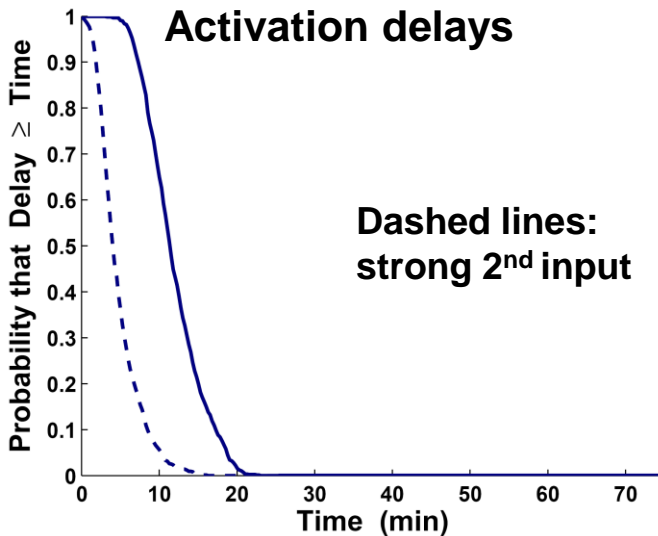
Strong second input speeds up activation and slows down deactivation of the connector-mediated pathway



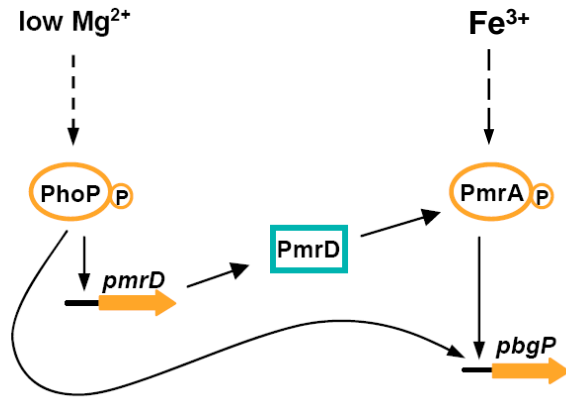
Direct regulation
(reference architecture)



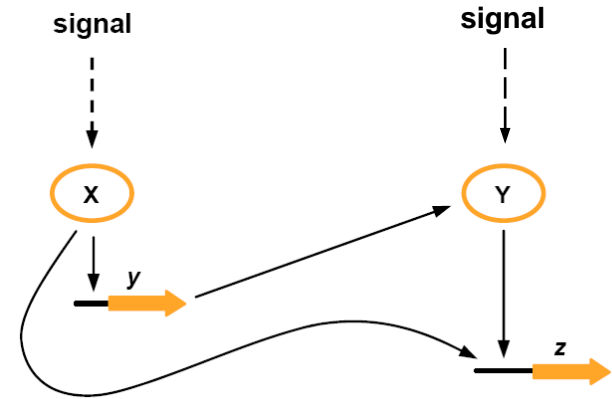
Connector-mediated pathway



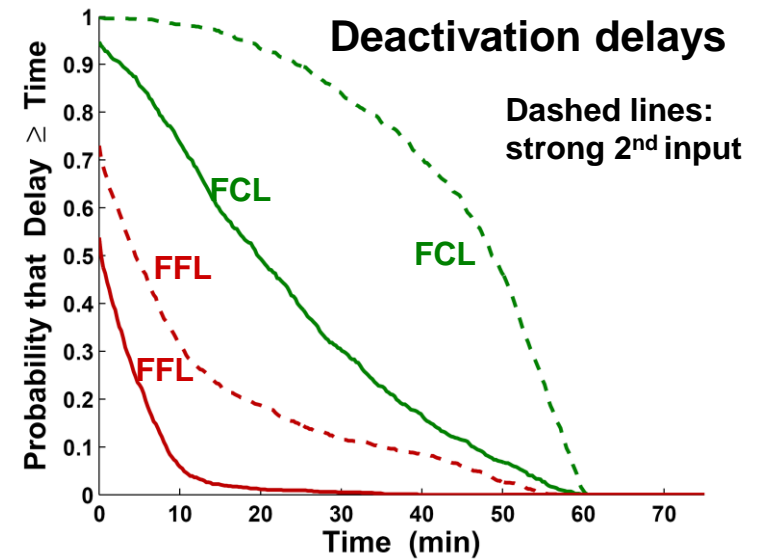
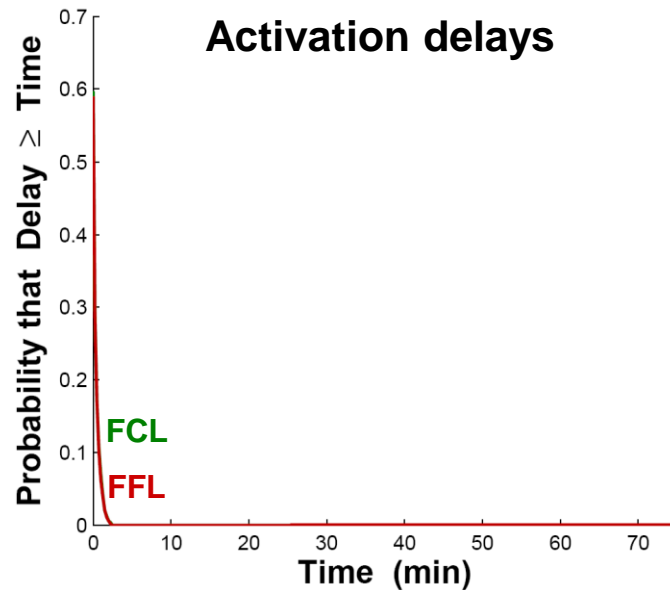
Strong activation of second input increases deactivation delays



Feedforward connector loop (FCL)



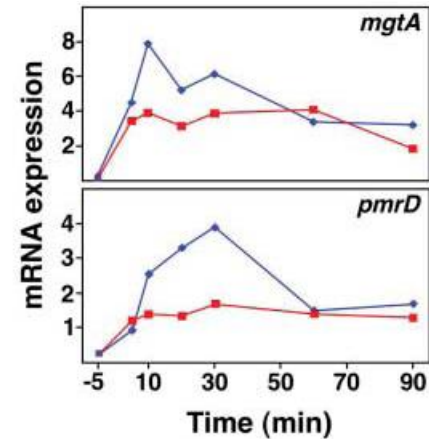
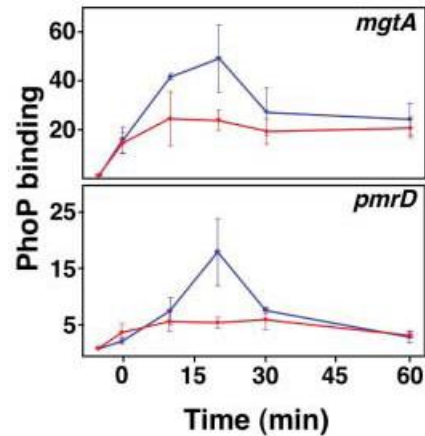
Feedforward loop (FFL)



Shape of a dynamic response curve determines the ability of *Salmonella enterica* to cause disease

PhoP: major regulator of *S. enterica* virulence

— wild type
— mutant



S. enterica infection in a mouse model:

