This repository contains MATLAB scripts to generate **Figures 4G, 4H, 4I, and 4J**

The following codes generate **Figure 4G**

**Main Script**

* **Code\_FIG4G.m**  
  This code computes and plots the **probability distribution of the fraction of CpGs methylated** across a selected genomic region  
    
  You can choose the genomic region by selecting a subset of rows in the input matrix. This selection can correspond to **specific time points** (lines 24-25) or **genomic bins (lines 53-54).**

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The following codes generate **Figures 4I**

**Main Script**

* **Code\_FIG4I.m**  
  This code generates a **correlation plot** between **gene expression** and **CpG methylation fraction**, including statistical analysis.  
    
  To correctly visualize the output distributions on a **logicle scale**, make sure to include the **@logicleTransform** folder in the same directory or MATLAB path.

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The following codes generate **Figures 4H**

**• Code\_FIG4H\_J.m**

This is the main script to run the simulations.  
You can modify or tune:

* **Initial conditions** (e.g., initial level of DNA methylation): lines 55–60
* **Simulation parameters** (e.g., number of simulations, time points for histogram output)

**• SSA\_FIG\_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.

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The following codes generate **Figures 4J**

**Workflow:**  
To generate Figure 4J:

* First, run Code\_FIG4H\_J.m, which saves the necessary .mat files for gene expression and DNA methylation statistics at different timepoints (e.g., first time point and second time point).
* Then, use Code\_FIG4I.m **replacing the hardcoded mean/stdev vectors with the saved variables** to replicate the simulation-based version of the correlation plot.