A Measure-Valued Approach to a Multilayer Epidemic Model with Households and Workplaces

Fabián Domínguez López

September 9, 2025

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Abstract

This report investigates the large-population limit of a multilayer stochastic epidemic model that incorporates both household and workplace structures. The model extends the classical SIR framework by explicitly accounting for infections occurring within small, tightly connected groups, as well as through global interactions. Building on the preprint [Kub23], we provide a detailed construction of the individual-based process and establish its convergence to a deterministic, measure-valued limit. Special attention is given to technical issues that arise in the limiting system, such as the treatment of ratios that may become indeterminate when the number of susceptibles vanishes, and the consistency between household- and workplace-based representations of the susceptible population. We derive auxiliary lemmas, and provide additional results ensuring the well-posedness of the model. Together, these results clarify the mathematical foundations of multilayer epidemic models and highlight their potential for capturing structured social interactions in large populations.

1 Introduction

Epidemic modeling plays a crucial role in understanding the spread of infectious diseases and in evaluating intervention strategies. Traditional models often assume homogeneous mixing among individuals (see, e.g., [KM27], [AM91]), which fails to account for the influence of structured social interactions. To address this limitation, recent approaches introduce heterogeneous contact patterns, particularly by modeling interactions within small, tightly connected social groups such as households and workplaces (e.g., [BP19]).

The preprint "Large population limit for a multilayer SIR model including households and workplaces" by Madeleine Kubasch [Kub23] presents a rigorous analysis of a stochastic SIR model incorporating two levels of interaction: global (uniform random contacts across the population) and local (structured by households and workplaces). The paper introduces an individual-based stochastic process and establishes its convergence, as the population size grows, to a deterministic measure-valued limit. In the case where infectious periods follow an exponential distribution, the limiting process reduces to a finite-dimensional system of ordinary differential equations (ODEs).

This report aims to carefully examine the structure, mathematical formulation, and main results of Kubasch's model. The focus is placed on the construction of the stochastic process, its convergence to a deterministic limit, and the interpretation of the resulting dynamical system. Rather than proposing modifications or extensions, the goal is to develop a deep and rigorous understanding of the framework, serving as a foundation for future theoretical or computational investigations.

Throughout this report, we use the following notation: Given a measurable space $(E, \mathcal{E})$, we let $\mathcal{M}_P(E)$ denote the set of point measures on E, $\mathcal{M}_F(E)$ the set of finite measures, and $\mathcal{M}_1(E)$ the set of probability measures. We define $\mathcal{M}_{P,1}(E) := \mathcal{M}_P(E) \cap \mathcal{M}_1(E)$ as the set of point probability measures on E. For a measure μ on E and a suitable function f, we write $\langle \mu, f \rangle := \int_E f \, d\mu$. The Dirac measure at $x \in E$ is denoted by δ_x. For any metric space E and integer m, we let $\mathcal{C}(E, \mathbb{R}^m)$ be the set of continuous functions $f : E \to \mathbb{R}^m$, and $\mathcal{C}_b(E, \mathbb{R}^m)$ the subset of bounded continuous functions. Finally, $\mathcal{C}_b^1(E, \mathbb{R}^m)$ denotes the set of bounded differentiable functions with bounded and continuous derivatives.

2 Model Overview

The model considers a population of fixed size K, where each individual belongs to exactly one household and one workplace. These affiliations are assigned independently according to fixed size distributions π^H and π^W. Within each layer (households, workplaces, general population), contacts occur at different rates:

- λ_H: contact rate within households,
- λ_W: contact rate within workplaces,

- β_G: global contact rate across the population, scaled by $1/K$.

Individuals evolve according to classical SIR dynamics: they begin as susceptible (S), may become infected (I), and eventually recover (R). The infectious period of each individual is independently drawn from a general distribution ν, which allows for both Markovian (exponential) and non-Markovian (non-exponential) settings. This generality is key to capturing a broader range of epidemic behaviors.

2.1 Model Construction

Let $(\Omega, \mathbb{P}, \mathcal{F})$ be a probability space. Let $K \in \mathbb{N}$ be the population size. For each $\omega \in \Omega$, we define a random multilayer graph $G^K(\omega)$ that encodes the structure of households and workplaces.

Let $n_{\text{max}} \in \mathbb{N}$ be fixed, representing the maximum allowed size for any household or workplace. Denote by

$$\pi^H = (\pi_1^H, \pi_2^H, \cdots, \pi_{n_{max}}^H), \quad \pi^W = (\pi_1^W, \pi_2^W, \cdots, \pi_{n_{max}}^W)$$

the household and workplace size distributions, respectively.

Let $\{X_n\}_n$ be an i.i.d. sequence of random variables on Ω, with distribution $X_n \sim \pi^H$. That is,

$$\mathbb{P}(X_n = i) = \pi_i^H, \quad \forall i \in \{1, \cdots, n_{max}\}.$$

These variables will help us determine the sizes of households in the population.

The construction proceeds as follows: the size of the first household is $X_1(\omega)$ if $X_1(\omega) \leq K$; otherwise, it is truncated at K. We randomly assign individuals to form this household. The remaining individuals are then used to form the next household using $X_2(\omega)$, and so on, until all individuals have been assigned to a household. An analogous procedure is used to form the workplaces, using another i.i.d. sequence $\{Y_n\}_{n\geq 1} \sim \pi_W$.

Example 2.1. ***Constructing $G^K(\omega)$ with $K = 6$ individuals.***
Assumptions:

- $n_{max} = 3$ *(maximum size for both households and workplaces).*
- *Household size distribution:* $\pi^H = (0.2, 0.5, 0.3)$.
- *Workplace size distribution:* $\pi^W = (0.1, 0.6, 0.3)$.

Household formation:
Start with 6 unassigned individuals. Simulate i.i.d. $X_i \sim \pi^H$*:*

1. $X_1 = 2 \rightarrow$ *Household of size 2: pick individuals A, E; 4 remain.*
2. $X_2 = 3 \rightarrow$ *Household of size 3: pick individuals B, D, F; 1 remains.*

3. $X_3 = 3 \to$ *Household of size 1 (truncated): individual C; none remain.*

Resulting households:

- *Household 1:* $\{A, E\}$
- *Household 2:* $\{B, D, F\}$
- *Household 3:* $\{C\}$

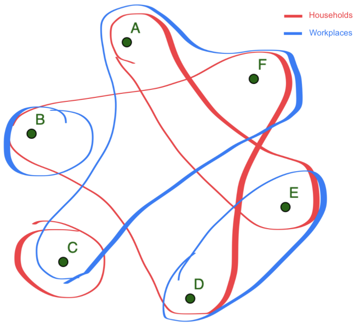
Workplace formation:

The same procedure is carried out independently for workplace assignments, using $Y_i \sim \pi^W$*, again starting with all 6 individuals:*

1. $Y_1 = 3 \to \{A, C, F\}$*; 3 remain.*
2. $Y_2 = 2 \to \{D, E\}$*; 1 remains.*
3. $Y_3 = 2 \to \{B\}$ *(truncated); none remain.*

Resulting workplaces:

- *Workplace 1:* $\{A, C, F\}$
- *Workplace 2:* $\{D, E\}$
- *Workplace 3:* $\{B\}$



3 Mathematical Framework

3.1 Types

To analyze the model in the large population limit, the dynamics are formulated as a measure-valued stochastic process. Each household or workplace is described by a type, represented as a triplet (n, s, τ), where:

- $n \in \{1, \cdots, n_{max}\}$ is the fixed size of the group,
- $s \in \{0, \cdots, n\}$ is the number of susceptible individuals,
- $\tau \in \mathbb{R}^{n_{max}}$ is a vector encoding the infection status of the non-susceptible members of the structure. Each entry τ_j corresponds to the time remaining until recovery (if positive) or the time elapsed since recovery (if negative) of an individual. Entries beyond the number of non-susceptible members are set to zero.

This representation encodes both the epidemiological state of each structure and the correlations arising from individuals belonging simultaneously to a household and a workplace, which are crucial for accurately modeling transmission dynamics.

Let $\omega \in \Omega$ and fix a population size $K \geq 1$. Denote by K_W and K_H the number of workplaces and households in the population, respectively. These are determined by $G^K(\omega)$, although their dependence on ω is suppressed in notation.

Define the set

$$E := \{(n, s, \tau) \in \{1, \cdots, n_{max}\} \times \{0, \cdots, n_{max}\} \times \mathbb{R}^{n_{max}} : s \leq n; \forall j > n - s, \tau_j = 0\}.$$

At any time $t \geq 0$, the state of the k-th household is given by:

$$x_k^H(t) = \left(n_k^H, s_k^H(t), \tau_k^H(t)\right) \in E.$$

Here:

- n_k^H is the fixed size of the household.
- $s_k^H(t)$ is the number of susceptibles at time t.
- $\tau_k^H(t)$ is a vector that encodes the epidemiological status of the $n - s$ non-susceptible individuals (either infected or recovered).

Each entry $\tau_{k,j}^H(t)$, for $j = 1, \ldots, n - s$, corresponds to a non-susceptible individual. If $\tau_{k,j}^H(t) > 0$, the individual is currently infected and will recover in $\tau_{k,j}^H(t)$ units of time. If $\tau_{k,j}^H(t) \leq 0$, the individual has already recovered, and the recovery occurred at time $t - |\tau_{k,j}^H(t)|$. The ordering of the entries in τ is arbitrary and does not reflect any specific assignment or label of individuals; it is introduced solely to allow consistent indexing and tracking of infection status within the structure.

For indices beyond the number of infected and recovered individuals (i.e. $j > n_k^H - s_k^H(t)$), $\tau_{k,j}^H(t)$ is defined as 0 for convenience.

Workplaces are defined analogously. The ℓ-th workplace has type

$$x_\ell^W(t) = \left(n_\ell^W, s_\ell^W(t), \tau_\ell^W(t)\right) \in E.$$

Example 3.1. ***Types and their evolution***

To illustrate how types (n, s, τ) are defined and how they evolve over time, we continue the previous example with a population of 6 individuals labeled A through F.

Assume the following epidemic state at time $t = 0$:

- *A is infected, and its remaining infection period is 3.7 units of time.*
- *B is recovered, having recovered 1.2 time units ago.*
- *C is susceptible.*
- *D is infected, and its remaining infection period is 2.5 units of time.*
- *E is susceptible.*
- *F is infected, and its remaining infection period is 4.8 units of time.*

Based on the groupings previously constructed, the household types at time $t = 0$ are as follows:

- *Household 1 (A, E): size $n = 2$, with $s = 1$ susceptible (E) and one infected (A).*

  $$x_1^H(0) = (2, 1, (3.7, 0, 0)).$$

- *Household 2 (B,D,F): size $n = 3$ and three non-susceptible: D (infected, 2.5 units left), B (recovered 1.2 units ago), and F (infected, 4.8 units left).*

  The order of τ is arbitrary. One possible representation:

  $$x_2^H(0) = (3, 0, (2.5, -1.2, 4.8))$$

- *Household 3 (C): size $n = 1$, with C susceptible.*

  $$x_3^H(0) = (1, 1, (0, 0, 0)).$$

Similarly, the workplace types at time $t = 0$ are:

- *Workplace 1 (A,C,F):*
$$x_1^W(0) = (3, 1, (3.7, 4.8, 0)).$$
- *Workplace 2 (D,E):*
$$x_2^W(0) = (2, 1, (2.5, 0, 0)).$$
- *Workplace 3 (B):*
$$x_3^W(0) = (1, 0, (-1.2, 0, 0)).$$

Now suppose that at time $t = 0.7$*, E becomes infected during a workplace contact and receives an infectious period of 2.9 time units. The updated types at time* $t = 0.7$ *are:*

- *Household 1 (A, E): now both individuals are infected, so* $s = 0$*. A has 3 units left (was 3.7), and E starts with 2.9.*
$$x_1^H(0.7) = (2, 0, (3, 2.9, 0)).$$
- *Workplace 2 (D,E): both members now infected. D has 1.8 units remaining, and E has just been infected.*
$$x_2^W(0.7) = (2, 0, (1.8, 2.9, 0)).$$

The rest of workplaces and households are just affected by the passing of time. For instance, at time $t = 0.7$*, the type of Household 2 is* $x_2^H(0.7) = (3, 0, (1.8, -1.9, 4.1))$*.*

3.2 Stochastic Process

Throughout this section, we assume that the underlying random graph is fixed. In other words, we fix $\omega \in \Omega$ and a population size $K \geq 1$, and study the epidemic process conditional on this realization of the graph.

Before formally defining the stochastic process that describes the evolution of the epidemic, we introduce the key ideas and notation used in its construction.

Denote by $\{e_k\}_{1 \leq k \leq n_{max}}$ the canonical basis of $\mathbb{R}^{n_{max}}$. For any $0 \leq t \leq T$ and $x = (n, s, \tau) \in E$, define

$$\Psi(x, T, t) := \left(n, s, \tau - \sum_{k=1}^{n-s} (T - t) e_k\right) \in E. \tag{3.1}$$

The function $\Psi(x, T, t)$ is introduced to model the natural evolution of a structure (household or workplace) over time in the absence of new infections. In other words, suppose a structure is in the state x at time t. Then, at time T, it will be in the state $\Psi(x, T, t)$ if no infection occurs in the meantime.

However, infections do occur, and when they do, they immediately alter the type of both the individual's household and workplace. The model assumes that whenever an infection happens, the infectious period of the newly infected individual is drawn randomly from a distribution ν, independently of the current state. If the newly infected individual belongs to the k-th household and the ℓ-th workplace, and receives an infectious period $\sigma \sim \nu$, then the type of both the household and the workplace undergoes a jump defined by the function:

$$j(x, \sigma) := (n, s - 1, \tau + \sigma e_{n-s+1}). \tag{3.2}$$

This reflects that the number of susceptibles s decreases by 1, and a new entry σ is inserted into the infectious period vector τ at position $n - s + 1$, corresponding to the newly infected individual.

We are now in a position to define the stochastic process $(\zeta_t^K = (\zeta_t^{H|K}, \zeta_t^{W|K}))_{t \geq 0}$, which takes values in the product space $\mathfrak{M}_{P,1} := \mathcal{M}_{P,1}(E) \times \mathcal{M}_{P,1}(E)$. Here, $\zeta_t^{H|K}$ and $\zeta_t^{W|K}$ denote the empirical distributions of household and workplace types at time t, respectively. More precisely, for any $t \geq 0$ and $X \in \{H, W\}$, the measure $\zeta_t^{X|K}$ is given by

$$\zeta_t^{X|K} = \frac{1}{K_X} \sum_{k=1}^{K_X} \delta_{x_k^X(t)},$$

where $x_k^X(t)$ is the type of the k-th structure (household or workplace) at time t.

Since each household and workplace is represented by a type $x = (n, s, \tau)$, it is possible to compute population-level quantities such as the average number of susceptibles and infecteds per structure.

Given a type $x = (n, s, \tau)$, the number of infected individuals it contains is:

$$i(\tau) := \sum_{k=1}^{n-s} \mathbb{1}_{\tau_k > 0},$$

that is, we count all non-susceptible individuals whose remaining infectious period is still positive.

Then, at time t, the average number of infected individuals per household is defined as:

$$I_H(t) := \frac{1}{K_H} \sum_{k=1}^{K_H} i(\tau_k^H(t)).$$

Similarly, one defines the average number of infecteds per workplace $I_W(t)$, using the workplace types $\tau_\ell^W(t)$.

Likewise, the average number of susceptibles per household is given by

$$S_H(t) := \frac{1}{K_H} \sum_{k=1}^{K_H} s_k^H(t),$$

and analogously for $S_W(t)$.

The total number of infecteds and susceptibles at time t is then

$$I(t) = K_X \cdot I_X(t), \quad S(t) = K_X \cdot S_X(t), \quad \text{for } X \in \{H, W\}.$$

This motivates the following consistency condition, which must hold for the model to be coherent:

$$K_H S_H(t) = K_W S_W(t), \quad K_H I_H(t) = K_W I_W(t), \quad \text{for all } t \geq 0. \tag{3.3}$$

In other words, the total number of susceptibles and infecteds is the same whether counted by household or by workplace.

Let $N_H := \frac{K}{K_H}$ denote the average household size, which is fixed over time. Similarly, define $N_W := \frac{K}{K_H}$ for workplaces. Then,

$$\frac{I(t)}{K} = \frac{I_X(t)}{N_X}, \quad \text{for } X \in \{H, W\}.$$

This identity will be useful for simplifying certain expressions later on.

It is important to emphasize that the initial configuration ζ_0^K must encode these structural properties of the population. For example, it must ensure that the total number of susceptibles and infecteds match between the household and workplace representations.

Additionally, a key condition must hold: for each initially infected or recovered individual, their remaining infectious period must be the same in both their household and their workplace type. That is, almost surely,

$$\{\tau_{k,j}^H(0) : 1 \leq k \leq K_H, 1 \leq j \leq n_k^H - s_k^H(0)\} = \{\tau_{\ell,j}^W(0) : 1 \leq \ell \leq K_W, 1 \leq j \leq n_\ell^W - s_\ell^W(0)\}. \tag{3.4}$$

This ensures that the infectious dynamics are coherent across layers, and will later be justified rigorously in Lemma 3.1.

To describe the evolution of the epidemic through time, we model infection events as points in Poisson point processes over appropriate spaces. These spaces encode the necessary variables for each possible type of infection: global (G), within-household (H), and within-workplace (W).

Each potential infection event is characterized by a tuple u that contains:

- A time-related random mark $\theta \in \mathbb{R}_+^d$, whose dimension d depends on the type of infection (global, household, or workplace). The components of θ are continuous random variables, used to determine whether the infection occurs and to assign the individual to a household and a workplace.
- An index $k \in \{1, \ldots, K_H\}$ identifying a household structure. If the infection occurs, the newly infected individual will be placed in household k, and the household type will be updated accordingly.

- An index $\ell \in \{1, \ldots, K_W\}$ identifying a workplace structure, used similarly to update the workplace type after infection.
- A sampled infectious period $\sigma \in \mathbb{R}_+$, drawn independently from the distribution ν, and assigned to the newly infected individual.

In summary, each tuple $u = (\theta, k, \ell, \sigma)$ fully specifies a potential infection event: when it might occur, who is infected, which structures are affected, and for how long the infection will last.

We now define the event spaces used to represent each type of infection:

For global infections, the event space is

$$U_G := (\mathbb{R}_+)^3 \times \{1, \cdots, K_H\} \times \{1, \cdots, K_W\} \times \mathbb{R}_+. \tag{3.5}$$

Here, the components of $\theta = (\theta_1, \theta_2, \theta_3) \in \mathbb{R}_+^3$ are used to determine whether the infection occurs (θ_1) and the assignments of the household (θ_2) and workplace (θ_3).

For household or workplace infections, the space is:

$$U := (\mathbb{R}_+)^2 \times \{1, \cdots, K_H\} \times \{1, \cdots, K_W\} \times \mathbb{R}_+, \tag{3.6}$$

where $\theta = (\theta_1, \theta_2) \in \mathbb{R}_+^2$ plays a similar role, adapted to the layer where the infection originates. We will denote this space by $U_H = U_W := U$ when referring specifically to household and workplace infections, respectively.

Each of these spaces is endowed with a product measure:

$$\mu_Y(du) = d\theta \otimes \mu^{\#}(dk) \otimes \mu^{\#}(d\ell) \otimes \nu(d\sigma), \quad Y \in \{H, W, G\},$$

where $d\theta$ is the Lebesgue measure on $\mathbb{R}_+^2$ or $\mathbb{R}_+^3$, $\mu^{\#}$ is the counting measure over household/workplace indices, and ν is the distribution of infected periods.

For any $t \geq 0$ and any event $u = (\theta, k, \ell, \sigma) \in U_G$ with $\theta = (\theta_1, \theta_2, \theta_3)$, we define the function $\mathcal{I}_G(t, u)$ to decide whether the event triggers an actual infection:

$$\mathcal{I}_G(t, u) := \mathbb{1}_{\left\{\theta_1 \leq \frac{\beta_G}{K} S(t) I(t), \theta_2 \leq \frac{s_k^H(t)}{S(t)}, \theta_3 \leq \frac{s_\ell^W(t)}{S(t)}\right\}}. \tag{3.7}$$

This means that an infection occurs with rate $\frac{\beta_G}{K} S(t) I(t)$, and the individual is assigned to household k and workplace ℓ proportionally to the number of susceptibles.

Next, for any $t \geq 0$ and any $u = (\theta, k, \ell, \sigma) \in U$ with $\theta = (\theta_1, \theta_2)$, we define

$$\mathcal{I}_H(t, u) := \mathbb{1}_{\left\{\theta_1 \leq \lambda_H s_k^H(t) i(\tau_k^H(t)), \theta_2 \leq \frac{s_\ell^W}{S(t)}\right\}}. \tag{3.8}$$

This indicates that an infection occurs within the k-th household with rate $\lambda_H s_k^H(t) i(\tau_k^H(t))$, and the individual belongs to the ℓ-th workplace with probability $\frac{s_\ell^W}{S(t)}$.

Similarly, we define

$$\mathcal{I}_W(t,u) := \mathbb{1}_{\left\{\theta_1 \leq \lambda_W s^W_\ell(t) i(\tau^W_\ell(t)), \theta_2 \leq \frac{s^H_k(t)}{S(t)}\right\}}. \tag{3.9}$$

When an infection does occur, the corresponding structure (household or workplace) must update its type. Thus, for any $T \geq t \geq 0$ and $u = (\theta, k, \ell, \sigma) \in U_G$, we define

$$\Delta_H(u,T,t). = \delta_{\left(\Psi(j(x^H_k(t-),\sigma),T,t))\right)} - \delta_{\left(\Psi(x^H_k(t-),T,t))\right)}$$

and

$$\Delta_W(u,T,t) := \delta_{\left(\Psi(j(x^W_\ell(t-),\sigma),T,t))\right)} - \delta_{\left(\Psi(x^W_\ell(t-),T,t))\right)},$$

where Ψ and j are respectively given by (3.1) and (3.2).

Finally, for any $T \geq t \geq 0$ and $u \in U$, we define $\Delta_H(u,T,t)$ and $\Delta_W(u,T,t)$ as before.

Proposition 3.1. *Define on the same probability space as ζ^K_0, and independently from ζ^K_0, three independent Poisson point measures Q_Y on $\mathbb{R}_+ \times U_Y$ with intensity $dt\mu_Y(du)$, for $Y \in \{H, W, G\}$. Then $\zeta^K = (\zeta^{H|K}, \zeta^{W|K})$ is defined as the unique strong solution taking values in $\mathbb{D}(\mathbb{R}_+, \mathfrak{M}_{P,1})$ (the space of càdlàg functions from $\mathbb{R}_+$ to $\mathcal{M}_{P,1}(E)^2$, equipped with the Skorokhod topology) of the following equation: For any $X \in \{H, W\}$ and $T \geq 0$,*

$$\zeta^{X|K}_T = \frac{1}{K}\Big(\sum_{j=1}^{K_X} \delta_{\Psi(x^X_j(0),T,0)} + \sum_{Y \in \{H,W,G\}} \int_0^T \int_{U_Y} \mathcal{I}_Y(t-,u)\Delta_X(u,T,t)Q_Y(dt,du)\Big), \tag{3.10}$$

where U_G and $U_H = U_W = U$ are defined by Equations (3.5) and (3.6), respectively.

Proof. We construct the process ζ^K as the unique strong solution of the stochastic equation by defining it recursively over a sequence of jump times generated by a dominating Poisson process.

At any time t, the evolution of ζ^K is governed by infection events from three independent Poisson point measures Q_H, Q_W, and Q_G, associated to household, workplace, and global infections respectively.

Each event, if it triggers an infection, causes a jump in the process. Between jumps, the system evolves deterministically according to the flow Ψ, which linearly decreases the remaining infectious periods of non-susceptible individuals.

To control the process, we introduce a uniform upper bound on the total rate of infection events, regardless of the current state:

$$\lambda_{\max} := n_{\max}\left(\lambda_H n_{\max} + \lambda_W n_{\max} + \beta_G\right).$$

This dominates all possible instantaneous rates of infection from the three sources.

Let $(T_n)_{n\geq 1}$ be the jump times of a homogeneous Poisson process $N = (N_t)_{t\geq 0}$ on $\mathbb{R}_+$ with rate $\lambda_{\max}$, and define $T_0 := 0$. Then, the inter-arrival times $S_n := T_n - T_{n-1}$ are i.i.d. exponential random variables with mean $1/\lambda_{\max}$, and $T_n \to \infty$ almost surely.

This gives a sequence of countable and locally finite jump times: in any finite time interval $[0, T]$, the number of jumps is almost surely finite.

The process starts from an initial condition ζ_0^K, which satisfies the consistency conditions described earlier.

For any interval $[T_n, T_{n+1})$, no infection occurs, so the system evolves deterministically. That is, for each structure $x \in E$, its type at time $t \in [T_n, T_{n+1})$ is given by:

$$x(t) = \Psi(x(T_n), t, T_n).$$

This corresponds to linearly decreasing all nonzero entries in τ at unit speed, representing the progression of infectious periods.

At each jump time T_n, we must determine:

1. Which type of infection occurs (household, workplace, or global),
2. Which structures are affected,
3. Whether the infection is accepted (via $I_Y(T_n^-, u)$).

To do this, we simulate a uniform random variable $U \sim \mathcal{U}[0, \lambda_{\max}]$ and partition the interval $[0, \lambda_{\max}]$ into disjoint segments associated to each source:

- Household infection if $U \in [0, \lambda_H n_{\max}^2]$,
- Workplace infection if $U \in [\lambda_H n_{\max}^2, \lambda_H n_{\max}^2 + \lambda_W n_{\max}^2]$,
- Global infection otherwise.

Let $Y \in \{H, W, G\}$ denote the selected infection type. We then sample a mark $u = (\theta, k, \ell, \sigma)$ from the intensity measure $\mu_Y(du)$, and evaluate the indicator function $I_Y(T_n^-, u)$.

- If $I_Y(T_n^-, u) = 0$, no infection occurs and the state remains unchanged.
- If $I_Y(T_n^-, u) = 1$, the infection is accepted and the types of the affected structures (household k, workplace ℓ) are updated by applying the transition map $\Delta^X(u, T, T_n)$, with $X \in \{H, W\}$.

We apply this procedure iteratively over all jump intervals $[T_n, T_{n+1})$, which defines the process $\zeta^K = (\zeta_t^{H|K}, \zeta_t^{W|K})_{t\geq 0}$ for all $t \geq 0$.

By construction, the process is càdlàg (right-continuous with left limits). Moreover, it takes values in $\mathcal{M}_{P,1}(E)^2$, since the number of households and workplaces is finite and fixed.

The stochastic equation (3.10) holds by design of the jump mechanism and the form of the Poisson point measures.

Once the realizations of the Poisson point measures Q_H, Q_W, Q_G are fixed; that is, once the jump times and event marks are given, the entire path of the process ζ^K is uniquely determined. This guarantees strong (pathwise) uniqueness of the solution.

The construction follows the general framework of piecewise deterministic Markov processes (PDMPs) as introduced by [Dav84], where the process evolves deterministically between random jump times generated by Poisson events.

□

The proof of the following result relies on the construction of the process and the consistency conditions imposed on the initial state (particularly equation (3.4)). We do not include the proof here, but it can be found in [Kub23]. The key point is that infection events always update both the household and the workplace of the newly infected individual, preserving this consistency over time.

Lemma 3.1. *Suppose that almost surely, $K_H S_H(0) = K_W S_W(0)$ and equation (3.4) holds. Then for any $t \geq 0$, $K_H S_H(t) = K_W S_W(t)$ and $K_H I_H(t) = K_W I_W(t)$, almost surely.*

With this framework in place, we are now in a position to examine the large population limit of the model and derive its deterministic approximation, as presented in the next sections.

4 Asymptotic Properties of the Population

We now turn to the analysis of the large-population limit of the model's structural components. The goal is to describe the asymptotic behavior of the empirical distributions of household and workplace sizes, as well as certain ratios that will be fundamental in the main convergence results.

4.1 Convergence of Empirical Size Distributions

We begin by proving that the empirical household and workplace size distributions converge almost surely to their theoretical counterparts as the population size grows. Define

$$\Omega^* := \left\{ \omega \in \Omega : (\pi^{H|K}, \pi^{W|K})_{K \geq 1} \xrightarrow[K \to \infty]{} (\pi^H, \pi^W) \right\},$$

where $\pi^{H|K}$ and $\pi^{W|K}$ are the empirical household and workplace size distributions observed in G^K.

The following Lemma ensures that $(\pi^{H|K}, \pi^{W|K})_{K \geq 1}$ converges $\mathbb{P}$-almost everywhere to (π^H, π^W).

Lemma 4.1. *Let $\pi^{H|K}$ and $\pi^{W|K}$ be the empirical household and workplace size distributions observed in G^K. Then,*

$$(\pi^{H|K}, \pi^{W|K})_{K\geq 1} \xrightarrow[K\to\infty]{\mathbb{P}-a.s.} (\pi^H, \pi^W).$$

Proof. We focus on the convergence of $\pi^{H|K}$, as the argument for $\pi^{W|K}$ is analogous.

Let $n_{\max}$ be fixed. Denote the true household size distribution by $\pi^H = (\pi_1^H, \pi_2^H, \cdots, \pi_{n_{max}}^H)$, where π_i^H is the probability of a household having size $i \in \{1, \cdots, n_{max}\}$.

Let $\{X_n\}_n$ be a sequence of i.i.d. random variables with distribution π^H. i.e.,

$$\mathbb{P}(X_n = i) = \pi_i^H, \quad \forall i \in \{1, \cdots, n_{max}\}.$$

Fix $m \in \{1, \cdots, n_{max}\}$. For $n \geq 1$, let $Z_n := \mathbb{1}_{\{X_n = m\}}$. Since the variables X_n are i.i.d, so are the variables Z_n. Moreover,

$$\mathbb{E}[Z_n] = \mathbb{P}(X_n = m) = \pi_m^H, \quad \forall n \in \mathbb{N}.$$

By the Law of large numbers,

$$M_n := \frac{1}{n}\sum_{k=1}^{n} Z_k \xrightarrow[n\to\infty]{a.s.} \pi_m^H.$$

Define the set

$$\Omega_m^* := \{\omega \in \Omega : M_n(\omega) \xrightarrow[n\to\infty]{} \pi_m^H\}.$$

Now, for each $K \geq 1$, define

$$N_K := \min\Big\{n : \sum_{i=1}^{n} X_i \geq K\Big\}. \tag{4.1}$$

This represents the number of full households needed to cover at least K individuals.

Define the empirical frequency (excluding the possible incomplete last household):

$$\tilde{\pi}_m^{H|K} := M_{N_K}(\omega).$$

Note that $N_K \to \infty$ as $K \to \infty$. Thus, since $M_n(\omega) \to \pi_m^H$ for $\omega \in \Omega_m^*$, it follows that

$$\tilde{\pi}_m^{H|K} \xrightarrow[K\to\infty]{} \pi_m^H.$$

Let $S_{N_K} := K - \sum_{n=1}^{N_K - 1} X_n(\omega)$ be the size of the (possibly incomplete) last household. Then, the true empirical proportion of households of size m among the N_K used is

$$\pi_m^{H|K} = \tilde{\pi}_m^{H|K} + \frac{1}{N_k}\Big[\mathbb{1}_{\{S_{N_K} = m\}} - \mathbb{1}_{\{X_{N_K}(\omega) = m\}}\Big]. \tag{4.2}$$

It follows that

$$\left|\pi_m^{H|K} - \tilde{\pi}_m^{H|K}\right| \leq \frac{1}{N_K},$$

and since $N_K \to \infty$ as $K \to \infty$, we conclude that

$$\pi_m^{H|K} \xrightarrow[K\to\infty]{} \pi_m^H, \quad \text{for all } \omega \in \Omega_m^*.$$

Define $\Omega_H^* = \cap_{m=1}^{n_{max}} \Omega_m^*$. Then, for every $\omega \in \Omega_H^*$, we have convergence of the full vector:

$$\pi^{H|K} = (\pi_1^{H|K}, \cdots, \pi_{n_{max}}^{H|K}) \xrightarrow[K\to\infty]{} \pi^H.$$

A completely analogous argument gives that $\pi^{W|K} \to \pi^W$ almost surely. Thus, $(\pi^{H|K}, \pi^{W|K}) \to (\pi^H, \pi^W)$ almost surely. $\square$

4.2 Numerical Illustration of Convergence

To illustrate the almost sure convergence established in Lemma 4.1, we present a numerical simulation showing how the empirical household size distribution approaches the true distribution for increasing population sizes.

Suppose the true household size distribution is given by

$$\pi^H = (\pi_1^H, \pi_2^H, \pi_3^H) = (0.2, 0.5, 0.3).$$

We simulate a sequence of households according to this distribution and keep adding them until we reach a total population size K. For each value of K, we compute the empiricial household size distribution $\pi^{H|K}$ and compare it with the true distribution π^H.

Simulation

```python
import numpy as np
import matplotlib.pyplot as plt

# True household size distribution
pi_H = np.array([0.2, 0.5, 0.3])
sizes = [1, 2, 3]

# Simulate a large sequence of household sizes
np.random.seed(42)
X = np.random.choice(sizes, p=pi_H, size=10000)

# Define a range of K values to evaluate convergence
K_values = np.linspace(100, 7000, 100, dtype=int)

# Store empirical proportions for each household size across K
empirical_curves = {size: [] for size in sizes}

for K in K_values:
```

```
    total = 0
    i = 0
    household_counts = {1: 0, 2: 0, 3: 0}
    while total < K and i < len(X):
        size = X[i]
        if total + size > K:
            break
        household_counts[size] += 1
        total += size
        i += 1
    N_K = sum(household_counts.values())
    for size in sizes:
        empirical_curves[size].append(household_counts[size] / N_K if N_K > 0 else 0)

# Plotting the convergence curves
plt.figure(figsize=(8, 5))
for size in sizes:
    plt.plot(K_values, empirical_curves[size], label=f"Size {size}", lw=2)

# Plot horizontal lines for true proportions
for i, true_val in enumerate(pi_H):
    plt.axhline(y=true_val, linestyle=’dashed’, color=’black’, alpha=0.6,
                label=f"True pi^H" if i == 0 else None)

plt.xlabel("Total population size K")
plt.ylabel("Empirical proportion")
plt.title("Convergence of Empirical Household Size Distribution to True pi^H")
plt.legend()
plt.grid(True)
plt.tight_layout()
plt.show()
```

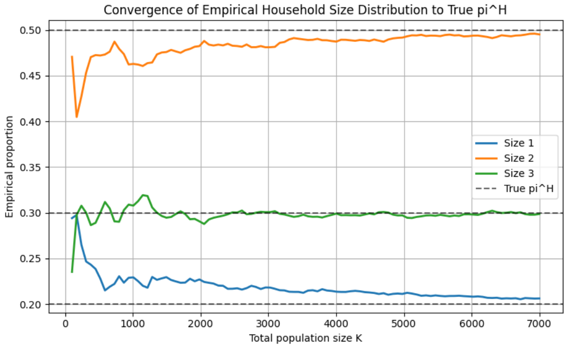


Figure 1: Output of the simulation code: convergence of empirical household size distributions.

Figure 4.2 above shows the empirical household size distribution $\pi^{H|K}$ computed from simulations for increasing values of K. As K grows, each empirical frequency converges to the corresponding component of the true distribution $\pi^H = (0.2, 0.5, 0.3)$, consistent with the Law of Large Numbers. Dashed horizontal lines indicate the true values.

4.3 Limiting Ratios of Households and Workplaces

Next, we determine the limiting ratios of the number of households and workplaces to the total population size.

Let X be a random variable with distribution π^H. Note that

$$0 < \mathbb{E}[X] = \sum_{n=1}^{n_{\max}} n \cdot \mathbb{P}[X = n] < \infty.$$

Proposition 4.1. *Let X be a random variable with distribution π^H. Then, as $K \to \infty$,*

$$\frac{K_H}{K} \xrightarrow{a.s.} \alpha_H := \frac{1}{\mathbb{E}[X]}.$$

Proof. Recall that households are constructed from an i.i.d. sequence $\{X_n\}_n \sim \pi^H$. For $m \in \mathbb{N}$, let $S_m := \sum_{i=1}^{m} X_i$ be the cumulative number of individuals after m households. By the Strong Law of Large Numbers,

$$\frac{S_m}{m} \xrightarrow{a.s.} \alpha_H^{-1} \quad \text{as } m \to \infty. \tag{4.3}$$

For $K \geq 1$, define

$$N_K := \min\Big\{n : \sum_{i=1}^{n} X_i \geq K\Big\}.$$

By construction, $K_H = N_K$ and we have

$$S_{K_H - 1} < K \leq S_{K_H}.$$

Dividing the inequality by K_H gives

$$\frac{S_{K_H-1}}{K_H} < \frac{K}{K_H} \leq \frac{S_{K_H}}{K_H}.$$

Since $K_H \to \infty$ as $K \to \infty$, (4.3) implies

$$\frac{S_{K_H}}{K_H} \xrightarrow[K\to\infty]{a.s.} \alpha_H^{-1}.$$

Moreover,

$$\frac{S_{K_H-1}}{K_H} = \frac{S_{K_H}}{K_H} - \frac{X_{K_H}}{K_H} \xrightarrow[K\to\infty]{a.s.} \alpha_H^{-1},$$

because X_{K_H} is bounded and $K_H \to \infty$.

Applying the squeeze theorem, we deduce that

$$\frac{K}{K_H} \xrightarrow[K\to\infty]{a.s.} \alpha_H^{-1}.$$

Taking the reciprocals yields

$$\frac{K_H}{K} \xrightarrow[K\to\infty]{a.s.} \alpha_H.$$

This completes the proof. □

Proceeding analogously for workplaces, we obtain the following proposition:

Proposition 4.2. *Let Y be a random variable with distribution π^W. Then, as $K \to \infty$,*

$$\frac{K_W}{K} \xrightarrow{a.s.} \alpha_W := \frac{1}{\mathbb{E}[Y]}.$$

The previous two results establish the asymptotic ratios of the number of households and workplaces to the total population size. As a direct consequence, we can also describe the relationship between the average number of susceptibles computed from each layer.

Lemma 4.2. *For every $t \geq 0$,*

$$\langle \eta_t^H, s\rangle = 0 \quad \iff \quad \langle \eta_t^W, s\rangle = 0.$$

Proof. Recall that for a population of size K,

$$\langle \zeta_t^{H|K}, s\rangle = \frac{S(t)}{K_H}, \quad \langle \zeta_t^{W|K}, s\rangle = \frac{S(t)}{K_W},$$

where $S(t)$ denotes the total number of susceptible individuals. Since $\zeta_t^{H|K} \to \eta_t^H$ almost surely and $s \in C_b(E)$, it follows that

$$\frac{S(t)}{K_H} \xrightarrow[K\to\infty]{a.s.} \langle \eta_t^H, s\rangle.$$

If $\langle \eta_t^H, s\rangle = 0$, then $S(t)/K_H \to 0$ almost surely. Using that $\frac{K_H}{K} \to \alpha_H > 0$, we deduce

$$\frac{S(t)}{K} = \frac{K_H}{K} \cdot \frac{S(t)}{K_H} \xrightarrow[K\to\infty]{a.s.} 0.$$

Consequently,

$$\frac{S(t)}{K_W} = \frac{S(t)}{K} \cdot \frac{K}{K_W} \xrightarrow[K\to\infty]{a.s.} 0,$$

whcih implies $\langle \eta_t^W, s\rangle = 0$. The converse follows by symmetry.

□

Remark 4.1. ***Interpretation of Lemma 4.2.***

This result confirms that if no susceptibles remain in households, then none remain in workplaces (and vice versa). In other words, both representations are consistent and vanish simultaneously.

5 Main Results

In this section, we summarize the key assumptions and results of [Kub23] describing the large population limit of the model. We begin by outlining the required regularity of initial conditions, then present the main convergence result and its reduction to a dynamical system in the Markovian case.

5.1 Assumptions on Initial Conditions

To ensure tightness and identify the limit, we impose the following regularity assumption on the sequence of initial conditions $(\zeta_0^K)_{K\geq 1}$.

Assumption 5.1. *For any $X \in \{H, W\}$ and $T \geq 0$,*

(i)

$$\lim_{N\to\infty} \sup_{K\geq 1} \mathbb{E}\left[\sup_{0\leq t\leq T} \frac{1}{K_X} \sum_{k=1}^{K_X} \sum_{i=1}^{n_{max}} \mathbb{1}_{\left\{n_k^X - s_k^X(0)\geq i, |\tau_{k,i}^X(0)-t|\geq N\right\}} \right] = 0.$$

(ii) For any $c \in \mathbb{R}$ and $i \in \{1, \cdots, n_{max}\}$,

$$\lim_{\epsilon\to 0} \sup_{K\geq 1} \mathbb{E}\left[\frac{1}{K_X} \sum_{k=1}^{K_X} \mathbb{1}_{\left\{n_k^X - s_k^X(0)\geq i, |(\tau_{k,i}^X(0)-T)-c|\leq \epsilon\right\}} \right] = 0.$$

These conditions ensure that the initial distributions of infectious periods are well-behaved: (i) prevents extreme values from concentrating, and (ii) avoids mass accumulation at specific time points. Together, they guarantee regularity in the initial data.

5.2 Convergence to the Deterministic Limit

We now turn to the large population limit of the measure process $(\zeta^K)_{K\geq 1}$.

Let $f \in \mathcal{C}_b^1(\mathbb{R}_+ \times E, \mathbb{R})$ and define, for every $t \geq 0$ and $x = (n, s, \tau) \in E$,

$$f_t(x) := f(t, x), \quad f_t^{\mathcal{I}}(x) := \langle \nu, f_t(j(x, \cdot))\rangle. \tag{5.1}$$

We introduce the differential operator $\mathcal{A}$, which governs the evolution of test functions under the deterministic flow (i.e., in the absence of new infections). For $x = (n, s, \tau) \in E$,

$$\mathcal{A}f_t(x) := \partial_t f(t, x) - \sum_{k=1}^{n-s} \partial_{\tau_k} f(t, x). \tag{5.2}$$

Let $\mathfrak{M}_1 := \mathcal{M}_1(E)^2$ be the space of pairs of probability measures on E, and let $\mathbf{n}(x) = n$, $\mathbf{s}(x) = s$, $\mathbf{i}(x) = i(\tau)$ denote the total number of individuals, the number of susceptibles, and the number of infectious individuals in a structure of type x, respectively.

We are now ready to state the main convergence theorem:

Theorem 5.1. *Let $\omega \in \Omega^*_{\mathcal{G}}$. Suppose that $(\zeta_0^K)_{K\geq 1}$ satisfies Assumption 5.1 and converges in law to $\eta_0 \in \mathfrak{M}_1$. Then $(\zeta^K)_{K\geq 1}$ converges in $\mathbb{D}(\mathbb{R}_+, \mathcal{M}_1(E))^2$ to $\eta = (\eta^H, \eta^W)$ defined as the unique solution of the following system of equations: For any $f \in \mathcal{C}_b^1(\mathbb{R}_+ \times E, \mathbb{R})$, for any $T \geq 0$,*

$$\begin{aligned}\langle \eta_T^X, f_T\rangle =& \langle \eta_0^X, f_0\rangle + \int_0^T \langle \eta_t^X, \mathcal{A} f_t\rangle dt + \lambda_X \int_0^T \langle \eta_t^X, \mathbf{si}(f_t^{\mathcal{I}} - f_t\rangle dt \\ &+ \lambda_{\bar{X}} \int_0^T \frac{\langle \eta_t^{\bar{X}}, \mathbf{si}\rangle}{\langle \eta_t^{\bar{X}}, \mathbf{s}\rangle} \langle \eta_t^X, \mathbf{s}(f_t^{\mathcal{I}} - f_t)\rangle dt + \beta_G \int_0^T \frac{\langle \eta_t^H, \mathbf{i}\rangle}{\langle \eta_0^H, \mathbf{n}\rangle} \langle \eta_t^X, \mathbf{s}(f_t^{\mathcal{I}} - f_t)\rangle dt.\end{aligned} \tag{5.3}$$

This equation describes the evolution of the limiting measure η^X. Each term represents a different mechanism of change: The first integral corresponds to natural aging of infectious periods and time variation. The second integral captures within-layer infections. The third term reflects cross-layer infections from the other structure type. The final term accounts for global infections in the population.

Let $s(t)$ and $i(t)$ denote the proportions of susceptible and infectious individuals in the population at time t, according to the distribution η_t. We define the set

$$\mathbb{S} := \{(n - i, i) : 2 \leq n \leq n_{\max}, 0 \leq i \leq n - 1\}.$$

For $(S, I) \in \mathbb{S}$, let $n^H_{S,I}(t)$ be the proportion of households containing S susceptible individuals and I infectious individuals at time t, according to the distribution η_t^H. Similarly, define $n^W_{S,I}(t)$ for workplaces.

We also define, for $X \in \{H, W\}$,

$$\tau_G(t) = \beta_G\, i(t), \quad \tau_X(t) = \frac{\lambda_X}{m_X} \sum_{(S,I)\in\mathbb{S}} SI\, n^X_{S,I}(t).$$

In [Kub23], it is shown that if the distribution ν of infectious periods is exponential with parameter γ, then, as the population size grows, the proportion of susceptible and infectious individuals converges to the solution of a deterministic dynamical system. In this setting, at time $t = 0$, a fraction ϵ of uniformly chosen individuals are infected in an otherwise susceptible population. Furthermore, the remaining infectious period of each initially infected individual is assumed to be distributed according to ν, independently of all other individuals.

Theorem 5.2. *Let $\epsilon > 0$ and suppose that η satisfies equation (5.3) with $\eta_0 = \eta_{0,\epsilon}$. Then, the functions $(s, i, \eta^X_{S,I} : X \in \{H, W\}, (S, I) \in \mathbb{S})$ are characterized as being the unique solution of the following dynamical system: for any $t \geq 0$, $X \in \{H, W\}$ and $(S, I) \in \mathbb{S}$,*

$$
\begin{aligned}
\frac{d}{dt}s(t) =& -(\tau_H(t) + \tau_W(t) + \tau_G(t)s(t)),\\
\frac{d}{dt}i(t) =& -\frac{d}{dt}s(t) - \gamma i(t),\\
\frac{d}{dt}\eta^X_{S,I}(t) =& -\left(\lambda_X SI + \tau_{\bar{X}}\frac{S}{s(t)} + \tau_G(t)S + \gamma I\right)\eta^X_{S,I}(t)\\
&+ \gamma(I+1)\eta^X_{S,I+1}(t)\mathbb{1}_{\{}S + I < n_{max}\}\\
&+ \left(\lambda_X(S+I)(I-1) + \gamma_{\bar{X}}\frac{S+1}{s(t)} + \tau_G(t)(S+I)\right)\eta^X_{S+1,I-1}(t)\mathbb{1}_{\{}I \geq 1\},
\end{aligned}
\tag{5.4}
$$

with initial conditions given by

$$
s(0) = 1 - \epsilon; \quad i(0) = \epsilon; \quad \eta^X_{S,I}(0) = \binom{S+I}{I}\pi^X_{S+I}(1-\epsilon)^S\epsilon^I. \tag{5.5}
$$

Remark 5.1. ***Interpretation of system* (5.4)*.*** *The first equation of the dynamical system describes the decrease in the proportion of susceptible individuals whenever a new infection occurs, either in the general population or within a household or workplace. The second equation accounts for the flow of individuals from the susceptible state to the infected state, who then leave the infected class at rate γ. Finally, the third equation governs the evolution of the distribution of structures: a structure of type (S, I) changes its composition either when one of its susceptible members becomes infected (in any layer of the graph) or when one of its infected members recovers. These events respectively produce transitions $(S, I) \to (S, I+1)$ and $(S, I) \to (S+1, I-1)$.*

Remark 5.2. *In several expressions throughout the model, we encounter ratios of the form:*

$$
R^{H|X}_t := \frac{\langle \zeta^{H|X}_t, \mathbf{si}\rangle}{\langle \zeta^{H|X}_t, \mathbf{s}\rangle}, \quad X \in \{H, W\},
$$

interpreted as the average number of infectious individuals per susceptible in structures of type X at time t. A similar expression appears in the limiting system:

$$
R^X_t := \frac{\langle \eta^X_t, \mathbf{si}\rangle}{\langle \eta^X_t, \mathbf{s}\rangle}.
$$

These ratios are well-defined as long as $\langle \zeta^{X|K}_t, \mathbf{s}\rangle$ or $\langle \eta^X_t, \mathbf{s}\rangle$ are strictly positive. However, as the epidemic progresses and the number of susceptibles decreases, it may happen that

$\langle\zeta_t^{X|K}, \mathbf{s}\rangle = 0$ *or* $\langle\eta_t^X, \mathbf{s}\rangle = 0$. *In such cases, the numerator must also vanish, since there can be no susceptible-infectious pairs, and the ratio becomes the indeterminate form* $\frac{0}{0}$.

To resolve this, we adopt the convention:

$$R_t^{X|K} := 0 \quad \textit{whenever} \quad \langle\zeta_t^{X|K}, \mathbf{s}\rangle = 0,$$

and analogously for R_t^X. *This choice ensures that the model remains well-defined and consistent with the epidemic dynamics. Indeed, if no susceptibles remain in layer* X, *no within-layer infections can occur. Thus, the infection rate per susceptible becomes irrelevant, and assigning the ratio the value zero accurately reflects the absence of further risk.*

This convention is particularly important in the limiting system, where one encounters cross-layer infection terms of the form:

$$\frac{\langle\eta_t^X, \mathbf{si}\rangle}{\langle\eta_t^X, \mathbf{s}\rangle} \cdot \langle\eta_t^{\bar{X}}, \mathbf{s}(f_t^{\mathcal{I}} - f_t)\rangle,$$

with $\bar{X}$ *denoting the complementary layer (i.e.,* $\bar{H} = W$, $\bar{W} = H$*). These terms describe the contribution of layer* X *to the infection rate in layer* $\bar{X}$. *However, if* $\langle\eta_t^X, \mathbf{s}\rangle = 0$, *layer* X *cannot exert any epidemiological influence on other layers, and the corresponding contribution should vanish. Defining* $0/0 := 0$ *ensures this behavior, preserving the continuity and boundedness of the equations, and avoiding singularities or discontinuities in degenerate scenarios.*

6 Proof of Theorem 5.1

In this section, we outline the main ideas in the proof of the convergence of the stochastic process $\zeta^K = (\zeta_t^{H|K}, \zeta_t^{W|K})$ to the deterministic limit $\eta = (\eta_t^H, \eta_t^W)$, as stated in Theorem 5.1. The proof involves two main steps: establishing uniqueness and continuity of the limit, and proving tightness of the sequence (ζ^K) in the Skorokhod space. As we will explain in the proof of Proposition 6.1, some arguments in the proof of uniqueness provided by [Kub23] seem problematic and would require further justification. Unfortunately, we were unable to write a complete and detailed proof based on it.

6.1 Uniqueness and Continuity of the Solution of Equation (5.3)

To establish the uniqueness of the solution of equation (5.3), we will need the following Lemma:

Lemma 6.1. *Let* $f \in \mathcal{C}_b(E, \mathbb{R})$. *There exists a sequence* $\{f_k\}_{k\geq 1}$ *taking values in* $\mathcal{C}_b^1(E, \mathbb{R})$ *such that* f_k *converges pointwise to* f *and* $\sup_{k\geq 1} \|f_k\|_\infty \leq \|f\|_\infty$.

Proof. Let $\psi \in C_c^\infty(\mathbb{R}^{n_{max}})$ be a standard mollifier, i.e., a nonnegative, smooth function with compact support and such that $\int_{\mathbb{R}^{n_{max}}} \psi(x)dx = 1$. For $k \geq 1$, define the rescaled mollifier

$$\psi_k(x) := k^{n_{max}} \psi(kx).$$

The sequence $\{\psi_k\}_{k\geq 1}$ satisfies $\lim_{k\to\infty} \psi_k = \delta_0$ in the sense of distributions; that is, for any test function $\phi \in C_c^\infty(\mathbb{R}^{n_{max}})$,

$$\int \phi(x)\psi_k(x)dx \to \phi(0) \quad \text{as } k \to \infty.$$

Let $f \in C_b(E, \mathbb{R})$. For $k \geq 1$, define the function $f_k : E \to \mathbb{R}$ by convolving f with ψ_k in the last variable:

$$f_k(n, s, \tau) := (f(n, s, \cdot) * \psi_k)(\tau).$$

Since $f \in C_b(E, \mathbb{R})$, it follows that, for every $x \in E$, $\lim_{k\to\infty} f_k(x) = f(x)$. Moreover, as $\int_{\mathbb{R}^{n_{max}}} \psi_k(x)dx = 1$ for any $k \geq 1$, we have that $\|f_k\|_\infty \leq \|f\|_\infty$. Finally, as the convolution of a bounded function with a smooth mollifier yields a smooth function, each f_k is smooth in the variable τ. The partial derivatives are also bounded due to the boundedness of f and the properties of ψ_k. Therefore, $f_k \in C_b^1(E, \mathbb{R})$ for all $k \geq 1$. □

For an element $\eta = (\eta_1, \eta_2) \in \mathfrak{M}_1$, we define its total variation norm by $\|\eta\|_{TV} = \|\eta_1\|_{TV} \vee \|\eta_1\|_{TV}$.

Proposition 6.1. *Let $\eta_* \in \mathfrak{M}_1$. Then, equation (5.3) admits at most one measure-valued solution η which belongs to $\mathcal{C}(\mathbb{R}_+, (\mathfrak{M}_1, \|\cdot\|_{TV}))$, such that $\eta_0 = \eta_*$.*

Proof. In [Kub23], a complete proof is provided; however, upon attempting to reconstruct the argument, we observed that certain nontrivial terms (particularly those involving quotients) require additional justification. It seems that some intermediate steps are either omitted or left implicit in the original source. For this reason, we do not reproduce the full derivation here. □

6.2 Tightness of $(\zeta^K)_{K\geq 1}$

We will now focus on proving the tightness of $(\zeta^K)_{K\geq 1}$ in $\mathbb{D}(\mathbb{R}_+, (\mathcal{M}_F(E), v))^2$, where v denotes the vague topology on $\mathcal{M}_F(E)$. In order to do this, we will introduce some preliminary results.

Lemma 6.2. *Let $f \in \mathcal{C}_b^1(\mathbb{R}_+ \times E, \mathbb{R})$. Then, for any $T \geq t_0 \geq 0$ and any $x \in E$,*

$$f(T, \Psi(x, T, t_0)) = f(t_0, x) + \int_{t_0}^{T} \mathcal{A}f(t, \Psi(x, t, t_0))dt,$$

where Ψ and $\mathcal{A}$ are defined by (3.1) and (5.2), respectively.

Proof. Fix $x = (n, s, \tau) \in E$ and $t_0 \in \mathbb{R}_+$, and consider the function $g_{t_0,x} : [t_0, \infty) \to \mathbb{R}$ defined by

$$g_{t_0,x}(T) := f(T, \Psi(x, T, t_0)).$$

We will show that $g_{t_0,x} \in C^1(\mathbb{R}_+)$, and that its derivative satifies

$$\frac{d}{dT} g_{t_0,x}(T) = \mathcal{A}f(T, \Psi(x, T, t_0)),$$

which yields the result upon integration.

To compute the derivative, define the auxiliary function $f_{n,s} : \mathbb{R}_+ \times \mathbb{R}^{n_{max}} \to \mathbb{R}$ by $f_{n,s}(u, v) := f(u, (n, s, v))$, and define $h_{t_0,x} : \mathbb{R}_+ \to \mathbb{R}_+ \times \mathbb{R}^{n_{max}}$ by

$$h_{t_0,x}(t) := \left(t, \tau - \sum_{k=1}^{n-s} (t - t_0) e_k \right),$$

where e_k is the k-th canonical basis vector in $\mathbb{R}^{n_{max}}$. Then we can write $g_{t_0,x}(t) = f_{n,s}(h_{t_0,x}(t))$, and since both $f_{n,s}$ and $h_{t_0,x}$ are continuously differentiable, so is their composition.

Using the chain rule, we compute

$$\frac{d}{dt} g_{t_0,x}(t) = \partial_1 f_{n,s}(h_{t_0,x}(t)) - \sum_{k=1}^{n-s} \partial_{k+1} f_{n,s}(h_{t_0,x}(t)),$$

where the negative signs appear because each component τ_k is decreasing with t. Note that $\partial_1 f_{n,s}(u, v) = \partial_t f(u, (n, s, v))$, and $\partial_{k+1} f_{n,s}(u, v) = \partial_{\tau_k} f(u, (n, s, v))$. Therefore, the derivative of $g_{t_0,x}$ satisfies

$$\frac{d}{dt} g_{t_0,x}(t) = \mathcal{A}f(t, \Psi(x, t, t_0)).$$

Integrating both sides from t_0 to T, we obtain

$$f(T, \Psi(x, T, t_0)) = f(t_0, x) + \int_0^T \mathcal{A}f(t, \Psi(x, t, t_0)) dt.$$

as claimed. □

We introduce the notation $\mathcal{S} = \{H, W, G\}$. Additionally, for any $f \in \mathcal{C}_b(\mathbb{R}_+ \times E, \mathbb{R})$, any $t \geq 0$ and $u = (\theta, k, \ell, \sigma) \in \bigcup_{Y \in \mathcal{S}} U_Y$ (with the spaces U_Y defined by (3.6) and (3.5)), we define

$$f^H_{t,u} := f(t, j(x^H_k(t), \sigma) - f(t, x^H_k(t)) \quad \text{and} \quad f^W_{t,u} := f(t, j(x^W_\ell(t), \sigma)) - f(t, x^W_\ell(t)). \quad (6.1)$$

Proposition 6.2. *Let* $f \in \mathcal{C}_b^1(\mathbb{R}_+ \times E, \mathbb{R})$*, and let* $f_t(\cdot) := f(t, \cdot)$*. Then, for all* $T \geq 0$ *and* $X \in \{H, W\}$*,*

$$\left\langle \zeta_T^{X|K}, f_T \right\rangle = \left\langle \zeta_0^{X|K}, f_0 \right\rangle + \int_0^T \left\langle \zeta_t^{X|K}, \mathcal{A} f_t \right\rangle dt + \frac{1}{K_X} \sum_{Y \in \mathcal{S}} \int_0^T \int_{U_Y} \mathcal{I}_Y(t-u) f^X_{t-,u} Q_Y(dt, du), \tag{6.2}$$

where the functions I_Y *are given by* (3.7)*,* (3.8) *and* (3.9)*.*

Proof. Let $f \in \mathcal{C}_b^1(\mathbb{R}_+ \times E, \mathbb{R})$ and $T \geq 0$. We will prove the result for $X = H$, since the case for $H = W$ is analogous. By equation (3.10), we have

$$\begin{aligned} \left\langle \zeta_T^{H|K}, f_T \right\rangle =& \frac{1}{K_H} \sum_{j=1}^{K_H} f_T(\Psi(x_j^H(0), T, 0)) \\ &+ \frac{1}{K_H} \sum_{Y \in \{H,W,G\}} \int_0^T \int_{U_Y} \mathcal{I}_Y(t-, u) \langle \Delta_H(u, T, t), f_T \rangle Q_Y(dt, du). \end{aligned} \tag{6.3}$$

Applying Lemma (6.2), we can write the first summand as

$$\frac{1}{K_H} \sum_{j=1}^{K_H} \left(f_0(x_j^H(0)) + \int_0^T \mathcal{A} f_t(\Psi(x_j^H(0), t, 0)) dt \right).$$

On the other hand, recall that, for any $u = (\theta, k, \ell, \sigma) \in \bigcup_{Y \in \mathcal{S}} U_Y$ and any $0 \leq t \leq T$,

$$\langle \Delta_H(u, T, t), f_T \rangle = f_T(\Psi(j(x_k^H(t-), \sigma), T, t)) - f_T(\Psi(x_k^H(t-), T, t)). \tag{6.4}$$

Thus, we can write the second summand in (6.3) as

$$\frac{1}{K_H} \sum_{Y \in \mathcal{S}} \int_0^T \int_{U_Y} \mathcal{I}_Y(t-, u) \big[f_T(\Psi(j(x_k^H(t-), \sigma), T, t)) - f_T(\Psi(x_k^H(t-), T, t)) \big] Q_Y(dt, du).$$

Using (6.2), this becomes

$$\begin{aligned} &\frac{1}{K_H} \sum_{Y \in \mathcal{S}} \int_0^T \int_{U_Y} \mathcal{I}_Y(t-, u) \left(\int_t^T \big[\mathcal{A} f_z(\Psi(j(x_k^H(t-), \sigma), z, t)) - \mathcal{A} f_z(\Psi(x_k^H(t-), z, t)) \big] \right) Q_Y(dt, du \\ &+ \frac{1}{K_H} \sum_{Y \in \mathcal{S}} \int_0^T \int_{U_Y} \mathcal{I}_Y(t-, u) \big[f(t, j(x_k^H(t-), \sigma)) - f(t, x_k^H(t-)) \big] Q_Y(dt, du). \end{aligned}$$

By (6.4) and (6.1), we conclude that

$$\begin{aligned}\left\langle \zeta_T^{H|K}, f_T \right\rangle =& \frac{1}{K_H}\sum_{j=1}^{K_H}\left(f_0(x_j^H(0)) + \int_0^T \mathcal{A}f_t(\Psi(x_j^H(0),t,0))dt \right) \\ &+ \frac{1}{K_H}\sum_{Y\in\mathcal{S}}\int_0^T\int_{U_Y}\mathcal{I}_Y(t-,u)\left(\int_t^T \langle \Delta_H(u,z,t), \mathcal{A}fz\rangle dz\right)Q_Y(dt,du) \\ &+ \frac{1}{K_H}\sum_{Y\in\mathcal{S}}\int_0^T\int_{U_Y}\mathcal{I}_Y(t-,u)f^X_{t-,u}Q_Y(dt,du).\end{aligned}$$

Then, as f and the indicator functions $\mathcal{I}_Y$ are bounded, we can apply Fubini's Theorem and obtain:

$$\begin{aligned}\left\langle \zeta_T^{H|K}, f_T \right\rangle =& \frac{1}{K_H}\sum_{j=1}^{K_H} f_0(x_j^H(0)) + \frac{1}{K_H}\sum_{Y\in\mathcal{S}}\int_0^T\int_{U_Y}\mathcal{I}_Y(t-,u)f^X_{t-,u}Q_Y(dt,du) \\ &+ \frac{1}{K_H}\int_0^T\left(\sum_{j=1}^{K_H}\mathcal{A}f_z(\Psi(x_j^H(0),z,0)) + \sum_{Y\in\mathcal{S}}\int_0^z\int_{U_Y}\mathcal{I}_Y(t-,u)\langle\Delta_H(u,z,t),\mathcal{A}f_z\rangle Q_Y(dt,du)\right)dz.\end{aligned}$$

This expression coincides exactly with equation (6.2). □

For $Y \in \mathcal{S}$, let

$$\tilde{Q}_Y(dt,du) = Q_Y(dt,du) - dt\mu_Y(du)$$

be the compensated martingale-measure associated to Q_Y. Then, for $f \in \mathcal{C}_b^1(\mathbb{R}_+ \times E, \mathbb{R})$ and $X \in \{H, W\}$,

$$\left\langle \zeta_T^{X|K}, f_T \right\rangle = M_T^{X|K}(f) + V_T^{X|K}(f),$$

where

$$M_T^{X|K} := \frac{1}{K_X}\sum_{Y\in\mathcal{S}}\int_0^T\int_{U_Y}\mathcal{I}_Y(t-,u)f^X_{t-,u}\tilde{Q}_Y(dt,du)$$

and

$$V_T^{X|K}(f) := \left\langle \zeta_0^{X|K}, f_0 \right\rangle + \int_0^T \left\langle \zeta_t^{X|K}, \mathcal{A}f_t \right\rangle dt + \frac{1}{K_X}\sum_{Y\in\mathcal{S}}\int_0^T\int_{U_Y}\mathcal{I}_Y(t,u)f^X_{t,u}\mu_Y(du)dt.$$

Proposition 6.3. *Let $f \in \mathcal{C}_b^1(\mathbb{R}_+ \times E, \mathbb{R})$ and let $X \in \{H, W\}$. Then the process $(M_T^{X|K}(f))_{T\geq 0}$ is a square-integrable martingale, with quadratic variation*

$$\left\langle M^{X|K}(f)\right\rangle_T = \frac{1}{K_X}\int_0^T \left\langle \zeta_t^{X|K}, \mathcal{H}_t^X((f_t^2)^{\mathcal{I}} - 2f_t^{\mathcal{I}}f_t + f_t^2)\right\rangle dt,$$

where, for each $t \geq 0$ *and* $x \in E$*,*

$$\mathcal{H}_t^X(x) = \beta_G \frac{I_H(t)}{N_H} \mathbf{s}(x) + \lambda_X \mathbf{s}(x)\mathbf{i}(x) + \lambda_{\bar{X}} \frac{\left\langle \zeta_t^{\bar{X}|K}, \mathbf{si} \right\rangle}{S_{\bar{X}}(t)} \mathbf{s}(x).$$

Proof. Let $f \in \mathcal{C}_b^1(\mathbb{R}_+ \times E, \mathbb{R})$ and $X \in \{H, W\}$. Note that $M_T^{X|K}(f)$ can be decomposed as:

$$M_T^{X|K}(f) = \sum_{Y \in \mathcal{S}} M_{Y,T}^{X|K}(f),$$

where, for each $Y \in \mathcal{S}$ and $T \geq 0$,

$$M_{Y,T}^{X|K}(f) := \int_0^T \int_{U_Y} \frac{1}{K_X} \mathcal{I}_Y(t-, u) f_{t,u}^X \tilde{Q}_Y(dt, du).$$

Since f is bounded, for each $Y \in \mathcal{S}$, we have

$$\mathbb{E}\left[\int_0^T \int_{U_Y} \left(\frac{1}{K_X} \mathcal{I}_Y(t, u) f_{t,u}^X\right)^2 \mu_Y(du)dt\right] < \infty.$$

Thus, each process $(M_{Y,T}^{X|K}(f))_{T\geq 0}$ is square-integrable, and so is the sum $(M_T^{X|K}(f))_{T\geq 0}$.

Since the Poisson measures $Q^{H,K}$, $Q^{W|K}$ and $Q^{G|K}$ are independent, the total quadratic variation decomposes as

$$\left\langle M^{X|K}(f) \right\rangle_T = \sum_{Y \in \mathcal{S}} \left\langle M_Y^{X|K}(f) \right\rangle_T.$$

We now compute the quadratic variation explicitly in the case $X = H$, starting with $Y = H$:

$$\begin{aligned}
&\mathbb{E}\left[\left\langle M_H^{H|K}(f) \right\rangle_T\right] \\
&= \mathbb{E}\left[\int_0^T \int_{U_H} \left(\frac{1}{K_H} \mathcal{I}_H(t, u) f_{t,u}^H\right)^2 \mu_H(du)dt\right] \\
&= \frac{1}{K_H^2} \mathbb{E}\left[\int_0^T \int_{U_H} \mathcal{I}_H(t, u)(f_{t,u}^H)^2 \mu_H(du)dt\right].
\end{aligned}$$

We compute the inner integral:

$$\begin{aligned}
&\int_{U_H} \mathcal{I}_H(t,u)(f^H_{t,u})^2\mu_H(du)\\
&=\sum_{k=1}^{K_H}\sum_{\ell=1}^{K_W}\lambda_H s^H_k(t)i(\tau^H_k(t))\cdot\frac{s^W_\ell(t)}{S(t)}\int(f(t,j(x^H_k(t),\sigma))-f(t,x^H_k(t)))^2\nu(d\sigma)\\
&=\sum_{k=1}^{K_H}\lambda_H s^H_k(t)i(\tau^H_k(t))\int(f(t,j(x^H_k(t),\sigma))-f(t,x^H_k(t)))^2\nu(d\sigma),
\end{aligned}$$

where the second equality follows from the fact that $\sum_{\ell=1}^{K_W} s^W_\ell(t)=S(t)$.

Since, for any $k\in\{1,\cdots,K_H\}$ and $t\in[0,T]$, $s^H_k(t)\le n_{max}$ and $i^H_k(t)\le n_{max}$ almost surely, we obtain the bound

$$\mathbb{E}\Big[\Big\langle M^{H|K}_H(f)\Big\rangle_T\Big]\le\frac{1}{K_H}\lambda_H(n_{max})^2 4\|f\|^2_\infty T. \tag{6.5}$$

Moreover, as $K_H\ge\frac{K}{n_{max}}$ and $\|f\|_\infty<\infty$, we get

$$\mathbb{E}\Big[\Big\langle M^{H|K}_H(f)\Big\rangle_T\Big]\le\frac{4}{K}\lambda_H(n_{max})^3\|f\|^2_\infty T<\infty,$$

which confirms square integrability.

Next, observe the identity:

$$\begin{aligned}
&\int\left(f(t,j(x,\sigma))-f(t,x)\right)^2\nu(d\sigma)\\
&=\int f(t,j(x,\sigma))^2\nu(d\sigma)-2f(t,x)\int f(t,j(x,\sigma))\nu(d\sigma)+f(t,x)^2\\
&=(f_t^2)^{\mathcal{I}}(x)-2f_t(x)\cdot f_t^{\mathcal{I}}(x)+f_t(x)^2.
\end{aligned}$$

Thus, by definition of $\zeta^{H|K}_t$, we have

$$\begin{aligned}
&\frac{1}{K_H}\sum_{k=1}^{K_H}s^H_k(t)i(\tau^H_k(t))\int\left(f(t,j(x^H_k(t),\sigma))-f(t,x^H_k(t))\right)^2\nu(d\sigma)\\
&=\left\langle\zeta^{H|K}_t,\mathbf{si}\left((f_t^2)^{\mathcal{I}}-2f_t^{\mathcal{I}}f_t+f_t^2\right)\right\rangle.
\end{aligned}$$

Putting everything together, the quadratic variation is given by

$$\begin{aligned}
\Big\langle M^{H|K}_H(f)\Big\rangle_T&=\int_0^T\int_{U_H}\left(\frac{1}{K_H}\mathcal{I}_H(t,u)f^H_{t,u}\right)^2\mu_H(du)dt\\
&=\frac{\lambda_H}{K_H}\int_0^T\left\langle\zeta^{H|K}_t,\mathbf{si}\left((f_t^2)^{\mathcal{I}}-2f_t^{\mathcal{I}}f_t+f_t^2\right)\right\rangle dt.
\end{aligned}$$

Similarly, $\left(M_{W,T}^{H|K}(f)\right)_{T\geq 0}$ and $\left(M_{G,T}^{H|K}(f)\right)_{T\geq 0}$ are square integrable martingales with quadratic variations given by

$$\left\langle M_W^{H|K}(f)\right\rangle_T = \frac{\lambda_W}{K_H}\int_0^T \frac{\left\langle \zeta_t^{W|K}, \mathbf{si}\right\rangle}{S_W(t)}\left\langle \zeta_t^{H|K}, \mathbf{s}\left((f_t^2)^{\mathcal{I}} - 2f_t^{\mathcal{I}} f_t + f_t^2\right)\right\rangle dt$$

and

$$\left\langle M_G^{H|K}(f)\right\rangle_T = \frac{\beta_G}{K_H}\int_0^T \frac{I_H(t)}{N_H}\left\langle \zeta_t^{H|K}, \mathbf{s}\left((f_t^2)^{\mathcal{I}} - 2f_t^{\mathcal{I}} f_t + f_t^2\right)\right\rangle dt.$$

This completes the argument for $(M_T^{H|K}(f))_{T\geq 0}$. An analogous reasoning applies to $(M_T^{W|K}(f))_{T\geq 0}$, thereby completing the proof. □

Now, we will proceed to prove the tightness of $(\zeta^K)_{K\geq 1}$, endowing $\mathcal{M}_F(E)$ with the vague topology.

Proposition 6.4. *Under the assumptions of Theorem 5.1, the sequence $(\zeta^K)_{K\geq 1}$ is tight in $\mathbb{D}(\mathbb{R}_+, (\mathcal{M}_F(E), v))^2$.*

Proof. Rather than following the proof strategy used in [Kub23], we adopt an approach similar to that of [GZN25, Lemma 4.6]. In particular using the tightness criterion stated in [GZN25, Lemma 4.5].

Let $T > 0$. As stated in [GZN25], it suffices to prove that for any $f \in \mathcal{C}_0(E) \cap \mathcal{C}_b^1(E)$, the sequence $\left(\langle \zeta^{H|K}, f\rangle\right)_{K\geq 1}$ is tight in $\mathbb{D}([0,T], \mathbb{R})$. We will use the tightness criterion in [GZN25, Lemma 4.5] to prove this. That is, we will prove that for any $\epsilon > 0$,

$$\lim_{\delta\to 0}\limsup_{K\to\infty}\sup_{t\in[0,T]}\frac{1}{\delta}\mathbb{P}\left(\sup_{0\leq r\leq s}|\langle \zeta_{t+r}, f\rangle - \langle \zeta_t, f\rangle| > \epsilon\right) = 0.$$

Let $\epsilon > 0$. Define $C := 4\lambda_H(n_{max})^3\|f\|_\infty^2$ and take $\delta = \frac{\epsilon}{2(\|Af\|_\infty + C\|f\|_\infty)}$. It follows from (6.5) that, for any $t, r \geq 0$,

$$\mathbb{E}\left[\langle M(f)\rangle_{t+r} - \langle M(f)\rangle_t\right] \leq \frac{r\cdot C}{K}\|f\|_\infty.$$

Thus, by Doob's inequality, we have

$$\begin{aligned}\mathbb{P}\left(\sup_{0\leq r\leq\delta}|M_{t+r}(f) - M_t(f)| > \frac{\epsilon}{2}\right) \leq& \frac{4}{\epsilon^2}\mathbb{E}\left[\left(M_{t+\delta}(f) - M_t(f)\right)^2\right]\\ =& \frac{4}{\epsilon^2}\mathbb{E}\left[\langle M(f)\rangle_{t+\delta} - \langle M(f)\rangle_t\right]\\ \leq& \frac{4\delta\cdot C_1}{\epsilon^2 K}\|f\|_\infty.\end{aligned} \tag{6.6}$$

On the other hand, for any $t, s \geq 0$,

$$\begin{aligned}|V_{t+r}(f) - V_t(f)| =& \int_t^{t+r} \langle \zeta_t, \mathcal{A} f_t \rangle dt + \frac{1}{K_H} \sum_{Y \in \mathcal{S}} \int_t^{t+r} \mathcal{I}_Y(t,u) f^H_{t,u} \mu_Y(du) dt \\ \leq& \|\mathcal{A} f\|_\infty \cdot r + \frac{1}{K_H} \sum_{Y \in \mathcal{S}} \int_t^{t+r} \mathcal{I}_Y(t,u) f^H_{t,u} \mu_Y(du) dt.\end{aligned}$$

Doing a similar process as in (6.5), we conclude that

$$|V_{t+r}(f) - V_t(f)| \leq \|\mathcal{A} f\|_\infty r + C \|f\|_\infty r.$$

Thus, by definition of δ,

$$\sup_{0 \leq r \leq \delta} |V_{t+r}(f) - V_t(f)| \leq \|\mathcal{A} f\|_\infty \delta + C \|f\|_\infty \delta \leq \frac{\epsilon}{2}.$$

Consequently,

$$\mathbb{P}\left(\sup_{0 \leq r \leq \delta} |V_{t+r}(f) - V_t(f)| > \frac{\epsilon}{2} \right) = 0. \tag{6.7}$$

From (6.6) and (6.7), it follows that

$$\begin{aligned}&\frac{1}{\delta} \mathbb{P}\left(\sup_{0 \leq r \leq s} |\langle \zeta_{t+r}, f \rangle - \langle \zeta_t, f \rangle| > \epsilon \right) \\ &\leq \frac{1}{\delta} \left[\mathbb{P}\left(\sup_{0 \leq r \leq \delta} |M_{t+r}(f) - M_t(f)| > \frac{\epsilon}{2} \right) + \mathbb{P}\left(\sup_{0 \leq r \leq \delta} |V_{t+r}(f) - V_t(f)| > \frac{\epsilon}{2} \right) \right] \\ &\leq \frac{4C}{\epsilon^2 K} \|f\|_\infty.\end{aligned}$$

Therefore,

$$\lim_{\delta \to 0} \limsup_{K \to \infty} \sup_{t \in [0,T]} \frac{1}{\delta} \mathbb{P}\left(\sup_{0 \leq r \leq s} |\langle \zeta_{t+r}, f \rangle - \langle \zeta_t, f \rangle| > \epsilon \right) = 0.$$

Thus, the sequence $(\zeta^K)_{K \geq 1}$ is tight in $\mathbb{D}(\mathbb{R}_+, (\mathcal{M}_F(E), v))^2$. □

Having established tightness using an approach inspired by [GZN25], we now recall two additional results from [Kub23] that will be used in the proof of Theorem 5.1.

For completeness, we reproduce the statements of [Kub23, Proposition 4.7] and [Kub23, Proposition 4.8]. The proofs are omitted here and can be found in the original article.

Proposition 6.5. *Under the assumptions of Theorem 5.1, the sequence* $(\zeta^K)_{K \geq 1}$ *is tight in* $\mathbb{D}(\mathbb{R}_+, (\mathcal{M}_F(E), w))^2$.

Proposition 6.6. *Under the assumptions of Theorem 5.1, all limiting values of* $(\zeta^K)_{K\geq 1}$ *in* $\mathbb{D}(\mathbb{R}_+, (\mathcal{M}_F(E), w))^2$ *are continous with regard to the total variaton norm, and solutions of Equation (5.3).*

We are now in a position to prove Theorem 5.1.

Proof of Theorem 5.1. By Proposition 6.5, every subsequence of $(\zeta^K)_{K\geq 1}$ admits a further subsequence converging in $\mathbb{D}(\mathbb{R}_+, (\mathcal{M}_F(E), w))^2$. Proposition 6.6 guarantees that any such limit is a solution of (5.3) and is continuous with respect to the total variation norm. Since we assume that ζ_0^K converges in law to $\eta_0 \in \mathfrak{M}_1$, Proposition 6.1 implies that all possible limits coincide. Therefore, the whole sequence $(\zeta^K)_{K\geq 1}$ converges in $\mathbb{D}(\mathbb{R}_+, (\mathcal{M}_F(E), w))^2$ to the unique solution of (5.3) with initial condition η_0. Finally, Proposition 6.1 ensures that this limit belongs to $\mathbb{D}(\mathbb{R}_+, \mathcal{M}_1(E))^2$, which completes the proof. □

7 Additional Results on Uniqueness

In this section, we study the uniqueness of solutions to the dynamical system (5.4).

Our goal is to prove that the system admits at most one solution, following the approach presented by [Kub23, Theorem 4.10]. To this end, we first rewrite the system in the form of a Cauchy problem and explicitly define all the involved terms.

Let $y \in C^1(\mathbb{R}_+, \mathbb{R}^d)$ and $f : \mathbb{R}^d \to \mathbb{R}^d$ be such that the system (5.4) can be expressed as

$$y'(t) = f(y(t)), \quad \forall t \geq 0,$$

where $d = 2 + 2\#\mathbb{S}$.

We denote by s, i and $n^X_{S,I}$ (respectively f_s, f_i and $f^X_{S,I}$) the components of y (and of f), for $X \in \{H, W\}$ and $(S, I) \in \mathbb{S}$.

We define the following rates:

$$\tau_G(y) := \beta_G i, \quad \tau_X(y) := -\frac{\lambda_X}{m_X} \sum_{(S,I)\in\mathbb{S}} SI\, n^X_{S,I}, \quad X \in \{H, W\}.$$

Then $f : \mathbb{R}^d \to \mathbb{R}^d$ is given by

$$f_s(y) = -\big(\tau_H(y) + \tau_W(y) + \tau_G(y)\big)\, s, \quad f_i(y) = -f_s(y) - \gamma i, \tag{7.1}$$

and, for all $X \in \{H, W\}$ and $(S, I) \in \mathbb{S}$,

$$\begin{aligned} f_{X,S,I}(y) = &- \left[\left(\lambda_X I + \frac{\tau_{\bar{X}}(y)}{s} + \tau_G(y)\right) S - \gamma I\right] n^X_{S,I} + \gamma(I+1) n^X_{S,I+1} \mathbb{1}_{\{S+I<n_{max}\}} \\ &+ \left(\lambda_X (I-1) + \frac{\gamma_{\bar{X}}(y)}{s} + \gamma_G(y)\right)(S+1) n^X_{S+1,I-1} \mathbb{1}_{\{I\geq 1\}}. \end{aligned} \tag{7.2}$$

Natural constraints arise from the fact that the population is partitioned into susceptible, infected, and removed individuals, and that each individual belongs to exactly one household and one workplace. We thus have:

$$s + i \leq 1, \quad \sum_{(S,I)\in\mathbb{S}} n^X_{S,I} \leq 1, \quad \sum_{(S,I)\in\mathbb{S}} S\, n^X_{S,I} \leq m_X s, \quad \forall X \in \{H, W\}, \tag{7.3}$$

where

$$m_X := \sum_{j=0}^{n_{\max}} j\pi^X_j.$$

We define the admissible set:

$$V := \left\{ y \in [0,1]^d : s + i \leq 1, \sum_{(S,I)\in\mathbb{S}} n^X_{S,I} \leq 1,\, m_X s - \sum_{(S,I)\in\mathbb{S}} S\, n^X_{S,I} \geq 0, \forall X \in \{H, W\} \right\}.$$

Proposition 7.1. *Let $y^* \in V$. Then the following asssertions hold:*

(i) Suppose that there exists a solution y of the Cauchy problem (5.4) with initial condition $y(0) = y^*$. Then $y(t) \in V$ for any $t \geq 0$ for which y is well defined.

(ii) For any $T \geq 0$, this problem admits at most a unique solution y on $[0, T]$.

(iii) In particular, for any $\epsilon > 0$, the dynamical system (5.4) endowed with initial condition (5.5) admits at most a unique solution.

Proof. In what follows, we prove only Assertions (ii) and (iii). The proof of Assertion (i) can be found in [Kub23, Theorem 4.10] and is not reproduced here.

(i) Fix $T \geq 0$ and let $y = (s, i, n^X_{S,I} : X \in \{H, W\}, (S, I) \in \mathbb{S})$ be a solution of the Cauchy problem $y'(t) = f(y(t))$ with initial condition $y(0) = y^* \in V$.

From (5.4), we have

$$s'(t) \geq -[(\lambda_H + \lambda_W)n_{max} + \beta_G]s(t).$$

Since $s \in \mathcal{C}^1(\mathbb{R}_+)$, it follows from a comparison argument that

$$s(t) \geq \epsilon_T := s(0) \exp(-[(\lambda_H + \lambda_W)n_{max} + \beta_G]T). \tag{7.4}$$

We consider two cases:

Case 1: s(0) = 0.

If $s(0) = 0$, then $s(t) = 0$ for all $t \geq 0$. Consequently, $n^X_{S,I}(t) = 0$ for all $t \geq 0$, for every $X \in \{H, W\}$ and $(S, I) \in \mathbb{S}$. In this situation, the equation for $i(t)$ reduces to

$$i'(t) = -\gamma\, i(t), \quad t \geq 0,$$

whose unique solution is fully determined by $i(0)$, thereby ensuring the uniqueness of $y(t)$ on $\mathbb{R}_+$.

Case 2: s(0) > 0.

By inequality (7.4), $y(t) \in V_T := V \cap \{s \geq \epsilon_T\}$ for any $t \in [0, T]$. Our aim is to prove that f is Lipschitz continous on V_T. Let

$$y = (s, i, n^X_{S,I} : X \in \{H, W\}, (S, I) \in \mathbb{S}), \quad \hat{y} = (\hat{s}, \hat{i}, \hat{n}^X_{S,I} : X \in \{H, W\}, (S, I) \in \mathbb{S})$$

be two points in V_T.

Recall that the components of f are f_s, f_i and $f_{X,S,I}$ (for $X \in \{H, W\}$) given by (7.1) and (7.2).

First, we focus in the component f_s:

For $X \in \{H, W\}$, define

$$c_X := \frac{\lambda_X \# \mathbb{S} (n_{max})^2}{m_X}.$$

By the definition of τ_X and the triangle inequality, we obtain

$$|\tau_X(y) - \tau_X(\hat{y})| \leq \frac{\lambda_X}{m_X} \sum_{(S,I) \in \mathbb{S}} SI |n^X_{S,I} - \hat{n}^X_{S,I}| \leq c_X \|y - \hat{y}\|_\infty.$$

On the other hand, we have

$$|\tau_G(y)s - \tau_G(\hat{y})\hat{s}| \leq \beta_G(|i||s - \hat{s}| + |i - \hat{i}||\hat{s}|) \leq 2\beta_G \|y - \hat{y}\|_\infty.$$

Therefore,

$$|f_s(y)s - f_s(\hat{y})| \leq |\tau_H(y) - \tau_H(\hat{y})| + |\tau_W(y) - \tau_W(\hat{y})| + |\tau_G(y)s - \tau_G(\hat{y})\hat{s}| \leq c_s \|y - \hat{y}\|_\infty,$$

where $c_s := c_H + c_W + 2\beta_G$.

Next, letting $c_i := c_s + \gamma$, we have

$$|f_i(y) - f_i(\hat{y})| \leq |f_s(y) - f_s(\hat{y})| + \gamma |i - \hat{i}| \leq c_i \|y - \hat{y}\|_\infty.$$

Finally, we focus on the components $f_{X,S,I}$. For $X \in \{H, W\}$, define $c'_X := (2\lambda_X n_{max} + 2\beta_G + 2\gamma) n_{max}$. By definition of $f_{X,S,I}$ and using the fact that $|n^X_{S,I} - \hat{n}^X_{S,I}| \leq \|y - \hat{y}\|_\infty$, we obtain that

$$\begin{aligned} |f_{X,S,I}(y) - f_{X,S,I}(\hat{y})| \leq c'_X \|y - \hat{y}\|_\infty &+ \left| \frac{\tau_{\bar{X}}(y)}{s} S n^X_{S,I} - \frac{\tau_{\bar{X}}(\hat{y})}{\hat{s}} S \hat{n}^X_{S,I} \right| \\ &+ \left| \frac{\tau_{\bar{X}}(y)}{s} (S+1) n^X_{S+1,I-1} - \frac{\tau_{\bar{X}}(\hat{y})}{\hat{s}} (S+1) \hat{n}^X_{S+1,I-1} \right| \mathbb{1}_{\{I \geq 1\}}, \end{aligned} \tag{7.5}$$

for any $X \in \{H, W\}$ and $(S, I) \in \mathbb{S}$.

Now, for $X \in \{H, W\}$, let $k_X := \lambda_{\bar{X}} n_{max} m_X$ and define the set

$$D_X := \{(x, y) : \epsilon_T \le y \le 1, 0 \le x \le k_X y^2\}.$$

Notice that, for any $(S, I) \in \mathbb{S}$, $(\tau_{\bar{X}}(y) S n^X_{S,I}, s) \in D_X$. Indeed, by inequalities (7.3), we have

$$|\tau_{\bar{X}}(y)| = \frac{\lambda_{\bar{X}}}{m_{\bar{X}}} \sum_{(S,I)\in\mathbb{S}} SIn^{\bar{X}}_{S,I} \le \frac{\lambda_{\bar{X}}}{m_{\bar{X}}}(n_{max} m_{\bar{X}} s) = \lambda_{\bar{X}} n_{max} s, \quad Sn^X_{S,I} \le \sum_{(S,I)\in\mathbb{S}} SIn^X_{S,I} \le m_X s.$$

Therefore,

$$\tau_{\bar{X}}(y) S n^X_{S,I} \le k_X s^2.$$

Thus, as $y \in V_T$, we conclude that $(\tau_{\bar{X}}(y) S n^X_{S,I}, s) \in D_X$.

It follows from definition of D_X that for any $(x, y), (u, v) \in D_X$, we have

$$\left|\frac{x}{y} - \frac{u}{v}\right| \le \frac{1}{v}\left(\frac{x}{y}|v - y| + |x - u|\right) \le \frac{1}{\epsilon_T}(1 \vee k_X)(|v - y| + |x - u|).$$

Consequently, for any $X \in \{H, W\}$ and $(S, I) \in \mathbb{S}$,

$$\left|\frac{\tau_{\bar{X}}(y)}{s} S n^X_{S,I} - \frac{\tau_{\bar{X}}(\hat{y})}{\hat{s}} S \hat{n}^X_{S,I}\right| \le \frac{1}{\epsilon_T}(1 \vee k_X)(|\tau_{\bar{X}}(y) S n^X_{S,I} - \tau_{\bar{X}}(\hat{y}) S \hat{n}^X_{S,I}| + |s - \hat{s}|) \le k_{X,T}\|y - \bar{y}\|_\infty,$$

where $k_{X,T} := \frac{1}{\epsilon_T}(1 \vee k_X)(\lambda_X n^3_{max}/m_X + 1)$.

Similarly,

$$\left|\frac{\tau_{\bar{X}}(y)}{s}(S + 1) n^X_{S+1,I-1} - \frac{\tau_{\bar{X}}(\hat{y})}{\hat{s}}(S + 1)\hat{n}^X_{S+1,I-1}\right| \mathbb{1}_{\{I \ge 1\}} \le k_{X,T}\|y - \bar{y}\|_\infty.$$

Hence, from (7.5), we obtain that

$$|f_{X,S,I}(y) - f_{X,S,I}(\hat{y})| \le (c'_X + 2k_{X,T})\|y - \hat{y}\|_\infty.$$

Therefore, f is Lipschitz continuous on V_T with Lipschitz constant $c_T := \max\{c_s, c_i, c'_H + 2K_{H,T}, c'_W + 2k_{W,T}\}$.

Now, suppose that there are two solutions of (5.4), y_1 and y_2, on $[0, T]$ with the same initial condition y^*. By Lipschitz continuity, we have

$$\|y(T) - \hat{y}(T)\|_\infty \le \int_0^T \|f(y(t)) - f(\hat{y}(t))\|_\infty dt \le c_T \int_0^T \|y(t) - \hat{y}(t)\|_\infty.$$

By Gronwall's Lemma, it follows that $y_1 \equiv y_2$ on $[0, T]$. Hence, for any $T \ge 0$, the Cauchy problem admits at most one solution on $[0, T]$.

To verify condition (iii), it remains to show that the initial condition y^*, as defined in equation (5.5), belongs to V.

For any $X \in \{H, W\}$, using equation (5.5) we have

$$\sum_{(S,I)\in\mathbb{S}} n_{S,I}^X(0) = \sum_{n=2}^{n_{max}} \pi_n^X \sum_{I=0}^{n-1} \binom{n}{I} \epsilon^I (1-\epsilon)^{n-I} = \sum_{n=2}^{n_{max}} \pi_n^X (1-\epsilon^n) \leq 1.$$

Similarly,

$$\sum_{(S,I)\in\mathbb{S}} S n_{S,I}^X(0) = \sum_{n=2}^{n_{max}} \pi_n^X \sum_{I=0}^{n-1} (n-I) \binom{n}{I} \epsilon^I (1-\epsilon)^{n-I} = \sum_{n=2}^{n_{max}} \pi_n^X n(1-\epsilon),$$

where in the last equality we used the fact that $\mathbb{E}[n-B] = n(1-\epsilon)$ when $B \sim \mathcal{B}(n,\epsilon)$. This can be rewritten as

$$\sum_{(S,I)\in\mathbb{S}} S n_{S,I}^X(0) = (m_X - \pi_1^X)(1-\epsilon) \leq m_X s(0),$$

where we used that $s(0) = 1-\epsilon$.

Since the remaining conditions of V follow directly from equation (5.5), we conclude that $y^* \in V$. $\square$

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