This repository contains MATLAB scripts to generate **Figure SM.8**.

* **FIGURE\_SM\_8.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, input range, FACS day)

(Optional) The final section of the script (currently commented out) allows you to plot **high** and **low** gene expression distributions separately.

To use this, ensure you have the files:  
LowX.mat  
HighX.mat

These files store precomputed distributions and are necessary to replicate Figure SM.8.

* **SSA\_FIG\_SM\_8.m**  
  This file implements the **stochastic simulation algorithm (SSA)** using Gillespie’s method.  
  You can modify or tune:
  + **Model parameters**, including reaction rates (e.g., p.ktprime, p.kea, p.kma, etc.)
  + **External input**:
    - The simulation supports three types of inputs: **KRAB**, **DNMT3**, and **TET1**.
    - Depending on the input of interest, **you must comment/uncomment the appropriate lines inside SSA\_FIG\_SM\_8.m**:
      * Lines 140–141: enable/disable KRAB
      * Lines 159–160: enable/disable DNMT3
      * Lines 171–172: enable/disable TET1
* To correctly visualize the output distributions on a **logicle scale**, make sure to include the **@logicleTransform** folder in the same directory or MATLAB path.
* **Required Input Files**: to run the full simulation pipeline, the following .mat files are required as **inputs** for initial condition sampling:
* IntermediateD10.mat
* IntermediateD220.mat
* IntermediateD120.mat
* IntermediateDA0.mat
* Intermediatem0.mat
* IntermediateX0.mat

These represent intermediate distributions from prior simulations and are used to generate our starting states.