This repository contains MATLAB scripts to generate **Figures SM.2, SM.1B, and 2M**

* **FIGURE\_SM\_2.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)
* **SSA\_FIG\_SM\_2.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.
* To correctly visualize the output distributions on a **logicle scale**, make sure to include the **@logicleTransform** folder in the same directory or MATLAB path.