Q1

Warrick Ma

$\gamma_j = k_{ej} (G_j : R_x)_0$

Assume $(G_j : R_x)_0$ steady state

$[G_j : R_x]_0 = \frac{k_{I,j} [G_j : R_x]_c}{k_{A,j} + k_{E,j}} \rightarrow [G_j : R_x]_c = \tau_{x,j} [G_j : R_x]_0$

Assume $[G_j : R_x]_c$ Steady state

$k_{I,j} \cdot [G_j : R_x]_c + k_{-j} \cdot [G_j : R_x]_c = k_{+j} [G_j][R_x]^0$

$[G_j : R_x]_c = K_{x,j}^{-1} \cdot [G_j][R_x]^0 \Rightarrow \tau_{x,j} [G_j : R_x]_0 = K_{x,j}^{-1} [G_j][R_x]^0$

$R_{x,T} = R_x^0 + [G_j : R_x]_c + [G_j : R_x]_0 + \sum_{i=1,j}^{N} [(G_i : R_x)_c + (G_i : R_x)_0]$

$= R_x^0 + (1 + \tau_{x,j}) [G_j : R_x]_0 + \sum_{i=1,j}^{N} [(1 + \tau_{x,i})(G_i : R_x)_0]$

$[R_x]^0 = \frac{\tau_{x,j} [G_j : R_x]_0}{K_{x,j}^{-1} [G_j]}$

$[G_j : R_x]_0 = \frac{G_j (R_{xT} - \sum [(1 + \tau_{xi}) [G_i : R_x]_0])}{(1 + \tau_{x,j}) G_j + \tau_{x,j} K_{x,j}}$

$\cancel{G_j \cdot \sum ([G_i : R_x]_c + [G_i : R_x]_0)}$ $G_j \sum [(1 + \tau_{xi}) [G_i : R_x]_0]$

$[G_i : R_x]_0 = \frac{[R_x]^0 [G_i]}{\tau_{xi} K_{xi}} = \frac{\tau_{xj} K_{xj} [G_j : R_x]_0 [G_i]}{[G_j] \tau_{xi} \cdot K_{xi}}$

$\sum (1 + \tau_{x,i}) \frac{\tau_{xj} K_{x,j} [G_j : R_x]_0 [G_i]}{\tau_{xi} K_{xi}}$

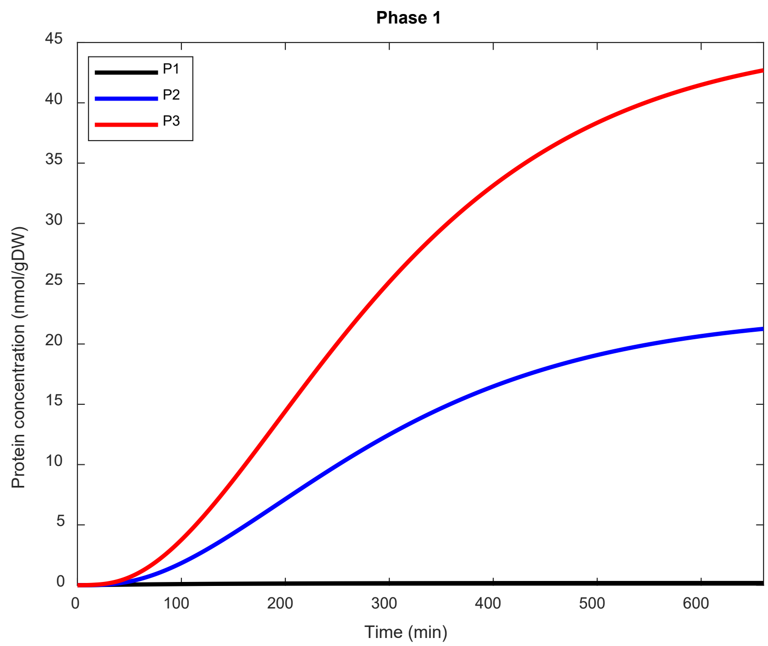
$\therefore [G_j : R_x]_0 = \frac{G_j \cdot R_{xT} - [G_j : R_x]_0 \cancel{\sum (1 + \tau_{xi})} \, \varepsilon_j}{(1 + \tau_{xj}) G_j + \tau_{xj} K_{xj}}$

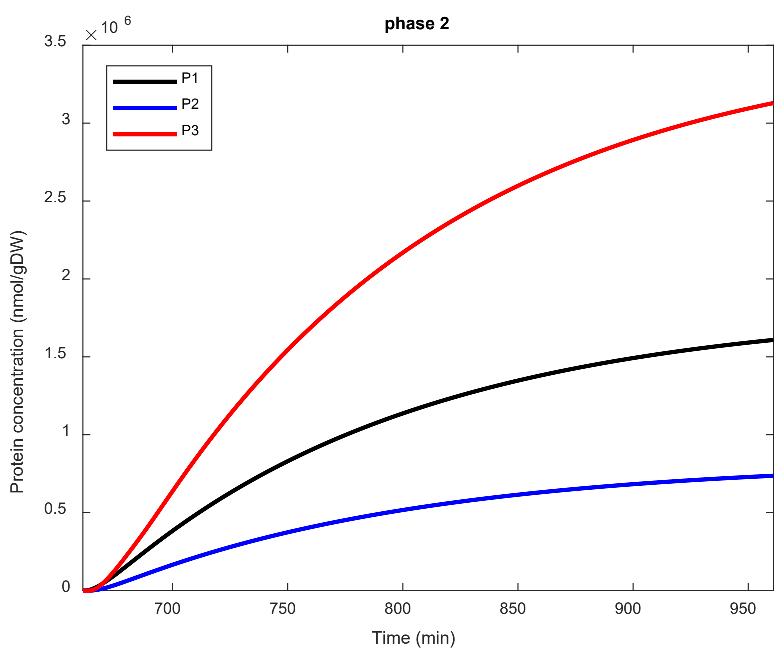
$[G_j : R_x]_0 = \frac{G_j \cdot R_{xT}}{(1 + \tau_{xj}) G_j + \tau_{xj} \cdot K_{xj} + \varepsilon_j}$

$\therefore \gamma = \frac{k_{ej} \cdot G_j \cdot R_{xT}}{(1 + \tau_{xj}) G_j + \tau_{xj} \cdot K_{xj} + \varepsilon_j}$

When $K_{x,i} \cdot \tau_{x,i} \gg K_{x,j} \cdot \tau_{xj}$

Q2





Inducer was added at the beginning of phase 2.

Part b:

See Matlab output. S1 matrix for sensitivity array time function of phase 1

S2 matrix for sensitivity array time function of phase 2

Part c:

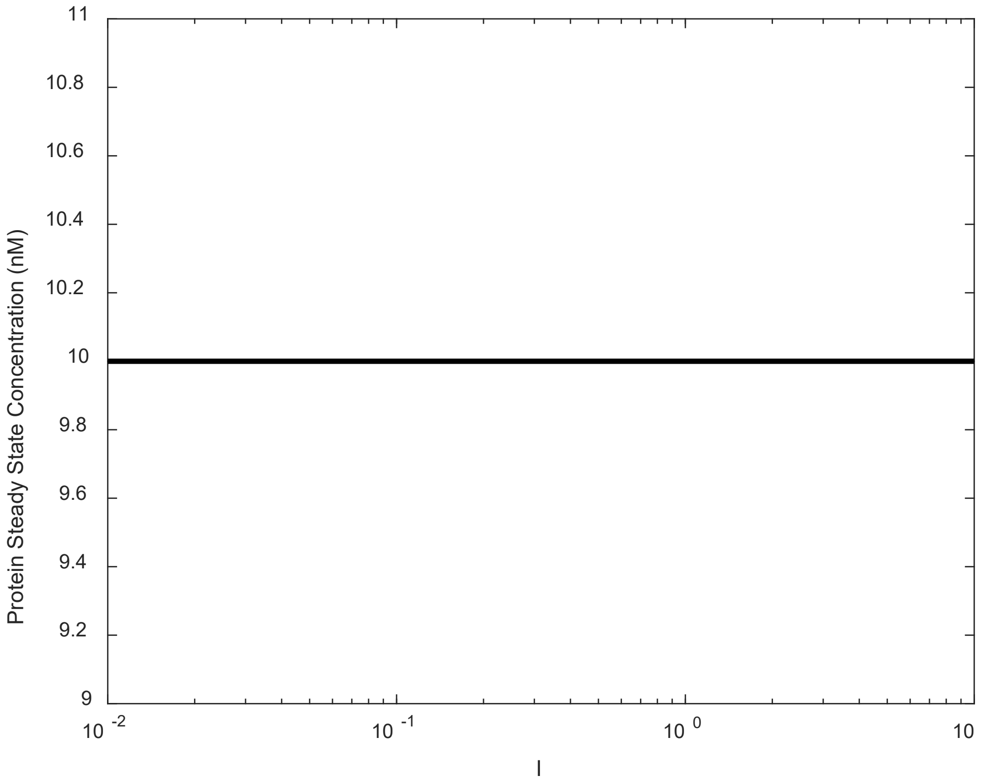
Importance of species in phase 1: P1>P3>P2

Importance of species in phase 2: P3>P2>P1

Q3

	v1	v2	v3	v4	v5	v6	b1	b2	b3	b4	b5	b6	b7	b8	b9
G	-1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
RNAP	-1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
G*	1	-1	0	0	0	0	0	0	0	0	0	0	0	0	0
NTP	0	-924	0	0	0	0	0	-1	0	0	0	0	0	0	0
Pi	0	1848	0	0	616	2	0	0	0	0	0	0	0	0	1
NMP	0	0	924	0	0	0	0	0	0	1	0	0	0	0	0
mRNA	0	1	-1	-1	1	0	0	0	0	0	0	0	0	0	0
rib	0	1	-1	-1	1	0	0	0	0	0	0	0	0	0	0
tRNA	0	0	0	0	308	-1	0	0	0	0	0	0	0	0	0
rib*	0	0	0	1	-1	0	0	0	0	0	0	0	0	0	0
GTP	0	0	0	0	-616	0	0	0	0	0	0	0	-1	0	0
AAtRNA	0	0	0	0	-308	1	0	0	0	0	0	0	0	0	0
protein	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
GDP	0	0	0	0	616	0	0	0	0	0	0	0	0	1	0
ATP	0	0	0	0	0	-1	0	0	0	0	-1	0	0	0	0
AA	0	0	0	0	0	0	-1	0	0	0	0	0	0	0	0
AMP	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0

```
xd=8.35;% mRNA degradation rate constant based on 2.1 min half life unit h ^(-1)
pd=9.9*10^(-3); %h^(-1)
p_conc=5*10^(-3); % gene p concentration in microM
rnap_conc=0.15; % rnap concentration in microM
ribo_conc=1.6; % ribosome concentration in microM
e_x=60*3600;kel=e_x/924; % 60 nt/sec; compute for enlongation rate constant ke
tau1=2.7;% time constant for transcription
tau2=0.8;%time constant for translation
K_x=0.3;%dissociation constant of RNAP in microM
K_L=57;%dissociation constant of ribosome in microM
n=1.5;Kd=0.3; % Kd (disocciation constant of inducer) is in mM
f1=I^n/(Kd^n+I^n);
u1=(0.26+300*f1)/(1+0.26+300*f1);
r_x=(rnap_conc*kel/tau1*(p_conc/(p_conc+K_x)))*u;
r_L=mRNA*ribo_conc/K_L*(16.5*3600/308);
```



The graph doesn’t look right but the linprog kept giving me a constant max protein production value.

Don’t know how to answer part c