This repository contains MATLAB scripts to generate **Figures SM.3C, SM.3E, SM.1E, and 2L**

* **FIGURE\_SM\_3.m**  
  This is the **main script** to run the simulations.  
  You can modify:
* **Initial conditions** (e.g., number of Da, DR1, DR2, DR12 nucleosomes, etc.)
  + Based on the input of interest (DNMT3 or TET1), you must set the correct initial conditions. See lines **61–73** for guidance.
* **Simulation parameters** (e.g., number of simulations, time points for histogram output)
* **External input range** (lines 35–44).

The last part of the script can optionally be uncommented to generate **Y1 distributions**, replicating the **RHS panel of Figure SM.1E**.

**• SSA\_FIG\_SM\_5\_3.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.kea, p.kma, etc.)
* **External input control**:
  + The code supports **DNMT3** and **TET1** inputs.
  + Depending on the input of interest, you must **comment/uncomment the corresponding lines**:
    - **Lines 115–116**: enable/disable DNMT3
    - **Lines 125–126**: 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.