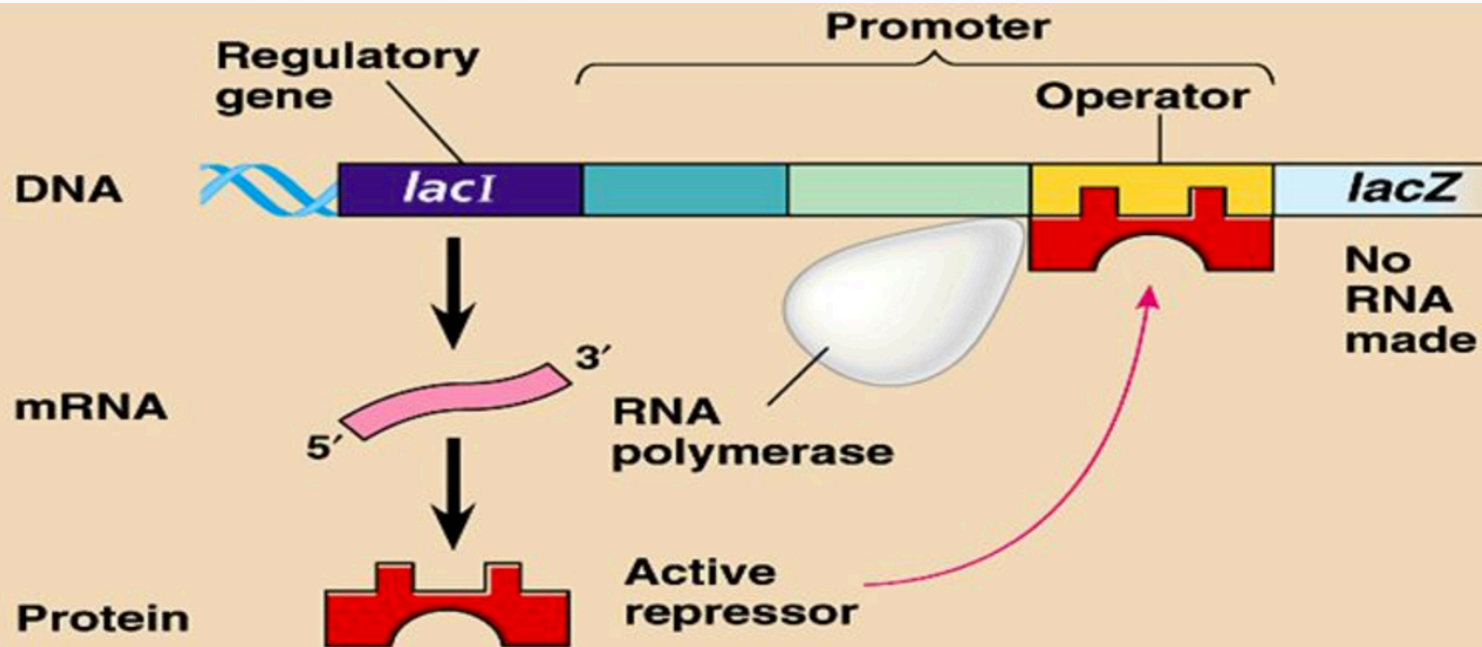


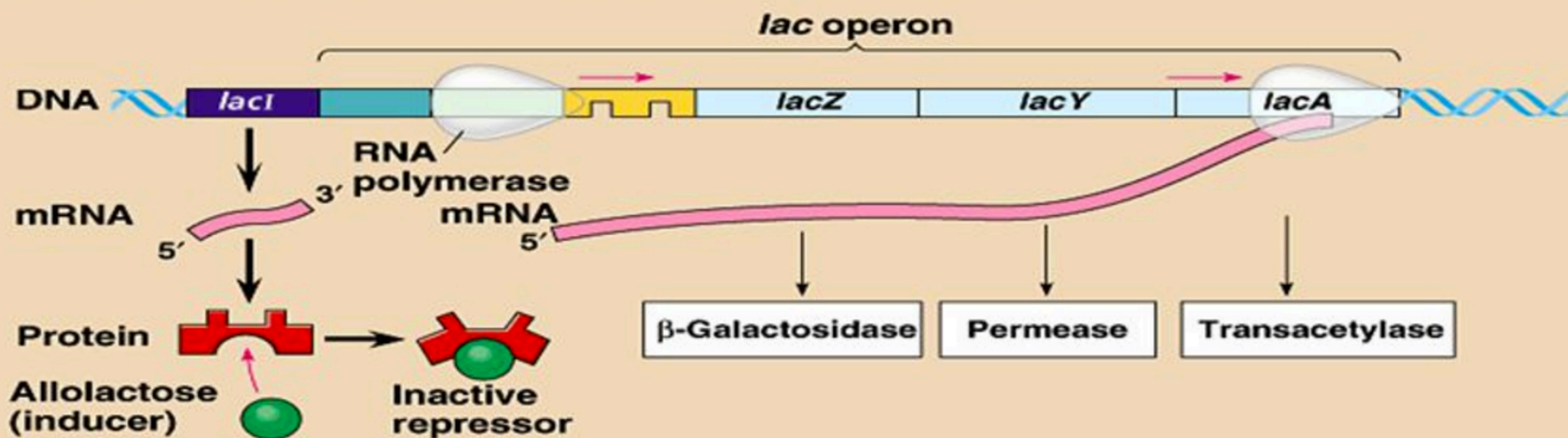
# The *lac* operon in *E. coli*

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# The *lac* operon



(a) Lactose absent, repressor active, operon off



(b) Lactose present, repressor inactive, operon on

# *lac* operon, with lactose present

- Lactose is brought into the cell by the *lac* permease transporter protein
- $\beta$ -galactosidase breaks up lactose into glucose and galactose..
- $\beta$ -galactosidase also converts lactose into allolactose.
- Allolactose binds to the *lac* repressor protein, preventing it from binding to the operator region of the genome.
- Transcription continues: mRNA encoding the *lac* genes is produced.
- Lac proteins are produced, and more lactose is brought into the cell. (The operon is ON.)
- Eventually, all lactose is used up, so there will be no more allolactose.
- The *lac* repressor can now bind to the operator, so mRNA transcription stops. (The operon has turned itself OFF.)

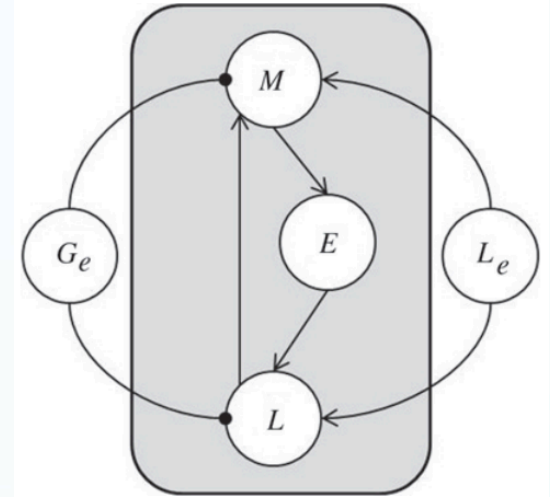
# Our first simple Boolean model

- At the bare minimum, we should expect:
  - Lactose absent => operon OFF.
  - Lactose present, glucose absent => operon ON.
  - Lactose and glucose present => operon OFF.

$$x_M(t+1) = f_M(t+1) = \overline{G_e} \wedge (L(t) \vee L_e)$$

$$x_E(t+1) = f_E(t+1) = M(t)$$

$$x_L(t+1) = f_L(t+1) = \overline{G_e} \wedge [(L_e \wedge E(t)) \vee (L(t) \wedge \overline{E(t)})]$$



- The state space (or phase space) is the directed graph  $(V, T)$ , where

$$V = \{(x_M, x_E, x_L) : x_i \in \{0,1\}\} \quad T = \{(x, f(x)) : x \in V\}$$

- We drew the state space for all four choices of the parameters:
  - $(L_e, G_e) = (0, 0)$ . Every state ended up in the “OFF” fixed point  $(0,0,0)$ .
  - $(L_e, G_e) = (0, 1)$ . Every state ended up in the “OFF” fixed point  $(0,0,0)$ .
  - $(L_e, G_e) = (1, 0)$ . Every state ended up in the “ON” fixed point  $(1,1,1)$ .
  - $(L_e, G_e) = (1, 1)$ . Every state ended up in the “OFF” fixed point  $(0,0,0)$ .

# A more refined model

- Our model only used 3 variables: mRNA (M), enzyme (E), and lactose (L).
- Let's propose a new model with 5 variables:
  - M: mRNA
  - B:  $\beta$ -galactosidase
  - A: allolactose
  - L: intracellular lactose
  - P: *lac* permease (transporter protein)
- Assumptions
  - Translation and transcription require one unit of time.
  - Protein and mRNA degradation require one unit of time
  - Lactose metabolism require one unit of time
  - Extracellular lactose is always available.
  - Extracellular glucose is always unavailable.

$$f_M = A$$

$$f_B = M$$

$$f_A = A \vee (L \wedge B)$$

$$f_L = P \vee (L \wedge \bar{B})$$

$$f_P = M$$

# Using ADAM to compute the state space

$$f_M = A$$

$$f_B = M$$

$$f_A = A \vee (L \wedge B)$$

$$f_L = P \vee (L \wedge \bar{B})$$

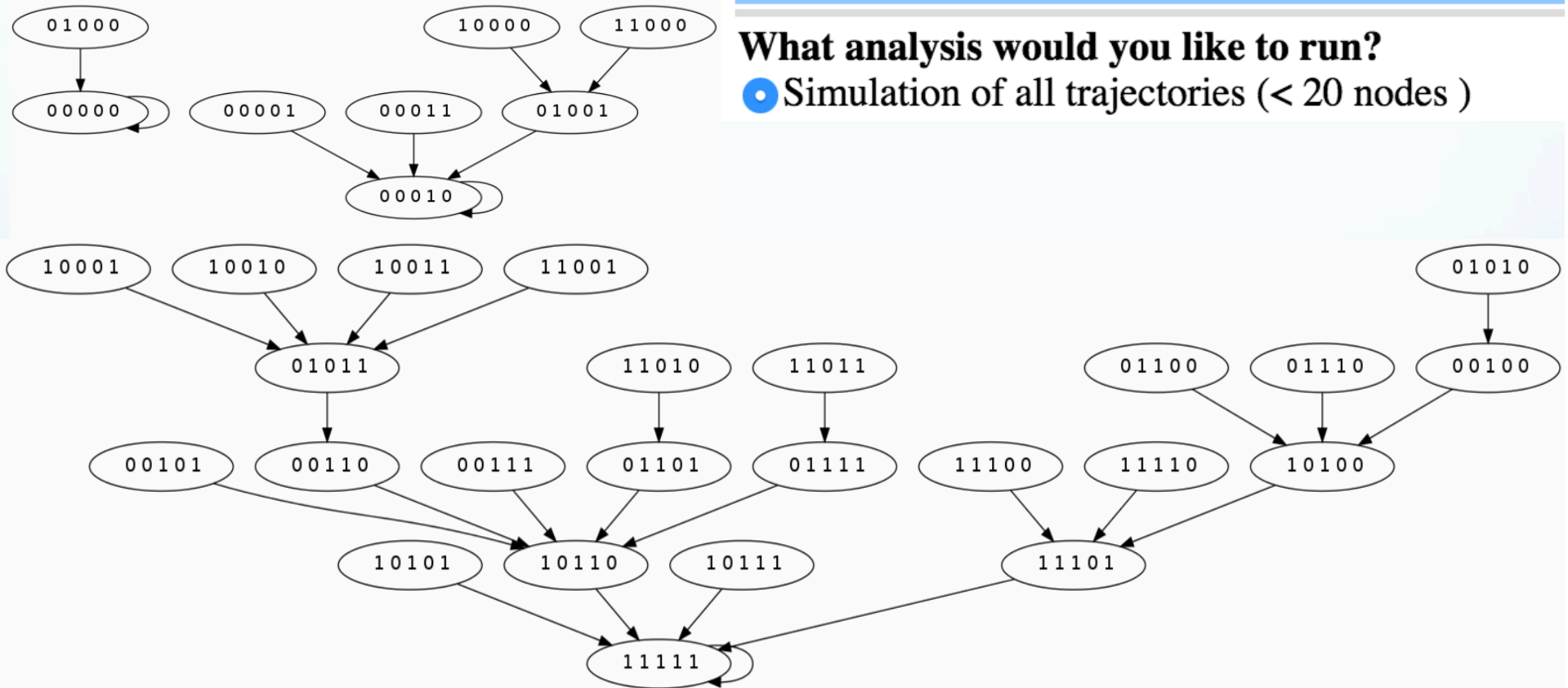
$$f_P = M$$

```
f1 = x3
f2 = x1
f3 = x3+x4*x2+x3*x4*x2
f4 = x5+x4*(1+x2)+x5*x4*(1+x2)
f5 = x1
```

4)

**What analysis would you like to run?**

- Simulation of all trajectories (< 20 nodes )



# Problems with our refined model

- Model variables:

- M: mRNA
- B:  $\beta$ -galactosidase
- A: allolactose
- L: intracellular lactose
- P: *lac* permease (transporter protein)

$$f_M = A$$

$$f_B = M$$

$$f_A = A \vee (L \wedge B)$$

$$f_L = P \vee (L \wedge \bar{B})$$

$$f_P = M$$

- Problems:

- The fixed point  $(M,B,A,L,P) = (0,0,0,0,0)$  should not happen with lactose present but not glucose. [though let's try to justify this...]
- The fixed point  $(M,B,A,L,P) = (0,0,0,1,0)$  is not biologically feasible: it would describe a scenario where the bacterium does not metabolize intracellular lactose.

- Conclusion: *The model fails the initial testing and validation, and is in need of modification.* (Homework!)

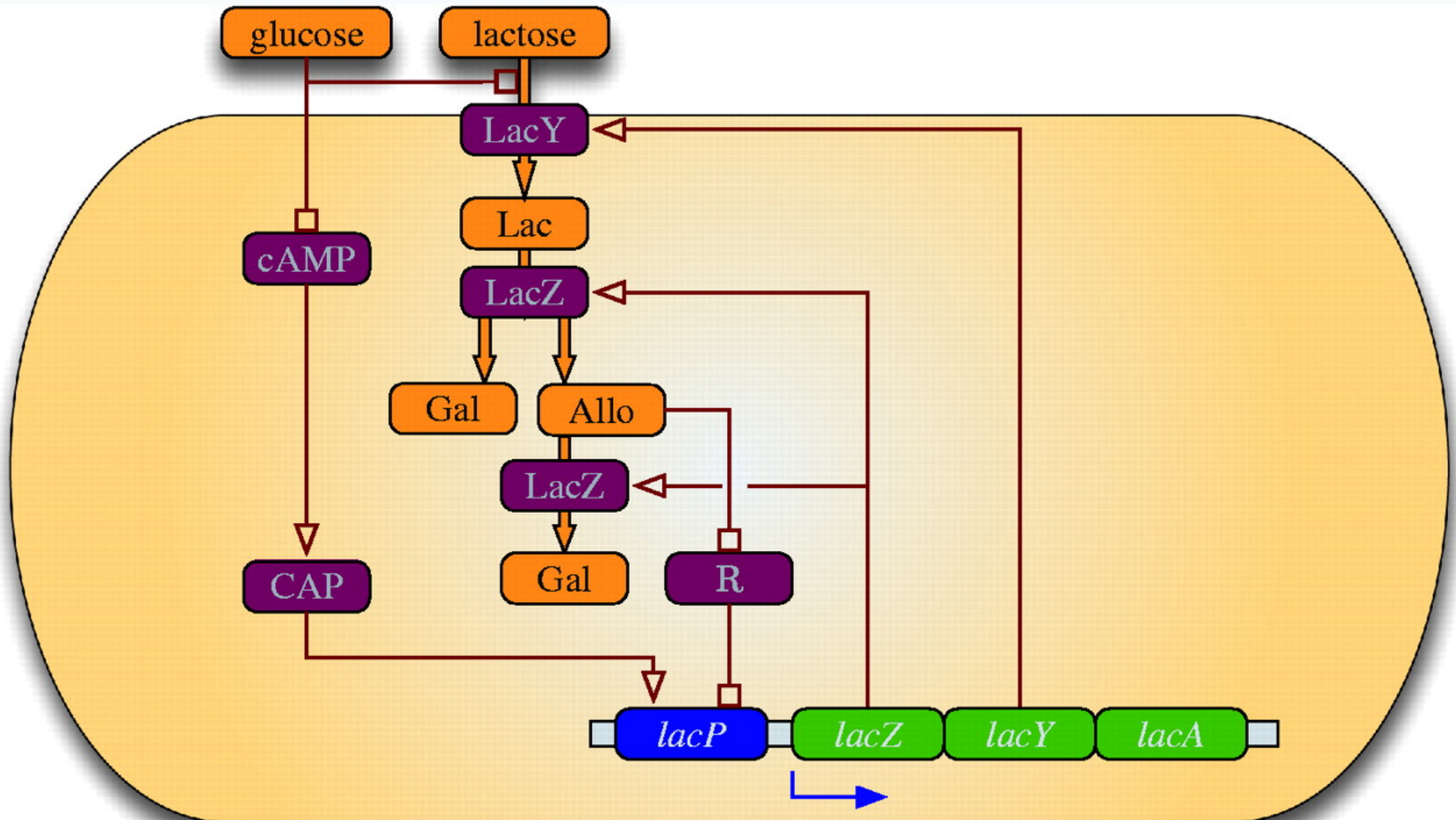


# Catabolite repression

- We haven't yet discussed the cellular mechanism that turns the *lac* operon OFF when both glucose and lactose are present. This is done by **catabolite repression**.
- The *lac* operon promoter region has **2 binding sites**:
  - One for RNA polymerase (this “unzips” and reads the DNA)
  - One for the **CAP-cAMP** complex. This is a complex of two molecules: catabolite activator protein (CAP), and the **cyclic AMP receptor protein** (cAMP, or *crp*).
- Binding of the CAP-cAMP complex is required for transcription for the *lac* operon.
- Intracellular glucose causes the cAMP concentration to decrease.
- When cAMP levels get too low, so do CAP-cAMP complex levels.
- Without the CAP-cAMP complex, the promoter is inactivated, and the *lac* operon is OFF.



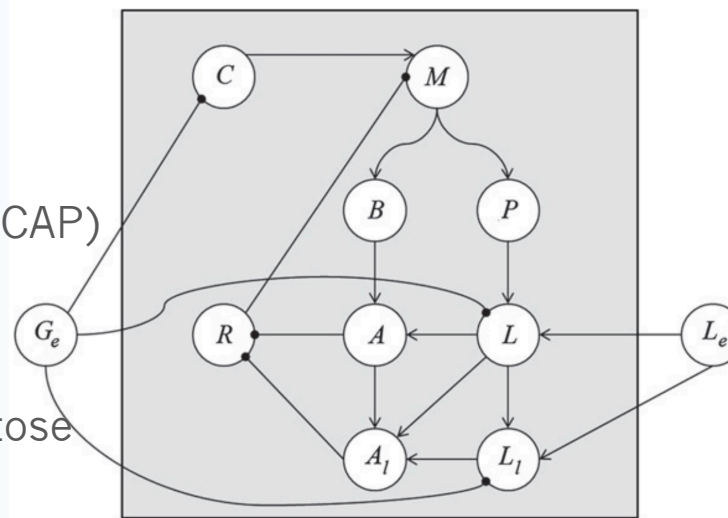
# Lac operon gene regulatory network



# A more refined model

- Variables:

- M: mRNA
- P: *lac* permease
- B:  $\beta$ -galactosidase
- C: catabolite activator protein (CAP)
- R: repressor protein (LacI)
- A: allolactose
- $A_l$ : at least low levels of allolactose
- L: intracellular lactose
- $L_l$ : at least low levels of intracellular lactose



$$f_M = \bar{R} \wedge C$$

$$f_P = M$$

$$f_B = M$$

$$f_C = \bar{G}_e$$

$$f_R = \bar{A} \wedge \bar{A}_l$$

$$f_A = L \wedge B$$

$$f_{A_l} = A \vee L \vee L_l$$

$$f_L = \bar{G}_e \wedge P \wedge L_e$$

$$f_{L_l} = \bar{G}_e \wedge (L \vee L_e)$$

- Assumptions:

- Transcription and translation require one unit of time.
- Degradation of all mRNA and proteins occur in one time-step.
- High levels of lactose or allolactose at any time  $t$  imply at least low levels for the next time-step  $t+1$ .

# A more refined model

- This 9-variable model is about as big as ADAM can render a state space.
- In fact, it doesn't work using the "Open Polynomial Dynamical System (oPDS)" option (variables + parameters).
- Instead, it works under "Polynomial Dynamical System (PDS)", if we manually enter numbers for the parameters.
- Here's a sample piece of the state space:

$$f_M = \bar{R} \wedge C$$

$$f_P = M$$

$$f_B = M$$

$$f_C = \bar{G}_e$$

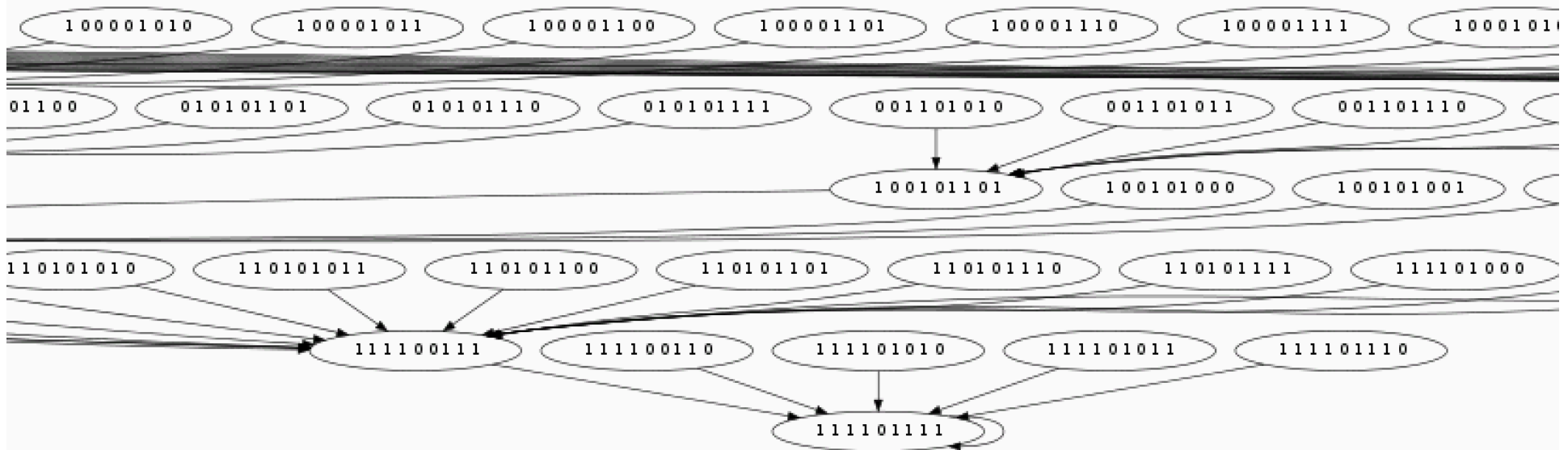
$$f_R = \bar{A} \wedge \bar{A}_l$$

$$f_A = L \wedge B$$

$$f_{A_l} = A \vee L \vee L_l$$

$$f_L = \bar{G}_e \wedge P \wedge L_e$$

$$f_{L_l} = \bar{G}_e \wedge (L \vee L_e)$$



# What if the state space is too big?

- The previous 9-variable model is about as big as ADAM can handle.
- However, many gene regulatory networks are much bigger.
  - A Boolean network model (2006) of T helper cell differentiation has 23 nodes, and thus a state space of size  $2^{23} = 8,388,608$ .
  - A Boolean network model (2003) of the segment polarity genes in *Drosophila melanogaster* (fruit fly) has 60 nodes, and a state space of size  $2^{60} \approx 1.15 \times 10^{18}$ .
  - There are many more examples...
- For systems like these, we would like to be able to analyze them without actually constructing the entire state space.
- One of the first goals is how to find the fixed points. This amounts to solving a system of equations:

$$\begin{cases} f_{x_1} = x_1 \\ f_{x_2} = x_2 \\ \vdots \\ f_{x_n} = x_n \end{cases}$$

$$f_M = \bar{R} \wedge C$$

$$f_P = M$$

$$f_B = M$$

$$f_C = \bar{G}_e$$

$$f_R = \bar{A} \wedge \bar{A}_l$$

$$f_A = L \wedge B$$

$$f_{A_l} = A \vee L \vee L_l$$

$$f_L = \bar{G}_e \wedge P \wedge L_e$$

$$f_{L_l} = \bar{G}_e \wedge (L \vee L_e)$$

# How to find the fixed points

- Let's rename variables:  $(M, P, B, C, R, A, A_l, L, L_l) = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9)$
- Writing each function in polynomial form, and then  $f_{x_i} = x_i$  for each  $i=1, \dots, 9$  yields the following system:

$$\begin{array}{l}
 f_M = \bar{R} \wedge C = M \\
 f_P = M = P \\
 f_B = M = B \\
 f_C = \bar{G}_e = C \\
 f_R = \bar{A} \wedge \bar{A}_l = R \\
 f_A = L \wedge B = A \\
 f_{A_l} = A \vee L \vee L_l = A_l \\
 f_L = \bar{G}_e \wedge P \wedge L_e = L \\
 f_{L_l} = \bar{G}_e \wedge (L \vee L_e) = L_l
 \end{array}
 \left\{ \begin{array}{l}
 x_1 + x_4 x_5 + x_4 = 0 \\
 x_1 + x_2 = 0 \\
 x_1 + x_3 = 0 \\
 x_4 + (G_e + 1) = 0 \\
 x_5 + x_6 x_7 + x_6 + x_7 + 1 = 0 \\
 x_6 + x_3 x_8 = 0 \\
 x_6 + x_7 + x_8 + x_9 + x_8 x_9 + x_6 x_8 + x_6 x_9 + x_6 x_8 x_9 = 0 \\
 x_8 + x_2 L_e (G_e + 1) = 0 \\
 x_9 + (G_e + 1)(x_8 + x_8 L_e + L_e) = 0
 \end{array} \right.$$

- We need to solve this for all 4 combinations:  $(G_e, L_e) = (0, 0), (0, 1), (1, 0), (1, 1)$

# How to find the fixed points

- Let's first consider the case when  $(G_e, L_e) = (1, 1)$
- We can solve the system by typing the following commands into Sage (<https://cloud.sagemath.com/>), the free open-source mathematical software:

```
1
2 P.<x1,x2,x3,x4,x5,x6,x7,x8,x9> = PolynomialRing(GF(2), 9, order='lex'); P
3     Multivariate Polynomial Ring in x1, x2, x3, x4, x5, x6, x7, x8, x9 over Finite Field of size 2
4
5 Le=1;
6 Ge=1;
7 print "Le =", Le;
8 print "Ge =", Ge;
9
9     Le = 1
10    Ge = 1
11
12 I = ideal(x1+x4*x5+x4, x1+x2, x1+x3, x4+(Ge+1), x5+x6*x7+x6+x7+1, x6+x3*x8,
13 x6+x7+x8+x9+x8*x9+x6*x8+x6*x9+x6*x8*x9, x8+Le*(Ge+1)*x2, x9+(Ge+1)*(Le+x8+Le*x8)); I
14
15 Ideal (x1 + x4*x5 + x4, x1 + x2, x1 + x3, x4, x5 + x6*x7 + x6 + x7 + 1, x3*x8 + x6, x6*x8*x9 +
16 x6*x8 + x6*x9 + x6 + x7 + x8*x9 + x8 + x9, x8, x9) of Multivariate Polynomial Ring in x1, x2,
17 x3, x4, x5, x6, x7, x8, x9 over Finite Field of size 2
18
19 B = I.groebner_basis(); B
20
21 [x1, x2, x3, x4, x5 + 1, x6, x7, x8, x9]
```



# What those Sage commands mean

Let's go over what the following commands mean:

- `P.<x1,x2,x3,x4,x5,x6,x7,x8,x9> = PolynomialRing(GF(2),9,order='lex');`
  - Define P to be **the polynomial ring** over 9 variables,  $x_1, \dots, x_9$ .
  - $\text{GF}(2) = \{0,1\}$ , and so the coefficients are binary.
  - `order='lex'` specifies a **monomial order**. More on this later.

- `Le=1; Ge=1; print "Le =", Le; print "Ge =", Ge;`
  - This defines two constants  $(G_e, L_e) = (1, 1)$  and prints them.

- `I = ideal(x1+x4*x5+x4, x1+x2, x1+x3, x4+(Ge+1), x5+x6*x7+x6+x7+1, x6+x3*x8, x6+x7+x8+x9+x8*x9+x6*x8+x6*x9+x6*x8*x9, x8+Le*(Ge+1)*x2, x9+(Ge+1)*(Le+x8+Le*x8)); I`
  - Defines I to be the **ideal** generated by those following 9 polynomials, i.e.,

$$I = \{p_1 f_1 + \dots + p_k f_k : p_k \in P\}$$

- `B = I.groebner_basis(); B`
  - Define B to be the **Gröbner basis** of I w.r.t. the **lex monomial order**. (More on this later)



# What does a Gröbner basis tell us?

The output of `B = I.groebner_basis();` B is the following:

$$[x_1, x_2, x_3, x_4, x_5+1, x_6, x_7, x_8, x_9]$$

This is short-hand for the following system of equations:

$$\{x_1 = 0, x_2 = 0, x_3 = 0, x_4 = 0, x_5 + 1 = 0, x_6 = 0, x_7 = 0, x_8 = 0, x_9 = 0\}$$

This simple system has the **same set of solutions** as the much more complicated system we started with:

$$\left\{ \begin{array}{l} x_1 + x_4 x_5 + x_4 = 0 \\ x_1 + x_2 = 0 \\ x_1 + x_3 = 0 \\ x_4 + (G_e + 1) = 0 \\ x_5 + x_6 x_7 + x_6 + x_7 + 1 = 0 \\ x_6 + x_3 x_8 = 0 \\ x_6 + x_7 + x_8 + x_9 + x_8 x_9 + x_6 x_8 + x_6 x_9 + x_6 x_8 x_9 = 0 \\ x_8 + x_2 L_e (G_e + 1) = 0 \\ x_9 + (G_e + 1)(x_8 + x_8 L_e + L_e) = 0 \end{array} \right.$$

# Gröbner bases vs. Gaussian elimination

✧ Gröbner bases are a generalization of Gaussian elimination, but for systems of polynomials (instead of systems of linear equations)

✧ In both cases:

- The input is a complicated system that we wish to solve.
- The output is a simple system that we can easily solve by inspection.

✧ Consider the following example:

- Input: The 2x2 system of linear equations 
$$\begin{cases} x + 2y = 1 \\ 3x + 8y = 1 \end{cases}$$
- Gaussian elimination yields the following:

$$\left[ \begin{array}{cc|c} 1 & 2 & 1 \\ 3 & 8 & 1 \end{array} \right] \rightarrow \left[ \begin{array}{cc|c} 1 & 2 & 1 \\ 0 & 2 & -2 \end{array} \right] \rightarrow \left[ \begin{array}{cc|c} 1 & 0 & 3 \\ 0 & 2 & -2 \end{array} \right] \rightarrow \left[ \begin{array}{cc|c} 1 & 0 & 3 \\ 0 & 1 & -1 \end{array} \right]$$

- This is just the much simpler system with the same solution! 
$$\begin{cases} x + 0y = 3 \\ 0x + y = -1 \end{cases}$$

# Back-substitution & Gaussian elimination

- ✧ Note that we don't necessarily need to do Gaussian elimination until the matrix is the identity. As long as it is **upper-triangular**, we can back-substitute and solve by hand.

- ✧ For example: 
$$\begin{cases} x + z = 2 \\ y - z = 8 \\ 0 = 0 \end{cases}$$

- ✧ Similarly, when Sage outputs a Gröbner basis, it will be in “upper-triangular form”, and we can solve the system easily by back-substituting.
- ✧ We'll do an example right away. For this part of the class, you can think of Gröbner bases as a mysterious “**black box**” that does what we want.
- ✧ We'll study them in more detail shortly, and understand what's going on behind the scenes.

# Gröbner bases: an example

✧ Let's use Sage to solve the following system:

$$\begin{cases} x^2 + y^2 + z^2 = 1 \\ x^2 - y + z^2 = 0 \\ x - z = 0 \end{cases}$$

```
17 P.<x,y,z>=PolynomialRing(RR,3,order='lex'); P
18      Multivariate Polynomial Ring in x, y, z over Real Field with 53 bits of precision
19
20 I = ideal(x^2+y^2+z^2-1, x^2-y+z^2, x-z); I
21      Ideal (x^2 + y^2 + z^2 - 1.000000000000000, x^2 - y + z^2, x - z) of Multivariate Polynomial
      Ring in x, y, z over Real Field with 53 bits of precision
22
23 B = I.groebner_basis(); B
24      [x - z, y - 2.000000000000000*z^2, z^4 + 0.500000000000000*z^2 - 0.250000000000000]
```

✧ From this, we get an “upper-triangular” system:

✧ This is something we can solve by hand.

$$\begin{cases} x - z = 0 \\ y - 2z^2 = 0 \\ z^4 + .5z^2 - .25 = 0 \end{cases}$$

## Gröbner bases: an example (cont.)

✧ To solve the reduced system:

$$\begin{cases} x - z = 0 \\ y - 2z^2 = 0 \\ z^4 + .5z^2 - .25 = 0 \end{cases}$$

▪ Solve for  $z$  in Eq. 3:  $z = \pm \sqrt{\frac{-1 + \sqrt{5}}{4}}$

▪ Plug  $z$  into Eq. 2 and solve for  $y$ :  $y = 2z^2 = \frac{-1 + \sqrt{5}}{2}$

▪ Plug  $y$  &  $z$  into Eq. 1 and solve for  $x$ :  $z = \pm \sqrt{\frac{-1 + \sqrt{5}}{4}}$

✧ Thus, we get 2 solutions to the original system:

$$\begin{cases} x^2 + y^2 + z^2 = 1 \\ x^2 - y + z^2 = 0 \\ x - z = 0 \end{cases}$$

$$(x_1, y_1, z_1) = \left( \sqrt{\frac{-1 + \sqrt{5}}{4}}, \frac{-1 + \sqrt{5}}{2}, \sqrt{\frac{-1 + \sqrt{5}}{4}} \right)$$

$$(x_2, y_2, z_2) = \left( -\sqrt{\frac{-1 + \sqrt{5}}{4}}, \frac{-1 + \sqrt{5}}{2}, -\sqrt{\frac{-1 + \sqrt{5}}{4}} \right)$$

# Returning to the *lac* operon

- We have 9 variables:  $(M, P, B, C, R, A, A_l, L, L_l) = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9)$
- Writing each function in polynomial form, we need to solve the system  $f_{x_i} = x_i$  for each  $i=1, \dots, 9$ , which is the following:

$$\begin{array}{l}
 f_M = \bar{R} \wedge C = M \\
 f_P = M = P \\
 f_B = M = B \\
 f_C = \bar{G}_e = C \\
 f_R = \bar{A} \wedge \bar{A}_l = R \\
 f_A = L \wedge B = A \\
 f_{A_l} = A \vee L \vee L_l = A_l \\
 f_L = \bar{G}_e \wedge P \wedge L_e = A_l \\
 f_{L_l} = \bar{G}_e \wedge (L \vee L_e) = L_l
 \end{array}
 \left\{ \begin{array}{l}
 x_1 + x_4 x_5 + x_4 = 0 \\
 x_1 + x_2 = 0 \\
 x_1 + x_3 = 0 \\
 x_4 + (G_e + 1) = 0 \\
 x_5 + x_6 x_7 + x_6 + x_7 + 1 = 0 \\
 x_6 + x_3 x_8 = 0 \\
 x_6 + x_7 + x_8 + x_9 + x_8 x_9 + x_6 x_8 + x_6 x_9 + x_6 x_8 x_9 = 0 \\
 x_8 + x_2 L_e (G_e + 1) = 0 \\
 x_9 + (G_e + 1)(x_8 + x_8 L_e + L_e) = 0
 \end{array} \right.$$

- We need to solve this for all 4 combinations:  $(G_e, L_e) = (0, 0), (0, 1), (1, 0), (1, 1)$  (we already did (1,1)).

# Returning to the *lac* operon

- Again, we use variables  $(M, P, B, C, R, A, A_l, L, L_l) = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9)$  and parameters  $(G_e, L_e) = (0, 0)$
- Here is the output from Sage:

```
1
2 P.<x1,x2,x3,x4,x5,x6,x7,x8,x9> = PolynomialRing(GF(2), 9, order = 'lex'); P
3   Multivariate Polynomial Ring in x1, x2, x3, x4, x5, x6, x7, x8, x9 over Finite Field of size 2
4
5 Le=0;
6 Ge=0;
7 print "Le =", Le;
8 print "Ge =", Ge;
9
9   Le = 0
   Ge = 0
10
11 I = ideal(x1+x4*x5+x4, x1+x2, x1+x3, x4+(Ge+1), x5+x6*x7+x6+x7+1, x6+x3*x8,
12 x6+x7+x8+x9+x8*x9+x6*x8+x6*x9+x6*x8*x9, x8+Le*(Ge+1)*x2, x9+(Ge+1)*(Le+x8+Le*x8)); I
13
12   Ideal (x1 + x4*x5 + x4, x1 + x2, x1 + x3, x4 + 1, x5 + x6*x7 + x6 + x7 + 1, x3*x8 + x6, x6*x8*x9 +
   x6*x8 + x6*x9 + x6 + x7 + x8*x9 + x8 + x9, x8, x8 + x9) of Multivariate Polynomial Ring in x1, x2
   , x3, x4, x5, x6, x7, x8, x9 over Finite Field of size 2
13
14 B = I.groebner_basis(); B
15
15   [x1, x2, x3, x4 + 1, x5 + 1, x6, x7, x8, x9]
```

- $(M, P, B, C, R, A, A_l, L, L_l) = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9) = (0, 0, 0, 1, 1, 0, 0, 0, 0)$



# Returning to the *lac* operon

- Again, we use variables  $(M, P, B, C, R, A, A_l, L, L_l) = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9)$  and parameters  $(G_e, L_e) = (1, 0)$
- Here is the output from Sage:

```
1 |
2 | P.<x1,x2,x3,x4,x5,x6,x7,x8,x9> = PolynomialRing(GF(2), 9, order = 'lex'); P
3 |   Multivariate Polynomial Ring in x1, x2, x3, x4, x5, x6, x7, x8, x9 over Finite Field of size 2
4 |
5 | Le=0;
6 | Ge=1;
7 | print "Le =", Le;
8 | print "Ge =", Ge;
9 |
9 |   Le = 0
9 |   Ge = 1
10 |
11 | I = ideal(x1+x4*x5+x4, x1+x2, x1+x3, x4+(Ge+1), x5+x6*x7+x6+x7+1, x6+x3*x8,
11 | x6+x7+x8+x9+x8*x9+x6*x8+x6*x9+x6*x8*x9, x8+Le*(Ge+1)*x2, x9+(Ge+1)*(Le+x8+Le*x8)); I
12 |
12 |   Ideal (x1 + x4*x5 + x4, x1 + x2, x1 + x3, x4, x5 + x6*x7 + x6 + x7 + 1, x3*x8 + x6, x6*x8*x9 +
12 | x6*x8 + x6*x9 + x6 + x7 + x8*x9 + x8 + x9, x8, x9) of Multivariate Polynomial Ring in x1, x2,
12 | x3, x4, x5, x6, x7, x8, x9 over Finite Field of size 2
13 |
14 | B = I.groebner_basis(); B
15 |
15 | [x1, x2, x3, x4, x5 + 1, x6, x7, x8, x9]
```

- $(M, P, B, C, R, A, A_l, L, L_l) = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9) = (0, 0, 0, 0, 1, 0, 0, 0, 0)$

# Returning to the *lac* operon

- Again, we use variables  $(M, P, B, C, R, A, A_l, L, L_l) = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9)$  and parameters  $(G_e, L_e) = (0, 1)$
- Here is the output from Sage:

```
1
2 P.<x1,x2,x3,x4,x5,x6,x7,x8,x9> = PolynomialRing(GF(2), 9, order = 'lex'); P
3   Multivariate Polynomial Ring in x1, x2, x3, x4, x5, x6, x7, x8, x9 over Finite Field of size 2
4
5 Le=0;
6 Ge=1;
7 print "Le =", Le;
8 print "Ge =", Ge;
9
10   Le = 0
11   Ge = 1
12
13 I = ideal(x1+x4*x5+x4, x1+x2, x1+x3, x4+(Ge+1), x5+x6*x7+x6+x7+1, x6+x3*x8,
14 x6+x7+x8+x9+x8*x9+x6*x8+x6*x9+x6*x8*x9, x8+Le*(Ge+1)*x2, x9+(Ge+1)*(Le+x8+Le*x8)); I
15
16   Ideal (x1 + x4*x5 + x4, x1 + x2, x1 + x3, x4, x5 + x6*x7 + x6 + x7 + 1, x3*x8 + x6, x6*x8*x9 +
17   x6*x8 + x6*x9 + x6 + x7 + x8*x9 + x8 + x9, x8, x9) of Multivariate Polynomial Ring in x1, x2,
18   x3, x4, x5, x6, x7, x8, x9 over Finite Field of size 2
19
20 B = I.groebner_basis(); B
21
22   [x1, x2, x3, x4, x5 + 1, x6, x7, x8, x9]
```

$$(M, P, B, C, R, A, A_l, L, L_l) = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9) = (1, 1, 1, 1, 0, 1, 1, 1, 1)$$

# Fixed point analysis of the *lac* operon

Using the variables  $(M, P, B, C, R, A, A_l, L, L_l) = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9)$

we got the following fixed points for each choice of parameters  $(G_e, L_e)$

- Input:  $(G_e, L_e) = (0, 0)$   
Fixed point:  $(x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9) = (0, 0, 0, 1, 1, 0, 0, 0, 0)$
- Input:  $(G_e, L_e) = (1, 0)$   
Fixed point:  $(x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9) = (0, 0, 0, 0, 1, 0, 0, 0, 0)$
- Input:  $(G_e, L_e) = (1, 1)$   
Fixed point:  $(x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9) = (0, 0, 0, 0, 1, 0, 0, 0, 0)$
- Input:  $(G_e, L_e) = (0, 1)$   
Fixed point:  $(x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9) = (1, 1, 1, 1, 0, 1, 1, 1, 1)$

All of these fixed points make biological sense!