Markovian SIR model for opinion propagation

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Abstract—In this work, we propose a new model for the dynamics of single opinion propagation at a size-limited location with a low population turnover. This means that a maximum number of individuals can be supported by the location and that the allowed individuals have a long sojourn time before leaving the location. The individuals can have either no opinion (S), a strong opinion that they want to spread (I), or an opinion that they keep for themselves (R); the letters stem from the popular Susceptible-Infectious-Recovered (SIR) epidemic model. Furthermore, we consider a variable opinion transmission rate. Hence, the opinion spreading is modelled as a Markovian non-standard SIR epidemic model with stochastic arrivals, departures, infections and recoveries. We evaluate the system performance by two complementary approaches: we apply a numerical but approximate solution approach which relies on Maclaurin series expansions and we investigate the fluid limit of the system at hand. Finally, we illustrate our approach by some numerical examples.

I. Introduction

Given the rapid growth of companies in the internet sector that base their revenue model on advertisement (such as Google, Facebook, etc.) and the ascent of social networks in particular, the study of opinion spreading is a trending topic, and there is a very strong interest in understanding how new opinions spread through a community. In this paper, we study opinion spreading at a specific location. This can be understood as either a virtual location, as on a group page in a social network, or a physical location, for example at an airport where mobile users interact and receive personalised ads. As these locations have a (geographically or virtually) constrained space, we consider a limited population size.

During the last decades, the main approach for modelling such opinion spreading is the contagion approach, which is based on the spreading of diseases. Most models for the transmission of infectious diseases descend from the classical SIR model [12]. SIR is an abbreviation for susceptible (S), infectious (I) and recovered (R). These are consequently the only possible states that an individual can be in when we discuss SIR type diseases, and the possible transitions between these states follow the order S → I → R. In particular, the SIR model suggests that if a healthy individual encounters a sick individual, there is a specific probability that the healthy individual will get infected and there is a specific probability that an infected individual will recover from the disease. Opinion spreading can be interpreted as behaving like a disease: if an individual without a specific opinion about a topic (a non-opinionated individual) will encounter a strongly opinionated individual, the first individual will, with some probability, get also strongly opinionated. Afterwards, strongly opinionated individuals may, with some probability, become opinionated: they stop transmitting their opinion to other non-opinionated individuals and keep their own opinion.

In the classical stochastic SIR epidemic model, many unrealistic assumptions are made ([2], [4]). For example, one assumes that the population is constant and that the contact times and the recovery times are exponentially distributed. As a consequence, many modifications of the model have been introduced and analysed in literature, each contribution relaxing some of the different assumptions. In Britton's paper [4], a general SIR epidemic model is used where the traditional contact rate is replaced by a cyclically varying renewal process with k states. Clémençon [5] studies a specific stochastic epidemic model that accounts for the effect of contact tracing on the spread of an infectious disease. In particular, the situation is investigated in which individuals identified as infected may contribute to detecting other infectious individuals by providing information related to individuals with whom they have had possibly infectious contacts.

In the present paper, we consider a location area where at most L individuals can be present and where individuals of individual type k arrive according to a Poisson process with parameter λ_k. Individuals remain at the location for an exponentially distributed amount of time with mean $1/\mu$ and then leave. Furthermore, the probability for non-opinionated individuals to become strongly opinionated depends on the number of individuals of the different types present at the location. In particular, the higher the relative number of individuals that want to transmit their opinion, the higher the probability that an individual without an opinion will get one. We also assume that the higher the number of non-opinionated individuals, the higher the probability that one of them gets a strong opinion. Concerning the recovery rate, we assume that each strongly opinionated individual has a fixed probability to become opinionated and also that, the more strongly opinionated individuals there are, the higher the probability that one of them becomes opinionated. Further explanation and the motivation on the above assumptions is given in section II. For ease of understanding, non-opinionated, strongly opinionated and opinionated individuals are further described as susceptible (S), infected (I) and recovered (R) individuals, respectively.

This paper investigates approximations for the defined SIR epidemic system. In particular, we propose a numerical evaluation method for this Markovian epidemic system which relies on a Maclaurin series expansion of the steady-state probability vector. For an overview on the technique of series expansions in stochastic systems, which is also known under the names light traffic analysis or stochastic perturbation, we refer the reader to the survey in [3]. One of the methods to establish series expansions of stochastic models is given via an updating formula in [10]. In [7], cases for which numerical computation of the steady-state vector is possible through a Maclaurin expansion in a parameter μ are given and

the approach is illustrated by a practical example of a paired queueing system.

In addition to the MacLaurin series approach, we also derive a fluid limit of the Markov chain. Fluid limits are a popular mathematical technique (see e.g. [8], [9]) which (when a good scaling is found) allow to focus on the salient features of the stochastic process while discarding 'second-order fluctuations' around this main trend. In the present paper, it helps to make the link with more standard deterministic SIR models. Also, the fluid scaling applied for this model (arrival rates and location capacity are sent to infinity), is highly different and complementary to the MacLaurin series expansion limit (which holds for low departure rates μ). We thus aim to view this difficult-to-analyse Markov model from different limiting cases, and gain new insights by combining them. We also note that the derivation of the fluid limit as performed in this paper also lends itself naturally to refinements in the form of diffusion results, but this is considered to be outside of the scope of the current paper.

The remainder of this paper is organised as follows. In section II, the model is described and special cases are discussed. Next, in section III the numerical series expansion approach is applied to the opinion propagation system at hand. In section IV we derive a formally justified fluid model from the original Markov model. To illustrate both approaches, section V considers various numerical examples. Finally, conclusions are drawn in section VI.

II. MARKOV CHAIN MODEL

As arrivals of the 3 types of individuals are modelled by Poisson processes and the lifetime distribution of an individual at the location is exponential, the state of the system can be described by a vector $\mathbf{i} = (i_R, i_I, i_S) \in \mathcal{L}$ where i_R, i_I and i_S are respectively equal to the number of recovered, infected and susceptible individuals. We let $\mathcal{L} = \{(i_R, i_I, i_S) \in \mathbb{N}^3 | s(\mathbf{i}) \leq L\}$ denote the state space of this Markov chain and the sum of all the individuals at the location $s(\mathbf{i}) = \sum_{k \in K} i_k \leq L$, $k \in K = \{R, I, S\}$ must be smaller than or equal to the maximum number of individuals L. Let $\pi(\mathbf{i})$ denote the steady-state probability distribution of the Markov chain which satisfies the following balance equations:

$$\pi(\mathbf{i})\Big(\sum_{k \in K} \mathbb{1}_{\{i_k > 0\}} \mu i_k + \sum_{k \in K} \mathbb{1}_{\{s(\mathbf{i}) < L\}} \lambda_k$$
$$+ \mathbb{1}_{\{i_S > 0\}} \alpha_{si}(i_R, i_I, i_S) + \mathbb{1}_{\{i_I > 0\}} \alpha_{ir}(i_I) \Big)$$
$$= \sum_{k \in K} \pi(\mathbf{i}_{\mathrm{up},k}) \mu(i_k + 1) \mathbb{1}_{\{s(\mathbf{i}) < L\}} + \sum_{k \in K} \pi(\mathbf{i}_{\mathrm{down},k})$$
$$\lambda_k \mathbb{1}_{\{i_k > 0\}} + \pi(i_R, i_I - 1, i_S + 1) \alpha_{si}(i_R, i_I - 1, i_S + 1)$$
$$\mathbb{1}_{\{(i_R, i_I - 1, i_S + 1) \epsilon \mathcal{L}\}} + \pi(i_R - 1, i_I + 1, i_S) \alpha_{ir}(i_I + 1)$$
$$\mathbb{1}_{\{(i_R - 1, i_I + 1, i_S) \epsilon \mathcal{L}\}}. \quad (1)$$

Indeed, as previously mentioned, we assume that the general state-dependent infection rates are captured in the function $\alpha_{si}(i_R, i_I, i_S)$, and the recovery rates, which depend only on the number of infected individuals i_I, are captured in the function $\alpha_{ir}(i_I)$. Finally, the notations $\mathbf{i}_{\mathrm{up},k}$ and $\mathbf{i}_{\mathrm{down},k}$ describe respectively the increase and the decrease of the element i_k of the vector $\mathbf{i}$ by one.
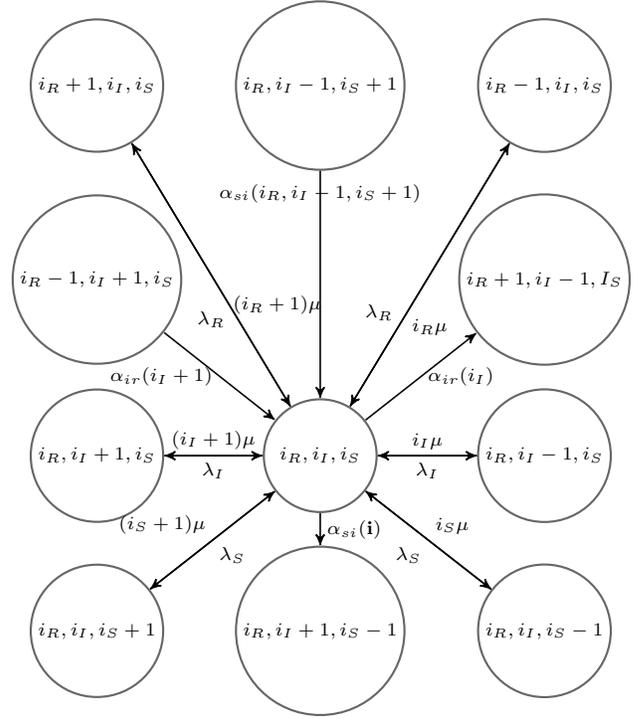

Figure 1. Transition rate diagram of state (i_R, i_I, i_S).

To calculate the Maclaurin series expansion in μ in section III, we need to assume that one of the arrival rates λ_k with $k = \{R, I, S\}$, the infection rate α_{si} and the recovery rate α_{ir} are positive.

Fig. 1 shows a fragment of the transition rate diagram of the opinion spreading model in state (i_R, i_I, i_S). For this figure, we assume that the sum of all individuals at each given state is equal to or is less than the maximum number of individuals L.

Special case 1

If we assume that each susceptible and infected individual has respectively a constant probability to get infected or recovered, i.e. $\alpha_{si}(i_R, i_I, i_S) = i_S \alpha_{si}$ and $\alpha_{ir}(i_I) = i_I \alpha_{ir}$, then the mean number of each type in steady state can be calculated explicitly. Indeed, as the departure rate of each individual is equal to μ, the total number of individuals is distributed as in a classic $M/M/L/L$ queue, with arrival rate $\lambda = \lambda_R + \lambda_I + \lambda_S$ and departure rate μ, for which the steady-state distribution can be found in every queueing-theory textbook. We then compute the stationary fractions of each type p_R, p_I and p_S as follows:

$$p_R = \frac{\lambda_R}{\lambda} + \frac{\lambda_I}{\lambda} \frac{\alpha_{ir}}{\alpha_{ir} + \mu} + \frac{\lambda_S}{\lambda} \frac{\alpha_{ir}\alpha_{si}}{(\alpha_{ir} + \mu)(\alpha_{si} + \mu)},$$
$$p_I = \frac{\lambda_I}{\lambda} \frac{\mu}{\alpha_{ir} + \mu} + \frac{\lambda_S}{\lambda} \frac{\mu \alpha_{si}}{(\alpha_{ir} + \mu)(\alpha_{si} + \mu)},$$
$$p_S = \frac{\lambda_S}{\lambda} \frac{\mu}{\alpha_{si} + \mu}.$$

Indeed, the fraction of susceptible individuals p_S is given by the fraction of arriving susceptible individuals multiplied by

the fraction of time during which it has turned into one of the other types. It can be checked that $p_R + p_I + p_S = 1$. As we know the distribution of the total number of individuals (denoted as $\Pr[Q = \ell]$) by the Erlang loss formula, we can then compute the distribution of the number Q_k of individuals of a certain type $k \in K = \{R, I, S\}$ as follows:

$$\Pr[Q_k = n] = \sum_{\ell=n}^{L} \binom{\ell}{n} \Pr[Q = \ell] p_k^n (1 - p_k)^{\ell-n}. \quad (2)$$

Special case 2

In the numerical examples and for the fluid model, we often consider the following special case for the functions $\alpha_{si}(i_R, i_I, i_S)$ and $\alpha_{ir}(i_I)$:

$$\alpha_{si}(i_R, i_I, i_S) = \left(\alpha_{si}^0 + \alpha_{si}^1 \frac{i_I}{i_R + i_I + i_S} \right) i_S,$$

$$\alpha_{ir}(i_I) = \alpha_{ir}^0 i_I.$$

where α_{si}^0, α_{si}^1 and α_{ir}^0 are given (positive) rates. The motivation behind this special case is as follows. Firstly, we assume that the higher the relative number of infected individuals at the location, the higher the rate at which the infection spreads. In the case of opinion spreading, the rate that a not opinionated individual gets an opinion increases as the number of individuals that want to transmit their opinion, i.e. strongly opinionated individuals, increases. Secondly, we also add a constant term α_{si}^0 so that susceptible individuals may become infected by themselves (i.e. without the presence of other infected individuals). Finally, we assume that infected individuals may eventually get recovered: a strongly opinionated individual may, after a while, stop transmitting his opinion and keep it for himself with rate α_{ir}^0.

While the former system of equations (1) is easily solved with a low maximum number of individuals, the state space explodes for even a reasonable L and a direct solution is computationally infeasible.

III. MACLAURIN SERIES EXPANSIONS

To mitigate the state space explosion problem, we rely on a Maclaurin series expansion in μ. If $\pi(\mathbf{i})$ is analytic in $\mu = 0$, it admits the representation,

$$\pi(\mathbf{i}) = \sum_{n=0}^{\infty} \pi_n(\mathbf{i}) \mu^n,$$

for $0 \le \mu < \mu_0$ and for $\mathbf{i} \in \mathcal{C}$.

Substituting the former expression in the balance equations,

we get

$$\sum_{n=0}^{\infty} \pi_n(\mathbf{i}) \mu^n \Big(\sum_{k \in K} \mathbb{1}_{\{i_k > 0\}} \mu i_k + \sum_{k \in K} \mathbb{1}_{\{s(\mathbf{i}) < L\}} \lambda_k$$
$$+ \mathbb{1}_{\{i_S > 0\}} \alpha_{si}(i_R, i_I, i_S) + \mathbb{1}_{\{i_I > 0\}} \alpha_{ir}(i_I) \Big)$$
$$= \sum_{n=0}^{\infty} \sum_{k \in K} \pi_n(\mathbf{i}_{\text{up},k}) \mu^{n+1} (i_k + 1) \mathbb{1}_{\{s(\mathbf{i}) < L\}}$$
$$+ \sum_{n=0}^{\infty} \sum_{k \in K} \pi_n(\mathbf{i}_{\text{down},k}) \lambda_k \mu^n \mathbb{1}_{\{i_k > 0\}}$$
$$+ \sum_{n=0}^{\infty} \pi_n(i_R, i_I - 1, i_S + 1) \alpha_{si}(i_R, i_I - 1, i_S + 1) \mu^n$$
$$\times \mathbb{1}_{\{(i_R, i_I - 1, i_S + 1) \epsilon \mathcal{L}\}}$$
$$+ \sum_{n=0}^{\infty} \pi_n(i_R - 1, i_I + 1, i_S) \alpha_{ir}(i_I + 1) \mu^n$$
$$\times \mathbb{1}_{\{(i_R - 1, i_I + 1, i_S) \epsilon \mathcal{L}\}}. \quad (3)$$

For $\mathbf{i} \in \mathcal{L}^* = \mathcal{L} \setminus \{(L, 0, 0)\}$, comparison of the terms in μ^0 on both sides of the former equation yields

$$\pi_0(\mathbf{i}) = 0, \quad (4)$$

whereas comparison of the terms in μ^n for $n > 0$ gives

$$\pi_n(\mathbf{i}) =$$
$$\frac{1}{\Delta(\mathbf{i})} \Big(\sum_{k \in K} \pi_{n-1}(\mathbf{i}_{\text{up},k})(i_k + 1) \mathbb{1}_{\{s(\mathbf{i}) < L\}}$$
$$+ \sum_{k \in K} \pi_n(\mathbf{i}_{\text{down},k}) \lambda_k \mathbb{1}_{\{i_k > 0\}}$$
$$+ \pi_n(i_R, i_I - 1, i_S + 1) \alpha_{si}(i_R, i_I - 1, i_S + 1)$$
$$\times \mathbb{1}_{\{(i_R, i_I - 1, i_S + 1) \epsilon \mathcal{L}\}}$$
$$+ \pi_n(i_R - 1, i_I + 1, i_S) \alpha_{ir}(i_I + 1)$$
$$\times \mathbb{1}_{\{(i_R - 1, i_I + 1, i_S) \epsilon \mathcal{L}\}}$$
$$- \mathbb{1}_{\{n > 0\}} \pi_{n-1}(\mathbf{i}) \sum_{k \in K} i_k \mathbb{1}_{\{i_k > 0\}} \Big), \quad (5)$$

with,

$$\Delta(\mathbf{i}) = \sum_{k \in K} \Big(\mathbb{1}_{\{s(\mathbf{i}) < L\}} \lambda_k + \mathbb{1}_{\{i_I > 0\}} \alpha_{ir}(i_I)$$
$$+ \mathbb{1}_{\{i_S > 0\}} \alpha_{si}(i_R, i_I, i_S) \Big). \quad (6)$$

As detailed in [7], we can use the above equation to compute new terms very efficiently, by iterating over the state space in lexicographic fashion, as on the RHS only entries of either order $n - 1$ or entries of order n but with a lower lexicographic index are present.

Performance measures

Once the series expansion of the steady-state distribution has been obtained, the expansion of various performance

measures directly follows. Let $\mathbf{X} \sim \pi$, then for a performance measure $J = \mathrm{E}[f(\mathbf{X})]$, we have

$$J = \sum_{\mathbf{i} \in \mathcal{L}} f(\mathbf{i})\pi(\mathbf{i}) = \sum_{\mathbf{i} \in \mathcal{L}} f(\mathbf{i}) \sum_{n=0}^{\infty} \pi_n(\mathbf{i})\mu^n$$

$$= \sum_{n=0}^{\infty} \sum_{\mathbf{i} \in \mathcal{L}} f(\mathbf{i})\pi_n(\mathbf{i})\mu^n = \sum_{n=0}^{\infty} J_n \mu^n, \quad (7)$$

for $0 \leq \mu < \mu_0$, with

$$J_n = \sum_{\mathbf{i} \in \mathcal{L}} f(\mathbf{i})\pi_n(\mathbf{i}).$$

The interchange of the summations is justified by the finiteness of $\mathcal{L}$ and the convergence of $\sum_n \pi_n(\mathbf{i})\mu^n$ for all $\mathbf{i} \in \mathcal{L}$. As such, any term J_n in the expansion of a performance measure J can be calculated from the corresponding vector π_n of the expansion of the steady-state vector π. Performance measures of interest include amongst others the jth order moment of the queue content of the kth queue ($f(\mathbf{i}) = i_k{}^j$).

IV. FLUID LIMIT

In this section, we develop a fluid limit for the model described in this contribution. To this end, we make use of the versatile random time-change formulation as proposed by Ethier and Kurtz in their book [8].

Basically, our task consists of two steps: first we write down a time-change formulation of the Markov process at hand, and then we use a strong law of large numbers for Poisson processes so as to transform the stochastic process into a differential equation. For completeness, we state this result here as a lemma.

Lemma 1. *Let Y be a unit rate Poisson process. Then for any $U > 0$,*

$$\lim_{M \to \infty} \sup_{0 \leq u \leq U} |M^{-1}Y(Mu) - u| = 0.$$

Let $\{X_r^M(t), X_i^M(t), X_s^M(t)\}$ denote a continuous-time Markov process, the three components respectively denoting the number of recovered, infected, susceptible individuals at time t. Here M denotes the scaling parameter, which affects the system in the following way: arrival rates of the three types are scaled by M ($\lambda_* \mapsto M \cdot \lambda_*$), and the capacity L of the system is likewise scaled with $M : L \mapsto M \cdot L$. We consider in this section both finite and infinite capacity systems; in the latter case of course no capacity scaling is needed. For notational convenience, we introduce

$$X^M(t) = X_r^M(t) + X_i^M(t) + X_s^M(t).$$

The number of susceptible individuals present at time t consists of: (1) the number of susceptible individuals present at time $t = 0$, which we denote as $X_s^M(0)$; (2) susceptible individuals arriving during the interval $(0, t]$ with rate $M\lambda_S$; (3) minus the susceptible individuals that get infected (with a rate that depends on all three processes X_r^M, X_i^M, X_s^M); (4) lastly, we need to subtract the individuals that have left the system due to service completion.

We formulate this in terms of a number of independent unit rate Poisson processes Y_{**} as follows, where the subscripts

denote the source and destination of the process at hand with s, i, r, o denoting susceptible, infected, recovered and outside respectively. This manner of writing Markov processes in terms of Poisson processes evaluated at times which depend on the past of said Markov process (aptly denoted as the random time-change method in [8]) is very handy when it comes to smoothly establishing the corresponding fluid models. We have that

$$X_s^M(t) = X_s^M(0) + Y_{os}\Big(M\lambda_S \int_0^t \mathbb{1}_{\{X^M(\tau) < M \cdot L\}} d\tau\Big)$$

$$- Y_{si}\Big(\int_0^t \alpha_{si}^M(X_r^M(\tau), X_i^M(\tau), X_s^M(\tau))$$

$$- Y_{so}\Big(\mu \int_0^t X_s^M(\tau)d\tau\Big).$$

Likewise, for the process of the number of infected individuals, we have at time t: (1) individuals present at time 0; (2) arrivals of infected individuals in $(0, t]$ (when there is room); (3) susceptible individuals getting infected. Departures occur because of (4) infected individuals recovering and (5) infected individuals leaving the system. This leads to

$$X_i^M(t) = X_i^M(0) + Y_{oi}\Big(M\lambda_I \int_0^t \mathbb{1}_{\{X^M(\tau) < M \cdot L\}} d\tau\Big)$$

$$+ Y_{si}\Big(\int_0^t \alpha_{si}^M(X_r^M(\tau), X_i^M(\tau), X_s^M(\tau))d\tau\Big)$$

$$- Y_{ir}\Big(\int_0^t \alpha_{ir}^M(X_i^M(\tau))d\tau\Big)$$

$$- Y_{io}\Big(\mu \int_0^t X_i^M(\tau)d\tau\Big).$$

And for the process of the number of recovered individuals, we have

$$X_r^M(t) = X_r^M(0) + Y_{or}\Big(M\lambda_R \int_0^t \mathbb{1}_{\{X^M(\tau) < M \cdot L\}} d\tau\Big)$$

$$+ Y_{ir}\Big(\int_0^t \alpha_{ir}^M(X_i^M(\tau))d\tau\Big)$$

$$- Y_{ro}\Big(\mu \int_0^t X_r^M(\tau)d\tau\Big).$$

Next, we introduce the scaled processes $\bar{X}_s := M^{-1}X_s^M$, $\bar{X}_i := M^{-1}X_i^M$, $\bar{X}_r := M^{-1}X_r^M$ and $\bar{X} := M^{-1}X^M$. For the state-dependent infection rates α_{si}, we assume that asymptotically as $M \to \infty$,

$$M^{-1}\alpha_{si}^M(Mi_R, Mi_I, Mi_S) \to \bar{\alpha}_{si}(i_R, i_I, i_S),$$

and likewise for the recovery rates α_{ir}. It can be easily checked that both special cases of section II agree with the above assumption.

Furthermore, we assume that $M^{-1}X_*^M(0)$ converges to the deterministic constant $x_*(0)$ as $M \to \infty$ (for $*$ equal to i_R, i_I, i_S). If we introduce the scaled processes in the equations

for $X_*^M(t)$, then we

$$\bar{X}_s(t) = M^{-1}X_s^M(0) + M^{-1}Y_{os}\left(M\lambda_S \int_0^t \mathbb{1}_{\{\bar{X}(\tau)<L\}}d\tau\right)$$

$$- M^{-1}Y_{si}\left(M \int_0^t \bar{\alpha}_{si}(\bar{X}_r(\tau), \bar{X}_i(\tau), \bar{X}_s(\tau))d\tau\right)$$

$$- M^{-1}Y_{so}\left(M\mu \int_0^t \bar{X}_s(\tau)d\tau\right);$$

$$\bar{X}_i(t) = M^{-1}X_i^M(0) + M^{-1}Y_{oi}\left(M\lambda_I \int_0^t \mathbb{1}_{\{\bar{X}(\tau)<L\}}d\tau\right)$$

$$+ M^{-1}Y_{si}\left(M \int_0^t \bar{\alpha}_{si}(\bar{X}_r(\tau), \bar{X}_i(\tau), \bar{X}_s(\tau))d\tau\right)$$

$$- M^{-1}Y_{ir}\left(M \int_0^t \bar{\alpha}_{ir}(\bar{X}_i(\tau))d\tau\right)$$

$$- M^{-1}Y_{io}\left(M\mu \int_0^t \bar{X}_i(\tau)d\tau\right).$$

$$\bar{X}_r(t) = M^{-1}X_r^M(0) + M^{-1}Y_{or}\left(M\lambda_R \int_0^t \mathbb{1}_{\{\bar{X}(\tau)<L\}}d\tau\right)$$

$$+ M^{-1}Y_{ir}\left(M \int_0^t \bar{\alpha}_{ir}(\bar{X}_i(\tau))d\tau\right)$$

$$- M^{-1}Y_{ro}\left(M\mu \int_0^t \bar{X}_r(\tau)d\tau\right).$$

As every term is either deterministic or of the form $M^{-1}Y_*(M\cdots)$, we can apply Lemma 1, and state that in the limit the process $(\bar{X}_r(t), \bar{X}_i(t), \bar{X}_s(t))$ converges to a deterministic limit $(x_r(t), x_i(t), x_s(t))$ (with $x(t) := x_r(t) + x_i(t) + x_s(t)$) satisfying the following integral equations:

$$x_s(t) = x_s(0) + \lambda_S \int_0^t \mathbb{1}_{\{x(\tau)<L\}}d\tau$$

$$- \int_0^t \bar{\alpha}_{si}(x_r(\tau), x_i(\tau), x_s(\tau))d\tau - \mu \int_0^t x_s(\tau)d\tau;$$

$$x_i(t) = x_i(0) + \lambda_I \int_0^t \mathbb{1}_{\{x(\tau)<L\}}d\tau$$

$$+ \int_0^t \bar{\alpha}_{si}(x_r(\tau), x_i(\tau), x_s(\tau))d\tau$$

$$- \int_0^t \bar{\alpha}_{ir}(x_i(\tau))d\tau - \mu \int_0^t x_i(\tau)d\tau;$$

$$x_r(t) = x_r(0) + \lambda_R \int_0^t \mathbb{1}_{\{x(\tau)<L\}}d\tau$$

$$+ \int_0^t \bar{\alpha}_{ir}(x_i(\tau))d\tau - \mu \int_0^t x_r(\tau)d\tau.$$

These in turn can be formulated as a system of (non-linear) differential equations:

$$\dot{x}_s(t) = \lambda_S \mathbb{1}_{\{x(t)<L\}} - \bar{\alpha}_{si}(x_r(t), x_i(t), x_s(t))$$
$$- \mu x_s(t);$$
$$\dot{x}_i(t) = \lambda_I \mathbb{1}_{\{x(t)<L\}} + \bar{\alpha}_{si}(x_r(t), x_i(t), x_s(t))$$
$$- \bar{\alpha}_{ir}(x_i(t)) - \mu x_i(\tau);$$
$$\dot{x}_r(t) = \lambda_R \mathbb{1}_{\{x(t)<L\}} + \bar{\alpha}_{ir}(x_i(t)) - \mu x_r(t).$$

This can be solved efficiently with one of the numerous well-honed numerical toolboxes for differential equations. We also note that the equilibrium points (i.e. set $\dot{x}_*(t)$ equal to zero in the LHS of the above equations) for special case 2 and $L = \infty$ can be found explicitly as the solutions of a quadratic equation, but we omit the exact expressions due to space constraints.

V. NUMERICAL RESULTS

To illustrate our numerical approach, we now assess the accuracy of the series expansion technique by means of some numerical examples. First, consider a system with a maximum number of individuals L equal to 5. Moreover, the arrival intensity of each type of individual is equal to 1 and we consider the second special case with α_{ir}^0, α_{si}^0 and α_{si}^1 all equal to 3. Figs. 2, 3 and 4 depict respectively the mean recovered queue content, the mean infected queue content and the mean susceptible queue content versus the lifetime rate μ. Series expansions of various orders N are depicted as indicated ($N = 1, 5, 10$), as well as simulation results which allow to assess the accuracy of the series expansions. As expected, the mean number of recovered individuals decreases and the mean number of infected and susceptible individuals increase as the departure rate increases. Moreover, for $\mu = 0$, the population consists only of recovered individuals as their lifetime is infinite such that all individuals get recovered eventually. Also, we observe that the approximation method is fairly accurate for low orders of the expansions (e.g. highly accurate for $N = 10$ in Fig. 4). Finally, for these parameter settings, the mean number of infected and susceptible individuals have a non-linear behaviour in μ. This is not the case for Fig. 2; the mean number of recovered individuals has a linear behaviour in μ such that a series expansion with $N = 1$ gives an accurate result.

Special case 1

In contrast to the previous part, we now look at the first special case as described in section II, where the mean number of each individual type are calculated explicitly. Figs. 5 and 6 depict the mean number of individuals of type I and S versus the arrival rate of infected individuals λ_I for different values of the infection rate α_{si}. Moreover, the maximum number of individuals allowed at the location L equals 10, the arrival intensity of recovered and susceptible individuals and the recovery rate are equal to 3, the lifetime rate μ equals 0.01 and the order of the series expansion N equals 10. As expected, the higher the arrival rate of infected individuals λ_I, the lower the mean number of susceptible individuals and the higher the mean number of infected individuals. This trend is strengthened when the infection rate α_{si} increases.
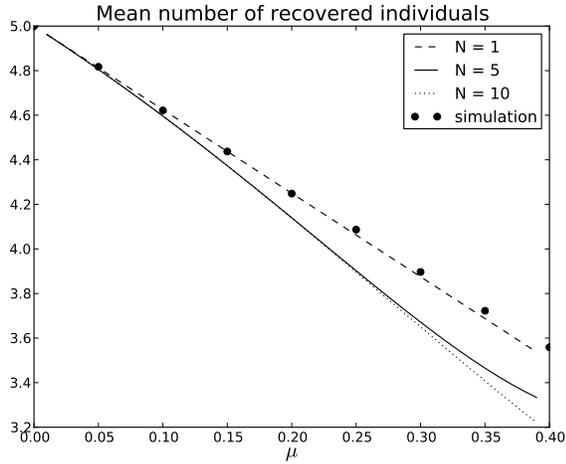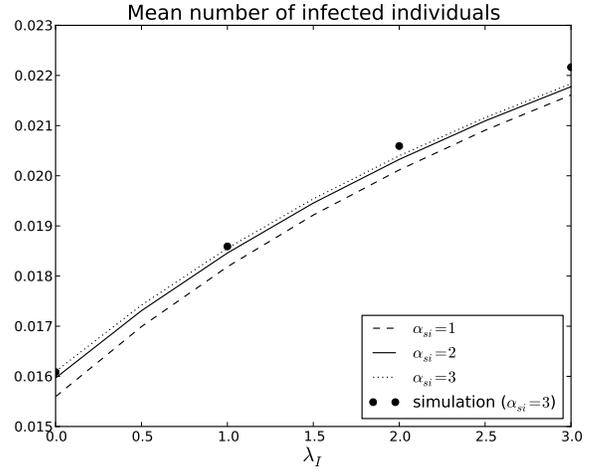
Figure 2. Mean number of recovered individuals.

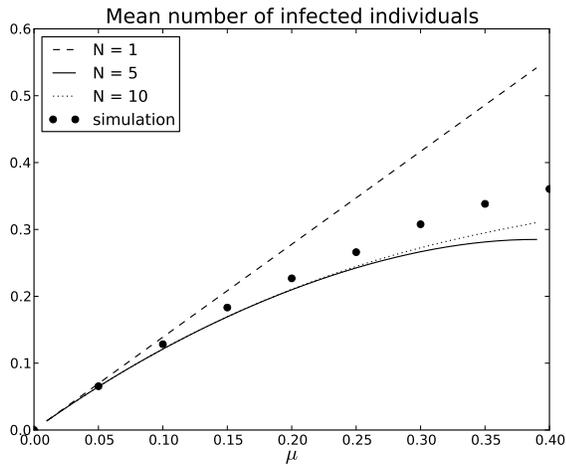Figure 3. Mean number of infected individuals.

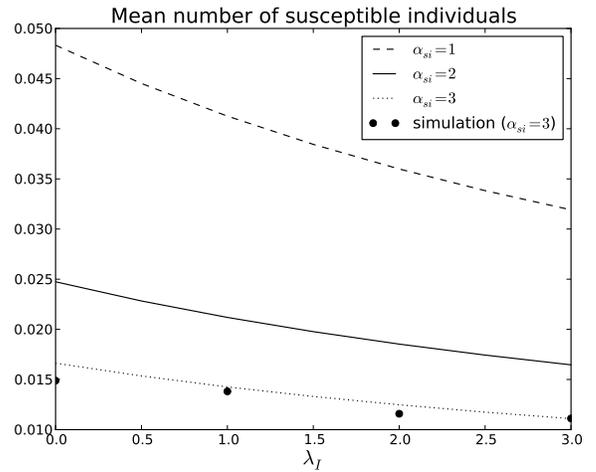Figure 4. Mean number of susceptible individuals.

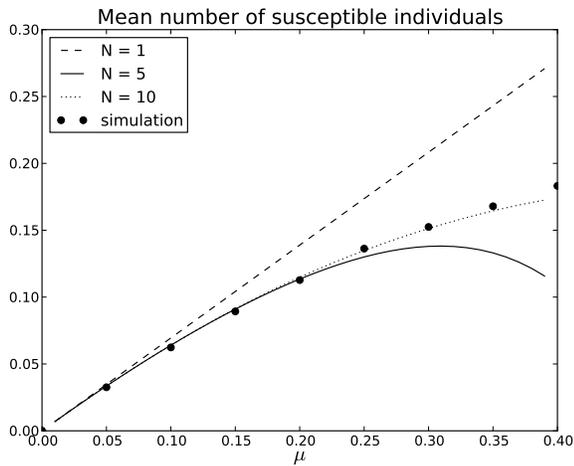Figure 5. Mean number of infected individuals.

Figure 6. Mean number of susceptible individuals.

Fluid limit

We look at the fluid approximation for the second special case in Figs. 7 and 8. In the first plot we start from a large number of infected individuals which quickly leads to many recovered individuals, whereas in the second plot the large number of recovered individuals prevents a large infected population to build up. We see good correspondence with the simulations.

VI. CONCLUSION

In this paper, we evaluate the propagation of a single opinion in a size-limited location that has a low population turnover. This means that the allowed individuals remain there on average for a long period. Furthermore, we assume that individuals can have either no opinion (S), a strong opinion that they want to spread (I) or an opinion that they keep for themselves (R). Moreover, the rate at which an individual without an opinion may get an opinion varies according to the number of individuals of the different types present at
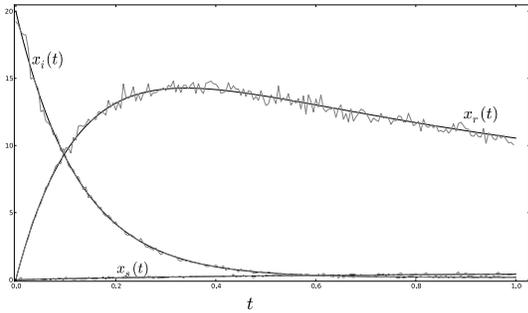
Figure 7. Fluid model and simulations for $M = 100$, $\lambda_R = \lambda_I = \lambda_S = 1$, $\mu = 1$, $\alpha_{si}^0 = \alpha_{si}^1 = \alpha_{ir}^1 = 3$.
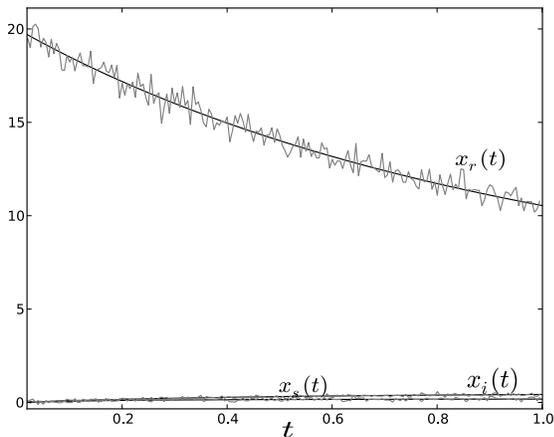

Figure 8. Fluid model and simulations for $M = 100$, $\lambda_R = \lambda_I = \lambda_S = 1$, $\mu = 1$, $\alpha_{si}^0 = \alpha_{si}^1 = \alpha_{ir}^1 = 3$.

the location. To cope with the inherent state space explosion, we propose an approximative numerical algorithm for the queueing system at hand. In particular, a numerical algorithm is applied which calculates the first N coefficients of the Maclaurin series expansion of the steady-state probability vector. From the numerical results we may conclude that the series expansion is quite a good approximation for the opinion model only when the departure rate is small. Future work will focus on expanding the system to a multiple opinion propagation model and deriving diffusion approximations.

VII. Acknowledgement

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