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The largest eigenvalue of the matrix describing a network's contact structure is often important in predicting the behavior of dynamical processes. We extend this notion to hypergraphs and motivate the importance of an analogous eigenvalue, the expansion eigenvalue, for hypergraph dynamical processes. Using a mean-field approach, we derive an approximation to the expansion eigenvalue in terms of the degree sequence for uncorrelated hypergraphs. We introduce a generative model for hypergraphs that includes degree assortativity, and use a perturbation approach to derive an approximation to the expansion eigenvalue for assortative hypergraphs. We define the dynamical assortativity, a dynamically sensible definition of assortativity for uniform hypergraphs, and describe how reducing the dynamical assortativity of hypergraphs through preferential rewiring can extinguish epidemics. We validate our results with both synthetic and empirical datasets.

susceptible-infected-susceptible (SIS) model on hypergraphs,[28] and we believe it will also prove useful in relating hypergraph assortative mixing patterns to other dynamical processes.

Our approach is as follows: first, we define and motivate the importance of the expansion eigenvalue on dynamical processes; second, we derive a mean-field approximation of this eigenvalue for hypergraphs without assortativity; third, we present a generative model for assortative hypergraphs; fourth, we employ a perturbation approach to derive the effect of degree–degree mixing on the eigenvalue and define the dynamical assortativity; and last, we show how our results can be used to modify hypergraph dynamics through preferential rewiring of hyperedges.

We start by defining terminology. A hypergraph is a mathematical object that describes group interactions among a set of nodes. We represent it as $H = (V, E)$, where V is the set of nodes and E is the set of hyperedges, which are subsets of V and represent unordered interactions of arbitrary size. We call a hyperedge with cardinality m an m-hyperedge and a hypergraph with only m-hyperedges an m-uniform hypergraph. It is useful to consider weighted hypergraphs, where each hyperedge e has an associated positive weight $\ _e$. We define the hyperdegree sequence as in Ref. 15, where the mth order hyperdegree of node i, $k_i^{(m)}$, is the number of m-hyperedges to which it belongs.

We now define the expansion eigenvalue and discuss its relevance to dynamical processes on hypergraphs. For a weighted hypergraph, the expansion eigenvalue and associated eigenvector $\mathbf{u}$ are defined by the eigenvalue equation

$$u_i = \square_{e=\{i,i_1,\ldots,i_{m\ 1}\}\ E}\ {}_e(u_{i_1} + \cdots + u_{i_{m\ 1}}), \qquad (1)$$

where and $\mathbf{u}$ are the Perron–Frobenius eigenvalue and eigenvector of the non-negative matrix associated to linear equation (1).

Here, we present some applications of the expansion eigenvalue. First, just like the Perron–Frobenius eigenvector of a network, the adjacency matrix represents eigenvector centrality;[29] in the unweighted case (i.e., $\ _e = 1$ for every hyperedge e), the eigenvector $\mathbf{u}$ corresponds to the Clique motif Eigenvector Centrality, a generalization of eigenvector centrality for hypergraphs.[30] Second, just as the largest eigenvalue of a network's adjacency matrix influences network dynamics, the expansion eigenvalue plays an important role in dynamical processes on hypergraphs. For example, consider an SIS process on a hypergraph, where a healthy node can get infected via a hyperedge e to which it belongs at rate $\ _e$ if at least one other node in e is infected (the case referred to as individual contagion in Ref. 15) and heals spontaneously at rate . As discussed in Ref. 28 in Theorem 9.1, the extinction threshold for the exact stochastic process can be bounded above by that for the mean-field dynamics. The mean-field equation for x_i, the probability that node i is infected, is given by

$$\frac{dx_i}{dt} = \ x_i + (1\ \ x_i) \times \square_{e=\{i,i_1,\ldots,i_{m\ 1}\}\ E}\ {}_e[1\ \ (1\ \ x_{i_1}), \ldots, (1\ \ x_{i_{m\ 1}})]. \qquad (2)$$

By inspection, $x_i = 0$ for all

and only if and v solve the eigenvalue equation $v = Kv$. Notice that in the m-uniform case, we recover the expression we previously derived. Consider the network formed by specifying hyperedge sizes ($m = 2, \ldots, M$) to be the nodes and constructing a link between two sizes m_1 and m_2 if at least one node in the original hypergraph is a member of a hyperedge of size m_1 and a hyperedge of size m_2. K is irreducible if and only if this network is strongly connected. If this is the case, by the Perron–Frobenius theorem, the eigenvalue with largest magnitude is positive and has a corresponding positive eigenvector, and they correspond, respectively, to and v.

In contrast with the uncorrelated case, we now assume that nodes are connected with an arbitrary function f_m determining the connection probability. We define

$$f_m(k_1, \ldots, k_m) = f_m^{(0)}(k_1, \ldots, k_m)\left[1 + g_m(k_1, \ldots, k_m)\right], \quad (13)$$

where is a parameter which will later assume to be small and g_m an assortativity function for m-uniform hypergraphs. The assortativity function $g_m(k_1, \ldots, k_m)$ determines how likely it is that nodes with degrees $k_1, \ldots, k_m$ are joined by a m-hyperedge; if $g_m > 0$ ($g_m < 0$), it is more (less) likely than it would be expected if they were connected at random. In order to preserve the expected degree sequence, g_m must satisfy $\sum_{k_1,\ldots,k_m} f_m^{(0)}(k_1, \ldots, k_m) g_m(k_1, \ldots, k_m) = 0$.

We now assume that the parameter is small and develop perturbative approximations to the eigenvalue and its eigenvector u_k. To first order, these approximations are

$$\begin{aligned} &= {}^{(0)} + {}^{(1)}, \\ u_k &= u_k^{(0)} + u_k^{(1)}, \end{aligned} \quad (14)$$

where ${}^{(0)} = (m \quad 1$ .md [(k)0.339757d (D)Tj /R53i8.99999 Tf 3.55508 0 Td(u)0Td [(m)0.1.35 Td J /R6rs8.99999 Tf 3.35703 0 Td(u)

We validate our results with numerical simulations on both synthetic and empirical hypergraphs. For both types of data, we modify the dynamical assortativity of the datasets by performing preferential double hyperedge swaps on the hypergraphs.

For each dataset hypergraph H, we focus on an m-uniform partition H_m


−0.1
0.0
0.1
0.

In particular, higher-order dynamical correlations might be missed by this approach. The second (related) limitation is that, since this eigenvalue is, by definition, a quantity related to linear processes, its applicability is restricted in principle only to certain dynamical regimes. However, approaches that reduce a hypergraph to an effective pairwise network have been successful and found application in clustering,

We multiply both sides by $k P(k)/\Delta k$ and sum over k, which yields

$$
\begin{aligned}
&{}^{(0)} \sum_k P(k)\frac{k u_k^{(1)}}{\Delta k} + {}^{(1)} \sum_k P(k)\frac{k^2}{\Delta k} \\
&= (m-1) \sum_k P(k)\frac{k^2}{\Delta k} \sum_{k_1} P(k_1)\frac{k_1 u_{k_1}^{(1)}}{\Delta k} \\
&\quad + (m-1) \sum_{k,k_1,\ldots,k_{m-1}} N(k)N(k_1),\ldots,N(k_{m-1}) \\
&\quad \times \frac{k^2 k_1^2 k_2,\ldots,k_{m-1}}{(N\Delta k)^m} g_m(k,k_1,\ldots,k_{m-1}).
\end{aligned}
$$

Because ${}^{(0)} = (m-1)/\Delta k^2 \Delta k$, the first terms on both sides are equal and we cancel them, yielding

$$
\begin{aligned}
{}^{(1)} &= (m-1)\frac{\Delta k}{\Delta k^2} \sum_{k,k_1,\ldots,k_{m-1}} N(k)N(k_1),\ldots,N(k_{m-1}) \\
&\quad \times \frac{k^2 k_1^2,\ldots,k_{m-1}}{(N\Delta k)^m} g_m(k,k_1,\ldots,k_{m-1}). \qquad \text{(A2)}
\end{aligned}
$$

We can use the relation that $f_m(k_1,\ldots,k_m) = (m-1)!k_1,\ldots,k_m/(N\Delta k)^{m-1} 1 + g_m(k_1,\ldots,k_m)$ to remove the reference to g_m, obtaining

$$
\begin{aligned}
{}^{(1)} &= \frac{(m-1)\Delta k}{(m-1)!\Delta k^2} \sum_{k,k_1,\ldots,k_{m-1}} N(k)N(k_1),\ldots,N(k_{m-1}) \\
&\quad \times \frac{k k_1}{N\Delta k} f_m(k,k_1,\ldots,k_{m-1}) \\
&\quad (m-1)\frac{\Delta k}{\Delta k^2} \sum_{k,k_1} P(k)P(k_1)\frac{k^2 k_1^2}{\Delta k^2}.
\end{aligned}
$$

The term

$$
\begin{aligned}
&\frac{1}{2!(m-2)!} \sum_{k,k_1,\ldots,k_{m-1}} N(k)N(k_1),\ldots,N(k_{m-1}) \\
&\quad \times k k_1 f_m(k,k_1,\ldots,k_{m-1})
\end{aligned}
$$


1.
0.5
0.0
0.1
0.2
0.3
0.4

susceptible and infected nodes as well as the rates of each mechanism. We repeat these steps until either t exceeds a maximum specified time or the number of infected nodes is zero. We refer to this termination time as T and the corresponding number of discrete data points as N_T. Modeling the SIS contagion process as a CTDS process can be more efficient than a DTDS process when R

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