This repository contains MATLAB scripts to generate **Figure SM.5**.

* **FIGURE\_SM\_5.m**  
  This is the **main script** to run the simulations.  
  You can modify:
  + Initial conditions (e.g., number of Da, DR1, DR2, DR12 nucleosomes)
  + Simulation parameters (e.g., number of simulations, time points for histogram output)
  + Depending on the input of interest, **you must comment/uncomment the appropriate lines, associated with the presence of DAPG, inside FIGURE\_SM\_5.m** (lines 43-44)
* **SSA\_FIG\_SM\_5.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** and **DNMT3**.
    - Depending on the input of interest, **you must comment/uncomment the appropriate lines inside SSA\_FIG\_SM\_5.m**:
      * Lines 102–103: enable/disable KRAB
      * Lines 121–122: enable/disable DNMT3
* To correctly visualize the output distributions on a **logicle scale**, make sure to include the **@logicleTransform** folder in the same directory or MATLAB path.