

Problem 1

a)

Starting from RNAP balance:

$$R_{X,T} = R_X + (G_j : R_X)_C + (G_j : R_X)_O + \sum_{i=1,j}^N [(G_i : R_X)_C + (G_i : R_X)_O] \quad (1)$$

From JDV's class notes: Deterministic Mathematical Models of Transcription:

$$K_{X,j}^{-1} \equiv \frac{k_+}{k_- + k_I} \quad (2)$$

$$\tau_{X,j}^{-1} \equiv \frac{k_I}{k_A + k_E} \quad (3)$$

Closed complex for gene j :

$$(G_j : R_X)_C = \frac{k_+}{k_- + k_I} (G_j)(R_X) = K_{X,j}^{-1} (G_j)(R_X) \quad (4)$$

Open complex for gene j :

$$(G_j : R_X)_O = \frac{k_I}{k_A + k_E} (G_j : R_X)_C = \tau_{X,j}^{-1} (G_j : R_X)_C \quad (5)$$

$$(G_j : R_X)_O = \tau_{X,j}^{-1} K_{X,j}^{-1} (G_j)(R_X) \quad (6)$$

Closed complex for gene i :

$$(G_i : R_X)_C = \frac{k_+}{k_- + k_I} (G_i)(R_X) = K_{X,i}^{-1} (G_i)(R_X) \quad (7)$$

Open complex for gene i :

$$(G_i : R_X)_O = \frac{k_I}{k_A + k_E} (G_i : R_X)_C = \tau_{X,i}^{-1} (G_i : R_X)_C \quad (8)$$

$$(G_i : R_X)_O = \tau_{X,i}^{-1} K_{X,i}^{-1} (G_i)(R_X) \quad (9)$$

New RNAP balance:

$$R_{X,T} = R_X + K_{X,j}^{-1}(G_j)(R_X) + \tau_{X,j}^{-1} K_{X,j}^{-1}(G_j)(R_X) + \sum_{i=1,j}^N [K_{X,i}^{-1}(G_i)(R_X) + \tau_{X,i}^{-1} K_{X,i}^{-1}(G_i)(R_X)] \quad (10)$$

Solving for free RNAP concentration:

$$R_X = \frac{R_{X,T}}{1 + K_{X,j}^{-1}(G_j) + \tau_{X,j}^{-1} K_{X,j}^{-1}(G_j) + \sum_{i=1,j}^N [K_{X,i}^{-1}(G_i) + \tau_{X,i}^{-1} K_{X,i}^{-1}(G_i)]} \quad (11)$$

Divide top and bottom by $\tau_{X,j}^{-1} K_{X,j}^{-1}$:

$$R_X = \frac{R_{X,T} \tau_{X,j} K_{X,j}}{\tau_{X,j} K_{X,j} + \tau_{X,j}(G_j) + (G_j) + \sum_{i=1,j}^N \frac{\tau_{X,j} K_{X,j}}{\tau_{X,i} K_{X,i}} (1 + \tau_{X,i})(G_i)} \quad (12)$$

$$\varepsilon_j = \sum_{i=1,j}^N \frac{\tau_{X,j} K_{X,j}}{\tau_{X,i} K_{X,i}} (1 + \tau_{X,i})(G_i) \quad (13)$$

Open complex of gene j in terms of total RNAP:

$$(G_j : R_X)_O = \tau_{X,j}^{-1} K_{X,j}^{-1}(G_j)(R_X) = \frac{R_{X,T} G_j}{\tau_{X,j} K_{X,j} + (\tau_{X,j} + 1)(G_j) + \varepsilon_j} \quad (14)$$

Kinetic rate of transcription:

$$r_{X,j} = k_{E,j} (G_j : R_X)_O \quad (15)$$

$$r_{X,j} = k_{E,j} R_{X,T} \frac{G_j}{\tau_{X,j} K_{X,j} + (\tau_{X,j} + 1)(G_j) + \varepsilon_j} \quad (16)$$

b) For an N-gene system to be approximately equivalent to the 1-gene system, the ε_j term needs to be minimized. The quantity $(1 + \tau)$ will never be smaller than 1, so trying to minimize it would serve little purpose. A very small G_i to G_j ratio means that there is a relatively low concentration of other genes besides j in the system; however, this case seems like the trivial answer, since the system could be approximated as a 1-gene system, especially if G_j is orders of magnitude larger than G_i . If τ for all other genes except j is much larger than it is for j , transcription of all those other genes is initiation limited, or inactivated.