We provide two Matlab scripts to help process the raw results into straightforward numbers. Matlab 2018 is required to run the scripts. To use the scripts, change Matlab working directory into the **result** folder of a simulation.

process_fitness

This function uses *evo_summary_x.txt* to calculate the fitness of the evolved genotype, and plot fitness over evolutionary steps.

Syntax

fitness_statistics = process_fitness(simulation_id,window_size)

Description

`simulation_id` : the "x" in *evo_summary_x.txt*.

`window_size` : the number of evolutionary steps used to average fitness in a simulation; the last window_size evolutionary steps are used.

fitness_statistics: a 1x6 array, in which the first three entries are the fitness under the two environments and their weighted-average, averaged over `window_size`, and the last three are the variance of the three fitness over the `window_size`.

calc_motif_occurrence

This function uses *N_motifs.txt* to calculate the occurrence of different motifs in the evolved genotypes. Occurrence is defined as the proportion of evolutionary steps in which at least one motif is present.

Syntax

occurrence=calc_motif_occurrence(window_size)

Description

`window_size` : the number of evolutionary steps used to calculate the occurrence of motifs; the last window_size evolutionary steps are used.

`occurrence` : a 1x36 array. Each entry is the occurrence of a motif that corresponding to *N_motifs.txt*; please refer to the readme of output files for the content of *N_motifs.txt*.

calc_Near_AND_gate

This function uses N_motifs.txt and N_Near_AND_gate_motifs.txt to calculate the proportion of evolutionary steps that contain AND-gated motifs and/or near AND-gated motifs, among the last X evolutionary steps. It also calcuate the proportions of near-AND-gated motifs that are fast-TF-controlled, slow-TF-controlled, or OR-gated.

Syntax

[occurrence, contribution_from_different_logic]=calc_Near_AND_gate(window_size)

Description

`window_size` : the number of evolutionary steps used to calculate the occurrence of motifs; the last window_size evolutionary steps are used.

`occurrence` : a 1x16 array. The columns are:

Col1: the proportion of steps with AND-gated isolated C1-FFLs only

Col2: the proportion of steps with near-AND-gated isolated C1-FFLs only

Col3: the prorportion of steps with both AND-gated and near-AND-gated isolated C1-FFLs

Col4: the proportion of steps with either AND-gated or near-AND-gated

isolated C1-FFLS

Col5: the proportion of steps with AND-gated C1-FFLs that depend on weak TFBSs in effector genes (if these weak TFBSs are excluded in scoring motifs, the corresponding C1-FFLs will be lost)

Col6-10: similar summaries about FFL-in-diamond

Col11-15: similar summaries about isolated diamond

Col16: the proportion of steps that contain at least one of AND-gated isolated C1-FFLs, near-AND-gated isolated C1-FFLs, AND-gated isolated diamonds, and near-AND-gated isolated diamonds

contribution_from_different_logi: a 1x9 array. Columns are

Col1: the average proportion of near-AND-gated isolated C1-FFLs that are slow-TF-controlled

Col2: the average proportion of near-AND-gated isolated C1-FFLs that are fast-TF-controlled

Col3: the average proportion of near-AND-gated isolated C1-FFLs that are OR-gated

Col4-6: similar summaries about FFL-in-diamond

Col7-9: similar summaries about isolated diamond

summarize_parameters

This function calculates the mean and variance of parameters in networks motifs. The function requires *parameters.txt*.

Syntax

[means, variances]=summarize_parameters(simulation_ids, sample_size)

Description

Different from the first 3 functions, summarize_parametes can batch

process results from multiple simulation replicates. To To use batch processing, organize results so such *parameters.txt* of replicate *x* is under "rep*x*/result/" and execute summarize_parameters in the directory that contains all repx.

`simulation_ids` : an integer array of the ids of simulation replicates.

`sample_size` : this is the number of resampling from a replicate.

`means` : a 4x6 matrix. Each entry is the mean value of a parameter, averaged over all samples of a replicate and over all replicates. Row 1 to 4 correponds to parameters of the fast TF, the slow TF, the effector, and the signal. Column 1 to 6 are

transition rate from active promoter to intermediate promoter, mRNA degradation rate, protein synthesis rate, protein degradation rate, locus length, and Kd of TFs.

`variances` : a 4x6 matrix. Each entry is the variance of a parameter in a batch of samples taken from each replicate, and then averaged over all replicates. Rows and columns of `variances` are similar to those `means` .