2018 IEEE Conference on Decision and Control (CDC)
Miami Beach, FL, USA, Dec. 17-19, 2018

A Robust Moment Closure for General Continuous-time Epidemic Processes

Nicholas J. Watkins, Cameron Nowzari, and George J. Pappas

***Abstract*— We develop a robust moment closure for a general class of continuous-time epidemic spreading processes, the elements of which are prevalent in the literature. Our moment closure method takes as input a general stochastic compartmental spreading process defined for n agents and m compartments, and produces a system of $2nm$ differential equations whose solutions provide nontrivial approximations to the marginal compartmental membership probabilities for each agent. This is an improvement over the commonly used mean-field type approximation, which provides no such guarantee. We demonstrate that our results provide useful predictions with examples performed on two models of competitive spreading processes, and find the developed closure to be more informative than mean-field approximations.**

I. Introduction

Compartmental epidemic spreading processes have been proposed as models for a broad class of complex systems, in which many system components interact in ways which are fundamentally nondeterministic in order to spread certain statuses throughout the agents. Typical examples include the spread of beliefs by way of social conversation [1], [2], the spread of messages through *ad hoc* wireless networks [3], and the proliferation of biological disease [4]. To enable a rigorous understanding of how best to interact with such systems, we must first develop an understanding of how the components of the system interact with each other. However, cultivating such an understanding is difficult.

This difficulty arises from the inherent complexity of the models. While it is possible to represent a broad class of compartmental epidemic spreading processes as finite state-space Markov chains, this is only possible through constructing a process with exponentially many (m^n) states (see, e.g. [5], [6]). This difficulty can be addressed without introducing approximations in the presence of very special structure in both the compartmental transition process and the processes' spreading graph. For example, if one is only concerned about the total number of agents who reside in each compartment at each time, and all spreading parameters of the process are homogeneous (i.e. they affect each agent identically), one can use lumping to reduce the complexity of the model [6, Section 2.4]. However, it is unclear whether or not such special structures exist in practice, and research has focus primarily on the case of heterogeneous spreading processes in recent years (see, e.g., [7] for a review).

In the case of general heterogeneous spreading processes, there are no currently known techniques for accurately approximating the evolution of the compartmental membership probabilities of the process with respect to time. Indeed, most prior works study compartmental epidemic spreading processes by way of a *mean-field* type approximation. Such approximations only provide weak guarantees that hold only in the case of processes with special structure. Indeed, the arguments used to justify the use of mean-field approximations most commonly appeal to a result from [8], which demonstrates that mean-field approximations are asymptotically equivalent to the expectation of the process, where the limit is taken with respect to the number of agents in a density-dependent system of stochastic differential equations. While this result does indeed apply to epidemic models on complete and homogeneous spreading graphs, it is unclear how to apply it to general, heterogeneous spreading processes.

Few results exist which formally demonstrate that mean-field approximations are good approximations to the statistics of spreading processes which demonstrate any significant heterogeneity [6]. While it can be shown that for the Susceptible-Infected-Recovered (SIR) process on tree graphs [9], [10], the mean-field model is equivalent to the expectation dynamics, this appears to be the only currently known case for which this is true. Likewise, while it is known that the mean-field approximation of the Susceptible-Infected-Susceptible (SIS) model provides an over-approximation of the probability of infection for each node on arbitrary spreading graphs, such a result seems peculiar to the SIS process, and the analysis used to demonstrate the result depends strongly on the structure of the model's compartmental transition process [11].

The primary contribution of this paper is a moment closure technique for general compartmental epidemic spreading processes which provides nontrivial approximations to the compartmental membership probabilities for every node in the graph regardless of the structure of the graph, or the compartmental transition process. In particular, given any compartmental epidemic spreading process model defined with n agents each taking membership in m compartments, our moment closure technique produces an approximate model consisting of a system of $2nm$ ordinary differential equations (ODEs), such that each compartmental membership probability of every agent is provided a rigorous and nontrivial approximation, i.e. an approximation more informative than membership in $[0, 1]$. This is important, as it is the first step required in developing controllers for epidemic processes with provable convergence guarantees, as we have done for $SEIV$ in [12]. Note that due to the limited size constraints of the venue, some technical arguments have been removed here. Analogous arguments for the special case in which the $SEIV$ process is considered are presented in detail in [12]. The full results will be presented in detail in a forthcoming thesis, which will be made publicly available.

Organization of Remainder: The remainder of the paper is organized as follows. In Section II, we formally

N.J. Watkins and G.J. Pappas are with the Department of Electrical and Systems Engineering, University of Pennsylvania, Philadelphia, PA 19104, USA, {nwatk,pappasg}@upenn.edu. C. Nowzari is with the Department of Electrical and Computer Engineering, George Mason University, Fairfax, VA 22030, USA, cnowzari@gmu.edu.

define the class of epidemic spreading processes considered, and formally state the problem studied. In Section III, we construct a robust moment closure to the general compartmental epidemic model. In Section IV, we demonstrate how to use the robust moment closure approximation to make optimal predictions about the compartmental membership probabilities for every node in the graph with respect to the bounds given by the robust moment closure. In Section V, we apply the developed tools to two models of competitive epidemics to demonstrate the benefits of our techniques as opposed to traditional mean-field approximation. •

Notation and Terminology: We use $\mathbb{R}_{\geqslant 0}$ to denote the set of non-negative real numbers, and $\mathbb{Z}_{\geqslant 0}$ denote the set of non-negative integers. We denote by $[k]$ the set of the first k positive integers, i.e. $[k] \triangleq \{1, 2, \dots, k\}$, and by $[k]_0$ the first $k+1$ natural numbers, i.e. $[k]_0 \triangleq \{0, 1, 2, \dots, k\}$.

We denote by $\mathbb{E}[X]$ the expectation of a random variable X. When clear from context, we omit the initial condition $X(0)$ of a stochastic process. When necessary, we explicitly include it as a part of the expectation's conditioning. •

II. Model and Problem Statement

In this section, we formally develop the model and the problem we study in this paper. The particular construction we present for the class of epidemic models we present here is our own (Section II-A), but we arrive at the same class of models as was discussed in [5], in which dynamics for mean-field models were proposed. In this work, we present dynamics which provide rigorous approximations to the compartmental membership probabilities of the process (Section III), from which good over- and under- approximations to each node's compartmental membership probabilities can be readily computed (Section IV).

A. General Compartmental Epidemic Model (GCEM)

We consider the dynamics of a general compartmental epidemic spreading model. In this model, each agent in a population is represented in a directed n-node spreading graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ by a particular node $i \in \mathcal{V}$. At each time in the process, every node belongs to one of a finite set of the model's *compartments*, which are described by the set of compartmental labels $\mathcal{L}$. Intuitively, a node being in a particular compartment ℓ represents the current status of an agent (e.g. belief state, infection stage).

We denote by $X(t)$ a stochastic vector containing the compartmental memberships of each node at time t. To make the notation as intuitive as possible, we index $X(t)$ in two dimensions: one which indicates the compartment which is being described, and the other the numerical label of the node. As such, we denote by $X_i^\ell(t)$ an indicator random variable, taking the value 1 if node i is in compartment ℓ, and 0 otherwise. In this way, we see that for all times t, we have that $\sum_{\ell \in \mathcal{L}} X_i^\ell(t) = 1$ for all i, as each node belongs to precisely one compartment at all times. We denote by $\mathcal{X}$ the set of states of the process. Figure 1 provides an illustration of a GCEM process with five compartments. Note that it is often the case in the literature that compartments are assigned alphabetical symbols bearing a mnemonic relation to the description of a particular status: S for "susceptible," I for "infected," R for "removed," and so forth (see, e.g., [5], [6], [13] and references therein). Our use of abstract labels ℓ_k here is due to the generality of our considerations: there is no assumed meaning to any compartment here. In our examples (Section V), we use alphabetical symbols to adhere to convention.

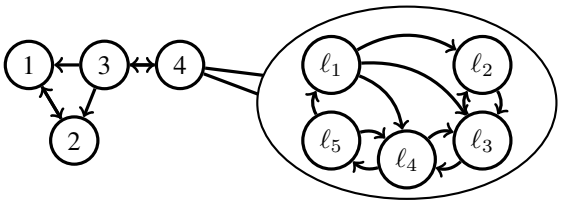


Fig. 1: A compartmental diagram of a GCEM process, in which each agent belongs to one of five compartments. The transition process for node 4 is explicitly illustrated, in which edges denote that a particular transition can occur with positive probability.

In general, GCEM processes can be posed as a system of Itô integrals taken with respect to measures of independent Poisson processes as

$$\begin{aligned} \mathrm{d}X_i^\ell = &\sum_{\ell' \in \mathcal{L}} X_i^{\ell'} \mathrm{d}\mathbb{P}_i^{\ell' \to \ell} - X_i^\ell \mathrm{d}\mathbb{P}_i^{\ell \to \ell'} \\ &+ \sum_{j \in \mathcal{V}} \sum_{\ell' \in \mathcal{L}} X_i^{\ell'} X_j^\ell \mathrm{d}\mathbb{Q}_{ij}^{\ell' \to \ell} - X_i^\ell X_j^{\ell'} \mathrm{d}\mathbb{Q}_{ij}^{\ell \to \ell'}, \end{aligned} \tag{1}$$

where the symbols $\mathrm{d}\mathbb{P}_i^{\ell' \to \ell}$ and $\mathrm{d}\mathbb{Q}_{ij}^{\ell' \to \ell}$ are the probability measures associated to transitions associated to internal effects (i.e. endogenous transitions), and transitions associated to external effects (i.e. exogenous transitions), respectively. Note that whenever a particular transition $\ell \to \ell'$ is not possible, we take the corresponding measure to instead be the constant zero, as doing so greatly simplifies notation.

We wish to study the expectation of the process (1). After some technical manipulations, we have these to be

$$\begin{aligned} \frac{\mathrm{d}\mathbb{E}[X_i^\ell]}{\mathrm{d}t} = &\sum_{\ell' \in \mathcal{L}} \mathbb{E}[X_i^{\ell'}] \lambda_i^{\ell' \to \ell} - \mathbb{E}[X_i^\ell] \lambda_i^{\ell \to \ell'} \\ &+ \sum_{j \in \mathcal{V}} \sum_{\ell' \in \mathcal{L}} \mathbb{E}[X_i^{\ell'} X_j^\ell] \mu_{ij}^{\ell' \to \ell} - \mathbb{E}[X_i^\ell X_j^{\ell'}] \mu_{ij}^{\ell \to \ell'}, \end{aligned} \tag{2}$$

where the terms $\lambda_i^{\ell' \to \ell}$ are the transition rates associated to the measures $\mathrm{d}\mathbb{P}_i^{\ell' \to \ell}$, and the terms $\mu_{ij}^{\ell' \to \ell}$ are the transition rates associated to the measures $\mathrm{d}\mathbb{Q}_{ij}^{\ell' \to \ell}$. It is important to note that the system of ordinary differential equations (2) is not closed. We have no expressions detailing the evolution of the second-order moments, which are required to evaluate the right-hand side of (2). However, there is no known method for closing the system (2) tractably without introducing the possibility of incorporating significant error. Explicit representation of the higher-order moments usually requires studying a Markov process with m^n states; approximate representations typically introduce errors which interact with the system in complicated and poorly understood ways [6]. In particular, most authors currently use mean-field type moment closures in the style of [5], [13], for which there are only accuracy guarantees in very special cases.

The problem we study in this paper is constructing a tractable method of rigorously approximating the solutions of (2)*, i.e. the trajectories of the compartmental membership*

probabilities for each node in the graph. To accomplish this, we construct a robust moment closure in Section III, wherein we take advantage of the structure of the process to bound the evolution of the probabilities. We then demonstrate how the optimal bounds which are admitted by the solutions of our approximation dynamics can be computed as a closed form output function of our system's states (Section IV).

III. Robust Moment Closures for GCEM

In this section, we construct a robust moment closure applicable to all GCEM processes. While to date, mean-field approximations such as those constructed in [5] have been used in the study of networked epidemic process, these come with no approximation accuracy guarantees outside of very special cases. Indeed, in Section V-A we see that for a simple model contained in GCEM, the mean-field approximation yields neither an over-approximation or an under-approximation to the compartmental membership probabilities of interest. As such, to design a controller which provides rigorous performance guarantees (as we have done in [12]), we need to construct a different moment closure. Our primary purpose in constructing a robust moment closure at this level of generality is to rigorously demonstrate that the concepts used to construct the moment closure in [12] can be readily adopted to any epidemic process.

We accomplish our goal in Theorem 1, however before stating it, we must first introduce some additional concepts and notation. Key in our result is the use of a well-known pair of inequalities which allow us to bound the joint probabilities of the form $\mathbb{E}[X_i^\ell X_j^{\ell'}]$ which appear in (2). We define the *Fréchet inequalities* as follows:

Definition 1 (Fréchet Inequalities) Let A and B be events, let $\Pr(A)$ and $\Pr(B)$ be the marginal probability of each event (respectively), and let $\Pr(A,B)$ denote the joint probability. Then, it holds that

$$\begin{aligned}\mathcal{F}_{\text{lwr}}(\Pr(A),\Pr(B)) &\triangleq \max\{0,\Pr(A)+\Pr(B)-1\}\\ &\leqslant \Pr(A,B),\end{aligned} \tag{3}$$

and

$$\begin{aligned}\Pr(A,B) &\leqslant \mathcal{F}_{\text{upr}}(\Pr(A),\Pr(B))\\ &\triangleq \min(\Pr(A),\Pr(B)),\end{aligned} \tag{4}$$

where $\mathcal{F}_{\text{lwr}}$ and $\mathcal{F}_{\text{upr}}$ are called the Fréchet bounds of the joint probability $\Pr(A,B)$. •

The Fréchet inequalities are interesting not only because they allow us to bound the joint probabilities $\Pr(A,B)$ with simple functions, but also because they are *optimal* in the sense that given only knowledge of the marginal probabilities $\Pr(A)$ and $\Pr(B)$, $\mathcal{F}_{\text{lwr}}$ is a tight lower bound, and $\mathcal{F}_{\text{upr}}$ is a tight upper bound [14]. That is, they give us the best pointwise approximation to the joint probabilities $\mathbb{E}[X_i^\ell X_j^{\ell'}]$ which we can reasonably expect without having to prove further distributional properties of a particular epidemic process. However, simply replacing the joint probabilities with an approximation without taking into account the effect of integrating the introduced error will lead to a needlessly conservative approximation (see [12, Section III.A]). We may have that the solutions of the resultant system of differential equations do not produce approximations which are valid probabilities (e.g. they can be greater than one).

With this in mind, we use *complement bounding operators* in such a way so as to guarantee that the induced system of differential equations always give us nontrivial probability estimates (i.e. estimates which always remain in the unit interval). We define the complement upper-bound operator:

Definition 2 (Complement Upper-Bounding Operator) Let ℓ and ℓ' be compartmental labels of a GCEM process. Suppose $\bar{x}_i^\ell$ and $\bar{x}_i^{\ell'}$ are valid upper-bounds of $\Pr(X_i^\ell=1)$ and $\Pr(X_i^{\ell'}=1)$, respectively. We define the complement upper-bounding operator as

$$\mathcal{B}_{\bar{x}_i^\ell}(\bar{x}_i^{\ell'}) \triangleq \min\{1-\bar{x}_i^\ell, \bar{x}_i^{\ell'}\}, \tag{5}$$

where we note that $\bar{x}_i^\ell = \Pr(X_i^\ell = 1)$ implies that $\mathcal{B}_{\bar{x}_i^\ell}(\bar{x}_i^{\ell'}) \geqslant \Pr(X_i^{\ell'}=1)$ holds. •

We see in the formal statement of our main result that the complement upper-bounding operator serves to prevent the over-approximation of the compartmental membership probabilities from becoming trivial, i.e. growing larger than one. This is important, as the over-approximations of compartmental membership probabilities appear in the dynamics of the approximating system we develop in nontrivial ways.

We now are ready to state our main result, which gives a system of $2mn$ ordinary differential equations that approximate the evolution of the compartmental membership probabilities of a given GCEM process.

Theorem 1 (Robust Moment Closure of GCEM) *Fix some GCEM process. Let $\underline{x}(0) = X(0) = \bar{x}(0)$, and consider the solutions of the system of ordinary differential equations*

$$\begin{aligned}
\dot{\bar{x}}_i^\ell &= \sum_{\ell'\in\mathcal{L}} \mathcal{B}_{\bar{x}_i^\ell}(\bar{x}_i^{\ell'})\lambda_i^{\ell'\to\ell} - \bar{x}_i^\ell\lambda_i^{\ell\to\ell'} +\\
&\sum_{j\in\mathcal{V}}\sum_{\ell'\in\mathcal{L}} \mathcal{F}_{upr}(\mathcal{B}_{\bar{x}_i^\ell}(\bar{x}_i^{\ell'}),\bar{x}_j^\ell)\mu_{ij}^{\ell'\to\ell} - \mathcal{F}_{lwr}(\bar{x}_i^\ell,\underline{x}_j^{\ell'})\mu_{ij}^{\ell\to\ell'},\\
\dot{\underline{x}}_i^\ell &= \sum_{\ell'\in\mathcal{L}} \underline{x}_i^{\ell'}\lambda_i^{\ell'\to\ell} - \underline{x}_i^\ell\lambda_i^{\ell\to\ell'} +\\
&\sum_{j\in\mathcal{V}}\sum_{\ell'\in\mathcal{L}} \mathcal{F}_{lwr}(\underline{x}_i^{\ell'},\underline{x}_j^\ell)\mu_{ij}^{\ell'\to\ell} - \mathcal{F}_{upr}(\underline{x}_i^\ell,\bar{x}_j^{\ell'})\mu_{ij}^{\ell\to\ell'}.
\end{aligned} \tag{6}$$

Then, for every compartment $\ell\in\mathcal{L}$ and each node $i\in\mathcal{V}$, the inclusions

$$\mathbb{E}[X_i^\ell(t)|X(0)] \in \left[\underline{x}_i^\ell(t),\bar{x}_i^\ell(t)\right] \subseteq [0,1], \tag{7}$$

hold for all $t\geqslant 0$.

Intuitively, we arrive at the dynamics (6) by replacing every occurrence of a joint probability $\mathbb{E}[X_i^\ell X_j^{\ell'}]$ with a Fréchet bound, where the particular bound used and the arguments passed depends on the manner in which the joint probability appears in the dynamics. When constructing dynamics for the over-approximation, we use the upper-bound when the joint probability appears in a term with a nonnegative coefficient, and the lower-bound when the joint probability appears in a term with a negative coefficient. When constructing dynamics for the under-approximation, we do the opposite. We then bound approximate probabilities which may cause components of solutions of the system

to leave the unit interval with appropriate complementarity bounds to prevent such an event from occurring.

Principally, the difficulty of proving Theorem 1 comes from determining that *despite* the fact the dynamics (6) do not adhere to an ordering point-wise in the system's state space, the solutions still obey the inclusion (7). Formally, this holds due to an extension of a comparison result from monotone systems theory [15], which has been demonstrated in [12]. Importantly, this result only requires the dynamics to obey an ordering on a small subset of the state space.

It is important to note that the argument used to prove Theorem 1 is conceptually similar to the argument used to prove the robust moment closure we construct in [12] for the $SEIV$ process. We have provided an explicit, general, result here in order to allow general use of our robust moment closure technique directly without having to develop *ad hoc* extensions for particular processes. We see the utility of Theorem 1 in Section V, where we demonstrate its application to two separate models of competitive epidemics, for which the mean-field approximations do not provide analytical accuracy guarantees, but our moment closure technique does.

IV. Optimal Set Membership Prediction

A principle reason that approximating the evolution of the compartmental membership probabilities rigorously is interesting is using the approximations to construct rigorous approximations to statistics of the process. For example, such statistics can be useful in predicting how many nodes are infectious after a certain amount of time has passed to ensure that an applied control realizes sufficient progress in driving the epidemic to extinction, as was done in [12]. Such statistics may also be used in predicting how many agents in a social system adopt a certain desirable behavior, for which we may like to compute a lower bound.

Our next result demonstrates that the optimal approximations of a particular statistic of the process, set membership expectations, can be expressed as closed-form functions of the state variables of (6).

Theorem 2 (Optimal Approximation of Set Membership Expectations) *Let $\underline{x}(0) = X(0) = \bar{x}(0)$, and consider the solutions $(\underline{x}, \bar{x})$ of (6) evaluated at time t. Define $\mathcal{S}(X)$ as the number of nodes belonging to compartments $S \subseteq \mathcal{L}$ in state X. It holds that*

$$\mathbb{E}[\mathcal{S}(X(t))|X(0)] \leqslant \sum_{i\in\mathcal{V}} \min\left\{ \sum_{\ell\in S} \bar{x}_i^\ell(t), 1 - \sum_{\ell\in\mathcal{L}\setminus S} \underline{x}_i^\ell(t) \right\}, \tag{8}$$

and that

$$\mathbb{E}[\mathcal{S}(X(t))|X(0)] \geqslant \sum_{i\in\mathcal{V}} \max\left\{ \sum_{\ell\in S} \underline{x}_i^\ell(t), 1 - \sum_{\ell\in\mathcal{L}\setminus S} \bar{x}_i^\ell(t) \right\}. \tag{9}$$

Moreover, the bounds are the tightest which can be derived from the inclusions generated by integrating (6).

The proof of Theorem 2 follows from forming variational characterizations of the optimal upper- and lower- bounds which can be derived on $\mathbb{E}[\mathcal{S}(X(t))|X(0)]$, given solutions of (6). Because the optimization problems formulated are highly structured, they admit analytical solutions. In particular, the solutions of these optimization problems give the inequalities (8) and (9).

We expect Theorem 2 to find use in generating predictions for use in controllers for epidemic processes, as was done for the particular case of $SEIV$ containment in [12]. As these predictions give both upper- and lower- bounds on the expectations, we can envision applications in which processes are controlled in such away so as to guarantee a certain minimum level of activity is maintained, as well as applications in which guarantees are provided that certain behaviors cannot persist.

V. Numerical Examples

In this section, we demonstrate the utility of our results by performing numerical simulations on two example processes.

A. SI_1SI_2S

In principle, the SI_1SI_2S process serves as a mathematical model for product or belief adoption for the case in which two products compete for market share. Each node in the network belongs to one of three compartments: susceptible (S), infected with contagion one (I_1), or infected with contagion two (I_2). Susceptible nodes are interpreted as disinterested by both products. Nodes infected with contagion one are supporters of product one. Nodes infected with contagion two are supporters of product two.

Transitions from the susceptible compartment to a state of infection occurs as a function of an exogenous process. Transitions from either infected compartment to the susceptible compartment occur as a function of an endogenous process. By specializing the general GCEM model (1) to this setting, one can verify that the corresponding stochastic differential equations for this process are given by

$$\begin{aligned} \mathrm{d}X_i^S = {} & X_i^{I_1}\mathrm{d}\mathbb{P}_i^{I_1\to S} + X_i^{I_2}\mathrm{d}\mathbb{P}_i^{I_2\to S} - \\ & \sum_{j\in\mathcal{V}} X_i^S X_j^{I_1}\mathrm{d}\mathbb{Q}_{ij}^{S\to I_1} - X_i^S X_j^{I_2}\mathrm{d}\mathbb{Q}_{ij}^{S\to I_2}; \end{aligned} \tag{10a}$$

$$\mathrm{d}X_i^{I_1} = \sum_{j\in\mathcal{V}} X_i^S X_j^{I_1}\mathrm{d}\mathbb{Q}_{ij}^{S\to I_1} - X_i^{I_1}\mathrm{d}\mathbb{P}_i^{I_1\to S}; \tag{10b}$$

$$\mathrm{d}X_i^{I_2} = \sum_{j\in\mathcal{V}} X_i^S X_j^{I_2}\mathrm{d}\mathbb{Q}_{ij}^{S\to I_1} - X_i^{I_2}\mathrm{d}\mathbb{P}_i^{I_2\to S}. \tag{10c}$$

By defining notations for mean-field approximation states ϕ_i^ℓ for all compartments $\ell \in \{S, I_1, I_2\}$, taking expectations, and replacing expectations of products with products of mean-field variables, we arrive at the mean-field approximation

$$\begin{aligned} \dot{\phi}_i^S = {} & \phi_i^{I_1}\lambda_i^{I_1\to S} + \phi_i^{I_2}\lambda_i^{I_2\to S} - \\ & \sum_{j\in\mathcal{V}} \phi_i^S\phi_j^{I_1}\mu_{ij}^{S\to I_1} - \phi_i^S\phi_j^{I_2}\mu_{ij}^{S\to I_2}; \end{aligned} \tag{11a}$$

$$\dot{\phi}_i^{I_1} = \sum_{j\in\mathcal{V}} \phi_i^S\phi_j^{I_1}\mu_{ij}^{S\to I_1} - \phi_i^{I_1}\lambda_i^{I_1\to S}; \tag{11b}$$

$$\dot{\phi}_i^{I_2} = \sum_{j\in\mathcal{V}} \phi_i^S\phi_j^{I_2}\mu_{ij}^{S\to I_1} - \phi_i^{I_2}\lambda_i^{I_2\to S}. \tag{11c}$$

Recognizing that $\dot{\phi}_i^S + \dot{\phi}_i^{I_1} + \dot{\phi}_i^{I_2} = 0$ and that if we initialize the mean-field approximation to an observed state

of the process, we have $\phi_i^S + \phi_i^{I_1} + \phi_i^{I_2} = 1$, we may remove the variables ϕ_i^S by substituting the expression $1 - \phi_i^{I_1} - \phi_i^{I_2}$. Doing so obtains the reduced mean-field approximation

$$\dot{\phi}_i^{I_1} = \sum_{j \in \mathcal{V}} (1 - \phi_i^{I_1} - \phi_i^{I_2}) \phi_j^{I_1} \mu_{ij}^{S \to I_1} - \phi_i^{I_1} \lambda_i^{I_1 \to S}, \quad \text{(12a)}$$

$$\dot{\phi}_i^{I_2} = \sum_{j \in \mathcal{V}} (1 - \phi_i^{I_1} - \phi_i^{I_2}) \phi_j^{I_2} \mu_{ij}^{S \to I_1} - \phi_i^{I_2} \lambda_i^{I_2 \to S}, \quad \text{(12b)}$$

which has been the object of study in prior works on SI_1SI_2S (see [1], [16]–[18] and references therein). As first noted in [17], the mean-field approximation is neither a reliable upper-bound or a reliable lower-bound of the expected probabilities of infection. We see this here in Figure 2, where contagion one spread on a 50 node Erdös-Rényi graph with connection probability 0.5 with $S \to I_1$ transition rate 7 and $I_1 \to S$ transition rates chosen uniformly at random from the interval $[0, 200]$, contagion two spread on a 50 node Erdös-Rényi graph with connection probability 0.5 with $S \to I_2$ transition rate 2 and $I_1 \to S$ transition rates chosen uniformly at random from the interval $[0, 50]$, where the two spreading graphs were generated independently.

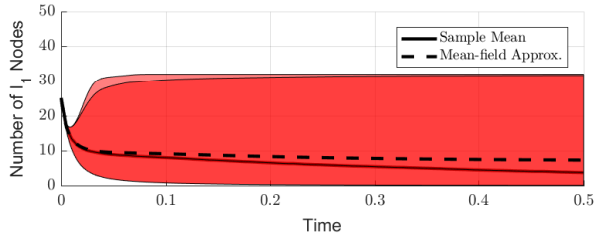
For this particular simulation, the mean-field approximation overestimates the probability of being infected by contagion one, and underestimates the probability of being infected by contagion two. We also see that the the predictions generated by the robust moment closure are nontrivial. Indeed, it restricts the expectation of the number of infected nodes for contagion one to roughly the interval $[0, 30]$, and the expectation of the number of infected nodes for contagion two to roughly the interval $[0, 35]$. In both cases, the upper bound is less than 50, the total number of nodes.

While even for this example the predictions given were nontrivial, one may wonder if the predictions given by the robust moment closure are always as coarse as those given in Figure 3. This is not the case. Often, they are substantially better. Consider the simulation results presented in Figure 3, where contagion one spread on a 100 node Erdös-Rényi graph with connection probability 0.75 with $S \to I_1$ transition rate 0.50 and $I_1 \to S$ transition rates chosen uniformly at random from the interval $[0, 1]$, contagion two spread on a 100 node Erdös-Rényi graph with connection probability 0.75 with $S \to I_2$ transition rate 0.05 and $I_1 \to S$ transition rates chosen uniformly at random from the interval $[0, 10]$, and the two spreading graphs were generated independently. In this case, the upper bound for contagion one is nearly tight, as is the lower bound for contagion two.

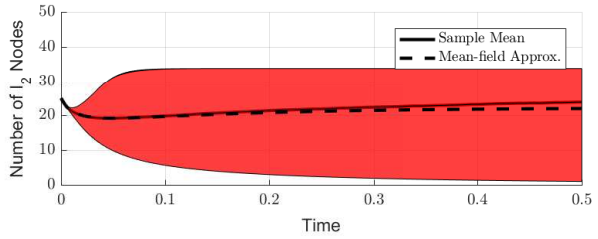
B. Direct Competition

For SI_1SI_2S, the mean-field approximations often seem to work well as a proxy for the expectation, despite not having a predefined ordering relation with the underlying expectation of the process. One may wonder if this is generally true. Here, we show by example that it is not. In particular, for a simple competitive epidemic model we call *direct competition*, a mean-field approximation is shown to be a poor proxy for the process' expectation.

For simplicity, we consider a model with two compartments such that transitions between each are due to exogeneous processes. Note that this is only a slight distinction from

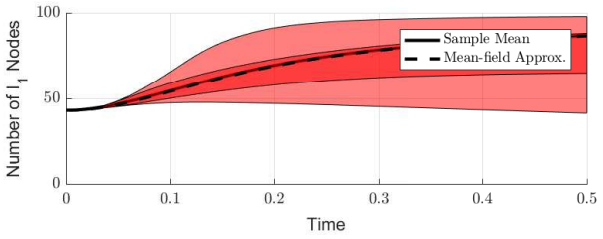


(a) Evolution of I_1 Nodes

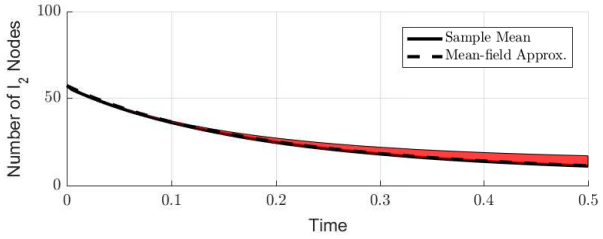


(b) Evolution of I_2 Nodes

Fig. 2: Comparison of the evolution of SI_1SI_2S statistics against predictions made by the robust moment closure dynamics and mean-field approximation (11), where the light red region gives the bounds from integrating (6), and the dark red region gives the bounds computed by applying Theorem 2. This demonstrates the lack of an ordering relation between the mean-field approximation and the expectation of the process. The mean-field approximation overestimates the number of nodes infected with contagion one, and underestimates the number of nodes infected with contagion two.



(a) Evolution of I_1 Nodes



(b) Evolution of I_2 Nodes

Fig. 3: Comparison of the evolution of SI_1SI_2S statistics against predictions made by the robust moment closure dynamics and mean-field approximation (11), where the light red region gives the bounds from integrating (6), and the dark red region gives the bounds computed by applying Theorem 2. One can see that the optimized predictions (from applying Theorem 2) are substantially better than those which come from direct integration, as they substantially reduce the uncertainty in the predictions of I_1 here.

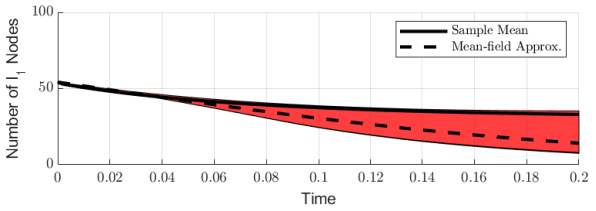


Fig. 4: Comparison of the evolution of the expectation of (13) against predictions made by the robust moment closure dynamics, and the mean-field approximation (14), where the light red region gives the bounds from integrating (6), and the dark red region gives the bounds computed by applying Theorem 2. It can be readily seen that the mean-field approximation differs significantly from the sample mean of the simulation, which is just below the upper-bound given by the robust moment-closure dynamics.

the SI_1SI_2S process, in that we now disallow people from taking neutral positions (i.e. susceptibility). As in Section V-A, we label the two infected compartments I_1 and I_2. Doing so allows us to write the corresponding specialization of (1) as the system of stochastic differential equations

$$\mathrm{d}X_i^{I_1} = \sum_{j\in\mathcal{V}} X_i^{I_1} X_j^{I_2} \mathrm{d}\mathbb{Q}_{ij}^{I_1\to I_2} - X_i^{I_2} X_j^{I_1} \mathrm{d}\mathbb{Q}_{ij}^{I_2\to I_1}, \quad (13a)$$

$$\mathrm{d}X_i^{I_2} = \sum_{j\in\mathcal{V}} X_i^{I_2} X_j^{I_1} \mathrm{d}\mathbb{Q}_{ij}^{I_2\to I_1} - X_i^{I_1} X_j^{I_2} \mathrm{d}\mathbb{Q}_{ij}^{I_1\to I_2}. \quad (13b)$$

As in Section V-A, we may take expectations and replace expectations of products by products of mean-field approximation variables to arrive at the mean-field approximation

$$\dot{\phi}_i^{I_1} = \sum_{j\in\mathcal{V}} \phi_i^{I_1}\phi_j^{I_2}\mu_{ij}^{I_1\to I_2} - \phi_i^{I_2}\phi_j^{I_1}\mu_{ij}^{I_2\to I_1}, \quad (14a)$$

$$\dot{\phi}_i^{I_2} = \sum_{j\in\mathcal{V}} \phi_i^{I_2}\phi_j^{I_1}\mu_{ij}^{I_2\to I_1} - \phi_i^{I_1}\phi_j^{I_2}\mu_{ij}^{I_1\to I_2}, \quad (14b)$$

where we may use the fact that $\dot{\phi}_i^{I_1} + \dot{\phi}_i^{I_2} = 0$ and $\phi_i^{I_1} + \phi_i^{I_2} = 1$ to eliminate $\phi_i^{I_2}$ to obtain the reduced representation

$$\dot{\phi}_i^{I_1} = \sum_{j\in\mathcal{V}} \phi_i^{I_1}(1-\phi_j^{I_1})\mu_{ij}^{I_1\to I_2} - (1-\phi_i^{I_1})\phi_j^{I_1}\mu_{ij}^{I_2\to I_1}. \quad (15)$$

Figure 4 is illustrative of a typical simulation in contagion one spreads on a 100 node Erdös-Rényi graph with connection probability 0.5 and $I_1 \to I_2$ rate 0.005, contagion two spreads on a 100 node Erdös-Rényi graph with connection probability 0.5 and $I_2 \to I_1$ rate 0.001, and the graphs are generated independently. The prediction given by the mean-field approximation and the sample mean of the process are substantially different. Indeed, the sample expectation of the process very nearly attains the upper bound provided by the robust moment closure, whereas the mean-field approximation comes near to the lower bound. This example demonstrates clearly that mean-field approximations should not be used as a proxy for the expectation of an epidemic process in general. They should only be trusted in particular cases, when approximation guarantees are demonstrated analytically. Our robust moment closure provides one method of providing such guarantees.

VI. Conclusions and Future Work

In this paper, we provide a general robust moment closure for a broad class of compartmental epidemic spreading processes. This is important, in that the mean-field approximations typically studied to date provide no formal accuracy guarantees. Since the robust moment closures provided here provide rigorously demonstrable upper- and lower- bounds on compartmental membership probabilities, they can be used readily to design control laws with provable convergence guarantees. We believe that designing such control laws is an interesting area for future work: as there is an extensive body of work which studies the control of epidemic processes under mean-field approximation, we expect that there can be an extensive body of work studying the control of epidemic processes using robust moment closures.

References

[1] X. Wei, N. C. Valler, B. Aditya Prakash, I. Neamtiu, M. Faloutsos, and C. Faloutsos, "Competing Memes Propagation on Networks: A Network Science Perspective," *IEEE Journal on Selected Areas in Communications*, vol. 31, no. 6, pp. 1049–1060, 2013.

[2] S. F. Ruf, K. Paarporn, P. E. Paré, and M. Egerstedt, "Dynamics of Opinion-Dependent Product Spread," in *2017 56th IEEE Conference on Decision and Control (CDC)*, pp. 2935–2940, 2017.

[3] S. Wang, M. H. R. Khouzani, B. Krishnamachari, and F. Bai, "Optimal Control for Epidemic Routing of Two Files with Different Priorities in Delay Tolerant Networks," in *IEEE American Control Conference*, (Chicago, IL, USA), pp. 1387–1392, 2015.

[4] N. T. J. Bailey, *The Mathematical Theory of Infectious Diseases and Its Applications*. High Wycombe, U.K.: Charles Griffin & Company, Ltd., 2nd ed., 1975.

[5] F. D. Sahneh, C. Scoglio, and P. V. Mieghem, "Generalized Epidemic Mean-Field Model for Spreading Processes Over Multilayer Complex Networks," *IEEE/ACM Transactions on Networking*, vol. 21, no. 5, pp. 1609–1620, 2013.

[6] I. Z. Kiss, J. C. Miller, and P. L. Simon, *Mathematics of Epidemics on Networks: From Exact to Approximate Models*. Cham, Switzerland: Springer Nature, first ed., 2017.

[7] C. Nowzari, V. M. Preciado, and G. J. Pappas, "Analysis and Control of Epidemics," *IEEE Control Systems Magazine*, vol. 36, no. 1, pp. 26–46, 2016.

[8] T. G. Kurtz, "Solutions of Ordinary Differential Equations as Limits of Pure Jump Markov Processes," *Journal of Applied Probability*, vol. 7, no. 1, pp. pp. 49–58, 1970.

[9] K. J. Sharkey, I. Z. Kiss, R. R. Wilkinson, and P. L. Simon, "Exact Equations for SIR Epidemics on Tree Graphs," *Bulletin of mathematical biology*, vol. 77, no. 4, pp. 614–645, 2015.

[10] I. Z. Kiss, C. G. Morris, F. Sélley, P. L. Simon, and R. R. Wilkinson, "Exact deterministic representation of Markovian SIR epidemics on networks with and without loops," *Mathematical Biology*, pp. 437–464, 2015.

[11] P. Simon and I. Z. Kiss, "On bounding exact models of epidemic spread on networks," *arXiv preprint*, pp. 1–18, 2017.

[12] N. J. Watkins, C. Nowzari, and G. J. Pappas, "Robust Economic Model Predictive Control of Continuous-time Epidemic Processes," *arXiv preprint*, no. arXiv:1707.00742, 2017.

[13] P. Van Mieghem, J. Omic, and R. Kooij, "Virus Spread in Networks," *IEEE/ACM Transactions on Networking*, vol. 17, no. 1, pp. 1–14, 2009.

[14] L. Rüschendorf, "Fréchet-Bounds and Their Applications," Tech. Rep. January, 1991.

[15] M. W. Hirsch and H. Smith, *Monotone Dynamical Systems*. 2006.

[16] F. Darabi Sahneh and C. Scoglio, "Competitive epidemic spreading over arbitrary multilayer networks," *Physical Review E - Statistical, Nonlinear, and Soft Matter Physics*, vol. 89, no. 6, 2014.

[17] N. J. Watkins, C. Nowzari, V. M. Preciado, and G. J. Pappas, "Optimal Resource Allocation for Competitive Spreading Processes on Bilayer Networks," *IEEE Transactions on Control of Network Systems*, vol. 5, no. 1, pp. 298–307, 2018.

[18] J. Liu, P. E. Paré, A. Nedic, C. L. Beck, and T. Basar, "On a Continuous-Time Multi-Group Bi-Virus Model with Human Awareness," in *2017 56th IEEE Conference on Decision and Control (CDC)*, (Melbourne, Australia), pp. 4124–4129, IEEE, 2017.