

"Coinfecting Phages Impede Each Other's Entry into the Cell"

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These scripts were developed using MATLAB versions 2019a–2023b (64-bit).

Important: For the dependent functions and parameter files to be correctly loaded, this folder (containing the two *.m files and this README document) must be set as the working folder of the current MATLAB session; this can be checked using the `pwd` command. In addition, this folder and all subfolders therein must be added to the search path of the current MATLAB session (see [MATLAB Documentation](#)).

This folder comprises two main MATLAB files:

1. **simulation_entry_vsanalytical_vsapprox.m**, used to simulate phage entry into the cell.
 - The algorithm behind this simulation is described in section “*Simulating the stochastic model*” in the STAR Methods of the publication.
 - In this script, the results of the stochastic simulation are also plotted and compared to the predictions by the analytical expressions of the model (described in section “*Stochastic model of phage entry kinetics*”) and the fits to the phenomenological expressions (described in section “*Measuring the numbers of adsorbed phages and intracellular phage genomes following bulk infection*”, subsection “*Data analysis*”). See **Figures S30–S35** in the preprint version of this paper on bioRxiv (doi.org/10.1101/2023.06.05.543643).
 - **Section description and execution order:**
 - i. Run sections 1 (“*Preparation [...]*”) and 2 (“*Simulation [...]*”) before sections 3.1–3.5 (where the results are plotted).
 - ii. Sections 3.1–3.5, examining the simulation results, are independent from one another and can be run in any order.
2. **simulation_cellfate_withentrydynamics.m**, used to simulate the infection outcome.
 - The algorithm behind this simulation is described in section “*Stochastic simulation of infection outcome in individual cells*” in the STAR Methods of the publication.
 - After the simulation, this script plots the trajectories of CI and Cro concentrations, the distributions of infection outcomes, and the MOI response curve with Hill fitting (see **Figures 6** and **S7** in the paper). This script also plots other observables not shown in the paper (e.g., MOI distribution, as in **Figure S27** in the preprint version).
 - **Section description and execution order:**
 - i. First, run sections 1.1–1.5 (in that order), which simulate phage entries in individual cells, then, the fate of those cells under different model assumptions.
 - ii. Section 2, preparing the instructions for plotting, must always be executed.
 - iii. Sections 3.1–3.2 examine the simulated distributions of cell size and MOI.
 - iv. Sections 4.1–4.5 examine the trajectories of CI and Cro, the infection outcome as a function of the input MOI, and changes to the Hill coefficients of the MOI response curves under different model assumptions.

The subfolder “*Dependent files*” contains the functions and parameter values required to run the two main MATLAB files above (see notes above regarding adding to the search path and setting the working folder).