A computational framework for evaluating the role of mobility on the propagation of epidemics on point processes

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Received: 1 October 2020 / Revised: 15 August 2021 / Accepted: 21 October 2021 / Published online: 20 December 2021
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Abstract
This paper is focused on SIS (Susceptible-Infected-Susceptible) epidemic dynamics (also known as the contact process) on populations modelled by homogeneous Poisson point processes of the Euclidean plane, where the infection rate of a susceptible individual is proportional to the number of infected individuals in a disc around it. The main focus of the paper is a model where points are also subject to some random motion. Conservation equations for moment measures are leveraged to analyze the stationary regime of the point processes of infected and susceptible individuals. A heuristic factorization of the third moment measure is then proposed to obtain simple polynomial equations allowing one to derive closed form approximations for the fraction of infected individuals in the steady state. These polynomial equations also lead to a phase diagram which tentatively delineates the regions of the space of parameters (population density, infection radius, infection and recovery rate, and motion rate) where the epidemic survives and those where there is extinction. A key take-away from this phase diagram is that the extinction of the epidemic is not always aided by a decrease in the motion rate. These results are substantiated by simulations on large two dimensional tori. These simulations show that the polynomial equations accurately predict the fraction of infected individuals when the epidemic survives. The simulations also show that the proposed phase diagram accurately predicts the parameter regions where the mean survival time of the epidemic increases (resp. decreases) with motion rate.

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Keywords Point process · Moment measures · Shot-noise process · Boolean model · Motion · Contact process · Epidemic · SIS model · Phase diagram · Markov process · Stationary regime

Mathematics Subject Classification 60G55 · 92D30 · 60K35

1 Introduction

This paper is focused on the use of the theory of point processes for the analysis of the propagation of an epidemic and of the policies to control it, in particular the reduction of individual motion (i.e., lockdown policies).

The general framework is that of a stochastic SIS (Susceptible, Infected, Susceptible) model on point processes of the Euclidean plane. In SIS, each individual has a state which is either Susceptible or Infected. It moves from $S$ to $I$ upon infection by another individual. From $I$, it moves to $S$ after some recovery time. Below we will use the terms SIS process and contact process equivalently. The model considered here is stochastic in several distinct ways:

1. The epidemic propagates on a random medium: the individuals are located at the points of a random point process on $\mathbb{R}^2$, which accounts for the random geometry of the problem, and in particular the fact that at any given time, the epidemic propagates more easily in more densely populated areas, and dies faster in sparsely populated ones;
2. The medium changes randomly over time: the individuals have some parameterizable random motion, which accounts for the randomness of displacement and allows one to study the effect of mobility reduction;
3. The infection process itself is a random phenomenon that takes into account the geometry of the configuration of other individuals around a susceptible individual through the sum over the infection rates of nearby infected individuals.

A longer version of this paper is available online (Baccelli and Ramesan 2020), and contains additional material that we will refer to in this paper when relevant.

1.1 Basic model

There is initially a single point process $\Xi_0$, which will here be Poisson homogeneous of intensity $\lambda$ in the Euclidean plane, with the points representing the initial location of individuals in the population. Individuals (hereafter referred to as points) move independently.

We will consider the following random waypoint motion model where, at any time, a point stays put for an exponential time and jumps from its current location to another location with rate $\gamma$; the displacements are random, i.i.d., and have a symmetrical distribution $D$ on $\mathbb{R}^2$. This leads to a location point process $\Xi_t$ at time $t$. Note that $\Xi_t$ is Poisson with intensity $\lambda$ for all $t$ thanks to the displacement theorem (Theorem 1.3.9 in Baccelli and Blaszczyszyn 2009). For the most part, we will consider the more specific case of a far random waypoint motion - where the displacements experienced
by points are very large (for example, if $D$ is a two dimensional Gaussian vector with i.i.d. coordinates $N(0, \sigma^2)$ with $\sigma^2$ tending to infinity).

There is an infection/contagion/viral charge function $f : \mathbb{R}^+ \rightarrow \mathbb{R}^+$. The special case

$$f(r) = \alpha 1_{r \leq a}$$

will be considered in the analysis. In this function, $\alpha > 0$ is the pairwise infection rate and $a > 0$ is the infection radius. In words, the rate at which a susceptible point is infected is proportional to the number of infected points that are at distance less than or equal to $a$ from it. More general functions (with bounded or unbounded support) can be considered in the theory and in the computational analysis.

The points of $\Xi_t$ can be in one of two states: 1 (or infected) or 0 (or susceptible). This leads to two point processes $\Phi_t$ and $\Psi_t$ such that

$$\Xi_t = \Phi_t + \Psi_t,$$

with $\Phi_t$ (resp. $\Psi_t$) the point process of infected (resp. susceptible) points. The SIS state dynamics is then as follows:

- At any time, the state of a susceptible point jumps to infected with a rate equal to the current value of the sum of $f$ over all infected points (sum of viral charges) at the susceptible point’s current location. That is, the transition rate of $X \in \Psi_t$ is

$$a(X, \Phi_t) = \sum_{Y \in \Phi_t} f(||X - Y||).$$

This accounts for the geographic locality of the infection mechanism, i.e., the higher chance of infection when surrounded by more infected points.

- At any time, the state of an infected point jumps to susceptible with a constant rate $\beta > 0$.

The above dynamics come in addition to the previously described motion of points. Expressed differently, our model is that of an SIS epidemic that evolves on a geometric random graph (where edges exist between points within distance $a$ of each other), and where the later evolves in time as its vertices move in space. In all cases described above, the pair $(\Phi_t, \Psi_t)$ is Markov on the space of counting measures, which is not a discrete space. Two equivalent representations of the basic model are presented in Appendix A of Baccelli and Ramesan (2020).

The system has four rate parameters: $\alpha, \beta, \lambda$, and $\gamma$. Since the focus is on the steady-state behaviour of the epidemic, without loss of generality, one of them can be taken equal to 1. When useful, we will take $\alpha = 1$ in what follows.

### 1.2 Aims and main results

The main aim of this paper is to study the role of motion on the equilibria, or steady-state behaviour of infection. The equilibria in question are mostly studied in the infinite Euclidean plane, which allows one to leverage the machinery of stationary point processes. In these infinite models, we answer the following two families of questions:
1. When do the aforementioned equilibria exist, i.e., when is there a non-zero fraction of infected points in steady state? Can we identify a phase diagram, namely critical values of the parameters that delineate regions where the epidemic almost surely (a.s.) dies out or has a positive probability to survive?

2. What is the fraction of infected points, $p$, in the steady state? What is the probability that a single infected point in a population causes a sustained epidemic?

**Results and Paper Structure:** Section 2, which is based on results in Liggett (1999), summarizes properties of the contact process that hold for deterministic graphs. These results are then generalized to our model, i.e., to random geometric graphs that evolve in time as points move. We establish that when fixing all parameters except $\beta$, there exists a deterministic threshold on $\beta$, $\beta_c$, such that the epidemic dies out for $\beta > \beta_c$ and survives for $\beta < \beta_c$. To use epidemiological terms, we show the existence of an epidemic threshold. We derive a necessary condition for the existence of a non-degenerate stationary regime (here non-degenerate means with a positive density of infected points) and establish a bound (Lemma 2) on the value of the epidemic threshold (eq., a necessary condition for the survival of the epidemic) in Sect. 3. In this last section, we also establish an infinite sequence of conservation equations that are satisfied by the dynamics. Of particular importance to what follows, Theorem 3 summarizes the relations that link moment measures of order one, two, and three. In Sect. 4, we introduce the second-order approximation of these conservation equations which allows one to obtain heuristic polynomial equations which in turn lead to estimates of the fraction $p$ of infected points in the stationary regime of the epidemic process (which is known as the endemic disease state in the epidemiology literature). The results established in Sect. 2 show that $p$ is also equal to the probability that a single infected point will cause a surviving epidemic - an important quantity for the study of real-world epidemics. These heuristics also lead to a tentative phase diagram (Fig. 1) that partitions the space of parameters ($\alpha$, $\beta$, $\gamma$, $\lambda$, $a$) into regions of survival and extinction of the epidemic. Throughout the paper, it will be convenient to introduce $\mu = \lambda \pi a^2$, where $\mu$ is the mean degree of a point in the underlying random geometric graph, and to discuss partitions of the ($\alpha$, $\beta$, $\gamma$, $\mu$) parameter space. We will identify a safe region, where there is extinction whatever the motion rate $\gamma$, a region which is unsafe and motion-insensitive, namely such that there is survival for all positive motion rates, and a region which is unsafe and motion-sensitive. This last region is the most surprising: when fixing all parameters except $\gamma$, there are two thresholds $0 < \gamma_c^- < \gamma_c^+$ such that there is survival for $\gamma < \gamma_c^-$ and for $\gamma > \gamma_c^+$ and extinction for $\gamma_c^- < \gamma < \gamma_c^+$. In other words, we find that, for certain subsets of the parameter space, a reduction in the motion of the population can be favorable to the propagation of the epidemic. Supporting simulation results for the accuracy of our heuristics and veracity of our phase diagram are distributed throughout Sect. 4.

Section 5 discusses model variants of practical importance to which the techniques of the present paper should be applicable. Finally, Sect. 6 gathers the list of conjectures that are made throughout the paper. An analysis, based on the same tools, of the model where there is no motion of points can be found in Sect. 5 of Baccelli and Ramesan (2020).
1.3 Related work

Previous work related to this paper broadly falls into two categories: the interacting particle system literature (in particular the literature on the contact process on graphs) and the mathematical epidemiology literature (in particular the literature on SIS epidemics over networks). In the present paper, the terms ‘contact process’ and ‘SIS epidemic’ will be used equivalently, as will be the terms ‘network’ and ‘graph’. We leverage the mathematical machinery that draws from the former body of literature. The moment closure heuristics we propose to estimate quantities of interest are linked to those considered in the latter body of work.

1.3.1 The contact process on graphs

In the absence of mobility, the problem was extensively studied in the particle system literature (see (Liggett 1999) and references therein). A basic dichotomy in this framework is between finite and infinite graphs. On finite graphs, the main question is that of the phase transition between a logarithmic and an exponential growth of the time till absorption (extinction of the epidemic). This was studied on deterministic graphs like finite grids and regular trees. There is a large corpus of results on infinite graphs such as...
grids and regular trees. This is well covered in the book of Liggett (1999). The contact process was also studied on infinite random graphs with unbounded degrees. It was first studied on the supercritical Bienaymé-Galton-Watson tree (Pemantle 1992) where it was shown that some critical values can be degenerate. Contact process models on Euclidean point processes were also thoroughly studied (see ex. Hao 2018; Ganesan 2015; Ménard and Singh 2015). The case without motion of the present paper ($\gamma = 0$) can be seen as the contact process on the random geometric graph.

1.3.2 The SIS epidemic on networks

Epidemics on networks have also been extensively studied. The focus here is on computationally tractable approaches allowing one to predict relevant epidemiological quantities and to derive qualitative properties of the epidemic. Pastor-Satorras et al. (2015) provides a comprehensive overview of methods and literature on the topic. In particular, the infinite collection of moment measure equations and subsequent heuristics to ‘close’ these equations described in Sect. 4.3 are similar in spirit to methods used in this literature for the analysis of SIS epidemics on (non-geometric, finite) graphs. An overview of the application of such techniques to the analysis of epidemics on graphs is contained in chapter 17 of Newman (2018), and relevant review articles include (Pastor-Satorras et al. 2015) (Section V.A) and Kuehn (2016). Examples of works that apply moment closure techniques in an epidemiological setting include (Krishnarajah et al. 2005; Wilkinson and Sharkey 2014), and Lloyd (2004). Epidemics with motion were extensively studied in the random graph setting (without considering geometry). The basic model for SIS on graphs is that where agents perform a random walk on the random graph and where agents meeting at a given point of the graph may infect each other - see (Figueiredo et al. 2020) and the references therein.

In the present paper, we focus on a point process model with the following far random waypoint motion: a point stays at a given location for an exponential time and then makes a jump with a large magnitude. This is inspired by the idea of a flight. We are not aware of previous research on previous studies on SIS epidemics on point processes with motion. The main difference with the literature on random geometric graphs is the fact that the structure of the random geometric graph evolves randomly over time in the case studied in the present paper, whereas it is fixed in Ganesan (2015) and the other references mentioned. Further, we derive accurate heuristics for quantities of interest, unlike most of the work in the interacting particle systems literature. The main difference with the literature on SIS epidemics on networks is that we explicitly model the effects of the geometry of the contact graph using the theory of point processes.

In summary, the main novelty of this paper is that it considers both the effects of the geometry that is inherent to populations affected by epidemics and the effects of population motion. To the best of the authors’ knowledge, the key results of the paper, namely the conservation equations of Theorem 3, the computational heuristics allowing to evaluate the fraction of infected points in steady state (Sect. 3.5), and the phase diagram alluded to above (Fig. 1), are new.
2 Basic properties of SIS dynamics and their implications

Deterministic graphs For the SIS dynamics (or contact process) on a fixed (deterministic) graph $\mathcal{G}$, the following results are summarized from Liggett (1999) and are obtained from the graphical representation of the dynamics explained therein. The underlying probability space is a product space with, for each point, a potential recovery Poisson process of rate $\beta$ and as many potential infection point processes of rate $\alpha$ as this point has neighbors. In these results, for all $A \subset \mathcal{G}$, $\Phi^A_t$ denotes the subset of infected points of $\mathcal{G}$ at time $t$ if the set of infected points at time 0 is $A$ and $\mathbb{P}^A$ is the measure that results from the set of infected points at time 0 being $A$. Using the coupling of the graphical representation of the dynamics, we have

- Monotonicity:

  \[
  \text{if } A \subset B, \text{ then } \Phi^A_t \subset \Phi^B_t, \text{ for all } t.
  \]

- Additivity:

  \[
  \Phi^{A \cup B}_t = \Phi^A_t \cup \Phi^B_t, \text{ for all } A, B, t.
  \]

- Self-duality

  \[
  \mathbb{P}^A(\Phi_t \cap B \neq \emptyset) = \mathbb{P}^B(\Phi_t \cap A \neq \emptyset), \text{ for all } A, B, t.
  \]

A direct consequence of monotonicity is the existence of a maximal (time) invariant measure which is obtained as the limiting measure when starting with all points infected. The existence of this limiting measure follows from the fact that the state measure is stochastically decreasing over time for this initial condition.

A useful consequence of self-duality is the fact that the probability that the epidemic survives when started from singleton $\{x\}$, with $x \in \mathcal{G}$, namely

\[
\lim_{t \to \infty} \mathbb{P}^{\{x\}}(\Phi_t \cap \mathcal{G} \neq \emptyset),
\]

coincides with the mass of the maximal time-invariant probability measure at $x$ (equivalently, the steady-state fraction of infected points), namely

\[
\lim_{t \to \infty} \mathbb{P}^{\mathcal{G}}(\Phi_t \cap \{x\} \neq \emptyset).
\]

One says that there is strong survival if, for some $x$, for the initial condition $\{x\}$, $x$ is infected infinitely often with positive probability. In the present paper, we concentrate on strong survival (the term survival will always mean strong survival). The most general structural result on the contact process states that if the probability that the epidemic strongly survives when started from the initial condition $\{x\}$ is positive for some $\beta$, then it is positive for all $\beta' < \beta$ and for all $x$. This is a consequence of monotonicity. Hence there exists a critical $\beta_c$ (not depending on $x$) such that for all
$\beta > \beta_c$, the epidemic dies out almost surely when starting from $x$, and when $\beta < \beta_c$, it (strongly) survives with a positive probability.

Now we generalize these existing results to random geometric graphs, in the three cases of no-motion, random waypoint motion and far random waypoint motion.

**Random geometric graph** We first generalize the above results to the case where the graph is random. The basic properties listed above hold conditionally on the graph topology. Assume that the graph is a random geometric graph of a stationary and ergodic point process $\Xi$. We equip the points of $\Xi$ with conditionally independent marks defined as above (for each point, one potential recovery Poisson point process and as many potential infection Poisson point processes as there are points in the ball of radius $a$ around it). Let $P_0$ denote the Palm probability of $\Xi$ on this probability space and let $\mathcal{F}$ denote the sigma algebra generated by $\Xi$. Then $P_0$ a.s.,

$$P_0(\Phi_t \cap \Xi \neq \emptyset \mid \mathcal{F}, \Phi_0 = \{x\}) = P_0(\Phi_t \cap \{x\} \neq \emptyset \mid \mathcal{F}, \Phi_0 = \Xi),$$

for all $t$ and $x \in \Xi$.

When letting $t$ tend to infinity, one gets that the (conditional) maximal time stationary measure on the random discrete set $\Xi$ puts a mass at $x \in \Xi$ equal to the (conditional) probability that the epidemic started at $x$ survives.

By unconditioning w.r.t. $\mathcal{F}$, one gets

$$P_0(\Phi_\infty \cap \Xi \neq \emptyset \mid \Phi_0 = \{0\}) = P_0(\Phi_\infty \cap \{0\} \neq \emptyset \mid \Phi_0 = \Xi).$$

The LHS is the probability that the epidemic survives when started from the typical point (the origin) or equivalently the spatial average of the probability of survival starting from a single point. The RHS is the probability that the origin is infected in the maximal stationary regime, or equivalently the fraction of infected points in a large ball under this maximal stationary regime.

Also, there exists a constant (this is a constant because of ergodicity) $\beta_c$ such that for $\beta > \beta_c$, the epidemic dies out when started from any point of the point process (or equivalently the maximal invariant measure is 0), whereas it survives with a positive probability otherwise (or equivalently the conditional maximal invariant random measure is positive a.s).

Note that, due to ergodicity, if the origin is infected i.o. with positive probability, it is with probability 1.

**Random geometric graph with point motion** Assume now that there is motion in the random waypoint sense defined above. We then have a random graph $\Xi_t$ that evolves with time, the evolution of which is not affected by the epidemic. One can endow the moving points of this graph with conditionally independent Poisson point processes of rate $\beta$ and $\alpha$ as above. We claim that monotonicity, additivity and self-duality hold for these dynamics. So all the conclusions extend to this case as well. In particular, there exists a critical $\beta_c$, there exists a maximal invariant measure, etc. The proof of this fact can be found in Appendix B.1 in Baccelli and Ramesan (2020).

**Random geometric graph with far random waypoint motion** The far random waypoint model studied in the present paper belongs to the class discussed above when
displacements are large. A natural instance is that of a two dimensional Gaussian vector with i.i.d. \( \mathcal{N}(0, \sigma^2) \) coordinates, with \( \sigma^2 \) large. Again, we claim that monotonicity, additivity and self-duality hold for these dynamics. All the conclusions hence extend to this case as well. We defer the proof to Appendix B.2 in Baccelli and Ramesan (2020).

3 Moment rate conservation Principle

3.1 First moment rate conservation principle

Assume that there exists a time-space stationary regime for the dynamics, with \((\Phi, \Psi)\) representatives of the time-space stationary point processes. Let \( p \) denote the (unknown) stationary fraction of infected points. That is, in this stationary regime, \( \Phi \) has spatial intensity \( \lambda p \) and \( \Psi \) has intensity \( \lambda(1 - p) \).

Let \( I_{\Phi}(x) = \sum_{X \in \Phi} f(||X - x||) \) denote the infection rate of locus \( x \in \mathbb{R}^2 \) at time \( t \). The time-space stationary assumption and the Campbell-Mecke theorem imply \( \mathbb{E}[I_{\Phi}(x)] = \lambda p F \), with \( F = 2\pi \int_0^\infty f(r)rdr \). In the special case (assumed here by default), \( F = \pi a^2 \alpha \).

Pick a subset \( D \) of the Euclidean space with volume 1. The spatial infection rate is defined as

\[
i = \mathbb{E}\left[ \sum_{Y \in \Psi \cap D} I_{\Phi}(Y) \right].
\]

From the Campbell-Mecke theorem

\[
i = \lambda(1 - p)\mathbb{E}^0_{\Psi}[I_{\Phi(0)}],
\]

with \( \mathbb{E}^0_{\Psi} \) the Palm distribution w.r.t. \( \Psi \). The spatial recovery rate is defined as

\[
r = \mathbb{E}\left[ \sum_{X \in \Phi \cap D} \beta \right] = \lambda p \beta.
\]

The Rate Conservation Principle (RCP, Baccelli and Brémaud 2003) gives that \( i = r \), namely

Lemma 1 Under the foregoing assumptions,

\[
p \beta = (1 - p)\mathbb{E}^0_{\Psi}[I_{\Phi(0)}].
\]

The last relation will be referred to as the first moment RCP.
### 3.2 A necessary condition for survival

A natural conjecture, backed by simulations, is that there is repulsion between \( \Phi \) and \( \Psi \), namely

\[
E_0^0 \{ I_\Phi(0) \} \leq E[I_\Phi(0)].
\]

In words, in the steady state, a typical susceptible point will see less infection than a typical locus in space. This will be referred to as the repulsion conjecture.

This and Lemma 1 give

\[
p\beta = (1 - p)E_0^0 \{ I_{\Phi(0)} \} \leq (1 - p)p \mu,
\]

that is, if \( p \neq 0 \),

\[
p \leq 1 - \frac{\beta}{\alpha \mu},
\]

with \( \mu = \lambda \pi a^2 \) the mean degree in the random geometric graph. This proves the following result on the critical value \( \beta_c \) defined in Sect. 2:

**Lemma 2** Under the \((\Phi, \Psi)\) repulsion conjecture,

\[
\beta_c \leq \alpha \mu. \tag{2}
\]

In words, assuming that the repulsion conjecture holds, if \( \beta > \alpha \mu \), then there is extinction a.s. (this is the safe region alluded to above) and the only invariant measure is the empty measure. As we shall see, according to our phase diagram, there are regions of the parameter space where \( \beta_c < \alpha \mu \). In addition either \( p = 0 \) or the fraction of infected points satisfies

\[
0 < p \leq 1 - \frac{\beta}{\alpha \mu}. \tag{3}
\]

Note that motion plays no role in this lemma. It is in fact hidden in the Palm expectation. Also note that the result holds for all stationary point processes (we did not use the Poisson assumption here). This will be used in the next subsection.

The result of Lemma 2 can be connected to the basic reproduction number \( (R_0) \) of epidemiology. This number is defined as the expected number of infections generated by a single infected point located in a population of all-susceptible points. In several epidemiological models, an emerging infection is predicted to die out in a population if \( R_0 \) is less than 1, and to survive if it is more then 1. Since a single infected point has an average degree \( \mu \), infects neighbours at rate \( \alpha \) and recovers at rate \( \beta \), it is easy to see that in the fast motion case (\( \gamma \) large), \( R_0 = \frac{\alpha \mu}{\beta} \). In this fast motion case, the bound of Lemma 2 should hence be the true value for \( \beta_c \), namely \( \beta_c = \alpha \mu \). However, as already mentioned above, there exist parameter regions where \( \beta_c < \alpha \mu \). In other words, in this...
random medium, random motion setting, $R_0$ is not the relevant parameter to predict whether the epidemic dies out or survives, in that the epidemic dies out in parameter regions where $R_0 > 1$.

### 3.3 A primer on moment measures

As already explained, we will establish conservation equations for higher order moment measures of the stationary (in time and in space) point processes of susceptible and infected points. This subsection summarizes some basic properties of these measures.

#### 3.3.1 Definition

The second factorial moment measure of a point process $\phi$, $\rho_{\phi}^{(2)}$, is defined by

\[
\mathbb{E} \left[ \sum_{X \neq X' \in \phi} g(X, X') \right] = \int_{\mathbb{R}^2} g(x, x') \rho_{\phi}^{(2)}(x, x') dx dx',
\]

for all measurable non-negative functions $g$. For a stationary point process of intensity $\lambda$,

\[
\rho_{\phi}^{(2)}(x, x') = \lambda^2 \xi_{\phi}^{(2)}(x' - x),
\]

with $\xi_{\phi}$ the pair correlation function of $\phi$.

Similarly, the joint moment measure of $(\phi, \psi)$, $\rho_{\phi, \psi}^{(2)}$, is defined by

\[
\mathbb{E} \left[ \sum_{X \in \phi, Y \in \psi} g(X, Y) \right] = \int_{\mathbb{R}^2} g(x, y) \rho_{\phi, \psi}^{(2)}(x, y) dx dy,
\]

for all measurable non-negative functions $g$. In the case of two jointly (space)-stationary point processes with intensities $\lambda$ and $\mu$,

\[
\rho_{\phi, \psi}^{(2)}(x, x') = \lambda \mu \xi_{\phi, \psi}^{(2)}(x' - x),
\]

with $\xi_{\phi, \psi}^{(2)}$ the cross-pair correlation function of $(\phi, \psi)$.

When the point processes are isotropic (as is the case in our model), we have

\[
\xi_{\phi, \psi}^{(2)}(x' - x) = \tilde{\xi}_{\phi, \psi}^{(2)}(||x' - x||).
\]

By abuse of notation, we will often drop the tilde in the RHS of the last relation.
3.3.2 A general relation between pair correlation functions

Let \((\upsilon, \phi, \psi)\) be three jointly stationary point processes such that \(\upsilon = \phi + \psi\). Let \(\lambda, \mu\) be the intensities of \(\phi\) and \(\psi\), respectively. Let \(p = \lambda / (\lambda + \mu)\). Then, for all \(r\),

\[
(1 - p)^2 \xi^{(2)}_{\psi, \psi}(r) + p^2 \xi^{(2)}_{\phi, \phi}(r) + 2p(1 - p) \xi^{(2)}_{\psi, \phi}(r) = \xi^{(2)}_{\upsilon, \upsilon}(r). \tag{4}
\]

where the RHS will depend on the fact that \(\upsilon\) is, e.g., a clustered or a repulsive point process. If \(\phi + \psi\) forms a Poisson point process, then

\[
(1 - p)^2 \xi^{(2)}_{\psi, \psi}(r) + p^2 \xi^{(2)}_{\phi, \phi}(r) + 2p(1 - p) \xi^{(2)}_{\psi, \phi}(r) = 1. \tag{5}
\]

Throughout the paper, we use the simplified notation \(\xi_{\psi, \psi}(r)\) in place of \(\xi^{(2)}_{\psi, \psi}(r)\) for the cross-pair correlation function of \((\phi, \psi)\).

3.4 Reformulation of RCP in terms of moment measures

It is possible to represent the Palm expectation used above in terms of moment measures. We have

\[
\mathbb{E}^0_{\psi} [I_{\Phi(0)}] = \lambda p \int_{\mathbb{R}^2} f(x) \xi_{\phi, \psi}(x) dx.
\]

So (1) can be rephrased in terms of the following integral equation:

\[
\beta = (1 - p)\lambda \int_{\mathbb{R}^2} \xi_{\psi, \phi}(x) f(||x||) dx. \tag{6}
\]

If the cross-pair correlation function \(\xi_{\psi, \phi}(\cdot)\) is constant equal to 1, which is the case when \(\Phi\) and \(\Psi\) are independent (possibly in the infinite velocity case), then this boils down to

\[
\beta = \alpha(1 - p)\mu, \tag{7}
\]

that is

\[
p = 1 - \frac{\beta}{\alpha\mu}, \tag{8}
\]

assuming that \(\frac{\beta}{\alpha\mu} < 1\). In other words, if there exists a non-degenerate stationary regime with \(\Phi\) and \(\Psi\) independent, then this achieves the upper bound in (3). We conjecture that this regime is achieved in the high velocity case provided \(\alpha\mu > \beta\), which is backed by simulations.
Let us come back to the general case for $\xi/\Psi_1/\Phi_1$. If we take the special case discussed above for $f$, we get

$$\beta = (1 - p)\lambda \alpha \int_{B(0,a)} \xi/\Psi_1/\Phi_1(x)dx.$$ 

Repulsion between $\Phi$ and $\Psi$ implies that

$$\int_{B(0,a)} \xi/\Psi_1/\Phi_1(x)dx \leq \pi a^2.$$ 

So for fixed $a$, $\alpha$, $\beta$, $\lambda$, any model with repulsion requires a smaller $p$ than the infinite velocity (or fast motion mean-field) model, which is in line with the bound in (3).

One can use isotropy to write (6) as

$$\lambda p \beta = \lambda (1 - p)\lambda p 2\pi \int_{\mathbb{R}^+} \xi/\Psi_1/\Phi_1(r)f(r)rdr. \quad (9)$$

Note the abuse of notation: we used the same notation as above for the cross-pair correlation functions in polar coordinates.

### 3.5 Higher moment rate conservation principle

The far random waypoint model features a mix of zero velocity and far away motion. Each point has an independent exponential clock with rate $\gamma$. When its clock ticks, the point jumps very far away. Arrivals are hence according to a Poisson rain (in space-time) with intensity $\lambda \gamma$ for type $I$ and an independent Poisson rain of intensity $\lambda (1 - p)$ for type $S$.

We recall the structural results listed in Sect. 2: assume all parameters fixed except $\beta$. There exists $\beta_c$ such that for $\beta > \beta_c$, the epidemic dies out for sure (or equivalently the maximal invariant measure is the zero measure), whereas for $\beta > \beta_c$ the epidemic might survive (or equivalently the maximal invariant measure is a positive measure).

Note that we do not know whether there exists a similar threshold on the parameter $\gamma$. At first glance, motion seems instrumental in the propagation of the epidemic by bringing infected points from far away. However, motion may also dissolve dense clusters where the epidemic survives for an arbitrarily long time. This is an important mathematical question, to which the tentative phase diagram obtained in this section gives a somewhat unexpected answer: in the proposed setting, motion is not always favoring the survival of the epidemic.

#### 3.5.1 RCP for second moment measures

One can see the LHS of the first moment RCP equation (1) as the “mass birth rate” of $\rho_\Psi^{(1)}$ (or equivalently the mass death rate of $\rho_\Phi^{(1)}$) and the RHS as the “mass death rate” of $\rho_\Psi^{(1)}$ (or equivalently the mass birth rate of $\rho_\Phi^{(1)}$). We see that this conservation law on the first moment measure involves a second moment measure.
One can think in the same terms for second moment measures. Let \( \mu(\Phi)^{0,r}_{\psi,\Phi}(x) \) denote the conditional density of \( \Phi \) at \( x \) given that \( \Psi \) has a point at \((0, 0)\) and \( \Phi \) a point at \((r, 0)\). Let also \( \mu(\Phi)^{0,r}_{\psi,\Phi}(x) \) denote the conditional density of \( \Phi \) at \( x \) given that \( \Psi \) has a point at \((0, 0)\) and a point at \((r, 0)\). The main result of this section is

**Theorem 3** Under the far random waypoint mobility model with jump rate \( \gamma \), if there exists a stationary regime, then the stationary pair correlation functions satisfy the following system of integral equations:

\[
\begin{align*}
p \xi_{\Phi, \Phi}(r)(\beta + \gamma) &= p \gamma + (1 - p) \xi_{\psi, \Phi}(r) \left( f(r) + \int_{\mathbb{R}^2} \mu(\Phi)^{0,r}_{\psi,\Phi}(x) f(||x||)dx \right) \\
p \xi_{\psi, \Phi}(r) \beta + (1 - p) \gamma &= (1 - p) \xi_{\psi, \psi}(r) \left( \gamma + \int_{\mathbb{R}^2} \mu(\Phi)^{0,r}_{\psi,\psi}(x) f(||x||)dx \right) \\
\beta &= \lambda (1 - p) 2\pi \int_{\mathbb{R}^+} \xi_{\psi, \Phi}(r) f(r) r dr \\
1 &= (1 - p)^2 \xi_{\psi, \psi}(r) + p^2 \xi_{\Phi, \psi}(r) - 2p(1 - p) \xi_{\psi, \Phi}(r).
\end{align*}
\]

(10)

**Proof** The last equation comes from the fact that \( \Xi_t \) is Poisson. Here is a sketch of the proof for the other equations. The “mass birth rate” in \( \rho^{(2)}_{\psi, \Phi}(r) \) is

\[
2\lambda p \lambda \rho \gamma + 2 \rho^{(2)}_{\psi, \Phi}(r) \left( f(r) + \int_{\mathbb{R}^2} \mu(\Phi)^{0,r}_{\psi,\Phi}(x) f(||x||)dx, \right)
\]

where we used the fact that arrivals of infected points are Poisson of intensity \( \lambda \gamma p \) (see the end of Sect. 2), and the “mass death rate” in \( \rho^{(2)}_{\psi, \Phi}(r) \) is \( 2 \rho^{(2)}_{\psi, \Phi}(r)(\beta + \gamma) \). The 2 comes from the fact that the recovery of motion of a point of \( \Phi \) deletes two infected points at a distance \( r \) of each other. The “mass death rate” in \( \rho^{(2)}_{\psi, \psi}(r) \) is

\[
p^2 \xi_{\Phi, \Phi}(r)(\beta + \gamma) \\
= p^2 \gamma + p(1 - p) \xi_{\psi, \Phi}(r) \left( f(r) + \int_{\mathbb{R}^2} \mu(\Phi)^{0,r}_{\psi,\Phi}(x) f(||x||)dx \right).
\]

(11)

Similarly, the “mass birth rate” in \( \rho^{(2)}_{\psi, \psi}(r) \) is

\[
2\rho^{(2)}_{\psi, \Phi}(r) \beta + 2\lambda^2 (1 - p)^2 \gamma,
\]

and the “mass death rate” in \( \rho^{(2)}_{\psi, \psi}(r) \) is

\[
2 \rho^{(2)}_{\psi, \psi}(r) \left( \gamma + \int_{\mathbb{R}^2} \mu(\Phi)^{0,r}_{\psi,\psi}(x) f(||x||)dx \right).
\]
Hence
\[ p(1 - p)\xi_{\psi, \Phi}(r)\beta + (1 - p)^2\gamma = (1 - p)^2\xi_{\psi, \Phi}(r) \left( \gamma + \int_{\mathbb{R}^2} \mu(\Phi)^0_r(\mathbf{x}) f(||\mathbf{x}||) d\mathbf{x} \right). \]
\[ (12) \]

If \( \xi \equiv 1 \), this leads to (7).

Assume that when \( \gamma \rightarrow \infty \), there is a finite limit for each \( \xi \) function. Then (11) implies that, when \( \gamma \) tends to infinity, \( \xi_{\psi, \Phi}(r) \) tends to 1 for all \( r \). By the same argument used on (12), one gets that, when \( \gamma \) tends to infinity, \( \xi_{\psi, \Phi}(r) \) tends to 1 for all \( r \). Hence, from (5), \( \xi_{\psi, \Phi}(r) \) tends to 1 for all \( r \) as well. But we know that for such pair correlation functions, the relation (7), \( \beta = (1 - p)\alpha\mu \), holds. In this sense, the last equations give the desired continuum between the no velocity and the high velocity cases.

### 3.5.2 RCP for higher order moment measures

The last theorem provides a conservation law on second moment measures which involves third moment measures. One can go along the path that would now consist in writing down a conservation law for third moment measures which will involve moment measures of order four and so on. This infinite hierarchy of integral equations (which was discussed in a different context in Baccelli et al. (2017)) should characterize the dynamics in an exact way. We will not pursue this line of thoughts here. We will rather follow a more computational path which consists in introducing various factorization heuristics for third moment measures which are introduced and analyzed below.

### 4 Heuristic analysis

We will see below that each factorization leads to a system of integral and polynomial equations jointly satisfied by the first and second order moment measures, which in turn provide computational approximations for these measures. Before introducing these factorizations, let us describe what they bring in the two next subsections.

#### 4.1 Prediction of the stationary fraction of infected points

Assume one wants to predict the fraction \( p \) of points that are infected in the steady state when there is survival, for a given set of parameters \((\alpha, \beta, \gamma, \mu)\).

Let us illustrate through one example among several others discussed below how to use some polynomial heuristic to do this. Let \( w \) be the value of the cross-pair correlation function at distance zero of the infected and susceptible point processes. The intuitive meaning of \( w \) is as follows: given that there is a susceptible point at the origin, the intensity of infected points in the near vicinity of the origin (near is understood w.r.t. \( a \)) is not \( \lambda p \) as it would be if there was no probabilistic dependence between infected and susceptible, but \( \lambda p w \) with \( w < 1 \). Then, we show that for each
one of the heuristic factorizations in question, the unknown variable $w$ satisfies some explicit polynomial equation that practically allow one to characterize $w$ and $p$ in closed form. For instance, for a certain factorization based on Bayes’ rule (see Sect. 4.4.1 below), $w$ is a positive number satisfying

$$
(2\gamma + \beta)((\alpha \mu w - \beta + 2\gamma)(w^2 \alpha^2 \mu^2 - 2\beta(\alpha \mu w - \beta)w) + w(\alpha \mu w - \beta)\beta^2 - 2\gamma \beta^2) = (\alpha \mu w - \beta)(\alpha \mu w - \beta + 2\gamma)(2\gamma(\alpha \mu w - \beta) + 2\alpha \beta w + \beta w(\alpha \mu w - \beta)),\quad (13)
$$

where $\gamma$ is the motion rate, $\beta$ the recovery rate, $\alpha$ the infection rate, and $\mu = \lambda \pi a^2$, with $\lambda$ the spatial intensity of the Poisson point process and $a$ is the infection radius. Once $w$ is determined through this polynomial equation, $p$ is then obtained through the formula

$$
p = 1 - \frac{\beta}{\alpha \mu w}. \quad (14)
$$

Discrete event simulation of the dynamics over large tori shows that the solution of this polynomial equation allows one to accurately predict the fraction of infected points as announced. Each factorization gives slightly different numerical results, as is natural for different heuristics, but always in line with the simulation results.

4.2 Prediction of criticality parameters and tentative phase diagram

As we shall see below, each of these polynomial equations also leads to a phase diagram determining the regions of the parameter space where there is survival or extinction. The boundaries between these regions are characterized by stating that $p = 0$ in the polynomial system. The rationale is as follows. Consider a region $P$ of the parameter space where $p > 0$ and another region $Q$ where $p = 0$. Assume that the boundary between these two regions forms a smooth curve $C$. The rationale is that when moving in $Q$ towards $C$, the value of $p$ should tend to 0. This continuity property is not granted for all phase transitions. In the present situation, this assumption is substantiated by simulations (see Table 11 for an example). This leads to further polynomial relations between the $(\alpha, \beta, \gamma, \mu)$ parameters which determine the boundaries between the regions where $p = 0$ and $p > 0$. The general shape of the resulting phase diagram is depicted in Fig. 1. The precise definitions of the boundaries between the regions again slightly vary depending on the chosen heuristic. The general structure is nevertheless common to all the considered heuristics.

Since this phase diagram is based on the polynomial heuristics, it is itself a heuristic. Its qualitative validity could not be proved within the framework of this paper. We explain in Sect. 4.8.3 how it can be partially substantiated by simulation on large tori. In particular, it is shown that, on any large torus, when picking a $\mu$ and a $\beta$ in the unsafe motion-insensitive region, the mean time to extinction sharply increases with motion rate in the vicinity of $\gamma^-_c$ and sharply decreases with this rate in the vicinity of $\gamma^+_c$. These monotonicity properties can be substantiated by simulation using confidence intervals on this mean time to extinction. In addition to partially substantiating the phase diagram (which deals with epidemics living on the infinite...
plane), these simulation results also show that the phase diagram accurately predicts the trends of the survival time of the epidemic when it lives on a large finite torus.

4.3 Heuristic factorizations of third moment measures

The announced heuristics are of two types: either based on Bayes’ formula and a conditional independence approximation, or based on a simple form of conditional dependence.

4.3.1 Heuristics based on Bayes’ formula and conditional independence

Below, we describe various heuristics which are all based on a conditional independence approximation and can be summarized as follows: the \( \mu \) densities, defined in relation with Theorem 3, are conditional densities of infected points at \( x \in \mathbb{R}^2 \) given the two events, e.g. that there is a susceptible point at \( 0 = (0, 0) \) and another susceptible point at \( r := (r, 0) \). We use Bayes’ formula to represent this in terms of the conditional probability that there is a susceptible point at \( 0 \) and another susceptible point at \( r \) given there is an infected point at \( x \). We then use the conditional independence approximation to represent the latter in terms of a product of pair correlation functions.

Consider first \( \mu(\Phi)^0_{\Psi,\Psi}(x) \), which we recall to be the conditional density of \( \Phi \) at \( x \) under the two point Palm probability of \( \Psi \) at \( (0, 0) \) and \( (0, r) \). Denote by \( \mu(\Psi, \Phi)^0_{\Psi}((0, x)) \) the joint density of \( (\Psi, \Phi) \) at \( (0, x) \) under the Palm of \( \Psi \) at \( r \) and use a similar notation for \( \mu(\Psi, \Phi)^0_{\Psi}(r, x) \) and \( \mu(\Psi, \Psi)^0_{\Psi}(0, r) \). The third moment density of \( (\Psi, \Psi, \Phi) \) at \( (0, r, x) \) is

\[
\mu(\Phi)^0_{\Psi,\Psi}(x) \xi_{\Psi,\Psi}(r) \lambda^2 (1 - p)^2
\]

and we have the following conditional representations of the latter:

\[
\mu(\Phi)^0_{\Psi,\Psi}(x) \xi_{\Psi,\Psi}(r) \lambda^2 (1 - p)^2 = \mu(\Psi, \Psi)^0_{\Psi}(0, r) \lambda p
\]

\[
= \mu(\Psi, \Phi)^0_{\Psi}(0, x) \lambda (1 - p)
\]

\[
= \mu(\Psi, \Phi)^0_{\Psi}(r, x) \lambda (1 - p),
\]

which is in essence Bayes’ rule rewritten in three different ways.

For three jointly stationary point processes \( \pi, \phi, \) and \( \psi \), let \( \rho^{(3)}_{\phi,\psi,\pi}(x, y, z) \) denote the the third moment density of \( (\phi, \psi, \pi) \) at \( (x, y, z) \). The use of Bayes’ rule is heuristically justified when interpreting

\[
\rho^{(3)}_{\phi,\psi,\pi}(x, y, z) \Delta x \Delta y \Delta z
\]

as the probability that \( \phi \) has one point in a small neighborhood of \( x \) of volume \( \Delta x \), \( \psi \) has one point in a small neighborhood of \( y \) of volume \( \Delta y \), and \( \pi \) has one point in a small neighborhood of \( z \) of volume \( \Delta z \).
So for all positive integers \( k \) and \( l \),

\[
\left( \mu(\Phi)_{\Psi, \Psi}(x)\xi_{\Psi, \Psi}(r)\lambda^2(1 - p)^2 \right)^{k+2l}
\]

\[
= (\mu(\Psi, \Phi)_{\Phi, \Phi}(0, r)\lambda p)^k (\mu(\Psi, \Phi)_{\Phi, \Phi}(0, x)\lambda)(1 - p)^l
\]

\[
= (\xi_{\Psi, \Psi}(||x||)\lambda(1 - p)\xi_{\Psi, \Phi}(||x - r||)\lambda(1 - p)\lambda p)^k
\]

\[
(\xi_{\Psi, \Psi}(r)\lambda(1 - p)\xi_{\Psi, \Phi}(||x - r||)\lambda p\lambda(1 - p))^l
\]

\[
(\xi_{\Psi, \Psi}(r)\lambda(1 - p)\xi_{\Psi, \Phi}(||x||)\lambda p\lambda(1 - p))^l
\]

where the last relation follows from the conditional independence heuristic. The meaning of \( k \) and \( l \), which will be used for the classification below, is the following: a bigger \( k \) puts in some sense more emphasis on the positive correlation structure. It follows that

\[
\mu(\Phi)_{\Psi, \Psi}(x) = \lambda p\xi_{\Psi, \Phi}(||x||)^{k+2l} \xi_{\Psi, \Phi}(||x - r||)^{k+2l} \xi_{\Psi, \Psi}(r)^{-k+2l}.
\]

Similarly

\[
\left( \mu(\Phi)_{\Phi, \Phi}(x)\xi_{\Phi, \Phi}(r)\lambda^2(1 - p)^2 \right)^{k+2l}
\]

\[
= (\mu(\Psi, \Phi)_{\Phi, \Phi}(0, r)\lambda p)^l (\mu(\Psi, \Phi)_{\Phi, \Phi}(0, x)\lambda)(1 - p)^l
\]

\[
= (\xi_{\Psi, \Phi}(||x||)\lambda(1 - p)\xi_{\Phi, \Phi}(||x - r||)\lambda p\lambda p)^l
\]

\[
(\xi_{\Psi, \Phi}(r)\lambda(1 - p)\xi_{\Phi, \Phi}(||x - r||)\lambda p\lambda p)^l
\]

\[
(\xi_{\Psi, \Phi}(r)\lambda p\xi_{\Phi, \Phi}(||x||)\lambda p\lambda(1 - p))^l
\]

Hence

\[
\mu(\Phi)_{\Phi, \Phi}(x) = \lambda p\xi_{\Phi, \Phi}(||x||)^{k+2l} \xi_{\Phi, \Phi}(||x - r||)^{2l} \xi_{\Psi, \Phi}(r)^{-l}.
\]

### 4.3.2 Heuristics based on mean values

Consider first \( \mu(\Phi)_{\Psi, \Psi}(x) \), which we recall to be the conditional density of \( \Phi \) at \( x \) under the two point Palm probability of \( \Psi \) at \( (0, 0) \) and \( \Phi \) at \( (0, r) \). Heuristically this, multiplied by \( \Delta x \), is the probability of of event \( A \) that there is a point in a region of small volume \( \Delta x \) around \( x \) given two events \( B \) and \( C \), that is \( P(A \mid B \cap C) \). The only data we have are \( P(A \mid B) \) and \( P(A \mid C) \). A natural heuristic is the geometric mean

\[
P(A \mid B \cap C) \sim \sqrt{P(A \mid B)P(A \mid C)}.
\]

A more general heuristic is

\[
P(A \mid B \cap C) \sim P(A \mid B)^\eta P(A \mid C)^{1-\eta},
\]
with $0 \leq \eta \leq 1$. One can also consider the arithmetic mean

$$ P(A \mid B \cap C) \sim \frac{P(A \mid B) + P(A \mid C)}{2}. $$

A more general heuristic is

$$ P(A \mid B \cap C) \sim P(A \mid B)\eta + P(A \mid C)(1 - \eta), $$

with $0 \leq \eta \leq 1$. The geometric mean leads to

$$ \mu(\Phi)_{\psi,\psi}^0(x) = \lambda p \xi_{\psi,\Phi}(||x||) \eta \xi_{\psi,\phi}(||x - r||)^{1-\eta} \quad (17) $$

and

$$ \mu(\Phi)_{\psi,\phi}^0(x) = \lambda p \xi_{\psi,\Phi}(||x||) \eta \xi_{\phi,\phi}(||x - r||)^{1-\eta}. \quad (18) $$

Note that a bigger $\eta$ puts more emphasis on the positive correlation. The arithmetic mean leads to

$$ \mu(\Phi)_{\psi,\psi}^0(x) = \lambda p \left( \eta \xi_{\psi,\Phi}(||x||) + (1 - \eta) \xi_{\psi,\phi}(||x - r||) \right) \quad (19) $$

and

$$ \mu(\Phi)_{\psi,\phi}^0(x) = \lambda p \left( \eta \xi_{\psi,\Phi}(||x||) + (1 - \eta) \xi_{\phi,\phi}(||x - r||) \right). \quad (20) $$

Here, a bigger $\eta$ puts more emphasis on the negative correlation.

### 4.3.3 Combining and classifying heuristics

These two broad type of heuristics admit several variants and combinations. For instance, the variants of Bayes’ heuristic are obtained by varying $k$ and $l$ in (16) and those based on mean values are obtained by choosing either a geometric or an arithmetic mean and by varying the parameter $\eta$ in (17)–(20). An example of combination is that where in the Bayes’ approach, one replaces the conditional independence step by the mean value heuristic. Mixtures of heuristics can also be used, for example by averaging two Bayes’ heuristics - we will see one such heuristic (named M2BI), below. We defer the full classification and naming of these heuristics to Appendix D in Baccelli and Ramesan (2020).

### 4.4 Terminology for functional and polynomial equations

**Integral Equations** When plugging any of the heuristics into the equations of (10), we get a system of integral equations, which will be referred to as the pairwise-interaction second moment measure functional equations.
**Polynomial Equations** Each of these functional equations in turn leads to polynomial equations satisfied by the value of the pair correlation functions close to zero. These will be referred to as the *pairwise-interaction second moment measure polynomial equations*. There is a functional and a polynomial equation for each heuristic of the classification. The setting for polynomial equations is as follows: it considers the special case with \( f(r) = \alpha_1 r < a \) and (with \( \mu = \lambda \pi a^2 \)), it assumes that \( \mu w > \beta \) and that

- \( \xi_{\psi, \phi}(.) \) is almost constant on \((0, a)\) and equal to \( w^1 \);
- \( \xi_{\phi, \phi}(.) \) is almost constant on \((0, a)\) and equal to \( v \).
- \( \xi_{\psi, \psi}(.) \) is almost constant on \((0, a)\) and equal to \( z \).

For numerical justifications of this heuristic, see Fig. 2 below.

The polynomial equations will be in the three variables \( v, w, z \). Note that (6) then reads

\[
\beta = \alpha \lambda (1 - p) \pi a^2 w = (1 - p) \alpha \mu w. \tag{21}
\]

So if there exists a stationary regime, with flat enough pair correlation functions in the said range, then necessarily the variables \( p, v, z \) and \( w \) will satisfy the announced ‘polynomial’ equation. Note that this is *not* sufficient for the functional equation to have a non-degenerate solution. We now provide and subsequently use two examples of heuristics: named M2BI (for Mixtures of 2 types of Bayes-Independent) and B1I (a Bayes-Independent heuristic) to see how the associated sets of functional equations yield polynomial equations and hence tentative phase diagrams. The other heuristics (B1G1, M\(\infty\)BI, M\(\infty\)B1G1, etc.) are listed and discussed in Appendix D.2 of Baccelli and Ramesan (2020).

**Terminology** Below and in Appendix D.2 of Baccelli and Ramesan (2020) we use the following code: \( f \) for functional and \( p \) for polynomial. For instance \( f\text{-b1i} \) means the functional equation associated to the B1I heuristic which is described below, \( p\text{-m}\infty\text{b1g1} \) means the polynomial equation of the M\(\infty\)B1G1 heuristic, etc.

### 4.4.1 Heuristic M2BI

This heuristic is obtained by mixing two Bayes-Independent heuristics (obtained by setting \( k = \infty \) and \( l = \infty \) respectively in (15), (16)), by taking their mean, to get:

\[
\mu(\Phi)^{0, r}_{\psi, \phi}(x) = \frac{\lambda p \xi_{\psi, \phi}(|x|) \xi_{\psi, \phi}(|x - r|)}{2 \xi_{\psi, \psi}(r)} + \frac{\lambda p \xi_{\psi, \phi}(|x|) \xi_{\psi, \phi}(|x - r|)}{2 \xi_{\phi, \phi}(|x|) \xi_{\psi, \psi}(r)} \tag{22}
\]

and

\[
\mu(\Phi)^{0, r}_{\psi, \phi}(x) = \frac{\lambda p \xi_{\psi, \phi}(|x|)}{2 \xi_{\psi, \psi}(r)} + \frac{\lambda p \xi_{\psi, \phi}(|x|) \xi_{\phi, \phi}(|x - r|)}{2 \xi_{\psi, \psi}(r) \xi_{\phi, \phi}(|x - r|)} \tag{23}
\]

---

1 Assuming that \( w < 1 \) is equivalent to what we called cluster or second repulsion above; more general assumptions should be considered in the no-motion case.
**Functional equation** Under Heuristic M2BI, the version of (10) is

\[(\beta + \gamma) p \xi_{\Phi, \Phi}(r) = p \gamma + (1 - p) \xi_{\Psi, \Phi}(r) f(r) + \frac{\lambda}{2} (1 - p) p \xi_{\Psi, \Phi}(r) \int_{\mathbb{R}^2} \xi_{\Psi, \Phi}(|\mathbf{x}|) f(|\mathbf{x}|) dx + \frac{\lambda}{2} (1 - p) p \xi_{\Psi, \Phi}(r) \frac{1}{2} \int_{\mathbb{R}^2} \xi_{\Psi, \Phi}(|\mathbf{x}|) \xi_{\Phi, \Phi}(||\mathbf{x} - \mathbf{r}||) f(||\mathbf{x}||) dx,\]

\[\beta p \xi_{\Psi, \Phi}(r) = (1 - p) \gamma \left( \xi_{\Psi, \Phi}(r) - 1 \right) + \frac{\lambda}{2} (1 - p) p \int_{\mathbb{R}^2} \xi_{\Psi, \Phi}(|\mathbf{x}|) \xi_{\Psi, \Phi}(||\mathbf{x} - \mathbf{r}||) f(||\mathbf{x}||) dx + \frac{\lambda}{2} (1 - p) p \xi_{\Psi, \Phi}(r) \int_{\mathbb{R}^2} \xi_{\Psi, \Phi}(|\mathbf{x}|) \xi_{\Phi, \Phi}(||\mathbf{x} - \mathbf{r}||) f(||\mathbf{x}||) dx.\]  

(24)

This should again be complemented by

\[p = 1 - \frac{\beta}{\lambda 2\pi \int_{\mathbb{R}^+} \xi_{\Psi, \Phi}(r) f(r) r dr},\]  

(25)

and

\[\xi_{\Psi, \Phi}(r) = \frac{1}{(1 - p)^2} \left( 1 - (p)^2 \xi_{\Phi, \Phi}(r) - 2 p (1 - p) \xi_{\Psi, \Phi}(r) \right).\]  

(26)

**Polynomial equation** The associated polynomial equations read

\[(2 \gamma + \beta) p v = 2 \gamma p + 2 \alpha (1 - p) w + \beta p w \]
\[\beta p w = (1 - p) \gamma (z - 1) + \frac{1}{2} \beta p w + \frac{1}{2} \beta p z \]
\[\beta = (1 - p) \alpha \mu w \]
\[1 = (1 - p)^2 z + 2 p (1 - p) w + p^2 v.\]  

(27)

Using the last and the second equations, we can eliminate \(z\) to get

\[\beta p (1 - p)^2 w = (1 - 2 p (1 - p) w - p^2 v) (2 \gamma (1 - p) + \beta p) - 2 \gamma (1 - p)^3.\]  

(28)
This in turn gives

\[(2\gamma + \beta)v(\alpha \mu w - \beta) = 2\gamma(\alpha \mu w - \beta) + 2\alpha \beta w + \beta w(\alpha \mu w - \beta)
\]

\[w(\alpha \mu w - \beta)\beta^2 = -2\gamma^2 \beta^2 + (\alpha \mu w - \beta + 2\gamma)(w^2\alpha^2\mu^2 - (\alpha \mu w - \beta)^2 v - 2\beta(\alpha \mu w - \beta)w).
\]

When now eliminating \(v\) in the last system, we get that \(w\) satisfies the degree 4 equation:

\[(2\gamma + \beta)((\alpha \mu w - \beta + 2\gamma)(w^2\alpha^2\mu^2 - 2\beta(\alpha \mu w - \beta)w) + w(\alpha \mu w - \beta)\beta^2 - 2\gamma\beta^2) = (\alpha \mu w - \beta)(\alpha \mu w - \beta + 2\gamma)(2\gamma(\alpha \mu w - \beta) + 2\alpha \beta w + \beta w(\alpha \mu w - \beta)). \tag{29}\]

### 4.4.2 Heuristic B1I

We arrive at this heuristic by setting \(l = k = 1\) in (15), (16) to get:

\[\mu(\Phi)^{0,r}_{\psi,\psi}(x) = \lambda p \xi_{\psi,\Phi}(||x||)^{\frac{2}{3}} \xi_{\psi,\Phi}(||x - r||)^{\frac{2}{3}} \frac{1}{\xi_{\psi,\Phi}(r)^{\frac{1}{3}}} \tag{30}\]

and

\[\mu(\Phi)^{0,r}_{\psi,\Phi}(x) = \lambda p \xi_{\psi,\Phi}(||x||)^{\frac{2}{3}} \xi_{\Phi,\Phi}(||x - r||)^{\frac{2}{3}} \frac{1}{\xi_{\Phi,\Phi}(r)^{\frac{1}{3}}}. \tag{31}\]

We then proceed exactly as we did in Sect. 4.4.1 to arrive at polynomial equations for the B1I heuristic that are as follows:

\[(\gamma + \beta)pv = \gamma p + \alpha(1 - p)w + \beta pw^\frac{2}{3}w^\frac{1}{3}
\]

\[\beta pw = (1 - p)\gamma(z - 1) + \beta p z^\frac{2}{3}w^\frac{1}{3}
\]

\[\beta = (1 - p)\alpha \mu w
\]

\[1 = (1 - p)^2z + 2p(1 - p)w + p^2v. \tag{32}\]

### 4.5 Numerical estimates of the fraction of infected points

In this section, we compare the fraction of infected points as estimated by our integral and polynomial systems and as obtained by discrete event simulation. For the latter, the system evolves on a square with edges wrapped around to form a torus so as to avoid border effects. Points move according to the mobility model defined above. The infection function is \(f(r) = \alpha 1_{r < a}\).

Tables 1, 2, and 3 study the effect of mobility for a variety of scenarios.

Instances of pair correlation functions obtained from the functional equation numerical scheme associated with Heuristic f-mb2i are given in Fig. 2. All numerical
solutions of integral equations lead to similar pictures, which justifies the polynomial heuristics.

We now briefly define a concept relevant to the subsequent sections. Boolean percolation is defined as the existence of an infinite connected component of the random graph that the epidemic evolves on. A well-known result for random geometric graphs states that such a component exists if and only if $\mu = \lambda \pi a^2 > \mu_*$, and the approxi-

Table 1  Effect of mobility. Way above Boolean-percolation. Fraction of infected points ($p$) obtained by simulation, the functional fixed point equation and the polynomial equation. This is for $\beta = 8$, $a = 2$, $\lambda = 1$ and $\alpha = 1$, so that $\mu \sim 12.56$. The agreement with simulation is good. Both $b_1$ and $m_2 b_i$ slightly overestimate $p$, with $b_1$ being here a bit closer than the others

| $\gamma$ | 0  | 0.2 | 1  | 5  | $\infty$ |
|----------|----|-----|----|----|---------|
| $p_{\text{sim}}$ | 0.26 | 0.28 | 0.29 | 0.33 | 0.36 |
| $p_{p-b_1i}$ | 0.313 | 0.315 | 0.323 | 0.341 | 0.363 |
| $p_{p-b_{1g1}}$ | 0.325 | 0.326 | 0.331 | 0.343 | 0.363 |
| $p_{p-m_2bi}$ | 0.328 | 0.328 | 0.329 | 0.341 | 0.363 |
| $p_{p-m_\infty bi}$ | 0.33 | 0.33 | 0.33 | 0.34 | 0.36 |
| $p_{p-h_0}$ | 0.23 | 0.28 | 0.29 | 0.32 | 0.36 |
| $p_{p-h_0}$ | 0.23 | 0.25 | 0.27 | 0.32 | 0.36 |

Table 2  Effect of mobility. Below Boolean percolation, medium recovery rate. Fraction of infected points ($p$) obtained by simulation, the functional fixed point equation and the polynomial equation. This is for $\beta = 2$, $a = 1$, $\lambda = 1$ and $\alpha = 1$, so that $\mu \sim 3.14$. Simulation is inefficient at low speeds. The agreement with simulation is again good when available. Both $b_1$ and $m_2 b_i$ slightly overestimate $p$ and provide similar results

| $\gamma$ | 0+ | 0.1 | 1 | 10 | $\infty$ |
|----------|----|-----|---|----|---------|
| $p_{\text{sim}}$ | 0.22 | 0.31 | 0.36 |
| $p_{p-b_1i}$ | 0.176 | 0.188 | 0.253 | 0.342 | 0.363 |
| $p_{p-b_{1g1}}$ | 0.205 | 0.213 | 0.264 | 0.348 | 0.363 |
| $p_{p-m_2bi}$ | 0.245 | 0.240 | 0.254 | 0.336 | 0.363 |
| $p_{p-m_\infty bi}$ | 0.26 | 0.26 | 0.27 | 0.34 | 0.36 |

Table 3  Effect of mobility. Below Boolean-percolation, low recovery rate. Fraction of infected points ($p$) obtained by simulation, the functional fixed point equation and the polynomial equation. This is for $\beta = 1$, $a = 1$, $\lambda = 1$ and $\alpha = 1$, so that $\mu \sim 3.14$. The agreement with simulation is again good when available and again provide similar results

| $\gamma$ | 0+ | 0.01 | 0.1 | 0.2 | 1 | 5 | 100 |
|----------|----|------|-----|-----|---|---|-----|
| $p_{\text{sim}}$ | | | | | | | |
| $p_{p-b_1i}$ | 0.478 | 0.503 | 0.523 | 0.599 | 0.657 | 0.68 |
| $p_{p-b_{1g1}}$ | 0.530 | 0.544 | 0.557 | 0.609 | 0.658 | 0.680 |
| $p_{p-m_2bi}$ | 0.523 | 0.538 | 0.551 | 0.605 | 0.656 | 0.680 |
| $p_{p-m_\infty bi}$ | 0.54 | 0.55 | 0.56 | 0.61 | 0.66 | 0.68 |
mate value of this percolation threshold is known to be $\mu_* \approx 4.512$ (Franceschetti and Meester 2007, chapter 2). Percolation is relevant for our discussions because, below percolation ($\mu < \mu_*$) and in the no-motion case ($\gamma = 0$), there is no steady-state where $p > 0$ - this is because the contact process a.s. dies out eventually on all finite connected graphs. Above percolation and in the no-motion case, however, there is a possibility of a non-degenerate steady state.

4.6 A tentative phase diagram

In this subsection, $\alpha$ is fixed (for instance taken equal to 1, without loss of generality). The polynomial systems described above lead to phase diagrams. The simplest instance is the $(\mu, \gamma)$-phase diagram, which is predicted by the monotonicity properties of the SIS dynamics: there exists a function $\beta_c = \beta_c(\mu, \gamma)$, which will be referred to as the extinction-survival critical recovery rate such that there is survival for all $\beta < \beta_c$ and extinction above. The main novelty here is an explicit expression for the function $\beta_c(\mu, \gamma)$, which is derived from the polynomial systems discussed above, and more precisely from the analysis of properties of the roots of these equations.

We will also discuss the $(\mu, \beta)$-phase diagram. This diagram is meant to investigate the influence of $\gamma$. The analysis of certain roots of our polynomial equations lead to the definition of a partition of the $(\mu, \beta)$ positive orthant in 3 disjoint regions:

- A safe region where the epidemic is always extinct regardless of the positive motion rate. This region is the wedge $\beta > \alpha \mu$.
- An unsafe region which is the geometric complement of the latter; in this region, there are motion rates such that the epidemic survives.

The unsafe region can in turn be partitioned into a motion-insensitive (UMI) and a motion-sensitive (UMS) region:

- In the UMI region, the epidemic always survives, regardless of the positive motion rate. This region is wedge-like too, of the form $\mu > \mu_0$, $\beta < \beta_0(\mu)$. Here $\mu_0$ is an absolute constant smaller than the percolation threshold $\mu_*$, and $\beta_0(\cdot)$ is a function to be specified, which will be referred to as the motion-sensitivity critical recovery rate.
  - In the part of the UMI region where $\mu < \mu_*$, the epidemic is extinct for 0 motion and survives for all non-zero motion rates.
In the part of the UMI region where $\mu > \mu_*$, the epidemic survives for all motion rates, including 0 motion.

- In the UMS region, the epidemic survives if motion is low or high enough. More precisely there exist functions $\gamma^+_{c}(\mu, \beta)$ (the upper extinction-survival critical motion rate) and $\gamma^-_{c}(\mu, \beta)$ (the lower extinction-survival critical motion rate), to be specified, such that there is survival if $\gamma < \gamma^-_{c}$ or $\gamma > \gamma^+_{c}$, and extinction otherwise. This region is a strip-like region of the form $\beta_0(\mu) < \beta < \alpha\mu$, with $\beta_0(\mu) = 0$ when $\mu < \mu_0$.

- In the part of the UMS region where $\mu < \mu_*$, the epidemic is extinct for 0 motion, survives for small enough motion rates, is extinct for intermediate motion rates, and survives for high enough motion rates.

- In the part of the UMS region above $\mu_*$, the epidemic survives for no and small enough motion rate, is extinct for intermediate motion rates, and survives for high enough motion rates.

This last phase diagram is depicted in Fig. 1.

As already mentioned, these phase diagrams are obtained when studying certain roots of the polynomial systems. The exact values of the constants and functions introduced above diagram depend on the heuristic, but the global picture is the same for all in spite of numerical discrepancies. The picture that emerges from this analysis is consistent for all heuristics and partially substantiated by simulation. Below, we first proceed with the analysis of the roots of the polynomial systems and then discuss the simulation validation.

### 4.7 Critical values of interest

It follows from the structural results of Sect. 2 that, for all $\gamma > 0$ and $\mu$, there is a critical value of $\beta$, a constant $\beta_c = \beta_c(\gamma, \mu)$ less than or equal to $\alpha\mu$, such that there is extinction (there is no positive invariant measure) if $\beta > \beta_c$ and survival (there is a positive invariant measure) if $\beta < \beta_c$.

In contrast, there is no mathematical argument showing the existence of a critical value $\gamma_c$ above which survival would hold and below which there would be extinction. In fact the analysis which follows suggests that this is not the case. However, when decreasing $\gamma$ from $\infty$ (where the epidemic should survives if $\mu\alpha > \beta$), if we are below Boolean percolation, there ought to be a $\gamma^+_{c}$ which is the largest $\gamma$ such that above this value the epidemic survives but not immediately below.

We now see through two examples how the polynomial heuristics can be used to derive the phase diagram and to estimate the critical values that form the boundaries between the regions of this phase diagram. The general idea is to leverage the fact substantiated by simulation that $p$ is continuous at the boundary of the regions of the phase diagram, that the density of the positive invariant maximal measure which exists in the survival region tends to 0 when getting close to the boundary between this region and the extinction region.
4.7.1 M2BI

\((\mu, \beta)\)-phase diagram A direct analysis of the roots of (27) around \(p \sim 0\) gives that \(p \sim 0\) is only possible if

\[
8(\mu\alpha - \beta)\gamma^2 + 2\beta(3(\mu\alpha - \beta) - 2\alpha)\gamma + \beta^2(\mu\alpha - \beta) = 0. \quad (33)
\]

This is easily obtained when showing that the first equation in (27) implies that

\[
v(p)p \to p \to 0 \frac{2\beta}{\mu(2\gamma + \beta)}
\]

and by using this fact in (28) when making an expansion in \(p\) close to 0.

When looking at (33) as a quadratic in \(\gamma\), we get that if there exists a positive (resp. negative) solution, then the other solution is positive (resp. negative). For real solutions to exist, it is necessary and sufficient to have either

\[
\mu\alpha - \beta \leq \frac{2\alpha}{3 + \sqrt{8}} \sim \alpha 0.343 \quad (34)
\]

or

\[
\mu\alpha - \beta \geq \frac{2\alpha}{3 - \sqrt{8}} \sim \alpha 11.65. \quad (35)
\]

This is easily obtained when studying the discriminant of (33). If these inequalities are not satisfied, then this discriminant is negative, so that there is no real valued \(\gamma\) solving (33). If (34) holds, then there are two positive roots. If (35) holds, then there are two negative roots, which for us is equivalent to no root.

Below, we focus on the region (34), which is the only one in which criticality is possible. Let

\[
\mu_0 = \alpha \eta := \alpha \frac{2}{3 + \sqrt{8}}. \quad (36)
\]

If \(\mu < \mu_0\), then (34) holds so that there exist two positive \(\gamma\) solving (33), say \(0 < \gamma^- < \gamma^+\).

If \(\mu > \mu_0\), then there exists a \(\beta_0(\mu, \alpha)\) defined by

\[
\beta_0 = \mu\alpha - \eta\alpha, \quad (37)
\]

such that if \(\beta < \beta_0\), then the quadratic equation (33) has no real root in \(\gamma\), which means that any positive motion results in survival,\(^2\) whereas if \(\beta > \beta_0\), then the roots \(0 < \gamma^- < \gamma^+\) exist. The upper phase transition w.r.t. \(\gamma\) takes place at \(\gamma^+_c\): Above

\(^2\) note that this is consistent with what we see in Tables 2 and 3, where the discrepancy between \(\mu\) and \(\beta/\alpha\) is above 0.343 and where the epidemics seems to persist for all \(\gamma > 0\).
\[ \gamma_c^+ \], there is survival, and below \( \gamma_c^+ \), there is extinction. Indeed, we conjecture that the system has a positive fraction of infected points for infinite \( \gamma \), and the threshold of interest is hence that obtained when decreasing \( \gamma \) from infinity and looking at the largest \( \gamma \) above which the epidemic survives. We have

\[
\gamma_c^+(\mu, \beta) = \beta \frac{2\alpha - 3(\mu\alpha - \beta) + \sqrt{(2\alpha - 3(\mu\alpha - \beta))^2 - 8(\mu\alpha - \beta)^2}}{8(\mu\alpha - \beta)} \tag{38}
\]

and

\[
\gamma_c^-(\mu, \beta) = \beta \frac{2\alpha - 3(\mu\alpha - \beta) - \sqrt{(2\alpha - 3(\mu\alpha - \beta))^2 - 8(\mu\alpha - \beta)^2}}{8(\mu\alpha - \beta)}. \tag{39}
\]

Since there is survival for \( \gamma > \gamma_c^+ \), it ought to be that for \( \gamma \in (\gamma_c^-, \gamma_c^+) \), there is extinction. By the same argument, for \( \gamma < \gamma_c^- \), there is survival.

Note that if \( \beta = \beta_0 \), then the corresponding value of \( \gamma_c^+ = \gamma_c^- \) is

\[
\gamma_0(\mu) = \frac{\beta_0(2\alpha - 3(\mu\alpha - \beta_0))}{8(\mu\alpha - \beta_0)} = \frac{(\mu\alpha - \eta\alpha)(2\alpha - 3\eta\alpha)}{8\eta\alpha} = \frac{\alpha(\mu - \eta)(2 - 3\eta)}{8\eta}. \tag{40}
\]

The last function is just an affine function in \( \mu \) with positive slope. It is strictly positive for \( \mu > \mu_0 \sim 0.343 \).

Hence we get the following m2bi \((\mu, \beta)\)-phase diagram:

**Result 4** Assume that \( \mu\alpha > \beta \).

- In the motion-subcritical regions, namely for all \( \mu < \mu_0 \), with \( \mu_0 \) given by (36), the system is motion-sensitive and there is survival for all values of \( \gamma \) larger \( \gamma_c^+ \) or smaller than \( \gamma_c^- \), and extinction for \( \gamma \) between these two values, with \( \gamma_c^+ \) and \( \gamma_c^- \) given by (38) and (39) respectively.

- In the motion-supercritical region, namely for all \( \mu > \mu_0 \),
  - if \( \beta < \beta_0 \), with \( \beta_0 \) defined in (37), the system is motion-insensitive in that there is survival for all positive values of \( \gamma \);
  - if \( \beta > \beta_0 \), then the system is motion sensitive.

Instances of the functions \( \beta \rightarrow \gamma_c^+(\mu, \beta) \) and \( \beta \rightarrow \gamma_c^- \) are depicted in Fig. 3.

\((\mu, \gamma)\)-phase diagram One can also use the same method to analyze the critical function \( \beta_c \). There are two ways of evaluating this quantity.

The first one is obtained from (33). The \( \beta_c \) function satisfies the following polynomial equation of degree 3 in \( \beta \):

\[
\beta^3 + \beta^2(6\gamma - \alpha\mu) + \beta 2\gamma(2\alpha - 3\mu\alpha + 4\gamma) - 8\mu\alpha\gamma^2 = 0. \tag{41}
\]

There is numerical evidence that this degree three equation has a single positive root that will be denoted \( \beta_c(\mu, \gamma) \).
Fig. 3 The p-m2bi $\beta \to \gamma^+(\mu, \beta)$ (green) and $\beta \to \gamma^- (\mu, \beta)$ (red) functions. The $x$-axis represents $\beta$. Left: $\alpha = 1$ and $\mu = 5 > \mu_0$; there is survival on the left of the curve and extinction on the right. If $\beta < \beta_0$, where $\beta_0$ is the largest $c$ such that the line $\beta = c$ does not intersect the $\gamma_c$ curves, the epidemic is motion-insensitive. Right: $\alpha = 1$ and $\mu = 25 < \mu_0$; there is survival above the green curve and below the red one. There is extinction between the two curves. There is no positive $\beta$ making the epidemic motion-insensitive. Notice that the $\gamma^-_c$ function is increasing for small $\beta$. It reaches a maximum and then decreases to 0 when $\beta$ is large.

Fig. 4 The p-m2bi $\gamma \to \beta_c(\mu, \gamma)$ function for $\alpha = 1$. On the $x$ axis, the variable is $\gamma$. Left: $\mu = 5$; there is extinction above the curve and survival below. Right: $\mu = 25$. The three roots are jointly represented. The interpretation of $\beta_c$ as the pseudo-inverse of $\gamma_c$ suggests that the $\beta_c$ function should be the upper envelope of these curves (this upper envelope is not depicted). To see this, use the fact that the function $\gamma^+_c$ is non-monotonic in this case. The discontinuity is at the point where $\gamma^-_c$ reaches its maximum.

The second approach consists in devising the local “inverse” of the $\beta \to \gamma_c(\beta)$ function discussed above. As illustrated by the left part of Fig. 3 for $\gamma$ small, the inverse function $\gamma \to \beta_c(\gamma)$ should be decreasing. It should then reach a minimum at $\gamma = \gamma_0$ and then increase to $\mu \alpha$ for $\gamma$ large. This is in line with what we see on Fig. 4. Hence we get the following p-m2bi $(\mu, \gamma)$-phase diagram:
Result 5 There is survival for all $\beta < \beta_c$ and extinction above with $\beta_c = \beta_c(\alpha, \mu, \gamma)$ solution of (41).

- If $\mu < \mu_0$, then the function $\gamma \rightarrow \beta_c(\alpha, \mu, \gamma)$ is discontinuous.
- If $\mu > \mu_0$, then the function $\gamma \rightarrow \beta_c(\alpha, \mu, \gamma)$ is continuous.

Instances of the function $\gamma \rightarrow \beta_c(\gamma)$ defined through (41) are plotted in Fig. 4 where we see that it is not monotonic in $\gamma$ in general.

4.7.2 B1I

$(\mu, \beta)$-phase diagram By an analysis of the polynomial system similar to that for m2bi above, we get that $p \sim 0$ is only possible if

$$2(\mu \alpha - \beta)\gamma^2 + (2\beta(\mu \alpha - \beta) + \beta^2(\rho - 1) - \beta \alpha)\gamma + \beta^3(\rho - 1) = 0, \quad (42)$$

with $\rho = \left(\frac{\alpha \mu}{\beta}\right)^2 > 1$. By looking at the discriminant of this quadratic, we get that a necessary (but not sufficient) condition for a positive real root to exists is that

$$\mu \alpha < \beta + 1 + \frac{\alpha}{2}. \quad \text{In words, } \mu \alpha \text{ has to be close enough to } \beta.$$

Here is a more precise analysis. There are two real roots (which are necessarily both positive) iff

$$\Delta := (2\beta(\mu \alpha - \beta) + \beta^2(\rho - 1) - \beta \alpha)^2 - 8(\mu \alpha - \beta)\beta^3(\rho - 1) > 0$$

and in this case,

$$\gamma_+^c(\mu, \beta) = \frac{\beta(\alpha - 2(\mu \alpha - \beta)) - \beta^2(\rho - 1) + \sqrt{\Delta}}{4(\mu \alpha - \beta)} \quad (43)$$

and

$$\gamma_-^c(\mu, \beta) = \frac{\beta(\alpha - 2(\mu \alpha - \beta)) - \beta^2(\rho - 1) - \sqrt{\Delta}}{4(\mu \alpha - \beta)}. \quad (44)$$

These two roots are plotted in Fig. 5.

For $\gamma > \gamma_+^c$ (in particular for $\gamma$ very large), there is survival. For $\gamma_-^c < \gamma < \gamma_+^c$, there is extinction, and when $0 < \gamma < \gamma_-^c$, there is survival again. We will give an interpretation of these phenomena below.

There exists a $\mu_0$ (for $\alpha = 1$, $\mu_0 \sim 0.263$ - for p-b1g1 0.306) such that (i) for $\mu < \mu_0$, and all $\beta < \alpha \mu$, $\Delta > 0$ and hence $\gamma_+^c$ and $\gamma_-^c$ exist, and (ii) for all values of $\mu > \mu_0$, there exists a minimal $\beta$, say $\beta_0 = \beta_0(\alpha \mu)$, for $\Delta$ to be positive and hence
Fig. 5  The p-bli functions $\beta \rightarrow \gamma_c^+(\mu, \beta)$ (in green) and $\beta \rightarrow \gamma_c^-(\mu, \beta)$ (in red) for $\alpha = 1$. Left: $\mu = 5$. Right: $\mu = .25$

Fig. 6  Left: The p-bli function $\mu \rightarrow \beta_0(\mu)$ for $\alpha = 1$. Right: The p-bli function $\gamma_0(\mu)$ for $\alpha = 1$

for non-degenerate $\gamma_c^+$ and $\gamma_c^-$ to exist. In the latter case, the function $\alpha \mu \rightarrow \beta_0(\alpha \mu)$ is solution of

$$
(2\beta(\mu \alpha - \beta) + Tr^{2}(\rho - 1) - Tr \alpha)^2 = 8(\mu \alpha - \beta)Tr^{3}(\rho - 1).
$$

The $\beta_0$ function is plotted in Fig. 6.

At $\beta_0$, $\gamma_c^+ = \gamma_c^- := \gamma_0$, with $\gamma_0$ strictly positive. The function $\gamma_0$ is $\gamma_c$ for $\beta = \beta_0$. It is plotted in Fig. 6.

We summarize this in the following p-bli $(\mu, \beta)$-phase diagram:

**Result 6** Assume that $\mu \alpha > \beta$. 

*: Springer*
In the motion-subcritical region $\mu < \mu_0$, the discriminant is positive and there is survival for values of $\gamma$ larger than $\gamma_c^+(\alpha \mu, \beta)$ given by (43) or smaller than $\gamma_c^-(\alpha \mu, \beta)$ and extinction for $\gamma$ between these two values.

In the motion-supercritical region $\mu > \mu_0$,

- If $\beta < \beta_0(\alpha \mu)$, with $\beta_0$ solution of (45), we have motion-insensitivity;
- If $\beta > \beta_0(\alpha \mu)$, then there motion sensitivity as above.

**Result 7** There is survival for all $\beta < \beta_c$ and extinction above with $\beta_c = \beta_c(\alpha, \mu, \gamma)$ solution of (42) which can be seen as a degree 9 polynomial in $\beta$.

This function is depicted in Fig. 7.

### 4.8 Simulation validation

#### 4.8.1 Stationary densities

This subsection gives simulation based fractions of infected points in various regions of the phase diagram and compares them to the polynomial solutions.

**Motion-insensitive, Boolean subcritical example** In this region, any positive motion instantly transforms the epidemic from extinct to surviving. This is illustrated by the results of Tables 4 and 5 (where simulation and second order heuristics concur).

**Motion-sensitive and Boolean-subcritical example** In this region, for $\gamma$ equal to 0, the epidemic dies out; for positive but small values of $\gamma$ (more precisely, for $0 < \gamma < \gamma_c^-$ with $\gamma_c^- > 0$), the epidemic survives; for intermediate values of $\gamma$ ($\gamma_c^- < \gamma < \gamma_c^+$), the epidemic is extinct; for $\gamma > \gamma_c^+$, the epidemic survives again. A
Table 4  Effect of mobility. Boolean-subcritical ($\mu = 3$), motion-supercritical ($\mu > \mu_0$), motion-insensitive ($\beta < \beta_0$) case. Fraction of infected points ($p$) obtained by simulation, the functional fixed point equation and the polynomial equation. This is for $\beta = 2$, $a = 1$, $\lambda \sim 0.955$ and $\alpha = 1$, so that $\mu = 3$. According to p-b1i, p-b1g1, and p-m2bi, the threshold $\gamma_c$ is equal to 0. This means that the epidemic survives for all positive speeds $\gamma$, in spite of the fact that it dies out for $\gamma = 0$.

| $\gamma$ | .1  | .5  | 1   | 2   | 5   | 10  | 100 | $\infty$ |
|----------|-----|-----|------|-----|-----|-----|-----|---------|
| $p_{\text{sim}}$ | 0.04 | 0.14 | 0.20 | 0.23 | 0.28 |
| $p_{\text{p-b1g1}}$ | 0.18 | 0.21 | 0.23 | 0.26 | 0.29 | 0.31 | 0.33 | 0.33 |
| $p_{\text{p-m2bi}}$ | 0.21 | 0.21 | 0.22 | 0.25 | 0.28 | 0.30 | 0.33 | 0.33 |

Table 5  Effect of mobility, way below Boolean-percolation. Boolean-subcritical ($\mu = 1$), motion-supercritical ($\mu > \mu_0$), motion-insensitive ($\beta < \beta_0$) case. Fraction of infected points ($p$) obtained by simulation, the functional fixed point equation and the polynomial equation. This is for $\beta = 0.4$. According to p-b1i, p-b1g1, and p-m2bi, $\gamma_c = 0$. The epidemic survives for all positive speeds $\gamma$, in spite of the fact that it dies for $\gamma = 0$.

| $\gamma$ | .1  | .5  | 1   | 2   | 5   | 10  | 100 | $\infty$ |
|----------|-----|-----|------|-----|-----|-----|-----|---------|
| $p_{\text{sim}}$ | 0.09 | 0.47 |       |     |     |   |       |         |
| $p_{\text{p-b1g1}}$ | 0.18 | 0.36 | 0.45 | 0.52 | 0.57 | 0.58 | 0.60 | 0.60 |
| $p_{\text{p-m2bi}}$ | 0.21 | 0.37 | 0.45 | 0.52 | 0.56 | 0.58 | 0.60 | 0.60 |

Table 6  Effect of mobility. Below percolation, recovery rate close to $\mu$. Fraction of infected points ($p$) obtained by simulation, the functional fixed point equation and the polynomial equation. This is for $\beta = 3$, $a = 1$, $\lambda = 1$ and $\alpha = 1$, so that $\mu \sim 3.14$. No simulation results are possible for this case. According to p-b1i, the threshold is $\gamma_c^+ \sim 2.65$. According to p-b1g1, the threshold is $\gamma_c^+ \sim 3.12$. According to p-m2bi, the threshold is $\gamma_c^+ \sim 8.15$. So again m2bi is more resistant to the epidemic than m1bi; b1g1 is intermediate.

| $\gamma$ | 2.6 | 2.7 | 3.3 | 8.2 | 8.3 | 8.6 | 10 | $\infty$ |
|----------|-----|-----|-----|-----|-----|-----|----|----------|
| $p_{\text{sim}}$ | $3 \times 10^{-4}$ | $2 \times 10^{-2}$ | $2 \times 10^{-2}$ | $2 \times 10^{-2}$ | $0.045$ |
| $p_{\text{p-b1i}}$ | 0 | $3 \times 10^{-4}$ | $2 \times 10^{-2}$ | $2 \times 10^{-2}$ | $0.045$ |
| $p_{\text{p-b1g1}}$ | 0 | 0 | $7 \times 10^{-5}$ | $2 \times 10^{-2}$ | $2 \times 10^{-2}$ | $0.045$ |
| $p_{\text{p-m2bi}}$ | 0 | 0 | 0 | $4 \times 10^{-4}$ | $2 \times 10^{-3}$ | $6 \times 10^{-4}$ | $0.045$ |

motion-supercritical instance of this situation is given in Table 6 (where $\mu \sim 3.14$ and $\beta = 3 > \beta_0$).

**Motion-sensitive and Boolean-supercritical example**  In this region, for $\gamma$ equal to 0, there is survival; for small but positive values of $\gamma$ (more precisely, for $0 < \gamma < \gamma_c(\beta)$ with $\gamma_c(\beta) > 0$), there is extinction; from $\gamma_c$ on, one starts having survival and, above this value, the fraction of infected points is strictly increasing in $\gamma$. In other words, in this case, moderate motion stops the survival present in the no-motion case.

One possible explanation is that, in the no-motion Boolean-supercritical case, the persistence of well connected clusters helps maintaining the epidemic and motion dissolves these clusters and makes it more challenging for the epidemic to survive. For
Table 7 Threshold \( \beta_0 \). Below \( \beta_0 \) there is survival for all motions. Above \( \beta_0 \) one needs high enough motion for the epidemic to survive. This is for \( \alpha = 1 \). For this controllability criterion, \( m_{2bi} \) is more resistant than \( b_{1i} \) and \( b_{1g1} \) is intermediate.

| \( \alpha \mu \) | 0.5 | 1  | 5  | 10 | 20 |
|-----------------|-----|-----|-----|----|----|
| \( \beta_{0, \text{sim}} \) |     |     |     |    |    |
| \( \beta_{0,p-b_{1i}} \) | 0.291 | 0.796 | 4.798 | 9.798 | 19.798 |
| \( \beta_{0,p-b_{1g1}} \) | 0.265 | 0.772 | 4.777 | 9.777 | 19.777 |
| \( \beta_{0,p-m_{2bi}} \) | 0.157 | 0.657 | 4.657 | 9.657 | 19.657 |

Table 8 Threshold \( \gamma_c \) for \( \beta > \beta_0 \). Below \( \gamma_c \) there is extinction, above, there is survival. This is for \( \alpha = 1 \) and \( \mu = 5 \). Once more, \( m_{2bi} \) is more resistant than \( b_{1g1} \) which is more resistant than \( b_{1i} \).

| \( \beta \) | 4.75 | 4.80 | 4.85 | 4.90 | 4.95 |
|-------------|------|------|------|------|------|
| \( \gamma_{c, \text{sim}} \) |     |     |     |     |     |
| \( \gamma_{c,p-b_{1i}} \) | 0    | 3.298 | 8.824 | 17.517 | 42.711 |
| \( \gamma_{c,p-b_{1g1}} \) | 0    | 6.265 | 10.808 | 19.379 | 44.557 |
| \( \gamma_{c,p-m_{2bi}} \) | 5.417 | 8.042 | 12.290 | 20.680 | 45.720 |

Table 9 Threshold \( \gamma_0 \) when \( \mu > \mu_0 \). Below \( \gamma_0 \), \( \beta_c = \beta_0 \) and survival/extinction is insensitive to \( \gamma \). This is for \( \alpha = 1 \). We see than \( m_{2bi} \) is more sensitive to gamma than \( b_{1g1} \), which is in turn more sensitive than \( b_{1i} \).

| \( \alpha \mu \) | 0.5 | 1  | 5  | 10 | 20 |
|-----------------|-----|-----|-----|----|----|
| \( \gamma_{0, \text{sim}} \) |     |     |     |    |    |
| \( \gamma_{0,p-b_{1i}} \) | 0.158 | 0.450 | 2.514 | 5.599 | 11.309 |
| \( \gamma_{0,p-b_{1g1}} \) | 0.121 | 0.370 | 2.467 | 4.857 | 9.818 |
| \( \gamma_{0,p-m_{2bi}} \) | 0.055 | 0.232 | 1.647 | 3.417 | 6.955 |

Table 10 Threshold \( \beta_c(\gamma) \) slightly above Boolean-percolation (\( \alpha = 1 \) and \( \mu = 5 \)). For \( \beta < \beta_c \) there is survival. For \( \beta > \beta_c \), there is extinction. The function \( \beta_c \) is constant equal to \( \beta_0 \) for \( \gamma < \gamma_0 \) and increases otherwise. Results are quite close with here \( b_{1g1} \) more resistant than \( b_{1i} \) and \( b_{1i} \) more resistant than \( m_{2bi} \). High enough values of \( \gamma \), motion again helps for survival. This situation is illustrated in Figs. 4 and 7.

| \( \gamma \) | 0.2 | 1  | 5  | 10 | 100 | \( \infty \) |
|-------------|-----|-----|-----|----|-----|----------|
| \( \beta_{c, \text{sim}} \) |     |     |     |    |     |         |
| \( \beta_{c,p-b_{1i}} \) | 4.798 | 4.798 | 4.814 | 4.859 | 4.976 | 5        |
| \( \beta_{c,p-b_{1g1}} \) | 4.932 | 4.811 | 4.802 | 4.854 | 4.976 | 5        |
| \( \beta_{c,p-m_{2bi}} \) | 4.657 | 4.657 | 4.740 | 4.826 | 4.976 | 5        |

4.8.2 Comparison of heuristics

In this subsection, we numerically compare the various heuristics. The estimates of \( \mu_0 \) are 0.263 for \( b_{1i} \), 0.306 for \( b_{1g1} \), and 0.343 for \( m_{2bi} \). Table 7 compares \( \beta_0(\mu) \) for \( \mu > \mu_0 \) for the various heuristics. Table 8 compares \( \gamma_c(\mu, \beta) \) for the three heuristics. Table 9 compares \( \gamma_0 \) for the three heuristics. Finally, Table 10 compares \( \beta_c \) for the three heuristics.
Table 11  Effect of recovery rate $\beta$. Below Boolean-percolation, medium mobility. Fraction of infected points ($p$) obtained by simulation, the functional fixed point equation and the polynomial equation. This is for $\gamma = 1$, $a = 1$, $\lambda = 1$ and $\alpha = 1$, so that $\mu \sim 3.14$. According to p-b1i, $\beta_c \sim 2.94$ (2.93 for p-b1g1). According to p-m2bi, $\beta_c \sim 2.82$. So, for these values, m2bi is a bit more ‘resistant’ to the epidemic than b1i. The simulator yields an estimate for this threshold around 2.7 (see Sect. 4.8.3). Note that the three estimates by b1 and m2bi are quite close and consistent with simulation

| $\beta$ | 0   | .2  | 1   | 2   | 2.5 | 2.78 | 2.86 | 2.88 | 2.95 |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| $p_{\text{sim}}$ | 1   | 0.92| 0.59| 0.22| 0   | 0   | 0   | 0   | 0   |
| $p_{\text{p-b1i}}$ | 0.915| 0.598| 0.254| 0.103| 0.028| 0.011| 0.007| 0   |
| $p_{\text{p-b1g1}}$ | 0.921| 0.609| 0.264| 0.109| 0.029| 0.011| 0.006| 0   |
| $p_{\text{p-m2bi}}$ | 1   | 0.918| 0.605| 0.254| 0.092| 0.006| 0   | 0   |
| $p_{\text{p-m2bi}}$ | 0.92 | 0.61 | 0.27 | 0.12 | 0.046 | 0.028 | 0 | 0 |

4.8.3 Simulation close to criticality

Simulating the SIS evolution close to criticality is a challenge. By definition, the criticality region is that with a vanishing fraction of infected points. By construction the behavior of the epidemic in this region is very sensitive to the size of the torus. Consider parameters such that the infinite system exhibits survival. For all finite size tori with these parameters, the epidemic ends up dying out in finite time, and random fluctuations make this time shorter when decreasing the size of the torus. Since there is no way to simulate arbitrarily large tori, there is hence no direct way of checking by simulation where the exact value of the critical parameters are located in general.

Here are however two natural ways to assess where the threshold lies, which are both based on the Mean Time Till Absorption (MTTA) and which are used to derive the values in the tables of the last sections.

The MTTA is a function of the parameter of interest (say $\gamma$), the torus side, say $L$, and the initial condition. To normalize things, we take as initial condition that with all points infected. The first method to separate the subcritical and the supercritical regions consists in fixing a large $L$ and in checking the value of the parameter for which there is a clear inflection of the MTTA. The second one leverages the idea that the MTTA should grow slowly with $L$ in the subcritical case (e.g., logarithmically on a grid) and fast in the supercritical case (e.g. exponentially on a grid). Unfortunately, the exact behavior of the MTTA on a torus is not known, so that this method cannot be used for a proof at this stage.

Example of estimate of $\beta_c$ The setting is that of Table 11, that is $\mu = 5$ and $\gamma = 1$. Note that $(\mu, \gamma)$ belongs to UMI region and to the Boolean-percolation region.

Figure 8 illustrates the two methods. Both give a $\beta_c$ between 2.5 and 2.6. We recall that according to p-b1i, $\beta_c \sim 2.94$ (2.93 for p-b1g1) and according to p-m2bi, $\beta_c \sim 2.82$.

Note also that Table 11 lends experimental support to the continuity assumption on phase transitions that we made and described in Sect. 4.2.

Examples of estimate of $\gamma_c$ The first example is in the UMS region. The setting is that of Table 8 with $\alpha = 1$, $\beta = 4.8$ and $\mu = 5$. For p-b1i, $\gamma_c^+ \sim 3.3$ (6.3 for...
p-b1g1), while for p-m2bi, $\gamma_c^+ \sim 8.0$. When using the methodology described above, simulation suggests a value of $\gamma_c^+$ around 3 (see Fig. 9 left). For $\gamma_c^-$, the value predicted by p-mb2i is 0.36 and that by p-bli 2.3, while simulation suggests a value around 0.4 (Fig. 9 right).

The second example is in the motion-subcritical UMS region. The setting is $\mu = 1/4$ ($\lambda = 1/\pi, \alpha = 1/2$), $\alpha = 1$, and $\beta = 1/5$. The value of $\gamma_c^+$ predicted by p-b1i is 1.73. That predicted by p-mb2i is 1.84. When using the methodology described above, Method 1 suggests a value of $\gamma_c^+$ around 2.5 (see Fig. 10, left). For $\gamma_c^-$, the value predicted by p-mb2i is 0.003 and that by p-bli 0.007. Simulation suggests a value of $\gamma_c^-$ around 0.1 (see Fig. 10, right).

Method 2 is illustrated for $\gamma_c^-$ and the same case on Fig. 11.

Let us stress once more that none of these methods provides a proof of the $(\mu, \gamma)$-phase diagram. Nevertheless, we can deduce from Method 1 (together with confidence intervals) that in the UMS region, the MTTA in a large torus is a decreasing function of $\gamma$ around $\gamma_c^-$ and an increasing function of $\gamma$ around $\gamma_c^+$. The former property in itself is a surprising fact. We illustrate this using 95% confidence intervals in Fig. 12.

The physical explanation is that already mentioned: due to the randomness of the configurations, there are clusters with high connectivity; for lower motion rates, these clusters persist for a longer time, which in turn favors the survival of the epidemic.

5 Model variants

5.1 Epidemic model variants

In relation with certain epidemics, the basic model described above is unsatisfactory in several ways.
Fig. 9 Here, $\beta = 4.8$, $\alpha = 1$ and $\mu = 5$, with $\lambda = 1$, $a = 1.261$. Top: Illustration of Method 1 (dependency on the parameter $\gamma$). On the $x$ axis, $\gamma$. On the $y$ axis, the MTTA averaged out over the cases $L = 40$ and $L = 50$. Left: whole curve. Right: region for the evaluation of $\gamma^c$. Bottom: Illustration of Method 2: On the $x$ axis, $L$. On the $y$ axis, the MTTA averaged out over 10 samples. Bottom left: the top curve is for $\gamma = 0.001$, the bottom one for $\gamma = 0.5$. Bottom right: the top curve is for $\gamma = 15$, the bottom one for $\gamma = 0.5$

Fig. 10 Here, $\beta = 0.2$, $\alpha = 1$ and $\mu = 0.25$, with $\lambda = 1/\pi$, $a = 1/2$. Illustration of Method 1 (dependency on the parameter $\gamma$). On the $x$ axis, $\gamma$. On the $y$ axis, the MTTA averaged out over the cases $L = 40$ and $L = 50$. Left: region for the evaluation of $\gamma^c$. Right: region for the evaluation of $\gamma^c$
Fig. 11 Here, $\beta = 0.2, \alpha = 1$ and $\mu = 0.25$, with $\lambda = 1/\pi, a = 1/2$. Illustration of Method 2 (dependency on the parameter $\gamma$) for $\gamma_c^-$. On the $x$ axis, $L$. On the $y$ axis, the MTTA averaged out over 10 runs. The upper curve is for $\gamma = 0.001$; the lower one is for $\gamma = 1$.

Fig. 12 Left: the parameters are those of Fig. 9: $\beta = 4.8, \alpha = 1$ and $\mu = 5$, with here $\lambda = 0.8, a = 1.41$. The torus side is $L = 40$. Right: the parameters are those of Fig. 9: $\beta = .2, \alpha = 1$ and $\mu = .25$, with here $\lambda = 1/\pi, a = 1/2$. The torus side is $L = 40$. In both cases, the $x$-axis gives the log of $\gamma$. The $y$ axis gives the MTTA with 95% confidence intervals. The MTTA is a unimodal function which decreases around $\gamma_c^-$ and increases around $\gamma_c^+$.

First the SIS dynamics is not sufficient. SIR (or further variants like SEIR) would be more satisfactory.

In addition, points should be compartmented in at least two classes, say at risk $A$ and not at risk $N$. Points not at risk would go along the SIS cycle (or their variants). In a first model, points at risk die when exposed to a high viral charge. For modelling this in the Markov SIS framework, a point $X$ of type $A$ in state $S$ has a death rate equal to
\[ \mathcal{D}(X, \tilde{\Phi}_t) = \sum_{Y \in \tilde{\Phi}_t} g(||X - Y||). \]

Here, we could take \( g = f \) or \( g = \delta f \), with \( \delta \) a positive constant. Another (and more favorable) variant is that where points at risk become sick at rate

\[ \mathcal{D}(X, \tilde{\Phi}_t) = \sum_{Y \in \tilde{\Phi}_t} g(||X - Y||) \]

and where the result of sickness is death with probability \( \nu \) and recovery with probability \( 1 - \nu \). This compartmenting can be combined with SIR or extensions.

Since we will analyze stationary regimes, the compartmental model is more interesting when there is a birth rate of points, with births representing either births in the biological sense or arrivals from far away. In the absence of births, all points at risk eventually die and the steady state boils down to that of the SIS model for points of type \( N \), namely the basic model. A natural model for births is that of a Poisson rain with intensity \( \lambda \). Newborns have a given probability to be in any state of \( \{N, A\} \times \{I, S\} \).

Some of these variants will be discussed in the note. However the basic model will be the basic one.

### 5.2 Far random waypoint and death

One can combine the setting of Sect. 3.5 with that of deaths as described in the last subsection. The model features external births with a rate \( \eta \), with say only susceptible points, migration with a rate \( \gamma \), and death with probability \( \nu \) upon infection. If \( \nu = \eta = 0 \), we obtain the last model. In this new case, the point process \( \Xi \) (we should say \( \tilde{\Xi} \) but decided to drop the tilde) is not Poisson any longer and both its intensity \( \lambda \) and its pair correlation functions are unknown. The equations are

\[
\begin{align*}
p \xi_{\Phi, \Phi}(r)(\beta + \gamma) &= p \gamma + (1 - p)(1 - \nu) \xi_{\Psi, \Phi}(r)(f(r) + \int_{\mathbb{R}^2} \mu_{\Phi, \Phi}(x) f(||x||) dx) \\
\lambda \xi_{\Psi, \Phi}(r) + \lambda(1 - p) \gamma + \eta &= \lambda(1 - p) \xi_{\Psi, \Psi}(r) \left( \gamma + \int_{\mathbb{R}^2} \mu_{\Psi, \Psi}(x) f(||x||) dx \right).
\end{align*}
\]

We also have

\[
\begin{align*}
\beta &= \lambda(1 - p)(1 - \nu) 2\pi \int_{\mathbb{R}^+} \xi_{\Psi, \Phi}(r) f(r) r dr \\
\eta &= \lambda^2 (1 - p) p \nu 2\pi \int_{\mathbb{R}^+} \xi_{\Psi, \Phi}(r) f(r) r dr,
\end{align*}
\]

which is the first moment RCP in this case (the first equation says that the rate of entrance in the susceptible state is the rate of infections that do not lead to death, and the second one that the external birth rate is the total death rate), and

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\[ \xi_{\Xi, \Xi}(r) = (1 - p)^2 \xi_{\Psi, \Psi}(r) + p^2 \xi_{\Phi, \Phi}(r) + 2p(1 - p) \xi_{\Psi, \Phi}(r), \quad (48) \]

which is the conservation equation discussed above. We also have

\[
\begin{align*}
\lambda^2 \gamma + \lambda \eta &= \gamma \lambda^2 \xi_{\Xi, \Xi}(r) + \nu \lambda^2 (1 - p)^2 \xi_{\Psi, \Psi}(r) \int_{\mathbb{R}^2} \mu(\Phi)^{0,r}_{\Psi, \Psi}(x)f(||x||)dx \\
&+ \nu \lambda^2 (1 - p) p \xi_{\Psi, \Phi}(r) \left( f(r) + \int_{\mathbb{R}^2} \mu(\Phi)^{0,r}_{\Psi, \Phi}(x)f(||x||)dx \right). \quad (49)
\end{align*}
\]

This is obtained by balancing the mass birth and death rates in \( \rho^{(2)}_{\Xi, \Xi} \).

So we have 4 unknown pair correlation functions, 2 unknown parameters (\( \lambda \) and \( p \)), and 6 equations relating them.

Associated with this model, one can define a functional equation based on any of the Bayes’ heuristics discussed above as well as a polynomial equation.

6 List of conjectures

We list here the three main conjectures stated in the present paper: (1) the repulsion conjecture in Sect. 3.2; (2) the high velocity conjecture in Sect. 3.4; (3) the \((\mu, \beta)\)-phase diagram in Sect. 4.6. The first two conjectures are strongly backed by simulation. The last one is partly backed by simulation. The three conjectures are mutually compatible: (i) the repulsion vanishes in the high velocity regime; (ii) everywhere in the unsafe region, high velocity leads to survival.

Acknowledgements The authors would like to thank Charles Radin and Fabien Mathieu for their valuable suggestions on this preprint. The authors acknowledge the support of the Texas Advanced Computing Center for providing access to computing resources that were used to carry out simulations. F. Baccelli was supported by the Simons Math+X Chair Grant (#197982) to the University of Texas at Austin and by the ERC NEMO grant, under the European Union’s Horizon 2020 research and innovation programme, grant agreement number 788851 to INRIA.

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