Motif-based mean-field approximation of interacting particles on clustered networks

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Interacting particles on graphs are routinely used to study magnetic behaviour in physics, disease spread in epidemiology, and opinion dynamics in social sciences. The literature on mean-field approximations of such systems for large graphs typically remains limited to specific dynamics, or assumes cluster-free graphs for which standard approximations based on degrees and pairs are often reasonably accurate. Here, we propose a motif-based mean-field approximation that considers higher-order subgraph structures in large clustered graphs. Numerically, our equations agree with stochastic simulations where existing methods fail.

With applications in as disparate branches of science as statistical physics [1], epidemiology [2–9], chemistry and systems biology [10,11], social science [12,13], and computer science [14–16], interacting particles on complex networks constitute an important class of models in the mathematician’s and physicist’s toolkit [17–20]. They describe systems where individual entities (particles), endowed with local states, interact with a subset of other entities (neighbors) and transition from one state to another as time evolves. For instance, in epidemiology the local state space consists of immunological statuses, such as susceptible, infected, removed etc. Who interacts with whom defines a graph with the particles as the vertices.

The time evolution of the ensemble of particle states is often described by a continuous-time Markov jump process, for which discrete-time analysis can be insufficient [21]. As the number of particles increases, the exponentially growing combinatorial state space renders exact stochastic analysis prohibitive. To this end, the standard mean-field theoretic approach has been to describe the non-equilibrium dynamics of interacting particle systems via Ordinary Differential Equations (ODEs) for the proportions of particles in each state. Together with control [22], learning-based methods [23,24] and graph limit theory [25,28], mean-field models can enable analysis of otherwise intractable settings [29–31]. More advanced mean-field approximations, such as heterogeneous mean-fields [32], pair approximations [33,34] or approximate master equations (AME) [35,41] and extensions thereof [42–45], acknowledge the heterogeneity of the particles’ behaviors due to the graph structure and incorporate vertices’ degrees and edge counts (pairs). Though they provide reasonable accuracy for a number of applications, they are generally not asymptotically exact in that they do not agree with the Functional Law of Large Numbers (FLLN) limits of the corresponding stochastic processes, agreeing only in certain special cases [46,47]. Even for calculations of critical parameter values, standard mean-field approximations are often inaccurate [48]. Nevertheless, their simplicity and intuitiveness have commonly justified mean-field approaches despite their inexactness.

In this paper, we propose a simple and elegant derivation of a general motif-based mean-field approximation for interacting particles on bounded-degree graphs to address two crucial shortcomings of the state-of-the-art: (i) The implicit assumption of cluster-free graphs [49]. In practice, graphs encountered are far from cluster-free and exhibit complex structures [14,50,52] (e.g., neural and transportation networks [53]), which greatly affect e.g. cascades in correlated networks [54]. Here, we go beyond correlation coefficients and account for arbitrary subgraph structures called motifs [55] beyond standard degree and edge-based calculations. (ii) The restriction to special cases (e.g. SIR epidemics, [56]) or dynamics driven by simple neighborhood counts. For instance, infection rates are often assumed to depend only on the number of infected neighbors, while in practice shared connections among neighbors and the shape of the induced neighborhood subgraph are too important to neglect (e.g., simplicial dynamics [14,57]). Though there exist a multitude of works on the analysis of clustered graphs [49,58,61], to the best of our knowledge, we provide the first general approximation that takes into account both of these aspects into a single coherent mean-field framework. We now introduce the mathematical model before explaining how our approximation addresses the above two issues.

a. Model A convenient way of generating random graphs is via the Configuration Model (CM) [20,62], which allows specifying either a degree sequence or probability law from which the degrees are sampled. Each vertex is assigned as many half-edges as its degree. We may need to add or drop a parity edge if the degree sequence is not graphical, but its contribution is negligible in large graphs [20, Section 7.6, pp. 239]. The configuration model graph is then constructed by uniformly-at-random matching of all available half-edges. As $N$, the number of vertices, grows to infinity, the numbers of self-loops and multiple edges have independent Poisson limits whose means depend only on the first two moments of the degree distribution [19, Theorem 3.1.2]. Therefore, their contributions to the limits of various counts scaled by
we iteratively sample hyperstubs of each motif vertex role with $N_2$ in $G$ considered in standard mean-field approximations. To subgraph and its coloring up to isomorphism (not only... consider the set of all vertices participating in $G_t, \ldots, G_M$, with $N_1, \ldots, N_M$ vertices, we construct an ECM on $N$ vertices by specifying higher-order motif participation counts (hyperstub degrees) $(d_1, \ldots, d_N)$, where $d_v \equiv (d_{v,1}, \ldots, d_{v,M}) \in D$, $d^i \equiv (d^i_1, \ldots, d^i_N)$, and $d^{i,j} \in N_0$ denotes the number of participations (hyperstubs) as the $j$-th vertex (role) in the motif $G^{(i)}$ (see Figure 1). As in the standard CM, hyperstubs are first generated for each node in accordance with a limiting hyperstub degree distribution $P(d)$. Subsequently, for each possible motif, we iteratively sample hyperstubs of each motif vertex role and add edges wherever the underlying motif has an edge, repeating until no hyperstubs are left.

To describe the dynamics of the interacting system, we will consider time-indexed colored ECM graphs $\{G_t\}_{t \geq 0}$. Each vertex is endowed with a local (finite) state space $X$. Denote the state of vertex $v$ at time $t$ — interpreted as color — as $G_t[v]$, and define the colored neighborhoods $N_t(v)$ as colored subgraphs of $G_t$ with fixed center vertex $v$, induced by the set of all vertices participating in motifs with $v$. Treated as a stochastic process, $G_t$ is a Markov jump process with infinitesimal rates $\lambda^{x \rightarrow y}(N_t(v))$, depending on $v$ only via its colored neighborhood configuration, i.e. the rate for vertex $v$ to jump from state $x$ to $y (\neq x)$ is given by

$$P(G_{t+h}[v] = y | G_t[v] = x, N_t(v)) = \lambda^{x \rightarrow y}(N_t(v))h + o(h). \quad (1)$$

Note that the rate functions $\lambda^{x \rightarrow y}$ depend on the entire subgraph and its coloring up to isomorphism (not only neighbor state counts), and therefore generalize those considered in standard mean-field approximations. To illustrate this, define the neighbor evaluation function

$$\psi(N_t(v), f) \equiv \sum_{n \in V(N_t(v))} f(N_t(v)[n]) \quad (2)$$

for any $f : X \rightarrow \mathbb{R}$ and colored neighborhood $N_t(v)$. Then, the simplicial susceptible-infected-susceptible (SIS) model [14], which imposes additional higher-order terms on the infection rates of vertices, can be modeled as

$$\lambda^{S \rightarrow I}(N_t(v)) = \tau_S \psi(N_t(v), 1)$$

$$\lambda^{I \rightarrow S}(N_t(v)) = \gamma,$$

for pairwise infection rate $\tau$, triangle (clique) infection rate $\tau_D$, recovery rate $\gamma$ and indicator function $1_A$. Here, the summation is over all unique triangles $\Delta_v$ involving $v$. This model is more realistic than the standard SIS model when shared acquaintances meet more often (see Figure 1 [53]). In our experiments, we also consider the standard SIS model where $\tau_D = 0$, which can also be understood as a result of microscopic contact processes [53], for which we similarly imagine higher-order interactions to be of interest. For a susceptible-infected-removed (SIR) model, $\lambda^{I \rightarrow S}$ is replaced by jumps to a third terminal state $R$. Finally, we consider the Ising Glauber dynamics $\Pi$ with states $\{U, D\}$ and

$$\lambda^{U \rightarrow D}(N_t(v)) = 1 - \lambda^{D \rightarrow U}(N_t(v))$$

$$= \left(1 + \exp \frac{2J}{T} \psi(N_t(v), (-1)^{1_U[v]}) \right)^{-1} \quad (5)$$

for interaction strength $J > 0$ and temperature $T > 0$.

b. Mean-Field Approximation While the exact colored graphs $G_t$ can be evolved through their probability laws or their associated operator semigroup $M$, an exact analysis is typically prohibitive due to the combinatorial state space. In the limit of large graphs ($N \to \infty$), our aim will thus be to approximate by a system of ODEs $M'$ the evolution of certain population fractions, obtained by aggregating the colored graphs via some aggregation function $\varphi$ — e.g. densities of different colors $\varphi_x(G) \equiv \frac{1}{N} \sum_v 1_{\{x\}}(G[v])$ — such that the diagram

$$\begin{array}{cccc}
G_t & \xrightarrow{\varphi} & G_t \\
\rho_0 & \xrightarrow{M'} & \rho_t
\end{array}$$

commutes: The goal is to find a system of ODEs $M'$ that accurately models the evolution of population fractions $\rho$, such that aggregating population fractions through $\varphi$ and then applying $M'$ is equivalent to first exactly evolving the system and then aggregating.

Since the degrees are bounded, the jumps of $G_t$ are also bounded. Therefore, one expects the jumps of various
where the color of the center vertex is changed from $v$ to $y$, Moreover, each $z \in \{x, d\}$ determines the colored neighborhood (up to isomorphism) of a center vertex with color $x$ and hyperstub degree $d$.

Aggregating colored ECMs over equivalence classes from the quotient space $G/\sim$, where $G$ is the space of all colored ECMs, is tantamount to keeping track of proportions $\rho_t(x, d, z)$ of vertices in $G_t$ with color $x \in X$, hyperstub degree $d$, and counts of neighboring motif colorings $z \in \{x, d\}$. Note that although $z$ already contains all information about $x, d$, for notational convenience we track proportions of $(x, d, z)$. As $N \to \infty$, these proportions can be described by deterministic ODEs, which we shall call the motif-based mean-field (MMF) equations.

This leads us to our main result: The MMF master equations for the limiting proportions $\rho_t$ constitute a system $M^0$ of ODEs in $\{x, d, z\}$ with an accuracy going beyond existing mean field approximations, and are given by

$$
\rho_t(x, d, z) = \sum_{y \in X} (\Lambda^{x \to y} - I) \rho_t(x, d, z) \lambda^{x \to y}(z) + \sum_{y \in X} \sum_{i,j,k,v \neq j} \left( \Lambda_{i,j,k,v}^{x \to y} - I \right) \rho_t(x, d, z) \gamma^{x \to y}_{i,j,k,v} (7)
$$

where we aggregate rates $\lambda^{x \to y}(z)$ and $\gamma^{x \to y}_{i,j,k,v}$ over equivalence classes corresponding to each center vertex configuration $z$ (since $z$ uniquely defines the colored neighborhood up to isomorphism) and each coloring $k$ of neighboring motifs $G^{(i)}$ respectively. Here, we defined limit operators $I$ and influx step operators $\Lambda^{x \to y}, \Lambda_{i,j,k,v}^{x \to y}$ acting on functions $f(x, d, z, y, f(x, d, z, y, k)$ such that we have influx by center vertex jumps from configurations $\Pi^{\to y}[z]$.

$$
[\Lambda^{x \to y} f](x, d, z, y) = f(y, d, \Pi^{\to y}[z], x) \quad (8)
$$

and similarly influx by jumps of all neighboring motifs’
vertices that are not the center vertex (v ≠ j)
\[
\Lambda_{i,j,k,v}^{\rightarrow y}(x, d, z, y, k)
= f(x, d, \Pi_{i,j,k,v}^{\rightarrow y}[z], X_{i,k}^{v}, \Omega_{i,v}^{\rightarrow y}[k])
\]
where \(\Omega_{i,v}^{\rightarrow y}[k]\) denotes the motif coloring resulting from changing the color of vertex v to y in motif i with coloring k. The jump rates of any neighbors in role v of motif G(1) with coloring k from the corresponding state \(\hat{x} = X_{i,k}^{v}\) to y are approximated by the averaged jump rate over all such colored motif occurrences
\[
\tilde{\lambda}_{i,k,v}^{\rightarrow y} = \frac{\sum_{d,z} \rho_t(\hat{x}, d, z) z_{k}^{i,v} \lambda_{x}^{\rightarrow y}(z)}{\sum_{d,z} \rho_t(\hat{x}, d, z) z_{k}^{i,v}},
\]
(10)
since a vertex in configuration z participates \(z_{k}^{i,v}\) times in the considered motif coloring. See Figure 2 for a visualization. Finally, sampling i.i.d. initial states from vertices that are not the center vertex (\(v = 0\))

\[
\rho_0(x, d, z) = P_0(x)P(d)
\]
\[
\prod_{i,j,k,v\neq j} \left[ P_0(X_{i,k}^{v}) \cdot \mathbb{1}_{\{z\}}(X_{j,k}^{v}) \right] z_{i,v}^{j},
\]
(11)
where \(\theta^0 = 1\). The fractions of vertices in any state x are then given by \(\rho_t(x) = \sum_{d,z} \rho_t(x, d, z)\).

The biggest appeal of the MMF equations (7) is their simplicity and intuitiveness. While they may generally not be asymptotically exact, experimentally we find that they are quite accurate. Note that as a special case, we obtain classical approximations such as AME 38 and thereby coarser approximations 39 for degree distributions \(P: \mathbb{N}_0 \rightarrow [0,1]\) by considering only the edge motif G(1), assuming binomial role distributions and aggregating equivalent terms, i.e. \(P(d^{1,1}, d^{1,2}) = \tilde{P}(d^{1,1} + d^{1,2}) \cdot \left(\frac{\theta^{1,1}}{\theta^{1,2}}\right) \left(\frac{1}{\theta^{1,1}}\right)^d \left(\frac{1}{\theta^{1,2}}\right)^d\).

\[\text{FIG. 3. Mean-field approximations in the SIS model using the edge and triangle graphs as motifs. (a-c)}: \text{Results for } \tau = 0.3, \gamma = 0.9. (a): P_{\theta}^{0.3}, P_\theta(I) = 0.2, (b): P_{\theta}^{0.3}, P_\theta(I) = 0.3, (c): P_{\theta}^{0.4}, P_\theta(I) = 0.4. (d-f): \text{Results for } P_{\theta}^{0.3}, (d): \tau = 0.3, \gamma = 0.9, P_\theta(I) = 0.2, (e): \tau = 0.5, \gamma = 0.7, P_\theta(I) = 0.6, (f): \tau = 0.65, \gamma = 0.55, P_\theta(I) = 0.75.\]

\[\text{FIG. 4. Mean-field approximations in the Ising Glauber model using the edge and triangle graphs as motifs. (a-c): Results for } T J^{-1} = 3. (a): P_{\theta}^{0.3}, P_\theta(D) = 0.2, (b): P_{\theta}^{0.3}, P_\theta(D) = 0.3, (c): P_{\theta}^{0.4}, P_\theta(D) = 0.4. (d-f): \text{Results for } P_{\theta}^{0.3}, P_\theta(D) = 0.33. (d): T J^{-1} = 1, (e): T J^{-1} = 3 (f): T J^{-1} = 4.\]

c. Numerical Evaluation
For numerical purposes, we generate equations only for P-supported hyperstub degrees d and simulate rescaled proportions \(\rho_t(x, z | d) \equiv \rho_t(x, d, z)/P(d)\). For fast ECM graph generation, we drop leftover hyperstubs (in our experiments, this amounts to less than 0.5% of all generated stubs, leading to only slight inaccuracies) instead of resampling until cardinality constraints are satisfied and allow but ignore self-loops and multi-edges. We use a third-order numerical integrator and compare MMF against the approximate master equations (AME) 38, the heterogeneous pair approximation (HPA) 35, the heterogeneous mean-field approximation (HMF) 32 and exact Gillespie simulations on graphs of size N = 100000. For use by the wider community, Python code is available at 68.

For two given, arbitrary network motifs G(1), G(2) we consider the three parametrized families of anti-diagonal, uniform and diagonal hyperstub degree distributions \(P_{\theta}^{a}, P_{\theta}^{u}, P_{\theta}^{d}\) with parameter \(\theta \in \mathbb{N}^3\). For \(P_{\theta}^{a}\), we put uniform mass \(1/(\theta + 1)\) on each case where \(\sum d^{1,j} = k\) and \(\sum d^{2,j} = \theta - k\) for \(k = 0, 1, \ldots, \theta\). In each case, we shall assume a uniform distribution over motif roles, resulting in a product of multinomials \(P_{\theta}^{a}(d) \equiv \frac{1}{(\theta + 1)} \sum_{k=0}^{\theta} \mathbb{1}_{\{k\}}(\sum_j d^{1,j} + \)
Fraction of infected \((I)\) 

0.2 0.4 0.6 0.8

0.3 0.4 0.5

Similar assertions hold for the Ising Glauber dynamics outperforms other approximation methods over a range of the SIS dynamics (3, 4) in Figure 3, our approximation put equal probability mass whenever \(\sum P_{2,N} = 1\). For the numerical simulation in the SIR model using the edge and triangle motifs \((a)\), \((b)\), \((c)\):

- \((a)\): \(\tau = 0.3, \gamma = 0.9, 1 - P_0(S) = P_0(I) = 0.2\).
- \((b)\): \(\tau = 0.5, \gamma = 0.7, 1 - P_0(S) = P_0(I) = 0.6\).
- \((c)\): \(\tau = 0.6, \gamma = 0.5, 1 - P_0(S) = P_0(I) = 0.5\).

\(d^2) \cdot \prod_{i \in \{1, 2\}} \text{Mult}(d^i | k, \frac{1}{N_i} 1_{N_i})\), where \(1_{N_i}\) is the \(N_i\)-dimensional one-vector. For \(P_{d^0,}\) and \(P_{d^i,}\) we similarly put equal probability mass whenever \(\sum_j d^1,j + \sum_j d^2,j \leq \theta\) and \(\sum_j d^1,j = \sum_j d^2,j = \theta\) respectively.

On the ECM graphs with edge and triangle motifs \((G^{(1)}, G^{(2)})\) from Figure 1, we find that our approximation matches well with the numerical Gillespie simulation. For the SIS dynamics \((3, 4)\) in Figure 3, our approximation outperforms other approximation methods over a range of (hyperstubs) degree distributions and dynamics parameters. Similar assertions hold for the Ising Glauber dynamics in Figure 4, where existing mean-field approximations become highly inaccurate near the critical point due to the high clustering of the considered graphs. Furthermore, our approximations remain quite accurate also e.g. for graphs with edge and square motifs \((G^{(1)}, G^{(3)})\) in Figure 1 as seen in Figure 5.

For the simplicial version of the SIS dynamics, in Figure 6 we find that the accuracy of our approximations is acceptable, while existing degree-based approximations are unable to handle simplicial dynamics by design. Finally, we verify the accuracy of our proposed framework on the SIR dynamics model in Figure 7 with non-binary states, where the Gillespie simulation for \(N = 100000\) is almost indiscernible from the predicted mean-field proportions, showing the generality of our approach.

**d. Discussion**

We have proposed motif-based mean-field equations for arbitrary neighborhood-dependent jump dynamics on a highly adjustable random graph model, considering both higher-order graph structures and dynamics. Numerical examples show that our approximations are quite accurate. Potential extensions include the consideration of general \(k\)-hop neighborhoods with \(k > 1\), control and lumping of equations under additional assumptions on motif roles to improve tractability. Finally, for applications, estimating hyperstubs degree distributions constitutes another important problem, as an identifiability problem arises from counting larger motifs that include smaller motifs.

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[1] R. J. Glauber, Time-dependent statistics of the ising model, Journal of Mathematical Physics 4, 294 (1963).
[2] I. Z. Kiss, J. C. Miller, and P. L. Simon, Mathematics of Epidemics on Networks: From Exact to Approximate Models Vol. 46 (Springer, 2017).
[3] F. Darabi Sahneh, C. Scoglio, and P. Van Mieghem, Generalized epidemic mean-field model for spreading processes over multilayer complex networks, IEEE/ACM Transactions on Networking 21, 1609 (2013).
[4] R. Pastor-Satorras and A. Vespignani, Epidemic spreading in scale-free networks, Phys. Rev. Lett. 86, 3200 (2001).
[5] R. Pastor-Satorras, C. Castellano, P. Van Mieghem, and A. Vespignani, Epidemic processes in complex networks, Rev. Mod. Phys. 87, 925 (2015).
[6] J. Sanz, C.-Y. Xia, S. Meloni, and Y. Moreno, Dynamics of interacting diseases, Phys. Rev. X 4, 041005 (2014).
[7] J. S. Juul and S. H. Strogatz, Descendant distributions for the impact of mutant contagion on networks, Phys. Rev. Research 2, 033005 (2020).
[8] B. F. Nielsen, L. Simonsen, and K. Sneppen, Covid-19 superspreading suggests mitigation by social network modulation, Phys. Rev. Lett. 126, 118301 (2021).
[9] J. Hindes and T. B. Schwartz, Epidemic extinction and control in heterogeneous networks, Phys. Rev. Lett. 117, 028302 (2016).
[10] D. F. Anderson and T. D. Nguyen, Prevalence of deficiency zero reaction networks in an erdos-renyi framework, arXiv:1910.12723 (2019).
[11] D. F. Anderson and T. D. Nguyen, Deficiency zero for random reaction networks under a stochastic block model framework, Journal of Mathematical Chemistry 59, 2063 (2021).
[12] K. Sugishita, M. A. Porter, M. Beguerisse-Díaz, and N. Masuda, Opinion dynamics on tie-decay networks, Phys. Rev. Research 3, 023249 (2021).
[13] J. S. Juul and M. A. Porter, Hipsters on networks: How a minority group of individuals can lead to an antiestablishment majority, Phys. Rev. E 99, 022313 (2019).
[14] D. Bruneo, M. Scarpa, A. Bobbio, D. Cerotti, and M. Gribaudo, Markovian agent modeling swarm intelligence algorithms in wireless sensor networks, Perform. Eval. 69, 135–149 (2012).
[15] M. Gribaudo, D. Cerotti, and A. Bobbio, Analysis of on-off policies in sensor networks using interacting markovian agents, in 2008 Sixth Annual IEEE International Conference on Pervasive Computing and Communications (PerCom) (2008) pp. 300–305.
[16] P. Van Mieghem, J. Omic, and R. Kooij, Virus spread in networks, [IEEE/ACM Transactions on Networking 17, 1 (2009).]
[17] R. Albert and A.-L. Barabási, Statistical mechanics of complex networks, Reviews of modern physics 74, 47 (2002).
[18] A. Barrat, M. Barthlemy, and A. Vespignani, Dynamical Processes on Complex Networks (Cambridge University Press, USA, 2008).
[19] R. Durrett, Random Graph Dynamics (Cambridge University Press, USA, 2006).
[20] R. van der Hofstad, Random Graphs and Complex Networks: Volume 1 (Cambridge University Press, USA, 2016).
[21] P. G. Fennell, S. Melnik, and J. P. Gleeson, Limitations of discrete-time approaches to continuous-time contagion dynamics, Phys. Rev. E 94, 052125 (2016).
[22] J.-M. Lasry and P.-L. Lions, Mean field games, Japan. J. Math 2, 229 (2007).
[23] X. Guo, A. Hu, R. Xu, and J. Zhang, Learning mean-field games, in Advances in Neural Information Processing Systems Vol. 32, edited by H. Wallach, H. Larochelle, A. Beygelzimer, F. d’Alché-Buc, E. Fox, and R. Garnett (Curran Associates, Inc., 2019).
[24] K. Cui and H. Koeppl, Approximately solving mean field games flock! the reinforcement learning way, arXiv:2105.07933 (2021).
[25] V. Sood and S. Redner, Voter model on heterogeneous graphs, Phys. Rev. Lett. 94, 178701 (2005).
[26] D. A. Rand, Correlation equations and pair approximations for spatial ecologies, in Advanced Ecological Theory (John Wiley & Sons, Ltd, 1999) Chap. 4, pp. 100–142.
[27] F. Vaquez and V. M. Eguíluz, Analytical solution of the voter model on uncorrelated networks, New Journal of Physics 10, 063011 (2008).
[28] E. Fugleise and C. Castellano, Heterogeneous pair approximation for voter models on networks, [EPL (Europhysics Letters) 88, 58004 (2009).]
[29] D. H. Silva, S. C. Ferreira, W. Cota, R. Pastor-Satorras, and C. Castellano, Spectral properties and the accuracy of mean-field approaches for epidemics on correlated power-law networks, Phys. Rev. Research 1, 033024 (2019).
[30] P. Van Mieghem, J. Omic, and R. Kooij, Virus spread in networks, [IEEE/ACM Transactions on Networking 17, 1 (2009).]
[31] J. Lindquist, J. Ma, P. Van den Driessche, and F. H. Willeboorde, Effective degree network disease models, Journal of Mathematical Biology 52, 143 (2011).
[32] A. F. Peralta and R. Toral, System-size expansion of the moments of a master equation, Chaos: An Interdisciplinary Journal of Nonlinear Science 28, 106303 (2018).
[33] A. F. Peralta and R. Toral, Binary-state dynamics on complex networks: Stochastic pair approximation and beyond, Phys. Rev. X 3, 021004 (2013).
[34] P. G. Fennell and J. P. Gleeson, Multistate dynamical processes on networks: Analysis through degree-based approximation frameworks, SIAM Review 61, 92 (2019).
[35] J. P. Gleeson, Binary-state dynamics on complex networks: Pair approximation and beyond, Phys. Rev. X 3, 021004 (2013).
[36] P. G. Fennell and J. P. Gleeson, Multistate dynamical processes on networks: Analysis through degree-based approximation frameworks, SIAM Review 61, 92 (2019).
[37] J. Lindquist, J. Ma, P. Van den Driessche, and F. H. Willeboorde, Effective degree network disease models, Journal of Mathematical Biology 52, 143 (2011).
[38] A. F. Peralta and R. Toral, System-size expansion of the moments of a master equation, Chaos: An Interdisciplinary Journal of Nonlinear Science 28, 106303 (2018).
[39] A. F. Peralta and R. Toral, Binary-state dynamics on complex networks: Stochastic pair approximation and beyond, Phys. Rev. Research 2, 043370 (2020).
[40] P. Farkhooi and W. Stannat, Complete mean-field theory for dynamics of binary recurrent networks, Phys. Rev. Lett. 119, 208301 (2017).
[41] C.-R. Cai, Z.-X. Wu, M. Z. Q. Chen, P. Holme, and J.-Y. Guan, Solving the dynamic correlation problem of the susceptible-infected-susceptible model on networks, Phys. Rev. Lett. 116, 258301 (2016).
[42] K. A. Jacobsen, M. G. Burch, J. H. Tien, and G. A. Rempala, The large graph limit of a stochastic epidemic model on a dynamic multilayer network, Journal of Biological Dynamics 12, 746 (2018).
[43] W. R. KhudaBuksh, C. Woroszylo, G. Rempala, and H. Koeppl, A functional central limit theorem for SI processes on configuration model graphs, Advances in Applied Probability (2022), (to be published), arXiv:1703.06328.
[44] S. Chatterjee and R. Durrett, Contact processes on random graphs with power law degree distributions have critical value 0, The Annals of Probability 37, 2332 (2009).
[45] J. P. Gleeson, S. Melnik, J. A. Ward, M. A. Porter, and P. J. Mucha, Accuracy of mean-field theory for dynamics on real-world networks, Phys. Rev. E 85, 026106 (2012).
[46] F. Battiston, G. Cencetti, T. Iacoboni, V. Latora, M. Lucas, A. Patania, J.-G. Young, and G. Petri, Networks beyond pairwise interactions: Structure and dynamics, Physics Reports 874, 1 (2020).
[51] G. St-Onge, H. Sun, A. Allard, L. Hébert-Dufresne, and G. Bianconi, Universal nonlinear infection kernel from heterogeneous exposure on higher-order networks, Phys. Rev. Lett. 127, 158301 (2021).
[52] G. St-Onge, V. Thibeault, A. Allard, L. J. Dubé, and L. Hébert-Dufresne, Social confinement and mesoscopic localization of epidemics on networks, Phys. Rev. Lett. 126, 098301 (2021).
[53] A. R. Benson, D. F. Gleich, and J. Leskovec, Higher-order organization of complex networks, Science 353, 163 (2016).
[54] J. P. Gleeson, Cascades on correlated and modular random networks, Phys. Rev. E 77, 046117 (2008).
[55] A. C. Schwarz and M. A. Porter, Motifs for processes on networks, SIAM Journal on Applied Dynamical Systems 20, 2516 (2021).
[56] M. Ritchie, L. Berthouze, and I. Z. Kiss, Beyond clustering: mean-field dynamics on networks with arbitrary subgraph composition, Journal of Mathematical Biology 72, 255 (2016).
[57] G. St-Onge, V. Thibeault, A. Allard, L. J. Dubé, and L. Hébert-Dufresne, Master equation analysis of mesoscopic localization in contagion dynamics on higher-order networks, Phys. Rev. E 103, 032301 (2021).
[58] N. Persky, R. Ben-Av, I. Kanter, and E. Domany, Mean-field behavior of cluster dynamics, Phys. Rev. E 54, 2351 (1996).
[59] V. Vlasov and A. Bifone, Hub-driven remote synchronization in brain networks, Scientific reports 7, 1 (2017).
[60] C. G. Assisi, V. K. Jirsa, and J. A. S. Kelso, Synchrony and clustering in heterogeneous networks with global coupling and parameter dispersion, Phys. Rev. Lett. 94, 018106 (2005).
[61] A. Fronczak, P. Fronczak, and J. A. Holyst, Mean-field theory for clustering coefficients in barabási-albert networks, Phys. Rev. E 68, 046126 (2003).
[62] M. Newman, Networks (Oxford University Press, USA, 2018).
[63] B. Karrer and M. E. J. Newman, Random graphs containing arbitrary distributions of subgraphs, Phys. Rev. E 82, 066118 (2010).
[64] M. Ritchie, L. Berthouze, and I. Z. Kiss, Generation and analysis of networks with a prescribed degree sequence and subgraph family: higher-order structure matters, Journal of Complex Networks 5, 1 (2017).
[65] S. Gómez, A. Arenas, J. Borge-Holthoefer, S. Meloni, and Y. Moreno, Discrete-time markov chain approach to contact-based disease spreading in complex networks, EPL (Europhysics Letters) 89, 38009 (2010).
[66] T. G. Kurtz, Approximation of Population Processes (Society for Industrial and Applied Mathematics, 1981).
[67] J. Jacod and A. Shiryaev, Limit Theorems for Stochastic Processes (Springer, Berlin, Heidelberg, 2003).
[68] K. Cui, W. R. KhudaBukhsh, and H. Koeppl, Motif-based mean-field equations (2022), https://doi.org/10.5281/zenodo.5653343.
[69] G. Großmann, C. Kyriakopoulos, L. Bortolussi, and V. Wolf, Lumping the approximate master equation for multistate processes on complex networks, in International Conference on Quantitative Evaluation of Systems (Springer, 2018) pp. 157–172.
[70] W. R. KhudaBukhsh, A. Auddy, Y. Disser, and H. Koeppl, Approximate lumpability for markovian agent-based models using local symmetries, Journal of Applied Probability 56, 647 (2019).