

1.

2. Assumptions:

- Circuit encoded on plasmid present at a constant 200 copies per cell
- Characteristic lengths $\mathcal{L}_X = 1000$ nt, $\mathcal{L}_T = 333$ AA
- Promoter controls follow Moon and Voigt formulation
- Translation operates at kinetic limit
- RNAP and ribosome levels constant
- $\mathcal{L}_{X,1} = 1200$ nt, $\mathcal{L}_{X,2} = 2400$ nt, $\mathcal{L}_{X,3} = 600$ nt

(a) Looking first at the mRNA...

$$\begin{aligned}\frac{dm_1}{dt} &= r_{X,1}u_1 - k_{X,1}^d m_1 - m_1 \mathcal{B}^{-1} \dot{\mathcal{B}} \\ \frac{dm_2}{dt} &= r_{X,2}u_2 - k_{X,2}^d m_2 - m_2 \mathcal{B}^{-1} \dot{\mathcal{B}} \\ \frac{dm_3}{dt} &= r_{X,3}u_3 - k_{X,3}^d m_3 - m_3 \mathcal{B}^{-1} \dot{\mathcal{B}}\end{aligned}$$

We can use the substitution $\mu = \mathcal{B}^{-1} \dot{\mathcal{B}}$

$$r_{X,j} = k_{E,j}^X R_{X,T} \left(\frac{G_j}{\tau_{X,j} K_{X,j} + (\tau_{X,j} + 1) G_j} \right)$$

$$\begin{aligned}u_1 &= \frac{W_{R_T,1} + W_I f_I}{1 + W_{R_T,1} + W_I f_I} \\ u_2 &= \frac{W_{R_T,2} + W_{12} f_{12} + W_{32} f_{32}}{1 + W_{R_T,2} + W_{12} f_{12} + W_{32} f_{32}} \\ u_3 &= \frac{W_{R_T,3} + W_{13} f_{13} + W_{23} f_{23}}{1 + W_{R_T,3} + W_{13} f_{13} + W_{23} f_{23}}\end{aligned}$$

And now at the protein...

$$\begin{aligned}\frac{dp_1}{dt} &= r_{L,1}w_1 - k_{L,1}^d p_1 - p_1 \mathcal{B}^{-1} \dot{\mathcal{B}} \\ \frac{dp_2}{dt} &= r_{L,2}w_2 - k_{L,2}^d p_2 - p_2 \mathcal{B}^{-1} \dot{\mathcal{B}} \\ \frac{dp_3}{dt} &= r_{L,3}w_3 - k_{L,3}^d p_3 - p_3 \mathcal{B}^{-1} \dot{\mathcal{B}}\end{aligned}$$

$$r_{L,j} = k_{E,j}^L R_{L,T} \left(\frac{m_j}{\tau_{L,j} K_{L,j} + (\tau_{L,j} + 1) m_j} \right)$$

$w_j = 1$ (since operating at kinetic level)

$$\frac{d\mathbf{x}}{dt} = \mathbf{A}\mathbf{x} + \mathbf{S}\mathbf{r}$$

$$\begin{aligned}\frac{d}{dt} \begin{bmatrix} m_1 \\ m_2 \\ m_3 \\ p_1 \\ p_2 \\ p_3 \end{bmatrix} &= - \begin{bmatrix} k_{X,ex}^d & 0 & 0 & 0 & 0 & 0 \\ 0 & k_X^d + \mu & 0 & 0 & 0 & 0 \\ 0 & 0 & k_X^d + \mu & 0 & 0 & 0 \\ 0 & 0 & 0 & k_{L,ex}^d & 0 & 0 \\ 0 & 0 & 0 & 0 & k_L^d + \mu & 0 \\ 0 & 0 & 0 & 0 & 0 & k_L^d + \mu \end{bmatrix} \begin{bmatrix} m_1 \\ m_2 \\ m_3 \\ p_1 \\ p_2 \\ p_3 \end{bmatrix} \\ &+ \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \hat{r}_{X,1} \\ \hat{r}_{X,2} \\ \hat{r}_{X,3} \\ \hat{r}_{L,1} \\ \hat{r}_{L,2} \\ \hat{r}_{L,3} \end{bmatrix}\end{aligned}$$

(b) Solving for parameters...

$$k_{E,j}^X = \frac{e^X}{\mathcal{L}_j} \text{ (from last week)}$$

$$k_{E,j}^X = \frac{42}{\mathcal{L}_j}$$

$$\mu = \frac{\ln 2}{t_d}$$

$$\mu = \frac{\ln 2}{30 \text{ min}}$$

$$\mu = 0.0231 \text{ min}^{-1} = 3.85 \times 10^{-4} \text{ s}^{-1}$$

$$\tau_{X,j}^{-1} \equiv \left(\frac{k_I}{k_A + k_E} \right)$$

$$\tau_{X,j}^{-1} \equiv \left(\frac{0.04}{k_{E,j}^X} \right)$$

This gives us time constants $\tau_{E,1}^X = 0.875$, $\tau_{E,2}^X = 0.4375$, $\tau_{E,3}^X = 1.75$

$$\kappa_{X,j}^{-1} \equiv \left(\frac{k_+}{k_- + k_I} \right)$$

$$\kappa_{X,j}^{-1} = \left(\frac{10.42}{0.01 + 0.04} \right)$$

$$\kappa_{X,j} = 0.0048$$

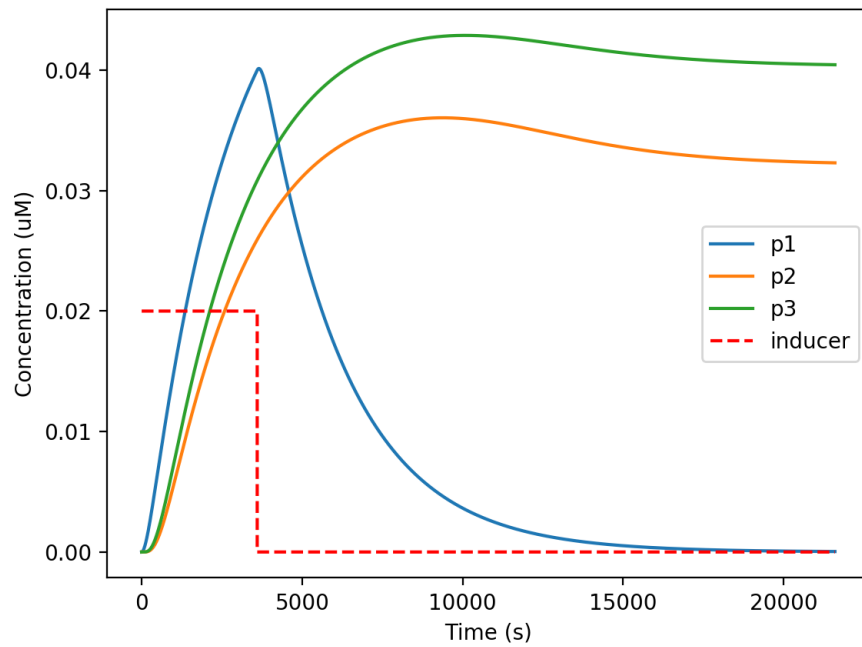
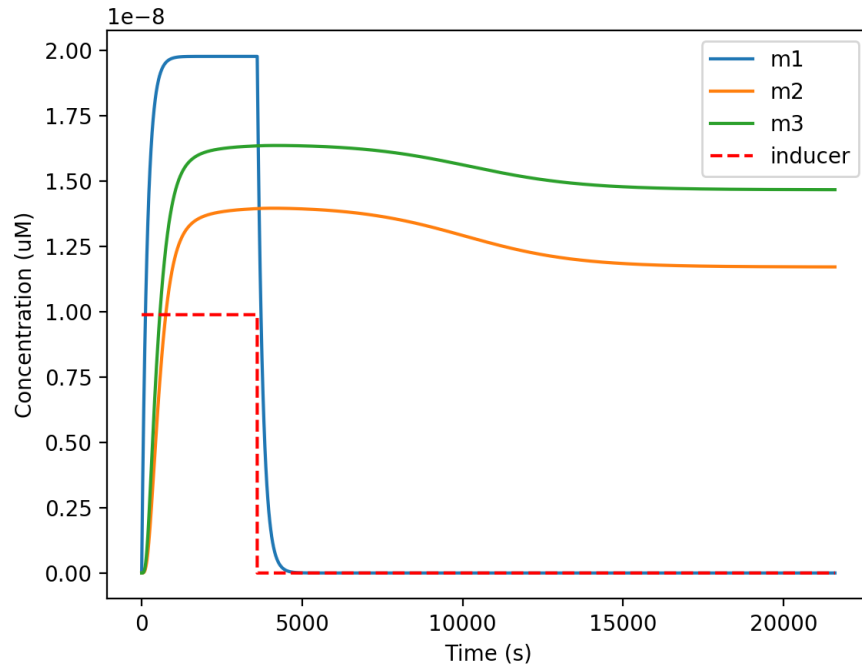
We need the copy number, RNA polymerase concentration, and ribosome concentrations in μM units:

$$200 \frac{\text{plasmids}}{\text{cell}} \left(\frac{1 \text{ mol}}{6.02 \times 10^{23} \text{ plasmids}} \right) \left(\frac{1 \text{ cell}}{6.7 \times 10^{-10} \mu L} \right) \left(\frac{10^6 \mu L}{1 L} \right) \left(\frac{10^6 M}{1 \mu M} \right) = 0.496 \mu M$$

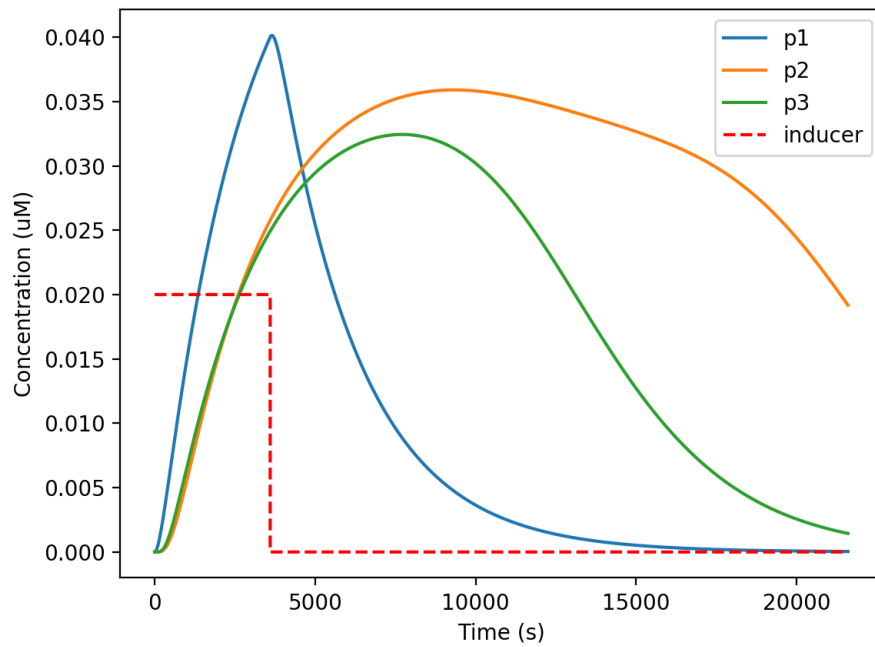
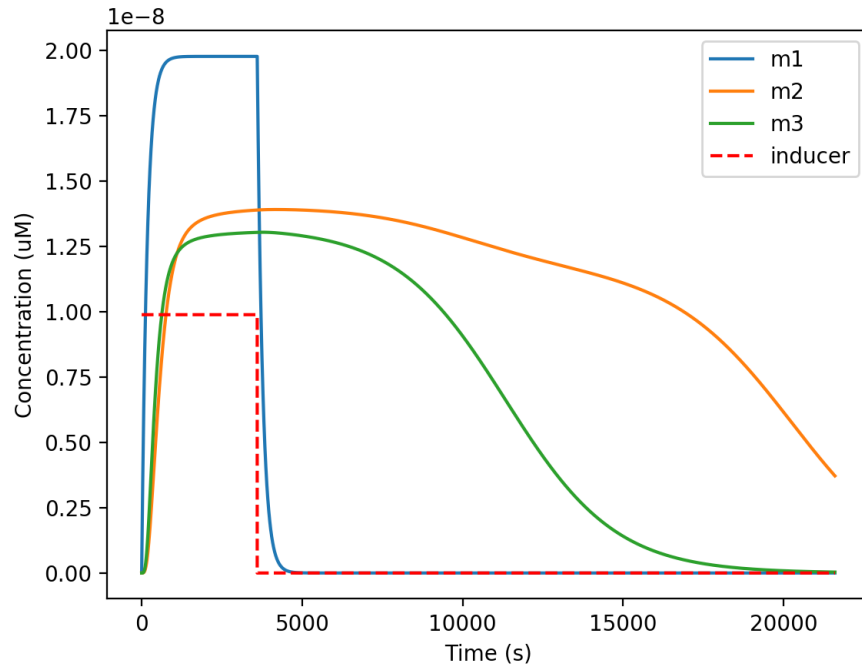
We can derive the RNAP and ribosome concentrations similarly

| Parameter | Symbol | Value | Units | Source |
|-----------------------------------|---------------------|-----------------------|----------------|--------------------|
| Specific growth rate | μ | 3.85×10^{-4} | s^{-1} | Given |
| mRNA elongation rate | e_X | 42 | nt/s | PS1 |
| Gene 1 length | $\mathcal{L}_{X,1}$ | 1200 | nt | Given |
| Gene 2 length | $\mathcal{L}_{X,2}$ | 2400 | nt | Given |
| Gene 3 length | $\mathcal{L}_{X,3}$ | 600 | nt | Given |
| TX elongation rate constant | $k_{E,1}^X$ | 0.035 | s^{-1} | See above |
| TX elongation rate constant | $k_{E,2}^X$ | 0.0175 | s^{-1} | See above |
| TX elongation rate constant | $k_{E,3}^X$ | 0.07 | s^{-1} | See above |
| TX initiation rate constant | k_I^X | 0.04 | s^{-1} | PS1 |
| TX abortive rate constant | k_A^X | 0 | s^{-1} | PS1 |
| TX time constant | $\tau_{X,1}$ | 0.875 | n/a | See above |
| TX time constant | $\tau_{X,2}$ | 0.4375 | n/a | See above |
| TX time constant | $\tau_{X,3}$ | 1.75 | n/a | See above |
| TX saturation constant | $\kappa_{X,123}$ | 0.0048 | μM | See above |
| Gene concentration | G_{123} | 200 | plasmids/cell | Given |
| Gene concentration | G_{123} | 0.496 | μM | See above |
| RNAP Concentration | $R_{X,T}$ | 8,000 | molecules/cell | Bremer [1] |
| RNAP Concentration | $R_{X,T}$ | 19.8 | μM | See above |
| Ribosome Concentration | $R_{L,T}$ | 50,000 | ribosomes/cell | Mackie [2] |
| Ribosome Concentration | $R_{L,T}$ | 123.96 | μM | See above |
| Basal transcription rate | $W_{R_T,123}$ | 0.00001 | | |
| Translation elongation rate | e_L | 14.5 | aa/s | Dalbow [3] |
| Peptide 1 length | $\mathcal{L}_{L,1}$ | 400 | aa | Given |
| Peptide 2 length | $\mathcal{L}_{L,2}$ | 800 | aa | Given |
| Peptide 3 length | $\mathcal{L}_{L,3}$ | 200 | aa | Given |
| TX elongation rate constant | $k_{E,1}^L$ | 0.03625 | s^{-1} | See above |
| TX elongation rate constant | $k_{E,2}^L$ | 0.0181 | s^{-1} | See above |
| TX elongation rate constant | $k_{E,3}^L$ | 0.0725 | s^{-1} | See above |
| TL time constant | $\tau_{L,123}$ | | | Defined same as TX |
| TL saturation constant | $\kappa_{L,123}$ | | | Defined same as TX |
| mRNA degradation rate constant | k_d^X | 5.5×10^{-3} | s^{-1} | Tanagachi [4] |
| Protein degradation rate constant | k_d^L | 3.85×10^{-6} | s^{-1} | Maurizi [5] |

For the unbroken circuit, we found the expected result that this circuit functions as a memory circuit. Even after the inducer is removed from the surroundings, thus deactivating the transcription of P1, we still have P2 and P3 being transcribed since they are able to induce each other's transcription.



However, when we break the circuit, preventing P2 from inducing P3, we see that P3's expression drops shortly after the inducer is removed from the system. And without P3 present to induce P2, P2 also drops soon after.



References

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- [4] Y. Taniguchi, P. J. Choi, G.-W. Li, H. Chen, M. Babu, J. Hearn, A. Emili, and X. S. Xie, "Quantifying e. coli proteome and transcriptome with single-molecule sensitivity in single cells," *Science*, vol. 329, no. 5991, pp. 533–538, 2010.
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