

Description for the attached code:

1. Deterministic and stochastic simulation of WT and mutant phenotype (Figures 2B-G, 3B, 3C, 3G, S3B, S4B, and S9)  
File : run “**stochastic simulation.m**” in the folder: “./stochastic simulation/
  - 1.1 (stochastic simulation.m) switch “gene switch” to “0” for setting gene mutation
  - 1.2 (stochasticsim\_mod27det.m and stochasticsim\_mod27sc.m) switch the “noise tuning” to “0” for deterministic simulation
  - 1.3 (stochasticsim\_mod27det.m and stochasticsim\_mod27sc.m) Switch from 'LogicgeneX' to 'LogicgeneX\_noAC' (in the regulatory function of gene X to exclude BLMP-1 activation of *lin-29* through regulating gene X.
- 2 nullcline\_analysis (Figure 4)  
File : run “**nullcline\_analysis.m**”
  - 2.1 generate the phase map by setting the ratio of maximum LIN-42, SCF-DRE-1, and DAF-12 ligand production
  - 2.2 Set the parameter 'neg\_strength\_BLMP1rp geneX' to '0' to include BLMP-1 activation of *lin-29*, or set it to '1' to exclude BLMP-1 activation of *lin-29*.
- 3 SCF-DRE-1 activity variation (Figures 5Bii and 5Biii)  
File : run “**Dre1\_activity\_variation.m**” in the folder: “./ Dre-1 activity variation/
  - 3.1 (Dre1\_activity\_variation.m) Choose either 'K\_Dre1\_re\_Blmp1\_sc' or 'gama\_Dre1\_re\_Blmp1\_sc' for plotting the output when tuning either the threshold of BLMP-1 degradation or the degradation rate of BLMP-1 regulated by SCF-DRE-1, respectively.
  - 3.2 (para28.m) To tune either the threshold of BLMP-1 degradation or the degradation rate of BLMP-1 by SCF-DRE-1, multiply the scaling factor for either parameter 'K\_Dre1\_re\_Blmp1\_sc' or 'gama\_Dre1\_re\_Blmp1\_sc', respectively.
- 4 Dre-1 onset time variation (Figure 5Bii)  
File : run “**Dre1\_onset\_time\_variation.m**” in the folder: “./ Dre-1\_onset\_time\_variation /
- 5 noise induced switching test (using constant LIN-42 level as input) (Figures 6Ai and 6Bi ) File : run “**noise induced switching\_constant LIN-42.m**” in the folder: “./ noise induced switching constant LIN-42 /

- 5.1 (noise induced switching\_constant LIN-42.m) use the parameter “L42\_sc” for setting the ratio of maximum LIN-42 production.
- 5.2 (noise induced switching\_constant LIN-42.m) switch “gene switch” to “0” for setting gene mutation
- 5.3 (stochasticsim\_mod27det.m and stochasticsim\_mod27sc.m) switch the “noise tuning” to “0” for deterministic simulation
- 5.4 Compare the simulation results by running “swithingplot.m”
- 6 noise induced switching test (using constant LIN-42 level as input) (Figure 6Aii-iii and 6Bii-iii) File : run “**noise\_induced\_switching\_cyclicLIN42.m**” in the folder: “./ noise induced switching cyclic LIN-42 /”
  - 6.1 (noise induced switching\_constant LIN-42.m) switch “gene switch” to “0” for setting gene mutation
  - 6.2 (stochasticsim\_mod27det.m and stochasticsim\_mod27sc.m) switch the “noise tuning” to “0” for deterministic simulation
  - 6.3 (stochasticsim\_mod27det.m and stochasticsim\_mod27sc.m) Set gamma\_L42 to 5 times its default value to increase the LIN-42 noise frequency by fivefold.
  - 6.4 Run 'plotnetworkI.m' to compare the distribution of DTC turning times simulated with either 1X (default) or 5X LIN-42 noise frequency.
  - 6.5 Run “plotnetworkII.m” to compare the heatmap of DTC turning time simulated with 1X (default) or 5X LIN-42 noise frequency.
- 7 Bistability analysis (Figures S7 and S8)
 

File : run “**bistability\_analysis.m**” in the folder: “./bistability analysis/”

  - 7.1 (bistability\_analysis.m) switch the “gene switch” to “0” for gene mutation
  - 7.2 (bistability\_analysis.m) run the “deterministic\_mod30.m” and “deterministic\_mod30\_noAC.m” for simulating from a high UNC-5 level. The file with “\_noAC” indicating the simulation of circuit excluding BLMP-1 activation of *lin-29*.
  - 7.3 (bistability\_analysis.m) run the “deterministic\_mod30m.m” and “deterministic\_mod30m\_noAC.m” for simulating from a low UNC-5 level. The file with “\_noAC” indicating the simulation of circuit excluding BLMP-1 activation of *lin-29*.
- 8 Simple regulation test (Figure S10)
 

File : run “**simple model.py**”

  - 8.1 For stochastic simulation of the gene circuit with BLMP-1 activation of *lin-29*, use the regulatory function 'f\_as\_g' to simulate a 'low to

high' LIN-42 transition, or use 'f\_de\_r' to simulate a 'high to low' LIN-42 transition.

- 8.2 For stochastic simulation of the gene circuit excluding BLMP-1 activation of *lin-29*, use the regulatory function 'f\_noAC\_as\_g' to simulate a 'low to high' LIN-42 transition, or use 'f\_noAC\_de\_r' to simulate a 'high to low' LIN-42 transition.