MIGRATION–CONTAGION PROCESSES

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Abstract

Consider the following migration process based on a closed network of $N$ queues with $K_N$ customers. Each station is a $\cdot$/M/$\infty$ queue with service (or migration) rate $\mu$. Upon departure, a customer is routed independently and uniformly at random to another station. In addition to migration, these customers are subject to a susceptible–infected–susceptible (SIS) dynamics. That is, customers are in one of two states: $I$ for infected, or $S$ for susceptible. Customers can swap their state either from $I$ to $S$ or from $S$ to $I$ only in stations. More precisely, at any station, each susceptible customer becomes infected with the instantaneous rate $\alpha Y$ if there are $Y$ infected customers in the station, whereas each infected customer recovers and becomes susceptible with rate $\beta$. We let $N$ tend to infinity and assume that $\lim_{N \to \infty} K_N/N = \eta$, where $\eta$ is a positive constant representing the customer density. The main problem of interest concerns the set of parameters of such a system for which there exists a stationary regime where the epidemic survives in the limiting system. The latter limit will be referred to as the thermodynamic limit. We use coupling and stochastic monotonicity arguments to establish key properties of the associated Markov processes, which in turn allow us to give the structure of the phase transition diagram of this thermodynamic limit with respect to $\eta$. The analysis of the Kolmogorov equations of this SIS model reduces to that of a wave-type PDE for which we have found no explicit solution. This plain SIS model is one among several companion stochastic processes that exhibit both random migration and contagion. Two of them are discussed in the present paper as they provide variants to the plain SIS model as well as some bounds and approximations. These two variants are the departure-on-change-of-state (DOCS) model and the averaged-infection-rate (AIR) model, which both admit closed-form solutions. The AIR system is a classical mean-field model where the infection mechanism based on the actual population of infected customers is replaced by a mechanism based on some empirical average of the number of infected customers in all stations. The latter admits a product-form solution. DOCS features accelerated migration in that each change of SIS state implies an immediate departure. This model leads to another wave-type PDE that admits a closed-form solution. In this text, the main focus is on the closed stochastic networks and their limits. The open systems consisting of a single station with Poisson input are instrumental in the analysis of the thermodynamic limits and are also of independent interest. This class of SIS dynamics has incarnations in virtually all queueing networks of the literature.
Keywords: Queueing theory; stochastic network; migration process; propagation of epidemics; susceptible–infected–susceptible dynamics; extinction; survival; point process; rate conservation principle; mean-field limit; thermodynamic limit; Poisson hypothesis; nonlinear Markov processes; phase transition; Markov jump processes; stationary regime; coupling; partial differential equations; wave equation; joint generating function

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1. Introduction

The model described in the abstract aims to quantify the role of migration in the propagation of epidemics on the simplest possible migration model, namely a closed network of $\cdot/M/\infty$ queues, and for the simplest epidemic process, namely the susceptible–infected–susceptible (SIS) model. The thermodynamic limit discussed in the abstract is considered in order to further simplify the problem.

The epidemic interpretation of the SIS thermodynamic model is as follows: individuals move from place (station) to place, where places are indexed by, say, $\mathbb{Z}$. The overall density of individuals is $\eta$ (i.e., the mean number of individuals per station is $\eta$). An individual stays at a place for an independent random time which is exponentially distributed with parameter $\mu$. The last parameter can be seen as the migration rate. The departure rate of individuals from a given place is hence $\lambda = \mu \eta$. When it leaves a place, an individual migrates to a place chosen independently and ‘at random’. At each station, individuals are subject to the SIS dynamics with parameters $(\alpha, \beta)$. Infections and recoveries take place in stations and conditionally on the state of the stations.

In order to answer the question of the abstract, we first consider the problem of a single open station of the $M/M/\infty$ type, referred to as the $M/M/\infty$ SIS reactor. The input features two types of customers, infected and susceptible. The customer states change according to the mechanisms described in the abstract. The question is about the steady state of this queue. Of particular interest to us is the proportion $p_0$ of infected customers in the stationary output point process of this reactor in the steady state. This system has its steady state with a joint generating function characterized as a solution of a second-order wave-type partial differential equation (PDE) for which we have found no closed-form solution. We nevertheless derive several structural properties of this open system, which are of independent interest.

The connection of the SIS reactor with the problem of the abstract is the following: Fix all parameters $\lambda, \mu, \alpha,$ and $\beta$ of the thermodynamic limit as defined in the abstract. If the latter has a non-degenerate steady state (namely a steady state with survival), then there must exist a $0 < p < 1$ such that the open system with infected proportion $p$ in input has a proportion of infected in output, $p_0$, equal to $p$ in the steady state. Conversely, if the SIS reactor has a stationary regime where $p_0(p) = p$, for some $p = p^* > 0$, then the thermodynamic limit has a stationary regime where the epidemic persists for appropriate initial conditions. In addition, it will be shown that if the SIS reactor admits no $p$ such that $p_0(p) = p$, then for all initial conditions, when time tends to infinity, the proportion of infected customers tends to 0 in the thermodynamic limit. This is why we study the conditions on the parameters $\lambda, \mu, \alpha,$ and $\beta$ under which such a $p$ exists, a situation that we will call survival, as well as conditions under which no such $p$ exists, a situation that we call weak extinction.

More precisely, we prove that the SIS thermodynamic limit admits the following phase transition diagram: fix all parameters other than $\eta$; there exists a non-degenerate function $\eta_c(\alpha, \beta, \mu)$ such that, for $\eta \leq \eta_c$, there is strong extinction, whereas for $\eta > \eta_c$, there is survival. We also derive bounds on the steady states of both the single open station model and the thermodynamic model. For instance, we give bounds on $\eta_c$ and $p^*$ for the latter. Some of these bounds are established under a hypothesis of negative correlation which is substantiated by simulation but not proved at this stage.

All the structural results on the SIS reactor are proved. All the results on the thermodynamic limit are proved under the assumption that the limits defining them exist—which we conjecture. This will be referred to as the thermodynamic propagation of chaos ansatz.
We also study the following variants of the SIS reactor:

- The departure-on-change-of-state (DOCS) reactor, where the infection rate is the same as above, but where (a) an infection immediately leads to a departure, and (b) a recovery immediately leads to a departure. This problem is simpler in that the associated PDE can be solved.

- The averaged-infection-rate (AIR) reactor, where (a) the infection rate of any susceptible is constant (rather than proportional to the actual number of infected), and (b) the recovery mechanism is as in the SIS case. This last model is a product-form Jackson network and admits a simple product-form solution.

In contrast to the plain SIS case, the stationary regimes of these two other open systems admit closed-form expressions. These two open-loop models in turn lead to thermodynamic limits. More precisely, the DOCS reactor leads to the DOCS thermodynamic limit, where customers leave the station as soon as they change their state and are immediately routed to another station chosen at random while keeping their new state. The AIR reactor leads to the AIR thermodynamic limit, which is a closed network (similar to the plain SIS thermodynamic limit) where, in any station, susceptible customers get infected with a rate that is proportional to the mean number of infected customers in all stations. The closed-form solutions alluded to above are used to quantify the phase diagram of the last two thermodynamic limits.

The AIR system is conjectured to provide bounds to the plain SIS system. These bounds are in the following sense. Consider two thermodynamic limits $A$ and $A'$ with the same parameters $\alpha, \beta, \mu$ and with varying $\eta$. System $A$ will be said to have more infection in mean than system $A'$ if the mean number of infected customers is greater in $A$ than in $A'$ in steady state. Assume that system $A$ (resp. $A'$) admits a critical value $\eta_c$ (resp. $\eta'_c$) such that if $\eta > \eta_c$ (resp. $\eta > \eta'_c$), then there is survival, whereas otherwise there is extinction. System $A'$ will be said to be safer than system $A$ if $\eta'_c \geq \eta_c$. If $A$ has more infection in mean than $A'$, then $A'$ is safer than $A$. The converse is not true in general. It will be proved that, under a certain negative correlation conjecture which is backed by simulation, DOCS is safer than AIR. There is numerical evidence that plain SIS can be safer than DOCS, or vice versa, depending on the parameters.

The main probabilistic tools used in the paper are stochastic comparison, coupling, the rate conservation principle (RCP), various classes of Markov processes with both discrete and continuous state spaces, mean-field limits, and branching processes. The PDEs alluded to above are instrumental for finding solutions to the Kolmogorov equations of the generating functions of the discrete-state-space Markov chains in question.

The paper is structured as follows. A summary of the models (single-station models and thermodynamic limit models) is given in Section 2, so as to make navigation between them easier. The open SIS reactor is studied in Section 3. Its stationary generating function satisfies a wave-type PDE for which we have not found a closed-form solution so far. We then establish rate conservation equations which are useful throughout the paper. Section 4 discusses the DOCS open reactor and Section 5 the AIR open reactor. Both models can be solved in closed form. The wave-type PDE of the DOCS reactor has a closed-form solution, whereas the AIR reactor reduces to a product-form queueing network for which an explicit solution is already known. The closed-form expressions provide bounds on the SIS dynamics. Section 6 gathers results on the thermodynamic mean-field limit of the SIS dynamics. The analysis is based on structural properties of the open SIS reactor. The main result is a characterization of the structure of the phase diagram. The same is done in Sections 7 and 8 for the AIR and the DOCS thermodynamic limits, respectively. Section 9 gives a probabilistic interpretation for the phase transition thresholds in terms of branching conditions. Finally, Section 10 gathers additional numerical observations based on discrete event simulation.

The appendix contains the proofs of several central and auxiliary results. The extended arXiv version of the paper [2] contains further material and in particular inequalities that would follow from the conjectured property of anti-association (negative correlation) of certain random variables in this SIS dynamics.
We conclude this introduction with a brief overview of the relevant literature. In the absence of mobility, the problem has been extensively studied in the particle system literature [11], where the model is referred to as the contact process. This literature contains a large corpus of results on the phase diagrams of infinite graphs with finite degrees such as grids and regular trees. The problem has also been studied on finite deterministic graphs, where the main question is that of the separation between logarithmic and exponential growth of the time till extinction with respect to the size of the graph. There is also a series of studies of SIS epidemic models on populations partitioned into households and, in particular, on their correlation structure and time to extinction; see e.g. [5] and [4] and references therein.

The SIS dynamics has also been extensively studied on finite random graphs. For overviews on this class of questions, see e.g. [14] and [13]. Moment closure techniques [10, 9] provide an important tool in this context. The contact process has also been studied on infinite random graphs with unbounded degrees. The supercritical Bienaymé–Galton–Watson tree was studied in [15], where it was shown that some critical values can be degenerate. It has also been extensively studied on Euclidean point processes [7, 8, 12].

The analysis of the case with mobility is more recent. The situation where agents perform a random walk on a finite graph and agents meeting at a given point of the graph may infect each other was studied in [6]. The situation where agents form a Poisson point process and migrate in the Euclidean plane was studied in [3], which proposed a computational framework based on moment closure techniques for evaluating the role of mobility in the propagation of epidemics.

The queueing model studied here may be seen as a discrete version of the model in [3], or as a thermodynamic limit of that of [6].

2. The models

2.1. The open models

All models in this subsection feature an open queueing system with two types of customers. There are two independent Poisson external arrival point processes: that of susceptible customers, with intensity $\lambda q$, and that of infected customers, with intensity $\lambda p$, with $q = 1 - p$.

2.1.1. The plain SIS reactor. The SIS reactor features a single M/M/$\infty$-type station (that will be referred to as a reactor). Service times of all customers in this queue are exponential with parameter $\mu$. While waiting in the reactor, each susceptible customer becomes infected with the instantaneous rate $\alpha n$ when there are $n$ infected customers, and each infected customer recovers and becomes susceptible with rate $\beta$. It is because of this interaction that we call the queue a reactor (see the left panel of Figure 1).
Let $X$ (resp. $Y$) denote the number of susceptible (resp. infected) customers in the steady state of the SIS reactor. By classical arguments, one gets that for all $0 \leq x \leq 1, 0 \leq y \leq 1$, the joint generating function $\Phi(x, y) = E[x^X y^Y]$ satisfies the PDE

$$
(\lambda(q(1 - x) + \lambda p(1 - y))) \Phi(x, y) = \mu(1 - x)\Phi_x(x, y) + (\mu(1 - y) + \beta(x - y)) \Phi_y(x, y) + \alpha y(y - x)\Phi_{xy}(x, y).
$$

(1)

The term in $\Phi_{xy}(x, y)$, which comes from the infection rate in $XY$, allows one to link this equation to the one-dimensional wave equation.

**Remark 1.** The one-dimensional wave equation reads $U_{tt} = c^2 U_{zz}$, with $c$ velocity, $t$ time, and $z$ space. The last PDE leads (after a change of variables) to a relation between second derivatives of the form $\Psi_{xx} = \left(\frac{\Psi_y}{\Psi_x}\right)^2 \Psi_{yy}$ plus additional lower-order terms—that is, a velocity of $\frac{\Psi_y}{\Psi_x}$ when interpreting $x$ as time and $y$ as space. In this sense, the wave equation satisfied by the joint generating function involves a velocity that is not determined by the parameters of the dynamics but only by the variables of the joint generating function.

2.1.2. The AIR reactor. The AIR model features a network of two M/M/$\infty$ stations. All infected arrivals are routed to the second station (that of the infected). The service rate in this station is $\nu = \mu + \beta$. When a customer leaves this station, it leaves the network with probability $\frac{\mu}{\mu + \beta}$ and is routed to the first station otherwise. All susceptible customers are routed to the first station (that of the susceptible). At time $t$, the service rate in this station is $\mu + \gamma(t)\alpha$, where $\gamma(t)$ is a positive deterministic function that can be fixed at will. When a customer leaves this station, it leaves the network with probability $\frac{\mu}{\mu + \gamma(t)\alpha}$ and is routed to the second station with probability $\frac{\gamma(t)\alpha}{\mu + \gamma(t)\alpha}$. This is depicted in the right panel of Figure 1.

The main difference from the SIS reactor is that the infection rate of a susceptible is a state-independent deterministic function here. In particular, when $\gamma(t)$ is constant, we will not need the PDE here but will rather use the theory of product-form queueing networks (see Section 5).

2.1.3. The averaging mean-field limit of the SIS reactor. The averaging mean-field limit of the SIS model is defined as the following limit of open networks. Consider a system with $K$ stations. Each station is an M/M/$\infty$ queue with service rate $\mu$ and arrival rate $\lambda$. Each arrival is independently declared infected with probability $p$ and susceptible otherwise. In each station, an infected customer turns susceptible with rate $\beta$, and a susceptible customer turns infected with rate $\frac{\nu}{\mu + \gamma(t)\alpha} \sum_{k=1}^K Y_k(t)$, where $Y_k(t)$ is the number of infected nodes in station $k$ at time $t$. So in this model, which is depicted in the left panel of Figure 4, conditionally on the state, the infection rate of a susceptible in a station is proportional to the empirical mean of the number of infected customers in all stations (rather than to the number of infected customers in the same station in the SIS reactor). The averaging mean-field limit of SIS is obtained by letting $K \to \infty$. The empirical mean in question then converges to a constant, which is also the mean number of infected customers in the typical station. When it exists, this limit features a typical station which is an AIR model with the constraint that $\gamma(.)$ must be such that $\gamma(t) = E_{N(.)}[Y(t)]$ for all $t$, where $F_{N(.)}$ is the distribution at time $t$ of the system with parameter $\gamma(.)$, and $Y(t)$ is the number of infected customers at time $t$ in the AIR station. The construction of such a system is discussed in Appendix D. A single AIR station where $\gamma(.) = E_{N(.)}[Y(t)]$ will be referred to as an AIR averaging mean-field (AIR-AMF) reactor.

2.1.4. The DOCS reactor. The DOCS model features a single station as in the SIS case. The infection mechanism of the SIS model is replaced by a simultaneous infection and departure mechanism with the following characteristics: if the number of infected is $Y(t)$, each susceptible gets infected with rate $\alpha Y(t)$ and, upon infection, it immediately leaves the system for good. There is also a ‘natural’ departure rate of susceptible customers, denoted by $\mu$. The total departure rate of infected customers is hence $\nu = \mu + \beta$, since when an infected customer recovers, it immediately leaves the system. Equivalently, the total departure rate is $\mu + \beta$, and upon departure, the infected customer keeps its state with probability $\frac{\mu}{\mu + \beta}$ or swaps to susceptible with the complementary probability. See the left panel of Figure 2.
In fact, if one just needs to determine $E(X)$ in the DOCS reactor, the state of departing customers does not matter. Therefore, we may (and will) analyze a more general scheme where there are no recoveries but a general departure rate $\nu$ of infected customers, and where $\nu$ and $\mu$ are not linked as above.

The associated PDE for the stationary generating function of the general DOCS reactor is

$$\frac{\lambda q (1 - x) + \lambda p (1 - y)}{\Phi_1(x, y)} = \frac{\mu (1 - x)}{\Phi_1(x, y)} + \frac{\nu (1 - y)}{\Phi_1(x, y)} + \frac{\alpha y (1 - x)}{\Phi_1(x, y)}.$$  \hspace{1cm} (2)

**Remark 2.** A wave-type equation shows up in the DOCS and the plain SIS systems, whereas it does not in the AIR model. This comes from the nonlinear infection rate of the form $\alpha XY$ whenever the state is $(X, Y)$. This leads to the $\frac{\partial}{\partial x}$ and $\frac{\partial}{\partial y}$ terms in the corresponding PDEs, which in turn lead to the corresponding wave equations. In contrast, in the AIR system, this nonlinearity is replaced by the linear rate $\alpha X \mathbb{E}[Y]$, with $\mathbb{E}[Y]$ seen as a parameter determined by a nonlinear relationship, which explains why the wave equation does not show up.

### 2.2. The routing mean-field limit of the DOCS reactor

The **DOCS routing reactor**, which will be essential below, is a variant of the DOCS reactor. It is based on a DOCS routing mean-field limit, which should not be confused with the DOCS thermodynamic limit (defined in Subsection 2.3 below). This routing mean-field limit is defined as follows. Consider first a network made of $N$ DOCS reactors, as depicted in the right panel of Figure 2. For this network, the state variables in station $1 \leq n \leq N$ will be denoted by $\hat{X}_n(t)$ and $\hat{Y}_n(t)$. Each station is a $\cdot$/M/$\infty$ station with service rate $\mu$ and external arrival rate $\lambda$. There is an external Poisson arrival process to each station, and each external arrival is independently declared infected with probability $p$ and susceptible otherwise. In each station, an infected customer turns susceptible with rate $\beta$. But rather than staying in the station (as in SIS), this newly susceptible customer instantaneously leaves, and rather than leaving for good as in the DOCS open reactor, it joins another station chosen at random and independently among the $N$ stations. Similarly, in station $n$, a susceptible customer turns infected with rate $\alpha \hat{Y}_n(t)$ at time $t$. But rather than staying in this station, the newly infected customer instantaneously joins another station chosen at random and independently among the $N$ stations.

When $N$ tends to infinity, we get the DOCS routing mean-field limit, which is a system with both external arrivals and internal customer routing. Again, the existence of this limit will not be discussed in the present paper. In the steady state of this limit, the overall arrival point process of infected customers in a typical station is Poisson with rate $\lambda p + \alpha \mathbb{E}[\hat{X}]$ (sum of external and internal rates), and that of susceptible customers is independent and Poisson with rate $\lambda q + \beta \mathbb{E}[\hat{Y}]$ (sum of external and internal rates again). Here $\hat{X}$ and $\hat{Y}$ represent the stationary state variables of a typical station in this limit. Here and in what follows, we use a hat on these variables to distinguish them from those of the DOCS reactor.
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FIGURE 3. On the left, a closed network of three SIS reactors. On the right, the SIS TL.

FIGURE 4. On the left, a closed network of three AIR reactors. On the right, the AIR TL.

We will use the term routing DOCS reactor to refer to the typical station in question, namely a station which behaves as a DOCS reactor but where, in addition to an external infected (resp. susceptible) Poisson input point process of intensity \( \lambda p(t) \) (resp. \( \lambda q(t) \)), there is an additional ‘re-routing’ infected (resp. susceptible) Poisson point process of intensity \( \alpha \mathbb{E}\{\hat{X}(t)\hat{Y}(t)\} \) (resp. \( \beta \mathbb{E}\{X(t)\} \)).

For all \( 0 \leq x \leq 1, 0 \leq y \leq 1 \), in steady state, the joint generating function \( \hat{\Phi}(x, y) = \mathbb{E}\{x\hat{X}y\hat{Y}\} \) satisfies the PDE

\[
\frac{1}{x} \left( \left( \lambda q + \beta \mathbb{E}\{\hat{Y}\} \right)(1-x) + \left( \lambda p + \alpha \mathbb{E}\{\hat{X}\} \right)(1-y) \right) \hat{\Phi}(x, y) = \mu(1-x)\hat{\Phi}_x(x, y) + (\mu + \beta \mathbb{E}\{\hat{Y}\})(1-y)\hat{\Phi}_y(x, y) + \alpha y(1-x)\hat{\Phi}_{xy}(x, y).
\]

(3)

This PDE is an instance of the DOCS PDE in (2) with the following specific parameters: \( \lambda q \) is replaced by \( \lambda q + \beta \mathbb{E}\{\hat{Y}\} \), \( \lambda p \) by \( \lambda p + \alpha \mathbb{E}\{\hat{X}\} \), and \( \nu \) is taken equal to \( \mu + \beta \).

Here are a few observations on the routing DOCS models. Consider first the prelimin model with \( N \) stations. Consider the whole system as a single system. Any customer has an exponential lifetime in the queue with parameter \( \mu \). During its lifetime, an individual changes state but stays in the system. Since the total arrival rate to the system is \( \lambda N \), the total number of customers in the stationary regime is Poisson with parameter (and mean) \( \lambda N/\mu \). Because of the symmetry, the mean number of all customers in any station is hence \( \lambda/\mu \). Letting \( N \) tend to infinity and noting that uniform integrability holds, we conclude that the mean number of customers stays equal to \( \lambda/\mu \) in the infinite system too. For all fixed \( N \), in the stationary regime, the pairs of \( (\hat{X}, \hat{Y}) \) vectors at different stations form an exchangeable family of dependent random vectors, with all coordinates summing up to a Poisson random variable.

2.3. The thermodynamic limits

2.3.1. Definition. The thermodynamic limits pertain to a family of closed networks as illustrated for SIS in the left panel of Figure 3 or for DOCS in the left panel of Figure 5.
They are all infinite-dimensional Markov systems. They can also be seen as certain nonlinear Markov processes (see Appendix D). Consequently, a wide range of asymptotic behaviors are possible for any given initial condition. For instance the dynamics could, e.g., converge to a stationary measure, or be periodic, or admit an attractor.

In this paper, for all cases considered, we assume that the thermodynamic limit exists and satisfies the following properties on any compact of time: (i) stations have independent dynamics; (ii) in each station, the arrival point process of susceptible (resp. infected) customers is (possibly non-homogeneous) Poisson, with these two processes being independent. This set of properties will be referred to as the thermodynamic propagation of chaos ansatz.

2.3.2. Examples. In all examples below, the prelimit is a closed system of \( N \) stations. Each station is again a \( \cdot /M/\infty \) queue with departure rate \( \mu \). There is a total of \( KN \) customers, and we assume that \( \lim_{N \to \infty} KN/N = \lambda/\mu = \eta \). Here \( \eta \) and \( \lambda \) are positive constants representing the mean population per station and the arrival rate in a station, respectively. The routing is independent and uniform at random to all stations.

**Plain SIS.** We will call the SIS thermodynamic limit (SIS TL) the infinite-dimensional system obtained by letting \( N \) tend to infinity, assuming \( KN \) behaves as described above. This limit is illustrated in the right panel of Figure 3.

**AIR.** The AIR thermodynamic limit (AIR TL) is best described as the following variant of the closed system of the abstract, which is depicted in the left panel of Figure 4. There are \( N \) stations, with state variables \( \tilde{X}_n \) and \( \tilde{Y}_n \). In any station, each susceptible customer swaps to infected with the instantaneous rate \( \alpha \frac{1}{N} \sum_{k=1}^{N} \tilde{Y}_k \) if there are \( \tilde{Y}_k \) infected customers in station \( k \), whereas each infected customer recovers and becomes susceptible with rate \( \beta \). Letting \( N \to \infty \), one gets a variant of the SIS TL (again assumed to hold here), where stations are independent. In this limit, which is depicted in the right panel of Figure 4, each station behaves as an AIR AMF reactor (with \( y(t) = \mathbb{E}[\tilde{Y}(t)] \)) with the following constraint on the parameters: the external arrival rate of susceptible customers is equal to \( \mu \mathbb{E}[\tilde{X}(t)] \), and that of infected customers is \( \mu \mathbb{E}[\tilde{Y}(t)] \).

**DOCS.** The DOCS thermodynamic limit (DOCS TL) features a closed queueing network with \( N \) DOCS stations and a total of \( KN \) customers, as illustrated in the left panel of Figure 5. If station \( n \) has \( X_n \) susceptible and \( Y_n \) infected customers, each susceptible customer swaps to infected with the instantaneous rate \( \alpha Y_n \); upon infection, it simultaneously leaves this station and is routed to one of the \( N \) stations chosen at random. Similarly, each infected customer becomes susceptible with rate \( \beta \); upon recovery, it simultaneously leaves and is routed to a station chosen at random. In addition, as in the closed SIS network model, each customer (infected or susceptible) also leaves the station with a departure rate \( \mu \) and is then also routed to a station chosen at random. We let \( N \) tend to infinity and assume that \( KN \) is such that the total input rate to a station tends to \( \lambda \) (or equivalently that the density of customers is \( \eta \)). Then,
in the limit when it exists, each station behaves as a routing DOCS reactor as defined in Subsection 2.2, with the additional consistency property that, in the latter, the external infected arrival rate $\lambda p^\ast(t)$ should match the external infected departure rate $\mu \mathbb{E}\left[\hat{Y}(t)\right]$, and similarly, $\lambda q^\ast(t)$ should be equal to $\mu \mathbb{E}\left[\hat{X}(t)\right]$. This fixed point, which characterizes the stationary distribution of the DOCS TL, is illustrated on the right in Figure 5.

2.3.3. Survival versus extinction. Below, for all thermodynamic limits, we assume that propagation of chaos holds. We will show that under this assumption, the dynamics of the infinite-dimensional Markov systems in question can be reduced to that of a finite-dimensional nonlinear Markov process.

**Definition 1.** In any thermodynamic limit, we will say that there is *survival* if the associated Markov system has a steady-state distribution with a fraction $0 < p < 1$ of susceptible customers. We will say that there is *weak extinction* if there exists no such $p$. We will say that there is *strong extinction* if, for all initial conditions, the associated Markov system converges to a regime without infected customers.

**Remark 3.** Weak extinction does not mean that the epidemic vanishes in the infinite-dimensional system as time tends to infinity. It only means that there is no initial condition for the associated infinite-dimensional Markov system to converge to a limiting regime with a positive fraction of infected customers.

**Remark 4.** As in many other models, survival in the thermodynamic limit should translate to the fact that the time to extinction in the prelimit at $N < \infty$ grows exponentially in $N$, where $N$ is as defined in the abstract.

3. SIS reactor analysis

3.1. Preliminary observations

It is easy to check from the PDE (1) that $\Phi(z, z) = e^{-\lambda (1-z)}$. A direct probabilistic argument also gives that $X + Y \sim \text{Pois}(\lambda/\mu)$.

We were not able to solve this PDE. This is why we resort to other techniques based on the RCP [1]. A variety of conservation equations will be discussed. These are of independent interest and will also be used in what follows.

3.2. First-order relations

The simplest first-order relation states that the rate of arrivals, $\lambda$, should match the rate of departures, namely $\mu \mathbb{E}[X + Y]$. Note that there is no reason for the rate of arrivals of infected customers, $\lambda p$, to match that of departures of infected customers, namely $\mu \mathbb{E}[Y]$. This also holds for susceptible customers.

**Lemma 1.** The following relation holds:

$$\lambda p + \alpha \mathbb{E}[XY] = (\mu + \beta) \mathbb{E}[Y].$$

*Proof.* We get this relation by differentiating the PDE (1) with respect to $y$ and taking $x = y = 1$. □

This has a simple RCP interpretation. We recognize in the left-hand side of (4) the increase rate of the mean number of infected customers in steady state (due to arrivals and infections), whereas the right-hand side is the mean decrease rate of the same quantity due to recoveries and departures from the reactor.

Also note that by differentiating the PDE (1) with respect to $x$ and taking $x = y = 1$, we get

$$\lambda q + \beta \mathbb{E}[Y] = \mu \mathbb{E}[X] + \alpha \mathbb{E}[XY].$$

This equation is actually the same as that in the lemma (using the fact that $\mathbb{E}[X] + \mathbb{E}[Y] = \frac{\lambda}{\mu}$).
3.3. Second-order relations

Lemma 2. The following relations hold:

\[(\lambda p + \mu + \beta)\mathbb{E}[Y] + \alpha \mathbb{E}[XY^2] = (\mu + \beta)\mathbb{E}[Y^2],\tag{6}\]

and

\[(\lambda q + \mu)\mathbb{E}[X] + (\alpha + \beta)\mathbb{E}[XY] = \alpha \mathbb{E}[X^2Y] + \mu \mathbb{E}[X^2].\tag{7}\]

Proof. The first relation is obtained by differentiating the PDE (1) with respect to \(y\) twice and taking \(x = y = 1\), the second by differentiating the PDE with respect to \(x\) twice and taking \(x = y = 1\). \(\square\)

3.4. Higher-order relations

Lemma 3. For all non-negative integers \(m\) and \(n\), the RCP relation for \(X^mY^n\) reads

\[
\begin{align*}
\lambda p\mathbb{E}[X^m((Y + 1)^n - Y^n)] + \lambda q\mathbb{E}[(X + 1)^m - X^m]Y^n] + 
\beta\mathbb{E}[Y ((X + 1)^m(Y - 1)^n - (X^m Y^n))]
+ \alpha \mathbb{E}[XY ((X - 1)^m(Y + 1)^n - (X^m Y^n))]
+ \mu \mathbb{E}[X ((X - 1)^m - X^m)Y^n] + 
\mu \mathbb{E}[YX^m ((Y - 1)^n - Y^n)] &= 0. \tag{8}
\end{align*}
\]

The proof is based on Equations (54), (55), and (56) in Appendix A.

4. DOCS reactor analysis

4.1. Preliminary observations

We start with a few observations on this system:

- By either a simple probabilistic argument or a direct analytical derivation based on the PDE, we get that \(\Phi(1, y) = e^{-(\theta(1-y))}\); that is, \(Y\) is Poisson with mean \(\theta = \frac{\lambda p}{\nu}\) (the \(Y\) process is that of an autonomous M/M/\(\infty\) queue with input rate \(\lambda\) and service rate \(\nu\)).
- Here, the random variable \(X + Y\) has no reason to be Poisson.
- The stationary output rate of infected customers, \(\nu \mathbb{E}[Y]\), should match the input rate of infected customers \((\lambda p)\). This is because the infected customers evolve as those of an M/M/\(\infty\) queue.
- The stationary depletion rate of susceptible customers, \(\mu \mathbb{E}[X] + \alpha \mathbb{E}[XY]\), should match the increase rate of susceptible customers \((\lambda q)\). This is because the susceptible customers evolve as in a stationary queue.

We summarize the last two observations in the following conservation equations:

\[
\lambda p = \nu \mathbb{E}[Y], \quad \lambda q = \mu \mathbb{E}[X] + \alpha \mathbb{E}[XY]. \tag{9}
\]

4.2. Analytical solution

By differentiating Equation (2) with respect to \(x\) and taking \(x = 1\), we get

\[-\lambda q \Phi(1, y) + (\lambda p(1 - y) + \mu) \Phi_x(1, y) = (\nu(1 - y) - \alpha y) \Phi_y(1, y),\]

or equivalently, the function \(\Psi(y) := \Phi_x(1, y)\) satisfies the ordinary differential equation (ODE)

\[
(\nu(1 - y) - \alpha y) \Psi'(y) = (\lambda p(1 - y) + \mu) \Psi(y) - \lambda q e^{-\theta(1-y)}. \tag{10}
\]

This can be rewritten as the first-order ODE

\[
\Psi'(y) = h(y)\Psi(y) - g(y), \tag{11}
\]
with
\[ h(y) := \frac{\lambda p(1 - y) + \mu}{v(1 - y) - \alpha y}, \quad g(y) := \frac{\lambda qe^{-\theta(1 - y)}}{v(1 - y) - \alpha y}. \] (12)

Notice that the coefficients of this first-order ODE have a singularity at
\[ y = y^* := \frac{\nu}{v + \alpha} < 1. \]

One can nevertheless work out the solution of this ODE for \( y \) in a neighborhood of 1 not including \( y^* \). The homogeneous equation has for a solution
\[ T(y) := e^{\int_1^y h(z)dz}. \]

Hence, when looking for a solution of the form \( \Psi(y) = T(y)a(y) \), we get that
\[ a(y) = a(1) - \int_1^y g(u)e^{-\int_u^y h(z)dz}du. \]

Hence
\[ \Psi(y) = e^{\int_1^y h(z)dz} \left( \Psi(1) - \int_1^y g(u)e^{-\int_u^y h(z)dz}du \right). \] (13)

An expansion shows that for \( u \) in a right neighborhood of \( y^* \), \( e^{-\int_u^y h(z)dz} \sim K(u - y^*)^b \) with \( K \) a constant and
\[ b = \frac{\lambda p \alpha + \mu(\alpha + v)}{(\alpha + v)^2}. \]

Hence the integral
\[ \int_1^{y^*} g(u)e^{-\int_u^y h(z)dz}du \]
is well defined and finite despite the singularity of \( g \) at \( y^* \). This integral must match \( \Psi(1) \). Indeed, if this were not the case, the function \( \Psi \) would have a singularity at \( y^* \), which is not possible. Hence
\[ \Psi(1) = \int_1^{y^*} g(u)e^{-\int_u^y h(z)dz}du, \]

that is,
\[ E[X] = \int_1^{y^*} \frac{\lambda qe^{-\frac{\lambda p(1-u)}{v(1-u) - \alpha u}}}{\lambda p(1-u) + \mu} \exp \left( - \int_1^u \frac{\lambda p(1 - z) + \mu}{v(1 - z) - \alpha z}dz \right) du. \] (14)

Using the fact that
\[ \int_1^u \frac{\lambda p(1 - z) + \mu}{v(1 - z) - \alpha z}dz = -\frac{1}{v + \alpha} \left( \lambda p(1 - u) + \left( \mu + \frac{\lambda p \alpha}{v + \alpha} \right) \ln \left( \frac{u - y^*}{1 - y^*} \right) \right), \]
with \( y^* = \frac{\nu}{v + \alpha} \), we get that
\[ E[X] = \lambda q \int_1^{y^*} \frac{e^{-\frac{\lambda p(1-u)}{v(1-u) - \alpha u}}}{\lambda p \frac{u}{v + \alpha}} \frac{1}{v(1-u) - \alpha u} \left( \frac{u - y^*}{1 - y^*} \right) \left( \frac{u}{v + \alpha} \right)^{\frac{\mu}{v + \alpha} + \frac{\lambda p \alpha}{(v + \alpha)^2}} du. \]

That is,
\[ E[X] = \lambda q \left( \frac{\mu}{v + \alpha} \right)^{\frac{\mu}{v + \alpha} + \frac{\lambda p \alpha}{(v + \alpha)^2}} \times \int_1^{y^*} \frac{e^{-\frac{\lambda p(1-u)}{v(1-u) - \alpha u}}}{\lambda p \frac{u}{v + \alpha}} \frac{1}{v(1-u) - \alpha u} \left( \frac{u - y^*}{1 - y^*} \right) \left( \frac{u}{v + \alpha} \right)^{\frac{\mu}{v + \alpha} + \frac{\lambda p \alpha}{(v + \alpha)^2}} du. \] (15)
Applying the change of variables $u = t^\alpha \nu + \alpha + \nu^\alpha$, we get
\[ E[X] = \frac{\lambda q}{\nu} \int_0^1 e^{-\frac{\lambda q t^\alpha}{\nu(v+\alpha)^2}(1-t)} \int_0^\infty \frac{\alpha - \nu^\alpha + \nu^\alpha}{\nu(v+\alpha)^2} \, dt. \] (16)

4.3. Analysis of the routing DOCS reactor

Compared to the SIS reactor, the routing DOCS reactor (defined in Subsection 2.2) features much faster migration. This is because the natural departures (those happening with rate $\mu$ regardless of the state) are complemented by departures that are caused by a change of state. Because of the nature of the mean-field model, this goes with an increased arrival rate of both infected and susceptible customers, in that ‘external’ arrivals (those happening with rate $\lambda p(t)$ for infected and rate $\lambda q(t)$ for susceptible customers) are complemented by ‘internal’ arrivals (with respective rates $\alpha E[\hat{X}(t)\hat{Y}(t)]$ for infected and $\beta E[\hat{Y}(t)]$ for susceptible customers). As we shall see (Lemma 4 below), this accelerated migration (in and out) preserves the mean queue size in steady state when it exists.

4.3.1. Stationary regime of the routing DOCS reactor. An important question is whether there exists a stationary regime for this reactor. A necessary condition is that there exists a probabilistic solution to the PDE (2) satisfying the above consistency equations. If this is the case, it follows from the observations preceding the remark of Subsection 2.2 and the results of Subsection 4.1 that $\hat{Y}$ is Poisson with parameter
\[ \hat{\theta} = \frac{\lambda p + \alpha E[\hat{X}\hat{Y}]}{\mu + \beta}. \] (17)

The random variable $\hat{X} + \hat{Y}$ has no reason to be Poisson and the two terms of the sum have no reason to be independent. In fact we will see later on that they are neither Poisson nor independent.

4.3.2. First-order rate conservation. Assuming that the routing DOCS reactor has a stationary regime, one can apply the rate conservation equations to this system. The first-order RCP, which says that the input and output rates coincide, reads
\[ \lambda q + \beta E[\hat{Y}] = \mu E[\hat{X}] + \alpha E[\hat{X}\hat{Y}] \] (18)
for susceptible customers and
\[ \lambda p + \alpha E[\hat{X}\hat{Y}] = (\beta + \mu)E[\hat{Y}] \] (19)
for infected ones. Note that these match the first-order relations of the SIS reactor.

Lemma 4. In the stationary regime of the DOCS routing mean-field model, one also has
\[ E[\hat{Y}] + E[\hat{X}] = \frac{\lambda}{\mu}. \] (20)

Proof. The result is obtained by adding up the last two equations. □

The fact that the mean total population is the same as in the SIS model is remarkable, as here, and in contrast to the SIS reactor, $\hat{X} + \hat{Y}$ is not Poisson.

4.3.3. Higher-order rate conservation. The setting is that of the last subsection. The RCP for $\hat{Y}(\hat{Y} - 1)$ reads
\[ (\lambda p + \mu + \beta) E[\hat{Y}] + \alpha E[\hat{X}\hat{Y}]E[\hat{Y}] = (\beta + \mu)E[\hat{Y}^2]. \] (21)

Note that it is similar to (6), except that $E[XY^2]$ is replaced by $E[\hat{X}\hat{Y}]E[\hat{Y}]$. Similarly, the RCP for $\hat{X}(\hat{X} - 1)$ reads
\[ (\lambda q + \mu)E[\hat{X}] + \beta E[\hat{Y}]E[\hat{X}] + \alpha E[\hat{X}\hat{Y}] = \alpha E[\hat{X}^2\hat{Y}] + \mu E[\hat{X}^2]. \] (22)
which is similar to (7), except that \( \beta \mathbb{E}[XY] \) is replaced by \( \beta \mathbb{E}[^X][^Y] \). Finally, the RCP for \( ^X^Y \) reads

\[
(\lambda q + \beta \mathbb{E}[^Y]) \mathbb{E}[^Y] + (\lambda p + \alpha \mathbb{E}[^X^Y]) \mathbb{E}[^X] = (\beta + 2\mu) \mathbb{E}[^X^Y] + \alpha \mathbb{E}[^X^Y^2].
\] (23)

Note that the complexity of the last two equations remains similar to that of the corresponding equations in the initial system.

5. AIR reactor analysis

5.1. The reactor

Thanks to the linearity of the rates, the AIR queueing network defined in Section 2 has a product-form distribution in steady state which is the product of two Poisson distributions, with parameter \( \frac{\lambda_1}{\mu} \) in station 1 and \( \frac{\lambda_2}{\mu} \) in station 2. Direct computations based on the traffic equations

\[
\lambda_1 = \lambda q + \lambda_2 \frac{\beta}{\mu + \beta}, \quad \lambda_2 = \lambda p + \lambda_1 \frac{\alpha y}{\mu + \alpha y}
\]

give that

\[
\lambda_1 = \frac{(\mu + \alpha y)(\beta + \mu q)\lambda}{(\mu + \beta)(\mu + \alpha y) - \beta \alpha y}.
\]

We also have \( x = \frac{\lambda_1}{\mu + \alpha y} = \frac{\lambda}{\mu} - y \), with \( x \) the mean queue size in station 1.

5.2. The averaging mean-field case

Consider the averaging mean-field limit when it exists. Denote by \( \tilde{X} \) the stationary number of susceptible customers in the typical station and by \( \tilde{Y} \) the stationary number of infected ones in this system. By arguments similar to those in Subsection 3.2, these state variables satisfy the relations

\[
\lambda q + \beta \mathbb{E}[\tilde{Y}] = \mu \mathbb{E}[\tilde{X}] + \alpha \mathbb{E}[\tilde{X}] \mathbb{E}[\tilde{Y}],
\] (24)

where the independence comes from the fact that in the limit, the infection rate is constant and equal to \( \alpha y = \alpha \mathbb{E}[\tilde{Y}] \). Using this and the fact that \( \mathbb{E}[\tilde{X}] = \frac{\lambda}{\mu} - y \), one gets

\[
\lambda q = \mu \left( \frac{\lambda}{\mu} - y \right) - \beta y + \alpha y \left( \frac{\lambda}{\mu} - y \right).
\] (25)

Thus, in the averaging mean-field version of the SIS reactor,

\[
\mathbb{E}[\tilde{X}] = \frac{\mu + \beta + \alpha \frac{\lambda}{\mu} - \sqrt{(\mu + \beta + \alpha \frac{\lambda}{\mu})^2 - 4\alpha \lambda \left( q + \frac{\beta}{\mu} \right)}}{2\alpha}
\] (26)

and

\[
\mathbb{E}[\tilde{Y}] = \frac{\lambda}{\mu} - \frac{\mu + \beta + \alpha \frac{\lambda}{\mu} - \sqrt{(\mu + \beta + \alpha \frac{\lambda}{\mu})^2 - 4\alpha \lambda \left( q + \frac{\beta}{\mu} \right)}}{2\alpha}.
\] (27)

6. SIS TL analysis

The natural parameters of the SIS TL are \((\eta, \mu, \alpha, \beta)\) with \( \eta \) the density parameter (that is, the mean number of customers per station, whatever their state), \( \mu \) the motion rate, \( \alpha \) the infection rate, and \( \beta \) the recovery rate. Note that the arrival rate in a station (whatever the state) is then \( \lambda = \eta \mu \). Another natural parameterization is hence \((\lambda, \mu, \alpha, \beta)\).
6.1. Fixed-point equations for the SIS reactor

If this thermodynamic model admits a stationary regime, then there exists, in the open-loop SIS reactor with parameters \( \eta, \mu, \alpha, \beta \), a value of \( p \), say \( p^* \), such that, for this value of \( p \), the external arrival rate \( \lambda p \) of infected customers matches the external departure rate of infected customers, namely \( \lambda p^* = \mu \mathbb{E}[Y] \) (or equivalently \( g(p^*) = p^* \)). Similarly, we should also have \( \lambda q^* = \mu \mathbb{E}[X] \).

Note that since the total arrival rate of infected customers, \( \lambda p^* + \alpha \mathbb{E}[XY] \), necessarily matches the total departure rate of infected customers, \( (\mu + \beta) \mathbb{E}[Y] \), the fact that \( \lambda p^* = \mu \mathbb{E}[Y] \) is equivalent to the fact that \( \alpha \mathbb{E}[XY] = \beta \mathbb{E}[Y] \).

6.1.1. Arrival versus departure rate of infected customers. Let \( p_0 \) denote the proportion of infected customers in the departure process of the SIS reactor in steady state, namely \( p_0 = \frac{\mathbb{E}[Y]}{\mathbb{E}[X]} \). Here is another representation of \( p_0 \) obtained by considering departures within the first busy cycle of an M/M/\( \infty \) queue (i.e., the cycle starting when the queue moves from empty to busy and ending at the next event of this type). By the strong law of large numbers, \( p_0 \) may be represented as \( p_0 = \frac{E[D_I(T)]}{E[T]} \), where \( T \) is the duration of a typical busy cycle, \( D_I(T) \) the number of customers served within the cycle, and \( D_I(T) \) the number of customers departed from the system in the infected state within the cycle.

Let us fix strictly positive parameters \( \mu, \alpha, \) and \( \beta \) and consider \( p_0 \) as a function of \( p \) and \( \eta \) only, say \( p_0 = g(p, \eta) \). If \( \eta \) is fixed too, then we write \( g(p) \) instead of \( g(p, \eta) \). Clearly, \( g(0) = 0 \) and \( g(1) < 1 \).

The next lemmas are proved in Appendix B.

Lemma 5. The function \( g \) is an increasing, strictly concave, and differentiable function on \([0, 1]\).

Lemma 6. Depending on the parameters \( \eta, \mu, \alpha, \) and \( \beta \), either there is only one solution \( p = 0 \) to the equation

\[
p = g(p) \tag{28}
\]

or there are exactly two solutions, \( p = 0 \) and \( p^* \equiv p^*(\eta, \mu, \alpha, \beta) \in (0, 1) \). Let \( g'(0) \) denote the right derivative of the function \( g(p) \) at 0, which exists by the previous lemma. Then \( p^* \) exists if and only if \( g'(0) > 1 \).

6.1.2. Main results on fixed point. In this subsection, we consider \( p_0 \) as a function of the two parameters \( p \) and \( \eta \), i.e., \( p_0 = g(p, \eta) \). The proof of the following lemma is given in Appendix B.

Lemma 7. The function \( \eta \to g'(0, \eta) \) is strictly increasing.

Corollary 1. There exists a function \( \eta_c^{(s)}(\alpha, \beta, \mu) = \eta_c(\alpha, \beta, \mu) \in [0, \infty) \cup \{\infty\} \) such that

- \( g'(0, \eta) \leq 1 \iff p = 0 \) is the only solution to (28) \( \iff \eta \leq \eta_c \);
- \( g'(0, \eta) > 1 \iff \text{there are two solutions to Equation (28), } p = 0 \text{ and } p^* > 0, \iff \eta > \eta_c \).

Proof. These results follow directly from the previous lemmas. \( \square \)

6.2. Bounds

In this subsection, we provide sufficient conditions for the existence and the non-existence of solutions \( p^* > 0 \) to the equation \( p_0(p) = p \). We also show that \( \eta_c^{(s)} \) is finite and strictly positive.

Lemma 8. Fix the set of parameters \( \alpha, \beta, \) and \( \mu \). For \( \eta \) (or equivalently \( \lambda \)) large enough, there exists \( p_1 > 0 \) such that if \( 0 < p < p_1 \), then the fraction of infected customers of the output is larger than that of the input, namely \( p_0 > p \).

Proof. An infected individual is guaranteed to leave infected if it departs before it recovers. The probability of this is \( \mu / (\mu + \beta) \). A susceptible individual (referred to as the target individual in what follows in this paragraph) is guaranteed to leave infected if (a) an infected individual (referred to as such
in what follows in this paragraph) arrives before the target susceptible individual departs (the probability of this is \( \frac{\lambda p}{\mu + \beta} \)); then (b) the infected individual infects the target individual before the departure of either of them and before the recovery of the infected one (the probability of this is \( \frac{\alpha}{\alpha + 2\mu + \beta} \)); and then either (c) the target individual departs before its own recovery (the probability of this is \( \frac{\mu}{\mu + \beta} \)), or (c’) the target individual recovers before the departure of either one and before the recovery of the infected one (the probability of this is \( \frac{\beta}{(2\mu + 2\beta)} \)) but gets infected by the infected one again, and so on. Thus,

\[
p_o \geq p \left( \frac{\mu}{\mu + \beta} + (1 - p) \frac{\lambda p}{\frac{\mu}{\mu + \beta} + \frac{\beta}{2(\mu + \beta)}} \right),
\]

where

\[
\kappa = \frac{\alpha}{\alpha + 2\mu + \beta} \left( \frac{\mu}{\mu + \beta} + \frac{\beta}{2(\mu + \beta)} \right) = \frac{2\alpha \mu}{2(\mu + \beta)(\alpha + 2\mu + \beta) - \alpha \beta}.
\]

Note that \( p_o > p \) follows if the right-hand side of \( 29 \) is strictly bigger than \( p \), which is equivalent to \( \frac{\mu}{\mu + \beta} + (1 - p) \cdot \frac{\lambda p}{\frac{\mu}{\mu + \beta} + \frac{\beta}{2(\mu + \beta)}} > 1 \), or to \( (1 - p) \frac{\lambda p}{\frac{\mu}{\mu + \beta} + \frac{\beta}{2(\mu + \beta)}} > \frac{\beta}{\mu + \beta} \).

Assume that, for some \( C > 1 \),

\[
\lambda \kappa > \frac{C \mu \beta}{\mu + \beta};
\]

then \( p_o > p \) for \( p < p_1 \equiv \frac{C - 1}{\lambda \kappa} \), so that there exists a \( p^* > 0 \) solving \( p_o(p) = p \).

\[
\square
\]

**Corollary 2.** It follows from Lemma 8 that for all \( \alpha, \beta, \mu \), the value of \( \eta^{(\text{s})}_c \) in Corollary 1 is finite, and more precisely

\[
\eta^{(\text{s})}_c \leq \frac{1}{\kappa} \frac{\beta}{\mu + \beta},
\]

with \( \kappa \) defined in \( 30 \).

Here is another observation.

**Lemma 9.** Fix the set of parameters \( \alpha, \beta, \) and \( \mu \). For \( \eta \) (or equivalently \( \lambda \)) small enough, \( p_o < p \) for all \( p \).

**Proof.** An individual is guaranteed to leave the system as susceptible in one of two scenarios. In the first scenario, it arrives as susceptible, finds no infected individuals in the system upon its arrival, and leaves before the arrival of an infected individual. The probability of this is \( (1 - p)\mathbb{P}(Y = 0) \cdot \frac{\mu}{\mu + \beta} \), which can be bounded from below by

\[
(1 - p)(1 - \mathbb{E}(Y)) \left( 1 - \frac{\lambda p}{\mu + \lambda p} \right) = (1 - p) \left( 1 - p_o \frac{\lambda}{\mu} \right) \left( 1 - p \frac{\lambda}{\mu} \right)
\]

Finally, for a fixed \( \mu \) and a small \( \varepsilon > 0 \), one can take \( \lambda \leq \varepsilon \mu \) so that the above is bounded from below by

\[
1 - p(1 + \varepsilon) - \varepsilon p_o.
\]

In the second scenario, an individual arrives infected, finds no other individual in the system, recovers before any other individual arrives and then leaves before any infected individual arrives. The probability of this is

\[
p \frac{e^{-\lambda}}{\beta + \lambda + \mu} \cdot \frac{\mu}{\beta + \lambda + \mu} \geq p \left( 1 - \frac{\lambda}{\mu} \right) \frac{\beta}{\beta + \lambda + \mu} \left( 1 - \frac{\lambda p}{\frac{\mu}{\beta + \lambda + \mu}} \right) \geq p \left( 1 - \frac{\lambda}{\mu} \right)^2 \frac{\beta}{\beta + \lambda + \mu}.
\]

With the choice of small \( \lambda \) already made, the above is bounded from below by

\[
p(1 - \varepsilon)^2 \frac{\beta}{\beta + \mu + \varepsilon \mu} \geq p(1 - \varepsilon)^2 \frac{\beta}{\beta + \mu} \left( 1 - \varepsilon \frac{\mu}{\beta + \mu} \right) \geq pc(1 - 3\varepsilon),
\]
where \( c = \frac{\beta}{(\beta + \mu)} \). Combining the two scenarios, we conclude

\[
1 - p_0 \geq 1 - p(1 + \varepsilon) - \varepsilon p_0 + pc(1 - 3\varepsilon),
\]

or equivalently

\[
p_0 \leq p \frac{1 - c + 3c\varepsilon}{1 - \varepsilon} < p,
\]
as long as \( \varepsilon < c/(2 + 3c) \).

From the proof of Lemma 9, one gets the following bound.

**Corollary 3.** For all \( \alpha, \beta, \mu \), the value of \( \eta_c^{(s)} \) in Corollary 1 is strictly positive, and more precisely

\[
\eta_c^{(s)} \geq \frac{\beta}{2\mu + 5\beta}.
\]  

**Remark 5.** Note that the last lower bound does not depend on \( \alpha \). This may look surprising at first glance. The fact that this bound holds even for \( \alpha = \infty \) can be explained as follows. For any fixed \( \eta > 0 \), in the \( \text{M}/\text{M}/\infty \) queue, there are busy cycles with only one customer. The smaller \( \eta \) is, the closer to 1 is the probability \( \mu / (\lambda + \mu) \) that a typical busy cycle will have only one customer to be served. Call such a cycle a 1-cycle. If a customer enters the queue as infected and if it is served in a 1-cycle, it has a chance close to \( \beta / (\beta + \mu) \) of recovering before leaving the queue; and if it susceptible, it leaves the queue susceptible after service in a 1-cycle queue. So \( p_0 > p \) uniformly in all values of \( \alpha \), for all \( \eta \) sufficiently small.

### 6.3. Survival versus extinction

The limiting system has only three parameters. Indeed, one can always take, say, \( \beta = 1 \) by a time rescaling, so that only the other three parameters remain. Consider the parameterization \((\alpha, \mu, \eta)\) and the associated positive orthant.

#### 6.3.1. Phase diagram in \( \eta \)

The following two results rely on the definitions of extinction and survival given in Definition 1. They show that the SIS TL admits a simple phase diagram with respect to \( \eta \), with critical value equal to \( \eta_c^{(s)} \) as defined above.

**Theorem 1.** If the SIS thermodynamic propagation of chaos ansatz holds, then, in the SIS TL, there exists a constant \( \eta_c \) such that there is survival if \( \eta > \eta_c^{(s)} \).

**Proof.** From Corollary 1, if \( \eta > \eta_c^{(s)} \), there exists \( p^* > 0 \) such that \( g(p^*) = p^* \). If the ansatz holds, take as initial distribution in the nonlinear Markov representation of the SIS TL the law of the open SIS reactor with infected input rate \( p = p^* \). This distribution is a stationary distribution of this system. \( \square \)

**Theorem 2.** If the SIS thermodynamic propagation of chaos ansatz holds, then, in the SIS TL, there is strong extinction if \( \eta \leq \eta_c^{(s)} \).

**Proof.** The proof is given in Appendix E. \( \square \)

**Remark 6.** Theorem 1 only shows that there exists an initial distribution \( \mathcal{P}^* \) of the SIS TL that makes this limiting system stationary. A stronger result is proved in Corollary 6 in the appendix: for all initial distributions which are stochastically larger than \( \mathcal{P}^* \), the distribution of the SIS TL converges to \( \mathcal{P}^* \) as time tends to infinity.

#### 6.3.2. Phase diagrams in \( \alpha \) and in \( \beta \)

Consider the SIS reactor. Fix all parameters except \( \alpha \) (resp. \( \beta \)) and consider \( 0 < \alpha_1 < \alpha_2 \) (resp. \( 0 < \beta_2 < \beta_1 \)). It is shown in Appendix C that there exists a coupling of the two associated models such that \( X_1(t) + Y_1(t) = X_2(t) + Y_2(t) = N(t) \) and \( Y_1(t) \leq Y_2(t) \) almost surely (a.s.), for all \( t \geq 0 \), given that the two models start from the same initial condition \( X_1(0) = X_2(0) \) and \( Y_1(0) = Y_2(0) \) a.s.
Consider now a finite closed network of SIS reactors with $N$ stations and $K_N$ customers. It is shown in Appendix C that the same monotonicity properties hold.

By arguments similar to those used with respect to $\eta$, we have the following result.

**Theorem 3.** If the SIS thermodynamic propagation of chaos ansatz holds, then, in the SIS TL, there exists a constant $\alpha^{(s)}_c$ (resp. $\beta^{(s)}_c$) such that there is survival if $\alpha > \alpha^{(s)}_c$ (resp. $\beta < \beta^{(s)}_c$) and strong extinction otherwise.

6.3.3. Other phase diagrams. Phase diagrams with respect to $\mu$ will only be discussed numerically in Section 10. An example of a question of interest is whether there is a simple (monotonic as above) phase diagram with respect to $\mu$ when $\alpha$, $\beta$, and $\eta$ are fixed.

6.4. First- and second-order relations in the thermodynamic limit

In the thermodynamic limit, the first-order relation of Lemma 1 simplifies to

$$\alpha \mathbb{E}[XY] = \beta \mathbb{E}[Y].$$

Consider now the second-order relations of Lemma 2. Equation (6) can be rewritten as

$$(\eta \mu + \mu + \beta) p \eta + \alpha \mathbb{E} \left[ XY^2 \right] = (\mu + \beta) \mathbb{E}[Y^2]$$

or equivalently

$$(\mu + \beta)(\mathbb{E}[Y^2] - \mathbb{E}[Y]^2 - \mathbb{E}[Y]) = \alpha \mathbb{E}[XY] \mathbb{E} \left[ Y \frac{\alpha XY}{\mathbb{E} \left[ \alpha XY \right]} \right] - \beta \mathbb{E}[Y]$$

$$= \beta \mathbb{E}[Y](\mathbb{E}_0^0[Y^2] - \mathbb{E}[Y]).$$

Similarly, (7) can be rewritten as

$$(\eta \mu + \mu + \beta) q + (\alpha + \beta) \mathbb{E}[XY] = \alpha \mathbb{E} \left[ X^2 Y \right] + \mu \mathbb{E}[X^2]$$

or equivalently

$$\mu \left( \mathbb{E}[X^2] - \mathbb{E}[X]^2 - \mathbb{E}[X] \right) (\alpha + \beta) \mathbb{E}[XY] - \alpha \mathbb{E}[XY] \mathbb{E} \left[ X \frac{\alpha XY}{\mathbb{E} \left[ \alpha XY \right]} \right]$$

$$= \mathbb{E}[XY] \alpha \left( 1 + \beta \frac{\alpha}{\alpha} - \mathbb{E}_0^0[X^-] \right) = \mathbb{E}[XY] \alpha \left( \beta - \mathbb{E}_0^0[X^+] \right).$$

Similarly, Equation (57) can be simplified to

$$\beta(\mathbb{E}_0^0[Y^-] - \mathbb{E}_R^0[Y^+]) = \mu \mathbb{E}_D^0[Y^+] - \eta \mu p,$$

whereas (58) can be simplified to

$$\beta(\mathbb{E}_R[X^-] - \mathbb{E}_L[X^+]) = \mu p \mathbb{E}_D^0[X^+] - \eta \mu q \frac{q}{p}.$$
thermodynamic limit, $E[\hat{X}] = \frac{\beta}{\alpha}$, $E[\hat{Y}] = \eta - \frac{\beta}{\alpha}$, $1 - \tilde{p}^* = \frac{\tilde{q}^*}{\tilde{p}} = \frac{\beta}{\alpha}$, and $\hat{X}$ and $\hat{Y}$ are independent and Poisson. In addition, the departure rate from a station is $\lambda = \eta \mu$.

If there is extinction, in the stationary regime, $E[\hat{X}] = \frac{\beta}{\alpha}$, $E[\hat{Y}] = 0$, $1 - \tilde{p}^* = \tilde{q}^* = 1$, and $\hat{X}$ is Poisson.

Proof. Assuming existence of the thermodynamic limit and its convergence to a stationary distribution, the result is immediate from plugging in $y = \frac{\beta}{\alpha}$ in (25).

The AIR phase diagram is hence quite explicit. We have $\eta_c = \frac{\beta}{\alpha}$, which does not depend on $\mu$.

In addition, the following continuity property holds: when $\eta \downarrow \eta_c$, $E[\hat{Y}] \downarrow 0$. Similar statements can be formulated with respect to any parameter other than $\eta$.

8. DOCS TL analysis

Since the behavior of a station in the DOCS TL is a specific instance of that of a station in the routing mean-field model, the following two results hold on the former: (i) The assumption that the ‘external’ arrival rate is $\lambda$ is equivalent to the assumption that the mean number of customers (of both types) in a station in steady state is $\frac{\lambda}{\mu}$ (see Equation (20)). By symmetry, this is equivalent to assuming that $\lim_{N \to \infty} \frac{K_N}{N} = \lambda / \mu := \eta$ in the DOCS TL. (ii) The condition $\lambda p^* = \mu E[\hat{Y}]$ is equivalent to $\alpha E[\hat{X}]^2 = \beta E[\hat{Y}]$ in view of (19). In words, in the DOCS TL, the stationary rate of ‘in-station’ infections matches the stationary rate of ‘in-station’ recoveries.

8.1. Analytical solution

In this section we use $p$ in place of $p^*$ to lighten the notation.

8.1.1. Rate conservation equations. As shown above, in the thermodynamic limit, we have

$$\lambda p = \mu E[\hat{Y}]$$

(42)

(in words, the rate of ‘natural’ migration of infected customers matches that of ‘external’ arrivals of infected customers),

$$\lambda q = \mu E[\hat{X}]$$

(43)

(in words, the rate of ‘natural’ migration of susceptible customers matches that of ‘external’ arrivals of susceptible customers), and

$$\alpha E[\hat{X}\hat{Y}] = \beta E[\hat{Y}]$$

(44)

(in words, the rate of ‘infections’ matches that of ‘recoveries’).

It follows that

$$E[\hat{Y}] = \hat{\theta} = \frac{\lambda p + \alpha E[\hat{X}\hat{Y}]}{\mu + \beta} = \frac{\lambda p + \beta \tilde{\theta}}{\mu + \beta};$$

that is, $\hat{\theta} = \frac{\lambda p}{\mu}$, which is consistent with (42).

As for second-order relations, when using the fact that $\hat{Y}$ is Poisson, one gets that (21) brings no information, whereas (22) leads to

$$\mu \left( E[\hat{X}^2] - E[\hat{X}] - E[\hat{X}]^2 \right) = \alpha \left( E[\hat{X}\hat{Y}] E[\hat{X}] + E[\hat{X}\hat{Y}] - E[\hat{X}^2\hat{Y}] \right)$$

(45)

and (23) to

$$\lambda q E[\hat{Y}] + \lambda p E[\hat{X}] + \beta E[\hat{Y}] \frac{\lambda}{\mu} = (\beta + 2 \mu) \frac{\beta}{\alpha} E[\hat{Y}] + \alpha E[\hat{X}\hat{Y}].$$

(46)
8.1.2. Analytic treatment based on the DOCS ODE solution. The explicit solution of the open
DOCS model is now used to analyze this thermodynamic limit. We recall that, in the DOCS TL, each
station behaves as an open DOCS reactor with susceptible input rate

$$\lambda q + \beta [\hat{E}] = \mu [\hat{X}] + \frac{\beta}{\mu} \lambda p = \lambda q + \frac{\beta}{\mu} \lambda p,$$

infected input rate

$$\lambda p + \alpha [\hat{X}] = (\mu + \beta) [\hat{Y}] = \frac{\mu + \beta}{\mu} - \lambda p,$$

and susceptible departure rate $v = \mu + \beta$. Hence, it follows from (16) that

$$[\hat{X}] = \frac{\lambda q + \beta}{\mu + \beta + \alpha} \int_0^1 e^{-\frac{\lambda q^2}{\alpha(\mu + \beta + \alpha)^2}(1-t)} \frac{\mu}{t^{\mu + \beta + \alpha} + \lambda p \frac{\alpha(\mu + \beta + \alpha)^2}{\mu(\mu + \beta + \alpha)^2}} - 1 dt. \quad (47)$$

Since $\mu [\hat{X}] = \lambda q$, we have the following.

**Proposition 1.** In the DOCS TL, $q$ satisfies the fixed-point relation

$$q = \frac{q\mu + p\beta}{\mu + \beta + \alpha} \int_0^1 e^{-\frac{q^2}{\alpha(\mu + \beta + \alpha)^2}(1-t)} \frac{\mu}{t^{\mu + \beta + \alpha} + \beta p \frac{\alpha(\mu + \beta + \alpha)^2}{\mu(\mu + \beta + \alpha)^2}} - 1 dt, \quad (48)$$

where the right-hand side is the analytic expression for $\frac{[\hat{X}]}{\eta}$ in this context.

8.1.3. Monotonicity and convexity properties. Here we study the properties of the right-hand side of
Equation (48) with respect to various parameters.

We consider the dependence on $\eta$ first. Rewriting the right-hand side of Equation (48) as

$$q = \frac{q\mu + p\beta}{\mu + \alpha + \beta} \int_0^1 e^{-\frac{q^2}{\alpha(\mu + \beta + \alpha)^2}(1-t)} \frac{\mu}{t^{\mu + \beta + \alpha} + \beta p \frac{\alpha(\mu + \beta + \alpha)^2}{\mu(\mu + \beta + \alpha)^2}} - 1 dt, \quad (49)$$

one gets that this right-hand side is a strictly decreasing function of $\eta$ when all other parameters are fixed.

The dependence on $\mu$ is more complicated. The integrand in the right-hand side of (48) is a monotonically
increasing function of $\mu$ since $\frac{q\mu + p\beta}{\mu + \alpha + \beta}$ as a function of $\mu$ is decreasing. However, the coefficient
$q\mu + p\beta$ is equal to $q + p\beta - q(a + \beta)$, which is either an increasing or decreasing function of $\mu$, depending
on the sign of $p\beta - q(a + \beta)$.

Consider now the dependence in $p$. Clearly,

$$p \rightarrow I(p) := \int_0^1 e^{-\frac{p\beta}{\alpha(\mu + \beta - \alpha)^2}(1-t)} \frac{\mu}{t^{\mu + \beta - \alpha} + \beta p \frac{\alpha(\mu + \beta - \alpha)^2}{\mu(\mu + \beta - \alpha)^2}} - 1 dt \quad (50)$$

is a positive and strictly decreasing function of $p$, when all other parameters $\eta, \mu, \alpha, \beta$ are fixed. The
quantity

$$I''(p) = \int_0^1 h^2_1(t) \exp(-ph_1(t))h_2(t) dt$$
is positive, since
\[ h_1(t) := \frac{\eta \alpha^2}{(\mu + \alpha + \beta)^2} (1 - t) + \frac{\eta (\mu + \beta) \alpha}{(\mu + \beta + \alpha)^2} |\log t| \quad \text{and} \quad h_2(t) := \frac{\mu}{(\mu + \beta + \alpha)^2} - 1 \]
are two strictly positive functions, and finite since \( \lim_{t \to 0} t^r \log t = 0 \) for any \( r > 0 \).

Furthermore, the numerator \( q \mu + p \beta \) in the prefactor of the right-hand side of (49) may be represented as \( \mu + p(\beta - \mu) \), which is strictly positive. Hence, if \( \beta \leq \mu \), the function in the right-hand side of (48) is strictly decreasing since its derivative with respect to \( p \) is
\[ D(p) := \frac{1}{\mu + \alpha + \beta} \left( (\beta - \mu) I(p) + (\mu + p(\beta - \mu)) I'(p) \right) < 0, \]
and strictly convex since its second derivative is
\[ \frac{1}{\mu + \alpha + \beta} \left( 2(\beta - \mu) I'(p) + (\mu + p(\beta - \mu)) I''(p) \right) > 0. \]

In particular,
\[ D(0) = \frac{\beta - \mu}{\mu} - 1 - \eta \left( \frac{\alpha (\mu + \beta)}{\mu (\mu + \alpha + \beta)} + \frac{\alpha^2}{(\mu + \alpha + \beta)(2\mu + \alpha + \beta)} \right) \]
\[ \equiv \frac{\beta - \mu}{\mu} - 1 - \eta \cdot \frac{\alpha}{\mu} \left( 1 + \frac{\alpha}{2\mu + \beta} \right)^{-1}. \]  
(51)

8.2. Phase diagram

Let
\[ \kappa_{c}^{(d)} := \frac{\beta \mu}{\alpha} \left( 1 + \frac{\alpha}{2\mu + \beta} \right), \quad \eta_{c}^{(d)} := \frac{\beta \mu}{\alpha} \left( 1 + \frac{\alpha}{2\mu + \beta} \right). \]  
(52)

Here is an analogue of Corollary 1 for DOCS.

Lemma 10. In the DOCS TL, if \( \beta \leq \mu \), then

\[ \bullet \ \text{p = 0 is the only solution to (48) \iff} \eta \leq \eta_{c}^{(d)}; \]

\[ \bullet \ \text{there are two solutions to Equation (48) (p = 0 and p* > 0) \iff} \eta > \eta_{c}^{(d)}. \]

Proof. The left-hand side and the right-hand side of (48) coincide at \( p = 0 \), where both are equal to 1. At \( p = 1 \), the left-hand side of (48) is 0, whereas the right-hand side of (48) is positive. By (51), we have \( D(0) < -1 \) if and only if \( \eta > \eta_{c}^{(d)} \). When \( \beta \leq \mu \), the right-hand side of (48) is a decreasing and convex function of \( p \). Hence, if the first derivative of the right-hand side of (48) at 0 is less than \(-1 \), then there is exactly one positive solution to (48), whereas if it is greater than or equal to \(-1 \), there is no such solution.

In the general case, there is at least one positive solution if the first derivative of the right-hand side of (48) at 0 is less than \(-1 \). \( \square \)

Theorem 5. Under the DOCS thermodynamic propagation of chaos ansatz, if \( \eta \leq \eta_{c}^{(d)} \), then there is weak extinction, whereas if \( \eta > \eta_{c}^{(d)} \), then there is survival.

Note that the statement on weak extinction in the last theorem is only proved under the assumption \( \beta \leq \mu \). There is numerical evidence that it also holds without this condition.
8.3. Interpretation of the results

Monotonicity. In DOCS, two contradictory phenomena are present:

1. A larger motion rate implies smaller population density, which lowers local epidemic spread.
2. A larger motion rate implies more global dissemination of the epidemic.

This possibly explains the following facts:

(a) The quantity \( \eta^{(d)} \) is decreasing in \( \mu \) (the motion rate); that is, if the population density per reactor is fixed, then increasing motion makes the system less safe. This is because only the phenomenon 2 is at play; the phenomenon 1 is blocked in this setting where \( \eta \) is fixed.

(b) The quantity \( \lambda^{(d)} \) is increasing in \( \mu \); that is, if the overall arrival rate in a reactor is fixed, then increasing motion leads to a safer system. In this case the phenomena 1 and 2 compete and our formula shows that the phenomenon 1 (or locality) dominates.

9. On the thresholds of the thermodynamic limits

Here is first a general observation on the connections between the properties of the open reactors and the thresholds (with respect to \( \eta \)) of the thermodynamic limits. We have shown that survival in a thermodynamic limit is guaranteed as soon as the derivative at 0 of the \( p \to p_0(p) \) function of the associated reactor is more than 1. Classical busy-cycle arguments show that the latter derivative can in turn be reinterpreted as the mean number of susceptible customers that a single infected customer arriving in the open reactor infects before leaving the reactor, given that the latter has only susceptible customers upon the arrival in question. This is precisely the \( R_0 \) parameter of epidemiologists. For SIS, the result is stronger: there is survival if the mean number of susceptible customers that a single infected customer infects is more than 1 and strong extinction otherwise. Of course, this mean number depends on the system considered. For AIR, the evaluation of this mean number is based on an averaging over the geometries of the random environments that a customer sees. For SIS or DOCS the evaluation takes the random and dynamic nature of the environment into account.

We now make some further observations on the thermodynamic limit thresholds in terms of the last mean value (or \( R_0 \)) interpretation when the scales of the \(( \lambda, \mu)\) or the \((\alpha, \beta)\) parameters, respectively, are changed.

Consider first a family of thermodynamic limits for DOCS indexed by \( n \), and assume that \( \lambda_n \) and \( \mu_n \) both tend to infinity in such a way that the limit of the ratio \( \lambda_n/\mu_n \) is a positive constant \( \eta \), whereas \( \alpha \) and \( \beta \) stay constant. Then \( \eta^{(d,n)} \) tends to \( \eta^{(a)} = \beta/\alpha \). Here is a probabilistic interpretation of this fact. Take a unique infected customer in a large closed network of DOCS reactors, and assume that apart from this infected customer, the system contains only susceptible customers. As \( \mu \) is very large, the infected customer travels very fast and visits many stations before recovering. The mean number of customers it infects before recovering is \( N := \eta \alpha/\beta \). This formula uses that fact that the recovery time has mean \( 1/\beta \), the infection rate is \( \alpha \), and some homogenization takes place over the population of susceptible customers seen before recovery, due to fast motion. In this limit (\( \lambda \) and \( \mu \) high), the condition \( \eta < \eta^{(d)} \) is then equivalent to the branching criticality condition \( N < 1 \), which is that of AIR. The argument should extend to SIS: under the same assumptions, the threshold for SIS \( \eta^{(s)} \) should tend to \( \eta^{(a)} = \beta/\alpha \) as well.

Consider now a family of DOCS TLs, also indexed by \( n \), and where \( \beta_n \) and \( \alpha_n \) both tend to infinity in such a way that the limit of the ratio \( \beta_n/\alpha_n \) is a positive constant \( \kappa \), whereas \( \lambda \) and \( \mu \) stay constant. It is easy to see that \( \eta^{(d)} \) tends to \( 1 + \kappa \). The condition \( \eta > \eta^{(d)} \) then reads \( M := \eta \alpha/(\alpha + \beta) > 1 \); that is, it is again like a branching condition stating that the mean number \( M \) of customers infected by a single infected customer is more than 1. Indeed, a single infected customer arriving at a station finds a mean of \( \eta \) susceptible customers. For a tagged susceptible customer, start two exponential clocks, one of parameter \( \alpha \) (for its own infection), and one of parameter \( \beta \) (for the departure of the infected customer). The chance that the tagged customer gets infected is hence \( \alpha/(\alpha + \beta) \). This justifies the interpretation of \( M \). Now
each infected customer then immediately leaves for another queue far away, where its fate is the same and independent. This justifies the branching (independence) interpretation. Note that \( \mu \) has disappeared because it is negligible with respect to \( \alpha \) and \( \beta \). This interpretation is specific to DOCS.

### 10. Comparison and numerical results

#### 10.1. Comparison of plain SIS TL and AIR TL

We conjecture that, in the stationary regime of the SIS TL, there is a negative correlation between \( X \) and \( Y \). This negative correlation property is substantiated by simulation but unproved at this stage. It is proved in the arXiv version of this paper [2] that if this negative correlation property holds, then \( \eta_{c}^{(s)} \geq \eta_{c}^{(a)} \), that is, SIS is safer than AIR. A potential interpretation is as follows: replacing the infection rate \( \alpha Y \) by \( \alpha \mathbb{E}[Y] \) at the same time decreases the infection rate when \( Y \) is large and increases it when \( Y \) is small. In the thermodynamic limit, this last fact dominates and makes it more likely for the epidemic to survive in AIR than in plain SIS.

#### 10.2. Comparison of plain SIS TL and DOCS TL

In this subsection, we use a mix of simulation and analysis to compare \( \eta_{c} \) in the thermodynamic limits of SIS and DOCS. The main conclusion is that depending on the parameters, either SIS or DOCS may be safer. The evaluation of \( \lambda_{c}^{(d)} \) is based on Theorems 1 and 2. The simulation of \( \eta_{c}^{(s)} \) is based on its characterization in Corollary 1 in terms of the derivative at 0 of the function \( p_{0}(p) \). For DOCS, we use the evaluation of \( \lambda_{c}^{(d)} \) in Lemma 10.

Figure 6 features a situation where both \( \alpha \) and \( \beta \) are moderate. We observe that \( \eta_{c}^{(d)} < \eta_{c}^{(s)} \), or equivalently, SIS is safer than DOCS.

The left panel of Figure 7 features a situation where \( \alpha \) is large and \( \beta \) moderate. We observe that \( \eta_{c}^{(s)} < \eta_{c}^{(d)} \), or equivalently, DOCS is safer than SIS. One possible explanation is that although the mean population in each system is the same, in DOCS, in any station with infection present, infected customers leave immediately, which is safer than the SIS case where they stay and infect all other susceptible customers present in the station.

One can observe in Figure 6 that the curve corresponding to the derivative at \( p = 0 \) for DOCS is higher (resp. lower) than that for SIS for low (resp. high) values of \( \lambda \) and, crucially, reaches 1 at a lower value of \( \lambda \). Both curves are produced by simulation. We also present the exact curve for DOCS that follows from our analytic results; this can be observed to agree with simulations.

The right panel of Figure 7 features a situation where \( \beta \) is large and \( \alpha \) moderate. Here SIS is safer than DOCS again. The interpretation is that although the mean number of individuals per station is the same in either case, in DOCS any station with many infected customers is more quickly depleted because of their fast recovery.

#### 10.3. Comparison of SIS-DOCS TL and AIR TL

It follows directly from the expressions for \( \eta_{c} \) in both cases that \( \eta_{c}^{(d)} > \eta_{c}^{(a)} \). This can be rephrased by saying that DOCS is safer than AIR. A possible interpretation is again that extinction happens when \( Y \) fluctuates to small values throughout all reactors of a large system. Fixing \( Y \) to its means as in AIR, in the thermodynamic limit, makes these fluctuations less likely. This possibly explains why the AIR system is less safe than the DOCS system.

#### 10.4. Phase diagram in \( \mu \)

For the SIS reactor and SIS TL, we have already characterized the phase diagrams: they turn out to be of the threshold type (survival in one interval, extinction in another). Another interesting question is what such a phase diagram looks like in \( \mu \). More specifically, one may be interested in fixing \( \eta, \alpha, \) and \( \beta \) and asking for which values of \( \mu \) the epidemic survives and for which it does not.
FIGURE 6. Comparison of $\eta_c^{(s)}$ and $\eta_c^{(d)}$ for $\mu = 1$, $\beta = 1$, and $\alpha = 1$.

FIGURE 7. Left: comparison of $\eta_c^{(s)}$ and $\eta_c^{(d)}$ for $\mu = 1$, $\beta = 1$, and $\alpha = 20$; Right: comparison of $\eta_c^{(s)}$ and $\eta_c^{(d)}$ for $\mu = 1$, $\beta = 10$, and $\alpha = 1$. On the left it is not clear which curve is higher at low values of $\lambda$, but it is clear that the curve corresponding to DOCS is lower for high values of $\lambda$ and that, crucially, it reaches 1 later than the curve for SIS. On the right it is clear that the curve corresponding to DOCS reaches 1 earlier than that corresponding to SIS. The curves in both panels are produced by simulation, and for DOCS we also provide the exact curve that follows from our analytical results.
We have shown that, in order to answer such a question, one needs to examine the derivative at \( p = 0 \) of the function \( g(p) \). Our findings were based on the monotonicity of this derivative with respect to the relevant parameters.

Numerical evidence shows that such monotonicity with respect to \( \mu \) does not always hold. Indeed, Figure 8 contains graphs of the derivative as a function of \( \mu \), when the other parameters are fixed, in two scenarios. On the right, \( \eta = 3, \alpha = 5, \beta = 1 \), and one can observe the absence of monotonicity and convexity. On the left, however, when \( \eta = \alpha = \beta = 1 \), it appears that the derivative is monotone. This evidence suggests that the phase diagram in \( \mu \) may be more complicated than in the case of other parameters. This is in line with what was observed in [3]. We plan to address the subject further in future research.

11. Conclusion and future research

We have rigorously proved the structure of the phase diagram of the SIS model under the assumption that the Poisson hypothesis holds. Future research on the basic model will consist in first proving the Poisson hypothesis (ansatz). Another key objective on the basic SIS model will be to establish the phase diagram for parameters other than population density. It would be nice to complement this with computational results like those established for the AIR and DOCS variants of the model. Several further variants of the basic model can also be considered, such as SIRS-type models where individuals go through a recovery phase (where they cannot be infected) before becoming susceptible again. We will also study further spatial SIS dynamics. Other basic queueing models, for instance finite-capacity queues, can also be considered. In fact, such epidemics can be devised on virtually all queueing network models in the literature.

Appendix A. Rate conservation

One can rewrite (6) as

\[
\lambda p \mathbb{E}[Y] + \alpha \mathbb{E} \left[ XY^2 \right] = \lambda p \mathbb{E}[Y] + \alpha \mathbb{E}[XY] \mathbb{E} \left[ \frac{\alpha XY}{\alpha \mathbb{E}[XY]} Y \right] = (\mu + \beta) \mathbb{E}[Y(Y - 1)].
\]

Let \( I \) denote the stationary infection epoch point process. Its intensity is \( a_i = \alpha \mathbb{E}[XY] \), and by Papangelou’s theorem [1],

\[
\mathbb{E} \left[ \frac{\alpha XY}{\alpha \mathbb{E}[XY]} Y \right] = \mathbb{E}_I^0[Y],
\]

with \( \mathbb{E}_I^0 \) denoting expectation with respect to the Palm probability with respect to \( I \) [1]. Hence the left-hand side of the last equality is \( \lambda p \mathbb{E}[Y] + a_i \mathbb{E}_I^0[Y] \), in which we recognize half of the increase rate of
\( \mathbb{E}[Y(Y - 1)] \). Let \( M_t \) denote the point process of recovery or departures of infected customers. The right-hand side of (53) can be rewritten as

\[
(\mu + \beta)\mathbb{E}[Y] \mathbb{E} \left[ \frac{(\mu + \beta)Y}{(\mu + \beta)\mathbb{E}[Y]} (Y - 1) = d_i \mathbb{E}_N[Y - 1], \right]
\]

with \( d_i \) the intensity of \( M_t \) and the same Palm probability notation as above. This is twice the decrease rate of \( Y(Y - 1) \). Hence (6) is nothing else than the RCP for \( \frac{1}{2} Y(Y - 1) \).

The RCP for \( Y^2 \) in turn reads

\[
\lambda p \mathbb{E}[2Y + 1] + \alpha \mathbb{E}[XY(2Y + 1)] = (\mu + \beta)\mathbb{E}[2Y(Y - 1)].
\]

By the same arguments, the right-hand side is half the decrease rate of the second factorial moment of \( X \) due to infection and departures. The left-hand side is half the increase rate of the same quantity due to arrivals of susceptible customers and recoveries of infected customers. This equation is hence the RCP for \( \frac{1}{2} X(X - 1) \). The RCP for \( X^2 \) reads

\[
\lambda q \mathbb{E}[X^2 + 1] + \beta \mathbb{E}[Y(2X + 1)] = \alpha \mathbb{E}[XY(2X - 1)] + \mu \mathbb{E}[X(2X - 1)].
\]

If we differentiate the PDE with respect to \( x \) and \( y \) (or \( y \) and \( x \)) and taking \( x = y = 1 \), we get

\[
\lambda p \mathbb{E}[X] + \lambda q \mathbb{E}[Y] + \beta \mathbb{E}[Y(Y - 1)] + \alpha(\mathbb{E}[XY(2X - 1)]) = 2\mu \mathbb{E}[XY].
\]

It is easy to check that inserting the two relations from the last lemma into the equation above does not give anything new. It just confirms that \( X + Y \) is Poisson-\( \lambda/\mu \). It is easy to check that this is in fact the RCP for \( XY \).

**Remark 7.** Using the Palm interpretation given above, and PASTA, it is easy to check that (6) can be rewritten as

\[
\lambda p \mathbb{E}_{A_i}[Y^-] + a_i \mathbb{E}_{D_i}[Y^+] = \mu_i \mathbb{E}_{D_i}[Y^+] + a_i \mathbb{E}_{R}[Y^+].
\]

with \( \mu_i = \mu \mathbb{E}[Y] \) the exogenous departure rate in this queue, \( a_i = \beta \mathbb{E}[Y] \) the recovery rate, and \( a_i = \alpha \mathbb{E}[XY] \) the infection rate. This is nothing but the classical property that, in the ‘infected queue’, the Palm expectation of the number of customers just before arrivals coincides with the Palm expectation of the number of customers just after departures. Similarly, (7) reads

\[
\lambda q \mathbb{E}_{A_i}[X^-] + a_i \mathbb{E}_{D_i}[X^+] = a_i \mathbb{E}_{D_i}[X^+] + \mu_i \mathbb{E}_{D_i}[X^+],
\]

with similar notation.

**Corollary 4.** The following relations hold:

\[
\lambda \left( \frac{q}{\mu} + \frac{\beta}{\alpha} \right) \left( 1 + \frac{\beta}{\alpha} \right) + \left( \lambda q - \frac{\beta}{\alpha} (\mu + \alpha + \beta) \right) \mathbb{E}[X] - \mu \mathbb{E}[X^2] = \alpha \mathbb{E}[X^2 Y] \tag{59}
\]

and

\[
\frac{\lambda}{\mu} \left( \lambda p + \frac{\mu + \beta}{\mu\alpha} (2\mu(\mu q + \beta) - \lambda \alpha) - \left( \lambda p + \mu + \beta + \frac{2}{\alpha} (\mu + \beta)^2 \right) \mathbb{E}[X] \right.
\]

\[
+ (\mu + \beta) \mathbb{E}[X^2] = -\alpha \mathbb{E}[XY^2]. \tag{60}
\]
Appendix B. Proofs of Lemmas 5, 6, and 7

Proof of Lemma 5. The proof consists of four steps: monotonicity, concavity, strict concavity, and differentiability.

Below, to make the proof more transparent, we use the notation $N_I(t)$ instead of $X(t)$ and $N_S(t)$ instead of $Y(t)$. In addition, the properties are expressed with respect to $\lambda = \eta \mu$ rather than $\eta$. Since $\mu$ is a constant, this is equivalent.

(1) Monotonicity. Consider the typical busy cycle. Assume that the first customer arrives at an empty system at time 0 and let $T > 0$ be the first time when the system becomes empty again. We have to show that the mean number of infected customers that depart from the system within the time interval $[0, T]$ is an increasing function of $\rho$.

For that, we consider two models, with input probabilities of being infected $p$ and $\tilde{\rho} > p$. For the input probability $p$ and for $0 \leq t \leq T$, we denote by $N(t)$ the total number of customers at time $t > 0$, by $N_I(t)$ the number of infected customers, and by $N_S(t)$ the number of susceptible customers. Clearly, $N(t) = N_I(t) + N_S(t)$. Let $\tilde{N}(t)$, $\tilde{N}_I(t)$, and $\tilde{N}_S(t)$ be the corresponding processes related to probability $\tilde{\rho}$, with $\tilde{N}(t) = \tilde{N}_I(t) + \tilde{N}_S(t)$ for $t \geq 0$.

We produce a coupling of the two processes such that, for all $0 \leq t \leq T$, $N(t) = \tilde{N}(t)$ a.s., while $\tilde{N}_I(t) \geq N_I(t)$ and, therefore, $\tilde{N}_S(t) \leq N_S(t)$. Thus, for the total numbers of departures of infected customers within the first busy cycle, we get $D_I(T) \leq \tilde{D}_I(T)$ a.s. Moreover, we will show that $\mathbb{P}(D_I(T) < \tilde{D}_I(T)) > 0$.

Let $t_n$, $n \geq 1$, be exponential-$\lambda$ random variables; let $\sigma_{n,j}$, $n, j \geq 1$, be exponential-$\mu$ random variables; let $a_{n,i,j}$ be exponential-$\alpha$ random variables; let $b_{n,j}$ be exponential-$\beta$ random variables; and let $u_n$ have a uniform distribution in the interval $(0, 1)$. We assume all these random variables to be mutually independent.

We introduce embedded epochs $T_0 = 0 < T_1 < T_2 < \ldots < T_\psi = T$, where $\psi$ is a random natural number representing the total number of events (jumps) that occur in both systems. This is not restrictive, as some of these events will be fictitious in either system. Both processes $(N_S(t), N_I(t))$ and $(\tilde{N}_S(t), \tilde{N}_I(t))$ are piecewise constant and may make jumps only at time instants $T_n$. We assume the processes to be right-continuous, and customers to be numbered in each group at any time, in a way that we will make precise in due time.

At time $T_0 = 0$, we let

$$N_S(0) = \mathbf{1}(u_1 > p) = 1 - N_I(0) \quad \text{and} \quad \tilde{N}_S(0) = \mathbf{1}(u_1 > \tilde{\rho}) = 1 - \tilde{N}_I(0)$$

and

$$D_S(0) = D_I(0) = \tilde{D}_S(0) = \tilde{D}_I(0) = 0.$$ 

Then we evaluate the values of the processes recursively: that is, we produce both time $T_{n+1}$ and their values at time $T_{n+1}$ given time $T_n$, their values at time $T_n$, and the values of $t_{n+1}$, $u_{n+1}$, $(\sigma_{n+1,j})_{j \geq 1}$, $(a_{n+1,i,j})_{i,j \geq 1}$, $(b_{n+1,j})_{j \geq 1}$.

Assume we have introduced both processes up to time $T_n$ and shown that $\tilde{N}_I(T_n) \geq N_I(T_n)$ and $\tilde{N}(T_n) = N(T_n)$. Assume that $\sigma_{n+1,j}$, $1 \leq j \leq N(T_n)$, are the remaining service times of all present customers, where customers numbered 1, \ldots, $N_I(T_n)$ are infected in both systems, customers numbered $N_I(T_n) + 1$, \ldots, $\hat{N}_I(T_n)$ are susceptible in the first system and infected in the second system, and customers numbered $\hat{N}_I(T_n) + 1$, \ldots, $\tilde{N}_I(T_n)$ are susceptible in both systems. Assume that the random variables $b_{n+1,j}$, for $j = N_I(T_n) + 1$, \ldots, $\hat{N}_I(T_n)$, represent the recovery times for the corresponding infected customers in the second system, and that for $j = 1, \ldots, N_I(T_n)$ they represent the recovery times.
for customers that are infected in both systems. Assume that if customer \( j \) is infected and customer \( i \) is susceptible at time \( T_n \), then \( \sigma_{n+1,j,i} \) is the instant when \( j \) may infect \( i \).

Consider the random sets of integers \( C_1(n) = \{ j : 1 \leq j \leq \tilde{N}_1(T_n) \} \), \( C_2(n) = \{ j : N_1(T_n) < j \leq \tilde{N}_1(T_n) \} \), and \( C_3(n) = \{ j : \tilde{N}_1(T_n) < j \leq N(T_n) \} \). For \( k = 1, 2, 3 \), let

\[
\Sigma_{n+1,k} = \min_{j \in C_k(n)} \sigma_{n+1,j} \quad \text{and} \quad B_{n+1,k} = \min_{j \in C_k(n)} b_{n+1,j},
\]

where \( \min_{\emptyset} = \infty \), by convention. Next, for \( k, l = 1, 2, 3 \), let

\[
A_{n+1,k,l} = \min_{j \in C_k(n), i \in C_l(n)} a_{n+1,i,j}.
\]

Finally, let

\[
\theta_{n+1} = \min (t_{n+1}, \min_{1 \leq k \leq 3} \Sigma_{n+1,k}, \min_{1 \leq k \leq 2} B_{n+1,k}, \min (A_{n+1,1,2}, A_{n+1,1,3}, A_{n+1,1,2})). \tag{61}
\]

Therefore, \( \theta_{n+1} \) is the next time instant when something happens in any of the systems—either the arrival of a new customer, the departure of a present customer, the recovery of a present customer, or the infection of one present customer by another one. Then

\[
T_{n+1} = T_n + \theta_{n+1}.
\]

If \( \theta_{n+1} = t_{n+1} \), i.e. a new customer arrives, then

\[
D_S(T_{n+1}) = D_S(T_n), \quad D_I(T_{n+1}) = D_I(T_n), \quad \tilde{D}_S(T_{n+1}) = \tilde{D}_S(T_n), \quad \tilde{D}_I(T_{n+1}) = \tilde{D}_I(T_n)
\]

and \( N(T_{n+1}) = \tilde{N}(T_{n+1}) + N(T_n) + 1, \)

\[
N_1(T_{n+1}) = N_1(T_n) + \mathbf{I}(u_{n+1} > \tilde{p}), \quad \tilde{N}_1(T_{n+1}) = \tilde{N}_1(T_n) + \mathbf{I}(u_{n+1} > \tilde{p}), \quad N_2(T_{n+1}) = N_2(T_n), \quad \tilde{N}_2(T_{n+1}) = \tilde{N}_2(T_n).
\]

If \( \theta_{n+1} = \min_{1 \leq k \leq 3} \Sigma_{n+1,k} \), then one of the present customers departs. If \( \Sigma_{n+1,1} \) is the smallest among the three, then there is a departure of a customer that is infected in both systems. Therefore, \( D_I(T_{n+1}) = D_I(T_n) + 1, \quad \tilde{D}_I(T_{n+1}) = \tilde{D}_I(T_n) + 1, \quad D_S(T_{n+1}) = D_S(T_n), \quad \tilde{D}_S(T_{n+1}) = \tilde{D}_S(T_n) \), and \( N_1(T_{n+1}) = N_1(T_n) - 1, \quad \tilde{N}_1(T_{n+1}) = \tilde{N}_1(T_n) - 1, \quad N_2(T_{n+1}) = N_2(T_n), \quad \tilde{N}_2(T_{n+1}) = \tilde{N}_2(T_n) \). By the symmetry, if \( \sigma_{n+1,1} \) is the smallest, then there is a departure of a customer that is susceptible in both systems. Therefore, \( D_S(T_{n+1}) = D_S(T_n) + 1, \quad \tilde{D}_S(T_{n+1}) = \tilde{D}_S(T_n) + 1, \quad D_I(T_{n+1}) = D_I(T_n), \quad \tilde{D}_I(T_{n+1}) = \tilde{D}_I(T_n), \)

and \( N_1(T_{n+1}) = N_1(T_n) - 1, \quad \tilde{N}_1(T_{n+1}) = \tilde{N}_1(T_n) - 1, \quad N_2(T_{n+1}) = N_2(T_n), \quad \tilde{N}_2(T_{n+1}) = \tilde{N}_2(T_n) \).

Next, if \( \Sigma_{n+1,2} \) is the smallest, then this means that the strict inequality \( N_1(T_n) < \tilde{N}_1(T_n) \) holds and there is a departure of a customer that is susceptible in the first system and infected in the second. Then \( D_I(T_{n+1}) = D_I(T_n), \quad \tilde{D}_I(T_{n+1}) = \tilde{D}_I(T_n) + 1, \quad D_S(T_{n+1}) = D_S(T_n) + 1, \quad \tilde{D}_S(T_{n+1}) = \tilde{D}_S(T_n) \), and \( N_1(T_{n+1}) = N_1(T_n), \quad \tilde{N}_1(T_{n+1}) = \tilde{N}_1(T_n) - 1, \quad N_2(T_{n+1}) = N_2(T_n) - 1, \quad \tilde{N}_2(T_{n+1}) = \tilde{N}_2(T_n) \). One can see that in all three cases

\[
N_1(T_{n+1}) \leq \tilde{N}_1(T_{n+1}) \quad \text{and} \quad D_I(T_{n+1}) \leq \tilde{D}_I(T_{n+1}). \tag{62}
\]

Similarly, if \( \theta_{n+1} = \min_{e=1,2} B_{n+1,k} \), then the numbers of departures do not change, and either (a) there is a simultaneous recovery of a customer that was infected in both systems, or (b) there was a customer that was susceptible in the first system and infected in the second, it has recovered in the second system, and nothing has changed in the first system. Again, one can see that the needed inequalities (62) continue to hold.

Finally, if \( \theta_{n+1} = \min (A_{n+1,1,2}, A_{n+1,1,3}, A_{n+1,1,2}) \), then the number of departures stays the same and there are again three scenarios. If \( A_{n+1,1,2} \) is the smallest among the three, then the set \( C_2(n) \) of customers
Remark 8. The monotonicity property discussed above can be extended in two ways:

1. Rather than comparing the two systems in a busy cycle, one compares them over the whole time half-axis. For this, one has to start the two systems at time $T_0 = 0$ with the same total population $N(T_0) = \tilde{N}(T_0)$ and with more infected customers in the dominating system than in the dominated one, i.e., with $N_l(T_0) \leq \tilde{N}_l(T_0)$ a.s. Based on the same arguments, one proves by induction over the overall jump times $\{T_n\}$ that in the coupling described above, for all $t$, $N(t) = \tilde{N}(t)$ a.s. and $N_l(t) \leq \tilde{N}_l(t)$ a.s.

2. The setting of the previous item can be extended to the situation where, rather than having constant fractions of the Poisson arrivals, $p$ and $\tilde{p}$, that are infected in the two systems, with $p \leq \tilde{p}$, one has deterministic time-varying fractions $p(t)$ and $\tilde{p}(t)$ of the Poisson arrivals which are infected in the two systems, with $p(.) \leq \tilde{p}(.)$. In this case we again have that, if $N_l(T_0) \leq \tilde{N}_l(T_0)$ a.s., then in the same coupling, $N(t) = \tilde{N}(t)$ a.s. and $N_l(t) \leq \tilde{N}_l(t)$ a.s. for all $t$.

(2) Concavity. We now introduce a slightly different coupling that allows us to consider simultaneously models with different parameters.

From now on, we do not enumerate customers. Instead, we consider a countable number $Z$ of ‘locations’ for them that coincide with ‘servers’. More precisely, we assume that an arriving customer chooses an empty server at random and stays there until its departure from the system.

We continue to consider a single busy cycle on the time interval $[0, T]$. We again denote by $T_0 < T_1 < T_2 < \ldots$ the time instants when the state of the systems may change. Hence, the state of the system $Z(t)$ at time $t$ is a collection of pairs $\{(z, c_z(t)), z \in Z\}$, where $z$ is a server and $c_z$ is its ‘color’. Here $c_z(t) = n$ (where ‘n’ means ‘no color’) if server $z$ is empty at time $t$, and $c_z(t)$ has one of several other colors otherwise. (The meanings of these colors will be explained in due time.) Let $\bar{N}(t) = \{z : c_z(t) \neq n\}$ be the set of occupied servers, and let $N(t) = \sum_{z \in \bar{Z}} 1(c_z(t) \neq n)$ denote its cardinality.

We introduce the following sequences of random variables:

- $\{u_n\}_{n \geq 0}$ are uniformly distributed in $(0, 1)$;
- $\{t_n\}_{n \geq 1}$ are exponential-$\lambda$;
- $\{\sigma_{n,z}\}_{n \geq 0, z \in Z}$ are exponential-$\mu$;
We assume that all these random variables are mutually independent.

Let $T_0 = 0$. Introduce recursively $\{\theta_k\}$ and $T_k = \sum_{j}^{k} \theta_j$. Let $N_k = \mathcal{N}(T_k + 0)$. For $n \geq 1$, assuming that $T_{n-1}$ is defined, we let $\Sigma_n = \min_{z \in N_{n-1}} \sigma_{n,z}$, $B_n = \min_{z \in \mathcal{N}_{n-1}} b_{n,z}$, $A_n = \min_{z \in N_{n-1}, z \neq v} a_{n,z,v}$. Then let

$$\theta_n = \min\{t_n, \Sigma_n, A_n, B_n\} \quad \text{and} \quad T_n = T_{n-1} + \theta_n.$$

Now we are ready to define a ‘three-color’ process. Let $p, q \geq 0$, $r > 0$ be numbers that sum up to 1, $p + r + q = 1$. We assume that each arriving customer gets the red color with probability $p$, the magenta color with probability $r$, and the green color with probability $q$. It occupies a server (that gets the same color as the customer).

We assume the process to be piecewise constant between time instants $T_n$. We introduce coloring by induction.

At time $T_0 = 0$, we color the arriving customer magenta if $u_0 \leq r$, red if $r < u_0 \leq r + p$, and green if $u_0 > r + p$, and we assume that the customer keeps its color within the time interval $(T_0, T_1]$.

Assume that coloring is done up to time $T_n$. Proceed with coloring for the time interval $(T_n, T_{n+1}]$.

If $\theta_n = t_n$, then we place an arriving customer at one of the empty servers and color the customer magenta if $u_0 \leq r$, red if $r < u_0 \leq r + p$, and green if $u_0 > r + p$.

If $\theta_n = \sigma_{n,z}$ for some $z \in N_n$, then customer $z$ leaves the system and the corresponding server becomes idle (‘no color’).

If $\theta_n = \beta_{n,z}$ for some $z \in N_n$, then customer $z$ becomes green, regardless of what color it had before.

If $\theta_n = A_n$, then we have to consider three cases. At time $T_n$, let $N_{n,m}$, $N_{n,r}$, $N_{n,g}$ be the sets of magenta, red, and green customers, where clearly

$$N_n = N_{n,m} \cup N_{n,r} \cup N_{n,g}.$$

Let $N_{n,m}$, $N_{n,r}$, and $N_{n,g}$ be the corresponding cardinalities. If $\theta_n = a_{n,z,v}$ for some $z \in N_{n,g}$, then (since green means susceptible) there is no new infection and all colors stay the same (one could say that this is a ‘false coloring’).

If $\theta_n = a_{n,z,v}$ for some $z \in N_{n,r}$, then customer $v$ (and the corresponding server) becomes red, whatever color it had before.

Finally, if $\theta_n = a_{n,z,v}$ for some $z \in N_{n,m}$, then customer $v$ (and the corresponding server) becomes magenta if it was either magenta or green before—or remains red if it was red before.

Thus, we have defined the three-color dynamics within the busy cycle.

As a result of the proposed coupling construction, one can observe the following.

1. If we do not distinguish between (i.e. we ‘merge’) the green and magenta colors (and recolor them as ‘new green’), then we get the two-color susceptible–infected model considered earlier, with the probability of green arrivals $r + q$ and the probability of red arrivals $p$; call this model the $(p, r + q)$ model.

2. If we do not distinguish between (i.e. we ‘merge’) the magenta and red colors (and recolor them as ‘new red’), then we get the two-color susceptible–infected model considered earlier, with the probability of green arrivals $q$ and the probability of red arrivals $r + p$; call this model the $(r + p, q)$ model.

This means that, for $0 \leq t \leq T$, the random variable $N_m(t)$ represents the ‘excess’ of the number of ‘red’ customers in the $(r + p, q)$ model in comparison with the $(p, r + q)$ model.

Assume now that $q > 0$ and consider the three-color $(r, \hat{p}, \hat{q})$-model with $\hat{p} > p$ and $r + \hat{p} + \hat{q} = 1$. Let $\widehat{N}_m(t)$ be the set of magenta customers at time $t$ in this model and $\widehat{N}_m(t)$ its cardinality. Then straightforward induction arguments show that $\widehat{N}_m(t) \subseteq \mathcal{N}_m(t)$ and, therefore, $\widehat{N}_m(t) \leq \mathcal{N}_m(t)$ a.s., for any $0 \leq t \leq T$. 

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In turn, this implies that the total number of departures within the first cycle of magenta customers in the corresponding systems, call them $D_m(T)$ and $\hat{D}_m(T)$, satisfy $D_m(T) \geq \hat{D}_m(T)$ a.s. Recall the notation $p_o = g(p)$. Then

$$g(p) = \frac{ED_g(T)}{ED(T)}, \quad g(p + r) = \frac{ED_g(T) + D_m(T)}{ED(T)},$$

$$g(\hat{p}) = \frac{ED_{g}(T)}{ED(T)}, \quad g(\hat{p} + r) = \frac{ED_{g}(T) + \hat{D}_m(T)}{ED(T)},$$

where, as before, $ED(T)$ is the mean number of customers served in the first busy cycle (which is the same as the total number of departures within the cycle). Since

$$g(p + r) - g(p) = \frac{ED_m(T)}{ED(T)} \geq \frac{ED_m(T)}{ED(T)} = g(\hat{p} + r) - g(\hat{p}),$$

we get the required concavity.

(3) **Strict concavity.** It is enough to consider the latter coupling construction and to justify that, for any $r > 0$ and any $0 \leq p < \hat{p} \leq 1 - r$, $P(D_m(T) > \hat{D}_m(T)) > 0$. One can see that this strict inequality holds on the following event, which has strictly positive probability:

$$\{u_0 \leq r, \quad \theta_1 = t_1, \quad u_1 \in (r + p, r + \hat{p}), \quad \theta_2 = a_{2,2,1}, \quad \theta_3 = \sigma_{3,0}, \quad \theta_4 = \sigma_{4,1}\}.$$  \hspace{1cm} (63)

The latter means that the following sequence of events occurs:

- The first customer gets the magenta color in both three-color systems.
- Then the second customer appears and gets the green color in the first system and red in the second.
- Then the second customer attempts to recolor the first one. This does not work in the first system, where we continue to have one green and one magenta; however, the attempt is successful in the second system, where we get two reds.
- Finally, the first customer leaves the system and then the second leaves the system; this ends the busy cycle.

One can see that $D_m(T) = 1 > \hat{D}_m(T) = 0$ on the event (63).

(4) **Differentiability.** Let $h > 0$ be small. For $p > 0$, introduce a four-color model with the colors green, violet, magenta, and red. Consider the second coupling construction introduced in the subsection ‘Concavity’ above. If we have an arrival at time $T_m$, then the new customer is colored green if $u_n < p - h$, violet if $p - h \leq u_n < p$, magenta if $p \leq u_n < p + h$, and red if $u_n \geq p + h$. Let $A_v$ be the event that there is only one violet arrival and no magenta arrival in the (first) busy cycle, and $A_m$ that there is only one magenta arrival and no violet arrival. These events have equal probabilities that are of order $ch + o(h)$, where $c = \mathbb{E}v$ and $v$ is the mean number of arrivals within a busy cycle; there appear only (at most) three colors (green, violet, and red) on the event $A_v$ and, similarly, at most three colors (green, magenta, and red) on the event $A_m$. Moreover, the dynamics of the process on the events $A_v$ and $A_m$ are identical, with the obvious swap of violet and magenta customers. Therefore, the mean number $\mathbb{E}(D_m(T) | A_v)$ of violet departures given the event $A_v$ coincides with the mean number $\mathbb{E}(D_m(T) | A_m)$ of magenta departures given the event $A_m$. Furthermore, the event that there are two or more violet and/or magenta arrivals has probability $O(h^2) = o(h)$. Since

$$g(p) - g(p - h) = \frac{ED_g(T)}{ED(T)} = ch \cdot \frac{ED_g(T) | A_v)}{ED(T)} + o(h)$$

$$= ch \cdot \frac{ED_m(T) | A_m)}{ED(T)} + o(h) = \frac{ED_m(T)}{ED(T)} + o(h) = g(p + h) - g(p) + o(h),$$
we get

\[ g(p) - g(p - h) \over h = {g(p + h) - g(p) \over h} + o(1). \]

By letting \( h \) tend to infinity, we obtain the desired differentiability of the function \( g \) at the point \( p \).

**Proof of Lemma 6.** The proof follows from the following arguments: when \( p = 1 \), we have \( p_0 < 1 \), and if \( p = 0 \), then \( p_n = 0 \). The function \( p_0 = g(p) \) is monotone increasing, strictly concave, and differentiable. If the right derivative \( g'(0) \) is less than or equal to 1, then there is no other solution to \( p = p_0 \) within \( (0, 1) \). If \( g'(0) > 1 \), there is exactly one other solution, say \( p^* \), to the fixed-point equation \( p = g(p) \equiv p_0 \), such that \( 0 < p^* < 1 \).

**Proof of Lemma 7.** Let \( 0 < \lambda < \hat{\lambda} \). By the splitting theorem for Poisson processes, a Poisson-\( \hat{\lambda} \) process may be obtained from a Poisson-\( \lambda \) process through independent and identically distributed thinning of points with acceptance probability \( r = \hat{\lambda}/\lambda \).

Consider the first busy cycle of length \( T \) for the infinite-server queue with input rate \( \lambda \); call it ‘system 1’. Let \( D \equiv D(T) \) be the number of customers that are served in/depart from system 1 within the time interval \([0, T]\). Then in ‘system 2’ with input rate \( \hat{\lambda} \), the total number \( \hat{D} \) of departures within \([0, T]\) has a conditional binomial distribution \( \text{Bin}(D, r) \); i.e., given any value \( D = k \), we have \( \hat{D} \sim \text{Bin}(k, r) \). Then \( \mathbb{E}\hat{D} = r\mathbb{E}D \).

Let \( D_I \) be the total number of infected departures from system 1 and \( \hat{D}_I \) from system 2, within the time interval \([0, T]\). Clearly, \( D_I \geq \hat{D}_I \) a.s.

We have \( G(h, \lambda) = \mathbb{E}\hat{D}_I \) and \( G(h, \hat{\lambda}) = r\mathbb{E}D \).

For small \( h \), given \( D \), the total number of arrivals of infected customers within \([0, T]\) to system 1 is 0 with probability \( 1 - hD + o(h) \), 1 with probability \( hD + o(h) \), and more than 1 with probability \( o(h) \). Let \( \kappa_i = 1 \) if the \( i \)-th arrival is infected and \( \kappa_i = 0 \) otherwise (here \( \mathbb{P}(\kappa_i = 1) = h \)). Let \( \zeta_i = 1 \) if the \( i \)-th arrival to system 1 is selected for system 2 and \( \zeta_i = 0 \) otherwise (here \( \mathbb{P}(\zeta_i = 1) = r \)). Then

\[ \mathbb{E}D_I = \sum_k \mathbb{P}(D = k) \sum_{i=1}^k \mathbb{P}(A_{k,i}) \mathbb{E}(D_I \mid D = k, A_{k,i}) = hC_\lambda + o(h), \]

where \( C_\lambda = \sum_k \mathbb{P}(D = k) \sum_{i=1}^k \mathbb{E}(D_I \mid D = k, A_{k,i}) \) and, for \( 1 \leq i \leq k, A_{k,i} = \{ \kappa_i = 1, \kappa_j = 0 \text{ for all } 1 \leq j < k \text{ and } j \neq i \} \). Next,

\[ \mathbb{E}\hat{D}_I = \sum_k \mathbb{P}(D = k) \mathbb{E}\left( \sum_{i=1}^k \hat{D}_I(A_{k,i}) \mathbb{I}(\zeta_i = 1) \mid D = k \right) + o(h) \leq \sum_k \mathbb{P}(D = k) \mathbb{E}\left( \sum_{i=1}^k D_I(A_{k,i}) \mathbb{I}(\zeta_i = 1) \mid D = k \right) + o(h) = r\mathbb{E}D_I + o(h), \]

and we get the needed monotonicity. In fact, there is strict inequality in the second line above, since the event \( \{ D = 2, \kappa_1 = 1, \kappa_2 = 0, \zeta_1 = 0, \zeta_2 = 1 \} \) has positive probability and, assuming the occurrence in system 1 of the sequence of events that (1) customer 1 infects customer 2, (2) customer 1 leaves, and (3) customer 2 leaves, we get \( D_I = 2 \) in the first system while \( \hat{D}_I = 0 \) in the second system.

**Appendix C. Monotonicity in \( \alpha \) and \( \beta \)**

The construction of the coupling for the SIS reactor is as follows. The two processes are piecewise constant and may change their states (jump) only at embedded epochs \( T_0 = 0 < T_1 < T_2 < \ldots \). Let \( X_{i,n} = X_i(T_n + 0) \) and \( Y_{i,n} = Y_i(T_n + 0) \), for \( i = 1, 2 \) and \( n = 0, 1, 2, \ldots \). Furthermore, let \( N_n = X_{1,n} + Y_{2,n} \). At each time \( T_n + 0 \), we set an exponential clock of rate \( \lambda \), \( N_n \) clocks of rate \( \mu \), \( N_n \) clocks of rate \( \beta \), and \( N_n(N_n - 1) \) clocks of rate \( \alpha \). We equip all customers, \( i = 1, \ldots, N_n \), with a \( \mu \)-clock and a \( \beta \)-clock, and all pairs of customers, say \( (i, j) \), with an \( \alpha \)-clock. All clocks are mutually independent.
Let $T_{n+1}$ be the time when the first of these clocks rings. If this is the $\lambda$-clock, then a new customer arrives and it (simultaneously) becomes either $I$, with probability $p$, or $S$, with probability $q = 1 - p$. If it is the $i$th $\mu$-clock, then the $i$th customer leaves both systems simultaneously. If it is the $i$th $\beta$-clock, then the $i$th customer becomes $S$ in both systems, regardless of its earlier state. And if it is the $(i, j)$th $\alpha$-clock, then, in the second system (that with infection parameter $\alpha_2$), the $j$th customer becomes $I$ if the $i$th customer is $I$, regardless of the history, and does not change its state if the $i$th was $S$. In the first system (with infection parameter $\alpha_1$), if the $i$th customer is $I$, then the $j$th customer becomes $I$ with probability $\alpha_1/\alpha_2$, and keeps its earlier state (no jump) in all other cases.

With this coupling, direct induction arguments provide the claimed monotonicity.

A similar coupling construction holds for the closed system with the following simplifications and modifications: here $N(t) \equiv N$, for any $t$; there is no $\lambda$-clock; the ringing of a $\mu$-clock means that the corresponding customer moves at random to any of $N$ stations, and we assume that in both systems, customers move to the same stations; when an $\alpha$-clock rings that corresponds to the pair of customers $(i, j)$, the $j$th customer becomes $I$ if $i$ and $j$ are located at the same station.

**Appendix D. The thermodynamic limits as nonlinear Markov processes**

In the transient thermodynamic limit of SIS, at time $t$, a station has a Poisson arrival process of infected (resp. susceptible) customers with an intensity equal to $\mu E[Y(t)]$ (resp. $\mu E[X(t)]$), where $Y(t)$ (resp. $X(t)$) is the number of infected (resp. susceptible) customers in the station at time $t$. The aim of this section is to show that this can be described in terms of a nonlinear Markov dynamics.

This is best explained when looking first at a discrete-time version of the problem. Time is slotted with increments of duration $h$. At time $k = 0$, choose an initial condition in the infinite-dimensional thermodynamic limit. The latter consists of a product-form distribution of customers over stations, with a fixed joint distribution $\mathcal{P}_0$ of infected and susceptible customers in any given station, such that the sum of the two coordinates is Poisson-$\eta$. The number of infected (resp. susceptible) arrivals in time slot 1 is Poisson with parameter $h\mu E[Y_0]$ (resp. $h\mu E[X_0]$), where the expectations are with respect to $\mathcal{P}_0$. In addition, each of the $Y_0$ infected customers tosses a three-face die with respective weights

$$1 - \exp(-h(\beta + \mu)), \quad \frac{\beta}{\beta + \mu} \exp(-h(\beta + \mu)), \quad \frac{\mu}{\beta + \mu} \exp(-h(\beta + \mu)).$$

If the outcome is 1, the customer stays and keeps its SIS state. If the outcome is 2, it stays and changes its SIS state. If the outcome is 3, it leaves. Similarly, conditionally on $Y_0$, each of the $X_0$ infected customers tosses a three-face die with respective weights

$$1 - \exp(-h(\alpha Y_0 + \mu)), \quad \frac{\alpha Y_0}{\alpha Y_0 + \mu} \exp(-h(\alpha Y_0 + \mu)), \quad \frac{\mu}{\alpha Y_0 + \mu} \exp(-h(\alpha Y_0 + \mu)).$$

If the outcome is 1, the customer stays and keeps its SIS state. If the outcome is 2, it stays and changes its SIS state. If the outcome is 3, it leaves. All these define a state $(X_1, Y_1)$. Let $\mathcal{P}_1$ be the distribution of $(X_1, Y_1)$.

The construction for all $k$ is then obtained by induction. Assume the triple $(X_k, Y_k, \mathcal{P}_k)$ is well defined. By applying the same dynamics to this triple, one gets at the same time a state $(X_{k+1}, Y_{k+1})$ and a distribution $\mathcal{P}_{k+1}$.

The key observations are then the following: (a) once the sequence of distributions $\{\mathcal{P}_k\}$ is determined, one can then see the evolution of $\{(X_k, Y_k)\}$ as that of a standard discrete-time discrete-space nonlinear Markov chain. (b) A stationary distribution is a distribution $\mathcal{P}$ such that if $\mathcal{P}_0 = \mathcal{P}$, then $\mathcal{P}_1 = \mathcal{P}$. (c) By tightness arguments, this can be extended to the continuous-time case by letting $h \to 0$.

**Appendix E. Proof of Theorem 2**

Below, $p^*$ is the maximum root of the fixed-point equation $p = g(p)$ for the plain SIS reactor. This means that if $g'(0) \leq 1$, then $p^* = 0$, whereas if $g'(0) > 1$, then $p^*$ is positive and there are two solutions to the fixed-point equation.
Consider an M/M/\infty system in the stationary regime on the time horizon [0, \infty), with input rate \lambda and service rate \mu. The number of customers in the system at any time \( t \), \( N(t) \), has a Poisson distribution with parameter \( \eta = \lambda / \mu \).

**Monotonicity.** Consider the SIS reactor with a Poisson input point process with a time-varying intensity like that discussed in Remark 8. Consider two variants of customer ‘coloring’ at time 0 and of input rates. In the first variant, there are initially \( Y(0) \) infected customers and the input point process of infected customers has an intensity equal to \( \lambda \hat{p}(.), \) while in the second variant there are initially \( \hat{Y}(0) \) infected customers and the intensity of infected customers is \( \lambda \hat{p}(.). \) Here \( p(t) \) and \( \hat{p}(t) \) are two given deterministic functions.

The next result follows from the monotonicity property established in Appendix B—more precisely, see Remark 8.

**Lemma 11.** If \( Y(0) \leq \hat{Y}(0) \) a.s. and \( p(.) \leq \hat{p}(.) \), then, under an appropriate coupling, for all \( t \), \( Y(t) \leq \hat{Y}(t) \) a.s.

In what follows, ‘by simple monotonicity arguments’ means ‘by applying Lemma 11’.

**The upper process.** We introduce an SIS model with a varying fraction of infected customers in the input process and instantaneous extra infections along the lines described in Remark 8.

Recall that we consider a total population dynamics which is that of an M/M/\infty system in the stationary regime on the time horizon \([0, \infty)\), with input rate \( \lambda \) and service rate \( \mu \).

Consider now the following infection/recovery mechanism. We introduce recursively deterministic times \( T^{(0)} = 0 < T^{(1)} < T^{(2)} < \ldots \) and probabilities \( p^{(1)} = 1 > p^{(2)} > \ldots \) such that

(i) \( p^{(n)} \downarrow p^* \) as \( n \to \infty \);

(ii) for any \( n = 1, 2, \ldots \), each customer that arrives in the system within the time interval \( (T^{(n-1)}, T^{(n)}) \) is infected with probability \( p^{(n)} \) and susceptible otherwise, independently of everything else;

(iii) for any \( n = 1, 2, \ldots \), at time \( T^{(n-1)} \), all customers present in the system become infected instantaneously.

In more detail, with \( n = 1, 2, \ldots \), we introduce recursively processes \( (\hat{X}^{(n)}(t), \hat{Y}^{(n)}(t)) \), for \( t \geq T^{(n-1)} \), and then let

\[
(\hat{X}(t), \hat{Y}(t)) = (\hat{X}^{(n)}(t), \hat{Y}^{(n)}(t)) \quad \text{for} \quad t \in [T^{(n-1)}, T^{(n)}].
\]

(64)

First we assume that, at time \( T^{(0)} = 0 \), all customers that are present in the system are infected, and that, starting from time 0, all arriving customers are infected too (i.e., each is infected with probability \( p^{(1)} = 1 \)). We have a time-homogeneous and irreducible Markov jump process on a countable state space, which is clearly aperiodic and positive recurrent. Therefore, there exists a unique stationary distribution which is the limit in law obtained for any initial state, and the speed of convergence to this stationary distribution is exponential. In the stationary regime, the output rate of infected customers is \( p^{(1)}_0 \), which is strictly less than \( p^{(1)} = 1 \). In particular, if one denotes by \( (\hat{X}^{(1)}(t), \hat{Y}^{(1)}(t)) \) the state process in this dynamics, one has \( \mathbb{E}\hat{Y}^{(1)}(t) \to p^{(1)}_0 \eta \) exponentially fast, as \( t \to \infty \).

Let \( \delta \in (0, 1) \) be arbitrarily small. We choose time \( T^{(1)} \) as

\[
T^{(1)} = \min\{t \geq T^{(0)} : \mathbb{E}Y(u)/\eta \leq p^{(1)}_0 + \delta\left(p^{(1)} - p^{(1)}_0\right)/2, \text{ for all } u \geq t\}.
\]

(65)

Then let \( p^{(2)} = p^{(1)}_0 + \delta\left(p^{(1)} - p^{(1)}_0\right)/2 \). By (64), this completes the description of the dynamics of the process \( (\hat{X}(t), \hat{Y}(t)) \) within the first time slot \([T^{(0)}, T^{(1)})\). Note that, by monotonicity and convexity of the function \( p_0 = g(p) \), we get \( p^{(1)}_0 > p^* \).
Assume we have introduced the processes \(\hat{X}(i)(t), \hat{Y}(i)(t)\) on the time intervals \([T^{(i-1)}, \infty)\), for \(i = 1, \ldots, n - 1\), and therefore have defined the process \(\hat{X}(t), \hat{Y}(t)\) on the interval \([0, T^{(n-1)}]\) via (64).

At the beginning of the \(n\)th time slot (at time \(T^{(n-1)}\)), we change all customers present in the system to infected and assume that, starting from this time, each arriving customer is either infected with probability \(p^{(n)} > p^*\), or susceptible otherwise. Then, starting from time \(T^{(n-1)}\), our system again behaves as an irreducible time-homogeneous Markov jump process whose distribution converges exponentially fast to its unique stationary distribution with output fraction of infected customers \(p^{(n)}_0\), which is strictly bigger than \(p^*\) (thanks again to monotonicity and convexity of the function \(g\)). We denote this process by \((\hat{X}^{(n)}(t), \hat{Y}^{(n)}(t)), t \geq T^{(n-1)}\). Then we let

\[
T^{(n)} = \min\{t \geq T^{(n-1)} : E\hat{Y}^{(n)}(u)/\eta \leq p^*_0(n) + \delta(p^{(n)} - p^*_0(n)) \cdot 2^{-n}, \forall u \geq t\}
\]

and \(p^{(n+1)} = p^*_0(n) + \delta(p^{(n)} - p^*_0(n)) \cdot 2^{-n}\). This completes the description of the process \((\hat{X}(t), \hat{Y}(t))\) within the \(n\)th time slot \([T^{(n-1)}, T^{(n)}]\). Again, thanks to monotonicity and convexity of the function \(p_0 = g(p)\), we get \(p^{(n)}_0 > p^{(n+1)}_0 > p^*\).

Thus, we have defined the process \((\hat{X}(t), \hat{Y}(t))\) for all \(t \geq 0\). It is left to explain the convergence (i). We know that there is no solution to the equation \(p_0 = g(p)\) bigger than \(p^*\), and the monotone sequences \(p^{(n)}_0\) and \(p^{(n)}_0^*\) converge to the same limit which is a solution to this fixed-point equation. The fact that this is the maximal solution proves the result.

**Comparison of the upper process and the thermodynamic limit process.**

As shown in Appendix D, under the propagation of chaos ansatz, the dynamics of any station in the SIS TL can be seen as a nonlinear Markov jump process \((X(t), Y(t))\) with a certain fraction \(p^*_0(t)\) of infected customers at time \(t\) (the fraction such that at any time \(t\), \(\lambda p^*_0(t) = \mu E[Y(t)]\)).

By construction, \(X(t) + Y(t) = N(t)\) for all \(t \geq 0\), where \(N(t)\) is the Poisson process describing the dynamics of the stationary M/M/\(\infty\) system and also \(N(t) = \hat{X}(t) + \hat{Y}(t)\) a.s. (where the latter are the state variables in the upper system described above).

**Proposition 2.** For all \(t \geq 0\), in a proper coupling, \(Y(t) \leq \hat{Y}(t)\) a.s. Therefore, \(\limsup_{t \to \infty} E[Y(t)] \leq p^*\).

**Proof.** First, by simple monotonicity arguments, \(Y(t) \leq \hat{Y}^{(1)}(t)\) a.s. for all \(t \geq 0\). In particular, \(E[Y(t)]/\eta \leq p^*\) for all \(t \geq T^{(1)}\). Consider now the time interval \([T^{(1)}, \infty)\) and compare the processes \((\hat{X}^{(2)}(t), \hat{Y}^{(2)}(t))\) and \((X(t), Y(t))\) within this interval. By construction, at the initial time \(T^{(1)}\) of this time period, \(\hat{Y}^{(2)}(T^{(1)}) \geq Y(T^{(1)})\) a.s., and for all \(t \geq T^{(1)}\), the input rate of infected customers in the auxiliary upper process is bigger than that in the thermodynamic limit. Then it follows from simple sample-path arguments that \(Y(t) \leq \hat{Y}^{(2)}(t)\) a.s. for all \(t \geq T^{(1)}\), and in particular, \(E[Y(t)] \leq E[\hat{Y}^{(2)}(t)]\), where the right-hand side is smaller than \(p^*_0(3)\), for all \(t \geq T^{(3)}\).

The induction argument implies that for any \(n = 1, 2, \ldots\) and any \(k < n\) and \(t \geq T^{(n-1)}\), the following inequalities hold a.s.: \(Y(t) \leq \hat{Y}^{(k)}(t)\), and therefore \(Y(t) \leq \hat{Y}(t)\). It is left to show that \(\lim p^{(k)} = p^*\). However, this is clear since \(p^*\) is the maximal solution to the equation \(p = g(p)\) and, by convexity, all \(p^{(k)} > p^*\) since \(p^{(k)}_0 = g(p^{(k)}_0) < p^*\).

**Corollary 5.** If \(g'(0) \leq 1\), then there is extinction of the infection process in that \(\lim_{t \to \infty} E[Y(t)] = 0\), for all initial distributions of infected customers in the system.

The next corollary follows from simple monotonicity arguments. Before stating it, we recall the following result on the fixed point of the SIS reactor. Assume \(g'(0) > 0\), which implies that \(p^* > 0\). Any SIS reactor is a time-homogeneous Markov process \((\hat{X}(t), \hat{Y}(t))\) with a countable state space, which is irreducible, positive recurrent, and ergodic. In particular, for \(p = p^*\), for all initial conditions \((\hat{X}(0), \hat{Y}(0))\), this Markov process converges to a limiting stationary Markov process with \(\mu E[Y] = p^*\lambda\). Denote this last stationary process by \((\hat{X}^*(t), \hat{Y}^*(t))\). This last process can be used to build a specific example \((X^*(t), Y^*(t), \mu_p^*), t \geq 0\), of the nonlinear Markov chain of Appendix D, where the initial distribution \(\mu_p^*\).
is that of $(\hat{X}^*(0), \hat{Y}^*(0))$. This distribution is invariant for this nonlinear dynamics. By this, we mean that it makes the Markov chain homogeneous and stationary, with an input rate of infected customers which is constant, equal to $\lambda p^*$, and equal to the mean output rate of infected customers.

**Corollary 6.** Consider the process $Y^*(t)$ defined above. Then $\hat{Y}(t) \geq Y^*(t)$ a.s. for all $t \geq 0$, and $\mathbb{P}(\hat{Y}(t) = Y^*(t)) \to 1$ as $t \to \infty$, where $\hat{Y}(t)$ is the upper process of Proposition 2.

Consider the nonlinear Markov process $Y(t)$ defined in Appendix D with any initial distribution such that $Y(0) \geq Y^*(0)$ a.s., with $Y^*(.)$ defined above. Then $\hat{Y}(t) \geq Y(t) \geq Y^*(t)$ a.s. and $\mathbb{P}(\hat{Y}(t) = Y(t) = Y^*(t)) \to 1$.

The only thing to comment upon is the last statement. It follows from the facts that all $Y$-variables are integer-valued and that the monotone convergence of integer-valued random variables is necessarily also a coupling (or total variation) convergence.

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**References**

[1] **Baccelli, F. and Brémaud, P.** (2003). *Elements of Queueing Theory: Palm Martingale Calculus and Stochastic Recurrences*, 2nd edn. Springer, Berlin, Heidelberg.

[2] **Baccelli, F., Foss, S. and Shneer, S.** (2022). Migration–contagion processes. Preprint. Available at [https://arxiv.org/abs/2208.03512](https://arxiv.org/abs/2208.03512).

[3] **Baccelli, F. and Ramesan, N.** (2022). A computational framework for evaluating the role of mobility on the propagation of epidemics on point processes. *J. Math. Biol.* 84, article no. 4.

[4] **Britton, T. and Neal, P.** (2010). The time to extinction for a stochastic SIS-household-epidemic model. *J. Math. Biol.* 61, 763–779.

[5] **Donnelly, P.** (1993). The correlation structure of epidemic models. *Math. Biosci.* 117, 49–75.

[6] **Figueiredo, D., Iacobelli, G. and Shneer, S.** (2020). The end time of SIS epidemics driven by random walks on edge-transitive graphs. *J. Statist. Phys.* 179, 651–671.

[7] **Ganesan, G.** (2015). Infection spread in random geometric graphs. *Adv. Appl. Prob.* 47, 164–181.

[8] **Hao, C. V.** (2018). Super-exponential extinction time of the contact process on random geometric graphs. *Combinatorics Prob. Comput.* 27, 162–185.

[9] **Krishnarajah, I., Cook, A., Marion, G. and Gibson, G.** (2005). Novel moment closure approximations in stochastic epidemics. *Bull. Math. Biol.* 67, 855–873.

[10] **Kuehn, C.** (2016). Moment closure—a brief review. In *Control of Self-Organizing Nonlinear Systems*, Springer, Cham, pp. 253–271.

[11] **Liggett, T. M.** (1999). *Stochastic Interacting Systems: Contact, Voter and Exclusion Processes*. Springer, Berlin, Heidelberg.

[12] **Ménard, L. and Singh, A.** (2016). Percolation by cumulative merging and phase transition for the contact process on random graphs. *Ann. Sci. École Norm. Sup.* 49, 1189–1238.

[13] **Newman, M. E. J.** (2018). *Networks*. Oxford University Press.

[14] **Pastor-Satorras, R., Castellano, C., Van Mieghem, P. and Vespignani, A.** (2015). Epidemic processes in complex networks. *Rev. Modern Phys.* 87, article no. 925.

[15] **Pemantle, R.** (1992). The contact process on trees. *Ann. Prob.* 20, 2089–2116.