Bistability and a differential equation model of the *lac* operon

Matthew Macauley

Department of Mathematical Sciences Clemson University http://www.math.clemson.edu/~macaule/

Math 4500, Fall 2016

A system is **bistable** if it is capable of resting in two stable steady-states separated by an unstable state.

A system is **bistable** if it is capable of resting in two stable steady-states separated by an unstable state.



From Wikipedia.

A system is bistable if it is capable of resting in two stable steady-states separated by an unstable state.



The threshold ODE: $y' = -ry(1 - \frac{y}{M})(1 - \frac{y}{T})$.

A system is **bistable** if it is capable of resting in two stable steady-states separated by an unstable state.



In the threshold model for population growth, there are three steady-states, 0 < T < M:

- *M* = carrying capacity (stable),
- T = extinction threshold (unstable),
- 0 = extinct (stable).

For an example of bistability, consider the *lac* operon.

For an example of bistability, consider the *lac* operon.

The expression level of the *lac* operon genes are either almost zero ("basal levels"), or very high (thousands of times higher).

For an example of bistability, consider the *lac* operon.

The expression level of the *lac* operon genes are either almost zero ("basal levels"), or very high (thousands of times higher). There's no "inbetween" state.

For an example of bistability, consider the *lac* operon.

The expression level of the *lac* operon genes are either almost zero ("basal levels"), or very high (thousands of times higher). There's no "inbetween" state.

The precise expression level depends on the concentration level of intracellular lactose. Let's denote this parameter by p.

For an example of bistability, consider the *lac* operon.

The expression level of the *lac* operon genes are either almost zero ("basal levels"), or very high (thousands of times higher). There's no "inbetween" state.

The precise expression level depends on the concentration level of intracellular lactose. Let's denote this parameter by p.

Now, let's "tune" this parameter.

For an example of bistability, consider the *lac* operon.

The expression level of the *lac* operon genes are either almost zero ("basal levels"), or very high (thousands of times higher). There's no "inbetween" state.

The precise expression level depends on the concentration level of intracellular lactose. Let's denote this parameter by p.

Now, let's "tune" this parameter. The result might look like the graph on the left.



For an example of bistability, consider the *lac* operon.

The expression level of the *lac* operon genes are either almost zero ("basal levels"), or very high (thousands of times higher). There's no "inbetween" state.

The precise expression level depends on the concentration level of intracellular lactose. Let's denote this parameter by p.

Now, let's "tune" this parameter. The result might look like the graph on the left.



This is reversible bistability. In other situations, it may be irreversible (at right).

In the case of reversible bistability, note that the *up-threshold* L_2 of p is higher than the *down-threshold* L_1 of p.



In the case of reversible bistability, note that the *up-threshold* L_2 of p is higher than the *down-threshold* L_1 of p.



This is hysteresis: a dependence of a state on its current state and past state.

In the case of reversible bistability, note that the *up-threshold* L_2 of p is higher than the *down-threshold* L_1 of p.



This is hysteresis: a dependence of a state on its current state and past state.

Thermostat example

Consider a home thermostat set for 72° .

In the case of reversible bistability, note that the *up-threshold* L_2 of p is higher than the *down-threshold* L_1 of p.



This is hysteresis: a dependence of a state on its current state and past state.

Thermostat example

Consider a home thermostat set for 72° .

If the temperature is T < 71, then the heat kicks on.

In the case of reversible bistability, note that the *up-threshold* L_2 of p is higher than the *down-threshold* L_1 of p.



This is hysteresis: a dependence of a state on its current state and past state.

Thermostat example

Consider a home thermostat set for 72° .

- If the temperature is T < 71, then the heat kicks on.
- If the temperature is T > 73, then the AC kicks on.

In the case of reversible bistability, note that the *up-threshold* L_2 of p is higher than the *down-threshold* L_1 of p.



This is hysteresis: a dependence of a state on its current state and past state.

Thermostat example

Consider a home thermostat set for 72° .

- If the temperature is T < 71, then the heat kicks on.
- If the temperature is T > 73, then the AC kicks on.
- If 71 < T < 73, then we don't know whether the heat or AC was on last.

If lactose levels are medium, then the state of the operon depends on whether or not a cell was grown in a lactose-rich environment.



If lactose levels are medium, then the state of the operon depends on whether or not a cell was grown in a lactose-rich environment.





If lactose levels are medium, then the state of the operon depends on whether or not a cell was grown in a lactose-rich environment.



Lac operon example

Let [L] denote the concentration of intracellular lactose.

If lactose levels are medium, then the state of the operon depends on whether or not a cell was grown in a lactose-rich environment.



Lac operon example

Let [L] denote the concentration of intracellular lactose.

• If $[L] < L_1$, then the operon is OFF.

If lactose levels are medium, then the state of the operon depends on whether or not a cell was grown in a lactose-rich environment.



Lac operon example

Let [L] denote the concentration of intracellular lactose.

- If $[L] < L_1$, then the operon is OFF.
- If $[L] > L_2$, then the operon is ON.

If lactose levels are medium, then the state of the operon depends on whether or not a cell was grown in a lactose-rich environment.



Lac operon example

Let [L] denote the concentration of intracellular lactose.

- If $[L] < L_1$, then the operon is OFF.
- If $[L] > L_2$, then the operon is ON.
- If $L_1 < [L] < L_2$, then the operon could be ON or OFF.

If lactose levels are medium, then the state of the operon depends on whether or not a cell was grown in a lactose-rich environment.



Lac operon example

Let [L] denote the concentration of intracellular lactose.

- If $[L] < L_1$, then the operon is OFF.
- If $[L] > L_2$, then the operon is ON.
- If $L_1 < [L] < L_2$, then the operon could be ON or OFF.

The region of bistability (L_1, L_2) has both induced and un-induced cells.

The Boolean network models we've seen are too simple to capture bistability.

The Boolean network models we've seen are too simple to capture bistability.

We'll see two different ODE models of the lac operon that exhibit bistability.

The Boolean network models we've seen are too simple to capture bistability.

We'll see two different ODE models of the lac operon that exhibit bistability.

These ODE models were designed using Michaelis–Menten equations from mass-action kinetics which we learned about earlier.

The Boolean network models we've seen are too simple to capture bistability.

We'll see two different ODE models of the lac operon that exhibit bistability.

These ODE models were designed using Michaelis–Menten equations from mass-action kinetics which we learned about earlier.

In a later lecture, we'll see how bistability can indeed be captured in a Boolean network system.

The Boolean network models we've seen are too simple to capture bistability.

We'll see two different ODE models of the lac operon that exhibit bistability.

These ODE models were designed using Michaelis–Menten equations from mass-action kinetics which we learned about earlier.

In a later lecture, we'll see how bistability can indeed be captured in a Boolean network system.

In general, bistable systems tend to have positive feedback loops (in their "wiring diagrams") or double-negative feedback loops (=positive feedback).

Modeling dilution in protein concentration due to bacterial growth

E. coli grows fast! It can double in 20 minutes.
E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

Let's define:

• V = average volume of an *E. coli* bacterial cell.

E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

Let's define:

- V = average volume of an *E. coli* bacterial cell.
- Let x = number of molecules of protein X in that cell.

E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

Let's define:

- V = average volume of an *E. coli* bacterial cell.
- Let x = number of molecules of protein X in that cell.

Assumptions about these derivatives:

E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

Let's define:

- V = average volume of an *E. coli* bacterial cell.
- Let x = number of molecules of protein X in that cell.

Assumptions about these derivatives:

• cell volume increases exponentially in time: $\frac{dV}{dt} = \mu V$.

E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

Let's define:

- V = average volume of an *E. coli* bacterial cell.
- Let x = number of molecules of protein X in that cell.

Assumptions about these derivatives:

- cell volume increases exponentially in time: $\frac{dV}{dt} = \mu V$.
- degradation of X is exponential: $\frac{dx}{dt} = -\beta x$.

E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

Let's define:

- V = average volume of an *E. coli* bacterial cell.
- Let x = number of molecules of protein X in that cell.

Assumptions about these derivatives:

- cell volume increases exponentially in time: $\frac{dV}{dt} = \mu V$.
- degradation of X is exponential: $\frac{dx}{dt} = -\beta x$.

$$\frac{d[x]}{dt} = (x'V - V'x)\frac{1}{V^2}$$

E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

Let's define:

- V = average volume of an *E. coli* bacterial cell.
- Let x = number of molecules of protein X in that cell.

Assumptions about these derivatives:

- cell volume increases exponentially in time: $\frac{dV}{dt} = \mu V$.
- degradation of X is exponential: $\frac{dx}{dt} = -\beta x$.

$$\frac{d[x]}{dt} = (x'V - V'x)\frac{1}{V^2} = (-\beta xV - \mu Vx)\frac{1}{V^2}$$

E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

Let's define:

- V = average volume of an *E. coli* bacterial cell.
- Let x = number of molecules of protein X in that cell.

Assumptions about these derivatives:

- cell volume increases exponentially in time: $\frac{dV}{dt} = \mu V$.
- degradation of X is exponential: $\frac{dx}{dt} = -\beta x$.

$$\frac{d[x]}{dt} = (x'V - V'x)\frac{1}{V^2} = (-\beta xV - \mu Vx)\frac{1}{V^2} = -(\beta + \mu)\frac{x}{V}$$

E. coli grows fast! It can double in 20 minutes. Thus, reasonable ODE models involving concentration shouldn't assume that volume is constant.

Let's define:

- V = average volume of an *E. coli* bacterial cell.
- Let x = number of molecules of protein X in that cell.

Assumptions about these derivatives:

- cell volume increases exponentially in time: $\frac{dV}{dt} = \mu V$.
- degradation of X is exponential: $\frac{dx}{dt} = -\beta x$.

$$\frac{d[x]}{dt} = \left(x'V - V'x\right)\frac{1}{V^2} = \left(-\beta xV - \mu Vx\right)\frac{1}{V^2} = -\left(\beta + \mu\right)\frac{x}{V} = -(\beta + \mu)[x].$$

Assumptions

• Lac repressor protein is produced at a constant rate.

Assumptions

- Lac repressor protein is produced at a constant rate.
- Laws of mass-action kinetics.

Assumptions

- Lac repressor protein is produced at a constant rate.
- Laws of mass-action kinetics.

Repressor binds to allolactose:

$$R + nA \rightleftharpoons_{1}^{K_1} RA_n$$

Assumptions

- Lac repressor protein is produced at a constant rate.
- Laws of mass-action kinetics.

Repressor binds to allolactose:

$$R + nA \stackrel{K_1}{\underset{1}{\longleftarrow}} RA_n \qquad \frac{d[RA_n]}{dt} = K_1[R][A]^n - [RA_n]$$

Assumptions

- Lac repressor protein is produced at a constant rate.
- Laws of mass-action kinetics.

Repressor binds to allolactose:

$$R + nA \stackrel{K_1}{\underset{1}{\longrightarrow}} RA_n \qquad \frac{d[RA_n]}{dt} = K_1[R][A]^n - [RA_n]$$

Assume the reaction is at equilibrium: $\frac{d[RA_n]}{dt} = 0$, and so $K_1 = \frac{[RA_n]}{[R][A]^n}$.

Assumptions

- Lac repressor protein is produced at a constant rate.
- Laws of mass-action kinetics.

Repressor binds to allolactose:

$$R + nA \stackrel{K_1}{\underset{1}{\longleftarrow}} RA_n \qquad \frac{d[RA_n]}{dt} = K_1[R][A]^n - [RA_n]$$

Assume the reaction is at equilibrium: $\frac{d[RA_n]}{dt} = 0$, and so $K_1 = \frac{[RA_n]}{|R||A|^n}$.

• The repressor protein binds to the operator region if there is no allolactose:

$$O + R \rightleftharpoons_{1}^{K_2} OR$$

Assumptions

- Lac repressor protein is produced at a constant rate.
- Laws of mass-action kinetics.

Repressor binds to allolactose:

$$R + nA \stackrel{K_1}{\underset{1}{\longleftarrow}} RA_n \qquad \frac{d[RA_n]}{dt} = K_1[R][A]^n - [RA_n]$$

Assume the reaction is at equilibrium: $\frac{d[RA_n]}{dt} = 0$, and so $K_1 = \frac{[RA_n]}{[R][A]^n}$.

• The repressor protein binds to the operator region if there is no allolactose:

$$O+R \underset{1}{\underbrace{K_2}} OR \qquad \frac{d[OR]}{dt} = K_2[O][R] - [OR].$$

Assumptions

- Lac repressor protein is produced at a constant rate.
- Laws of mass-action kinetics.

Repressor binds to allolactose:

$$R + nA \stackrel{K_1}{\underset{1}{\longleftarrow}} RA_n \qquad \frac{d[RA_n]}{dt} = K_1[R][A]^n - [RA_n]$$

Assume the reaction is at equilibrium: $\frac{d[RA_n]}{dt} = 0$, and so $K_1 = \frac{[RA_n]}{[R][A]^n}$.

The repressor protein binds to the operator region if there is no allolactose:

$$O+R \stackrel{K_2}{\underset{1}{\longleftarrow}} OR \qquad \frac{d[OR]}{dt} = K_2[O][R] - [OR].$$

Assume the reaction is at equilibrium: $\frac{d[OR]}{dt} = 0$, and so $K_2 = \frac{[OR]}{[O][R]}$.

Let O_{tot} = total operator concentration (a constant).

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

 $O_{tot} = [O] + [OR]$

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

 $O_{tot} = [O] + [OR] = [O] + K_2[O][R]$

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

 $O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

 $O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$

Therefore, $\frac{[O]}{O_{tot}} = \frac{1}{1+K_2[R]}$. "Proportion of free (unbounded) operator sites."

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

$$O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$$

Therefore, $\frac{[O]}{O_{tot}} = \frac{1}{1+K_2[R]}$. "Proportion of free (unbounded) operator sites."

Let R_{tot} be total concentration of the repressor protein (constant):

 $R_{tot} = [R] + [OR] + [RA_n]$

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

$$O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$$

Therefore, $\frac{[O]}{O_{tot}} = \frac{1}{1+K_2[R]}$. "Proportion of free (unbounded) operator sites."

Let R_{tot} be total concentration of the repressor protein (constant):

$$R_{tot} = [R] + [OR] + [RA_n]$$

Assume only a few molecules of operator sites per cell: $[OR] \ll \max\{[R], [RA_n]\}$:

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

$$O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$$

Therefore, $\frac{[O]}{O_{tot}} = \frac{1}{1+K_2[R]}$. "Proportion of free (unbounded) operator sites."

Let R_{tot} be total concentration of the repressor protein (constant):

$$R_{tot} = [R] + [OR] + [RA_n]$$

Assume only a few molecules of operator sites per cell: $[OR] \ll \max\{[R], [RA_n]\}$:

$$R_{tot} \approx [R] + [RA_n] = [R] + K_1[R][A]^n$$

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

$$O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$$

Therefore, $\frac{[O]}{O_{tot}} = \frac{1}{1+K_2[R]}$. "Proportion of free (unbounded) operator sites."

Let R_{tot} be total concentration of the repressor protein (constant):

$$R_{tot} = [R] + [OR] + [RA_n]$$

Assume only a few molecules of operator sites per cell: $[OR] \ll \max\{[R], [RA_n]\}$:

$$R_{tot} \approx [R] + [RA_n] = [R] + K_1[R][A]^n$$

Eliminating $[RA_n]$, we get $[R] = \frac{R_{tot}}{1 + K_1[A]^n}$.

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

$$O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$$

Therefore, $\frac{[O]}{O_{tot}} = \frac{1}{1+K_2[R]}$. "Proportion of free (unbounded) operator sites."

Let R_{tot} be total concentration of the repressor protein (constant):

$$R_{tot} = [R] + [OR] + [RA_n]$$

Assume only a few molecules of operator sites per cell: $[OR] \ll \max\{[R], [RA_n]\}$:

$$R_{tot} \approx [R] + [RA_n] = [R] + K_1[R][A]^n$$

Eliminating $[RA_n]$, we get $[R] = \frac{R_{tot}}{1 + K_1[A]^n}$.

Now, the proportion of free operator sites is:

$$\frac{[O]}{O_{tot}} = \frac{1}{1 + K_2[R]}$$

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

$$O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$$

Therefore, $\frac{[O]}{O_{tot}} = \frac{1}{1+K_2[R]}$. "Proportion of free (unbounded) operator sites."

Let R_{tot} be total concentration of the repressor protein (constant):

$$R_{tot} = [R] + [OR] + [RA_n]$$

Assume only a few molecules of operator sites per cell: $[OR] \ll \max{[R], [RA_n]}$:

$$R_{tot} \approx [R] + [RA_n] = [R] + K_1[R][A]^n$$

Eliminating $[RA_n]$, we get $[R] = \frac{R_{tot}}{1 + K_1[A]^n}$.

Now, the proportion of free operator sites is:

$$\frac{[O]}{O_{tot}} = \frac{1}{1 + K_2[R]} = \frac{1}{1 + K_2(\frac{R_{tot}}{1 + K_1[A]^n})}$$

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

$$O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$$

Therefore, $\frac{[O]}{O_{tot}} = \frac{1}{1+K_2[R]}$. "Proportion of free (unbounded) operator sites."

Let R_{tot} be total concentration of the repressor protein (constant):

$$R_{tot} = [R] + [OR] + [RA_n]$$

Assume only a few molecules of operator sites per cell: $[OR] \ll \max{[R], [RA_n]}$:

$$R_{tot} \approx [R] + [RA_n] = [R] + K_1[R][A]^n$$

Eliminating $[RA_n]$, we get $[R] = \frac{R_{tot}}{1 + K_1[A]^n}$.

Now, the proportion of free operator sites is:

$$\frac{[O]}{O_{tot}} = \frac{1}{1 + K_2[R]} = \frac{1}{1 + K_2(\frac{R_{tot}}{1 + K_1[A]^n})} \cdot \frac{1 + K_1[A]^n}{1 + K_1[A]^n}$$

Let O_{tot} = total operator concentration (a constant). Then, using $K_2 = \frac{[OR]}{[O][R]}$,

$$O_{tot} = [O] + [OR] = [O] + K_2[O][R] = [O](1 + K_2)[R].$$

Therefore, $\frac{[O]}{O_{tot}} = \frac{1}{1+K_2[R]}$. "Proportion of free (unbounded) operator sites."

Let R_{tot} be total concentration of the repressor protein (constant):

$$R_{tot} = [R] + [OR] + [RA_n]$$

Assume only a few molecules of operator sites per cell: $[OR] \ll \max\{[R], [RA_n]\}$:

$$R_{tot} \approx [R] + [RA_n] = [R] + K_1[R][A]^n$$

Eliminating $[RA_n]$, we get $[R] = \frac{R_{tot}}{1 + K_1[A]^n}$.

Now, the proportion of free operator sites is:

$$\frac{[O]}{O_{tot}} = \frac{1}{1 + K_2[R]} = \frac{1}{1 + K_2(\frac{R_{tot}}{1 + K_1[A]^n})} \cdot \frac{1 + K_1[A]^n}{1 + K_1[A]^n} = \underbrace{\frac{1 + K_1[A]^n}{K + K_1[A]^n}}_{:=f([A])},$$

where $K = 1 + K_2 R_{tot}$.

Summary

The proportion of free operator sites is

$$\frac{[O]}{O_{tot}} = \underbrace{\frac{1 + K_1[A]^n}{K + K_1[A]^n}}_{:=f([A])},$$

where $K = 1 + K_2 R_{tot}$.

Summary

The proportion of free operator sites is

$$\frac{[O]}{O_{tot}} = \underbrace{\frac{1 + K_1[A]^n}{K + K_1[A]^n}}_{:=f([A])},$$

where $K = 1 + K_2 R_{tot}$.

Remarks

Summary

The proportion of free operator sites is

$$\frac{[O]}{O_{tot}} = \underbrace{\frac{1 + K_1[A]^n}{K + K_1[A]^n}}_{:=f([A])},$$

where $K = 1 + K_2 R_{tot}$.

Remarks

• The function f([A]) is (almost) a Hill function of coefficient n.
Modeling of lactose repressor dynamics

Summary

The proportion of free operator sites is

$$\frac{[O]}{O_{tot}} = \underbrace{\frac{1 + K_1[A]^n}{K + K_1[A]^n}}_{:=f([A])},$$

where $K = 1 + K_2 R_{tot}$.

Remarks

- The function f([A]) is (almost) a Hill function of coefficient n.
- $f([A] = 0) = \frac{1}{\kappa} > 0$ "minimal basal level of gene expression."

Modeling of lactose repressor dynamics

Summary

The proportion of free operator sites is

$$\frac{[O]}{O_{tot}} = \underbrace{\frac{1 + K_1[A]^n}{K + K_1[A]^n}}_{:=f([A])},$$

where $K = 1 + K_2 R_{tot}$.

Remarks

- The function f([A]) is (almost) a Hill function of coefficient n.
- $f([A] = 0) = \frac{1}{\kappa} > 0$ "minimal basal level of gene expression."
- f is increasing in [A], when $[A] \ge 0$.

Modeling of lactose repressor dynamics

Summary

The proportion of free operator sites is

$$\frac{[O]}{O_{tot}} = \underbrace{\frac{1 + K_1[A]^n}{K + K_1[A]^n}}_{:=f([A])},$$

where $K = 1 + K_2 R_{tot}$.

Remarks

- The function f([A]) is (almost) a Hill function of coefficient n.
- $f([A] = 0) = \frac{1}{\kappa} > 0$ "minimal basal level of gene expression."
- f is increasing in [A], when $[A] \ge 0$.
- $\lim_{[A]\to\infty} f([A]) = 1$ "with lots of allolactose, gene expression level is max'ed."

The production of mRNA from DNA via transcription is not an instantaneous process; suppose it takes time $\tau > 0$.

The production of mRNA from DNA via transcription is not an instantaneous process; suppose it takes time $\tau > 0$.

Thus, the production rate of mRNA is not a function of allolactose at time t, but rather at time $t - \tau$.

The production of mRNA from DNA via transcription is not an instantaneous process; suppose it takes time $\tau > 0$.

Thus, the production rate of mRNA is not a function of allolactose at time t, but rather at time $t - \tau$.

Suppose protein P decays exponentially, and its concentration is p(t).

$$\frac{dp}{dt} = -\mu p$$

The production of mRNA from DNA via transcription is not an instantaneous process; suppose it takes time $\tau > 0$.

Thus, the production rate of mRNA is not a function of allolactose at time t, but rather at time $t - \tau$.

Suppose protein P decays exponentially, and its concentration is p(t).

$$\frac{dp}{dt} = -\mu p \implies \int_{t-\tau}^t \frac{dp}{p} = -\mu \int_{t-\tau}^t dt \, .$$

Integrating yields

 $\left| \ln p(t) \right|_{t-\tau}^{t}$

The production of mRNA from DNA via transcription is not an instantaneous process; suppose it takes time $\tau > 0$.

Thus, the production rate of mRNA is not a function of allolactose at time t, but rather at time $t - \tau$.

Suppose protein P decays exponentially, and its concentration is p(t).

$$\frac{dp}{dt} = -\mu p \quad \Longrightarrow \quad \int_{t-\tau}^t \frac{dp}{p} = -\mu \int_{t-\tau}^t dt \, .$$

Integrating yields

$$\ln p(t)\Big|_{t-\tau}^t = -\mu t\Big|_{t-\tau}^t dt$$

The production of mRNA from DNA via transcription is not an instantaneous process; suppose it takes time $\tau > 0$.

Thus, the production rate of mRNA is not a function of allolactose at time t, but rather at time $t - \tau$.

Suppose protein P decays exponentially, and its concentration is p(t).

$$\frac{dp}{dt} = -\mu p \quad \Longrightarrow \quad \int_{t-\tau}^t \frac{dp}{p} = -\mu \int_{t-\tau}^t dt \, .$$

Integrating yields

$$\left| \ln p(t) \right|_{t-\tau}^{t} = -\mu t \Big|_{t-\tau}^{t} dt = \ln \frac{p(t)}{p(t-\tau)}$$

The production of mRNA from DNA via transcription is not an instantaneous process; suppose it takes time $\tau > 0$.

Thus, the production rate of mRNA is not a function of allolactose at time t, but rather at time $t - \tau$.

Suppose protein P decays exponentially, and its concentration is p(t).

$$\frac{dp}{dt} = -\mu p \implies \int_{t-\tau}^t \frac{dp}{p} = -\mu \int_{t-\tau}^t dt \, .$$

Integrating yields

$$\ln p(t)\Big|_{t-\tau}^t = -\mu t\Big|_{t-\tau}^t dt = \ln \frac{p(t)}{p(t-\tau)} = -\mu [t-(t-\tau)] = -\mu \tau.$$

The production of mRNA from DNA via transcription is not an instantaneous process; suppose it takes time $\tau > 0$.

Thus, the production rate of mRNA is not a function of allolactose at time t, but rather at time $t - \tau$.

Suppose protein P decays exponentially, and its concentration is p(t).

$$\frac{dp}{dt} = -\mu p \implies \int_{t-\tau}^t \frac{dp}{p} = -\mu \int_{t-\tau}^t dt \, .$$

Integrating yields

$$\ln p(t)\Big|_{t-\tau}^t = -\mu t\Big|_{t-\tau}^t dt = \ln \frac{p(t)}{p(t-\tau)} = -\mu [t-(t-\tau)] = -\mu \tau.$$

Exponentiating both sides yields $\frac{p(t)}{p(t-\tau)} = e^{-\mu\tau}$,

The production of mRNA from DNA via transcription is not an instantaneous process; suppose it takes time $\tau > 0$.

Thus, the production rate of mRNA is not a function of allolactose at time t, but rather at time $t - \tau$.

Suppose protein P decays exponentially, and its concentration is p(t).

$$\frac{dp}{dt} = -\mu p \quad \Longrightarrow \quad \int_{t-\tau}^t \frac{dp}{p} = -\mu \int_{t-\tau}^t dt \, .$$

Integrating yields

$$\ln p(t)\Big|_{t-\tau}^t = -\mu t\Big|_{t-\tau}^t dt = \ln \frac{p(t)}{p(t-\tau)} = -\mu [t-(t-\tau)] = -\mu \tau.$$

Exponentiating both sides yields $\frac{p(t)}{p(t-\tau)}=e^{-\mu\tau},$ and so

$$p(t) = e^{-\mu\tau} p(t-\tau).$$

Consider the following 3 quantities, which represent concentrations of:

- M(t) = mRNA,
- $B(t) = \beta$ -galactosidase,
- A(t) =allolactose.

Consider the following 3 quantities, which represent concentrations of:

- M(t) = mRNA,
- $B(t) = \beta$ -galactosidase,
- A(t) =allolactose.

Assumption: Internal lactose (L) is available and is a parameter.

Consider the following 3 quantities, which represent concentrations of:

- M(t) = mRNA,
- $B(t) = \beta$ -galactosidase,
- A(t) =allolactose.

Assumption: Internal lactose (L) is available and is a parameter.

The model (Yildirim and Mackey, 2004)

$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$
$$\frac{dB}{dt} = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B$$
$$\frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

Consider the following 3 quantities, which represent concentrations of:

- M(t) = mRNA,
- $B(t) = \beta$ -galactosidase,
- A(t) =allolactose.

Assumption: Internal lactose (L) is available and is a parameter.

The model (Yildirim and Mackey, 2004)

$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$
$$\frac{dB}{dt} = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B$$
$$\frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

These are *delay differential equations*, with discrete time delays due to the transcription and translation processes.

ODE for β -galactosidase (B)

$$\frac{dB}{dt} = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B,$$

ODE for β -galactosidase (B)

$$\frac{dB}{dt} = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B,$$

Justification:

• $\tilde{\gamma}_B B = \gamma_B B + \mu B$ represents loss due to β -galactosidase degredation and dilution from bacterial growth.

ODE for β -galactosidase (*B*)

$$\frac{dB}{dt} = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B,$$

Justification:

• $\tilde{\gamma}_B B = \gamma_B B + \mu B$ represents loss due to β -galactosidase degredation and dilution from bacterial growth.

Production rate of β -galactosidase, is proportional to mRNA concentration.

ODE for β -galactosidase (*B*)

$$\frac{dB}{dt} = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B,$$

Justification:

- $\tilde{\gamma}_B B = \gamma_B B + \mu B$ represents loss due to β -galactosidase degredation and dilution from bacterial growth.
- \blacksquare Production rate of $\beta\text{-galactosidase,}$ is proportional to mRNA concentration.
- τ_B = time required for translation of β -galactosidase from mRNA, and $M_{\tau_B} := M(t \tau_B)$.

ODE for β -galactosidase (*B*)

$$\frac{dB}{dt} = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B,$$

Justification:

- $\tilde{\gamma}_B B = \gamma_B B + \mu B$ represents loss due to β -galactosidase degredation and dilution from bacterial growth.
- Production rate of β -galactosidase, is proportional to mRNA concentration.
- τ_B = time required for translation of β -galactosidase from mRNA, and $M_{\tau_B} := M(t \tau_B)$.
- $e^{-\mu\tau_B}M_{\tau_B}$ accounts for the time-delay due to translation.



ODE for mRNA (M)

$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1 (e^{\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$

Justification:

• $\tilde{\gamma}_M M = \gamma_M M + \mu M$ represents loss due to mRNA degredation and dilution from bacterial growth.

ODE for mRNA (M)

$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1 (e^{\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$

Justification:

- $\tilde{\gamma}_M M = \gamma_M M + \mu M$ represents loss due to mRNA degredation and dilution from bacterial growth.
- Production rate of mRNA is proportional to fraction of free operator sites,

$$\frac{[O]}{O_{tot}} = \frac{1 + K_1[A]^n}{1 + K_1[A]^n} = f([A]).$$

ODE for mRNA (M)

$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1 (e^{\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$

Justification:

- $\tilde{\gamma}_M M = \gamma_M M + \mu M$ represents loss due to mRNA degredation and dilution from bacterial growth.
- Production rate of mRNA is proportional to fraction of free operator sites,

$$\frac{[O]}{O_{tot}} = \frac{1 + K_1[A]^n}{1 + K_1[A]^n} = f([A]).$$

The constant $\tau_M > 0$ represents the time-delay due to transcription of mRNA from DNA. Define $A_{\tau_M} := A(t - \tau_M)$.

ODE for mRNA (M)

$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1 (e^{\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$

Justification:

- $\tilde{\gamma}_M M = \gamma_M M + \mu M$ represents loss due to mRNA degredation and dilution from bacterial growth.
- Production rate of mRNA is proportional to fraction of free operator sites,

$$\frac{[O]}{O_{tot}} = \frac{1 + K_1[A]^n}{1 + K_1[A]^n} = f([A]).$$

- The constant $\tau_M > 0$ represents the time-delay due to transcription of mRNA from DNA. Define $A_{\tau_M} := A(t \tau_M)$.
- The term $e^{-\mu\tau_M}A_{\tau_M}$ accounts for the concentration of A at time $t \tau_M$, and dilution due to bacterial growth.

ODE for allolactose (A)

$$\frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

ODE for allolactose (A)

$$\frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

Justification:

• $\tilde{\gamma}_A A = \gamma_A A + \mu A$ represents loss due to allolactose degredation and dilution from bacterial growth.

ODE for allolactose (A)

$$\frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

Justification:

- $\tilde{\gamma}_A A = \gamma_A A + \mu A$ represents loss due to allolactose degredation and dilution from bacterial growth.
- The first term models production of allolactose from the chemical reaction $lac \stackrel{\beta-gal}{\longrightarrow} allo$.

ODE for allolactose (A)

$$\frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

Justification:

- $\tilde{\gamma}_A A = \gamma_A A + \mu A$ represents loss due to allolactose degredation and dilution from bacterial growth.
- The first term models production of allolactose from the chemical reaction $lac \stackrel{\beta-gal}{\longrightarrow} allo$.
- The second term models loss of allolactose from the chemical reaction allo β-gal glucose & galactose.

Steady-state analysis

Steady-state analysis

To find the steady states, we must solve the nonlinear system of equations:

$$0 = \alpha_M \frac{1 + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$

$$0 = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B$$

$$0 = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

Steady-state analysis

To find the steady states, we must solve the nonlinear system of equations:

$$0 = \alpha_M \frac{1 + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$

$$0 = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B$$

$$0 = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

This was done by Yildirim et al. (2004). They set $L = 50 \times 10^{-3}$ mM, which was in the "bistable range."

Steady-state analysis

To find the steady states, we must solve the nonlinear system of equations:

$$0 = \alpha_M \frac{1 + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$

$$0 = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B$$

$$0 = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

This was done by Yildirim et al. (2004). They set $L = 50 \times 10^{-3}$ mM, which was in the "bistable range."

They also estimated the parameters through an extensive literature search.
Steady-state analysis

To find the steady states, we must solve the nonlinear system of equations:

$$0 = \alpha_M \frac{1 + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$

$$0 = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B$$

$$0 = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

This was done by Yildirim et al. (2004). They set $L = 50 \times 10^{-3}$ mM, which was in the "bistable range."

They also estimated the parameters through an extensive literature search.

Finally, they estimated $\mu=3.03\times 10^{-2}~{\rm min}^{-1}$ by fitting the ODE models to experimental data.

Steady-state analysis

To find the steady states, we must solve the nonlinear system of equations:

$$0 = \alpha_M \frac{1 + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu \tau_M} A_{\tau_M})^n} - \widetilde{\gamma}_M M$$

$$0 = \alpha_B e^{-\mu \tau_B} M_{\tau_B} - \widetilde{\gamma}_B B$$

$$0 = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

This was done by Yildirim et al. (2004). They set $L = 50 \times 10^{-3}$ mM, which was in the "bistable range."

They also estimated the parameters through an extensive literature search.

Finally, they estimated $\mu=3.03\times 10^{-2}~{\rm min}^{-1}$ by fitting the ODE models to experimental data.

Steady states	<i>A</i> * (mM)	<i>M</i> * (mM)	<i>B</i> * (mM)
Ι.	4.27×10^{-3}	4.57×10^{-7}	2.29×10^{-7}
II.	$1.16 imes 10^{-2}$	$1.38 imes10^{-6}$	$6.94 imes10^{-7}$
III.	$6.47 imes 10^{-2}$	$3.28 imes10^{-5}$	$1.65 imes 10^{-5}$



Figure: Bistability is (L, A^*) space. The *y*-axis is in logarithmic scale. For a range of *L* concentrations there are three coexisting steady states for the allolactose concentration.



Figure: Time series simulations of mRNA, β -galactosidase and allolactose concentrations. These were produced by numerically solving the 3-variable model using $L = 50 \times 10^{-3}$ mM, which is in the bistable region.

Consider the following 5 variables, which represent concentrations of:

- M(t) = mRNA,
- $B(t) = \beta$ -galactosidase,
- A(t) =allolactose.
- P(t) = lac permease.
- L(t) = intracellular lactose.

Consider the following 5 variables, which represent concentrations of:

- $\blacksquare M(t) = \mathsf{mRNA},$
- $B(t) = \beta$ -galactosidase,
- A(t) =allolactose.
- P(t) = lac permease.
- L(t) = intracellular lactose.

The model (Yildirim and Mackey, 2004)

$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1 (e^{-\mu\tau_M} A_{\tau_M})^n}{K + K_1 (e^{-\mu\tau_M} A_{\tau_M})^n} + \Gamma_0 - \widetilde{\gamma}_M M$$

$$\frac{dB}{dt} = \alpha_B e^{-\mu\tau_B} M_{\tau_B} - \widetilde{\gamma}_B B$$

$$\frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{A}{K_A + A} - \widetilde{\gamma}_A A$$

$$\frac{dP}{dt} = \alpha_P e^{-\mu(\tau_B + \tau_P)} M_{\tau_B + \tau_P} - \widetilde{\gamma}_P P$$

$$\frac{dL}{dt} = \alpha_L P \frac{L_e}{K_{L_e} + L_e} - \beta_{L_e} P \frac{L}{K_{L_e} + L} - \alpha_A B \frac{L}{K_L + L} - \widetilde{\gamma}_L L$$

Remarks

The only difference in the ODE for *M* is the extra term Γ₀ which describes the basal transcription rate (in the absence of extracellular lactose).

- The only difference in the ODE for M is the extra term Γ_0 which describes the basal transcription rate (in the absence of extracellular lactose).
- The ODEs for *B* and *A* are the same as in the 3-variable model.

- The only difference in the ODE for M is the extra term Γ_0 which describes the basal transcription rate (in the absence of extracellular lactose).
- The ODEs for *B* and *A* are the same as in the 3-variable model.
- The ODE for *P* is very similar to the one for *B*:

- The only difference in the ODE for M is the extra term Γ_0 which describes the basal transcription rate (in the absence of extracellular lactose).
- The ODEs for *B* and *A* are the same as in the 3-variable model.
- The ODE for *P* is very similar to the one for *B*:
 - production rate of *lac* permease is proportional to mRNA concentration, with a time-delay.

- The only difference in the ODE for M is the extra term Γ_0 which describes the basal transcription rate (in the absence of extracellular lactose).
- The ODEs for *B* and *A* are the same as in the 3-variable model.
- The ODE for *P* is very similar to the one for *B*:
 - production rate of *lac* permease is proportional to mRNA concentration, with a time-delay.
 - the 2nd term accounts for loss due to degredation and dilution.

Remarks

- The only difference in the ODE for *M* is the extra term Γ₀ which describes the basal transcription rate (in the absence of extracellular lactose).
- The ODEs for *B* and *A* are the same as in the 3-variable model.
- The ODE for *P* is very similar to the one for *B*:
 - production rate of *lac* permease is proportional to mRNA concentration, with a time-delay.
 - the 2nd term accounts for loss due to degredation and dilution.
- The ODE for lactose,

$$\frac{dL}{dt} = \alpha_L P \frac{L_e}{K_{L_e} + L_e} - \beta_{L_e} P \frac{L}{K_{L_1} + L} - \alpha_A B \frac{L}{K_L + L} - \widetilde{\gamma}_L L,$$

is justified by the following:

Remarks

- The only difference in the ODE for *M* is the extra term Γ₀ which describes the basal transcription rate (in the absence of extracellular lactose).
- The ODEs for *B* and *A* are the same as in the 3-variable model.
- The ODE for *P* is very similar to the one for *B*:
 - production rate of *lac* permease is proportional to mRNA concentration, with a time-delay.
 - the 2nd term accounts for loss due to degredation and dilution.
- The ODE for lactose,

$$\frac{dL}{dt} = \alpha_L P \frac{L_e}{K_{L_e} + L_e} - \beta_{L_e} P \frac{L}{K_{L_1} + L} - \alpha_A B \frac{L}{K_L + L} - \widetilde{\gamma}_L L,$$

is justified by the following:

The 1st term models gain due to transport of external lactose by *lac* permease.

Remarks

- The only difference in the ODE for *M* is the extra term Γ₀ which describes the basal transcription rate (in the absence of extracellular lactose).
- The ODEs for *B* and *A* are the same as in the 3-variable model.
- The ODE for *P* is very similar to the one for *B*:
 - production rate of *lac* permease is proportional to mRNA concentration, with a time-delay.
 - the 2nd term accounts for loss due to degredation and dilution.
- The ODE for lactose,

$$\frac{dL}{dt} = \alpha_L P \frac{L_e}{K_{L_e} + L_e} - \beta_{L_e} P \frac{L}{K_{L_1} + L} - \alpha_A B \frac{L}{K_L + L} - \widetilde{\gamma}_L L,$$

is justified by the following:

- The 1st term models gain due to transport of external lactose by *lac* permease.
- The 2nd term accounts for loss due to this process being reversible.

Remarks

- The only difference in the ODE for *M* is the extra term Γ₀ which describes the basal transcription rate (in the absence of extracellular lactose).
- The ODEs for *B* and *A* are the same as in the 3-variable model.
- The ODE for *P* is very similar to the one for *B*:
 - production rate of *lac* permease is proportional to mRNA concentration, with a time-delay.
 - the 2nd term accounts for loss due to degredation and dilution.
- The ODE for lactose,

$$\frac{dL}{dt} = \alpha_L P \frac{L_e}{K_{L_e} + L_e} - \beta_{L_e} P \frac{L}{K_{L_1} + L} - \alpha_A B \frac{L}{K_L + L} - \widetilde{\gamma}_L L,$$

is justified by the following:

- The 1st term models gain due to transport of external lactose by *lac* permease.
- The 2nd term accounts for loss due to this process being reversible.
- The 3rd term describes loss due to $lac \xrightarrow{\beta-gal} allo$.

- The only difference in the ODE for *M* is the extra term Γ₀ which describes the basal transcription rate (in the absence of extracellular lactose).
- The ODEs for *B* and *A* are the same as in the 3-variable model.
- The ODE for *P* is very similar to the one for *B*:
 - production rate of *lac* permease is proportional to mRNA concentration, with a time-delay.
 - the 2nd term accounts for loss due to degredation and dilution.
- The ODE for lactose,

$$\frac{dL}{dt} = \alpha_L P \frac{L_e}{K_{L_e} + L_e} - \beta_{L_e} P \frac{L}{K_{L_1} + L} - \alpha_A B \frac{L}{K_L + L} - \widetilde{\gamma}_L L,$$

- is justified by the following:
 - The 1st term models gain due to transport of external lactose by *lac* permease.
 - The 2nd term accounts for loss due to this process being reversible.
 - The 3rd term describes loss due to $lac \xrightarrow{\beta-gal} allo$.
 - the 4th term accounts for loss due to degredation and dilution.

To find the steady states, we set M' = A' = B' = L' = P' = 0 and solve the resulting nonlinear system of equations.

To find the steady states, we set M' = A' = B' = L' = P' = 0 and solve the resulting nonlinear system of equations.

This was done by Yildirim et al. (2004). They set $L_e = 50 \times 10^{-3}$ mM, which was in the "bistable range."

To find the steady states, we set M' = A' = B' = L' = P' = 0 and solve the resulting nonlinear system of equations.

This was done by Yildirim et al. (2004). They set $L_e = 50 \times 10^{-3}$ mM, which was in the "bistable range."

They also estimated the parameters through an extensive literature search.

To find the steady states, we set M' = A' = B' = L' = P' = 0 and solve the resulting nonlinear system of equations.

This was done by Yildirim et al. (2004). They set $L_e = 50 \times 10^{-3}$ mM, which was in the "bistable range."

They also estimated the parameters through an extensive literature search.

Finally, they estimated $\mu = 2.26 \times 10^{-2} \text{ min}^{-1}$ by fitting the ODE models to experimental data.

To find the steady states, we set M' = A' = B' = L' = P' = 0 and solve the resulting nonlinear system of equations.

This was done by Yildirim et al. (2004). They set $L_e = 50 \times 10^{-3}$ mM, which was in the "bistable range."

They also estimated the parameters through an extensive literature search.

Finally, they estimated $\mu = 2.26 \times 10^{-2} \text{ min}^{-1}$ by fitting the ODE models to experimental data.

SS's	A* (nM)	<i>M</i> * (mM)	<i>B</i> * (mM)	<i>L</i> * (mM)	<i>P</i> * (mM)
Ι.	$7.85 imes 10^{-3}$	$2.48 imes 10^{-6}$	$1.68 imes 10^{-6}$	$1.69 imes 10^{-1}$	$3.46 imes 10^{-5}$
II.	2.64×10^{-2}	$7.58 imes 10^{-6}$	$5.13 imes10^{-6}$	2.06×10^{-1}	$1.05 imes 10^{-4}$
III.	$3.10 imes 10^{-1}$	$5.80 imes 10^{-4}$	$3.92 imes 10^{-4}$	2.30×10^{-1}	$8.09 imes 10^{-3}$



Figure: Bistability is (L, A^*) space. The y-axis is in logarithmic scale. For a range of L_e concentrations there are three coexisting steady states for the allolactose concentration.

5-variable ODE model



Figure: Time series simulations of mRNA, β -galactosidase and allolactose concentrations. These were produced by numerically solving the 3-variable model using $L_e = 50 \times 10^{-3}$, which is in the bistable region.

M. Macauley (Clemson)