

Problem 1a) Convert  $\langle n \rangle$  values in Table 1 to specific volume basis (B): $\Rightarrow$  Given:- Sample size (V) = 1 mLCell count in sample @ OD600 = 0.1 ( $\hat{N}_c$ ) =  $1 \times 10^8$  cells/mL $\Rightarrow$  From Bionumbers (BID: 100008), average cell dry weight for E. coli ( $\langle m_c \rangle$ ) = 0.28 pg  
 $\approx 2.8 \times 10^{-13}$  gDW/cell $\therefore$  Specific Volume Basis (B) =  $\langle m_c \rangle \cdot \hat{N}_c \cdot V$ 

$$= 2.8 \times 10^{-13} \frac{\text{gDW}}{\text{cell}} \cdot 1 \times 10^8 \frac{\text{cells}}{\text{mL}} \cdot 1 \text{ mL}$$

$$\therefore B = 2.8 \times 10^{-5} \text{ gDW}$$

 $\Rightarrow$  To convert the  $\langle n \rangle$  values to nmol/gDW:-

$$\langle n \rangle \frac{\text{molec of mRNA}}{\text{cell}} \times 1 \times 10^8 \frac{\text{cells}}{\text{mL}} \times 1 \text{ mL} \times \frac{1 \text{ mol}}{6.022 \times 10^{23} \text{ molecules}} \times \frac{10^9 \text{ nmol}}{\text{mol}} \times \frac{1}{2.8 \times 10^{-5} \text{ gDW}}$$

↑  
Values of  $\langle n \rangle$   
in the table

$$(\langle n \rangle \times (5.93 \times 10^{-3})) \text{ nmol/gDW}$$

The corresponding table of values is listed below:-

IPTG (mM)	$\langle n \rangle$ (nmol/gDW)	low n (nmol/gDW)	high n (nmol/gDW)
0.000	0.113	0.107	0.119
0.001	0.125	0.101	0.154
0.005	0.243	0.219	0.261
0.012	0.397	0.385	0.409
0.053	0.510	0.498	0.522
0.216	0.552	0.540	0.563
1.0	0.552	0.546	0.557

b) Derive the gain function ( $K_x$ )

→ Starting with the mRNA balance:-

$$\dot{m}_i = \mu_{x,i} \bar{u}_i - (\mu + \sigma_{m,i}) m_i$$

At steady state;  $\dot{m}_i = 0$ , thus the eqn. reduces to:-

$$(\mu + \sigma_m) m^* = \mu_x \bar{u}$$

$$\therefore m^* = \frac{\mu_x}{(\mu + \sigma_m)} \cdot \bar{u}$$

→ Plugging in values for  $\mu_x$  & the promoter function  $\bar{u}$ :-

$$\textcircled{*} \mu_x = K_E^* \cdot R_{x,T} \left( \frac{G}{\tau_x \cdot K_x + (\tau_x + 1)G} \right)$$

$$\textcircled{*} \bar{u} = \frac{W_1 + W_2 f_I}{1 + W_1 + W_2 f_I}$$

$$\therefore m^* = \underbrace{\frac{K_E^* \cdot R_{x,T}}{(\mu + \sigma_m)} \left( \frac{G}{\tau_x K_x + (\tau_x + 1)G} \right)}_{\text{GAIN FUNCTION } (K_x)} \cdot \underbrace{\frac{W_1 + W_2 f_I}{1 + W_1 + W_2 f_I}}_{\text{PROMOTER FUNCTION } (\bar{u})} \quad \text{where } f_I = \frac{I^n}{K^n + I^n}$$

c) A table listing all parameter values, units and sources has been attached along with this prelim. These parameters yield:-

$$K_x = 0.552 \text{ nmol/gdw}$$

$$\bar{u} = \frac{0.26 + 266 f_I}{1 + 0.26 + 266 f_I}$$

$$\text{where } f_I = \frac{I^{1.49}}{(0.36)^{1.49} + I^{1.49}}$$

d) The model fit does have the same shape and is a good estimator for the converted  $\langle n \rangle$  values as a function of IPTG. The least squares error was minimized to  $\approx 4 \times 10^{-4}$  by optimizing the initial values of  $W_1, W_2, K$  and  $n$  in the promoter function. It is also important to note that an RNAP (total) abundance of 126 nM was required as the value of 30 nM from Bionumbers (possibly because it describes available RNAP) was not applicable with our data.