

readme

Systems Biology Assignment(2)

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This readme is part of the assignment to review the paper: J.Lewis (2003), *Autoinhibition with transcriptional delay: a simple mechanism for the zebrafish somitogenesis oscillator*, Current Biology **13**, 1398-1408. This assignment is part of the course 'Systems Biology' by Natal van Riel at the Eindhoven University of Technology, the Netherlands. <http://www.tue.nl>.

singlecell_nonoise.m

This file belongs to the paragraph and results of direct autoinhibition of gene expression. Table 1 shows the parameters that can be altered and their default values and range.

Table 1 - parameters belonging to the 'singlecell_nonoise.m' file. In red, the default values if there are more options. If there are square brackets '[', this indicates a range of possible values. The value in red then still denotes the default value.

parameter	explanation	default value / range
RR	Chooses the molecule of interest (1=her1, 2=her7)	1,2
MM	Chooses the attenuation of interest (0=normal, 1=1/10 th , 2=1/20 th)	1,2,3
tmher1	The delay in the mRNA transcription of her1	[10.2,31.5], 12 [min]
tpher1	The delay in the protein translation of her1	2.8 [min]
tmher7	The delay in the mRNA transcription of her7	[5.9,20.1], 7.1 [min]
tpher7	The delay in the protein translation of her7	1.7 [min]
a	The rate of production of new protein molecules	4.5 [mRNA ⁻¹ min ⁻¹]
b	The decay rate of the protein	0.23 [min ⁻¹]
c	The decay rate of the mRNA	0.23 [min ⁻¹]
k	Transcription rate per hour	33 [cell ⁻¹ min ⁻¹]
P ₀	The critical concentration	40 [-]

If the reader wants to alter the attenuation coefficient manually, more attenuation coefficients can be added to the 'aa' parameter in the matlab-file.

To reproduce the results in the papers; the values in table 2 should be used for the mentioned parameters, the other parameter-values should remain the same.

Table 2 - parameters to be set to these values in order to reproduce the results shown in the paper. If there are more values mentioned, the analysis has to be run for each of those numbers.

parameter	explanation	value
RR	Chooses the molecule of interest (1=her1, 2=her7)	1
MM	Chooses the attenuation of interest (0=normal, 1=1/10 th , 2=1/20 th)	1,2,3
tmher1	The delay in the mRNA transcription of her1	12 [min]
tmher7	The delay in the mRNA transcription of her7	7.1 [min]

singlecell_noise.m

This file belongs to the paragraph and results of noisy control of gene expression. Table 3 shows the parameters that can be altered and their default values and range.

Table 3 - parameters belonging to the 'singlecell_noise.m' file. In red, the default values if there are more options. If there are square brackets '[', this indicates a range of possible values. The value in red then still denotes the default value.

parameter	explanation	default value / range
RR	Chooses the molecule of interest (1=her1, 2=her7)	1,2
MM	Chooses the attenuation of interest (0=normal, 1=1/10 th , 2=1/20 th)	1,2,3
tmher1	The delay in the mRNA transcription of her1	[10.2,31.5], 12 [min]
tpher1	The delay in the protein translation of her1	2.8 [min]
tmher7	The delay in the mRNA transcription of her7	[5.9,20.1], 7.1 [min]
tpher7	The delay in the protein translation of her7	1.7 [min]
Koff	The mean life-time of a bound repressor	1 [min ⁻¹]
eps	The time step of the discrete analysis	0.1 [min]
a	The rate of production of new protein molecules	4.5 [mRNA ⁻¹ min ⁻¹]
b	The decay rate of the protein	0.23 [min ⁻¹]
c	The decay rate of the mRNA	0.23 [min ⁻¹]
k	Transcription rate per hour	33 [cell ⁻¹ min ⁻¹]
P _{crit}	The critical concentration	40 [-]

If the reader wants to alter the attenuation coefficient manually, more attenuation coefficients can be added to the 'aa' parameter in the matlab-file.

To reproduce the results in the papers; the following parameters should changes to the mentioned values, the other parameters values should remain the same:

Table 4 - parameters to be set to these values in order to reproduce the results sown in the paper. if there are more values mentioned, the analysis has to be run for each of those numbers.

parameter	explanation	value
RR	Chooses the molecule of interest (1=her1, 2=her7)	1
MM	Chooses the attenuation of interest (0=normal, 1=1/10 th , 2=1/20 th)	1,2,3
koff	The mean life-time of a bound repressor	1 [min ⁻¹]
eps	The time step of the discrete analysis	0.1 min
tmher1	The delay in the mRNA transcription of her1	12 [min]
tmher7	The delay in the mRNA transcription of her7	7.1 [min]

twocells_nonoise.m

This file belongs to the paragraph and results of delta-notch communication in adjacent cells. Table 5 shows the parameters that can be altered and their default values and range.

Table 5 - parameters belonging to the 'twocells_nonoise.m' file. In red, the default values if there are more options. If there are square brackets '[', this indicates a range of possible values. The value in red then still denotes the default value.

parameter	explanation	default value / range
RR	Chooses the molecule of interest (1=Pher1, 2=Pher7, 3=Pdeltac, 4=mher1, 5=mher7, 6=mdeltac)	1,2,3,4,5,6
MM	Chooses the coupling of interest (0=uncoupled, 1=coupled TN=36, 2=coupled TN=56)	1,2,3
lag	The array containing all delays in cell 1 (1: tphe1, 2: tphe7, 3: tpe1ac, 4: tme1, 5: tme7, 6: tpe1ac)	
lag1:1	The delay in the protein translation of her1	2.8 [min]
lag1:2	The delay in the protein translation of her7	1.7 [min]
lag1:3	The delay in the protein translation of deltaC	20.5 [min]
lag1:4	The delay in the mRNA transcription of her1	[10.2,31.5], 12 [min]
lag1:5	The delay in the mRNA transcription of her7	[5.9,20.1], 7.1 [min]
lag1:6	The delay in the mRNA transcription of deltac	[16,68] 16 [min]
r	The relative importance of manners of transcription for her1 and her7 (r:1+r:2+r:3+r:4=1)	
r:1	Relative importance of unregulated transcription	[0,1]
r:2	Relative importance of delta/notch activity	[0,1]
r:3	Relative importance of her1/her7 alone	[0,1] 1 (uncoupled)
r:4	Relative importance of combined delta/notch & her1/7	[0,1]
s	The relative importance of manners of transcription for deltaC (s:1+s:2+s:3+s:4=1)	
s:1	Relative importance of unregulated transcription	[0,1]
s:2	Relative importance of delta/notch activity	[0,1]
s:3	Relative importance of her1/her7 alone	[0,1] 1 (uncoupled)
s:4	Relative importance of combined delta/notch & her1/7	[0,1]
a	The rate of production of new protein molecules	4.5 [mRNA ⁻¹ min ⁻¹]
b	The decay rate of the protein	0.23 [min ⁻¹]
c	The decay rate of the mRNA	0.23 [min ⁻¹]
k	Transcription rate per hour	33 [cell ⁻¹ min ⁻¹]
P_{OH}	The critical concentration for her1 and her7	40 [-]
P_{OD}	The critical concentration for deltac	1000 [-]

If the reader wants to alter the relative importance of the manner of transcription, one can do this is the 'if' statement where they are declared. To reproduce uncoupled behavior, please enter:

r=[0,0,1,0] and s=[0,0,1,0]. For coupled behavior, please enter: r=[0,0,0,1] and s=[0,0,1,0] (these parameters come directly from the authors supplemental data).

To reproduce the results in the papers; the following parameters should changes to the mentioned values, the other parameters values should remain the same:

Table 6 - parameters to be set to these values in order to reproduce the results shown in the paper. if there are more values mentioned, the analysis has to be run for each of those numbers.

parameter	explanation	value
RR	Chooses the molecule of interest (1=her1, 2=her7)	6
MM	Chooses the attenuation of interest (0=normal, 1=1/10 th , 2=1/20 th)	1,2,3