

# Cellular Control Systems with Delays

Joseph M. Mahaffy

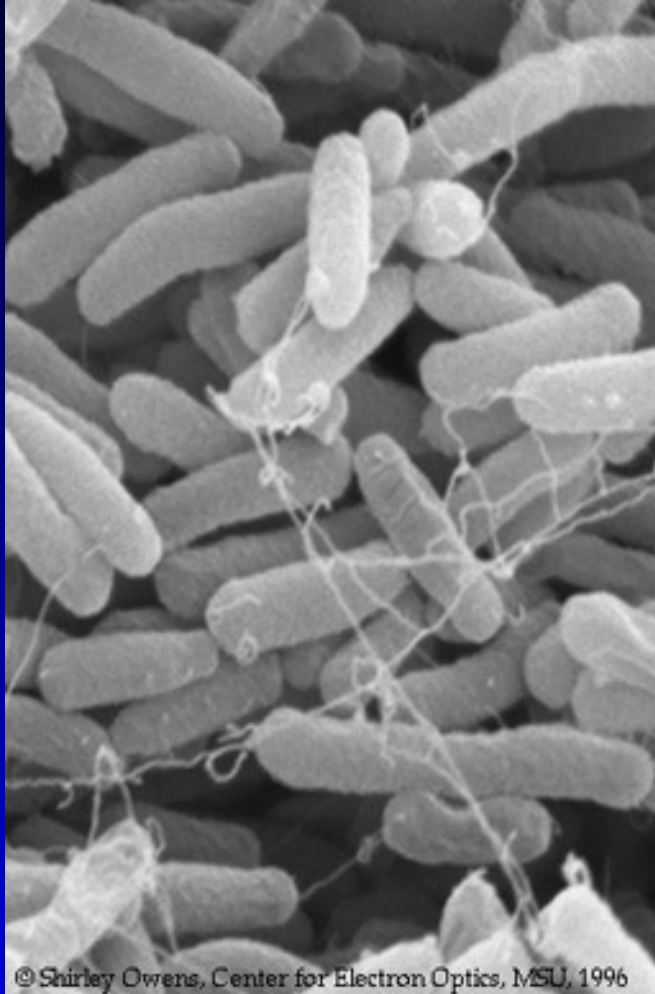
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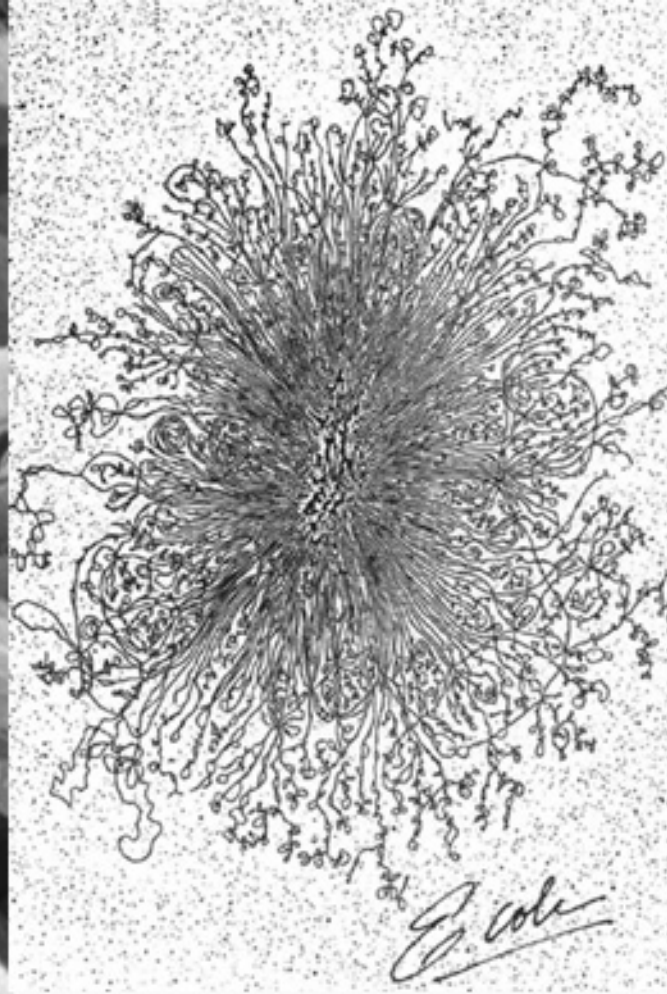
# Abstract

Genetic control models for *Escherichia coli* are presented with delays for transcription and translation. Feedback controls for induction and repression are developed using biochemical kinetics. These techniques are applied to develop models for the *lac* operon, including catabolite repression. Mathematical analyses of the models show Hopf bifurcations and hysteresis effects. The modeling techniques are extended to the regulation of DNA replication and cell growth in *E. coli*.

# *Escherichia coli*



Cells



DNA

# Outline

- Brief History of Induction and Repression Models
- Description of Repression
- Biochemical Kinetics
- Repression Models
- Cellular Control of *lac* Operon
- Models for *lac* Operon
- Results for the Models
- Future Directions

# Brief History

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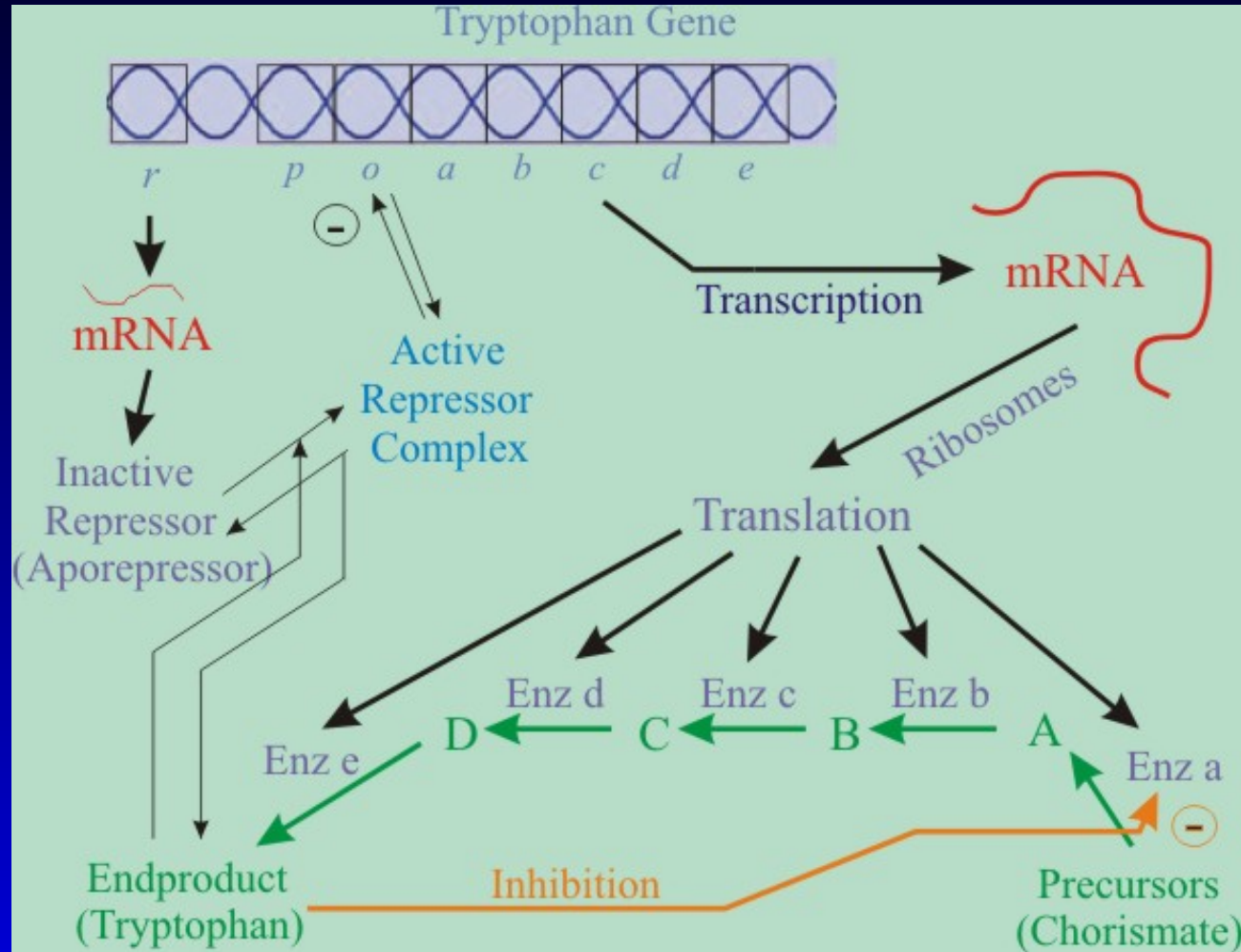
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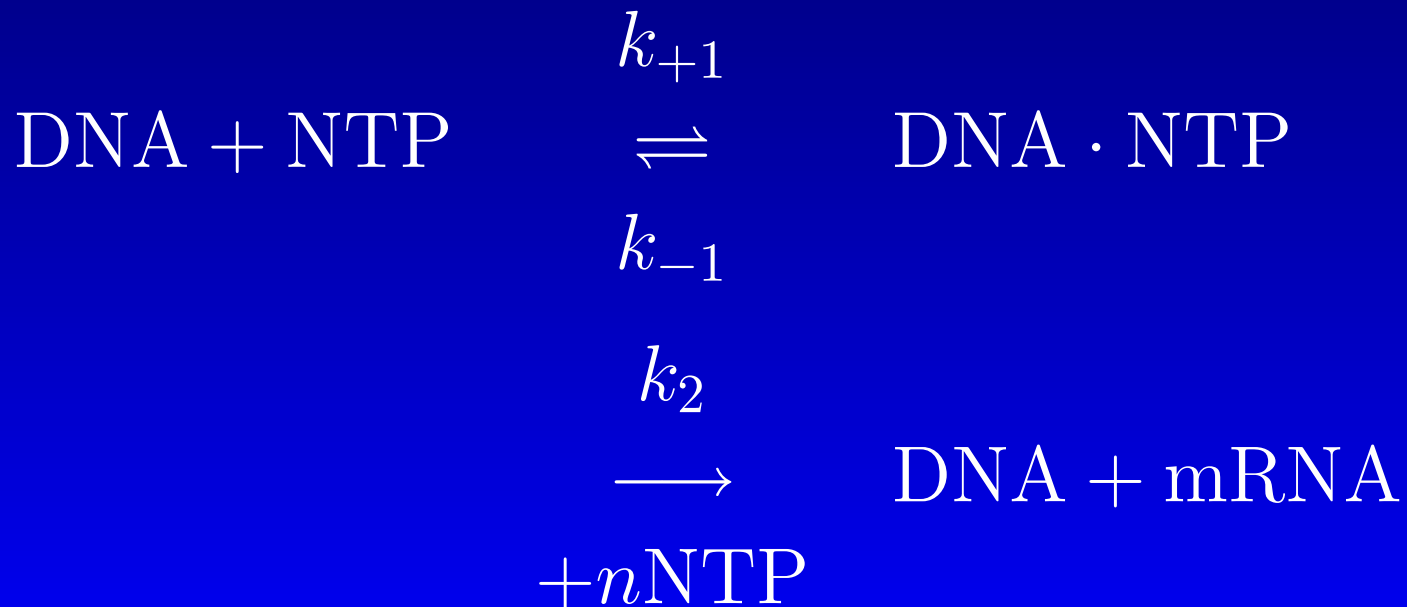
# Repression - *trp* Operon



# Biochemical Equations

## Transcription

With the  $\sigma_{70}$  factor, **RNA polymerase** melts the DNA to form an opening complex. The polymerase sequentially reads the DNA, adding nucleotide triphosphates (NTPs), to produce the completed mRNA.

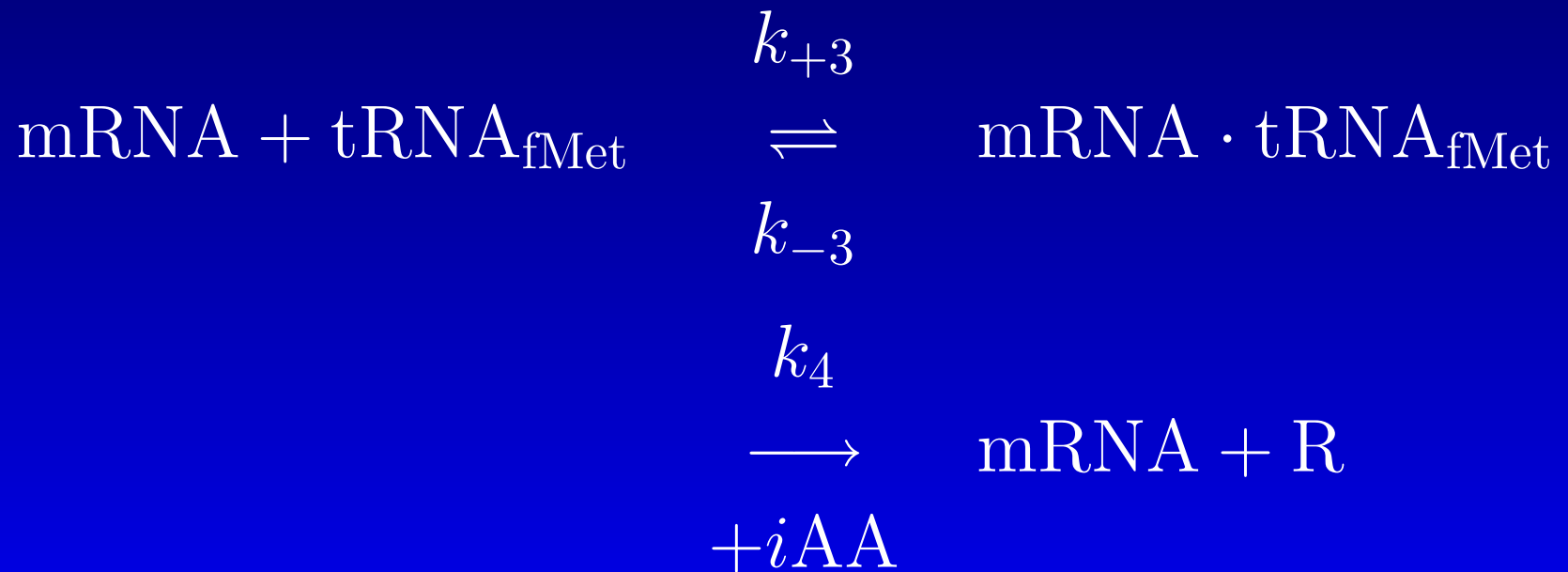




# Biochemical Equations

## Translation

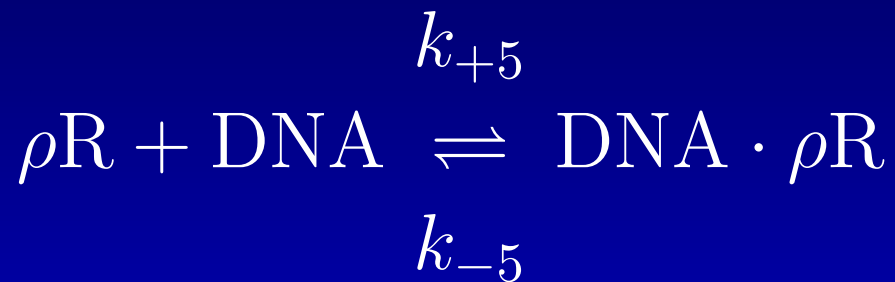
Shortly after transcription begins, **ribosomes** attach to the elongating mRNA and translate the triplet codons by accepting the appropriate charged tRNAs and adding amino acids (AA) to the new protein (R).



# Biochemical Equations

## Repressor Binding

This simplified model assumes that  $\rho$  molecules of the endproduct/repressor protein, **R**, bind to the **operator region** of the DNA to prevent transcription.



# Biochemical Kinetics

## Quasi-Steady State

Assume the intermediate complexes are formed rapidly and are essentially in equilibrium.

$$\begin{aligned} \frac{d[\text{DNA} \cdot \text{NTP}]}{dt} &= k_{+1}[\text{DNA}][\text{NTP}] \\ &\quad - (k_{-1} + k_2)[\text{DNA} \cdot \text{NTP}] = 0 \end{aligned}$$

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Thus, if  $K_1 = k_{+1}/(k_{-1} + k_2)$ ,

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Similar argument for the translation intermediate.

# Biochemical Kinetics

## Fast Equilibrium

Assume the repressor and operator region of tryptophan operon rapidly equilibrate.

$$\begin{aligned}\frac{d[\text{DNA} \cdot \rho\text{R}]}{dt} &= k_{+5}[\text{DNA}][\text{R}]^{\rho} - k_{-5}[\text{DNA} \cdot \rho\text{R}] \\ &= 0\end{aligned}$$

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Thus, if  $K_5 = k_{+5}/k_{-5}$ ,

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# Conservation Law

Assume the total DNA is in constant concentration and satisfies the conservation law

$$\begin{aligned} [\text{DNA}]_T &= [\text{DNA}] + [\text{DNA} \cdot \text{NTP}] + [\text{DNA} \cdot \rho\text{R}] \\ &= [\text{DNA}](1 + K_1[\text{NTP}] + K_5[\text{R}]^\rho) \end{aligned}$$



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Negative feedback by the repressor, **R**

# DE for Transcription

Let  $\mu$  be the **decay** and **dilution rate** for [mRNA], then from the kinetic equations above the differential equation describing the production of mRNA is

$$\begin{aligned}\frac{d[\text{mRNA}]}{dt} &= k_2[\text{DNA} \cdot \text{NTP}] - \mu[\text{mRNA}] \\ &= \frac{k_2[\text{DNA}]_T[\text{NTP}]}{1 + K_1[\text{NTP}] + K_5[\text{R}]^\rho} - \mu[\text{mRNA}]\end{aligned}$$

# Repression Models

Let  $x_1(t)$  be the concentration of mRNA and  $x_n(t)$  be the endproduct.

$$\dot{x}_1 = \frac{a_1}{1 + Kx_n^\rho} - b_1x_1$$

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Adding delays for transcription and translation

$$\dot{x}_1(t) = \frac{a_1}{1 + Kx_n^\rho(t - \tau)} - b_1x_1(t)$$

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  - Periodic solutions after Hopf bifurcation
  - Period of oscillation is 2-4 times delay

# Linear Analysis - DDE

$$\begin{pmatrix} \dot{x}_1(t) \\ \dot{x}_2(t) \end{pmatrix} = \begin{pmatrix} -b_1 & 0 \\ a_2 & -b_2 \end{pmatrix} \begin{pmatrix} x_1(t) \\ x_2(t) \end{pmatrix} + \begin{pmatrix} 0 & f'(\bar{x}_2) \\ 0 & 0 \end{pmatrix} \begin{pmatrix} x_1(t - \tau) \\ x_2(t - \tau) \end{pmatrix}$$

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Characteristic equation

$$\begin{vmatrix} -b_1 - \lambda & f'(\bar{x}_2)e^{-\lambda\tau} \\ a_1 & -b_2 - \lambda \end{vmatrix} = 0$$

or

$$(\lambda + b_1)(\lambda + b_2) - a_2 f'(\bar{x}_2) e^{-\lambda\tau} = 0$$

# Hopf Bifurcation

Since  $f'(\bar{x}_2) < 0$ , the characteristic equation with  $A \equiv -a_2 f'(\bar{x}_2)$  is

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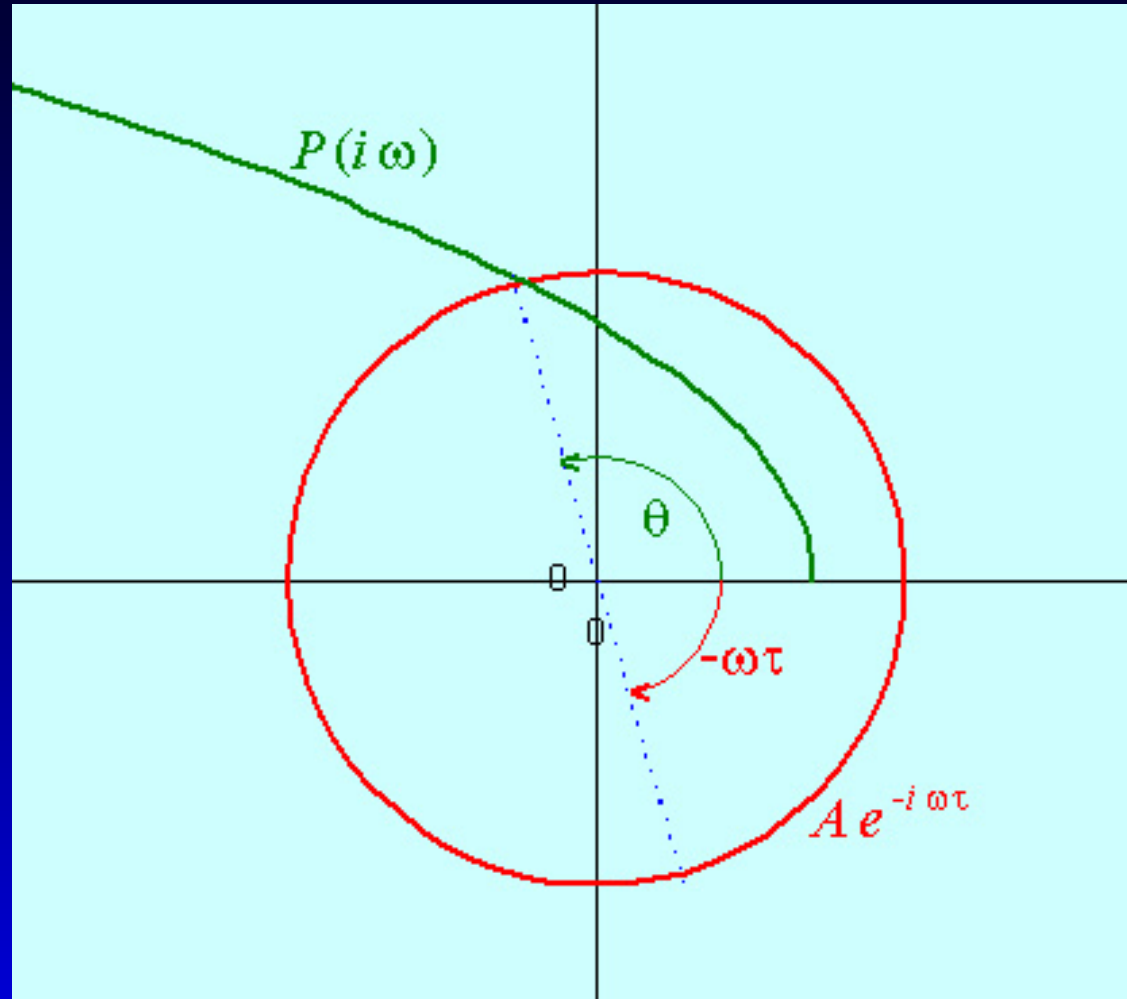
$$|P(i\omega)| = A$$

and

$$\arg(P(i\omega)) = \arctan\left(\frac{i\omega}{b_1}\right) + \arctan\left(\frac{i\omega}{b_2}\right)$$

$$\text{or } \theta = \pi - \omega\tau$$

# Hopf - Argument Principle



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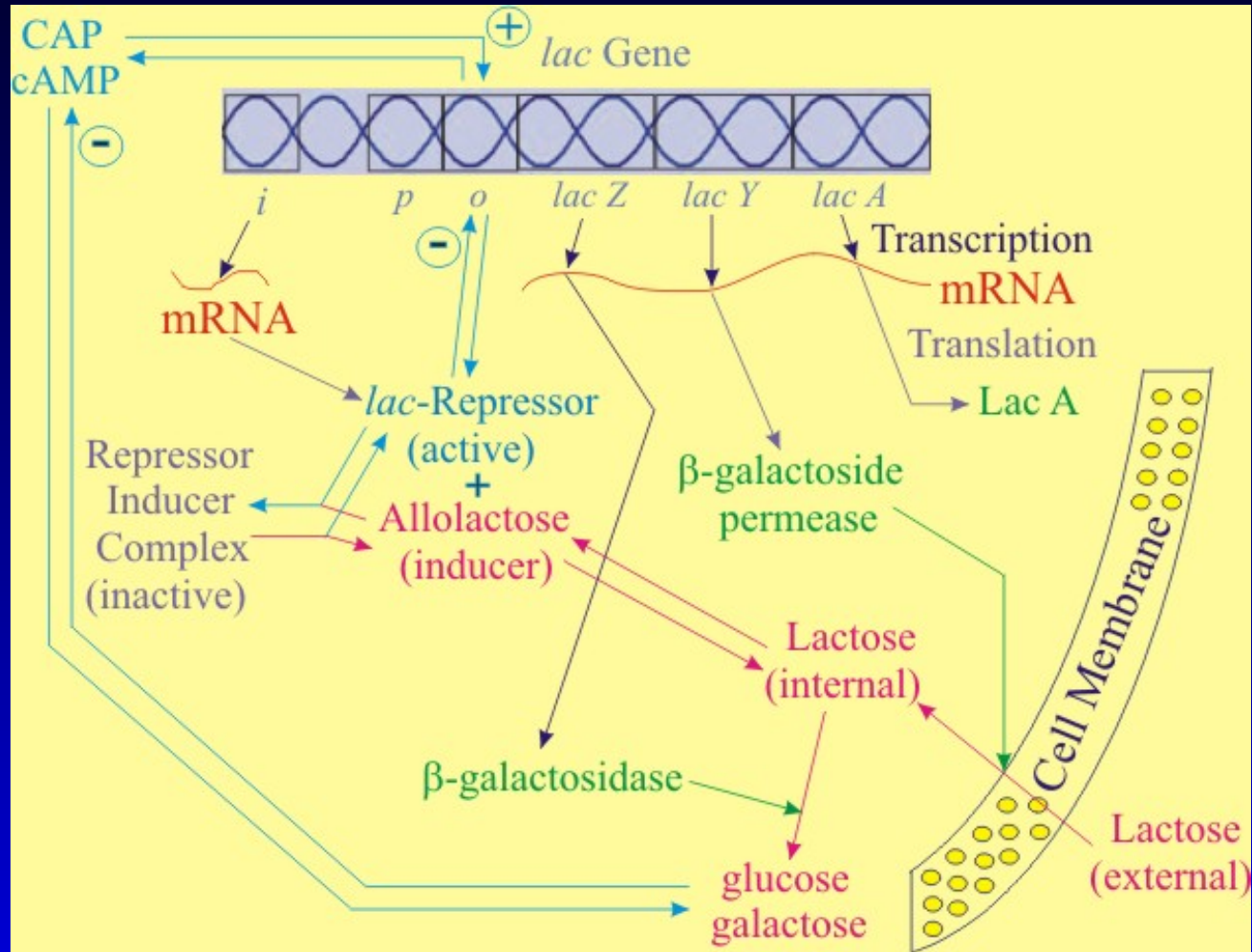
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  - Estimate Parameters from Experiments
  - Stable Model that matches Experiments

# The *lac* Operon



# Classic Induction Model

Let  $x_1(t)$  be the concentration of mRNA and  $x_n(t)$  be the endproduct

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Saturation enzyme kinetic or **S-curve** function

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- Delays destabilize the Model
- No oscillations in the Physiological range

# *lac* Model A - Mahaffy(1984)

Let  $x_1$  be [cAMP],  $x_2$  be [mRNA],  $x_4$  be [Lactose<sub>i</sub>],  
 $x_3$  be [ $\beta$ -galactosidase], and  $x_5$  be [Glucose]

$$\dot{x}_1(t) = \frac{1}{1 + x_5^\gamma(t - \tau_1)} - b_1 x_1(t)$$

$$\dot{x}_2(t) = \frac{x_1(t)(1 + K_2 x_4^\rho(t - \tau_2))}{(1 + K_3 x_1(t))(1 + K_4 x_4^\rho(t - \tau_2)) + K_5} - b_2 x_2(t)$$

$$\dot{x}_3(t) = x_2(t) - b_3 x_3(t)$$

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Assumes  $\beta$ -galactosidase is rate limiting.

# *lac* Model B - Mahaffy(1984)

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Simplified with no **catabolite repression**

Let  $x_1$  be [mRNA],  $x_2$  be [ $\beta$ -galactoside permease],  
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Examines the induction of both enzymes by lactose.

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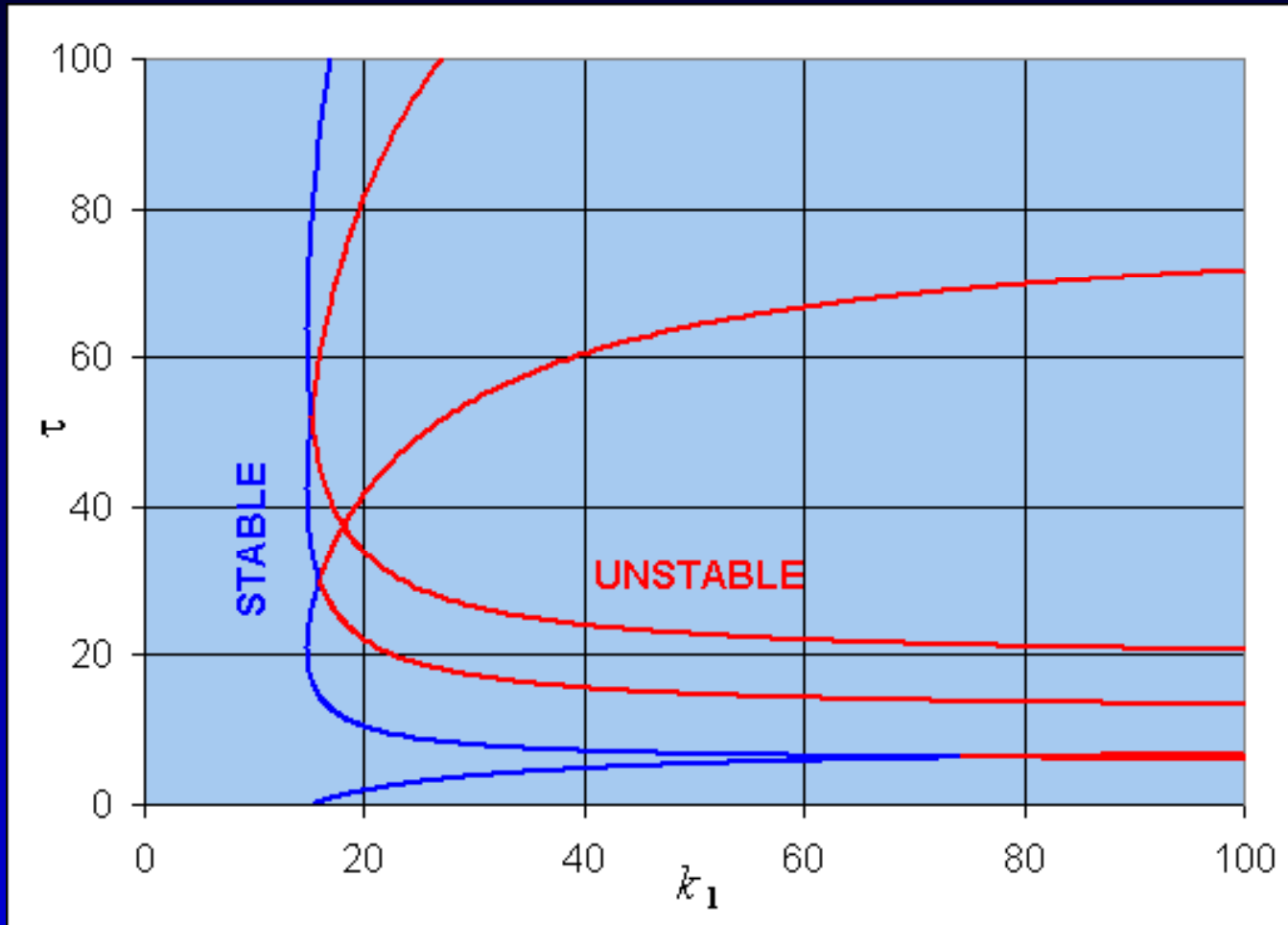
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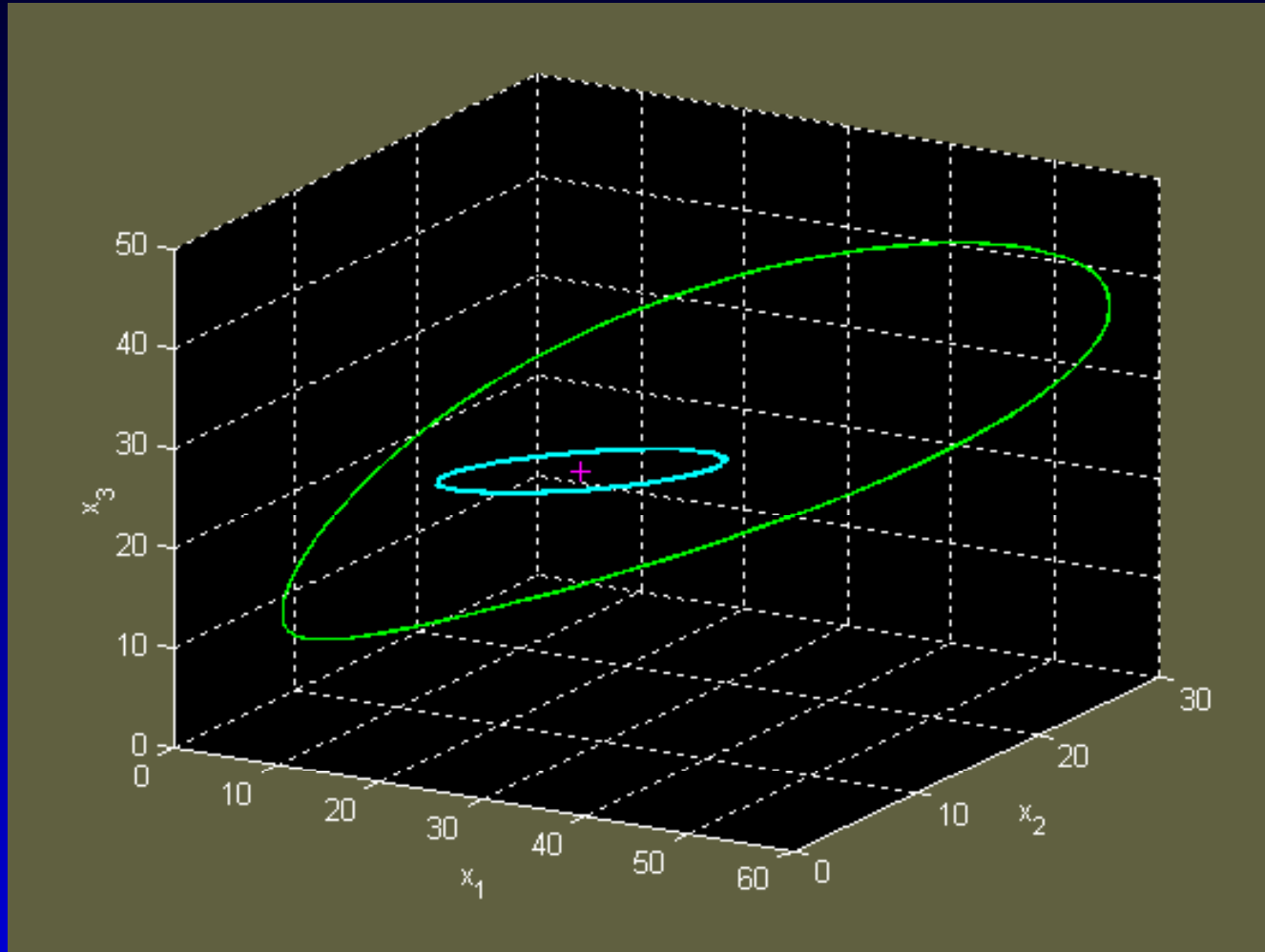
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# Bifurcation Diagram



# Model Simulation



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