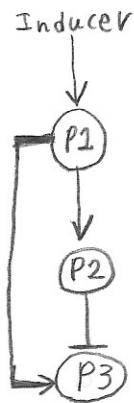


Prelim. Q 2.



Inducer \rightarrow Induction
 \rightarrow repression

\Rightarrow Want concentrations in $\frac{\text{nmol}}{\text{g DW}}$

\Rightarrow Want time in min

$\Rightarrow u_p = 1$, i.e. translation is at its kinetic limit (Assume iv)

\Rightarrow use assumption (iii)

$$T_d = 40 \text{ min} \Rightarrow \mu_{\text{cell}} = \frac{\ln(2)}{40 \text{ min}} = 0.0173 \text{ min}^{-1}$$

$$u_{m1}(I) = \frac{W_{11} + W_{I1} f_{m1}(I)}{1 + W_{11} + W_{I1} f_{m1}(I)}$$

$$f_{m1}(I) = \frac{I^{n_{I1}}}{K_{I1}^{n_{I1}} + I^{n_{I1}}} = \frac{I^{1.5}}{(0.30 \text{ mM})^{1.5} + I^{1.5}}$$

$$u_{m2}(P_1) = \frac{W_{22} + W_{12} f_{m2}(P_1)}{1 + W_{22} + W_{12} f_{m2}(P_1)}$$

$$f_{m2}(P_1) = \frac{P_1^{n_{12}}}{K_{12}^{n_{12}} + P_1^{n_{12}}} = \frac{(P_1)^{1.5}}{(1.0 \frac{\text{nmol}}{\text{g DW}})^{1.5} + (P_1)^{1.5}}$$

$$u_{m3}(P_1, P_2) = \frac{W_{33} + W_{13} f_{m3,1}(P_1)}{1 + W_{33} + W_{23} f_{m3,2}(P_2) + W_{13} f_{m3,1}(P_1)}$$

$$f_{m3,1}(P_1) = \frac{P_1^{n_{13}}}{K_{13}^{n_{13}} + P_1^{n_{13}}} = \frac{(P_1)^{1.5}}{(1.0 \frac{\text{nmol}}{\text{g DW}})^{1.5} + (P_1)^{1.5}}$$

$$f_{m3,2}(P_2) = \frac{P_2^{n_{23}}}{K_{23}^{n_{23}} + P_2^{n_{23}}} = \frac{(P_2)^{10}}{(10 \frac{\text{nmol}}{\text{g DW}})^{10} + (P_2)^{10}}$$

Control parameters:

$$W_{I1} = 100 \quad W_{13} = 5.0 \quad W_{33} = 10^{-6}$$

$$W_{11} = 10^{-6} \quad W_{22} = 10^{-1}$$

$$W_{12} = 10.0 \quad W_{23} = 50.0$$

{ aside w_{ii} is the basal expression level }

{ u increases/leads to transcription states }

{ all possible states }

{ aside I is the default microstate of the system }

{ The top terms of the regulation function represent the microstates and the possibility of being in that state as these states have a positive/helps in expression }

{ of the transcription in this case of the gene }

{ The bottom terms of the regulation function still represent the microstates and the possibility of being in those states but }

{ these terms are all possible states. And }

{ applies to both top and bottom terms } \rightarrow States that are associated with induction and repression have saturation functions

{ here Hill functions, based on the protein or inducer related to the repression or induction }

Prelim. Q2. continued.

$$\text{(i) } G_{P1} = G_{P2} = G_{P3} = 200 \frac{\text{copies}}{\text{cell}} \cdot \frac{1\text{mol}}{6.022 \times 10^{23} \text{copies}} \cdot \frac{1\text{nmoL}}{10^{-9}\text{mol}} \cdot \frac{1\text{cell}}{2.8 \times 10^{-13}\text{g}} \cdot \frac{0.39}{1\text{gDW}}$$

(vii)
and each cell is
70% water
 $\Rightarrow 30\%$ dry
 $g \cdot 0.3 = \text{gDW}$

$$\Rightarrow G_{P1} = G_{P2} = G_{P3} = 0.356 \frac{\text{nmoL}}{\text{gDW}}$$

assumption

$$\text{(ii) characteristic: } \frac{L_X}{\text{Length}} = 1000 \text{nt}$$

$$\frac{L_T}{\text{Length}} = 333 \text{AA}$$

$$(\text{assumption V}) \text{ RNAP} = R_X = 1150 \frac{\text{copies}}{\text{cell}} \cdot \frac{1\text{mol}}{6.022 \times 10^{23} \text{copies}} \cdot \frac{1\text{nmoL}}{10^{-9}\text{mol}} \cdot \frac{1\text{cell}}{2.8 \times 10^{-13}\text{g}} \cdot \frac{0.39}{1\text{gDW}}$$

Checking units

$$\frac{\text{copies}}{\text{cell}} \cdot \frac{\text{mol}}{\text{copies}} \cdot \frac{\text{nmoL}}{\text{mol}} \cdot \frac{\text{cell}}{\text{g}} \cdot \frac{\text{g}}{\text{gDW}} = \frac{\text{nmoL}}{\text{gDW}}$$

$$\Rightarrow R_X = 2.046 \frac{\text{nmoL}}{\text{gDW}}$$

$$(\text{assumption V}) \text{ Ribosomes} = R_T = 45,000 \frac{\text{copies}}{\text{cell}} \cdot \frac{1\text{mol}}{6.022 \times 10^{23} \text{copies}} \cdot \frac{1\text{nmoL}}{10^{-9}\text{mol}} \cdot \frac{1\text{cell}}{2.8 \times 10^{-13}\text{g}} \cdot \frac{0.39}{1\text{gDW}}$$

Checking units

$$\frac{\text{copies}}{\text{cell}} \cdot \frac{\text{mol}}{\text{copies}} \cdot \frac{\text{nmoL}}{\text{mol}} \cdot \frac{\text{cell}}{\text{g}} \cdot \frac{\text{g}}{\text{gDW}} = \frac{\text{nmoL}}{\text{gDW}}$$

$$\Rightarrow R_T = 80.06 \frac{\text{nmoL}}{\text{gDW}}$$

$$(\text{assumption Vi}) L_{X,1} = 1200 \text{nt}$$

$$\frac{L_{X,2} = 2400 \text{nt}}{L_{X,3} = 600 \text{nt}} \Rightarrow L_{L,i} \approx \frac{1}{3} L_{X,i} \Rightarrow L_{L,1} = 400 \text{AA}$$

$$\frac{L_{L,2}}{L_{L,3}} = 800 \text{AA}$$

$$L_{L,3} = 200 \text{AA}$$

$$(\text{assumption viii}) T_{d,1/2, \text{mRNA}} = 0.0333 \text{ hr} \Rightarrow k_{d, \text{mRNA}} = \frac{\ln(2)}{T_{d,1/2, \text{mRNA}}}$$

$$k_{d, \text{mRNA}} = 0.347 \text{ min}^{-1}$$

$$T_{d,1/2,p} = 24 \text{ hour} \cdot \frac{60 \text{ min}}{1 \text{ hour}} = 1440 \text{ min} \Rightarrow k_{d,p} = \frac{\ln(2)}{T_{d,1/2,p}}$$

$$k_{d,p} = 4.81 \times 10^{-4} \text{ min}^{-1}$$

Prelim.Q 2, Continued.

(assumption ix) RNAP elongation rate = $\dot{V}_X = \frac{60 \text{ nt}}{\text{s}} \cdot \frac{60 \text{ s}}{\text{min}} = \underline{\underline{\frac{3600 \text{ nt}}{\text{min}}} = \dot{V}_X}$

Ribosome elongation rate = $\dot{V}_L = 16.5 \frac{\text{AA}}{\text{s}} \cdot \frac{60 \text{ s}}{\text{min}} = \underline{\underline{\frac{990 \text{ AA}}{\text{min}}} = \dot{V}_L}$

(assumption X) $K_X = 0.24 \frac{\text{n mol}}{\text{g DW}}$ ← mRNA saturation constant

$K_L = 454.64 \frac{\text{n mol}}{\text{g DW}}$ ← Protein saturation constant

The kinetic limit of transcription is governed by,

$$V_{X,i} = K_{E,i} R_X \left(\frac{G_{pi}}{\tau_X K_X + (\tau_X + 1) G_{pi}} \right) \quad (1)$$

The kinetic rate of transcription is (1) multiplied by $u_{mi}(\dots)$

$$r_{X,i} = V_{X,i} u_{mi}(\dots) \quad (2)$$

The kinetic limit of translation is equal to the kinetic rate of translation as given by assumption iv.
Thus

$$r_{L,i} = K_{E,i} R_T \left(\frac{mRNA^*_i}{\tau_L K_L + (\tau_L + 1) mRNA^*_i} \right) \quad (3)$$

$mRNA$ at steady state

Prelim. Q2. continued.

As given in general and in data table #3,

$$\underline{T_x = 2.7}$$

$$\underline{T_L = 0.8}$$

$$mRNA^*_i = \underline{V_{x,i}}$$

$\lambda_{mRNA} \} \equiv$ Total "out flow" rate for mRNA
/ outflux

$$\lambda_{mRNA} = \text{degradation rate} + \text{dilution rate}$$

$$= k_{d,mRNA} + \mu_{cell}$$

$$\lambda_{mRNA} = 0.347 \text{ min}^{-1} + 0.0173 \text{ min}^{-1} = 0.3643 \text{ min}^{-1} = \underline{\lambda_{mRNA}}$$

λ_p Total "out flow" / outflux rate for Protein

$$\lambda_p = \text{degradation rate} + \text{dilution rate}$$

$$= k_{d,p} + \mu_{cell}$$

$$\lambda_p = 4.81 \times 10^{-4} \text{ min}^{-1} + 0.0173 \text{ min}^{-1} = 0.01778 \text{ min}^{-1} = \underline{\lambda_p}$$

$$k_{E,j,i} = \underbrace{\langle k_E \rangle}_{\frac{V_x}{L}} \left(\frac{L}{L_{x,i}} \right) = \frac{V_x}{L} \cdot \frac{L}{L_{x,i}} = \underline{\frac{V_x}{L_{x,i}}} = k_{E,j,i}$$

$$k_{Ex,j,i} = k_p \left(\frac{V_L}{L_{j,L}} \right) \Rightarrow k_{Ex,j,i} = \underline{\frac{V_L}{L_{j,L}}}$$

Poly some
amplification
number

→ Assumed to be 1

Prelim.Q2. continued.

Now, with the parameters listed before, Let's perform a mass balance around the mRNA's and the protein's in our system:

$$\text{rate produced} - \text{rate consumed} + \text{Accumulation} = \frac{\text{rate of change}}{\text{of general conserved quantity}}$$

$$\frac{dm_1}{dt} = V_{X,j1} u_{m1}(I) - k_{d,mRNA} m_1 - \mu_{cell} m_1$$

$$\frac{dm_2}{dt} = V_{X,j2} u_{m2}(P_1) - k_{d,mRNA} m_2 - \mu_{cell} m_2$$

$$\frac{dm_3}{dt} = V_{X,j3} u_{m3}(P_1, P_2) - k_{d,mRNA} m_3 - \mu_{cell} m_3$$

$$\frac{dP_1}{dt} = r_{L,j1}(I) - k_{d,p} P_1 - \mu_{cell} P_1$$

$$\frac{dP_2}{dt} = r_{L,j2}(P_1) - k_{d,p} P_2 - \mu_{cell} P_2$$

$$\frac{dP_3}{dt} = r_{L,j3}(P_1, P_2) - k_{d,p} P_3 - \mu_{cell} P_3$$

Simplified forms

$I \Rightarrow i$ in code

$$\frac{dm_1}{dt} = r_{X,j1}(I) - \lambda_{mRNA} m_1$$

$$\frac{dm_2}{dt} = r_{X,j2}(P_1) - \lambda_{mRNA} m_2$$

$$\frac{dm_3}{dt} = r_{X,j3}(P_1, P_2) - \lambda_{mRNA} m_3$$

$$\frac{dP_1}{dt} = r_{L,j1}(I) - \lambda_p P_1$$

$$\frac{dP_2}{dt} = r_{L,j2}(P_1) - \lambda_p P_2$$

$$\frac{dP_3}{dt} = r_{L,j3}(P_1, P_2) - \lambda_p P_3$$

Prelim, Q2. continued.

Now, modeling it descriptively like on pset #2

$$\underline{X}_{k+1} = \hat{\underline{A}} \underline{X}_k + \hat{\underline{S}} \underline{r}_k$$

$$\hat{\underline{A}} = \exp(\underline{A} \tau), \quad \tau \equiv \text{time-step size}$$

identity matrix

$$\hat{\underline{S}} = \underline{A}^{-1} [\hat{\underline{A}} - \underline{I}] \underline{S}_k$$

inverse of \underline{A}

"dilution" matrix

Stochastic matrix

$$\underline{A} = \begin{bmatrix} -\lambda_{\text{mRNA}} & 0 & 0 & 0 & 0 \\ 0 & -\lambda_{\text{mRNA}} & 0 & 0 & 0 \\ 0 & 0 & -\lambda_{\text{mRNA}} & 0 & 0 \\ 0 & 0 & 0 & -\lambda_p & 0 \\ 0 & 0 & 0 & 0 & -\lambda_p \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

"dil"

mRNA → protein

$$\underline{X}_k = \begin{bmatrix} m_1_k \\ m_2_k \\ m_3_k \\ p_1_k \\ p_2_k \\ p_3_k \end{bmatrix}$$

$$\underline{S} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

m_1
 m_2
 m_3
 p_1
⋮

$$\underline{r}_k = \begin{bmatrix} r_{x_1 k} \\ r_{x_2 k} \\ r_{x_3 k} \\ r_{L_1 k} \\ r_{L_2 k} \\ r_{L_3 k} \end{bmatrix}$$

$$T = 1.0 \text{ min}$$

Want to see response to 10 mM inducer
use the following protocol:

a.i) Graph's title (Model Ran to Steady state W/O Inducer)

Goal: run the model to steady-state without Inducer
 $(Y_1, \text{blue}) \equiv \text{protein } P_1$
 $(Y_2, \text{red}) \equiv \text{Protein } P_2$
 $(Y_3, \text{green}) \equiv \text{Protein } P_3$

for all plots
in Q2.

- saved as
Q2ai

a.ii) Graph's title (Phase 1)

Goal: from the steady-state, run the model without
inducer for an additional 60 min.

- saved as
Q2 aii

a.iii) Graph's title (phase 2)

Goal: add inducer and run the model for 300min.
- saved as Q2 aiii

a.Total) Graph's title (I1-FFL Q2.a.)

Goal: plot P_1, P_2 , and P_3 versus time

- saved as
Q2 a total

file for part Q2.a is called Q2Final.jl

Prelim. Q2. Continued

b.) phase 1's window is $\text{senp1}(i, j, t - 1019)$

↑ ↑ ↑
row column layer

phase 1's window is from
 $t = 1020 \text{ min}$ to $t = 1040 \text{ min}$

phase 2's windows is: $\text{senp2E}(i, j, t - 1074)$
early window

late window
 $\hookrightarrow \text{senp2L}(i, j, t - 1324)$

early window for phase 2 is from
 $t = 1075 \text{ min}$ to $t = 1095 \text{ min}$

late window for phase 2 is from
 $t = 1325 \text{ min}$ to $t = 1345 \text{ min}$

\Rightarrow perturbations in parameters set to 1% there
current value

$$\Rightarrow \text{using } s_{ij}(t) = \left(\frac{p_j}{x_i} \right) * \left. \frac{\partial x_i}{\partial p_j} \right|_t$$

run / include("Q2-runner.jl") with all files
in submission present in local directory.

Prelim. Q2. Continued.

(c) see julia code, Q2-runner.jl for $N_{ij} = \frac{1}{T} \int_0^T dt$
run/include
and the SVD and the U matrix analysis
 $\Delta_{ij}^{(t)} S_{ij}^{(t)}$
equal to the
matrixes calc. in
Q2.b.

using the trapezoidal rule to our 21 time layers

with $\Delta x = T = 1 \text{ min}$ \rightarrow
representing unique identifier depending on the time window
one is working in

$$\square N_{ij} = \frac{\Delta x}{2T} \cdot \left(1 \text{sen} \square (i, j, 1) + 2 \cdot 1 \text{sen} \square (i, j, 2) + \dots + 2 \cdot 1 \text{sen} \square (i, j, 20) + 1 \text{sen} \square (i, j, 21) \right)$$

\downarrow
20 in all
cases here

$$\square = P_1, P_2 E, \notin P_2 L$$

The SVD objects are $P_1, P_2 E, \notin P_2 L$

Ranking based on absolute magnitude of the first column of the U matrix for the 3 time windows:

From most sensitive to least goes:

For $|P_1|$: Protein 2 (0.607), mRNA2 (0.570),
Variable named \downarrow Protein 3 (0.404), mRNA3 (0.367),
 \downarrow up¹ Protein 1 (0.0856), mRNA1 (0.0448)

This ranking is reasonable \because the Proteins are sensitive to all the parameter changes that effect their corresponding mRNA's. Thus, they should and are as seen

above are more sensitive than their mRNAs. As the rest of the ranking it is reasonable as the main influence for mRNA1 is I and I is a state and thus is not considered in the sensitivity analysis, from mRNA1 having low sensitivity it follows that Protein 2 would also have low sensitivity. Then it is reasonable that mRNA3 is the next lowest sensitivity as it depends on Protein 1 and Protein 2, thus as (see next page)
 \downarrow 1 is regulated by

it would be the most sensitive species. As for protein 3 it reasons that as mRNA 3 is the most sensitive, protein 3 should be also. but note that mRNA 3 impact on protein 3 is damped by how it effects the translation rate as $R_{L3} = k_{EX,3} R + \frac{mRNA_3^*}{T_L k_L + (T_L + 1)mRNA_3^*}$, Thus as the sensitivity of

$$\left(\frac{mRNA_3^*}{T_L k_L + (T_L + 1)mRNA_3^*} \right)$$

mRNA₃ would effect both the numerator and the denominator, it creates a dampening type effect on the sensitivity of protein 3. Thus reasoning that as mRNA 3 is the most sensitive mRNA, protein 3 should be the least sensitive protein. As mentioned before as the regulation of mRNA 1 and mRNA 2 are only functions of one species, they will be less significantly sensitive compared to mRNA 3, and thus as the proteins are still sensitive wrt the parameters that their corresponding mRNA's are sensitive to and as these mRNA's the significant coupling mRNA 3 had it reasons that their proteins should be more sensitive than the mRNA's. Thus as for the same reasoning as for the time window for phase 1, mRNA 1 should be the least sensitive, followed by mRNA 2 as the least sensitive protein is protein 3 and thus since mRNA 2 & mRNA 1 have low sensitivity and protein 3's sensitivity is coupled to these species and more's sensitivity it follows that mRNA 2 will be the 2nd least sensitive followed by protein 3, and thus same as in time window for P1, protein 1 would be next sensitive as protein 2 should be more sensitive than protein 1, followed by protein 2 and the lastly mRNA 3 and this follows what the data/sensitivity analysis

mRNA2 is positively regulated by Protein 1, increases or decreases in Protein 1 would lead to increases or decreases in mRNA2 and thus Protein 2 and since protein 2 negatively regulates mRNA3 this would lead to a decrease or increase in expression but mRNA3 is also positively regulated by Protein 1 and thus these antagonistic effects lead/reason that mRNA3 would be less sensitive than mRNA2 and thus mRNA3 should as it is be the next least sensitive species, and this implies protein 3 is the next least sensitive species after mRNA3 and thus as mRNA2 and protein 2 are the only remaining species to be ranked it follows that mRNA2 will be the next least sensitive species after Protein 3 and thus the most sensitive species in phase 1 would be/is protein 2.

For IP2E.U1: mRNA3 (0.612), Protein2 (0.470), Protein1 (0.419)
variable name
saup2E Protein3 (0.339), mRNA2 (0.250), mRNA1 (0.227)

This ranking is reasonable as /because as mRNA3 has the most parameters and the largest regulation function which becomes significant when P1 and P2 concentrations become significant which happens when I_{inducer} is added. Thus it is reasonable that mRNA3 is the most sensitive to parameter changes. Now as previously talked about it would be a issue if Protein 3 was not more sensitive but that was only present when fluxiations in the regulatory functions are not present, as significant w.r.t time

In the early part of phase two the regulation function are undergoing significant changes and thus mRNA3 is effected by the sensitivity of all other species, except protein3. Thus it is reasonable that

Prelim. Q2. Continued.

predicted.

For IP2L, UI: Protein 3 (0.511), Protein 2 (0.498), Protein 1 (0.492),
Variable name
saup2L mRNA 3 (0.313), mRNA 2 (0.276), & mRNA 1 (0.274)

This ranking is reasonable as/ because at this point the proteins will be approaching their steady states and thus the sensitivity of the proteins should be greater than/ dependent on the same parameter / sensitive to the same parameters as their corresponding mRNA's. As mRNA 2 has the least coupling to other factors as its regulatory function U only depends on a state, I, it should be the least sensitive of the mRNA's, followed by mRNA 2 as it is influenced by the species α , i.e. it depends on more parameters and should be more sensitive than mRNA 1 as Protein 1 is effected by mRNA 1, then as mRNA 3 depends on both Protein 1 and Protein 2, it follows that mRNA 3 should be more sensitive than mRNA 2 and mRNA 1. Also as mRNA 3's regulatory function U, is a function of $C_{Protein 1}^{n_{03}}$ and $C_{Protein 2}^{n_{03}}$, at first thought it might seem as it would indicate that mRNA 3 would be more sensitive compared to protein 1 and protein 2 but as the effect the regulatory function as $\frac{(P_0)^{n_{03}}}{(K_{03})^{n_{03}} + (P_0)^{n_{03}}}$ thus creating a dampening effect on the variable dependency / sensitivity in Protein 2 and Protein 1. Thus indicating on a sensitivity scale Protein 1 and Protein 2 are more sensitive than mRNA 3 and as discussed previously Protein 3 is also more sensitive than mRNA 3. Now, as there are not significant fluctuations in the regulatory functions for the mRNA's wrt time, it follows that Protein 1's sensitivity > mRNA 3's sensitivity. In addition to that as the regulatory functions are significant in this time window, it follows that

Prelim. Q2. Continued.

Protein 1 will be the least sensitive of the proteins, and as Protein 3 has the most species coupled to its "expression" (the expression of mRNA 3 & the expression of Protein 1 not as normally used).

3), thus, without the significant fluctuations of mRNA 3's regulation function w.r.t time, the sensitivity of protein 3 is lacking the dampening characteristics seen previously. Thus it follows that protein 3 will be

the most sensitive species and from this it implies that protein 2 will be the 2nd most sensitive species. Thus from reasoning the sensitivity ordering/ranking of the species in phase 2 late window, should be

be from most to least sensitive: Protein 3, Protein 2, Protein 1, mRNA 3, mRNA 2, and mRNA 1. Thus the reasoning associated with the sensitivity is consistent with the ranking obtained by using single value decomposition on the time-averaged sensitivity array for Phase 2 Late, and analysing the absolute magnitude of the elements of the first column of \underline{U} .

Explanations for the shifts: The shift from the rankings seen in windows for phase 1 to both of the other time windows occur because as the regulatory functions for the mRNA's become significant (the $f_{mRNA}(...)$ are no longer $\ll 1$, and thus $U_{mRNA}(...)$ is no longer $\ll 1$), and how sensitive this function is w.r.t time in that time window (i.e. how much does the $U_{mRNA}(...)$ fluctuate over the time span of the time window).

The shift from the rankings seen in the time window for phase 2 Early comes from the fact that in this window the regulatory functions have significant fluctuations w.r.t time

Prelim.Q2.Final

and this characteristic /property is not seen in the other time windows which is why the rankings shift from phase 1 to phase 2E and from phase 2E to phase 2L as in both phase 1 and phase 2L the regulatory functions do not significantly fluctuate over the time span of the window. The shift in rankings seen in the time window for phase 2L comes from its regulatory function being significant (here significant meaning $U_{MO} \cancel{<} 1$), and that its regulatory function does not fluctuate significantly over the time span of the time window for phase 2 Late. These were some of the reasons behind the shift in the sensitivity rankings between time windows. (For more explicit explanations on how these individual properties /changes in the time windows effect the rankings, see the explanations for the rankings of each of the individual time-windows).

Overview of rankings:

Time window:	Phase 1	Phase 2 E	Phase 2 L
most sensitive:	Protein 2	mRNA 3	Protein 3
	mRNA 2	Protein 2	Protein 2
	Protein 3	Protein 1	Protein 1
	mRNA 3	Protein 3	mRNA 3
	Protein 1	mRNA 2	mRNA 2
least sensitive:	mRNA 1	mRNA 1	mRNA 1