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Spatially Inhomogeneous Host-Vector Disease Transmission using Configuration Space Analysis

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In this article we consider a microscopic model for the host-vector disease transmission based on configuration space analysis. We model transmission with a birth-death mechanism in the vector component and mobility in the host component. Our intension is to show that a Vlasov type scaling, which is a mean-field-like scaling of an interacting particle system, leads to the known equations used in epidemiology to model host-vector disease spread on the kinetic level. Configuration space analysis is here a very powerful tool. The concepts of harmonic analysis in this framework are used to derive first the dynamics of correlation functions - giving a hierarchical system of equations comparable to the well known BBGKY hierarchy in Hamiltonian dynamics. A proper Vlasov type scaling guaranties that the resulting Vlasov hierarchy is closed and possesses the property of preservation of chaos. The limiting system of time evolution equations is non-linear and strongly related to the well-known Fisher-KPP equations. A numerical analysis strengthens the analytical results. Moreover, the dynamics of case numbers over time gives qualitatively the solution of a SISUV-ODE system. The microscopic dynamics hence leads to the right behavior in the scaling limit.

KEYWORDS:
Heterogeneous Disease Models; Vector-Host Dynamics; Agent-Based Modelling.

1 | INTRODUCTION

In recent years much about the modeling and understanding of various types of disease spreading and epidemic behavior have been studied. In principle, one can distinguish two types of models for disease spread. On the one hand, there is the classical SIR model from Kermack and McKendrick (48) which describes the time evolution of the number of susceptible (S), infected (I) and recovered (R) individuals by a system of ordinary differential equations. This model has been developed and extended exhaustively in the last 90 years. Among those extensions are the introduction of new compartments to model vector-bourne diseases, see e.g. (60, 53), delay equations to model incubation time, e.g. (52), models considering the age and wealth structure etc. A main drawback of the models described above is that they do not provide any information about the spatial spread of a disease. Nevertheless, there have been various approaches to link many different SIR areas to obtain spatial behavior. In the SIR model case, an advection-diffusion equation has been identified as the limiting equation, see e.g. (15). Another approach in incorporating spatial information for the SIR model may also be found in (59). A series of different models for vector-bourne diseases such as Dengue fever including stochastic and deterministic models, fractional differential equations or the effect of climate on the mosquito have been proposed, see e.g. (51, 53, 30, 36, 34, 35, 40, 55, 33, 4, 5, 2, 14) and references therein.

Of course, there are also many models and far too many to have a comprehensive list, for other arboviruses like Malaria and Chikungunya which are comparable, see e.g. (1, 3, 12, 13).

Although the SIR-model and all its extensions are very flexible in describing the different aspects of disease dynamics, the modeling assumptions of the disease spread are purely on the macroscopic level. However, for many different diseases, the infection mechanism is only known on the microscopic, i.e., particle-to-particle or agent-to-agent level. Especially in disease spread, it is known how in principle the dynamics looks like on the agent-to-agent level. On the other side, the dynamics of case numbers like the SIR or SIRUV or SISUV model are very well studied and can be fitted to data at least on a small time scale. The modeling of spatial disease spread from a microscopic agent-to-agent model has been already done in a cancer model by (19) and in (8, 9) for a disease with no movement. Partial differential equation (PDE) models for a spatial dynamics have been proposed, however, up to the authors knowledge, there has not been shown yet, that these PDE models are well-defined scaling limits arising from a particle system model on the agent-to-agent-interaction, hence the microscopic level. Understanding the mechanism of disease transmission is one of the core ingredients in fighting diseases and epidemia. For a good forecast of the outbreak of a disease a sound and profound modeling of different aspects of the disease dynamics has to be done.

One way to consider both microscopical modeling and spatial resolution is to describe the disease dynamics by means of an interacting particle system on a proper state space with suitable interaction potentials. Fundamental in this area are dynamics in so-called marked configuration spaces (26, 29). The classical configuration spaces and their application have been studied by (39). On the note (18) an introduction into the geometry of configuration spaces is provided. The emphasis is given to the "lifting" procedure which turns out to coincide with the direct approach introduced in (7). The analysis and the geometry for a class of infinite dimensional manifolds, namely, compound configuration spaces have been exhibited (43). The paper (42) deals with Poisson measure on configuration spaces. The geometry on configuration spaces with marked Poisson measures used in statistical physics has been developed by (46). Before, Poisson spaces have been studied by e.g. (44). In (41) Gibbs measures on configuration spaces are investigated.

Configuration space analysis is a tool to give mathematical rigor to dynamics of particles interacting with each other. There are definitely more tools than that, see e.g. (32) and the references therein. The framework has, however, an advantage if one has interactions, which can not be expressed by Newton's law of motion. Typical examples are spin-flip processes, like magnetization in the Ising model (31), the voter model (16, 38), the contact process (37), or a model for a lattice gas (56). Further examples of such a type may be found e.g. in (49, 50, 58). From the modeling point of view, the systems can be compared to cellular automata but continuous in space. The rules are described by linear operators acting on functions or observables on subsets of a metric space. A refinement of the models can in many cases be achieved by introducing new aspects of the dynamics due to the incorporation of new Markov pre-generators. Since this can often be done by just adding the corresponding linear operators, the systems can be seen as modular. The configuration space techniques together with a proper scaling of the microscopic system, a so-called Vlasov type scaling, have been recently used to model the dynamics of cancer cells (19).
In our approach, the components of particle configurations consist of susceptible and infected/infectious particles that interact with one another. One may also easily incorporate other types of particles to model recovery or short time immunity. The microscopic dynamics then results from suitable "spin-flip"-processes (particle changes the type). The methods to construct dynamics on multi-component configuration spaces have been extensively developed in (29). One may also consider dynamics with birth, death, and mobility of particles. It is straightforward to include these parts by adding suitable Markov pre-generators in the evolution equations. In these models, disease transmission represents the contact between host individuals in directly transmitted diseases and between host and vector individuals in host-vector diseases.

The intent of this work is to apply a strategy to link suitable microscopic disease models with the classical disease models on the kinetic level via a scaling limit. Dynamical processes in large interacting systems are often approximately described by kinetic equations, see e.g. (57, 58). There is definitely a large number of scaling limit methods, such as diffusive scaling limit (27), Vlasov type scaling limits (28), hydrodynamic limits (47), etc. The proper choice of the method of scaling depends on the desired macro-, or mesoscopic quantity one wants to observe. A famous scaling limit method is the Vlasov scaling which is a proper scaling limit for infinite particle system of Hamiltonian motion. The convergence in the Vlasov scaling limit was shown by (10) for the Hamiltonian dynamics and by (17) for more general deterministic dynamical systems. A general strategy for the derivation of Vlasov type equations in the framework of continuous particle systems is described in (20). It is based on a proper scaling of the hierarchical equations for the evolution of correlation functions and can be interpreted in terms of the rescaled Markov generators. This scaling is actually of mean-field type which is adapted to preserve the spatial structure. A Vlasov type scaling for such a dynamics leads to a generalized Boltzmann nonlinear equation for the particle density (28). The existence of

the rescaled and limiting evolution of correlation functions and the convergence to the limiting evolution have been studied, see e.g. (21, 25, 24).

Our aim is to apply this approach to the framework of a host-vector disease dynamics with birth-death mechanism in the vector component and mobility in the host component. A Vlasov type scaling leads on to a time evolution of the underlying correlation functions. Considering correlation functional of a particular type and under a prescribed structure of initial distributions of the underlying interacting particle system, we obtain the corresponding kinetic equations. A kinetic description of disease spread dynamics is widely used and often a starting point of theoretical studies in epidemiology.

We first provide the basic notions that are necessary in order to develop the underlying setting. We give a brief overview of analysis in one-component configuration spaces. In particular, we describe the configuration space,

$$\Gamma := \left\{\gamma \subset \mathbb{R}^2 : \#(\gamma \cap \Lambda) < \infty \text{ for every compact } \Lambda \subset \mathbb{R}^2\right\},$$

and the finite configuration space $\Gamma_0 := \{\gamma \in \Gamma : \#(\gamma) < \infty\}$. For fixed Radon measure σ on $(\mathbb{R}^2, \mathcal{B}(\mathbb{R}^2))$, we derive the corresponding Lebesgue-Poisson measure λ_{σ_z} on $(\Gamma_0, \mathcal{B}(\Gamma_0))$ and the Poisson measure π_{σ_z} on $(\Gamma, \mathcal{B}(\Gamma))$. Furthermore, we define and present some properties of the K-transform, a mapping which maps functions defined on Γ_0 into functions defined on Γ. The main feature of this transform is its purely combinatorial property. We provide the dual operator of the K-transform, denoted by K^*. The mapping K^* maps probability measures μ on Γ into measures ρ_μ on Γ_0. Following the terminology used in statistical mechanics, we call the measures ρ_μ correlation measures. For the special case, ρ_μ being a measure on Γ_0 absolutely continuous with respect to the Lebesgue-Poisson measure, the corresponding Radon-Nykodym derivative yields the corresponding correlation functional k_μ. After introducing the concept of correlation measures and functionals, we use those to derive the time evolution of a particular type of correlation functionals from the corresponding Markov pre-generators representing our model for host-vector disease dynamics with birth-death mechanism in vector and mobility in host on the microscopic level. An approach to the study of such a dynamics is based on combinatorial harmonic analysis on configuration spaces. The use of the K-transform provides the relations between observables and states to quasi-observables and correlation measures. The starting point for this approach is the Markov pre-generator of the dynamics, denoted by L, related to the forward Kolmogorov (or Fokker Planck) equation for observables

$$\frac{d}{dt}F_t = LF_t, \quad F_t|_{t=0} = F_0.$$

We assume that the linear operator L determines a Markov process on Γ with initial distribution μ. The relations between observables, states, quasi-observables, correlation measures and correlation functionals yield a description of the underlying dynamics in terms of those elements, through the corresponding forward Kolmogorov or Fokker-Planck equations. We construct the multi-component configuration space needed in the modeling of host-vector disease transmission. The definition of configuration spaces can be extended to multi-component configuration spaces. For host-vector diseases a fundamental model in terms of ordinary differential equations is the SISUV model. Encoding the basic mechanisms of this model in a corresponding interacting particle system, we have four types of particles (compartments) that are susceptible host (S), infected host (I), susceptible vector (U), and infected vector (V). This results in the four-component configuration space,

$$\Gamma^4 := \left\{\gamma = \left(\gamma^S, \gamma^I, \gamma^U, \gamma^V\right) \in \Gamma^S \times \Gamma^I \times \Gamma^U \times \Gamma^V \ : \ \gamma^i \cap \gamma^j = \varnothing, \text{ for } i \neq j,\ i, j \in \{S, I, U, V\}\right\}.$$

We use the structure of the multi-component configuration spaces to model the disease spread. The interactions in the particle systems modeling a disease dynamics are described via interaction potentials. Therefore, we have a look at possible potentials and then on rates which indicate the influence of the surrounding configuration on an infection transition. In our model, we provide infection, recovery, birth, death, and jump dynamics of particles. A Vlasov type scaling limit is performed in terms of the stochastic evolution to the full system. This Vlasov type scaling yields the corresponding kinetic equations which provide a space-dependent mean-field-like approximate description of the evolution of large particle systems. The Vlasov type scaling leads on to an evolution of the underlying correlation functionals of particular type which reflects with the right choice of the potentials a classical kinetic description of the disease dynamics. Thereby, we explain the scaling for direct contact and host-vector disease transmission. The scaling of dynamics includes infection, recovery, birth, death, and jump transition. The Markov pre-generators are defined on a proper space of functions on the multi-component configuration space. Some numerical simulations of the host-vector disease dynamics are provided. We simulate and analyze the particle dynamics in spatial simulation. A comparison of the particle model and the kinetic model is shown. Both models are in good agreement for a large number of simulations and particles.

2 | PRELIMINARIES IN CONFIGURATION SPACE ANALYSIS

Configuration space analysis is a tool to give mathematical rigor to dynamics of agents interacting with each other. There are definitely more tools than that, see e.g. (32). The framework has however an advantage if one has interactions, which can not be expressed by Newton's law of motion. Typical examples are spin-flip processes, like magnetization in the Ising model or birth and death processes (27). From the modeling point of view the systems can be compared to cellular automata but continuous in space. The rules are described by linear operators acting on a proper space functions defined on configuration space, also called observables. A refinement of the models can in many cases be achieved by introducing new aspects of the dynamics due to the incorporation of new Markov pre-generators. Since this can often be done by just adding the corresponding operators, the systems can be seen as modular. We will give a brief introduction to (one-component) configuration spaces in this section. However we will not exceed the theory needed throughout this paper. For details we refer the interested reader to (7), (39), (45) and the references therein.

2.1 | One-component configuration space

In configuration space analysis one is dealing with locally finite subsets of an underlying metric space. Here the choice of the underlying metric space is the real plane, which is appropriate to model the spread of a disease. The metric is induced by the norm coming from the euclidean scalar product. This leads us to the following first definition.

Definition 1 (Configuration space)**.** The configuration space Γ over $\mathbb{R}^2$ is defined by

$$\Gamma := \Gamma_{\mathbb{R}^2} := \left\{\gamma \subset \mathbb{R}^2 : \#(\gamma \cap \Lambda) < \infty \text{ for every compact } \Lambda \subset \mathbb{R}^2\right\},$$

where $\#(\cdot)$ denotes the cardinality of a set.

The configurations are thus a union of singletons, which are of finite number if restricted to a compact set. However be aware that there can be infinite many singletons in a configuration.
The local finiteness (on a compact set) now leads to the fact, that one can identify each $\gamma \in \Gamma$ with the positive, integer-valued Radon measure

$$\sum_{x\in\gamma} \delta_x \in \mathcal{M}(\mathbb{R}^2).$$

Here δ_x is the Dirac measure at x, $\sum_{x\in\varnothing} \delta_x$ is the zero measure, and $\mathcal{M}(\mathbb{R}^2)$ denotes the space of all non-negative Radon measures on the Borel σ-algebra $\mathcal{B}(\mathbb{R}^2)$. In terminology of interacting particle systems one can see this measure as unnormalized empirical measure. Elements in $\mathbb{R}^2$ are by this procedure identified with analytic objects one can deal with. Indeed in this way, Γ can be endowed with the vague topology on $\mathcal{M}(\mathbb{R}^2)$, i.e. the coarsest topology on Γ with respect to which all mappings

$$\Gamma \ni \gamma \mapsto \langle f, \gamma\rangle := \int_{\mathbb{R}^2} f(x)\, d\gamma(x) = \sum_{x\in\gamma} f(x) \in \mathbb{R}, \quad f \in C_c(\mathbb{R}^2),$$

are continuous. Here $C_c(\mathbb{R}^2)$ denotes the set of all continuous functions on $\mathbb{R}^2$ having compact support. With respect to this topology, we can define the Borel σ-algebra over Γ which we will denote by $\mathcal{B}(\Gamma)$.

In order to provide more structure on Γ, we study at first configurations of a given number of particles, e.g. the 5 particle configurations. To obtain such statements we consider the so called space of finite configurations.

Definition 2 (Space of finite configurations)**.** We define

$$\Gamma_0 := \bigsqcup_{n=0}^{\infty} \Gamma^{(n)}, \text{ where } \Gamma^{(n)} := \left\{\gamma \in \Gamma : \#(\gamma) = n\right\}, n \in \mathbb{N} \quad \text{and} \quad \Gamma^{(0)} := \{\varnothing\},$$

and call it the space of finite configurations.

For $n \in \mathbb{N}$ there is a natural bijection between the spaces $\Gamma^{(n)}$ and the symmetrization $\widetilde{\left(\mathbb{R}^2\right)^n}/\mathbb{S}_n$ of $\widetilde{\left(\mathbb{R}^2\right)^n} := \left\{(x_1, \dots, x_n) \in \left(\mathbb{R}^2\right)^n \,\middle|\, x_i \neq x_j \text{ if } i \neq j\right\}$ under the permutation group $\mathbb{S}_n$ over $\{1, \dots, n\}$. That means we can identify elements from both spaces. As a direct consequence the particles in a configuration are considered as indistinguishable. To provide an analysis we can use the fact that this bijection induces a metrizable topology on $\Gamma^{(n)}$. We endow Γ_0 with the metrizable topology of disjoint

union of topological spaces. Again we can define Borel sets and denote the corresponding Borel-σ-algebra on $\Gamma^{(n)}$ and Γ_0 by $\mathcal{B}(\Gamma^{(n)})$ and $\mathcal{B}(\Gamma_0)$, respectively.

Let $\mathcal{B}_b(\mathbb{R}^2)$ denote the family of all bounded Borel sets of $\mathbb{R}^2$ and for $\Lambda \in \mathcal{B}_b(\mathbb{R}^2)$ let $\Gamma_\Lambda := \left\{\gamma \in \Gamma \,\middle|\, \gamma \subset \Lambda\right\}$. Evidently,

$$\Gamma_\Lambda = \bigsqcup_{n=0}^{\infty} \Gamma_\Lambda^{(n)}, \text{ where } \Gamma_\Lambda^{(n)} := \Gamma_\Lambda \cap \Gamma^{(n)}, \quad n \in \mathbb{N}_0 := \mathbb{N} \cup \{0\},$$

leading to a situation similar to the one of Γ_0, described above. We endow Γ_Λ again with the topology of disjoint union of topological spaces and with the corresponding Borel-σ-algebra $\mathcal{B}(\Gamma_\Lambda)$. With the help of the measurable spaces $\big(\Gamma_\Lambda, \mathcal{B}(\Gamma_\Lambda)\big)$ we are ready to define probability measures on the configuration space $(\Gamma, \mathcal{B}(\Gamma))$.

Let σ be a non-atomic Radon measure on $\big(\mathbb{R}^2, \mathcal{B}(\mathbb{R}^d)\big)$ with $\sigma(\mathbb{R}^2) = +\infty$. Consider e.g., the Lebesgue measure on $(\mathbb{R}^2, \mathcal{B}(\mathbb{R}^2))$. We equip $((\mathbb{R}^2)^n, \mathcal{B}((\mathbb{R}^2)^n))$ with the n-dimensional product measure $\sigma^{(n)} := \sigma_1 \otimes \cdots \otimes \sigma_n$. For $z \in (0, \infty)$ the Lebesgue–Poisson measure on $(\Gamma_0, \mathcal{B}(\Gamma_0))$ with intensity measure $\sigma_z := z\,\sigma$ is given by

$$\lambda_{\sigma_z} := \sum_{n=0}^{\infty} \frac{z^n}{n!} \widehat{\sigma^{(n)}},$$

where $\widehat{\sigma^{(n)}}$, $n \in \mathbb{N}$, is the image measure on $(\Gamma^{(n)}, \mathcal{B}(\Gamma^{(n)}))$ of the product measure $\sigma^{(n)}$ under the mapping

$$\mathrm{sym}^{(n)} : \widetilde{\left(\mathbb{R}^2\right)^n}/\mathbb{S}_n \ni \left(x_1, \dots x_n\right) \mapsto \left\{x_1, \dots x_n\right\} \in \Gamma^{(n)}.$$

For $n = 0$ one sets $\widehat{\sigma^{(0)}}\big(\{\varnothing\}\big) := 1$. Taking into account that

$$\lambda_{\sigma_z}\big(\Gamma_\Lambda\big) = \sum_{n=0}^{\infty} \frac{z^n}{n!} \widehat{\sigma^{(n)}}(\Gamma_\Lambda) = \sum_{n=0}^{\infty} \frac{z^n\, \sigma(\Lambda)^n}{n!} = \exp\big(\sigma_z(\Lambda)\big),$$

we define a probability measure $\pi_{\sigma_z}^\Lambda := \exp(-\sigma_z(\Lambda))\lambda_{\sigma_z}$ on $(\Gamma_\Lambda, \mathcal{B}(\Gamma_\Lambda))$. Using for $\Lambda \in \mathcal{B}_b(\mathbb{R}^2)$ the projection

$$\Gamma \ni \gamma \mapsto \mathbf{p}_\Lambda(\gamma) := \gamma \cap \Lambda \in \Gamma_\Lambda,$$

and applying a version of Kolmogorov's theorem for projective limit spaces we obtain a unique measure π_{σ_z} as the limit of the family $\{(\Gamma_\Lambda, \mathcal{B}(\Gamma_\Lambda)) \,:\, \Lambda \in \mathcal{B}_b(\mathbb{R}^2)\}$. π_{σ_z} is called Poisson measure on $(\Gamma, \mathcal{B}(\Gamma))$ with respect to the intensity measure σ_z.

Dealing with dynamics of configurations, hence Radon measures, a very important tool is a configuration space version of a Fourier transform. Indeed such a combinatorial version of the Fourier-transform is given by the so called K-transform.

Definition 3 (K-transform)**.** Let G be a $\mathcal{B}(\Gamma_0)$-measurable function with local support, i.e. $G|_{\Gamma\setminus\Gamma_\Lambda} \equiv 0$ for some bounded Borel set $\Lambda \subset \mathcal{B}_b(\mathbb{R}^2)$. The K-transform of G is the mapping

$$KG : \Gamma \to \mathbb{R}, \quad (KG)(\gamma) = \sum_{\substack{\eta \subset \gamma \\ \#(\eta) < \infty}} G(\eta).$$

The K-transform hence maps functions defined on Γ_0 into functions defined on Γ. Since in the above definition the sum has only a finite number of summands non-zero, due to the local support property, KG indeed is well defined. In particular $(KG)|_{\Gamma_\Lambda}$ is $\mathcal{B}(\Gamma_\Lambda)$-measurable and $(KG)|_{\Gamma_\Lambda}(\gamma_\Lambda) = (KG)(\gamma)$ for every configuration $\gamma \in \Gamma$, hence KG fulfills the properties of a cylinder function in the classical sense. In particular, in the case G is a bounded $\mathcal{B}(\Gamma_0)$-measurable function with bounded support, i.e. $G|_{\Gamma_0\setminus\bigsqcup_{n=0}^N \Gamma_\Lambda^{(n)}} \equiv 0$, for some natural number N and $\Lambda \in \mathcal{B}_b(\mathbb{R}^2)$, one finds $|(KG)(\gamma)| \le C(1 + |\gamma_\Lambda|)^N$, for $C \ge |G|$ and all $\gamma \in \Gamma$. Which means KG is polynomially bounded. Since this is a very special and important class in our consideration we define the following space:

Definition 4. The space of bounded $\mathcal{B}(\Gamma_0)$-measurable functions with bounded support is denoted by $B_{bs}(\Gamma_0)$.

As the K-transform can be seen as combinatorial version of the Fourier transform, indeed one can show the following theorem, linking cylinder functions and the K-transform.

Theorem 1 ((45, 39))**.** *The K-transform is a linear isomorphism which inverse mapping is defined on cylinder functions by*

$$(K^{-1}F)(\eta) := \sum_{\xi \subset \eta} (-1)^{|\eta\setminus\xi|} F(\xi), \quad \eta \in \Gamma_0.$$

Of all elements in the domain of the K-transform the so-called coherent states $e_\lambda(f)$ play a special role.

Definition 5 (coherent state)**.** A coherent state $e_\lambda(f)$ corresponding to a $\mathcal{B}(\mathbb{R}^n)$-measurable function f with compact support is defined by

$$e_\lambda(f,\eta) = \prod_{x\in\eta} f(x), \quad \eta \in \Gamma_0 \setminus \{\varnothing\}, \quad e_\lambda(f,\varnothing) := 1.$$

If f has compact support, then the image $e_\lambda(f)$ under the K-transform is a well-defined function on Γ given by

$$(Ke_\lambda(f))(\gamma) = \prod_{x\in\gamma}(1+f(x)), \quad \gamma \in \Gamma.$$

Our aim in Section 3 is to identify the dynamics on the configuration space as the time evolution of certain measures. For this purpose it is important to consider also the dual operator K^* of the K-transform K.

Definition 6. Let $\mathcal{M}^1_{fm}(\Gamma)$ denote the set of probability measures on $(\Gamma, \mathcal{B}(\Gamma))$ with finite local moments of all orders, i.e.

$$\int_\Gamma \#(\gamma\cap\Lambda)^n \, d\mu(\gamma) < \infty \quad \text{for all } n \in \mathbb{N} \text{ and all } \Lambda \in \mathcal{B}_b(\mathbb{R}).$$

For $\mu \in \mathcal{M}^1_{fm}(\Gamma)$ we define the correlation measure $\rho_\mu := K^*\mu$ corresponding to μ by

$$\int_{\Gamma_0} G(\eta)\, d\rho_\mu(\eta) = \int_\Gamma (KG)(\gamma)\, d\mu(\gamma), \quad G \in B_{bs}(\Gamma_0). \tag{1}$$

Observe that ρ_μ is a measure on $(\Gamma_0, \mathcal{B}(\Gamma_0))$ and $K|G|$ is μ-integrable under the above conditions, thus $B_{bs}(\Gamma_0) \subset L^1(\Gamma_0, \rho_\mu)$.

Moreover, by Definition 6, the inequality $\|KG\|_{L^1(\Gamma;\mu)} \le \|G\|_{L^1(\Gamma_0;\rho_\mu)}$ holds on $B_{\mathrm{bs}}(\Gamma_0)$, allowing an extension of the K-transform to a bounded linear operator $K : L^1(\Gamma_0;\rho_\mu) \to L^1(\Gamma;\mu)$ in such a way that (1) still holds for $G \in L^1(\Gamma_0;\rho_\mu)$. For the extended operator the explicit representation still holds now μ-a.e. Moreover, we have that ρ_μ is locally finite, i.e., $\rho_\mu\left(\Gamma^{(n)}_\Lambda\right) < \infty$ for all $n \in \mathbb{N}_0$ and $\Lambda \in \mathcal{B}_b(\mathbb{R}^2)$.

3 | THE GENERAL STRATEGY

In this section we provide the general strategy of our approach which will be applied in a later section to the particular problem of a host-vector disease dynamics. This approach is developed in (26) for stochastic dynamics in (one-component) configuration space and generalized in (29) to the situation of stochastic dynamics in a multi-component configuration space. A multi-component configuration space is serving as state space in our application. In this section we provide the ideas originated and worked out in detail in (26).

3.1 | Markov generators and related evolution equations

Heuristically, the stochastic evolution of an infinite particle system is described by a Markov process on Γ, which is determined by a Markov generator L defined on a proper space of functions on Γ.

In applications there is a need of knowledge on certain characteristics of the stochastic evolution in terms of mean values rather than point wise These characteristics concern e.g. observables, i.e., measurable functions defined on Γ for which expected values are given by

$$\langle F, \mu\rangle := \int_\Gamma F(\gamma)\, d\mu(\gamma),$$

where μ is a probability measure on $\mathcal{B}(\Gamma)$, i.e., a state of the system. Suppose that the initial distribution of particles in our system, i.e., the initial state of our system, is a probability measure μ_0 with all moments finite. For $t > 0$ let μ_t be the distribution of particles at time t, i.e., the state of the system at time t. This leads to the following time evolution problem on states,

$$\frac{d}{dt}\langle F, \mu_t\rangle = \langle LF, \mu_t\rangle, \quad \mu_t\Big|_{t=0} = \mu_0. \tag{2}$$

For F being of type $F = KG$ with some $G \in B_{\mathrm{bs}}(\Gamma_0)$ we use (1) to obtain

$$\int_{\Gamma_0} (K^{-1}LK)G(\eta)\, d\rho_{\mu_t}(\eta) = \int_{\Gamma} K(K^{-1}LKG)(\gamma)\, d\mu_t(\gamma) = \frac{d}{dt}\int_{\Gamma} KG(\gamma)\, d\mu_t(\gamma) = \frac{d}{dt}\int_{\Gamma_0} G(\eta)\, d\rho_{\mu_t}(\eta).$$

Moreover, setting $\hat{L} := K^{-1}LK$ we have

$$\int_{\Gamma_0} \hat{L}G(\eta)\, d\rho_{\mu_t}(\eta) = \frac{d}{dt}\int_{\Gamma_0} G(\eta)\, d\rho_{\mu_t}(\eta), \quad \rho_{\mu_t}\Big|_{t=0} = \rho_{\mu_0}. \tag{3}$$

Definition 7 (correlation functional)**.** If for $\mu \in \mathcal{M}^1_{\mathrm{fm}}(\Gamma)$ the corresponding correlation measure ρ_μ is absolutely continuous with respect to the Lebesgue-Poisson measure λ_σ on $\mathcal{B}(\Gamma_0)$, its Radon-Nikodym derivative $k_\mu := \frac{d\rho_\mu}{d\lambda_\sigma}$ is called the correlation functional corresponding to μ.

Now assuming that the correlation measures ρ_{μ_t} for $t \geq 0$ are absolutely continuous with respect to the Lebesgue-Poisson measure λ_σ, we can rewrite (3) in terms of correlation functionals $k_t := k_{\mu_t}$, $t \geq 0$, see Definition 7. This reads

$$\frac{d}{dt}\langle\langle G, k_t\rangle\rangle = \langle\langle \hat{L}G, k_t\rangle\rangle, \quad k_t\Big|_{t=0} = k_0, \tag{4}$$

where $\langle\langle \cdot, \cdot \rangle\rangle$ is the usual pairing

$$\langle\langle G, k_\mu\rangle\rangle := \int_{\Gamma_0} G(\eta)\, k_\mu(\eta)\, d\lambda_\sigma(\eta). \tag{5}$$

A strong version of Equation (4) is given by

$$\frac{d}{dt}k_t = \hat{L}^* k_t, \quad k_t\Big|_{t=0} = k_0, \tag{6}$$

with $\hat{L}^*$ being the dual operator of $\hat{L}$ in the sense defined in (5).

One may associate to any correlation functional k_μ on Γ_0 a sequence $\left\{k^{(n)}_\mu\right\}_{n\in\mathbb{N}_0}$, where

$$k^{(n)}_\mu := k_\mu\Big|_{\{\eta\in\Gamma_0\,:\,\#(\eta)=n\}}, \tag{7}$$

are symmetric functions on $(\mathbb{R}^2)^n$, $n \in \mathbb{N}_0$. These functions are called the n-point correlation functions corresponding to the measure μ.

Remark 1. For $n \in \mathbb{N}_0$, $k^{(n)}_\mu$ describes the n-th moment of the state μ and in the special case $n = 1$ the one point correlation function $k^{(1)}_\mu$ is the particle density of the system in state μ. This can be seen as follows. Let $A \subset \mathbb{R}^2$ be bounded and consider the observable

$$\Gamma \ni \gamma \mapsto N_A(\gamma) := \#(A \cap \gamma) \in \mathbb{N}_0,$$

i.e., we observe the number of particles in A. Moreover, we need the quasi-observable (a measurable function on Γ_0)

$$G : \Gamma_0 \to \mathbb{R}, \quad \eta \mapsto \begin{cases} \mathbb{1}_A(x) & \text{if } \eta = \{x\},\ x \in \mathbb{R}^2 \\ 0 & \text{else} \end{cases}.$$

Hence for a system in state μ the expected number of particles in A is given by

$$\int_{\Gamma} N_A(\gamma)\, d\mu(\gamma) = \int_{\Gamma} \sum_{x\in\gamma} \mathbb{1}_A(x)\, d\mu(\gamma) = \int_{\Gamma} (KG)(\gamma)\, d\mu(\gamma) = \int_{\Gamma_0} G(\eta)\, d\rho_\mu(\eta) = \int_A k^{(1)}_\mu(x)\, dx, \tag{8}$$

where here the intensity measure for the Lebesgue-Poisson measure is taken to be the Lebesgue measure, i.e., $\sigma := dx$ and $z := 1$. The right hand side of (8) is a measure on A and therefore, $k^{(1)}_\mu$ is the particle density of the system.

Related to (6) one has a countably infinite number of equations having a hierarchical structure,

$$\frac{d}{dt}k^{(n)}_t = \hat{L}^* k^{(n)}_t, \quad k^{(n)}_t\Big|_{t=0} = k^{(n)}_0, \quad n \in \mathbb{N}_0, \tag{9}$$

where each equation only depends on a finite number of coordinates. Let us stress that (9) is nothing else but a hierarchical system of equations corresponding to the Markov generator L. This system has the same meaning as the BBGKY hierarchy in the case

of Hamiltonian dynamics. As a result we have reduced the infinite dimensional problem (2) to the infinite system of equations (9). However, recall that due to (4) we are only interested in weak solutions to (9). To derive solutions to (2) from solutions to (4) an additional analysis is needed, namely, to distinguish the correlation functionals from the set of solutions to (4).

3.2 | Vlasov type scaling

The so-called Vlasov type scaling or kinetic scaling starts with scaling the Markov generator of the underlying dynamics with respect to a parameter $\varepsilon > 0$ in a proper way. Therefore, we get scaled versions of equations (6) and (9), i.e., $\hat{L}_\varepsilon^*$ instead of $\hat{L}^*$. The next important step in the Vlasov type scaling concerns the proper rescaling of the initial state of the system. Or, equivalently, in the language of n-point correlation functions, it means the proper rescaling of the initial conditions of the evolution of n-point correlation functions. More precisely, at the beginning we scale $k_0^{(n)}$ with parameter $\varepsilon > 0$ in such a way that the resulting functions $k_{0,\varepsilon}^{(n)}$ as $\varepsilon \to 0$ behave as follows

$$r_{0,\varepsilon}^{(n)}(\eta) := \varepsilon^n k_{0,\varepsilon}^{(n)}(\eta) \to r_0^{(n)}(\eta), \quad \varepsilon \to 0,\ \eta \in \Gamma_0, \tag{10}$$

where for $n \in \mathbb{N}_0$ the symmetric functions $r_0^{(n)}$ are a subject of choice for our concrete example.

An important case is to take

$$r_0^{(n)}(x_1, \dots, x_n) = \rho_0(x_1) \cdot \dots \cdot \rho_0(x_n) = e_\lambda(\rho_0, \{x_1, \dots, x_n\}), \quad \rho_0 : \mathbb{R}^2 \to (0, +\infty),$$

corresponding to an independent initial distribution of particles.

It is clear that such a rescaling of the initial condition leads to a singular function with respect to $\varepsilon > 0$. In applications, this fact can be interpreted as the growth of density of the system with $\varepsilon \to 0$. For $n \in \mathbb{N}_0$ we denote by $k_{t,\varepsilon}^{(n)}$ the solution of the functional evolution

$$\frac{d}{dt} k_{t,\varepsilon}^{(n)} = \hat{L}_\varepsilon^* k_{t,\varepsilon}^{(n)}, \quad k_{t,\varepsilon}^{(n)}\Big|_{t=0} = k_{0,\varepsilon}^{(n)}.$$

One can expect that this solution will be also singular with respect to $\varepsilon > 0$. Moreover, we should choose a type of scaling of the generators which preserves the order of this singularity. Namely, for $n \in \mathbb{N}_0$ and $\varepsilon > 0$ we consider

$$r_{t,\varepsilon}^{(n)} := \varepsilon^n k_{t,\varepsilon}^{(n)},$$

and assume that

$$r_{t,\varepsilon}^{(n)} \to r_t^{(n)}, \quad \varepsilon \to 0.$$

This is equivalent to investigating the Cauchy problem for the operators $\hat{L}_{\varepsilon,\mathrm{ren}}^* = R_\varepsilon \hat{L}_\varepsilon^* R_{\varepsilon^{-1}}$, $\varepsilon > 0$, where for $\delta > 0$ and a correlation functional k_μ we have $(R_\delta k_\mu)(\eta) := \delta^{\#(\eta)} k_\mu(\eta)$. Hence the associated Cauchy problem reads

$$\frac{d}{dt} r_{t,\varepsilon} = \hat{L}_{\varepsilon,\mathrm{ren}}^* r_{t,\varepsilon}, \quad r_{t,\varepsilon}\Big|_{t=0} = r_{0,\varepsilon},$$

where we use the identification via (7). We seek for the limit $\hat{L}_{\varepsilon,\mathrm{ren}}^* \to V$ as $\varepsilon \to 0$. Using the initial condition $r_t|_{t=0} = r_0$, where r_0 is associated to the sequence $(r_0^{(n)})_{n\in\mathbb{N}_0}$ in (10), the solution r_t of the Vlasov equation

$$\frac{d}{dt} r_t = V r_t, \quad r_t\Big|_{t=0} = r_0, \tag{11}$$

clearly implies that the associated sequence $\left(r_t^{(n)}\right)_{n\in\mathbb{N}_0}$ is again of the form

$$r_t^{(n)}(x_1, \dots, x_n) = \rho_t(x_1) \cdot \dots \cdot \rho_t(x_n) = e_\lambda(\rho_t, \{x_1, \dots, x_n\}), \quad \rho_t : \mathbb{R}^d \to (0, +\infty),$$

where ρ_t is determined by the kinetic equation

$$\frac{\partial}{\partial t} \rho_t = v(\rho_t) \tag{12}$$

and v is derived from the (nonlinear) limiting operator V.

In other words, considering the Vlasov equation (11) with initial condition r_0 of the form

$$r_0(\eta) := e_\lambda(\rho_0, \eta), \quad \eta \in \Gamma, \tag{13}$$

the solution r_t at time $t \geq 0$ is of the same type, i.e.

$$r_t(\eta) = e_\lambda(\rho_t, \eta), \quad \eta \in \Gamma, \tag{14}$$

and ρ_t is determined by the kinetic equation (12).

Remark 2. The fact that solutions of the Vlasov equation (11) with initial condition (13) are of type (14) for all times $t \geq 0$, is in literature known as preservation of chaos. Note that this property is guarantied when applying the above described Vlasov type scaling.

4 | MARKOV EVOLUTIONS IN A HOST-VECTOR DISEASE DYNAMICS

The application in this article is devoted to the vector-borne disease spread. We identify the agents (host and vector) with their corresponding positions in $\mathbb{R}^2$. Since host and vector have to be distinguished and moreover, since the fact that one can not be infected and susceptible at the same time should be a feature of the model, we put all of these agents in different compartments (we deal with particles of four types). For this purpose an appropriate state space for the disease spread dynamics turns out to be the four-component configuration space.

4.1 | Four-component configuration space

The underlying state space is built up with the help of the (one-component) configuration space Γ, see Subsection 2.1.

Definition 8 (state space for host-vector disease dynamics)**.** Let $\Gamma^S, \Gamma^I, \Gamma^U$ and Γ^V be four copies of the configuration space Γ. The configuration space for a host-vector disease spread model is defined as

$$\Gamma^4 := \left\{ \gamma = \left(\gamma^S, \gamma^I, \gamma^U, \gamma^V\right) \in \Gamma^S \times \Gamma^I \times \Gamma^U \times \Gamma^V \ : \ \gamma^i \cap \gamma^j = \varnothing, \text{ for } i \neq j, \ i,j \in \{S,I,U,V\} \right\},$$

and the finite configuration space as

$$\Gamma_0^4 := \left\{ \eta = \left(\eta^S, \eta^I, \eta^U, \eta^V\right) \in \Gamma_0^S \times \Gamma_0^I \times \Gamma_0^U \times \Gamma_0^V \ : \ \eta^i \cap \eta^j = \varnothing, \text{ for } i \neq j, \ i,j \in \{S,I,U,V\} \right\}.$$

We endow Γ^4 and Γ_0^4 with the product topology induced by the topological spaces $\Gamma^S, \Gamma^I, \Gamma^U, \Gamma^V$ and $\Gamma_0^S, \Gamma_0^I, \Gamma_0^U, \Gamma_0^V$, respectively, and with the corresponding Borel-σ-algebras. Moreover, we consider the corresponding product measures on $(\Gamma^4, \mathcal{B}(\Gamma^4))$ and $(\Gamma_0^4, \mathcal{B}(\Gamma_0^4))$, respectively, obtained from the constructed measures in the one-component situation.

Next we generalize the K-transform, well-known in the one-component case, to the four-component setting. We make use of functions with bounded support

$$B_{\mathrm{bs}}\left(\Gamma_0^4\right) := \Big\{ G : \Gamma_0^4 \to \mathbb{R} \text{ measurable } : \ G\Big|_{\Gamma_0^4 \setminus \left(\sqcup_{n=0}^{N^S} \Gamma^n_{\Lambda^S}\right) \times \left(\sqcup_{n=0}^{N^I} \Gamma^n_{\Lambda^I}\right) \times \left(\sqcup_{n=0}^{N^U} \Gamma^n_{\Lambda^U}\right) \times \left(\sqcup_{n=0}^{N^V} \Gamma^n_{\Lambda^V}\right)} \\ \text{for some compact } \Lambda^S, \Lambda^I, \Lambda^U, \Lambda^V \subset \mathbb{R}^d \text{ and } N^S, N^I, N^U, N^V \in \mathbb{N}_0 \Big\},$$

where a $\mathcal{B}(\Gamma_0^4)$-measurable function G is called quasi observable, to define the K-transform of G:

$$(KG)\left(\gamma^S, \gamma^I, \gamma^U, \gamma^V\right) := \sum_{\substack{\eta^S \subset \gamma^S \\ \#(\eta^S) < \infty}} \sum_{\substack{\eta^I \subset \gamma^I \\ \#(\eta^I) < \infty}} \sum_{\substack{\eta^U \subset \gamma^U \\ \#(\eta^U) < \infty}} \sum_{\substack{\eta^V \subset \gamma^V \\ \#(\eta^V) < \infty}} G\left(\eta^S, \eta^I, \eta^U, \eta^V\right).$$

Even in this more general situation, we have all the properties discussed in Subsection 2.1. In particular, $K : B_{\mathrm{bs}}(\Gamma_0^4) \to K(B_{\mathrm{bs}}(\Gamma_0^4))$ is a linear and positivity preserving isomorphism whose inverse mapping is defined by

$$\left(K^{-1}F\right)(\eta^S, \eta^I, \eta^U, \eta^V) := \sum_{\xi^S \subset \eta^S} \sum_{\xi^I \subset \eta^I} \sum_{\xi^U \subset \eta^U} \sum_{\xi^V \subset \eta^V} (-1)^{|\eta^S \setminus \xi^S| + |\eta^I \setminus \xi^I| + |\eta^U \setminus \xi^U| + |\eta^V \setminus \xi^V|} F(\xi^S, \xi^I, \xi^U, \xi^V).$$

The corresponding definitions of the correlation measures and the correlation functionals follow straight forward as in the one-component case.

4.2 | Markov generators and related evolution equations in host-vector disease dynamics

Heuristically, the stochastic evolution of an infinite four-component particle system is described by a Markov process on Γ^4, which is determined by a Markov generator L defined on a proper space of functions on Γ^4. In this section we provide the Markov pre-generator in the particular application of a host-vetor disease dynamics with birth-death mechanism in the vector components and mobility in the host components. We use the terminology of a Markov pre-generator, since we do not show

here, that the given linear operator is indeed the generator of an associated Markov process. Such a construction could be done using the theory of operator semi groups, see e.g. (23).

4.2.1 | Evolution of observables

We consider the host-vector disease transmission with birth-death in vector and mobility in host. We assume here that the lifespan of a host is much longer than that of the vector. Here we have humans and mosquitoes in mind. The model could also be adapted with birth-death dynamics of humans and mobility of vectors. However for the sake of simplicity these considerations are taken out from this article. For a short time span of some month the dynamics however will reflect the disease spread mechanism.
In the following we will introduce the different Markov pre-generators used for the modeling of the disease spread. All of them are combined in the complete model given by the Markov pre-generator $L := L_h + L_v$, where L_h is provided in (15) and L_v is given by (16).

Infection

The pre-generator of the infection has to cope the following reaction equation:

$$S + V \mapsto I + V,$$

with a certain rate. This means we have have a mechanism, which takes a particle at a location $x \in \mathbb{R}^2$ from the compartment of susceptible (S) and puts it in the compartment of infected hosts (I). The rate is dependent on the compartment of infected vectors (V). On the host level we obtain the pre-generator:

$$(L_{h,\mathrm{inf}}F)(\gamma) := \sum_{x\in\gamma^S} c_h\big(x,\gamma^V\big)\Big(F\big(\gamma^S\backslash x,\gamma^I\cup x,\gamma^U,\gamma^V\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big).$$

On the vector side, an infection of a vector occurs if an infected host gets in contact with a susceptible vector. The dynamics is an analogue to the one for the hosts. We obtain

$$(L_{v,\mathrm{inf}}F)(\gamma) := \sum_{x\in\gamma^U} c_v\big(x,\gamma^I\big)\Big(F\big(\gamma^S,\gamma^I,\gamma^U\backslash x,\gamma^V\cup x\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big).$$

Specification of the infection rate. In our model the prescribed flip from a healthy host (vector) getting infected by the surrounding infected vectors (hosts) happens with a certain rate of infection c_h (c_v). With $R \in (0,\infty)$ we denote the maximal distance of possible infection for a single healthy individual at direct contact with an infected one. Via the function

$$[0,\infty) \ni r \mapsto \phi_R(r) := \phi(r) \in [0,\infty),$$

we describe the potential of infection for a healthy individual depending on distance to a single infected individual, where ϕ_R is e.g. of the form given in Figure 1 . For fixed $x \in \mathbb{R}^2$ the rate of infection for host and vector are given by

$$c_h\big(x,\gamma^V\big) := \sum_{y\in\gamma^V} \beta_h\phi(|x-y|) \quad \text{and} \quad c_v\big(x,\gamma^I\big) := \sum_{y\in\gamma^I} \beta_v\phi(|x-y|),$$

where the constants $\beta_h, \beta_v \in [0,1]$ are risk of infection for host and vector, respectively.

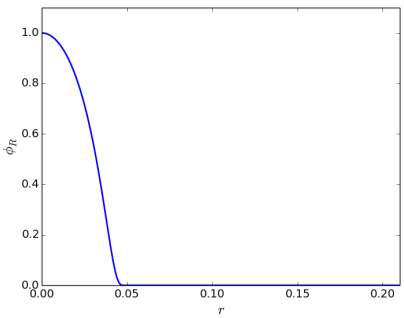

FIGURE 1 Distance dependent risk of infection for a susceptible individual in range of an infected one ($R = 0.05$)

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Mobility

The transport of particles is done by a so-called Kawasaki dynamics. In our model just the hosts move due to a kernel function depending on the configuration. We have thus to specify a mechanism taking a host from the susceptible or infected compartment at a location x and then put it back in the same compartment but in a location x'. We have:

$$(L_{h,\mathrm{mob}}F)(\gamma) := \sum_{x\in\gamma^S}\int_{\mathbb{R}^2} a^S(x,y)\Big(F\big(\gamma^S\backslash x\cup y,\gamma^I,\gamma^U,\gamma^V\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big)\,dy + \sum_{x\in\gamma^I}\int_{\mathbb{R}^2} a^I(x,y)\Big(F\big(\gamma^S,\gamma^I\backslash x\cup y,\gamma^U,\gamma^V\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big)\,dy.$$

Thus the disease dynamics on the agent-to-agent level for host and vector is provided by

$$\begin{aligned}(L_hF)(\gamma) := {} & \sum_{x\in\gamma^S} c_h\big(x,\gamma^V\big)\Big(F\big(\gamma^S\backslash x,\gamma^I\cup x,\gamma^U,\gamma^V\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big)\\ & + \sum_{x\in\gamma^I}\alpha_h\Big(F\big(\gamma^S\cup x,\gamma^I\backslash x,\gamma^U,\gamma^V\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big)\\ & + \sum_{x\in\gamma^S}\int_{\mathbb{R}^2} a^S(x,y)\Big(F\big(\gamma^S\backslash x\cup y,\gamma^I,\gamma^U,\gamma^V\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big)\,dy\\ & + \sum_{x\in\gamma^I}\int_{\mathbb{R}^2} a^I(x,y)\Big(F\big(\gamma^S,\gamma^I\backslash x\cup y,\gamma^U,\gamma^V\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big)\,dy\end{aligned} \tag{15}$$

and

$$\begin{aligned}(L_vF)(\gamma) := {} & \sum_{x\in\gamma^U} c_v\big(x,\gamma^I\big)\Big(F\big(\gamma^S,\gamma^I,\gamma^U\backslash x,\gamma^V\cup x\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big)\\ & + \int_{\mathbb{R}^2} b\Big(F\big(\gamma^S,\gamma^I,\gamma^U\cup x,\gamma^V\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big)\,dx\\ & + \sum_{x\in\gamma^U} d^U\Big(F\big(\gamma^S,\gamma^I,\gamma^U\backslash x,\gamma^V\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big)\\ & + \sum_{x\in\gamma^V} d^I\Big(F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\backslash x\big) - F\big(\gamma^S,\gamma^I,\gamma^U,\gamma^V\big)\Big),\end{aligned} \tag{16}$$

where the function $c_h\big(x,\gamma^V\big) \geq 0$ is infection rate for host, the constant $\alpha_h \in [0,1]$ is recovery rate for host, the function $c_v\big(x,\gamma^I\big) \geq 0$ is infection rate for vector, the constants $b \in [0,1]$ birth rate for vector, $d^U \in [0,1]$ death rate for susceptible vector, $d^V \in [0,1]$ death rate for infected vector, the functions $a^S(x,y)$ mobility rate for susceptible host and $a^I(x,y)$ mobility rate for infected host.

Since we now have the Markov pre-generator $L := L_h + L_v$, defined for suitable functions on Γ^4, in hand, we can state the time evolution problem on states

$$\frac{d}{dt}\langle F,\mu_t\rangle = \langle LF,\mu_t\rangle, \quad \mu_t\Big|_{t=0} = \mu_0,$$

where μ_0 is a probability measure on $(\Gamma^4,\mathcal{B}(\Gamma^4))$ with all moments finite describing the initial state of the system and μ_t is the state of the system at time $t > 0$.

4.3 | Evolution of correlation functions

Recall that our goal is to describe the time evolution of the particle density in our four-component system. Following the procedure as outlined in Section 3, we have to go for the time evolution of the corresponding 1-point-correlation functions. Thus we need to specify the time evolution problem for correlation functionals first. We obtain the following

Corollary 1. *The dual operator $\hat{L}_h^*$ corresponding to $\hat{L}_h := K^{-1}L_hK$ is given by*

$$\begin{aligned}(\hat{L}_h^*k)(\eta) = {} & \sum_{x\in\eta^S}\sum_{x\in\eta^V}\beta_h\phi(|x-y|)\,k\big(\eta^S\cup x,\eta^I\backslash x,\eta^U,\eta^V\big) - \sum_{x\in\eta^S}\sum_{x\in\eta^V}\beta_h\phi(|x-y|)\,k\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\\ & + \sum_{x\in\eta^S}\int_{\mathbb{R}^2}\beta_h\phi(|x-y|)\,k\big(\eta^S\cup x,\eta^I\backslash x,\eta^U,\eta^V\cup y\big)\,dy\\ & - \sum_{x\in\eta^S}\int_{\mathbb{R}^2}\beta_h\phi(|x-y|)\,k\big(\eta^S,\eta^I,\eta^U,\eta^V\cup y\big)\,dy\\ & + \sum_{x\in\eta^S}\alpha_h k\big(\eta^S\backslash x,\eta^I\cup x,\eta^U,\eta^V\big) - \#\eta^I\,\alpha_h k\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\end{aligned}$$

$$+\sum_{x\in\eta^S}\int\limits_{\mathbb{R}^2} a^S(x,y)\Big(k\big(\eta^S\backslash x\cup y,\eta^I,\eta^U,\eta^V\big)-k\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\Big)\,dy$$
$$+\sum_{x\in\eta^I}\int\limits_{\mathbb{R}^2} a^I(x,y)\Big(k\big(\eta^S,\eta^I\backslash x\cup y,\eta^U,\eta^V\big)-k\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\Big)\,dy$$

and the dual operator $\hat{L}_v^*$ *corresponding to* $\hat{L}_v := K^{-1}L_vK$ *is given by*

$$\begin{aligned}(\hat{L}_v^*k)(\eta) = {}& \sum_{x\in\eta^U}\sum_{x\in\eta^I}\beta_v\phi(|x-y|)\,k\big(\eta^S,\eta^I,\eta^U\cup x,\eta^V\backslash x\big)-\sum_{x\in\eta^U}\sum_{x\in\eta^I}\beta_v\phi(|x-y|)\,k\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\\ &+\sum_{x\in\eta^S}\int\limits_{\mathbb{R}^2}\beta_v\phi(|x-y|)\,k\big(\eta^S,\eta^I\cup y,\eta^U\cup x,\eta^V\backslash x\big)\,dy\\ &-\sum_{x\in\eta^S}\int\limits_{\mathbb{R}^2}\beta_v\phi(|x-y|)\,k\big(\eta^S,\eta^I\cup y,\eta^U,\eta^V\big)\,dy+\sum_{x\in\eta^U}b\,k\big(\eta^S,\eta^I,\eta^U\backslash x,\eta^V\big)\\ &-\#\eta^U\,d^U\,k\big(\eta^S,\eta^I,\eta^U,\eta^V\big)-\#\eta^V\,d^V\,k\big(\eta^S,\eta^I,\eta^U,\eta^V\big).\end{aligned}$$

Thus for $\hat{L} := K^{-1}LK$ *we have that* $\hat{L}^* = \hat{L}_h^* + \hat{L}_v^*$.

The corresponding time evolution of correlation functionals then reads

$$\frac{d}{dt}k_t = \hat{L}^*k_t,\quad k_t\Big|_{t=0} = k_0.$$

In order to examine the time evolution of the density of particles, we consider the time evolution of correlation functionals of the following type,

Definition 9 (1-point correlation functions in the host-vector disease spread model)**.**

$$\mathbb{R}^2\ni x\mapsto k^S(x) := \begin{cases} k(\eta^S,\eta^I,\eta^U,\eta^V) & \text{if } \eta=\{x\},\ \eta^I=\varnothing,\ \eta^U=\varnothing,\eta^V=\varnothing\\ 0 & \text{else}\end{cases}$$
$$= k^{(1,0,0,0)}\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\in\mathbb{R},$$

$$\mathbb{R}^2\ni x\mapsto k^I(x) := \begin{cases} k(\eta^S,\eta^I,\eta^U,\eta^V) & \text{if } \eta=\varnothing,\ \eta^I=\{x\},\ \eta^U=\varnothing,\eta^V=\varnothing\\ 0 & \text{else}\end{cases}$$
$$= k^{(0,1,0,0)}\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\in\mathbb{R},$$

$$\mathbb{R}^2\ni x\mapsto k^U(x) := \begin{cases} k(\eta^S,\eta^I,\eta^U,\eta^V) & \text{if } \eta=\varnothing,\ \eta^I=\varnothing,\ \eta^U=\{x\},\eta^V=\varnothing\\ 0 & \text{else}\end{cases}$$
$$= k^{(0,0,1,0)}\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\in\mathbb{R},$$

$$\mathbb{R}^2\ni x\mapsto k^V(x) := \begin{cases} k(\eta^S,\eta^I,\eta^U,\eta^V) & \text{if } \eta=\varnothing,\ \eta^I=\varnothing,\ \eta^U=\varnothing,\eta^V=\{x\}\\ 0 & \text{else}\end{cases}$$
$$= k^{(0,0,0,1)}\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\in\mathbb{R},$$

$$\mathbb{R}^2\times\mathbb{R}^2\ni(x,y)\mapsto k^{SV}(x,y) := \begin{cases} k(\eta^S,\eta^I,\eta^U,\eta^V) & \text{if } \eta^S=\{x\},\ \eta^I=\varnothing,\ \eta^U=\varnothing,\eta^V=\{y\}\\ 0 & \text{else}\end{cases}$$
$$= k^{(1,0,0,1)}\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\in\mathbb{R}$$

and

$$\mathbb{R}^2\times\mathbb{R}^2\ni(x,y)\mapsto k^{IU}(x,y) := \begin{cases} k(\eta^S,\eta^I,\eta^U,\eta^V) & \text{if } \eta^S=\varnothing,\ \eta^I=\{x\},\ \eta^U=\{y\},\eta^V=\varnothing\\ 0 & \text{else}\end{cases}$$
$$= k^{(1,0,0,1)}\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\in\mathbb{R}.$$

Using Definition 9 the resulting time evolution of these correlation functions at $x \in \mathbb{R}^2$ for $t \geq 0$ is given by

$$\begin{cases} \frac{d}{dt}k_t^S(x) = -\int_{\mathbb{R}^2} \beta_h \phi(|x-y|)\, k_t^{SV}(x,y)\, dy + \alpha_h k_t^I(x) + \int_{\mathbb{R}^2} a^S(x,y)\left(k_t^S(y) - k_t^S(x)\right)\, dy \\ \frac{d}{dt}k_t^I(x) = \int_{\mathbb{R}^2} \beta_h \phi(|x-y|)\, k_t^{SV}(x,y)\, dy - \alpha_h k_t^I(x) + \int_{\mathbb{R}^2} a^I(x,y)\left(k_t^I(y) - k_t^I(x)\right)\, dy \\ \frac{d}{dt}k_t^U(x) = -\int_{\mathbb{R}^2} \beta_v \phi(|x-y|)\, k_t^{IU}(y,x)\, dy + b - d^U k_t^U(x) \\ \frac{d}{dt}k_t^V(x) = \int_{\mathbb{R}^2} \beta_v \phi(|x-y|)\, k_t^{IU}(y,x)\, dy - d^V k_t^V(x). \end{cases} \tag{17}$$

Remark 3. The above system of equations (17) is not closed. I.e., the time evolution of the 1-point correlation functions k_t^S, k_t^I and k_t^U, k_t^V depends on the time evolution of the 2-point correlation functions k_t^{SV} and k_t^{IU}, respectively.

In order to close the time evolution of particle density, we apply the Vlasov type scaling method, described in Subsection 3.2 . We obtain the resulting renormalized pre-generator $V := V_h + V_v$ for the dynamics of correlation functionals, where V_h and V_v are given by

$$\begin{aligned} (V_h k)(\eta) = {} & \textstyle\sum_{x\in\eta^S} \int_{\mathbb{R}^2} \beta_h \phi(|x-y|)\, k\left(\eta^S \cup x, \eta^I \backslash x, \eta^U, \eta^V \cup y\right)\, dy - \sum_{x\in\eta^S} \int_{\mathbb{R}^2} \beta_h \phi(|x-y|)\, k\left(\eta^S, \eta^I, \eta^U, \eta^V \cup y\right)\, dy \\ & + \textstyle\sum_{x\in\eta^S} \alpha_h k\left(\eta^S \backslash x, \eta^I \cup x, \eta^U, \eta^V\right) - \#\eta^I\, \alpha_h k\left(\eta^S, \eta^I, \eta^U, \eta^V\right) \\ & + \textstyle\sum_{x\in\eta^S} \int_{\mathbb{R}^2} a^S(x,y)\Big(k\left(\eta^S \backslash x \cup y, \eta^I, \eta^U, \eta^V\right) - k\left(\eta^S, \eta^I, \eta^U, \eta^V\right)\Big)\, dy \\ & + \textstyle\sum_{x\in\eta^I} \int_{\mathbb{R}^2} a^I(x,y)\Big(k\left(\eta^S, \eta^I \backslash x \cup y, \eta^U, \eta^V\right) - k\left(\eta^S, \eta^I, \eta^U, \eta^V\right)\Big)\, dy \end{aligned}$$

and

$$\begin{aligned} (V_v k)(\eta) = {} & \textstyle\sum_{x\in\eta^S} \int_{\mathbb{R}^2} \beta_v \phi(|x-y|)\, k\left(\eta^S, \eta^I \cup y, \eta^U \cup x, \eta^V \backslash x\right) - \sum_{x\in\eta^S} \int_{\mathbb{R}^2} \beta_v \phi(|x-y|)\, k\left(\eta^S, \eta^I \cup y, \eta^U, \eta^V\right) \\ & + \textstyle\sum_{x\in\eta^U} b\, k\left(\eta^S, \eta^I, \eta^U \backslash x, \eta^V\right) - \sum_{x\in\eta^U} d^U k\left(\eta^S, \eta^I, \eta^U, \eta^V\right) - \sum_{x\in\eta^V} d^V k\left(\eta^S, \eta^I, \eta^U, \eta^V\right). \end{aligned}$$

Hence we analyze the Vlasov equation

$$\frac{d}{dt} r_t\left(\eta^S, \eta^I, \eta^U, \eta^V\right) = (V r_t)\left(\eta^S, \eta^I, \eta^U, \eta^V\right)$$

with initial condition

$$r_0\left(\eta^S, \eta^I, \eta^U, \eta^V\right) = e_\lambda\left(\rho_0^S, \rho_0^I, \rho_0^U, \rho_0^V, \eta^S, \eta^I, \eta^U, \eta^V\right)$$

with given initial densities $\rho_0^l : \mathbb{R}^2 \to \mathbb{R}$ for $l \in \{S, I, U, V\}$. For $t \geq 0$ in the particular situation where we pass to renormalized versions of 1-point correlation functions, as provided in Definition 9,

$$\begin{aligned} \mathbb{R}^2 \ni x \mapsto \rho_t^S(x) := r_t^{(1,0,0,0)}\left(\eta^S, \eta^I, \eta^U, \eta^V\right) \in \mathbb{R}, \\ \mathbb{R}^2 \ni x \mapsto \rho_t^I(x) := r_t^{(0,1,0,0)}\left(\eta^S, \eta^I, \eta^U, \eta^V\right) \in \mathbb{R}, \\ \mathbb{R}^2 \ni x \mapsto \rho_t^U(x) := r_t^{(0,0,1,0)}\left(\eta^S, \eta^I, \eta^U, \eta^V\right) \in \mathbb{R}, \\ \mathbb{R}^2 \ni x \mapsto \rho_t^V(x) := r_t^{(0,0,0,1)}\left(\eta^S, \eta^I, \eta^U, \eta^V\right) \in \mathbb{R}, \end{aligned}$$

this analysis results in the system of equations

$$\begin{cases} \frac{d}{dt}\rho_t^S(x) = -\beta_h \left(\phi * \rho_t^V\right)(x)\rho_t^S(x) + \alpha_h \rho_t^I(x) + \int_{\mathbb{R}^2} a^S(x,y)\left(\rho_t^S(y) - \rho_t^S(x)\right)\, dy \\ \frac{d}{dt}\rho_t^I(x) = \beta_h \left(\phi * \rho_t^V\right)(x)\rho_t^S(x) - \alpha_h \rho_t^I(x) + \int_{\mathbb{R}^2} a^I(x,y)\left(\rho_t^I(y) - \rho_t^I(x)\right)\, dy \\ \frac{d}{dt}\rho_t^U(x) = -\beta_v \left(\phi * \rho_t^I\right)(x)\rho_t^U(x) + b - d^U \rho_t^U(x) \\ \frac{d}{dt}\rho_t^V(x) = \beta_v \left(\phi * \rho_t^I\right)(x)\rho_t^U(x) - d^V \rho_t^V(x) \end{cases} \tag{18}$$

where $*$ denotes the convolution operator.

Remark 4. The system of equations (18) provides the kinetic description of the host-vector disease dynamics with birth-death and mobility mechanism obtained via a Vlasov type scaling.

Note that the scaled and renormalized dual operator $\hat{L}^*_{\epsilon,\mathrm{ren}}$ of the operator $\hat{L}^*$ as provided in Corollary 1 is given in Appendix APPENDIX A:. In this representation the particular nature of the proper scaling gets visible.

5 | NUMERICAL SIMULATION

To illustrate the above analytical considerations, we show computational results of both the particle system and the corresponding kinetic equations. However, one has to be careful about the direct comparison of the particle system in the numerical simulation and the dynamics of particles in the framework of configuration spaces. In the latter, one has that the configurations are locally finite but can indeed have infinite many particles, which is of course not possible in simulations. In addition to this fact, the particle dynamics is implemented with boundary conditions, leading to a dynamics in the unit square, which is also different from the setting in configuration space. However, using the above mentioned choice of the interaction potentials an increase of the number of particles approximates the resulting kinetic equations obtained from the Vlasov type scaling in the configuration space framework.

The spread of the disease is modeled via a flip from susceptible to infected states. The flip is performed according to an infection rate. Since the infected vectors (hosts) influence the infection rate of host (vector) at a certain point in the area, the computation of these rates is the main task during the numerical evaluation. After the infection rates of host (vector) are computed for every susceptible host (vector), a uniformly distributed random variable is chosen and compared to the infection rate of host (vector) in order to transmit the host (vector) from the susceptible to the infected state or not.

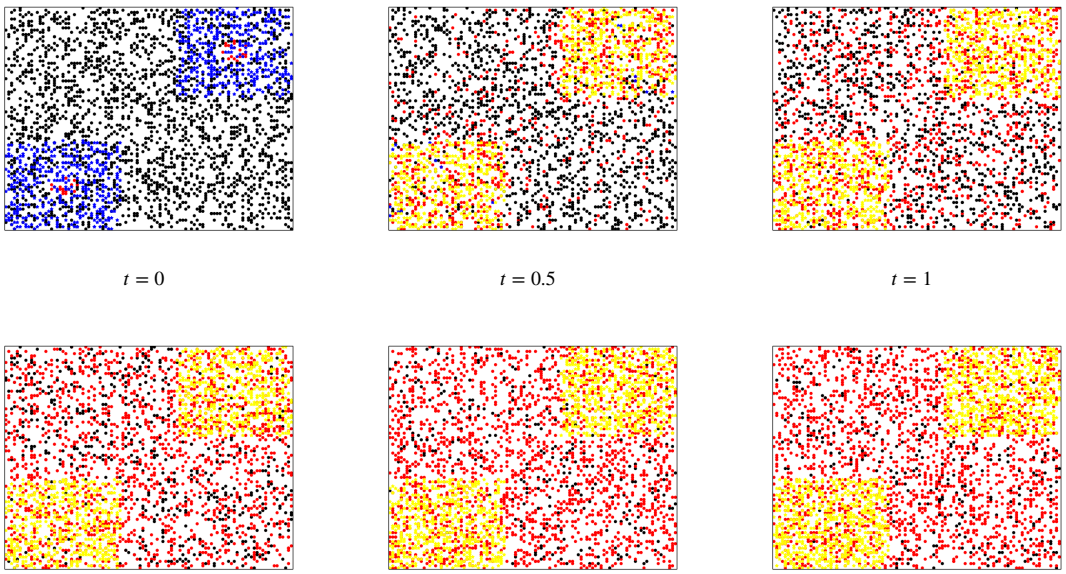

FIGURE 2 Microscopic system of host-vector disease transmission

In the particle simulation - as mentioned above - we consider the space $[0,1]\times[0,1]\subset\mathbb{R}^2$. We choose the risk of infection for host $\beta_h = 0.1$ and vector $\beta_v = 0.2$, the recovery rate for host $\alpha = 0.14$, the mobility rate for host from x to y $a^S(x,y) = a^I(x,y) = \int_{\mathbb{R}^2} \frac{1}{|y-x|^{\mu+1}}\,dx$ with $\mu = 0.2$, the birth rate for vector $b = 0.5$, and the death rate for vector $d^U = d^V = 0.3$. The potential of infection is ϕ_R as given in Figure 1 . As initial condition, we have 2500 hosts and 800 vectors. The spread of the disease is shown in Figure 2 . Susceptible hosts are depicted as black spots, infected hosts as red spots, susceptible vectors as blue spots, and infected vectors as yellow spots. In the simulation we fix two spaces for vector, i.e. the squares $[0,0.4]\times[0,0.4]$ and $[0.6,1]\times[0.6,1]$. Figure 2 shows a spatial distribution of hosts and vectors evolving in time. We also simulate the kinetic

equations to compare them with the particle simulation. For this purpose, we choose the same parameters as in the particle simulation. In order to tackle the problem numerically, we partition the domain $[0,1]\times[0,1]$ in 2500 sub-domains. The system of kinetic equations is solved via a standard finite differences method with $\Delta x = 0.02$ and $\Delta t = 0.01$. Figure 3 shows a spatial solution of the kinetic equations for infected hosts. For infected vectors, the spatial solution of kinetic equations is comparable with the one obtained from the particle dynamics averaged over hundred runs. The comparison between the dynamics in the kinetic and the particle approximation is shown in Figure 4 .

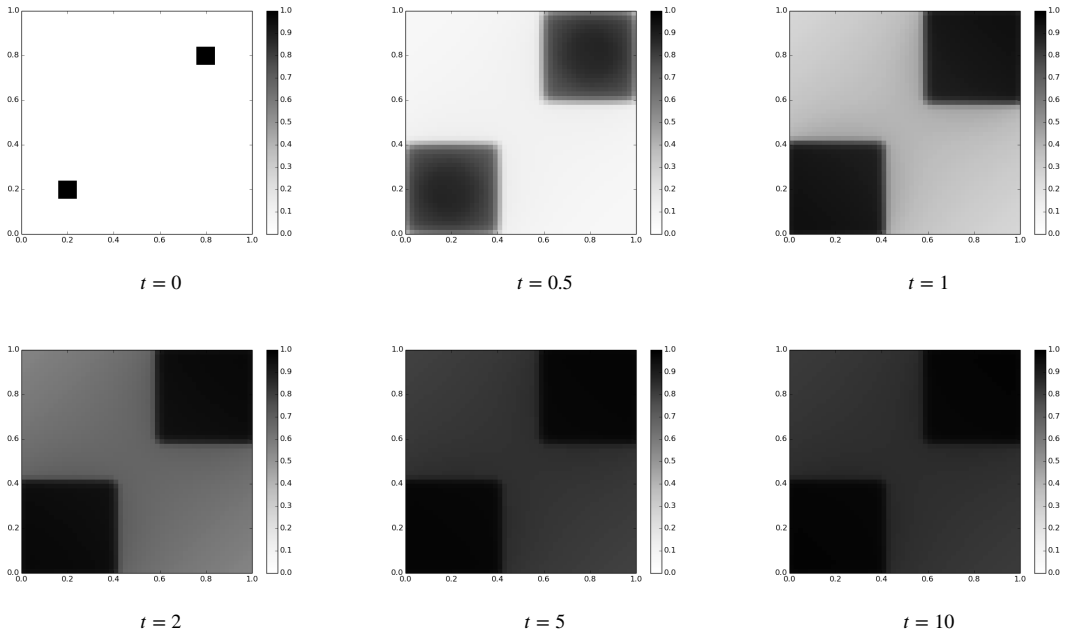

FIGURE 3 Numerical solution of the kinetic equations for the infected host

It is interesting to see, that the case numbers reflect the a standard SISUV system, see Fig.4. The kinetic equations and the particle dynamics vary slightly in comparison of case numbers. Especially in the host dynamics this difference is evident. The very good agreement in the case of vectors is due to the larger number of vectors compared to the number of hosts. Moreover, the average here is just performed over 100 runs with uniform initial conditions, which maybe is too few to really find the averaged particle dynamics in the asymptotic regime. Although the small number of simulations one finds both qualitatively already in good agreement. The influence of the initial conditions such as the number and spatial distribution of infected hosts and vectors reflects in the case numbers just in the speed of disease spread. In the classical SISUV model, different initial conditions would lead to a different infection rate. This can also be directly seen in the Vlasov type limit, namely in the convolution term, which is then - to obtain just the case numbers in time - integrated over the spatial variable.

6 | CONCLUSION

The intention of this article is to show that the Vlasov type scaling, which is a mean-field-like scaling of an interacting particle system, leads to the known equations used in epidemiology to model host-vector disease spread on the kinetic level. Configuration space analysis is here a very powerful tool to model the dynamics on the microscopic level using Markov pre-generators known from hop and flip processes. The concepts of harmonic analysis in this framework, established e.g. in (45), are used to derive first the dynamics of correlation functions - giving a hierarchical system of equations comparable to the well known BBGKY hierarchy in Hamiltonian dynamics. Then a proper Vlasov type scaling guaranties that the resulting Vlasov hierarchy is closed and possesses the property of preservation of chaos. The limiting system of time evolution equations is non-linear and

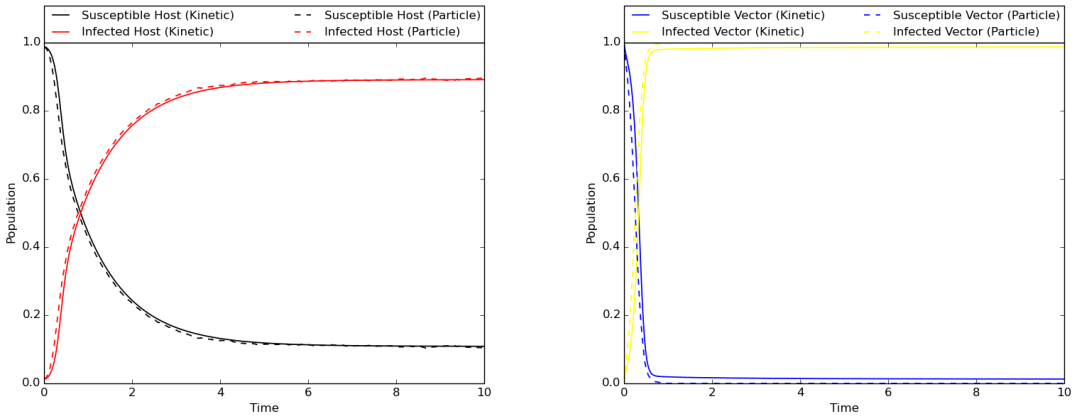

FIGURE 4 Dynamics of the particle model averaged over a hundred runs and the kinetic equations for susceptible and infected compartment of (a) host and (b) vector

strongly related to the well-known Fisher-KPP equations. A numerical analysis strengthens the analytical results. Moreover, the dynamics of case numbers over time gives qualitatively the solution of a SISUV-ODE system. The microscopic dynamics hence leads to the right behavior in the scaling limit.

It is however still an open question, if this is the only possible scaling leading to such a system of equations or if another kind of scaling procedure provides the same kinetic and hence mesoscopic dynamics. The spatial resolution of the problem however can give rise to study spatial control of such systems or predict outbreaks from spatially known microscopic data. These considerations will be postponed for a later study.

7 | ACKNOWLEDGMENTS

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□

APPENDIX A: RENORMALIZED SCALED DUAL OPERATORS FOR THE HOST-VECTOR DISEASE DYNAMICS

In order to close the time evolution of the particle density, we apply a Vlasov type scaling as described in Section 3.2. Here we provide the corresponding rescaled operators.

First, we scale the infection operator using $\phi_\varepsilon = \varepsilon\phi$,

$$
\begin{aligned}
&(\hat{L}^*_{h,\mathrm{inf},\varepsilon,\mathrm{ren}}k)\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\\
&\quad=\varepsilon^{\#(\eta^S)+\#(\eta^I)+\#(\eta^U)+\#(\eta^V)}\\
&\times\Bigg(\sum_{y\in\eta^I}\sum_{\tilde{y}\in\eta^V}\beta_h\,\phi_\varepsilon\big(|y-\tilde{y}|\big)\,\varepsilon^{-\left(\#(\eta^S\cup\{y\})+\#(\eta^I\setminus\{y\})+\#(\eta^U)+\#(\eta^V)\right)}\\
&\qquad\times k\big(\eta^S\cup\{y\},\eta^I\setminus\{y\},\eta^U,\eta^V\big)\\
&\quad-\sum_{x\in\eta^S}\sum_{\tilde{y}\in\eta^V}\beta_h\,\phi_\varepsilon\big(|x-\tilde{y}|\big)\,\varepsilon^{-\left(\#(\eta^S)+\#(\eta^I)+\#(\eta^U)+\#(\eta^V)\right)}k\big(\eta^S,\eta^I,\eta^U,\eta^V\big)\\
&\quad+\sum_{y\in\eta^I}\int_{\mathbb{R}^2}\beta_h\,\phi_\varepsilon\big(|y-\tilde{y}|\big)\,\varepsilon^{-\left(\#(\eta^S\cup\{y\})+\#(\eta^I\setminus\{y\})+\#\eta^U+\#(\eta^V\cup\{\tilde{y}\})\right)}
\end{aligned}
$$

$$
\begin{aligned}
&\times k\big(\eta^S \cup \{y\}, \eta^I \setminus \{y\}, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y} \\
&- \textstyle\sum_{x\in\eta^S} \int_{\mathbb{R}^2} \beta_h\, \phi_\varepsilon\big(|x-\tilde{y}|\big)\, \varepsilon^{-\left(\#(\eta^S)+\#(\eta^I)+\#(\eta^U)+\#(\eta^V\cup\{\tilde{y}\})\right)} \\
&\times k\big(\eta^S, \eta^I, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y}\Bigg) \\
&= \textstyle\sum_{y\in\eta^I} \sum_{\tilde{y}\in\eta^V} \beta_h\, \varepsilon\, \phi(|y-\tilde{y}|)\, k\big(\eta^S \cup \{y\}, \eta^I \setminus \{y\}, \eta^U, \eta^V\big) \\
&\quad - \textstyle\sum_{x\in\eta^S} \sum_{\tilde{y}\in\eta^V} \beta_h\, \varepsilon\, \phi(|x-\tilde{y}|)\, k\big(\eta^S, \eta^I, \eta^U, \eta^V\big) \\
&+ \textstyle\sum_{y\in\eta^I} \int_{\mathbb{R}^2} \beta_h\, \varepsilon\, \phi(|y-\tilde{y}|)\, \varepsilon^{-1} k\big(\eta^S \cup \{y\}, \eta^I \setminus \{y\}, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y} \\
&\quad - \textstyle\sum_{x\in\eta^S} \int_{\mathbb{R}^2} \beta_h\, \varepsilon\, \phi(|x-\tilde{y}|)\, \varepsilon^{-1} k\big(\eta^S, \eta^I, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y} \\
&= \textstyle\sum_{y\in\eta^I} \sum_{\tilde{y}\in\eta^V} \beta_h\, \varepsilon\, \phi(|y-\tilde{y}|)\, k\big(\eta^S \cup \{y\}, \eta^I \setminus \{y\}, \eta^U, \eta^V\big) \\
&\quad - \textstyle\sum_{x\in\eta^S} \sum_{\tilde{y}\in\eta^V} \beta_h\, \varepsilon\, \phi(|x-\tilde{y}|)\, k\big(\eta^S, \eta^I, \eta^U, \eta^V\big) \\
&+ \textstyle\sum_{y\in\eta^I} \int_{\mathbb{R}^2} \beta_h\, \phi(|y-\tilde{y}|)\, k\big(\eta^S \cup \{y\}, \eta^I \setminus \{y\}, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y} \\
&\quad - \textstyle\sum_{x\in\eta^S} \int_{\mathbb{R}^2} \beta_h\, \phi(|x-\tilde{y}|)\, k\big(\eta^S, \eta^I, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y}.
\end{aligned}
$$

Taking $\varepsilon \to 0$ we obtain the renormalized operator

$$
\begin{aligned}
(V_{h,\mathrm{inf}}k)\big(\eta^S, \eta^I, \eta^U, \eta^V\big) &:= \lim_{\varepsilon\to 0} (\hat{L}^*_{h,\mathrm{inf},\varepsilon,\mathrm{ren}}k)\big(\eta^S, \eta^I, \eta^U, \eta^V\big) \\
&= \textstyle\sum_{y\in\eta^I} \int_{\mathbb{R}^2} \beta_h\, \phi(|y-\tilde{y}|)\, k\big(\eta^S \cup \{y\}, \eta^I \setminus \{y\}, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y} \\
&\quad - \textstyle\sum_{x\in\eta^S} \int_{\mathbb{R}^2} \beta_h\, \phi(|x-\tilde{y}|)\, k\big(\eta^S, \eta^I, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y}.
\end{aligned}
$$

For the birth operator we consider $b_\varepsilon = \frac{b}{\varepsilon}$,

$$
\begin{aligned}
&(\hat{L}^*_{v,\mathrm{birth},\varepsilon,\mathrm{ren}}k)\big(\eta^S, \eta^I, \eta^U, \eta^V\big) \\
&= \varepsilon^{\#(\eta^S)+\#(\eta^I)+\#(\eta^U)+\#(\eta^V)} \\
&\times\Bigg(\textstyle\sum_{\tilde{x}\in\eta^U} b_\varepsilon\, \varepsilon^{-\left(\#(\eta^S)+\#(\eta^I)+\#(\eta^U\setminus\{\tilde{x}\})+\#(\eta^V)\right)} k\big(\eta^S, \eta^I, \eta^U \setminus \{\tilde{x}\}, \eta^V\big) \Bigg) \\
&= \varepsilon \textstyle\sum_{\tilde{x}\in\eta^U} \frac{b}{\varepsilon}\, k\big(\eta^S, \eta^I, \eta^U \setminus \{\tilde{x}\}, \eta^V\big) \\
&= \textstyle\sum_{\tilde{x}\in\eta^U} b\, k\big(\eta^S, \eta^I, \eta^U \setminus \{\tilde{x}\}, \eta^V\big).
\end{aligned}
$$

Taking $\varepsilon \to 0$ we obtain the renormalized operator

$$
\begin{aligned}
(V_{v,\mathrm{birth}}k)\big(\eta^S, \eta^I, \eta^U, \eta^V\big) &:= \lim_{\varepsilon\to 0} (\hat{L}^*_{v,\mathrm{birth},\varepsilon,\mathrm{ren}}k)\big(\eta^S, \eta^I, \eta^U, \eta^V\big) \\
&= \textstyle\sum_{\tilde{x}\in\eta^U} b\, k\big(\eta^S, \eta^I, \eta^U \setminus \{\tilde{x}\}, \eta^V\big).
\end{aligned}
$$

For the recovery, death and jump operator no scaling is needed. Finally, we obtain the renormalized generator for the dynamics of correlation functionals,

$$
\begin{aligned}
&(V_h k)\big(\eta^S, \eta^I, \eta^U, \eta^V\big) \\
&= \textstyle\sum_{y\in\eta^I} \int_{\mathbb{R}^2} \beta_h\, \phi(|y-\tilde{y}|)\, k\big(\eta^S \cup \{y\}, \eta^I \setminus \{y\}, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y} \\
&\quad - \textstyle\sum_{x\in\eta^S} \int_{\mathbb{R}^2} \beta_h\, \phi(|x-\tilde{y}|)\, k\big(\eta^S, \eta^I, \eta^U, \eta^V \cup \{\tilde{y}\}\big)\, d\tilde{y} \\
&+ \textstyle\sum_{x\in\eta^S} \alpha_h\, k\big(\eta^S \setminus \{x\}, \eta^I \cup \{x\}, \eta^U, \eta^V\big) - \#(\eta^I)\, \alpha_h\, k\big(\eta^S, \eta^I, \eta^U, \eta^V\big),
\end{aligned}
$$

and

$$
\begin{aligned}
&(V_v k)\big(\eta^S, \eta^I, \eta^U, \eta^V\big) \\
&= \textstyle\sum_{\tilde{y}\in\eta^V} \int_{\mathbb{R}^2} \beta_v\, \phi(|\tilde{y}-y|)\, k\big(\eta^S, \eta^I \cup \{y\}, \eta^U \cup \{\tilde{y}\}, \eta^V \setminus \{\tilde{y}\}\big)\, dy \\
&\quad - \textstyle\sum_{\tilde{x}\in\eta^U} \int_{\mathbb{R}^2} \beta_v\, \phi(|\tilde{x}-y|)\, k\big(\eta^S, \eta^I \cup \{y\}, \eta^U, \eta^V\big)\, dy \\
&+ \textstyle\sum_{\tilde{x}\in\eta^U} b\, k\big(\eta^S, \eta^I, \eta^U \setminus \{\tilde{x}\}, \eta^V\big) - \sum_{\tilde{x}\in\eta^U} d^U k\big(\eta^S, \eta^I, \eta^U, \eta^V\big) \\
&\quad - \textstyle\sum_{\tilde{y}\in\eta^V} d^V k\big(\eta^S, \eta^I, \eta^U, \eta^V\big).
\end{aligned}
$$

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