A Probabilistic Master–Equation Framework for Infection Spread Across Spatially Distributed Plots

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ABSTRACT

We present a probabilistic modelling framework that couples *within-plot* infection dynamics—described by plot-specific master equations—with *between-plot* transmission rules. Directional movement of the pathogen (or predator) is governed by two empirically tunable probability mass functions: a *threshold* distribution expressing the propensity of an infectious plot to transmit, and an *absorbency* distribution capturing the susceptibility of the recipient plot. Convolving these rules with the time-resolved internal state distributions yields probability density functions (PDFs) and cumulative distribution functions (CDFs) for infection arrival at every plot in the network. The approach is computationally tractable, interpretable, and applicable to ecological disease, epidemiological outbreaks, and information contagion on networks with heterogeneous nodes.

1 Introduction

Spatial contagion—whether in forest ecosystems, animal meta-populations, or online communities—depends on local heterogeneities. Constructing a monolithic compartmental model disregards these nuances, whereas an explicit joint master equation becomes computationally prohibitive. We therefore adopt a hybrid strategy: (i) model each plot with its own master equation that reflects the *internal* infection dynamics and (ii) connect plots through probabilistic transmission kernels that respect those local states.

2 Assumptions

1. **Markovian within-plot dynamics.** Each plot follows a continuous-time Markov chain (CTMC)—future changes depend only on the current state, not on the path taken to arrive there.
2. **Single-edge events.** During an infinitesimal time interval, at most one source–target transmission occurs because simultaneous jumps are negligibly rare.
3. **Locally known parameters.** Birth, death, recovery, or predation rates may vary across plots or through time, yet are assumed known (or separately estimable) when the process is simulated or fitted.
4. **Edge-wise independence.** When computing transmission on edge $(p \to q)$ we treat it independently of other edges; correlations can be accommodated later by expanding the transmission kernel to include those covariates.

3 Model

3.1 The Problem

Practitioners often ask, *“With what probability and at what time will infection reach plot q if it starts in plot p?”* Our goal is to produce the full set of arrival-time PDFs $\{f_{\mathrm{in},q}(t)\}$.

3.2 Within-plot master equation

Inside each plot, infection can grow, shrink, or disappear depending on biological processes such as birth, death, or predation. Mathematically, if $X_p(t) \in \{0,\ldots,N_p\}$ denotes the infectious load in plot p, then the probability vector

$$\mathbf{P}_p(t) = \big(P_p^{(0)}(t),\ldots,P_p^{(N_p)}(t)\big)^\top$$

evolves via the CTMC generator $\mathbf{A}_p$:

$$\frac{d\mathbf{P}_p}{dt} = \mathbf{A}_p \mathbf{P}_p(t), \qquad \sum_{i=0}^{N_p} P_p^{(i)}(t) = 1.$$

3.3 Threshold and absorbency distributions

A source plot is not always willing to send the pathogen, and a neighbour is not always willing to accept it. We capture these tendencies with

$$\theta_p(i) = \Pr[\text{attempt transmit} \mid X_p = i], \qquad \alpha_q(j) = \Pr[\text{accept} \mid X_q = j],$$

leading to an edge-specific probability

$$T_{p\to q}(i,j) = \theta_p(i)\,\alpha_q(j),$$

which can depend on any measurable covariate (population density, weather, resource level, management actions, *etc.*).

3.4 Time-resolved transmission PDF

Blending the internal state probabilities with the willingness to transmit and accept yields a timeline for one edge:

$$f_{p\to q}(t) = \sum_{i=1}^{N_p} \sum_{j=0}^{N_q} P_p^{(i)}(t)\,P_q^{(j)}(t)\,T_{p\to q}(i,j).$$

3.5 Network propagation via convolutions

If several neighbours can reach the same plot, the earliest arrival wins. For in-neighbours $\mathscr{N}(q)$ this competition is expressed as

$$f_{\text{in},q}(t) = 1 - \prod_{p\in\mathscr{N}(q)} \left[1 - F_{p\to q}(t)\right],$$

with $F_{p\to q}(t) = \int_0^t f_{p\to q}(\tau)\,d\tau$.

3.6 Within-plot marginal dynamics

Solving or integrating the master equation delivers the full distribution inside each plot:

$$\mathbf{P}_p(t) = \exp\!\big(\mathbf{A}_p t\big)\mathbf{P}_p(0) = \mathbf{P}_p(0) + \int_0^t \mathbf{A}_p \mathbf{P}_p(\tau)\,d\tau.$$

These marginals then feed into the edge-level computations above.

4 Results

To demonstrate the framework we use a predator–prey toy example: **wolves** (predators) roam between plots while hunting **bunnies** (prey). Four linearly connected plots (P=4) are simulated for $T_{\max}$=25 discrete time steps (Δt=0.1).

4.1 Individual master-equation dynamics

Figure 1 displays how the probability of observing a certain number of bunnies in plot 0 changes over time.

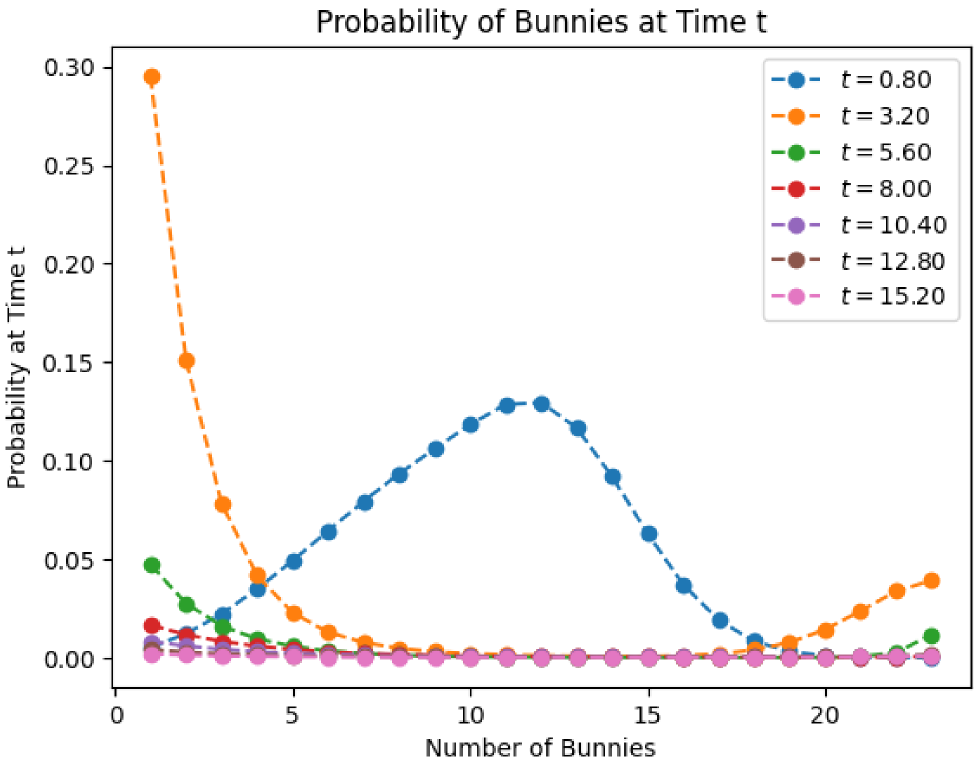
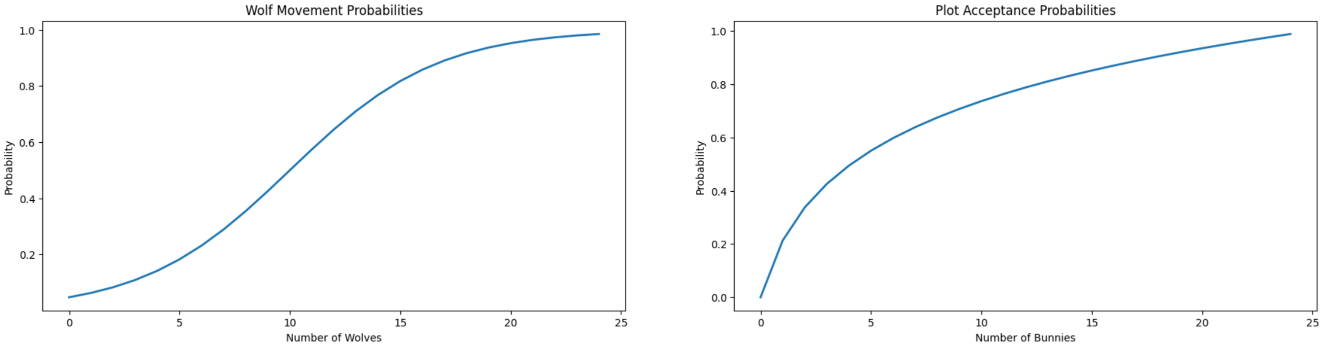


Figure 1. Probability of bunnies (prey) over time within plot 0. Other plots follow distinct distributions due to different initial conditions and local parameters.

4.2 Threshold and absorbency kernels

Threshold (wolf movement) and absorbency (plot acceptance) curves for the first edge are shown side-by-side in Fig. 2.



(a) Threshold: wolf leaving probability vs. #wolves

(b) Absorbency: acceptance probability vs. #bunnies

Figure 2. Example kernels for plots 0→ 1. In practice, each curve may depend on multiple factors—population counts, temperature, humidity, or active interventions.

4.3 Network-wide spread dynamics

Finally, Figure 3 aggregates all edges to present the probability of infection arrival in plots 0–2. The peak shifts later and broadens as distance from the initial infection increases, illustrating growing uncertainty.

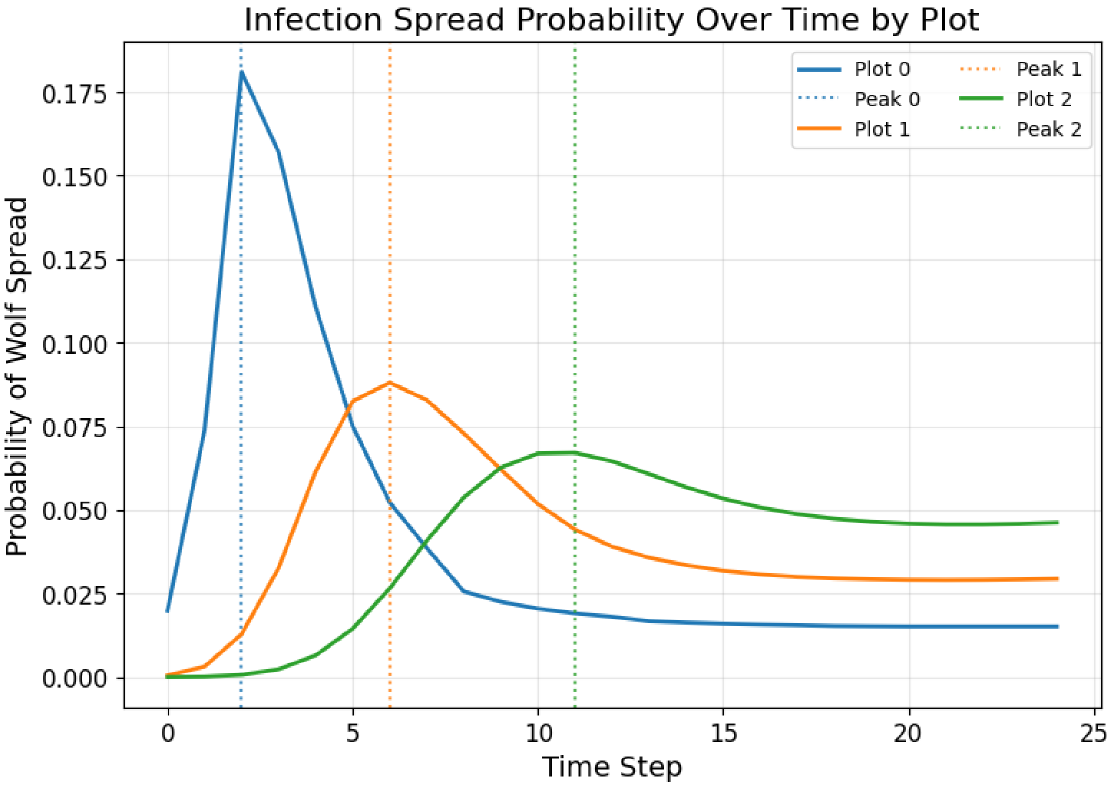


Figure 3. Probability of wolf spread over time by plot. Vertical dotted lines mark peak arrival times. Uncertainty grows and peaks shift right as the infection moves farther from its origin.

4.4 Validation checks

At every simulated time step we verified:

- Within each plot, $\sum_i P_p^{(i)}(t) = 1$
- For each edge, $\int_0^{T_{\max}} f_{p\to q}(t)\,dt \le 1$.

5 Discussion

Our hybrid approach converts detailed local dynamics into tractable landscape-level forecasts. Crucially, the *threshold* and *absorbency* distributions can be parametrised with *any* set of variables: host density, predator satiation, weather, resource availability, management interventions, or stochastic environmental noise. This flexibility makes the framework well-suited for rapid scenario testing without changing its mathematical backbone.

Current limitations—edge correlations, sub-plot spatial structure, and long-range jumps—offer clear avenues for future work. Coupling the arrival-time PDFs with costed intervention models is another practical direction.

Multiple shared neighbors in a plot/node may cause ’feedback’ loops which influence the probability of a plot/node spreading. Possible fixes are still being considered.

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Data and code availability

Scripts and source data for reproducing all figures are hosted at
- `https://github.com/scheuermann-daniel/Probabilistic-Infection-Spread-Model`

Competing interests

The author declares no competing interests.

References

1. van Kampen, N. G. *Stochastic Processes in Physics and Chemistry*. 3rd ed., Elsevier, Amsterdam (2007).
2. Gardiner, C. W. *Stochastic Methods: A Handbook for the Natural and Social Sciences*. 4th ed., Springer, Berlin (2009).
3. Gillespie, D. T. Exact stochastic simulation of coupled chemical reactions. *J. Phys. Chem.* **81**, 2340–2361 (1977).
4. Pastor-Satorras, R. & Vespignani, A. Epidemic spreading in scale-free networks. *Phys. Rev. Lett.* **86**, 3200–3203 (2001).
5. Newman, M. E. J. Spread of epidemic disease on networks. *Phys. Rev. E* **66**, 016128 (2002).
6. Keeling, M. J. & Rohani, P. *Modeling Infectious Diseases in Humans and Animals*. Princeton University Press, Princeton (2008).
7. Kiss, I. Z., Miller, J. C. & Simon, P. L. *Mathematics of Epidemics on Networks: From Exact to Approximate Models*. Springer, Cham (2017).
8. Andersson, H. & Britton, T. *Stochastic Epidemic Models and Their Statistical Analysis*. Lecture Notes in Statistics 151, Springer, New York (2000).