

Problem 1

A) $\langle m_c \rangle = 2.8 \times 10^{-13}$ gDW/cell <https://biomodels.hms.harvard.edu/biomodel.aspx?id=103905&ver=1.3&term=Cell+mass+E.coli&brw>
 $\hat{N}_c = 1 \times 10^8$ cell/mL
 $V = 1$ mL
 $\beta = \langle m_c \rangle \hat{N}_c V = 2.8 \times 10^{-5}$ gDW
 $\langle n_{\text{molecule}} \rangle = \langle n \rangle / A_0$ $A_0 = \text{Abogadro\#}$
 $\langle n \rangle \Rightarrow \langle n_{\text{molecule}} \rangle / \beta$ *See Excel Sheet for Table

B) $\dot{m}_i = r_{x,i} \bar{u}_i - (\mu + \theta_{m,i}) m_i$

P.55

$$0 = r_{x,i} \bar{u}_i - (\mu + \theta_{m,i}) m_i$$

$$m_i (\mu + \theta_{m,i}) = r_{x,i} \bar{u}_i$$

$$m_i = \frac{r_{x,i} \bar{u}_i}{(\mu + \theta_{m,i})}$$

$$r_{x,i} = K_E^x R_{x,T} \left(\frac{G_i}{T_{x,i} K_{x,i} + (C_{x,i} + 1) G_i} \right)$$

$$\Rightarrow m^* = \frac{r_{x,i} \bar{u}}{(\mu + \theta_{m,i})}$$

$$\bar{u} = \frac{w_1 + w_2 F}{1 + w_1 + w_2 F} \quad F = \frac{I^n}{K_d^n + I^n}$$

$$\Rightarrow m^* = K_x(G, \theta) \bar{u}(I, K)$$

C) Use boundary values as test

$$@ I_{\text{prom}} = 0 \Rightarrow F = 0 \Rightarrow \bar{u} = \frac{w_1}{1 + w_1}$$

$$m^* = K_x \bar{u} = K_x \frac{w_1}{1 + w_1} \quad K_x = 2.2474 \times 10^{-5} \text{ nmol/gDW}$$

See Matlab code PRELIM1_P1.m for parameter calc's

$$w_1 = 0.000507575 \quad \text{Wolfram Alpha}$$

Now we can do a curve fit with Matlab
for n, w_2 & K_d

See Curve file for curve and parameter values

$$r_{x,i} = K_E^x R_{x,T} \left(\frac{G_i}{T_{x,i} K_{x,i} + (C_{x,i} + 1) G_i} \right)$$

K_E^x = elongation rate constant

$R_{x,T}$ = total RNAP concentration = 2,000 RNAP/cell

<https://biomodels.hms.harvard.edu/biomodel.aspx?id=113700&ver=1.8&term=RNAP+concentration&brw>

G_i = copy # of gene = 2

$T_{x,i}$ = time constant for transcription $\approx K_E^x / \mu$

K_x = rate of initiation

$K_{x,i}$ = saturation constant for transcription

$K_{X,i}$ = saturation constant for transcription

$$V_{\epsilon}^x = e_x \cdot L^{-1}$$

L = length of gene (nt) characteristic transcription length = 400 nt

$e_x = \text{elongation rate (nt/s)} = 25 \text{ nt/sec}$ (also known as value of 27 nt/sec)

$$K_{\text{eff}} = \frac{K_1}{K_1 + K_2}$$

$$K_I = 4 \times 10^{-2} \text{ s}^{-1} \quad \text{From M. Clure \&}$$

$K_{x,i} = 0.036 \mu\text{M}$ Taken from P52 solns.

Cell volume = $1.46 \mu\text{m}^3$

$$K_d = 49.6 \mu M$$

Did not use this instead used matlab curve fit tool

d) My model has a good fit given by the r^2 value