

1.) a)  $V = \gamma_D / \gamma_N$  cell 1, or  $\gamma_N > \gamma_D$

$\frac{dN_1}{dt} \neq \frac{dN_2}{dt}$  approach 0 b/c  $\gamma_N N_{\text{tot}}$  term greater than  $F(D_{2,\text{ori}})$  term in equations below:

$$\frac{dN_1}{dt} = F(D_2) - \gamma_N N_1$$

$$\frac{dN_2}{dt} = F(D_1) - \gamma_N N_2$$

$$\frac{dN_1}{dt} = \frac{F(D_2)}{\gamma_N} - N_1$$

$$\frac{dN_2}{dt} = \frac{F(D_1)}{\gamma_N} - N_2$$

$\therefore @ \text{QSSA}$

$$N_1 = f(D_2)$$

$$N_2 = f(D_1)$$

$$\frac{dD_1}{dt} = (g(f(D_2)) - D_1)V$$

$$\frac{dD_2}{dt} = (g(f(D_1)) - D_2)V$$

b) \*phase portrait on doc  
nullclines:  $D_1 = g(f(D_2))$

$$= \frac{1}{1 + 10 \left( \frac{D_2^2}{0.1 + D_2^2} \right)}$$

$$D_2 = g(f(D_1))$$

$$= \frac{1}{1 + 10 \left( \frac{D_1^2}{0.1 + D_1^2} \right)}$$

The lateral inhibition works similarly as the case discussed in lecture with the fact that there are three steady states, and cell 1 wins when at the stable S.S. w/a higher concentration of  $D_2$  while cell 2 win when @ stable S.S. w/ a higher concentration of  $D_1$ .

$$2.) \text{a) } \frac{dL_c}{dt} = q + K_m(z)[L_b - L_c(z)] \frac{1}{n_c} + K_r R_s^* - K_f L_c(z) R_s$$

$$\textcircled{1} \text{ ss } \frac{dL_c}{dt} = 0$$

$$0 = q + K_m(z)[L_b - L_c(z)] \frac{1}{n_c} + K_r R_s^* - K_f L_c(z) R_s$$

$$K_f L_c(z) R_s + \frac{K_m(z)}{n_c} L_c(z) = q + \frac{K_m(z)}{n_c} L_b + K_r R_s^*$$

$$L_c(z) \left[ K_f R_s + \frac{K_m(z)}{n_c} \right] = q + \frac{K_m(z)}{n_c} L_b + K_r R_s^*$$

$$L_c(z) = q + \frac{K_m(z)}{n_c} L_b + K_r R_s^*$$

$$K_f R_s + \frac{K_m(z)}{n_c}$$

b)

for very small  $K_m$ ...

$$L_c = q + K_r R_s^*$$

$$K_f R_s$$

In this scenario, bulk  $K$  transport would not play a big factor into the  $L$  concentration at cell surfaces. Therefore, the concentration of  $L_c$  for each cell does not depend on position, just the chemical reactions, binding/unbinding with  $R_s/R_s^*$ , including and EGF production from the cell.

for very large  $K_m$ ...

$$L_c = \frac{\frac{K_m(z)}{n_c} L_b}{\frac{K_m(z)}{n_c}} = L_b$$

In this scenario, binding would not play a big factor into the  $L$  concentration at cell surfaces. Therefore, the concentration of  $L_c$  for each cell should be similar to  $L$  at the boundary since <sup>hardly</sup> any chemical reactions are taking place. This also does not depend on position since chemical reactions are not changing concentration as bulk occurs.

c) low concentration of L  $\Rightarrow L_c K_{ss} \ll 1$

$$L_c(z) = q + \frac{K_m(z)}{n_c} L_b + K_r R_s^*$$

$L_b = 0$   
 $K_r R_s^* + \frac{K_m(z)}{n_c}$

$$R_{\text{total}}^* = R_s^* + R_i^*$$

$$= \left( \frac{1}{K_e^*} + \frac{1}{k_{deg}} \right) \left( \frac{K_{ss} L_c(z)}{1 + K_{ss} L_c(z)} \right) V_s$$

$$= \left( \frac{1}{K_e^*} + \frac{1}{k_{deg}} \right) \left[ \frac{K_{ss} \left( q + K_r R_s^* \right)}{K_r R_s^* + \frac{K_m(z)}{n_c}} \right] V_s$$

$$+ K_{ss} \left( \frac{q + K_r R_s^*}{K_r R_s^* + \frac{K_m(z)}{n_c}} \right)$$

if low conc. of L, then  $K_r R_s^*$  &  $K_r R_s$  small...

$$R_{\text{tot}}^* = \left( \frac{1}{K_e^*} + \frac{1}{k_{deg}} \right) \left( \frac{K_{ss} \left( \frac{q n_c}{K_m(z)} \right)}{1 + K_{ss} \left( \frac{q n_c}{K_m(z)} \right)} \right) V_s$$

where  $K_{ss} = \frac{K_e^* K_f}{K_f (K_r + K_e^*)}$

d) setting to Sherwood #...

$$R_{\text{tot}}^* = \left( \frac{1}{K_e^*} + \frac{1}{k_{deg}} \right) \left( \frac{K_{ss} \left( \frac{q n_c}{(\dot{\gamma} z^2)^{1/3}} \right)}{\frac{z}{D_L} + K_{ss} \left( \frac{q n_c}{(\dot{\gamma} z^2)^{1/3}} \right)} \right) V_s$$

\* profile in doc

- 3.) Assumptions:
- i)  $\tau_d \approx 40$  min
  - ii)  $K_x \Rightarrow$  from prelim 1 Q1
  - iii)  $p^0 = 0.3 \text{ }\mu\text{M}$
  - iv)  $V_{cell} = 1 \text{ }\mu\text{m}^3$
  - v)  $\text{weight}_{cell} = 4.3 \times 10^{-13} \text{ g}$  & 70% water  
 $\hookrightarrow \text{dry weight: } 1.29 \times 10^{-13} \text{ g}$
  - vi)  $t_{1/2} = 24 \text{ hr for } p_i$
  - vii)  $(1 + T_{L,i})m_i \ll T_{L,i} K_L$
  - viii) t\_late initiation time = 1.5 s
  - ix)  $L_p = 333 \text{ aa}$
  - x) t\_late saturation coeff ( $K_{L,i}$ ) = 200  $\mu\text{M}$
  - xi)  $K_p$  unity?

a) @ S.S.  $\dot{p}_i = 0$

$$0 = r_{x,i} w_i^* - (\mu + \theta_{p,i}) p_i^*$$

$$p_i^* = \frac{r_{x,i} w_i^*}{N + \theta_{p,i}} = K_{x,i} w_i^* \quad \text{let } w_i^* = M_i^* w_i$$

depends on mRNA production...

@ S.S.  $m_i = 0$

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

$$m_i^* = \frac{r_{x,i} \bar{u}_i}{N + b_{m,i}} = K_{x,i} \bar{u}_i$$

$$\therefore p_i^* \approx K_{x,i} K_{x,i} \bar{u}_i w_i$$

b)  $p_i^*$  for 300 aa protein w/  $w_i = 1$  &  $\bar{u}_i$  profile from prelim 1:

$$\bar{u}(I) = 0.25 + 98.75 f_I \quad f_I = \frac{I^{1.85}}{1 + 0.25 + 98.75 f_I} \quad (9 \times 10^{-2})^{1.85} + I^{1.85}$$

$$\textcircled{1} \quad \bar{u}(I=0) = 0.2$$

$$\textcircled{2} \quad \bar{u}(I=5 \times 10^{-4}) = 0.204$$

$$\textcircled{3} \quad \bar{u}(I=0.005) = 0.418$$

$$\textcircled{4} \quad \bar{u}(I=0.012) = 0.720$$

$$\textcircled{5} \quad \bar{u}(I=0.053) = 0.965$$

$$\textcircled{6} \quad \bar{u}(I=0.216) = 0.988$$

$$\textcircled{7} \quad \bar{u}(I=1) = 0.990$$

$$m^{*,e} = \frac{\langle n_S \rangle (N_c V) \left( \frac{1 \times 10^9}{A_v} \right)}{(1-\alpha) \langle m_c \rangle (N_c V)}$$

Prelim 1:

①	$K_x = m^{*,e} (I = 0)$	= 0.245 nmol/gDW
②	$m^{*,e} (I = 5e^{-4})$	= 0.270
③	$m^{*,e} (I = 0.005)$	= 0.528
④	$m^{*,e} (I = 0.012)$	= 0.862
⑤	$m^{*,e} (I = 0.053)$	= 1.107
⑥	$m^{*,e} (I = 0.216)$	= 1.197
⑦	$m^{*,e} (I = 1)$	= 1.197

$$K_{L,i} = 200 \mu\text{mol} \left( \frac{1000 \text{ nano}}{1 \mu\text{m}} \right) \left( \frac{1 \text{ L}}{1 \times 10^{16} \text{ pm}^3} \right) \left( \frac{1 \text{ nm}^3}{1.29 \times 10^{-13} \text{ gDW}} \right)$$

$$= 1550.388 \text{ nmol/gDW}$$

	$\bar{u}_i (\text{AU})$	$p_i^* \text{ (nmol/gDW)}$
①	0.2	2.9841
②	0.264	3.3543
③	0.418	13.4407
④	0.720	37.7964
⑤	0.965	65.0558
⑥	0.988	72.0215
⑦	0.990	72.1673

\*profile on doc

c) The  $p_i^*$  curve moves up as a function of  $\bar{u}_i$  because as the  $T_{ri} \frac{K_{hi}}{K_p}$  term (in equation on next page) increases the translation limit (the numerator\* in this case) increases, thus increasing the  $p_i^*$  concentration for each  $\bar{u}_i$  value. If more ribosomes are able to read a message at once, then the protein concentration should increase.

\*numerator shown on next page

\* any values not given in final were taken from Prelim 1 solution or parameters from pset 2

$$\text{ribosome [J]} = 2.3 \text{ nm} \\ = 18.254 \frac{\text{nmol}}{\text{gDW}}$$

Numerator: t<sub>late</sub> limit

$$\text{Avg eln constant} = 16.5 / 333 = .0495 \text{ s}^{-1}$$

$$\text{prot eln constant} = 0.0495 * \frac{333}{300} = 0.055 \text{ s}^{-1}$$

$$t_{AV} = 0.055 (1.5) = 0.0825$$

changes for each profile ( $K_x$ )

$$\text{Numerator} = \text{prot eln constant} * 18.254 * \frac{(\text{m})}{\tau_{K_x} + m(\tau_{K_x} - \tau_{K_L})} * 3600$$

$\tau_{K_x}$  small compared to  $\tau_{K_x} - \tau_{K_L}$   
(assume 0)

denominator: degradation + dilution terms

$$\text{Growth rate} = (\log(2)/40) * 60 = 0.452 \text{ hr}^{-1}$$

$$\text{protein deg. const.} = -(\log(0.5)/24) = 0.0125 \text{ hr}^{-1}$$

$$\text{denominator} = \text{growth rate} + \text{protein deg. const.} \\ = 0.464 \text{ hr}^{-1}$$

$$\frac{\text{numerator}}{\text{denominator}} \neq w_i$$

" $K_x K_L w_i$ "

- 4.) Assumptions:
- $F6P = 0.1 \text{ mM}$ ,  $\frac{dF6P}{dt} = 0$
  - $[ATP] = 2.3 \text{ mM}$ ,  $\frac{d[ATP]}{dt} = 0$
  - $PFK(E_i) = 0.12 \text{ NM}$ ,  $\frac{dPFK(E_i)}{dt} = 0$
  - $K_{F6P} = 0.11 \text{ mM}$   
 $K_{ATP} = 0.42 \text{ mM}$
  - $K_{cat} = 0.45^{-1}$
- a) Activator = 3'-5' cyclic AMP

$W_2 \Rightarrow w/ 3'-5'-\text{AMP}$        $W_1 \Rightarrow n/o 3'-5'-\text{AMP}$

$$f_2 = \frac{\left(\frac{3'-5'-\text{AMP}_{\text{bind}}}{K_2}\right)^{n_2}}{1 + \left(\frac{3'-5'-\text{AMP}_{\text{bind}}}{K_2}\right)^{n_2}} \quad f_1 = 0 \quad \therefore \text{Activator} = 0$$

$\uparrow$                                    $b/c x = 0$

let activator = 0.405 [saturation]

$$\uparrow \quad \hat{r} = \frac{W_1}{1 + W_1} r_1$$

3.003

$$f_2 = \frac{\left(\frac{0.405}{K_2}\right)^{n_2}}{1 + \left(\frac{0.405}{K_2}\right)^{n_2}} \approx 1$$

Solve for  $W_1$ ...

$$W_1 \approx 0.0451$$

$$\hat{r} = \frac{0.0451 + W_2 f_2}{1 + 0.0451 + W_2 f_2} r_1$$

60.30%

Solve for  $W_2$ ...

$$W_2 \approx 0.8550$$

b) binding constant:  $115.1 \text{ NM} \Rightarrow 0.1151 \text{ mM}$

$$n = 12.27$$

$\uparrow$   
order parameter

solved in  
MATLAB

so, it works if

$\downarrow$  normalized.

c) \* plot in doc

The proposed model can describe the shape of the data, but the kinetic limit does not match the data's