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 1x39 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  $N_motifs$ .