

# Structured population dynamics with partial sampling

Lab Immersion

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# Introduction

Wright-Fisher model

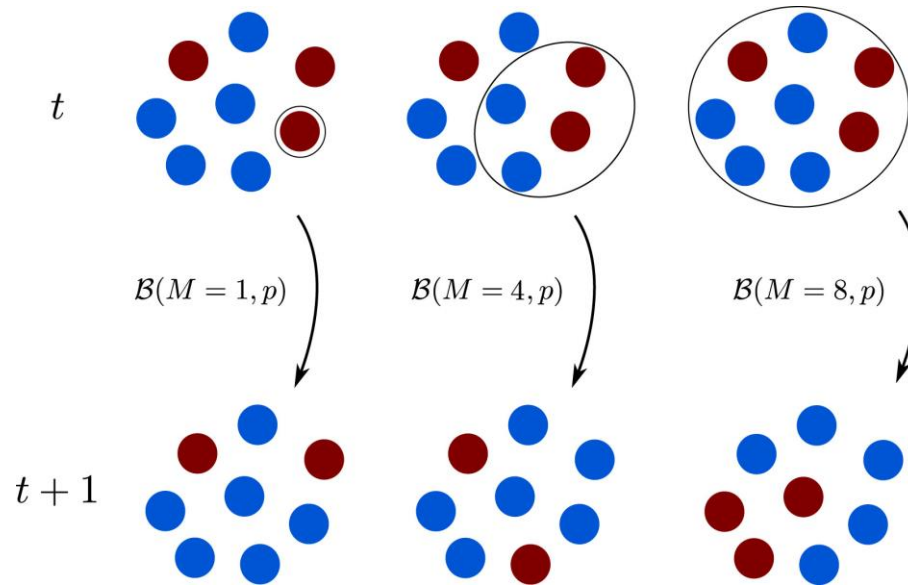
$$P_{i \rightarrow j} = \binom{N}{j} p^j (1-p)^{N-j}$$

$$\begin{cases} x = \frac{i}{N} \\ p = \frac{x(1+s)}{1+xs} \end{cases}$$

Moran model

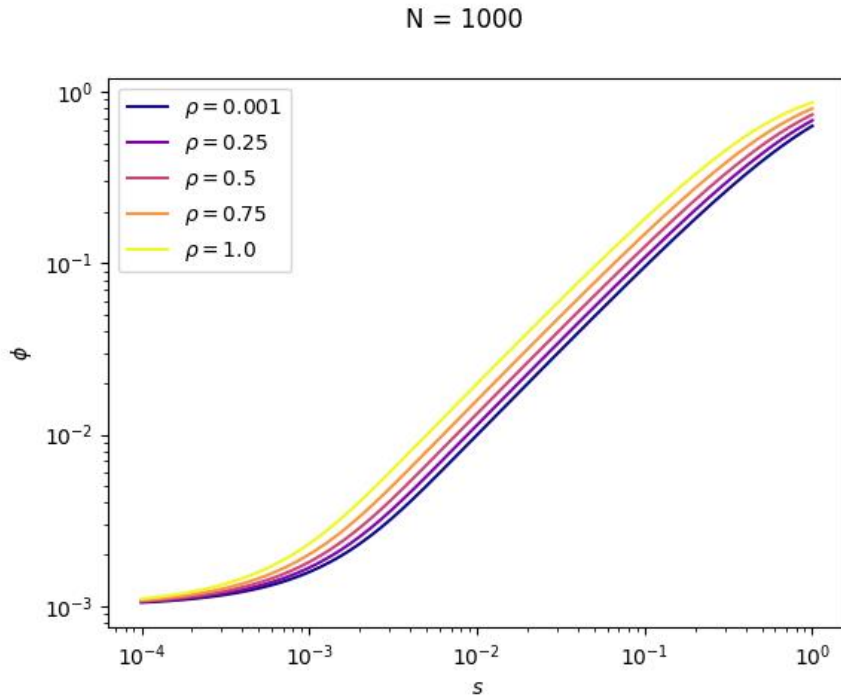
$$P_{i \rightarrow j} = \begin{cases} x(1-p) & \text{if } j = i - 1 \\ xp + (1-x)(1-p) & \text{if } j = i \\ p(1-x) & \text{if } j = i + 1 \\ 0 & \text{otherwise} \end{cases}$$

# Introduction: partial sampling



From Alexandre, Arthur, Alia Abbata, Cecilia Fruet, Claude Loverdo, and Anne-Florence Bitbol. "Bridging Wright-Fisher and Moran Models."

# Introduction: Fixation probability



- Probability to fixate starting from one mutant, given its relative fitness
- Under the diffusion approximation:

$$N \gg 1, s \sim \frac{1}{N}$$

$$\phi(s) = \frac{1 - \exp(-\frac{2}{2-\rho}s)}{1 - \exp(-\frac{2}{2-\rho}Ns)} \quad \text{with} \quad \rho := \frac{M}{N}$$

# Methods: Well-mixed case

## Simulations:

- Simulate a large number of runs
- Count the number of fixations, and the number of steps before extinction/fixation

## Matrix inversions:

- Compute the transition matrix  $P$ , and its limit by permutating some states

$$P = \begin{bmatrix} 1 & 0 & 0 \\ b_1 & A & b_2 \\ 0 & 0 & 1 \end{bmatrix} \in \mathbb{R}^{(N-1) \times (N-1)} \quad \leftrightarrow \quad \bar{P} = \begin{bmatrix} A & B \\ 0 & I_2 \end{bmatrix}$$

$$\bar{P}^n = \begin{bmatrix} A^n & B_n \\ 0 & I_2 \end{bmatrix} \quad \text{with} \quad B_n = \left( \sum_{k=0}^{n-1} A^k \right) B \xrightarrow{n \rightarrow \infty} (I_{N-1} - A)^{-1} B \quad \Rightarrow \quad \phi = [(I_{N-1} - A)^{-1} B]_{0,2}$$

Manhart, Michael, Allan Haldane, and Alexandre V. Morozov. "A Universal Scaling Law Determines Time Reversibility and Steady State of Substitutions under Selection."

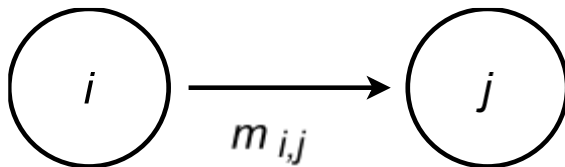
# Methods: Structured populations

- Consider a graph of  $D$  demes, each having  $N$  individuals
- For each deme, perform a partial sampling step with a weighted average:

$$\tilde{x}^{[i]} = \sum_{k=1}^D m_{k,i} x^{[k]}$$

- The structure is represented by the migration rate matrix  $m = (m_{i,j})_{1 \leq i,j \leq D}$

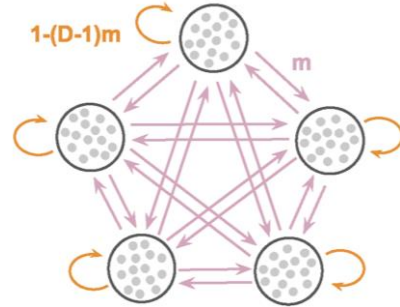
Such that  $0 \leq m_{i,j} \leq 1$ ,  $\sum_{k=1}^D m_{k,i} = 1$



# Methods: Graphs

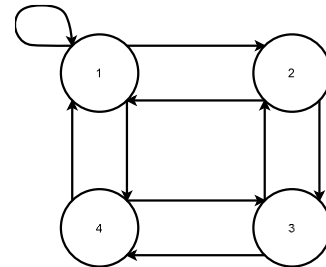
- **Clique:**

$$m_{i,j} = \begin{cases} 1 - (D - 1)m & \text{if } i = j \\ m & \text{otherwise} \end{cases}$$



- **Cycle:**

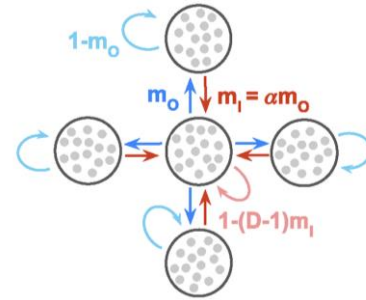
$$m_{i,j} = \begin{cases} m & \text{if } j = i - 1 \pmod D \\ 1 - (\alpha + 1)m & \text{if } j = i \pmod D \\ \alpha m & \text{if } j = i + 1 \pmod D \\ 0 & \text{otherwise} \end{cases}$$



# Methods: Graphs

- Star:

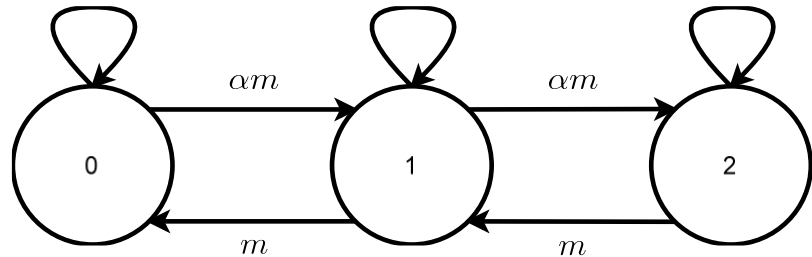
$$\forall i > 0, \quad m_{0,i} = m, \quad m_{i,0} = \alpha m, \quad m_{i,i} = 1 - m, \\ m_{0,0} = 1 - (D-1)\alpha m$$



- Line:

$$m_{0,0} = 1 - m \\ m_{D-1,D-1} = 1 - \alpha m$$

$$m_{i,i+1} = \alpha m \quad \text{if } i < D-1 \\ m_{i,i} = 1 - (1 + \alpha)m \quad \text{if } 0 < i < D-1 \\ m_{i,i-1} = m \quad \text{if } i > 0$$

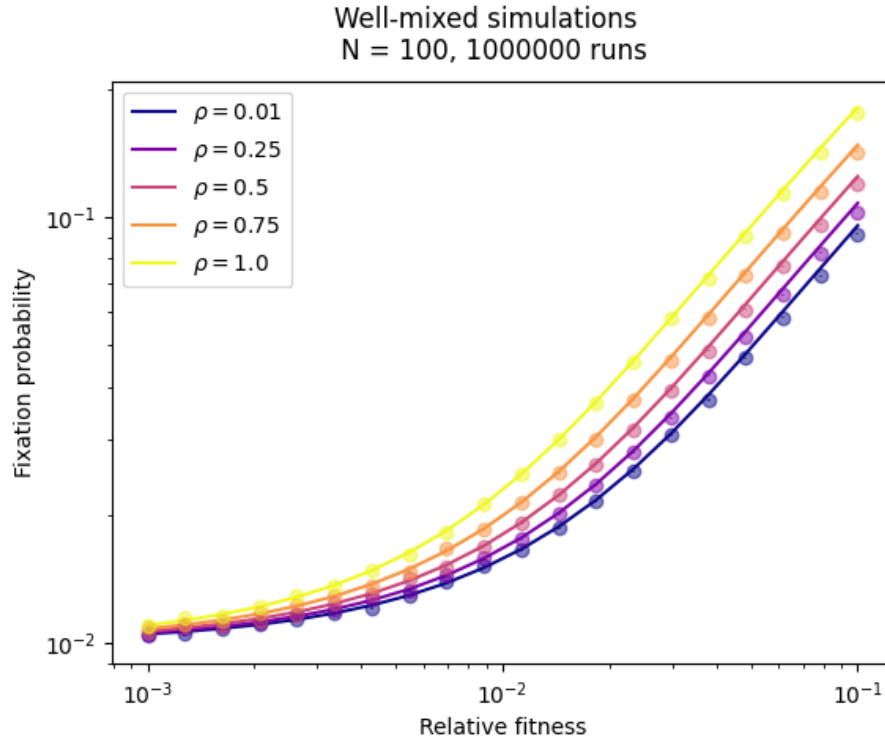




# Results: Well-mixed

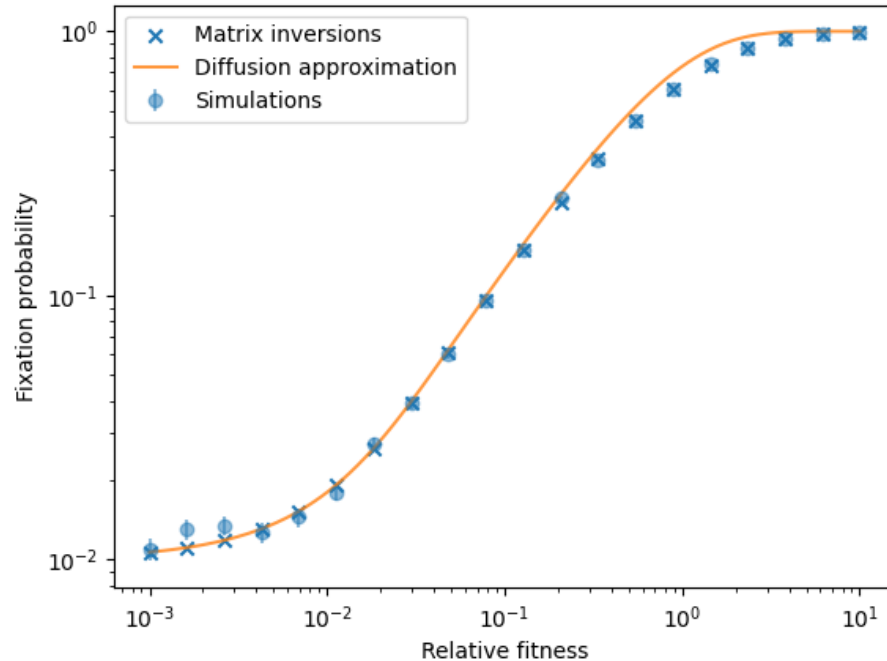
Dots: simulation  
results

Lines : Diffusion  
approximation



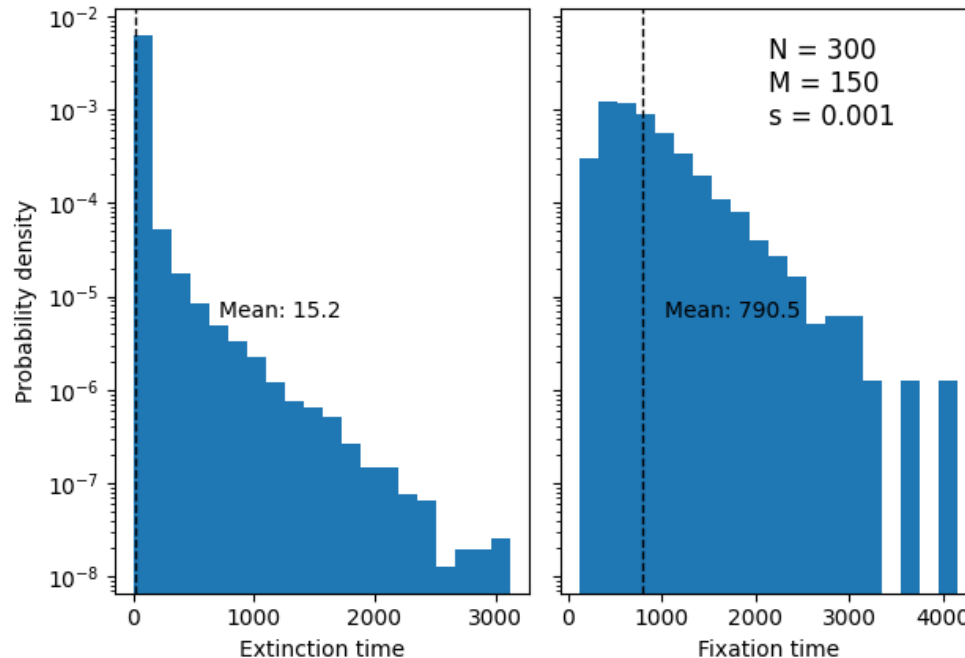
# Results: Well-mixed

Well-mixed,  $N = 100$ ,  $M = 50$ , 10000 simulations

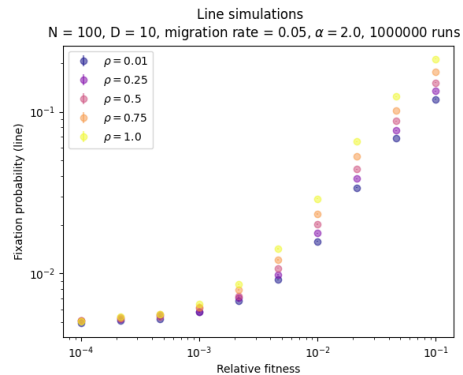
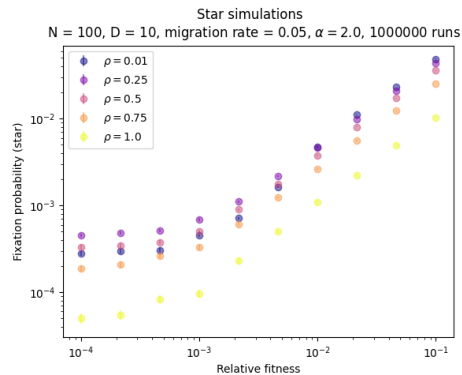
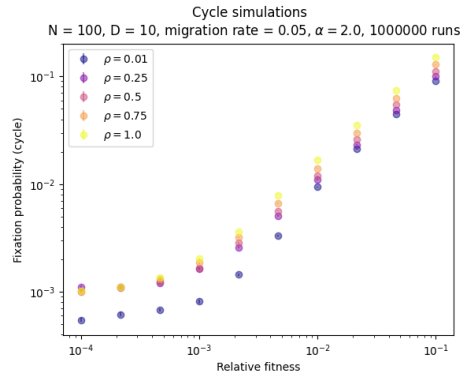
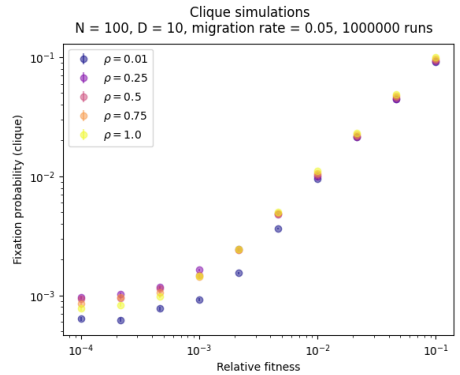


# Results: Well-mixed

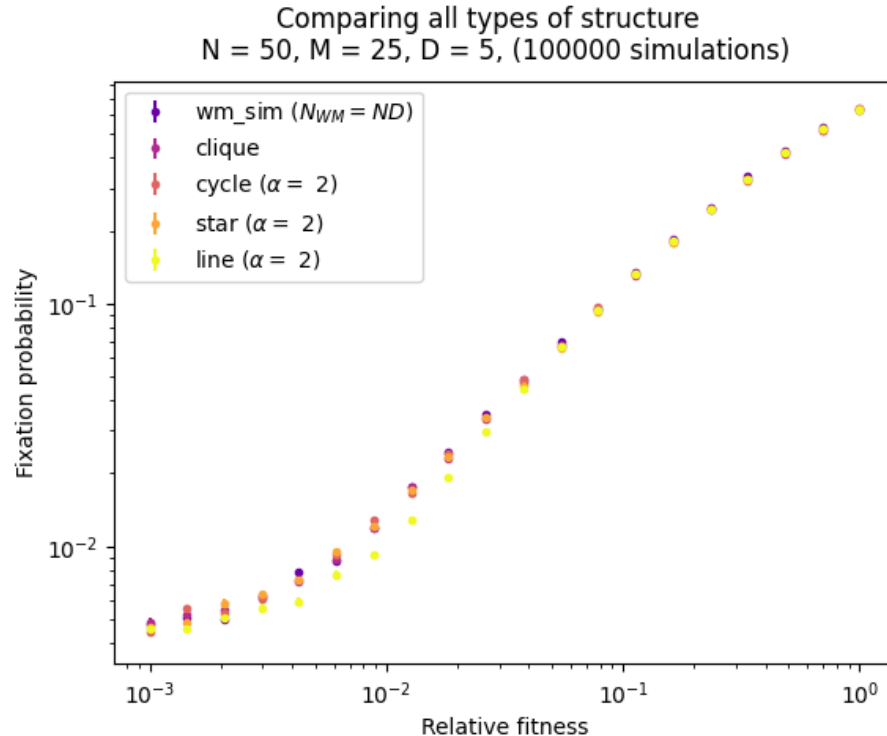
Well-mixed simulations (1000000 runs)



# Results: Graphs

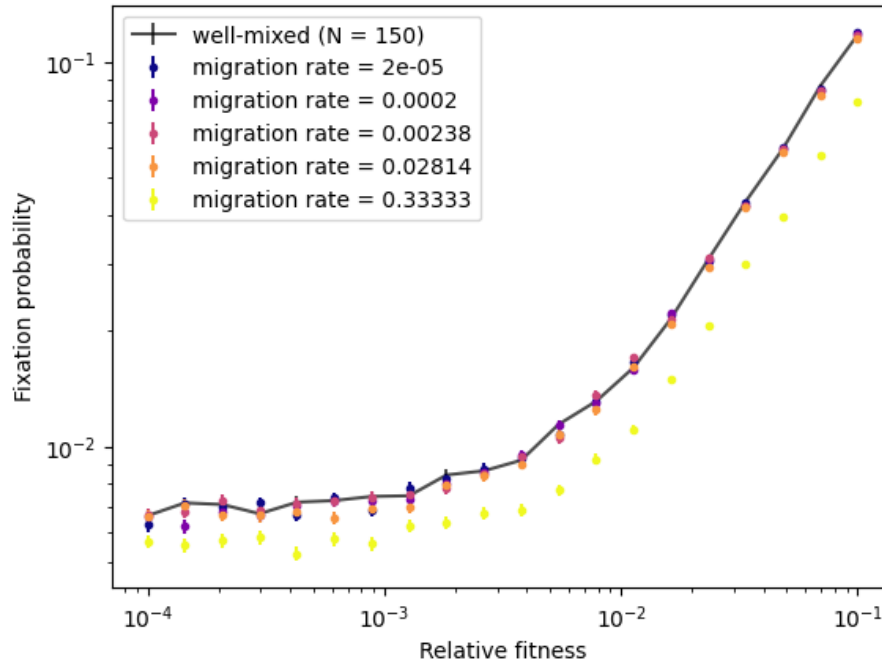


# Results: Graphs

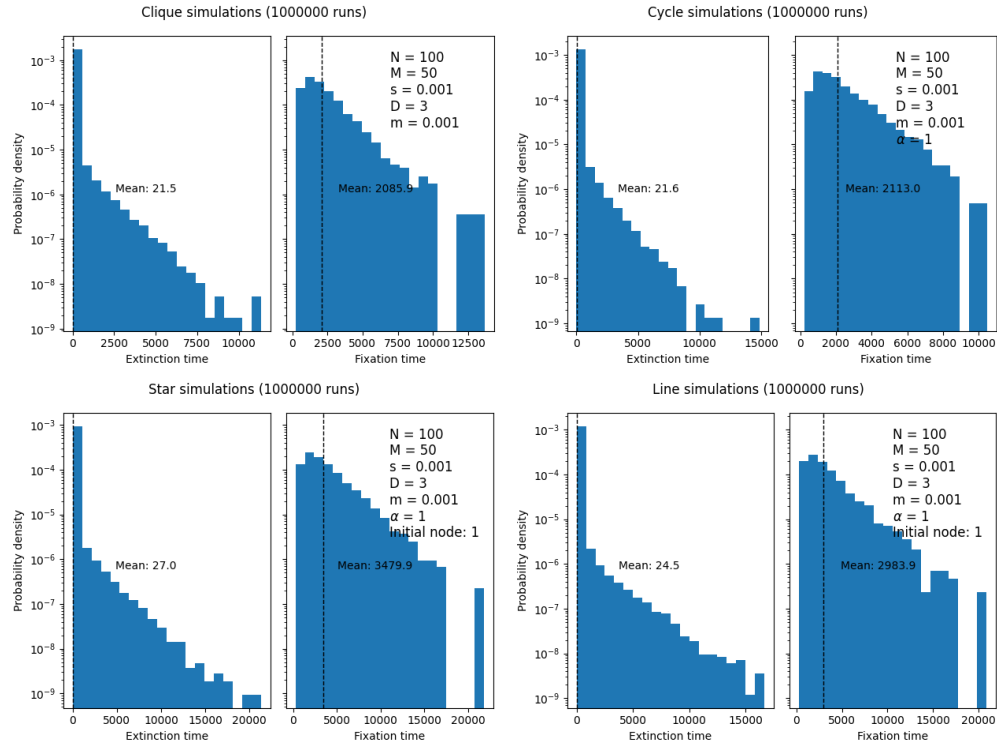


# Results: Graphs

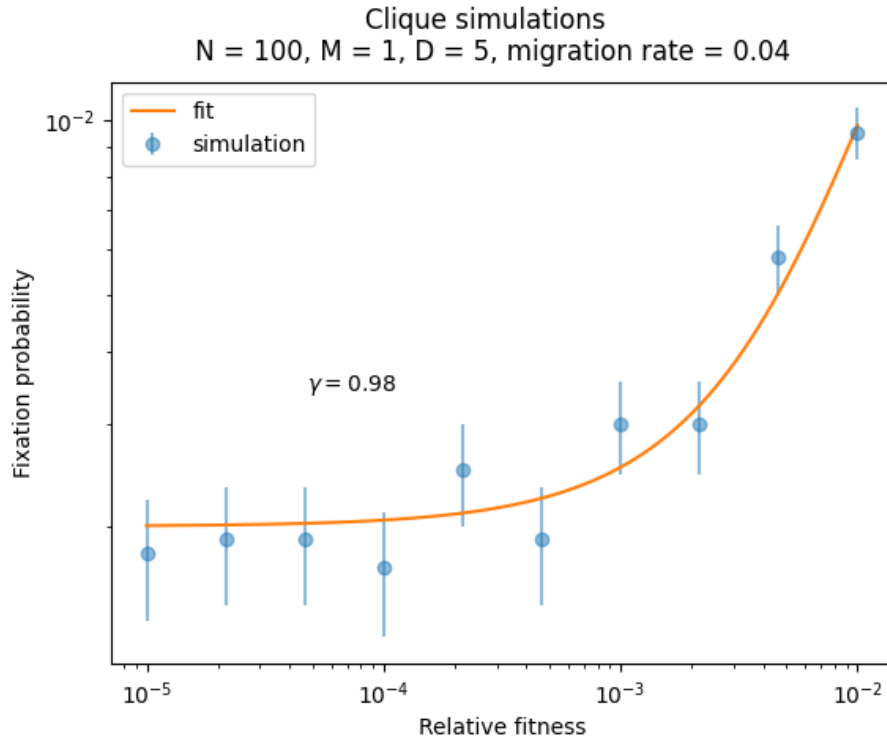
Comparing migration rates on Clique simulations  
 $N = 50$ ,  $M = 25$ ,  $D = 3$ , (100000 simulations)



# Results: Graphs



# Results: Fitting a model curve



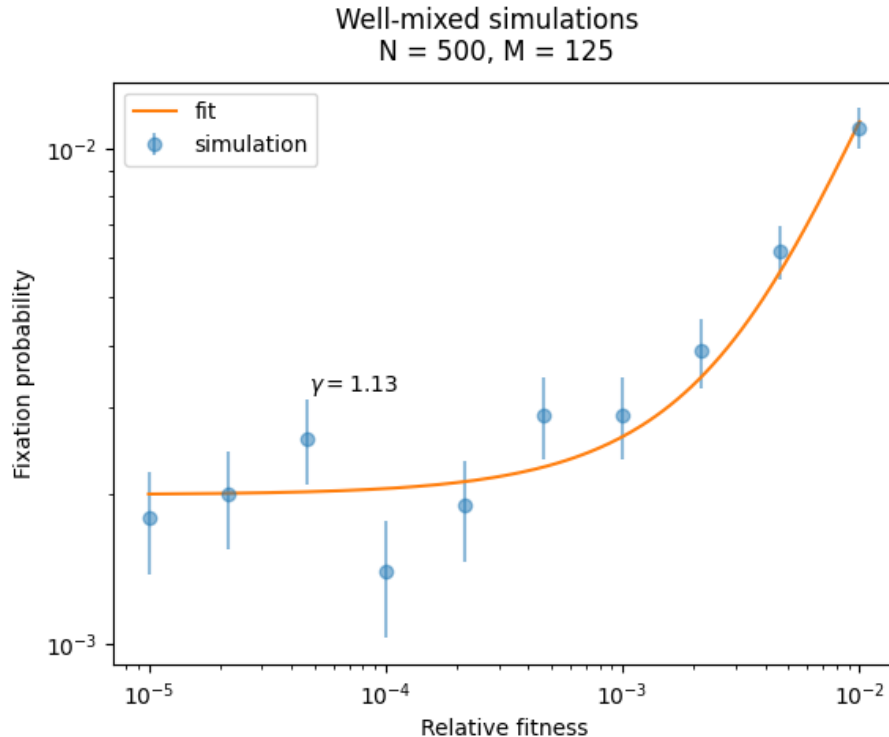
Model curve:

$$\phi_{\gamma}(s) = \frac{1 - \exp(-\gamma s)}{1 - \exp(-\gamma N D s)}$$

(10 000 runs)



# Results: Fitting a model curve (WM)



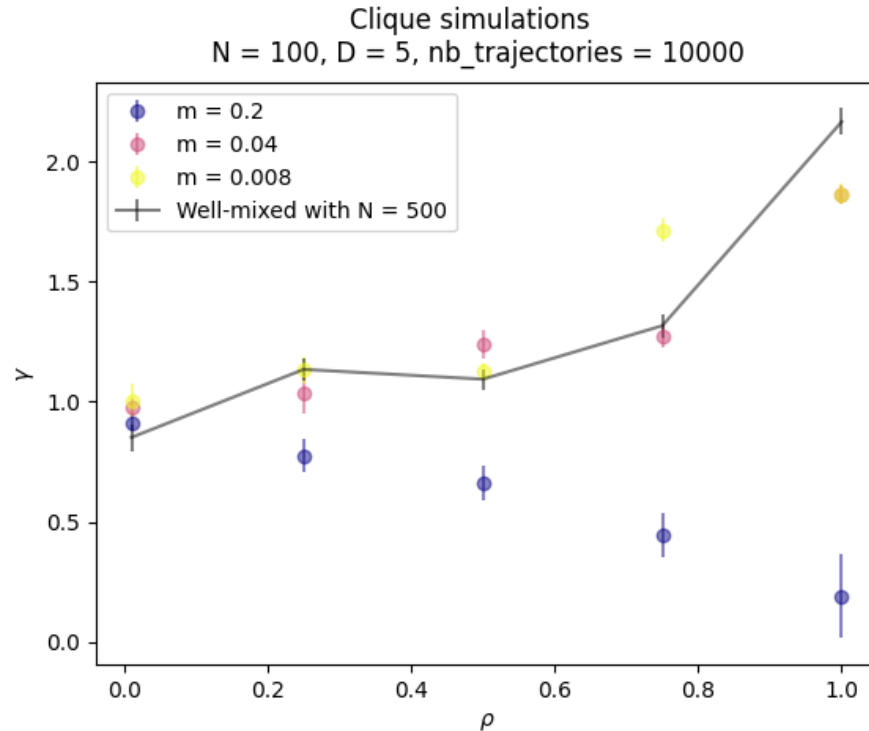
Model curve:

$$\phi_{\gamma}^{WM}(s) = \frac{1 - \exp(-\gamma s)}{1 - \exp(-\gamma N s)}$$

Under the diffusion approximation:

$$\gamma_{th} = \frac{2}{2 - \rho} \approx 1.14 \quad (N = 500, M = 125)$$

# Results: Fitting a model curve



# Conclusion

- Investigate the results for large migration rates (should behave like in the well-mixed case)
- Alternative ways to compute the weighted fraction:

$$p_i = \frac{\tilde{x}^{[i]}(1+s)}{1 + \tilde{x}^{[i]} \cdot s} \quad \text{with} \quad \tilde{x}^{[i]} = \sum_{k=1}^D m_{k,i} x^{[k]}$$

$$p'_i = \sum_{k=1}^D m_{k,i} \frac{\tilde{x}^{[k]}(1+s)}{1 + \tilde{x}^{[k]} \cdot s}$$

- Improve precision (more runs, larger N, D, more data points)

# References

- Abbara, Alia, and Anne-Florence Bitbol. “Frequent Asymmetric Migrations Suppress Natural Selection in Spatially Structured Populations.” *PNAS Nexus* 2, no. 11 (November 14, 2023): pgad392. <https://doi.org/10.1093/pnasnexus/pgad392>.
- Abbara, Alia, Lisa Pagani, Celia García-Pareja, and Anne-Florence Bitbol. “Mutant Fate in Spatially Structured Populations on Graphs: Connecting Models to Experiments.” *PLOS Computational Biology* 20, no. 9 (September 6, 2024): e1012424. <https://doi.org/10.1371/journal.pcbi.1012424>.
- Alexandre, Arthur, Alia Abbara, Cecilia Fruet, Claude Loverdo, and Anne-Florence Bitbol. “Bridging Wright–Fisher and Moran Models.” *Journal of Theoretical Biology* 599 (February 21, 2025): 112030. <https://doi.org/10.1016/j.jtbi.2024.112030>.
- Manhart, Michael, Allan Haldane, and Alexandre V. Morozov. “A Universal Scaling Law Determines Time Reversibility and Steady State of Substitutions under Selection.” *Theoretical Population Biology* 82, no. 1 (August 1, 2012): 66–76. <https://doi.org/10.1016/j.tpb.2012.03.007>.