This repository contains MATLAB scripts to generate **Figure SM.4**.

**Figure SM.4 – top panels**

* **SSA\_FIG\_SM\_4\_trajectories.m**  
  This is the **main script** to run the simulations. 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**: the simulation supports different values of Y1. Depending on the amount of interest, **you must set the variable rrrr accordingly (Line 33).**
* To correctly visualize the smoothed trajectories, if needed, make sure to include the function **movingmean.m** in the same directory or MATLAB path.

**Figure SM.4 – bottom panels**

* **FIGURE\_SM\_4.m**  
  This is the **main script** to run the simulations.  
  You can modify or tune:
  + **Initial conditions** (e.g., number of Da and DR2 nucleosomes)
  + **External input**: the simulation supports different values of Y1. Depending on the amount of interest, **you must set the variables l1,l2 accordingly (Lines 37, 38).**
  + **Simulation parameters** (e.g., number of simulations, time points for histogram output)
* **SSA\_FIG\_SM\_4.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.