Approximating Network Dynamics in Compartmental System Dynamics Models

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Over the past few decades the field of "network science" has exploded in popularity (Barabási, 2016). A fundamental tenant of this research is that network structure – who interacts with whom – matters for individual and collective outcomes (e.g. Watts and Strogatz, 1998; Newman, 2003; Burt, 2005). One criticism of compartmental system dynamics (CSD) models is the lack of an underlying network specifying the topological structure of interactions among individuals. Within compartments, individuals are assumed to be well-mixed and in many cases the interactions between compartments are assumed to occur at random. The effect of these assumptions can be substantial. For example, Rahmandad and Sterman (2008) show that for clustered network topologies the predicted dynamics of a standard contagion model differ significantly when simulated using an agent-based model (ABM) that fully accounts for network structure versus a CSD that does not. Despite this potential shortcoming, CSDs have many advantages over models with fully represented networks including computational efficiency, clarity of exposition, and more tractable analysis.

However, as this paper demonstrates, CSDs and networks are not mutually exclusive. We describe a framework developed primarily in theoretical biology, known as a *pair approximation* or *correlation model*, that can be readily implemented using standard CSD tools, thus retaining the speed, simplicity, and tractability of CSDs, while capturing a substantial portion of the effect of an underlying network structure. We illustrate the approach and its effectiveness using two examples, a standard SIS epidemiological model and a new model of social contagion that we call SIS2.

While the mathematics of the pair approximation have been substantially developed elsewhere (e.g. Keeling, Rand and Morris, 1997; Morris, 1997; Van Baalen, 2000), exploring this method in this special anniversary issue of the *System Dynamics Review* makes two important contributions. First, for system dynamics

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modelers, this paper introduces a relatively simple method of capturing the sometimes important effects of network structure while maintaining the many benefits of the CSD methodology. Second, we believe that with this tool in hand, experts in CSD modeling will be able to make new contributions to understanding phenomenon where networks matter. To date, applications of the pair approximation approach have been largely confined to analytic models in theoretical biology and physics, and while the mathematical analysis of the pair approximation is substantially more tractable than analysis of fully represented networks, in all but the simplest models analytic solutions remain unobtainable. The simulation toolkit of CSDs and interdisciplinary expertise of CSD modelers are perfectly suited to expanding the range of dynamic systems that can be represented and analyzed with this approximation method.

The basic idea behind the pair approximation is to move from compartments that represent individuals in a given state to compartments that represent connected pairs of individuals in pairs of states. For example, in the standard Susceptible-Infected-Susceptible (SIS) model from epidemiology, there are two compartments – S and I – representing the number of individuals in the population in the susceptible and infected states, respectively. In the pair approximation CSD, there are four compartments, SS, SI, IS, and II representing ordered connected susceptible-susceptible pairs, susceptible-infected pairs, infected-susceptible pairs, and infected-infected pairs, respectively.[1] Flows specify the rates of transitions between these pair types. As we show by comparing simulation results with CSD predictions from the standard SIS model and the pair approximation CSD, this modest increase in model complexity goes a long way towards closing the gap between the standard well-mixed CSD and the full blown ABM.

In addition to better approximating the ABM results, we show that the pair approximation SIS model provides additional insights into the dynamics of diffusion that are unobtainable with the standard SIS CSD model. Specifically, we derive an analog of the epidemic threshold for contagion that shows how concentration of infected individuals in pockets of the population can inhibit diffusion (or, alternatively spreading "seeds" of a new product or message widely can encourage its spread), and we demonstrate how the model can predict non-monotonic diffusion curves observed in ABM simulations.

The basic pair approximation introduces no new model parameters beyond

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[1] One can reduce this to three compartments using unordered pairs, but this makes maintaining units consistency less transparent. Because the population size remains constant, another state variable can be eliminated, and thus the system of equations is second-order as opposed to the first-order system of the standard SIS model.

those used in the standard CSD model, and thus requires no additional data for model calibration. A downside of this feature is that, like the standard CSD, the approximation cannot account for variability introduced by network structures that differ from one another in any way beyond average degree.[2] In particular, *network clustering*, the probability that two nodes in anetowkr with a connection in common are themselves connected, is a triadic property that is know to have strong effects on many network dynamics (Watts, 1999; Burt, 2005; Centola and Macy, 2007; Lamberson, 2015) that cannot be detected by either the standard CSD or the basic pair approximation. However, as we describe, by introducing one additional model parameter we obtain a "cluster corrected pair approximation" that improves the model fit in highly clustered networks and allows the researcher to examine the impact of network clustering on the predicted dynamics.

Finally, we apply the pair approximation CSD to a new model of social contagion that we call SIS2. In this model, just as infected individuals can transmit an infection to susceptible individuals, susceptible individuals can "cure" their infected contacts. This model of two-way influence may be a more accurate representation of how social contagions, such as rumors (Sunstein, 2014), emotional states (Kramer, Guillory and Hancock, 2014), or political behavior (Bond, Fariss, Jones, Kramer, Marlow, Settle and Fowler, 2012) spread. As we show, in a standard CSD two-contagion is equivalent to one-way contagion with a reduced infectivity parameter. But using an ABM, we demonstrate that in fact the dynamics of two-contagion are substantially different, and the pair approximation CSD accurately captures this discrepancy.

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[2] The degree of a node in a network is the number of links connected to that node. The average degree of a network is the average degree taken over all nodes.

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