This repository contains MATLAB scripts to generate **Figures SM.6B – E**

The following codes generate **Figures SM.6B**

* **FIGURE\_SM\_6.m**  
  This is the **main script** to run the simulations.  
  You can modify:
  + Initial conditions (e.g., number of Da, DR1, DR2, DR12 nucleosomes, mRNA level, Protein level)
  + Simulation parameters (e.g., number of simulations, time points for histogram output)
  + If needed, you can save the values of the variables at the final day of simulation. These distributions are then used in the script FIGURE\_SM\_6\_3bins.m to generate Figures SM.6C–E.  
    For convenience, the corresponding .mat files from our simulations have been saved and included in the folder:
* initialdistributionD1.mat
* initialdistributionD2.mat
* initialdistributionD12.mat
* initialdistributionDA.mat
* initialdistributionmx.mat
* initialdistributionx2.mat
* **SSA\_FIG\_SM\_6\_1.m**  
  This file implements the **stochastic simulation algorithm (SSA)** using Gillespie’s method.  
  You can tune **model parameters** (e.g., reaction rates) directly in this file.

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The following codes generate **Figures SM.6C-E**

* **FIGURE\_SM\_6\_3bins.m**  
  This is the **main script** to run the simulations from the saved intermediate gene expression level distributions.   
  You can modify or tune:
  + **Bin range** (lines 40 - 42)
  + **Simulation parameters** (e.g., number of simulations, time points for histogram output and violin plots)
* **SSA\_FIG\_SM\_6\_1.m**  
  (Same as above) This file implements the **stochastic simulation algorithm (SSA)** using Gillespie’s method.  
  You can tune **model parameters** (e.g., reaction rates) directly in this file.

**Additional notes**

* To correctly visualize the output distributions on a **logicle scale**, make sure to include the **@logicleTransform** folder in the same directory or MATLAB path.
* To generate **violin plots**, make sure to include the functions **Violin.m** and **violinplot.m** in the same directory or MATLAB path.