

Source codes and data files for computation (journal.pone.0104057)

This repository contains the source codes and the data files for computation in journal.pone.0104057. “FFL” folder contains the files for computation of FFL models. “AKT_pathway” folder contains the files for computation of AKT pathway model.

“FFL” folder contains the data files used for computation and draw figures. “step_10_data_points.data” file was used for parameter inference and model selection in Figure 2-7 and Table 1, and to draw Figure 1.C, 3 and 6. This file was also shown in Table S1. This file was renamed as “ref_time_point.data” when used for computation. “pulse_10_data_points.data” file was used to draw Figure 4 and 7. This file was also shown in Table S2. The data are put in order of time (Time = 1, 2,...,10) in these files. “step_100_data_points.data” file was used for parameter inference and model selection in Figure S1 and Text S3, and to draw Figure S1.A and S1.B. This file was renamed as “ref_time_point.data” when used for computation. “pulse_100_data_points.data” file was used to draw Figure S1.C and S1.D. The data are put in order of time (Time = 0.1, 0.2,...,9.9, 10) in these files.

“FFL” folder contains the source codes used for parameter inference and model selection. “model_selection” folder contains “population_annealing” folder and “rejection_sampler” folder. “10_data_points” folder contains the source codes for computation of Figure 2-7 and Table S1. “100_data_points” folder contains the source codes for computation of Figure S1 and Text S3. The number of “annealing_schedule” folder corresponds to the number in Table 1. For parameter inference, we wrote 10 population annealing source codes of 10000 particles computation with different random seed because of the lack of memory of used machine. Their simulated results were combined (totally 100000 particles) for parameter inference. For model selection, we wrote 20 population annealing source codes of 50000 particles computation with different random seed because of the lack of memory of used machine. Two by two of their simulated results were combined (totally 100000 particles for 1 independent computation) to calculate the mean and the standard deviation of 10 independent computations for model selection in Table 1 and Text S3. In ABC rejection sampler source codes for model selection, numerically-calculated accept particle number was divided by total particle number.

“AKT_pathway” folder contains the source codes used for parameter inference and model selection of Figure 8 and Table 2. “model_selection” folder contains

“population_annealing” folder and “rejection_sampler” folder. The number of “annealing_schedule” folder corresponds to the number in Table 2. In ABC rejection sampler source codes for model selection, numerically-calculated accept particle number was divided by total particle number. “AKT_pathway” folder does not contain the data file used for computation. This is because the data file can be freely downloaded from the web page of the group of Noguchi et al. (2013) Mol. Syst. Biol. study as mentioned in the main text.

For computation, the source codes were compiled with the files of Mersenne twister (mt19937ar.c, mt19937ar.h downloaded from Mersenne Twister Home Page, we thank Dr. Matsumoto and Dr. Nishimura for development) for random number generation. The source codes were compiled by GNU Compiler Collection. For example, they were compiled as “gcc -O2 pa1.c mt19937ar.c -lm” in FFL models and “gcc -O2 pa1.c mt19937ar.c function.c -lm” in AKT pathway model, where “-O2” is a compiler option and “function.c” file is needed for computation of AKT pathway model.

Note that comments in source codes are written in Japanese.