Generalised moment closure for multistate dynamics on networks

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In the study of dynamics on networks, moment closure is a commonly used method to obtain low-dimensional evolution equations amenable to analysis. The variables in the evolution equations are mean counts of subgraph states and are referred to as moments. Due to interaction between neighbours, each moment equation is a function of higher-order moments, such that an infinite hierarchy of equations arises. Hence, the derivation requires truncation at a given order, and, an approximation of the highest-order moments in terms of lower-order ones, known as a closure formula. Recent systematic approximations have either restricted focus to closed moment equations for SIR epidemic spreading or to unclosed moment equations for arbitrary dynamics. In this paper, we develop a general procedure that automates both derivation and closure of arbitrary order moment equations for dynamics with nearest-neighbour interactions on undirected networks. Automation of the closure step was made possible by our generalised closure scheme, which systematically decomposes the largest subgraphs into their smaller components. We show that this decomposition is exact if these components form a tree, there is independence at distances beyond their graph diameter, and there is spatial homogeneity. Testing our method for SIS epidemic spreading on lattices and random networks confirms that biases are larger for networks with many short loops in regimes with long-range dependence. A Mathematica script that automates the moment closure is available for download.

I. INTRODUCTION

Mathematical analysis of complex systems usually starts from high-dimensional models. While these may have more realism, they are harder to analyse than simpler low-dimensional models. Therefore, one often looks for a low-dimensional description via a coarse-graining method. The earliest coarse-graining methods were developed in statistical physics to study phase transitions in lattice models of materials [1–4] and are now known as mean-field approximations. The essence of mean-field approximations is that one can obtain a simpler description by neglecting some correlations in the system by replacing an average (sum) of products with a product of averages (sums). While this substitution was initially only applied to terms in the energy function of equilibrium lattice models [1–4], it eventually came to be applied as well to occurrence probabilities in kinetic equations of non-equilibrium lattice models derived from the master equation [5–7]. Its domain of application was extended from materials to spatial population dynamics in ecology and evolution [8–10], and to epidemic dynamics on networks [11, 12]. In this general context the methods of deriving and truncating kinetic equations for dynamics of chemical or biological species came to be known as moment closure [13].

For multistate dynamics on networks [14–16], moment closure consists of first deriving a system of ordinary differential equations (ODEs), also known as moment equations, representing the evolution of the expected frequency of small subgraph states known as network motifs. The derivation proceeds from smaller to larger sized-motifs, with dynamics of mean motif counts of size $m$ depending only on mean motif counts of size $m$ and $m + 1$ if the dynamics has only nearest-neighbour interactions. Hence, a system of ODEs obtained in such a manner for motif counts up to a maximum considered size $k$ (also referred to as the order of the moment closure) is always underdetermined, because it depends on motifs of size $k + 1$ but does not contain equations for them. Therefore, as the second step of moment closure, a closure approximation is applied by expressing counts of $(k + 1)$-size motifs as functions of counts of $\{1, \ldots, k\}$-size motifs, closing the system of ODEs. The underlying assumption that may justify such a substitution is that mean counts or probabilities of larger-sized motifs factorise in terms of smaller-sized ones when the latter are (conditionally) independent. For homogeneous networks, closures that are valid at the individual level (i.e. concerning states of given nodes) are also valid at the population level (i.e. concerning total counts or averages of states in the whole network) [17], which then permits a compact description in terms of population-level quantities. Yet, the number of motif types, and hence equations, increases combinatorially with $k$. It is then hoped that the derivation can be stopped at an order low enough for the resulting system of ODEs to be sufficiently amenable to analytical or numerical methods and high enough to satisfy the independence assumptions underlying the closure approximately.

Recent systematic procedures to obtain moment equations have either focused on closed equations for the specific case of SIR epidemic spreading [18, 19] or on unclosed equations for arbitrary dynamics [20]. For SIR epidemic spreading, the independence assumptions behind the required closure formulas are provably valid. In particular, Sharkey et al. [19] showed that an exact individual-level closure approximation exists for motifs that have an all-susceptible set of nodes which cuts all possible chains of infection between the remaining parts when removed. In tree networks, this is already possible with three nodes such that the largest required motif in
the moment equations is of size 2. In case of non-tree networks, larger motifs need to be taken into account, resulting in a larger number of equations. For large networks with many loops of various sizes, the individual-level approach would result in an impractically large system of equations, and therefore one quickly becomes obliged to work with population-level models instead. Population-level moment closure still provides a good approximation for mildly heterogeneous networks and even for dynamics that include reinfection \[15, 17, 21\], with a steady improvement of accuracy when the effect of short loops is taken into account by including network motifs that contain them \[19, 22, 23\]. While for dynamics other than SIR spreading, closure approximations continue to be only heuristically justified, one can still derive unclosed moment ODEs for them. An automated algorithm for this purpose, focusing on the general case of directed adaptive networks, was developed by Danos et al. \[20\].

In this paper, we provide a fully automated procedure for both derivation and closure of population-level moment equations up to any order and for dynamics on arbitrary undirected networks. Automation of the closure step was made possible by our generalised closure scheme, which systematically decomposes the largest subgraphs into their smaller components. We show that this approximation scheme is exact if the motifs that are decomposed by the closure form a tree and if there is independence beyond their graph diameter. The procedure consists of four main steps (Figure 1): (i) enumeration of all dynamically relevant motifs up to size \(k\), (ii) derivation of the ODEs for the subset of these motifs that will not be eliminated in the next step, (iii) elimination via conservation relations, and (iv) closure of the system of ODEs. We will refer to the final closed system of ODEs as the \(k\)-th order mean field, or MF\(k\) in short. We developed a Mathematica \[24\] package that derives MF\(k\) by performing steps (i)–(iv). The required inputs for this algorithm are: (i) the counts of all induced subgraphs in the underlying network up to size \(k\), and (ii) the matrices \(R^0\), \(R^1\) with conversion and interaction rates. The \texttt{html}\ output of an example is attached in Supplement S-VIII and the package is available for download.

The general underlying Markov chain for the network and its motifs are introduced in Sections II and III. Section IV explains the general formula (6) for step (ii), which follows from the master equation (for its derivation, see Supplement S-I). The conversion relations used for elimination of variables from the ODEs in step (iii) are shown in equations (8, 9) of Section V. The form of the system of moment equations up to a truncation order \(k\) (10) and the variable elimination are shown in Section VI, resulting in the unclosed system (14). Finally, general expressions to close the system of moment equations in step (iv) are derived in Section VII (equations (24) or (25)), resulting in form (15). In Section VIII we set up MF1-5 models of SIS epidemic spreading and compare their steady states to those of simulations on a selection of networks. We focus in particular on the square lattice, for which low-order moment closures and approximate master equation methods fail, due to its large number of loops of any size, and we compare against random networks and higher-dimensional lattices, for which the former methods work well.

II. THE UNDERLYING DISCRETE-STATE CONTINUOUS-TIME MARKOV CHAIN

We consider a dynamical system on a fixed undirected graph \(G\) with \(N\) nodes and adjacency matrix \(A \in \{0,1\}^{N \times N}\), where each node may have one out of \(n\) discrete states. We may see the nodes as locations and the states as species, such that the space at node \(i \in \{1,\ldots,N\}\) is occupied by exactly one species in \(\{1,\ldots,n\}\). We denote the state vector at time \(t\) by \(X(t)\) such that \(X_i(t)\in \{1,\ldots,n\}\). The type of dynamics we consider is a continuous-time Markov chain with two Poisson process transition types, with rates specified by a \(n \times n \times n\) tensor \(R^1\) and a \(n \times n \times n\) tensor \(R^0\):

1. \(R^0\) specifies spontaneous conversion rates. Any node with state \(a\) may change spontaneously into state \(b\), with rate \(R_{ab}^0\).
2. \(R^1\) specifies nearest-neighbour interaction rates. Any node with state \(a\) may change into state \(b\) for each link to a node with state \(c\), with rate \(R_{abc}\).

This corresponds to the reaction rules

\[
\circ \xrightarrow{R_{ab}^0} \bullet, \quad \circ \circ \xrightarrow{R_{abc}} \circ \bullet.
\]

A simple example is susceptible-infected-susceptible (SIS) epidemic spreading on a square two-dimensional lattice of \(\sqrt{N} \times \sqrt{N}\) nodes (say, periodic in both directions). For SIS spreading, each node may have one of two states, susceptible or infected, \(\{\bullet,\circ\} = \{1,2\}\), for \(t \in [0,\infty)\) and \(i \in \{1,\ldots,N\}\). \(S\) nodes can become infected at rate \(\beta\) per infected neighbour and \(I\) nodes recover spontaneously at rate \(\gamma\). Hence, for SIS spreading, the matrix \(R^0\) has a single non-zero entry \(R_{2,1}^0 = \gamma > 0\) (for spontaneous recovery) and the tensor \(R^1\) has a single non-zero entry \(R_{1,2,2}^1 = \beta > 0\) (for infection along IS links, denoted by the symbol \(\bullet \circ\) below), corresponding to the reaction rules

\[
\bullet \xrightarrow{\gamma} \circ, \quad \bullet \circ \xrightarrow{\beta} \circ \circ.
\]

III. NETWORK MOTIFS AND THEIR COUNTS

We define network motifs as (typically small) graphs with given state labels. The order of a motif is the number of nodes it has. E.g., in our example, \(I\) nodes and IS links are examples of first and second-order motifs. We use square brackets to denote the count of occurrences of motifs in \((G,X)\), i.e. the number of occurrences of \(I\)
FIG. 1. Mean-field models for multistate dynamics on networks via moment closure. Left: general form. Right: example (MF2 for SIS spreading). Input (top): network $G$, the considered process defined by the reaction rate matrices $R^0, R^1$. Output (bottom): closed system of differential equations representing mean frequencies of motif counts in the network up to a maximum size $k$. The four main steps are: (i) find all dynamically relevant motifs, (ii) derive the moment equations for the motifs that will not be eliminated, (iii) substitute to be eliminated terms via conservation relations, (iv) close the system via a closure scheme.

Nodes is $\{\bullet\}$. Hence, we can write e.g. respectively for $I$ nodes, $IS$ links and $ISI$ chains

$$
\bullet = \sum_{i \in \{1,\ldots,N\}} \delta_2(X_i), \\
\bullet \bullet = \sum_{i \neq j \in \{1,\ldots,N\}} \delta_1(A_{ij}) \delta_2(X_i) \delta_1(X_j), \\
\bullet \bullet \bullet = \sum_{i,j,k \neq \ell \in \{1,\ldots,N\}} \delta_1(A_{ij}) \delta_1(A_{jk}) \delta_0(A_{ik}) \delta_2(X_i) \delta_1(X_j) \delta_2(X_k),
$$

where we omitted the dependence on $t$. The Kronecker delta, $\delta_y(x)$, is 1 if $x$ equals $y$ and 0 otherwise. By construction, the motif counts on the left-hand side are random, since $X(t)$ is random. Generalizing the above examples, a network motif of order $m$, is a network with $m$ nodes, each of which are labelled with a state. It thus fully characterised by its connectivity pattern between nodes and its state labels on the nodes. The connectivity between motif nodes, i.e. the motif without labels, will be indicated by $a$, which, depending on the context, denotes the adjacency matrix of the motif, or a set $a \in \{1,\ldots,m\} \times \{1,\ldots,m\}^m$ of links between the $m$ nodes (the indices of the non-zero entries in the adjacency matrix of the motif such that $\mu \leq m(m-1)/2$, or a graphical representation of the connectivity. For instance, two linked nodes are displayed according to these representations as $\{0,1\}$, $\{(1,2)\}$, or $\circ \circ$ respectively. As we focus only on undirected networks, each pair in the pair representation is bidirectional, i.e. we write $\{(1,2)\}$ instead of $\{(1,2),(2,1)\}$. Motif labels will be indicated via a vector $x = (x_1,\ldots,x_m) \in \{1,\ldots,n\}^m$ with state labels $x_p$ at positions $p = 1,\ldots,m$. Hence, the pair of $x$ and $a$ describes the motif, which we write as $x^a$. For example $(2,1)^{(1,2)}$ is the $\bullet \bullet \bullet$ link, $(1,1,1)^{(1,2),(2,3),(1,3)} = (\bullet \bullet \bullet)^{(1,2),(2,3),(1,3)}$ is the motif of nodes with states $\bullet$ connected in a triangle, later written as $\bullet \bullet \bullet$.

For a general network motif $x^a$, the total count $[x^a] = [x^a](t)$ in the network $G$ with fixed adjacency $A$ and node labels $X = X(t)$ is

$$
[x^a] = \sum_{i \in S(m,N)} \delta_a(A_i) \delta_x(X_i),
$$

where $S(m,N)$ is the set of all $m$-tuples from $\{1,\ldots,N\}$ without repetition, which has size $|S(m,N)| = N!/(N-m)!$. For instance, $\sum_{i \in S(3,3)} = \sum_{i \in \{1,\ldots,3\}} \sum_{j \in \{1,\ldots,3\} \setminus \{i\}} \sum_{k \in \{1,\ldots,3\} \setminus \{i,j\}}$. For an index set $i \subset \{1,\ldots,N\}^m$ of length $m$ we use the convention that $A_i \in \{0,1\}^{m \times m}$ and $X_i \in \{1,\ldots,n\}^m$ are the
restrictions of matrix $A$ and vector $X$ to the index set $i$. We count exact matches between the motif and the subgraph in $(G, X)$. This means that the counted motif needs to have $a$ as induced subgraph of $G$, with matching state labels. Counting via (3) leads to multiple counting of motifs with symmetries (more precisely: automorphisms – see Supplement S-I), with multiplicity equal to the number of symmetries. For instance, $\circ-\circ$ is counted once; but $\circ-\circ$ or $\circ-\circ$ twice, and $\circ-\circ-\circ$ six times.

IV. DIFFERENTIAL EQUATIONS FOR MOTIF COUNTS

In our SIS spreading example, the expected rate of change for the count of infected nodes is well known to satisfy

$$
\frac{d}{dt} \langle \circ \rangle = -\gamma \langle \circ \rangle + \beta \langle \circ-\circ \rangle,
$$

where $\langle \cdot \rangle$ brackets denote expectations over many independent realisations of the underlying Markov chain. Relation (4) is exact for finite network sizes $N$ and can be derived from the Kolmogorov-forward (or master) equation for the Markov chain, see Supplement S-I. Note that the structure in (4) is such that the expected rate for the frequency of a motif of size $m = 1$ (here $\langle \circ \rangle$) depends on the counts of motifs of size $m = 1$ (here $\langle \circ \rangle$), from spontaneous conversions (here recovery) and size $m = 2$ (here $\langle \circ-\circ \rangle$) from nearest-neighbour-induced conversions (here infection).

This is true in general such that the count of a general motif $\langle \circ^a \rangle (t)$ of size $m$ satisfies an ordinary differential equation of form

$$
\frac{d}{dt} \langle \circ^a \rangle = F_{\circ^a} \left( \langle \circ_1^b \rangle, \langle \circ_2^b \rangle, \ldots \right),
$$

where $|y_i| \in \{m, m + 1\}$. On the right-hand side the $\langle \circ_1^b \rangle (t)$ stand for counts of motifs of size $m$ or $m + 1$ on which the dynamics of $\langle \circ^a \rangle (t)$ depend. Our package expresses the right-hand side of the differential equation (5) for arbitrary motifs $\circ^a$ of size $m$ in the general form

$$
\frac{d}{dt} \langle \circ^a \rangle = \sum_{y \in \mathcal{N}_p^c (\circ^a)} \frac{R_{xy}}{n} \langle \circ^a \rangle - \sum_{y \in \mathcal{N}_p^c (\circ^a)} \frac{R_{yx}}{n} \langle \circ^a \rangle + \frac{R_{xy}}{n} \langle \circ^a \rangle,
$$

Here, $x_{p-k}$ is the state label vector obtained by setting the state label of the $p$th element of $x$ to $k$. $\kappa_{p,c}^c$ is the $c$-degree at position $p$ in motif $\circ^a$, i.e. it is the number of connections node $p$ in motif $\circ^a$ has to nodes with state label $c$. The set $\mathcal{N}_p^c (\circ^a)$ contains all motifs $\circ^b$ of order $m + 1$ that extend the state label vector $x$ by one new node with state label $c$ and extend adjacency $a$ by links to the new node, namely

$$
\mathcal{N}_p^c (\circ^a) = \bigcup_{\ell=1}^{m+1} \{ \circ^b : y_{\ell} = c, y_{\ell+\theta} = \circ^a, (\ell, p) \in b \},
$$

where $y_{\ell+\theta}$ denotes the $m$th order connected motif obtained by deleting the $\ell$th node of $\circ^b$ and its links. The differential equation (6) shows how the expected count of $\circ^a$ is increased by transitions into $\circ^a$ – the positive terms – and decreased by transitions out of $\circ^a$ – the negative terms. This happens through spontaneous conversions (terms with $R^0$), through nearest-neighbour interaction between nodes within the motif (first two terms with $R^1$), or through nearest-neighbour interaction with nodes outside the motif (last two terms with $R^1$). Note that equivalent motifs up to permutation (isomorphic motifs – see Supplement S-I) result in the same equation, such that we choose the same representative node indexing for each equivalence class.

V. CONSERVATION RELATIONS

Conservation relations are linear algebraic relations between motif counts. E.g., for SIS spreading on a square lattice with periodic boundary conditions, we have for first and second-order motifs:

$$
[\circ (t)] + [\circ (t)] = N, \quad [\circ-\circ (t)] + [\circ-\circ (t)] + [\circ-\circ (t)] = 4N.
$$

Such conservation of node and link counts occurs because our graph $G$ is fixed. We can use the total counts on the right-hand side as normalising factors such that we may write

$$
[\circ (t)] + [\circ (t)] = 1, \quad [\circ-\circ (t)] + [\circ-\circ (t)] + [\circ-\circ (t)] = 1.
$$

where $[\cdot]$ is our notation for normalised motif counts. For networks with homogeneous degree, one can also write conservation equations of the type $[\circ (t)] = [\circ-\circ + [\circ-\circ]]$. 
In general, for each adjacency matrix \( a \) of possible motifs of size \( m \) the conservation relation

\[
\sum_{x:|x|=m} [x^a](t) = [a], \quad \text{where} \quad [a] = \sum_{i \in S(m,N)} \delta_a(A_i), \quad (7)
\]

holds. The overall count \([a]\) of induced subgraphs \( a \) in graph \( G \) is constant in time, and split up between all possible labellings. We can therefore use \([a]\) as a normalisation factor for the (variable) counts of motifs such that we may consider normalised motif counts

\[
[x^a] := [x^a]/[a], \quad \text{such that} \quad \sum_{x:|x|=m} [x^a](t) = 1 \quad (8)
\]

is the conservation relation for the normalized quantities. For networks with homogeneous degree there is the additional type of conservation relation

\[
\sum_{k=1}^{n} x_{p-k}^a = x_{p-0}^a, \quad (9)
\]

for each stub \( p \) of the motif \( x^a \) (a stub is a node with degree 1 in \( a \)). The conservation relations (8) and (9) can be used to reduce the number of variables in the moment equations via substitution. This can result in a substantial reduction in the number of moment equations (see Table S2).

**VI. TRUNCATION AND SUBSTITUTION**

When we use (6) to express expected rates of change for the set of motifs up to a chosen maximum size \( k \), we obtain a truncated hierarchy of moment equations. This linear system of differential equations has the form

\[
\dot{x} = Q \cdot x + c \quad (10)
\]

where \( x_m \) are vectors with all dynamically relevant motif counts of size \( m \), \( Q_m \) the coefficients for \( x_m := dx_m/dt \) with motifs of the same size, and \( Q_{m,m+1} \) the coefficients for \( x_m \) with motifs of the size \( m+1 \). The block diagonal form follows from the fact that the change of size-\( m \) motif counts depends only on motif counts of size \( m \) and of size \( m+1 \). We will show (10) in the more compact notation:

\[
\begin{bmatrix}
\dot{x}_1 \\
\dot{x}_2 \\
\vdots \\
\dot{x}_k
\end{bmatrix} =
\begin{bmatrix}
Q_{1} & Q_{12} & 0 & \cdots & 0 \\
0 & Q_{2} & Q_{23} & 0 & \cdots \\
\vdots & \vdots & \ddots & \ddots & \vdots \\
0 & \cdots & 0 & Q_{k-1} & Q_{k-1,k} \\
0 & \cdots & 0 & 0 & Q_{k}
\end{bmatrix}
\begin{bmatrix}
x_1 \\
x_2 \\
\vdots \\
x_k
\end{bmatrix} +
\begin{bmatrix}
x_1 \\
x_2 \\
\vdots \\
x_k
\end{bmatrix} \quad (11)
\]

In Supplement S-II, (10) is shown for SIS spreading up to a maximum motif size of \( k = 3 \).

The substitution via conservation relations can be written as

\[
\dot{x} = E \cdot \dot{\bar{x}} + c, \quad (12)
\]

where \( x = x_1, \ldots, x_k \), \( \bar{x} \) is \( x \) with the to be substituted elements omitted. \( E, c \) contain the coefficients of linear dependence from (7, 9), with their \( i \)th row/element corresponding to the identity transformation for motifs that are not substituted. Substituting this into (10) results in the system of equations for the remaining motifs \( \bar{x} \):

\[
\dot{\bar{x}} = Q' \cdot \begin{bmatrix}
\bar{x} \\
\bar{x}_{k+1}
\end{bmatrix} + \tilde{c}. \quad (14)
\]

For an example, see Section VIII A 2.

**VII. CLOSURE SCHEME**

Because in (14), counts for the largest motifs \( x_{k+1} \) appear on the right-hand side but not on the left-hand side, (14) is underdetermined. A closure scheme provides a way of expressing the undetermined parts \( \bar{x}_{k+1} \) in (10) through a nonlinear function \( \bar{x}_{k+1} \approx f(\bar{x}) \), creating a closed system of ODEs:

\[
\dot{\bar{x}} = Q' \cdot \begin{bmatrix}
\bar{x} \\
f(\bar{x})
\end{bmatrix} + \tilde{c}, \quad (15)
\]
where \( \bar{f} \) also depends on counts of induced subgraphs of order up to \( k + 1 \) ([\( g_{k+1}^{\bar{f}} \)] in Figure 1) if the motifs were not normalised in advance. In this section, we develop a closure scheme that decomposes \( x_{k+1} \) into its smaller-sized components. Our final formula generalises closures hitherto most commonly used, as shown in e.g. House et al. [22]. We will show that the decomposition is valid when: (i) counts of components are conditionally independent given the node states in their intersection and the adjacency structure between them is a tree, (ii) the network is spatially homogeneous, and (iii) the network is sufficiently large, such that the law of large numbers applies. We start with some introducing examples in Section VIIA and defer detailed explanation to Sections VII B, VII C. Examples are given in Sections VII D and S-V.

A. Introduction

When truncating the moment hierarchy at a chosen order \( k \), we approximate the order \( k + 1 \) motifs appearing in the equations for order \( k \) motifs in terms of lower-order motifs. E.g., looking at the moment equations for SIS spreading in Supplement S-II, when truncating at \( k = 1 \), we would need an expression of \([\bullet \bullet \bullet] \) in terms of \([\bullet \bullet \bullet] \) and \([\bullet] \). Using the shorthand \( x_i \) for the event \( X_i = x \), this is justified when there is a conditional independence relation of the form \( P(S_i, S_j, I_k) = P(S_i, S_j)P(S_j, I_k) \) and if the component probabilities are the same everywhere in the network, such that node indices \( i, j, k \) do not matter. This can be generalised to larger chains, such as e.g. \([\bullet \bullet \bullet \bullet \bullet] \propto [\bullet]([\bullet \bullet \bullet \bullet \bullet]/[\bullet \bullet \bullet]) \), which similarly follows from the assumed conditional independence relation \( P(S_i, S_j, I_k, I_l) = P(S_i, S_j, I_k)P(S_j, I_k|S_j, I_k) \) and homogeneity in the network.

It is possible to generalise the examples above to larger subgraphs by starting from the chain rule of probability, \( P(x) = P(x_{i_n} | x_{i_{n-1}}, ..., x_{i_2}, x_{i_1})P(x_{i_1}) \), where \( x \) is a vector of state labels on a given network motif, and subsequently simplify with assumed conditional independence relations. For instance, for our second example above, \([\bullet]([\bullet \bullet \bullet \bullet \bullet]/[\bullet \bullet \bullet]) \), we have \( P(S_i, S_j, I_k) = P(I_k|S_i, S_j)P(S_j|S_i)P(S_i) \). If now node \( k \) is conditionally independent of node \( i \), we substitute \( P(I_k|S_i, S_j) = P(I_k|S_j) \), such that we obtain the expression found above. In general, a simplification of the chain rule in terms of subgraphs is possible if we can order the chosen sets of subgraphs (with node indices \( i_1, ..., i_n \)) without creating loops and if the states of adjacent subgraphs are conditionally independent given their shared nodes. To make this precise, we need the concept of independence map. The independence map is a graph in which link absence between two nodes means that there is no direct dependence between them. For instance, if in the four-node graph shown in row 4 column 1 of Table I there is no direct dependence between nodes that are further than two steps removed, its independence map is the graph shown in row 4 column 3 of Table I. The condition mentioned above for simplification of the chain rule in terms of subgraphs reduces to the requirement that the independence map be chordal, because this allows a tree composition in terms of maximal cliques, as shown in column 4 of Table I. A graph is chordal if every loop greater than three is cut short by a link between two non-consecutive nodes of the loop.

In reality, we do not know the dependence structure between the graph nodes. However, the practical requirement of truncation of the moment hierarchy obliges us to assume an independence map for each of the largest motifs. In order to obtain a consistent decomposition method, we will choose as independence map the graph obtained by connecting all nodes to other nodes in their \( d-1 \) neighbourhood, where \( d \) is the diameter of the motif. The chain rule then leads to a decomposition in terms of (maximal) cliques of the independence map in the numerator and the node sets that separate them in the denominator. Table I shows example graphs, with their diameter, their assumed independence maps, their tree decomposition and the resulting closure formula. The choice of dependence within a distance \( d \) may in some cases result in non-chordal independence maps, such that the decomposition cannot be made. In the next sections, we will explain our method in detail and further show how one can treat motifs with a non-chordal independence map.

B. Definitions and background

We will rely on the theory of decomposable Markov networks, following mostly the terminology of Pearl [25, Ch. 3]. We generalise the decomposition from a factorisation involving (1-)cliques to one involving \( d \)-cliques. He definitions in this section apply to a general graph \( \mathcal{G} \) with nodes states \( X \), but we will apply the decomposition to motifs in Section VII C.

a. Separation Given a graph \( \mathcal{G}(\mathcal{V}, \mathcal{E}) \) and three disjoint subsets of nodes \( i, j, k \subset \mathcal{V} \), \( k \) separates \( i \) and \( j \) in \( \mathcal{G} \), written as \( i \perp \perp j \mid k \), if every path between \( i \) and \( j \) has at least one vertex in \( k \). Here, \( k \) is called a separator, or also, a node cut set of \( i \) and \( j \) in \( \mathcal{G} \).

b. Independence map An independence map \( \mathcal{M} \) is a graph that represents the independence between components of a set of random variables \( X \) such that separation in \( \mathcal{M} \) guarantees conditional independence between corresponding subsets of \( X \). More precisely, given three disjoint subsets of nodes \( i, j, k \subset \mathcal{V} \), \( X \) possesses a spatial
Markov property:
\[ i \perp_{M} j \mid k \implies X_i \perp X_j \mid X_k, \quad (16) \]
where the \( \perp \) notation on the right refers to independence of the random variables: \( P(X_i=x_i, X_j=x_j \mid X_k=x_k) = P(X_i=x_i \mid X_k=x_k)P(X_j=x_j \mid X_k=x_k) \). The pair \((X, M)\) defines what is known as a Markov network.

c. Independence beyond distance \( d \) Let \( G = (\mathcal{V}, E) \) be a graph where the nodes in \( \mathcal{V} \) have (random) states \( X \). We define \( G^d \) as the graph in which all nodes of \( G \) are neighbours if they are at most a shortest distance \( d \) away from each other, i.e.
\[ G^d = (\mathcal{V}, \mathcal{E}^d), \quad \text{with} \quad \mathcal{E}^d = \{ (i, j) \in \mathcal{V} : \text{dist}_G(i, j) \leq d \}. \quad (17) \]
We then say that \((G, X)\) has independence beyond distance \( d \) if \( G^d \) is the independence map of \( X \), or for all distinct subsets of nodes \( i, j, k \subset \mathcal{V} \) holds
\[ i \perp_{G^d} j \mid k \implies X_i \perp X_j \mid X_k. \quad (18) \]
This means that states of two non-neighbouring sets in \( G^d \), which by definition (17) are further than \( d \) steps apart in \( G \), are independent of each other given the state of their separator \( k \).

d. Maximal \( d \)-cliques and \( d \)-clique graph A maximal clique is a complete subgraph not contained in a larger complete subgraph \([26]\). As a generalisation, maximal \( d \)-cliques are maximal subgraphs with distance between any two nodes not greater than \( d \) \([24]\). Correspondingly, maximal cliques in \( G^d \) are maximal \( d \)-cliques in \( G \). The graph \( C^d \) is the \( d \)-clique graph of \( G \) if each node in \( C^d \) corresponds to a \( d \)-clique in \( G \) with links between nodes in \( C^d \) occurring when the corresponding \( d \)-cliques overlap. Hence, while nodes in \( C^d \) correspond to maximal \( d \)-cliques in \( G \), links in \( C^d \) correspond to intersections between overlapping maximal \( d \)-cliques in \( G \).

e. Junction graph of \( d \)-cliques A junction graph of \( G \)'s maximal \( d \)-cliques, denoted further as \( J^d(G) \), is a subgraph of the \( d \)-clique graph \( C^d \) obtained by removing redundant links from \( C^d \). Denoting \( d \)-cliques corresponding to nodes \( i, j \) in \( C^d \) as \( c_i, c_j \subset \mathcal{V} \), a link between \( i \) and \( j \) in \( C^d \) is redundant when there is an alternative path between \( i \) and \( j \) in \( C^d \) passing by a series of other nodes in \( C^d \) of which the corresponding \( d \)-cliques all contain \( c_i \cap c_j \). The junction graph \( J^d(G) \) is then obtained by iteratively removing redundant links from the \( C^d \) until there are no further redundant links. While the \( d \)-clique graph is unique, there may be several junction graphs \( J^d(G) \) of \( d \)-cliques for one graph \( G \). Note that for chord graphs (defined below), the junction graph equals what is known as a junction tree, which can also be obtained via the junction tree algorithm \([27]\), applied to the \( d \)-clique graph.

f. \( d \)-chordality A graph \( G \) is chordal when for every loop of length greater than 3, there exists a link in \( G \) between two non-consecutive nodes of the loop (thus, giving a short-cut, also called chord to the loop). As a generalisation, we will call a graph \( G \) \( d \)-chordal if \( G^d \) is chordal. If a graph \( G \) is \( d \)-chordal, then \( J^d(G) \) is a tree, or equivalently, if \( G^d \) is chordal, then \( J(G^d) \) is a tree. Non-chordal graphs can always be converted to a chordal graph via triangulation, i.e. adding chords to every chordless loop of length greater than 3. We will write below \( \text{tr}(G^d) \) as a minimal triangulation of a non-chordal

| subgraph | diameter | assumed independence map | tree decomposition | closure formula |
|----------|----------|--------------------------|------------------|---------------|
| 1-3-2-3 | 2        | 1-3-2                   | 1-3-2            | [3-1][3-2]    |
| 1-2-3-3 | 2        | 1-2-3                   | 1-2-3            | [1-2][1-3]    |
| 1-2-3-2 | 3        | 1-2-3                   | 1-2-3            | [1-2][1-3]    |
| 1-4-3-2 | 3        | 1-4-3                   | 1-4-3            | [1-4][2-3]    |
| 2-3-3-2 | 3        | 2-3-3                   | 2-3-3            | [2-3][2-4]    |
| 2-3-2-3 | 3        | 2-3-2                   | 2-3-2            | [2-3][2-4]    |

TABLE I. Examples of our method to obtain closure formulas. Because the closures can be written independent of the state labels, the decomposition is shown for node-indexed graphs without reference to particular node states.
\( G^d \), obtained by adding the smallest number of links that leads to chordality, unless stated otherwise.

\( g. \) Decomposability at distance \( d \) \hspace{1cm} If there is independence beyond distance \( d \) \((18)\) and \( G \) is \( d \)-chordal, then the joint probability of the network nodes of \( G \) being in a given state \( P(X=x) \) can be factorised over the \( d \)-cliques of \( G \). We will call this property of the graph \( G \) and its node states \( X \) decomposability at distance \( d \). We call \( J \) the set of \( d \)-cliques in \( G \), ordering its elements consistent with the resulting junction tree structure for \( G^d \) (such that \( J_i \) is the chosen root and parent nodes have lower index than their leaves), and call \( \text{pa}(J_i) \) the parent node of \( J_i \). In such cases, the factorisation is possible because the tree structure between \( d \)-cliques allows application of the chain rule of conditional probability.

\[
P(X=x) = \prod_{i=1}^{\vert J \vert} P(X_{J_i}=x_{J_i} \mid X_{\text{pa}(J_i)}=x_{\text{pa}(J_i)}) = \prod_{i=1}^{\vert J \vert} \frac{\prod_{j \in J_i} P(X_{J_i}=x_{J_i})}{\prod_{j \notin J_i} P(X_{J_i \cap J_j}=x_{J_i \cap J_j})}.
\]  

(19)

The steps in (19) are explained as follows. As chordality makes \( J^d(G) \) a tree and any \( d \)-clique separates its neighbours, one can recursively use conditional independence of children given parents (line 1). We use the convention that \( \text{pa}(J_i) = \emptyset \), such that the first factor is \( P(X_{J_i}=x_{J_i}) \). In line 2 we exploit that any two \( d \)-cliques in \( G \) are also separated by their intersection to condition instead on intersections.

\( h. \) Non-\( d \)-chordal graphs \hspace{1cm} There are two alternative ways to decompose non-\( d \)-chordal \( G \): (i) perform the decomposition (19) on the (more conservative) independence map after triangulation, \( \text{tr}(G^d) \). In this case, the factors in (19) may still contain subgraphs of diameter \( d+1 \), but of smaller size than \( G \), such that one may have to apply (19) recursively to achieve smaller diameter for all factors. Furthermore, the resulting decomposition will depend on the choice of triangulation. Alternatively, (ii), one can start from the non-tree \( J^d(G) \) and use the ad-hoc formula (without prior triangulation)

\[
P(X=x) \approx \zeta \frac{\prod_{i=1}^{\vert J \vert} P(X_{J_i}=x_{J_i})}{\prod_{i,j \neq i} P(X_{J_i \cap J_j}=x_{J_i \cap J_j})}.
\]  

(20)

Because the fraction in (20) does not result from application of the chain rule as in (19), it is not a product of conditional probabilities and hence it does not guarantee the property that each of the node states in \( x \) has to appear one more time in the numerator than in the denominator, which in turn leads to inconsistency between closure formulas that assume different \( d \). The factor \( \zeta \) in (20) corrects for this inconsistency – see Section VII C for more detail. After applying (ii) to non-chordal graphs, the nodes in the resulting \( d \)-clique tree are not all maximal \( d \)-cliques of \( G \) any more \((28)\). When applying (ii) to non-chordal graphs, the subgraphs in \( J^d(G) \) are still maximal \( d \)-cliques of \( G \) but the clique graph is not a tree, thus, violating the assumptions behind the decomposition (19).

\( i. \) Maximum motif diameter \hspace{1cm} The decomposition explained in this section implies that if independence beyond distance \( d \) is valid in the whole network \( (G, X) \), then we know that we only need to consider motifs up to diameter \( d \), justifying truncation of the moment hierarchy. Note, however, that truncation is usually done at a give size, not at a given diameter. We expand on this in point VII C e.

C. Motif decomposition

\( a. \) Decomposition of motifs at the individual level \hspace{1cm} We apply the decomposition (19) to motifs with connectivity \( a \) and chordal independence map \( a^d \) embedded in the network. For now, we ignore that this may in some cases break the independence assumption, but see section VIII C e for more detail on this issue. Considering a set \( i \) of nodes that have connectivity \( a \) in our network \( G \) and taking \( P(X_i=x) \) as the probability that these are in states with labels \( x \), we can write the decomposition (19) for of \( P(X_i=x) = \langle [x_i^a]\rangle \) to obtain

\[
\langle [x_i^a]\rangle = \frac{\prod_{j \in J_i} \langle [x_{i,j}\rangle}{\prod_{j=2} \langle [x_{i,\text{pa}(J_j)\cap J_j}\rangle},
\]  

(21)

where now \( J \) is the set of \( d \)-cliques in \( a \). Choosing \( d = \text{diam}(a) - 1 \) ensures that the decomposition results in component motifs with diameter decreased by one compared to the decomposed motif. For motifs with non-chordal \( a^d \) one can, as noted above, either triangulate \( a^d \) first or use the ad-hoc approximation (20). We relied on the package Chordal Graph [29] for triangulation of non-chordal \( a^d \). The ad-hoc formula (20) applied to the motif at \( i \) is

\[
\langle [x_i^a]\rangle \approx \frac{\prod_{j \in J_i} \langle [x_{i,j}\rangle}{\prod_{j \notin J_i} \langle [x_{i,\text{pa}(J_j)\cap J_j}\rangle} \prod_{j \in J_i} \langle [x_j]\rangle\gamma_j.
\]  

(22)

The consistency correction (written as \( \zeta \) in (20)) here equals \( \prod_{j \in J_i} \langle [x_i] \rangle \gamma_j \) and ensures that the ad-hoc extension of closures to motifs with non-chordal \( a^d \) does not result in inconsistency with MF1 [condition 1 of 9, Ch. 21] under independence between node states: when all motifs of order greater than one are replaced by products of order one motifs, i.e. \( \langle [x_i^a]\rangle \rightarrow \prod_{j \in J_i} \langle [x_j]\rangle \), the right hand side of (22) should reduce to MF1. Therefore, for each \( j \), \( \gamma_j \) is chosen such that this is fulfilled. These ad-hoc steps usually result in violation of the conservation relations of Section V [9]. In the approximations used in Section VIII, the bias introduced due to this violation is small. For mitigation of this problem, see [9, 23].
b. Decomposition of motifs at the population level

If we take the following spatial homogeneity assumption for all motifs \(x^a\) of sizes \(m\) up to our maximal considered size \(k\)

\[
\forall i, i' \in \mathcal{I}(a) : \langle [x^a_i] \rangle = \langle \frac{[x^a_i]}{a} \rangle = \langle [x^a] \rangle,
\]

(23)

where \(\mathcal{I}(a) := \{ j \in S(m, N) : A_j = a \}\), then (21, 22) are independent of \(i\), such that we can write (21) as

\[
\langle [x^a] \rangle \approx \frac{\prod_{j=1}^{|\mathcal{J}|} \langle [x^a_{J_j}] \rangle}{\prod_{j=2}^{|\mathcal{J}|} \langle [x^a_{\text{pa}(J_j) \cup J_j}] \rangle}
\]

(24)

and (22) as

\[
\langle [x^a] \rangle \approx \frac{\prod_{j=1}^{|\mathcal{J}|} \langle [x^a_{J_j}] \rangle}{\prod_{j,k}^{|\mathcal{J}|} \langle [x^a_{\text{pa}(J_j) \cup J_k}] \rangle} \prod_m \langle [x^a_p] \rangle^{\gamma p}
\]

(25)

which may be used to close the population-level equations (10). In (24, 25), node indexing of a motif is consistent with the node labels \(x\). Recall that we use a single consistent indexing for isomorphic motifs. The decomposition (24, 25) is not unique. If the independence assumptions are satisfied each of the alternative ways to decompose motif \(x^a\) should result in the same value. As we do not expect the independence to be perfectly valid, we take the average of the alternative ways of decomposing \(x^a\) if they exist.

c. Normalisation

We showed the closure formulas for normalised motifs, i.e. we first normalised the counts of motifs via (8), and then applied the closure. Hence, in this case, the counts of induced subgraphs in the network enter into the system of equations as normalisation factors in the unclosed system. One can also decide not to normalise (or to do it after applying closure). In this latter case, the subgraph counts enter into the final system of equations when applying closure, as the closure formulas for the non-normalised motif counts contain them (to see this, substitute each motif count in (24, 25) as \([y^b] \rightarrow [y^b]/|b|\)). Hence, structural information specific to the considered network enters the mean field equations either when normalising the motif counts or when applying closure. In simple cases, such as lattices or random graphs, the subgraph counts can be found by hand without much effort. In other cases, one can resort to subgraph counting algorithms. In Mathematica [24], we used the IGraph [30] command IGLADSubisomorphismCount\([g, G, \text{Induced} \rightarrow \text{True}]\), where \(G\) is the considered network and \(g\) the induced subgraph to be counted.

d. Law of large numbers

We will use the population-level closure to study the steady states in a single realisation of a given network. Motif counts are then assumed to be the total counts in a single network, instead of their expectations over many realisations. As the closure formulas apply to expectations, we make the additional assumption that motif counts are close to their expectations.

e. Additional bias

Decomposing the whole network \(\mathcal{G}\) at distance \(d\) is exact when \(\mathcal{G}\) is \(d\)-chordal and there is independence beyond distance \(d\) (Section VII B). Applying the decomposition to motifs embedded in \(\mathcal{G}\) instead of \(\mathcal{G}\) can be done without additional bias when \(a\) is a distance-hereditary subgraph of \(\mathcal{G}\) (i.e. distances between nodes in \(a\) are equal to those between corresponding nodes in \(\mathcal{G}\)) and conditional independence relations implied by \(a\) are also valid in \(\mathcal{G}\). As a counterexample for the former, take for \(\mathcal{G}\) the six-node graph \(\circ \bigcirc \circ \bigcirc \circ \bigcirc\) and for its induced subgraph consisting of nodes \(\{1, 2, 4, 6, 5\}\). Here, \(a\) is not distance-hereditary because \(\text{dist}_a(1, 5) = 4 \neq \text{dist}_G(1, 5) = 2\). As a counterexample for the latter, take for \(\mathcal{G}\) the square \(\bigcirc \bigcirc\) and for \(a\) the 3-node chain \(\{1, 2, 4\}\). In this case, \(a\) is distance hereditary, but, while (when assuming independence beyond distance \(d=1\)) within \(a\) we have the independence relation \(\{1\} \perp \{4\} | \{2\}\), this is not true in \(\mathcal{G}\), where \(\{1\} \perp \{4\} | \{2\}\), because the node cut set in \(\mathcal{G}\) for \(\{1\}\) and \(\{4\}\) is \(\{2, 3\}\). This occurs because the decomposed motifs are non-maximal \(d\)-cliques. Therefore, we expect a bias as a consequence of this in the closed mean-field equation hierarchy ((10) with (24) or (25) at population level under spatial homogeneity). This bias can be avoided when expressing the equations in terms of maximal \(p\)-cliques for \(p \in \{0, ..., k+1\}\) and truncating at given diameter instead of at given size.

D. Examples

Supplement S-V shows 13 application examples of (24, 25) in table form. As the closures can be written independent of the particular labels, they are shown for subgraphs only, with each node tagged with its index. We have also dropped the \(\langle \cdot \rangle\), assuming that the law of large numbers applies, such that the counts approach their expectations almost surely for increasing network size \(N\). The examples can be understood by reading the table from left to right. Below, we derive the normalisation factors and the non-normalised closures of examples 1-3 of Supplement S-V for different network types. Note that, unlike in Supplement S-V, we use letter labels below, for consistency with the main text and the literature.

1. \(x^2 = \bigcirc \bigcirc\): This diameter-2 motif has chordal independence map equal to \(a\) and decomposes with (24) as

\[
\langle \bigcirc \bigcirc \bigcirc \rangle \approx \frac{\langle \bigcirc \bigcirc \rangle \langle \bigcirc \bigcirc \rangle}{\langle \bigcirc \rangle}
\]

(26)

assuming conditional independence beyond distance \(d=1\). Via normalization (8) we obtain also the closure for the non-normalized counts:

\[
\langle \bigcirc \bigcirc \bigcirc \rangle \approx [\bigcirc \bigcirc \bigcirc] \frac{[\bigcirc \bigcirc]}{[\bigcirc]}.
\]

(27)
The counts of the induced subgraphs of size 2 and 1, required for normalisation, are

\[ [\bigcirc \bigcirc] = \kappa N, \quad [\bigcirc] = N, \quad (28) \]

and total number of triples (3-node motifs) in the network is

\[ [\bigotimes \bigotimes \bigotimes] + [\bigotimes \bigotimes] = \sum_{i}^{N} \kappa_i (\kappa_i - 1), \quad (29) \]

with \( \kappa_i \) the number of neighbours of node \( i \) and \( \kappa \) the mean number of neighbours over the whole network. For particular network types (29) can be simplified. Below are two examples.

(a) For a network with fixed degree without triangles (e.g., a square lattice), we have \( \forall i : \kappa_i = \kappa \) and \( \bigotimes \bigotimes = 0 \), such that

\[ [\bigotimes \bigotimes \bigotimes] = \kappa (\kappa - 1) N. \quad (30) \]

Using (27) and (30), we obtain

\[ [\bigotimes \bigotimes \bigotimes] \approx \frac{\kappa - 1}{\kappa} \frac{[\bigotimes \bigotimes]}{[\bigcirc]}, \quad (31) \]

An early use of this closure for networks can be found in Keeling et al. [11].

(b) In a large Erdős-Rényi random network, we have \( \kappa_i \sim \text{Pois}(\kappa) \) and \( \frac{[\bigotimes \bigotimes]}{([\bigotimes \bigotimes] + [\bigotimes \bigotimes \bigotimes])} \approx 0 \) [31]. Hence

\[ [\bigotimes \bigotimes \bigotimes] = \sum_{i}^{N} \frac{\kappa^2_i}{\kappa} - \sum_{i}^{N} \kappa_1, \approx \frac{\kappa^2}{\kappa} N, \quad (32) \]

where replacing the average by the expectation on the second line requires \( N \rightarrow \infty \) (law of large numbers), on the third line we used \( \text{Var}(\cdot) := E((\cdot)^2) - (E(\cdot))^2 \), and on the fourth line we used that, for \( \kappa_i \sim \text{Pois}(\kappa) \), we have \( E(\kappa_i) = \text{Var}(\kappa_i) = \kappa \). We could also have obtained this result directly from the large-\( N \) limit of chains [28]. Using (27) and (32), we obtain

\[ [\bigotimes \bigotimes \bigotimes] \approx \frac{[\bigotimes \bigotimes \bigotimes]}{[\bigotimes \bigotimes]}, \quad (33) \]

This closure was, to the best of our knowledge, first used for networks in Gross et al. [21].

2. \( \bigotimes \bigotimes \bigotimes \): This diameter-2 motif has chordal independence map \( a \) and decomposes with (24) as

\[ [\bigotimes \bigotimes \bigotimes] \approx \frac{[\bigotimes \bigotimes \bigotimes]}{[\bigotimes \bigotimes]}, \quad (34) \]

when assuming independence of nodes \( (d=0) \). With non-normalised counts, this becomes

\[ \left[ \bigotimes \bigotimes \bigotimes \right] \approx \frac{[\bigotimes \bigotimes \bigotimes]}{[\bigotimes \bigotimes \bigotimes]/[\bigotimes]^3}. \quad (35) \]

Alternatively, one can extend the usage of the ad-hoc formula (25) to include non-maximal cliques: using its three 1-cliques in (25), we obtain

\[ \left[ \bigotimes \bigotimes \bigotimes \right] \approx \frac{[\bigotimes \bigotimes \bigotimes]/[\bigotimes \bigotimes \bigotimes]}{[\bigotimes \bigotimes \bigotimes]/[\bigotimes]^3}. \quad (36) \]

which is known as the Kirkwood closure for triangles [17]. Using (8), we obtain for the closure with non-normalised counts

\[ \left[ \bigotimes \bigotimes \bigotimes \right] \approx \frac{[\bigotimes \bigotimes \bigotimes]/[\bigotimes \bigotimes \bigotimes]}{[\bigotimes \bigotimes \bigotimes]/[\bigotimes]^3}. \quad (37) \]

The frequency \( [\bigotimes \bigotimes \bigotimes] \) depends on the network type. For instance, if we use the definition of the clustering coefficient \( \phi := [\bigotimes \bigotimes]/([\bigotimes \bigotimes] + [\bigotimes \bigotimes \bigotimes]) \) [32], we have [via (28) and (29)] for a network with fixed degree \( [\bigotimes \bigotimes] = \phi \kappa (\kappa - 1) N \), such that

\[ \left[ \bigotimes \bigotimes \bigotimes \right] \approx \frac{\kappa - 1}{\kappa^2} \phi N \frac{[\bigotimes \bigotimes \bigotimes]/[\bigotimes \bigotimes \bigotimes]}{[\bigotimes \bigotimes \bigotimes]/[\bigotimes]^3}, \]

which was first used for networks by Keeling [32].

3. \( \bigotimes \bigotimes \bigotimes \): This diameter-2 motif has chordal independence map \( a \) and decomposes with (24) as

\[ \left[ \bigotimes \bigotimes \bigotimes \right] \approx \frac{[\bigotimes \bigotimes \bigotimes]}{[\bigotimes \bigotimes \bigotimes]}, \quad (38) \]

when assuming independence beyond distance \( d=1 \). Alternatively, extending the ad-hoc formula (25) to the three non-maximal 3-cliques, we obtain

\[ \left[ \bigotimes \bigotimes \bigotimes \right] \approx \frac{[\bigotimes \bigotimes \bigotimes]}{[\bigotimes \bigotimes \bigotimes]}, \quad (39) \]

where a consistency correction \( [\bigotimes] \) was required. The non-normalised form of this closure was first used in House et al. [22].

VIII. APPLICATION TO SIS EPIDEMIC SPREADING

We apply our method to SIS spreading, which is a continuous-time discrete-state Markov chain description of epidemic spreading through a population of susceptibles [e.g., 15]. As introduced in Section II, we have \( n = 2 \) species. The \( 2 \times 2 \) matrix \( \mathbf{R}^0 \) of spontaneous conversion rates and the \( 2 \times 2 \times 2 \) tensor \( \mathbf{R}^1 \) of conversion rates due to nearest-neighbour interaction for SIS spreading have only two non-zero entries, \( R_{2,1}^0 = \gamma > 0 \), \( R_{1,2,2}^1 = \beta > 0 \),
corresponding to reaction scheme (2). Hence, contagion of susceptibles $S$ occurs over IS links at rate $\beta$, whereas recovery occurs spontaneously at rate $\gamma$. In the study of phase transitions and interacting particle systems, SIS epidemic spreading is known as the contact process [33], which is typically studied on d-dimensional lattices. In this context, it was found to belong to the directed percolation universality class, of which scaling properties have been widely studied [5–7, 34].

We run the simulations with a Gillespie algorithm [35] and stabilise them via feedback control [36–38], such that steady states can be obtained in a more efficient manner than when running regular simulations (see Supplement S-III).

### A. Mean-field equations

We derived the mean-field models up to fifth order for the square lattice and up to second order for other networks, including cubic/hypercubic lattices, random regular networks and Erdős-Rényi random networks. In the main text, we only show a step-by-step derivation of the first and second-order mean-field models because they allow demonstration of our method in the simplest form. Recall that we write in the text $\langle \cdot \rangle$ as $[\cdot]$, assuming the LLN holds (in the Mathematica html files for MF4, attached in S-VIII, we use the notation $\langle \cdot \rangle$ instead).

To gain insight in the strength of dependence between neighbouring node states in simulations and higher-order mean-field models, we will observe the correlation between neighbouring node states $a$ and $b$ as in Keeling [32], defined by

$$C_{ab} = \frac{N \langle [a] [b] \rangle}{\kappa [a]}$$

(where $\kappa$ is the mean degree) or when motif counts are normalised,

$$C_{ab} = \frac{\langle [a] [b] \rangle}{[a] [b]}$$

They are uncentered correlations between species types that are separated by one link. Values greater than 1 indicate clustering and values less than 1 avoidance (compared to a uniform random distribution). For a generalisation of this correlation to arbitrary distances between end nodes, see Supplement S-IV.

#### 1. MF1

The first-order mean field originates from the molecular field approximation in statistical physics [1, 2] and is now commonly known as the ‘mean field model’ [14–16]. MF1 only considers node states ($k = 1$) and neglects correlations beyond distance 0. It provides a picture of the dynamics when species are well mixed throughout a large domain. One way to achieve this is when the domain is a complete network on which susceptibles and infecteds have contact rate $\kappa \beta / N$, and when $N \to \infty$ [15].

There are two motif types of size 1: $\circ$ and $\bullet$. Of these, only $\bullet$ is dynamically relevant. This means that we only need the equation:

$$\frac{d}{dt}[\bullet] = \beta [\circ \bullet] - \gamma [\bullet].$$

To close the system at order 1, $[\circ \bullet]$ needs to be expressed in terms of $[\circ]$ and $[\bullet]$. No correlation beyond distance 0 corresponds to (using (24)):

$$\kappa N \frac{[\circ]}{N} \Longrightarrow \frac{[\circ \bullet]}{[\bullet]} = \frac{\kappa}{N} (N - [\circ]),$$

where we have also used the conservation relation $[\circ] + [\bullet] = N$ to substitute $[\circ] = N - [\bullet]$. The final expression for the first-order mean field is

$$\frac{d}{dt}[\bullet] = \beta \frac{\kappa}{N} [\bullet] (N - [\circ]) - \gamma [\bullet],$$

which, after normalisation [via (8)], yields

$$\frac{d}{dt}[\bullet] = \beta \frac{\kappa}{N} [\bullet] (1 - [\circ]) - \gamma [\bullet].$$

The steady state solutions are then

$$[\bullet]_1^* = 0, [\bullet]_2^* = 1 - \frac{\gamma}{\kappa \beta}.$$

At $\beta / \gamma = \kappa^{-1}$, the solution $[\bullet]_1^*$ becomes unstable due to a transcritical bifurcation, also known as the epidemic threshold in epidemiology.

#### 2. MF2

The second-order mean field originates from the Bethe approximation in statistical physics [3] and is now commonly known as the ‘pair approximation’ [14–16]. MF2 neglects dependence beyond distance 1 and is obtained by considering all dynamically relevant motifs up to size 2. Noting that motifs without infecteds are dynamically irrelevant and omitting zero blocks, we obtain

$$\begin{pmatrix}
[\circ] & [\circ \circ] & [\circ \bullet] & [\bullet \circ] & [\bullet \bullet] & [\circ \circ \circ] & [\bullet \circ \bullet] & [\bullet \bullet \circ] & [\bullet \circ \circ]
\end{pmatrix}
\begin{pmatrix}
\gamma & \beta & 0 & \beta & \beta & \beta & \beta & \beta & \beta
\end{pmatrix}
\begin{pmatrix}
[\circ] & \circ \circ & \circ \bullet & \bullet \circ & \bullet \bullet & \circ \circ \circ & \circ \circ \bullet & \bullet \circ \circ & \bullet \bullet \circ
\end{pmatrix}
\begin{pmatrix}
\gamma & -\beta - \gamma & \beta & 0 & 2\beta & 0 & 2\beta & 0 & 2\beta
\end{pmatrix}$$

Hence, two types of order 3 motifs appear on the right-hand side: chains and triangles. For the networks we consider in this paper, triangular subgraphs are either not present (in case of square, cubic, hypercubic lattices)
or negligible for large $N$ (e.g. for Erdős-Rényi random networks [28]), so we only need to consider the system

\[
\begin{bmatrix}
\bullet \\
\bullet \\
\bullet
\end{bmatrix}
\begin{bmatrix}
\gamma & -\gamma & 0 \\
-\beta - \gamma & \gamma & \beta \\
2\beta & -2\gamma & 0 & 2\beta
\end{bmatrix}
\begin{bmatrix}
\bullet \\
\bullet \\
\bullet
\end{bmatrix}
\]

The number of conservation relations used for elimination depends on whether the networks have a homogeneous degree.

a. Networks with homogeneous degree In this case, the conservation relations are

\[
\begin{align*}
[\bullet] + [\bullet] &= N, \quad (44) \\
[\bullet\bullet] + [\bullet\bullet] &= \kappa[\bullet], \quad (45) \\
[\bullet\bullet] + [\bullet\bullet] &= \kappa[\bullet], \quad (46)
\end{align*}
\]

However, due to the dynamic irrelevance of $[\bullet]$ and $[\bullet\bullet]$, only (46) can be used to eliminate further variables. We use it to eliminate $[\bullet\bullet] = \kappa[\bullet] - [\bullet\bullet]$. Following (12-14), this means

\[
\begin{align*}
\mathbf{x} &= \begin{bmatrix}
[\bullet] \\
[\bullet] \\
[\bullet] \\
\end{bmatrix} \\
\mathbf{x}_3 &= \begin{bmatrix}
[\bullet\bullet] \\
\end{bmatrix},
\end{align*}
\]

and

\[
\mathbf{E} = \begin{bmatrix}
1 & 0 & 0 \\
0 & 1 & 0 \\
\kappa & -1 & 1
\end{bmatrix}, \quad \mathbf{c} = \begin{bmatrix}
0 \\
0 \\
0
\end{bmatrix}, \quad \tilde{Q}_{12,\ldots,21} = \begin{bmatrix}
-\gamma & \beta & 0 \\
0 & -\beta - \gamma & \gamma \\
2\beta & -2\gamma & 0
\end{bmatrix},
\]

\[
\tilde{Q}_{23} = [\beta - \beta],
\]

such that we can calculate $Q', \tilde{c}$ to obtain

\[
\begin{bmatrix}
\gamma & \beta \\
\beta & \gamma & -\beta - 2\gamma
\end{bmatrix}
\begin{bmatrix}
[\bullet] \\
[\bullet]
\end{bmatrix}
\begin{bmatrix}
[\bullet\bullet] \\
\bullet\bullet
\end{bmatrix}
\begin{bmatrix}
[\bullet\bullet\bullet] \\
[\bullet\bullet\bullet]
\end{bmatrix}
\]

(47)

Applying the closure (31) for degree-homogeneous networks [resulting from (24)],

\[
\begin{align*}
[\bullet\bullet\bullet] &\approx \kappa(N - 1)N \frac{\kappa\beta}{N} = \kappa - 1 \frac{[\bullet\bullet\bullet][\bullet]}{N} \\
[\bullet\bullet\bullet] &\approx \kappa(N - 1)N \frac{\kappa^2\beta^2}{N^2} = \kappa - 1 \frac{[\bullet\bullet\bullet]^2}{N}
\end{align*}
\]

(48)

we obtain the final nonlinear system

\[
\begin{bmatrix}
-\gamma & \beta \\
\beta & -\beta - 2\gamma
\end{bmatrix}
\begin{bmatrix}
[\bullet] \\
[\bullet]
\end{bmatrix}
\begin{bmatrix}
[\bullet\bullet] \\
\bullet\bullet
\end{bmatrix}
\begin{bmatrix}
[\bullet\bullet\bullet] \\
[\bullet\bullet\bullet]
\end{bmatrix}
\]

(49)

which, after elimination of $[\bullet]$ and $[\bullet\bullet]$ via (44-45) and normalisation via (8) becomes

\[
\begin{bmatrix}
-\gamma & \kappa\beta \\
\beta & -\beta - 2\gamma
\end{bmatrix}
\begin{bmatrix}
[\bullet] \\
[\bullet]
\end{bmatrix}
\begin{bmatrix}
[\bullet\bullet] \\
\bullet\bullet
\end{bmatrix}
\begin{bmatrix}
[\bullet\bullet\bullet] \\
[\bullet\bullet\bullet]
\end{bmatrix}
\]

(50)

From the steady state solutions (S33) we find that the epidemic threshold, is now located at $\beta/\gamma = (\kappa - 1)^{-1}$. We also derived non-trivial steady state correlations via (41) in (S34).

b. Networks with heterogeneous degree Here, (45) and (46) do not hold, but the total frequency of any given subgraph is still conserved. Hence, the conservation relations are (44) from order 1 and

\[
\begin{align*}
[\bullet\bullet\bullet] + [\bullet\bullet\bullet] + 2[\bullet\bullet\bullet] &= \kappa N. \quad (51)
\end{align*}
\]

This means that we cannot eliminate $[\bullet\bullet\bullet]$ here (unlike in case of networks with homogeneous degree), such that we have three instead of two equations. Also applying the closure for ER networks (33) [resulting from (24)],

\[
\begin{align*}
[\bullet\bullet\bullet] \approx \begin{bmatrix}
[\bullet] \\
\bullet\bullet\bullet
\end{bmatrix}, \quad [\bullet\bullet\bullet] \approx \begin{bmatrix}
[\bullet\bullet\bullet]^2
\end{bmatrix}, \quad (52)
\end{align*}
\]

we obtain

\[
\begin{bmatrix}
-\gamma & \beta & 0 \\
-\beta - \gamma & \gamma & \beta \\
2\beta & -2\gamma & 0 & 2\beta
\end{bmatrix}
\]

(53)

After substitution of $[\bullet]$ and $[\bullet\bullet\bullet]$ via the conservation relations (44, 51) and normalisation via (8), this becomes

\[
\begin{bmatrix}
-\gamma & \kappa\beta & 0 \\
-\beta - \gamma & \gamma & \kappa\beta \\
2\beta & -2\gamma & 0 & 2\kappa\beta
\end{bmatrix}
\]

(54)

There are three steady states, of which two are in the admissible range (S35). Here, the epidemic threshold is located at $\beta/\gamma = \kappa^{-1}$, as in the first-order mean field model. The steady state correlations are given in (S36).

3. MF3-MF5

Approximations of higher order than two correspond to cluster variation approximations in statistical physics [4]. MF3 results from neglecting dependence beyond distance 2 and is commonly known as the ‘triple approximation’ [15, 22]. Its step-by-step derivation for the square lattice is shown in Supplement S-VII and results
in four equations (after substitution with conservation relations). In Supplementary Materials S-VIII, we show the derivation of the unclosed MF4 for a general network as Mathematica notebook output. We also derived the closed MF4 and MF5 for the square lattice. The number of equations after elimination with conservation relations is respectively 14 and 37. The derivation of MF4 with closure is shown in Supplement S-VIII point 2. The steady states of MF4 and MF5 are shown in Figure 2 of Section VIII B.

B. Comparison to simulations

Here, we compare the steady states of MF1-5 of SIS epidemic spreading with those of the simulations on a selection of network types: lattices, regular random networks and Erdős-Rényi random networks.

a. Square lattice In Figure 2a, we show, for the square lattice, the steady state fraction of infecteds versus $\beta/\gamma$ for MF1-MF5 compared to simulations. The steady states of the mean-field models get closer to those of the simulation with increasing order. All mean-field models have an increasing bias in their non-trivial (endemic) steady states when approaching the critical value of $\beta/\gamma$ from above. Figure 2b compares the steady state distance-1 correlations between species types from MF2 and MF5 to those in simulations. Species of the same type cluster whereas different species tend to avoid each other (compared to a random distribution). The infected-infected correlation diverges when approaching the critical value of $\beta/\gamma$ from above and has a singularity at the bifurcation. E.g. for MF2, via (S34), we have $C_{II}^\ast(\beta/\gamma) \to \infty$ for $\beta/\gamma \searrow (\kappa - 1)^{-1}$ (limit from above in the endemic equilibrium). We recall that the errors in the mean-field models visible in Figure 2a can be due to violation of the statistical dependence assumption beyond distance $k$, non-chordality of the independence map, and violation of the spatial homogeneity assumption. Spatial homogeneity can be violated in two ways: via heterogeneity of structure and via heterogeneity of dynamics [17]. As the structure of a lattice is homogeneous and we only study steady states (i.e. there are no dynamics) that are spatially homogeneous (see Figure S2b), spatial inhomogeneity can not be a source of bias here. This leaves statistical dependence and non-chordality as only sources of bias. In the square lattice there are always loops with diameter larger than $d$ for any chosen $d$ along which unaccounted for information can spread, unless $d$ is greater than or equal to the graph diameter of the entire lattice. This means that mean-field models that do not consider motifs of size up to the network diameter minus one cannot be exact.

As MF1 assumes no correlation between the states of neighbouring nodes, the distance between the horizontal line through 1 and the + markers of the correlations in the simulations is a measure of the bias of MF1 due to neglect of correlations in MF1 closures. Likewise, the distance between the steady state MF2/MF5 correlations and the simulations is due to neglect of (higher-order and conditional) dependence in MF2/MF5 closures and higher-level non-chordality. All models have larger biases closer to the critical point, where higher-order correlations become more important. This is a well-known characteristic of continuous phase transitions, in which correlations occur on increasingly long ranges when approaching the phase transition (bifurcation). Figure S3 in Supplement S-IV shows the correlation as a function of distance from a central point [via (S30)], for various values of $\beta/\gamma$. It shows, as expected from phase transitions theory, that correlations at any distance are larger closer to the critical point. At the critical point, theory shows that correlations occur at all distances [6].

Comparing the square lattice to the 4-neighbour random regular graph, we can see that there is also a phase transition, but there is substantially less bias than in the square lattice (Figure 3 blue × vs +). This is because random regular graphs are locally treelike, and hence, unlike in the square lattice, correlations over longer distances can be captured well via a decomposition of larger motifs into links (MF2). The small remaining bias in the 4-regular random graph we suspect to be because the assumed conditional independence is not valid for all states [18, 19].

b. General cubic lattices and random regular networks We show in Figure 3 how the steady states and correlations in MF1, MF2 and simulations depend on the number of neighbours in d-dimensional cubic lattices and random regular networks. When d is the lattice dimension, the lattice degree is $\kappa = 2d$. The observations of the square lattice generalise to cubic/hypercubic lattices and random regular networks (at least up to $\kappa = 10$): i. there is a transcritical bifurcation at a particular value of $\beta/\gamma$, where $C_{II}^\ast$ becomes singular, ii. MF1 and MF2 capture qualitatively the steady state fraction of infecteds and correlations are captured qualitatively by MF2, iii. MF2 is less biased than MF1, vi. the bias is larger closer to the bifurcation. According to MF1, the bifurcation occurs at $\kappa^{-1} = (2d)^{-1}$ and according to MF2 at $(2d - 1)^{-1} = (\kappa - 1)^{-1}$ (see Sections VIII A1 and VIII A 2). Liggett [39] proved that for lattices, the critical value predicted by MF2 is a lower bound. Figure 3a shows that MF2 and this lower bound is approached increasingly closely when the lattice dimension increases. Due to higher clustering of neighbours, the epidemic threshold in lattices is higher than that in the corresponding random regular network [32], but this difference decreases with dimension/degree (Figure 3a). The steady states of a 5-dimensional hypercubic lattice and of a random regular network with degree 10 are indistinguishable from each other and from MF2. This is a consequence of the fact that two random walks in space of dimension 5 or higher have a finite number of intersections almost surely [40–42]. If the path along which an infection travels is seen as a random walk, having many intersections in $d \leq 4$ means that one cannot ignore alternative infec-
tion paths. In $d > 4$, it is harder for infections to travel via alternative paths to the same point, and hence those paths resemble trees more closely. Hence, as explained above and in Sharkey and Wilkinson [19], MF2 should then be more accurate.

c. Erdős-Rényi random networks Finally, we show in Figure 4 how the steady states and correlations in MF1, MF2 and simulations depend on the number of neighbours in an Erdős-Rényi random network. Recall that MF2 on an Erdős-Rényi random network is different from that of the networks above because it has one fewer conservation relation. As above, the behaviour of the steady state solutions is captured qualitatively by MF1 and MF2 and of the correlations by MF2 alone. Also as above, networks with a larger degree have lower biases and MF2 is better than MF1, but now there seems to be a slight increase of bias with $\beta/\gamma$, at least in the range inspected. Despite spatial heterogeneity of the degree in Erdős-Rényi random networks, there is considerably less bias than in lattices, confirming that the presence of loops beyond closure distance is the dominant cause for mean-field model biases in the steady states of SIS spreading.

IX. SUMMARY AND CONCLUSIONS

Previous work found that exact closed individual-level moment equations exist for SIR spreading on arbitrary networks, with the requirement to consider larger-sized motifs, and therefore more equations, for networks that are decreasingly tree-like [19]. While for other dynamics than SIR spreading it may not be possible to prove exactness for a finite number of closed moment equations, it is generally found that accuracy increases with the order of approximation [e.g. 15, 22] (which was confirmed here). Feasibility of automated derivation of exact closed moment equations for SIR epidemic spreading was shown by [19], while an automated procedure to derive unclosed moment equations for arbitrary dynamics was developed by [20]. We developed an automated procedure to both derive and close population-level moment equations for arbitrary dynamics on networks at any approximation order, allowing us to consider mean-field models of higher orders than typically derived by hand. For this purpose, we developed a method to derive closure schemes from predefined independence assumptions. Our closure formulas rely, besides the requirements of spatial homogeneity and large network size, on the assumption of conditional independence beyond distance $k$ and $k$-chordality of the considered network. Consistently, our simulations of SIS epidemic spreading showed that, at given approximation order, the largest biases occurred for networks with many short loops of any size, such as lattices, in parameter regimes with long-range correlations, such as near continuous phase transitions. Note however that, for lattices, we found the bias of mean-field models to decrease with lattice dimension, which is consistent with results in percolation and phase transitions theory, where it was shown that the importance of loops decreases with the lattice dimension [40–42]. We also showed that the conventional procedure of truncation at a maximum motif size instead of at a maximum motif diameter necessitates independence assumptions that are inconsistent for different approximated motifs or that may be incompatible with the network (see VII C e).

We expect our tool to lend itself well to study dynamics on networks with density and size of short loops larger than in random networks but smaller than in lattices, such as often observed in real-world networks [43], particularly when the network is structurally homogeneous. For networks with considerable degree heterogeneity and/or community structure, we expect approximate master equation methods [44–47] to be more efficient. While our treatment focused on static networks with at most nearest-neighbour interactions, it can be extended to adaptive networks such as those studied in [20, 21, 48, 49], and to dynamics with higher-order in-
FIG. 3. Comparison of the mean-field approximations (dotted lines: MF1, solid lines: MF2) and simulations (markers) of SIS epidemic spreading on lattices and random regular networks with number of neighbours 4,6,8,10 as a function of $\beta/\gamma$: (a) Nontrivial steady states, (b) Correlations: $C_{II}^*$ (above 1), $C_{SI}^*$ (below 1).

FIG. 4. Comparison of the mean-field approximations (dotted lines: MF1, solid lines: MF2) and simulations (markers) of SIS epidemic spreading on an Erdős-Rényi random network with number of neighbours 4,6,8,10 as a function of $\beta/\gamma$: (a) Nontrivial steady states, (b) Correlations: $C_{II}^*$ (above 1), $C_{SI}^*$ (below 1).

interactions [50] – requiring reaction rate tensors $R^p$ with $p \geq 2$. We also suspect that our generalisation of moment closure to higher approximation orders can be used to extend the use of message-passing methods [51–53] for epidemic modelling to graphs with loops.

To end, we list some of the many open questions that remain. How plausible are the independence assumptions at increasing orders for common dynamical processes on real-world networks and for different initial conditions? Does our closure scheme relate to the maximum entropy closure scheme [54]? Can one systematically include assumptions in closure schemes most appropriate to the particular process and network considered in order to improve the efficiency of moment closures?

ACKNOWLEDGMENTS

This work was supported by the UK Engineering and Physical Sciences Research Council (EPSRC) grants EP/N023544/1 and EP/V04687X/1.

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For an ER random network, the expected number of $m$-node loops and $m$-node chains (counting all ordered $m$-tuples without repetition) are $\mathcal{L}(N) = \frac{N^m}{(N-m)!} \left( \frac{1}{N-1} \right)^m$ and $\mathcal{C}(N) = \frac{N^m}{(N-m)!} \left( 1 - \frac{1}{N-1} \right) \left( \frac{1}{N-1} \right)^{m-1}$, where $\frac{1}{N-1}$ is the probability of having a link between two given nodes. Hence, $\lim_{N \to \infty} \mathcal{L}(N) = \kappa^m = O(1)$ and $\lim_{N \to \infty} \mathcal{C}(N) = \lim_{N \to \infty} \kappa^{m-1} N = O(N)$. Hence, as $\mathcal{L}(N)$ remains finite and $\mathcal{C}(N)$ grows with $N$, loops can be ignored in the limit of large $N$. In the case $m = 3$ (and $N$ large), we can hence safely assume that all triples are chains.

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SUPPLEMENT

S-I. DERIVATION OF THE MOMENT EQUATIONS

In this section, we derive expressions for the expected rate of change and conservation relations of motif counts, first shown in (8, 9) of Section V. Both can be seen as invariance relations, the former being of a differential type, and derived from the master equation for the Markov chain on the network, and the latter of an algebraic type, following from the property that the network is fixed.

a. Master equation for transitions in a Markov chain  
We recall that the state of the system for our network with \( N \) nodes is given by (using := for “defined as”) \( X := (X_1, X_2, ..., X_N) \in \{1, ..., n\}^N \), where \( X_i \) is the label of the species that occupies node \( i \). Hence, the total number of states is \( n^N \). The probabilistic transition from one state to another, following a discrete-state continuous-time Markov chain, defines an evolution equation for the probability of being in each of these states, the so-called master equation (also known as the Kolmogorov-forward equation for a Markov jump process [55]). The probability density \( P(X,t) \) for a particular state \( X \) at time \( t \) changes according to

\[
\frac{d}{dt} P(X,t) = \sum_{X' \neq X} [w(X' \rightarrow X)P(X',t) - w(X \rightarrow X')P(X,t)],
\]

where \( w \) denotes the transition rate between system states. If we define \( W \) as a \( n^N \times n^N \) transition rate matrix with non-diagonal entries \( w(X' \rightarrow X) \) and diagonal entries \( - \sum_{X' \neq X} w(X \rightarrow X') \), we can rewrite the master equation as

\[
\dot{P}(t) = WP(t),
\]

which describes the evolution of the density for all states as elements of a vector \( P \) (and not just of one particular state as in (S1)). Because almost surely at most one node can change state at any one time \( t \), only states differing from each other in one node can be directly transitioned between. Therefore, \( W \) must be sparse, having only \( N(n-1) \) entries in each row or column, as each of the \( N \) nodes can convert to any of the \( n-1 \) other species. This permits writing (S1) as

\[
\frac{d}{dt} P(X,t) = \sum_{i=1}^{N} \sum_{k \neq X_i} [w_i(X_{i+k} \rightarrow X)P(X_{i+k},t) - w_i(X \rightarrow X_{i+k})P(X,t)],
\]

where \( X \rightarrow X_{i+k} : (X_1, ..., X_i, ..., X_N) \rightarrow (X_1, ..., k, ..., X_N) \) is the operator that replaces the species at the \( i \)th node by species \( k \), and \( w_i(\cdot) \) is the conversion rate at node \( i \).

b. Motifs and their frequencies  
In what follows, we will derive from the master equation the evolution of the frequency (or total count) of the motifs \( x^a \), as defined in Section II. Recall that these motifs, are defined by their state label vector \( x \) of size \( m \) and the adjacency structure between motif nodes \( a \). We denote a single occurrence at a given \( i \in S(m,N) \) as

\[
[x_i^a](t) := \delta_a(A_i)\delta_x(X_i(t)),
\]

which requires an exact match of the adjacency \( a \) by \( A_i \) and state label vector \( x \) by \( X_i \). For example, if \( A \) contains a connected triangle between nodes 1, 2 and 3, then motifs with \( a = \{(1,2),(2,3)\} \) would not occur on \( i = (1,2,3) \). The total count of motifs in the large network is then the number of such exact matches, which is obtained by summing over all indices \( i \in S(m,N) \), as shown in (3). Since the large network structure is constant in time, we can use the counts of induced subgraphs \( [a] \) given by (8) as a normalisation factor for the (variable) counts of motifs such that we may consider normalised motif frequencies

\[
[[x^a]] := [x^a] / [a].
\]

c. Evolution of expected counts  
Total and normalised counts \( [x^a] \) and \( [[x^a]] \) refer to realisations of states \( X \) on the large random network such that they are random variables. Similarly, \( [x_i^a](X) \) is a random variable in \( \{0,1\} \) for each index vector \( i \in S(m,N) \) once we take the randomness of states \( X \) into account. Its expectation is

\[
\langle [x_i^a] \rangle = \sum_X [x_i^a](X)P(X,t).
\]
The master equation (S2) for the density $P$ implies that the expectation satisfies the differential equation

$$
\frac{d}{dt} \langle x_i^2 \rangle = \sum_X \left[ \langle x_i^2 \rangle (X) \frac{d}{dt} P(X, t) \right]
= \sum_X \left\{ \sum_{i' = 1}^N \sum_{k \neq X_{i'}} \left[ w_{i'}(X_{i' \to k}) P(X_{i' \to k}, t) - w_{i'}(X \to X_{i' \to k}) P(X, t) \right] \right\},
$$

where in the second step, we substituted $\delta_x(X_{i' \to k}) w_{i'}(X \to X_{i' \to k})$ for $\delta_x(X_{i' \to k}) w_{i'}(X \to X_{i' \to k}) P(X, t)$ which corresponds to a reordering of the terms in $\sum_X$, and where we have used the notation $\langle \cdot \rangle$ for the expectation $\sum_X \langle \cdot \rangle P(X, t)$. In the third step, we use the fact that only changes to the nodes belonging to $i$ matter. In the last step, we factored out the common elements in the delta functions corresponding to all but the $n$th element of $X_i$ and $\mathbf{x}$, and we used the subscript notation $\langle \cdot \rangle^p_{\mathbf{x} \neq i}$ to denote a vector with element $p$ removed. The expression on the right-hand side in (S6) can be understood independently of the prior algebraic manipulations: the expected change rate of $\langle x_i^2 \rangle$ equals the sum of expected rates for each of the nodes $i_p$ in $i$ changing its state to $x_p$, minus the rate of node $i_p$ changing its state from $x_p$.

$d. Conversion rates$ Next, we will insert the two types of admissible transitions (as discussed in Section II) into (S6), namely spontaneous conversions with rates given in matrix $R^0 \in \mathbb{R}^{n \times n}$, and, conversions due to interactions with a single nearest neighbour with rates given in $R^1 \in \mathbb{R}^{n \times n \times n}$. The diagonal entries of $R^0, R^1$ are zero without loss of generality. For these transition types, the rates $w_{i_p}$ in (S6) are

$$
w_{i_p}(X \to X_{i_p \to k}) = \sum_{a,c} R^1_{a,cp} \delta_a(X_{i_p}) \sum_j A_{i_p,j} \delta_c(X_j) + \sum_a R^0_{a,k} \delta_a(X_{i_p}). \tag{S7}
$$

With the rates in (S7), and noting that

$$
\delta_x(k) - \delta_x(x_{i_p}) = \begin{cases} 
1 & \text{if } x_p = k, \\
-1 & \text{if } x_p = x_{i_p}, \\
0 & \text{if } k \neq x_p \text{ and } x_p \neq x_{i_p},
\end{cases}
$$

the sum inside the averaging brackets in (S6) has the form

$$
\left[ \sum_{a,c} R^1_{a,cp} \delta_a(X_{i_p}) \sum_j A_{i_p,j} \delta_c(X_j) + \sum_a R^0_{a,k} \delta_a(X_{i_p}) \right] \delta_{x_p}(X_{i_p})
$$

$$
- \sum_{k \neq X_{i_p}} \sum_{c} R^1_{x_kpc} \sum_j A_{i_p,j} \delta_c(X_j) + R^0_{x_kk} \delta_x(X_{i_p}),
$$

where we used for the last two terms that $\delta_{x_p}(X_{i_p}) \delta_{x_{i_p}}(X_{i_p})$ can be combined to $\delta_x(X_{i_p})$.

c. Differential equations for motif counts When distributing the products and exploiting the linearity of the averaging brackets, the differential equation (S6) for the expected rate of change at $i$ becomes

$$
\frac{d}{dt} \langle x_i^2 \rangle = \delta_x(A_i) \sum_p \left[ \sum_{a,c} R^1_{a,cp} \left[ \delta_{x_p}(X_{i_p}) \delta_a(X_{i_p}) \sum_j A_{i_p,j} \delta_c(X_j) \right] + \sum_a R^0_{a,k} \delta_a(X_{i_p}) \delta_x(X_{i_p}) \right]
$$

$$
- \sum_{k \neq X_{i_p}} R^1_{x_kpc} \left[ \delta_x(X_k) \sum_j A_{i_p,j} \delta_c(X_j) \right] - \sum_{k \neq X_{i_p}} R^0_{x_kk} \left[ \delta_x(X_k) \right].
$$
After replacing index label \( a \) by \( k \), using the definition of \( [x^a_i] \) in (S3) and using \( (x^a_i)_{p-k} \) to indicate \( x^a_i \) with its \( p \)th element replaced by species \( k \), this becomes

\[
\frac{d}{dt} ([x^a_i]) = \sum_{p}^{m} \sum_{k}^{n} \left[ \sum_{c}^{n} R_{kx,c}^{1} \langle \delta_c(x^a_i) \rangle + R_{kx,c}^{0} \langle \delta_c(x^a_i) \rangle \right] - \sum_{p}^{m} \sum_{k}^{n} \left[ \sum_{c}^{n} R_{kx,c}^{1} \langle \delta_c(x^a_i) \rangle - R_{kx,c}^{0} \langle \delta_c(x^a_i) \rangle \right].
\]

This shows that \( \langle [x^a_i] \rangle \) can increase by a conversion from motifs that differ from \( x^a_i \) in only one node (first two terms), or decrease by having any of the nodes in \( x^a_i \) convert to another species (last two terms), with both increase and decrease possible via interaction with neighbours and via spontaneous conversion. The factors of form \( \langle [\cdot] \rangle \) located at \( i \) at node \( i_p \). The neighbouring node \( j \) with species \( c \) can be part of the motif \( [\cdot] \), or it can be outside of \( [\cdot] \), in which case it gives rise to higher-order motifs. Therefore, by splitting the neighbourhood sums as follows,

\[
\sum_{j}^{N} A_{i_p,j}\delta_c(X_j) = \sum_{j \in \mathcal{I}}^{N} A_{i_p,j}\delta_c(X_j) + \sum_{j \notin \mathcal{I}}^{N} A_{i_p,j}\delta_c(X_j),
\]

their products with \( [x^a_i] \) and \( (x^a_i)_{p-k} \) count contributions of \( c \)--neighbours from within versus from outside the motif separately:

\[
\langle [x^a_i] \rangle = \sum_{j}^{N} A_{i_p,j}\delta_c(X_j) = \sum_{j \in \mathcal{I}}^{N} A_{i_p,j}\delta_c(X_j) + \sum_{j \notin \mathcal{I}}^{N} A_{i_p,j}\delta_c(X_j),
\]

\[
\langle (x^a_i)_{p-k} \rangle = \sum_{j}^{N} A_{i_p,j}\delta_c(X_j) = \sum_{j \in \mathcal{I}}^{N} A_{i_p,j}\delta_c(X_j) + \sum_{j \notin \mathcal{I}}^{N} A_{i_p,j}\delta_c(X_j).
\]

On the right-hand side, \( e_p \) is an \( m \)--dimensional vector with a 1 at position \( p \) and zeroes elsewhere, and \( \delta_c(x) \) a vector Kronecker delta function that returns a vector of the size of \( x \) with ones where the elements equal \( c \) and zeroes elsewhere. Thus, the term \( \delta_c(x)e_p \) counts the number of \( c \)--connections at position \( p \) in the motif \( x^a \). We use the notation \( \mathcal{I}, \mathcal{J} \) for the vector \( i \) with an extra node index \( j \) appended at position \( m+1 \). We used \( \mathcal{N}^c_p(x^a) \) to denote the set of all \((m+1)\)--order connected motifs that can be obtained by linking a new \( c \)--node to the \( p \)th position in motif \( x^a \), i.e.,

\[
\mathcal{N}^c_p(x^a) := \bigcup_{\ell=1}^{m+1} \left\{ y^b : |y| = m+1, y_{\ell} = c, y^b_{\ell+\ell} = x^a, (\ell, p) \in b \right\},
\]

where \( y^b_{\ell+\ell} \) denotes the \( m \)th order connected motif obtained by deleting the \( \ell \)th node of \( y^b \). The sum over elements of \( \mathcal{N}^c_p(x^a) \) in (S9) results from the fact that any of the other motif nodes can also link to the new node. The types of higher-order motifs appearing in the differential equation depend on the considered motif. In Figure S1, we show this dependence structure (ignoring the labels).

With the substitutions from above, we obtain the individual-level moment equations:

\[
\frac{d}{dt} ([x^a_i]) = \sum_{p}^{m} \sum_{k}^{n} \left\{ \left( \sum_{c}^{n} \delta_c(x)e_p R_{kx,c}^{1} + R_{kx,c}^{0} \right) \langle [x^a_i] \rangle \right\} - \sum_{p}^{m} \sum_{k}^{n} \left\{ \sum_{c}^{n} \delta_c(x)e_p R_{kx,c}^{1} + R_{kx,c}^{0} \right\} \langle [x^a_i] \rangle.
\]

The population-level moment equations are then obtained by taking the sum \( \sum_{i \in S(m,N)} \) [see definitions of \( x^a \) and
FIG. S1. Dependence of moment equations of a given motif on motifs of one order higher due to nearest-neighbour interactions, up to order 4 (ignoring labels).

\[
\frac{d}{dt} \langle x^a \rangle = \sum_p n \sum_k c \left\{ \left( \frac{R^0_{x^p x^k}}{n} + \delta_c(x) a e_p R^1_{x^p x^c} \right) \langle \langle x^a \rangle \rangle - \left( \frac{R^0_{x^p x^k}}{n} + \delta_c(x) a e_p R^1_{x^p x^c} \right) \langle \langle x^a \rangle \rangle \right\} + \sum_{y^b \in N^c_{x^p} (x^a)} R^1_{x^p x^c} \langle \langle y^b \rangle \rangle - \sum_{y^b \in N^c_{x^p} (x^a)} R^1_{x^p x^c} \langle \langle y^b \rangle \rangle ,
\]

where we collected the sums at the front. In closing this section, we make the following remarks. i. The evolution of expected motif counts of size \( m \) is a function of expected motif counts of size \( m \) and \( m + 1 \). ii. Equation (S12) leads to the same equation for motifs in the network that are isomorphic, where we call two motifs \( x^a \) and \( y^b \) isomorphic if there exists a permutation \( \pi \) of their node indices that maps them onto each other, i.e. \( \forall x^a, y^b : x^a \simeq y^b \iff \exists \pi : \pi x = y, \pi a \pi^T = b \). Hence, different motifs that are isomorphic belong to the same equivalence class. Isomorphic motifs have equal total counts such that we may consider only one representative from each equivalence class. In our implementation, we therefore make sure that we count all isomorphic motifs under a single representative node indexing. iii. The summation in (3) over index tuples \( i \in S(m, N) \) that we used to go from (S11) to (S12) leads to multiple counting of motifs that possess automorphisms other than the identity transformation. A motif has an automorphism if it can be mapped onto itself by a permutation of its node indices. An automorphism is therefore an isomorphism with itself, i.e. \( \text{Aut}(x^a) := \{ \pi : \pi x = x, \pi a \pi^T = a \} \). The multiplicity with which a particular motif \( x^a \) is counted (via (3)) is then equal to \( |\text{Aut}(x^a)|\).

f. Conservation relations In fixed networks, the frequencies of induced subgraphs of a given type (e.g. nodes, links, polygons, chains) remain fixed. The sum over all possible motif label orderings then yields these fixed frequencies,
\[
\begin{array}{cccccc}
  k & n_{\text{ch}} & n_{\text{eq}} & n_4 & n_{4c} \\
  1 & 2 & 1 & 2 & 2 & 1 \\
  2 & 5 & 2 & 5 & 5 & 2 \\
  3 & 11 & 4 & 15 & 11 & 4 \\
  4 & 21 & 10 & 65 & 35 & 14 \\
  5 & 36 & 31 & 419 & 113 & 38 \\
\end{array}
\]

TABLE S2. Cumulative number of equations \( (n_{\text{ch}}, n_{\text{eq}}, n_{4c}) \) or motif types \( (n_g) \) as a function of order \( k \). \( n_{\text{ch}} \): number of chain motifs (if the number of species \( n = 2 \)), \( n_g \): number of subgraph types, \( n_{\text{eq}} \): total number of equations ignoring conservation relations (if \( n = 2 \)), \( n_4 \): number of equations for the square lattice (if \( n = 2 \)), \( n_{4c} \): number of equations for the square lattice after elimination via conservation relations (if \( n = 2 \)).

or using the notation from above,

\[
\sum_x [x^a] = [a], \quad \sum_x [x^a]^\top = 1, \quad (S13)
\]

where the right is the normalised form of the left [via (S4)]. For networks with homogeneous degree and motifs and every stub \( p \) of motif \( x^a \) (also called leaf), i.e. a node with degree 1, there is the additional conservation relation

\[
\sum_k [x^a_{p,k}] = \left[ \frac{[a]}{[a \setminus p]} \right] [x^a_{p,0}]^\top, \quad \sum_k [x^a_{p,k}] = [x^a_{p,\emptyset}], \quad (S14)
\]

where the right is again the normalised form of the left (via (S4)). Under the conditions mentioned above, \([a] / [a \setminus p]\) is the number of out-motif connections at the node that connects to the stub. As (S13) and (S14) can be derived for each motif up to the chosen truncation order, they form an additional system of equations that can be used to reduce the dimensionality of the mean-field model via elimination. To avoid multiplicity of equations while deriving relations (S14), we set up one equation per set of stubs that lead to isomorphic variants of the considered subgraph when their indices are permuted.

\textbf{g. Number of equations} A simple lower bound on the number of equations (before elimination) can be found by considering only chains. At each order there is only one chain graph. Order 1 contributes \( n \) equations, where \( n \) is the number of possible node states. Each chain of order \( m > 1 \) has \( \left( \begin{array}{c} n \\ m \end{array} \right) = \frac{(m+n-1)!}{(m-1)!n!} \) ways of labelling its \( m \) nodes with \( n \) species. The total number of equations from chains is then \( n_{\text{ch}} = 2 + \sum_{m=2}^k \left( \begin{array}{c} n \\ m \end{array} \right) \). For networks in which the number of short loops goes to zero with \( N \to \infty \), as in Erdős-Rényi random networks, the total number of equations is equal to this lower bound plus the number of equations due to non-chain trees. When loops need to be taken into account however, there will be additional connected motif types at each order; see Table S2 column \( n_g \) [26, Table 4.2.1]. To obtain the number of equations contributed by each of these, one has to consider all labelling orderings, knowing that some orderings lead to isomorphic motifs and hence do not add to the total. We have listed in Table S2 the total number of equations \( n_{\text{eq}} \) resulting from our enumeration algorithm for dynamics with \( n = 2 \), such as SIS epidemic spreading. For a particular network, these are still reduced by the number of motifs not occurring in the considered network and by the number of variables via the conservation relations. Column \( n_4 \) in Table S2 shows the number of equations for the square lattice and column \( n_{4c} \) shows the remaining number after eliminating variables by using conservation relations.

\textbf{S-II. MOMENT EQUATIONS FOR SIS SPREADING UP TO ORDER 3}

The moment equations up to third order can be written (via (11)) as

\[
\begin{bmatrix}
  x_1 \\ x_2 \\ x_3 \\ x_4
\end{bmatrix}
\begin{bmatrix}
  \dot{x}_1 \\ \dot{x}_2 \\ \dot{x}_3 \\ \dot{x}_4
\end{bmatrix}
\begin{bmatrix}
  Q_{11} & Q_{12} & 0 & 0 \\ 0 & Q_{22} & Q_{23} & 0 \\ 0 & 0 & Q_{33} & Q_{34}
\end{bmatrix}
\]

(S15)
Then, the coefficients for motifs up to order three are (omitting zero blocks)

while those for fourth-order motifs in $Q_{14}$ are

When written out, this corresponds to the equations:

$$\frac{d}{dt}[\text{a}] = -\gamma[\text{a}] + \beta[\text{a}]$$,  \hspace{1cm} (S16)

$$\frac{d}{dt}[\text{b}] = \gamma[\text{b}] - (\beta + \gamma)[\text{b}] + \beta[\text{b}] - \beta[\text{b}]$$,  \hspace{1cm} (S17)

$$\frac{d}{dt}[\text{c}] = 2\beta[\text{c}] - 2\gamma[\text{c}] + 2\beta[\text{c}] + 2\beta[\text{c}]$$,  \hspace{1cm} (S18)

$$\frac{d}{dt}[\text{d}] = \gamma[\text{d}] + \gamma[\text{d}] - (\beta + \gamma)[\text{d}] - \beta[\text{d}] + \beta[\text{d}] - \beta[\text{d}] - 2\beta[\text{d}] - \beta[\text{d}] + \beta[\text{d}]$$,  \hspace{1cm} (S19)

$$\frac{d}{dt}[\text{e}] = \gamma[\text{e}] - (\beta + 2\gamma)[\text{e}] + \beta[\text{e}] + \beta[\text{e}] - \beta[\text{e}] + \beta[\text{e}] + \beta[\text{e}] - \beta[\text{e}] + \beta[\text{e}]$$,  \hspace{1cm} (S20)

$$\frac{d}{dt}[\text{f}] = \gamma[\text{f}] - 2(\beta + \gamma)[\text{f}] + 2\beta[\text{f}] + 2\beta[\text{f}] - \beta[\text{f}] + 2\beta[\text{f}] + 2\beta[\text{f}] + 2\beta[\text{f}] + \beta[\text{f}] + 2\beta[\text{f}] + \beta[\text{f}]$$,  \hspace{1cm} (S21)

$$\frac{d}{dt}[\text{g}] = \gamma[\text{g}] - 2(\beta + \gamma)[\text{g}] + 2\beta[\text{g}] + 2\beta[\text{g}] - \beta[\text{g}] + 2\beta[\text{g}] + 2\beta[\text{g}] - \beta[\text{g}] + 2\beta[\text{g}]$$,  \hspace{1cm} (S22)

$$\frac{d}{dt}[\text{h}] = -3\gamma[\text{h}] + 2\beta[\text{h}] + 2\beta[\text{h}] + 2\beta[\text{h}] + 2\beta[\text{h}] + \beta[\text{h}] + 2\beta[\text{h}] + 2\beta[\text{h}]$$,  \hspace{1cm} (S23)

$$\frac{d}{dt}[\text{i}] = 2\gamma[\text{i}] - (\beta + \gamma)[\text{i}] - 2\beta[\text{i}] + \beta[\text{i}] - 2\beta[\text{i}] + 2\beta[\text{i}] - 2\beta[\text{i}] - 2\beta[\text{i}] + \beta[\text{i}]$$,  \hspace{1cm} (S24)

$$\frac{d}{dt}[\text{j}] = \gamma[\text{j}] - 2(\beta + \gamma)[\text{j}] + 2\beta[\text{j}] + 2\beta[\text{j}] - \beta[\text{j}] + 2\beta[\text{j}] + 2\beta[\text{j}]$$,  \hspace{1cm} (S25)

$$\frac{d}{dt}[\text{k}] = -3\gamma[\text{k}] + 6\beta[\text{k}] + 3\beta[\text{k}] + 6\beta[\text{k}] + 3\beta[\text{k}]$$,  \hspace{1cm} (S26)
FIG. S2. Feedback control of SIS epidemic spreading on a square lattice: (a) example time profiles of infected fraction $I$ and fraction of susceptible-infected links $SI$ in conventional (left) and controlled (right) simulation, (b) bifurcation diagram with control; insets: example spatial patterns; grid size 100×100 (white=susceptible, black=infected), gain $g \gg 1$, recovery rate $\gamma = 1$. Near the critical point, the conventional simulation shows large fluctuations and short extinction times (absorption event occurs at the end of the time series for $\beta \approx 0.43$ in green) whereas the controlled simulation has small fluctuations and no extinction.

S-III. OBTAINING STEADY STATES FROM SIMULATIONS

a. Feedback control

As we aim to compare the steady states of mean-field models to those of the simulation, we need a way to obtain the steady states of the simulations, even if they are unstable or marginally stable. Treating the simulation like an ideal physical experiment, the general approach to finding equilibria regardless of stability is to introduce a stabilizing feedback loop of the form

$$r(t) = r_0 + g([x^a](t) - [x^a]_{\text{ref}}),$$

(S27)

as was done in [36–38] for continuation of unstable vibrations in mechanical experiments. In (S27), $r$ is one of the conversion rates in $R_0$ or $R_1$. The feedback control [56] makes this rate time dependent by coupling it to the motif frequency $[x^a](t)$ of a chosen motif $x^a$ through the relation (S27). The factor $g$ is called the feedback control gain and is problem specific. When performing bifurcation analysis, it is convenient if the rate $r$ used as the control input is also the bifurcation parameter varied for the bifurcation diagram. In this case, whenever the simulation with feedback control (S27) settles to an equilibrium $(r^*_c, [x^a]_{c})$ (in the limit of large $N$) the point $(r^*_c, [x^a]_{c})$ will be on the equilibrium branch of the simulation without feedback control [57–59]. For SIS spreading, we choose

$$r = \beta, \quad x^a = \bullet, \quad g = \infty.$$  

(S28)

This limit for feedback control results in what is called the conserved contact process, as proposed by Tomé and De Oliveira [60]. While SIS spreading does not have any unstable steady states, points that are marginally stable, as near the continuous phase transition (epidemic threshold) are stabilised as well by the control. This stabilisation suppresses fluctuations, even close to the bifurcation, which results in faster convergence of the mean and absence of absorption for any positive $\bullet$.

b. Simulation algorithm

In the limit of infinite gain $g$, each recovery event forces a simultaneous infection event, such that the number of infected nodes $\bullet$ stays constant. In a simulation based on the Gillespie algorithm [35] this is done in the following steps:

1. start with a number of randomly distributed infected nodes,
2. recover an infected node selected uniformly at random,
3. infect a randomly selected susceptible node, with selection probability proportional to its number of infected neighbours,
4. advance time with $\Delta t = -\log(\xi)/(\gamma \bullet)$, (where $\xi$ is a uniform random variable on the interval $[0, 1]$),
5. go to step 2.

This loop runs until we observe that $\bullet$ is stationary (call this time $t_e$). Then for some additional time $T$ we observe the fluctuations of $\bullet$ around its mean. Tomé and De Oliveira [60] derived the effective infection rate $\tilde{\beta}$.
for each chosen count \([\bullet]\) of infected nodes by noting that, because for every infection event there is a recovery event, 
\[
\tilde{\beta}(\bullet\bullet) = \gamma [\bullet],
\]
where \(\langle \cdot \rangle\) is an average over many independent realisations, such that
\[
\tilde{\beta} = \gamma \langle [\bullet] \rangle,
\]
which they found to lead to the same nontrivial steady states \([\bullet]\) as \([\bullet]\) in the model without control. As the model with control is ergodic (no absorbing states exist) we need to run only a single realisation and compute the effective infection rate as
\[
\tilde{\beta} = \gamma \frac{[\bullet]}{\int_{t_u}^{t_u+T} \bullet\bullet(t)dt/T}.
\]
(S29)

In this manner, the error bars of estimates of \(\tilde{\beta}\) can be made arbitrarily small by increasing \(T\).

### S-IV. CORRELATIONS AT GIVEN DISTANCE

In Figure S3 we show for SIS epidemic spreading the correlation at given distance between two nodes (only between infected nodes shown). Its general definition is
\[
C_D^{ab} = \frac{N^2}{\sum_{ij} \mathbb{1}_{\text{dist}(i,j)=D}} \sum_{ij} [\bullet\bullet][\bullet\bullet]_{\text{dist}(i,j)=D},
\]
(S30)
or with normalised motifs:
\[
C_D^{ab} = \sum_{ij} [\bullet\bullet][\bullet\bullet]_{\text{dist}(i,j)=D},
\]
(S31)
where the distance \(\text{dist}(i,j)\) is the length of the shortest path between \(i\) and \(j\). Note that the correlations between neighbouring nodes (40) is a special case of this, i.e. \(C_{ab} = C_1^{ab}\). An alternative way to write (S31) is
\[
C_D^{ab} = \sum_{c_1,...,c_{D-1}} [a c_1...c_{D-1} b],
\]
(S32)
where \([a c_1...c_{D-1} b]\) is a chain motif of size \(D + 1\) with indicated states. This definition was used to derive \(C_D^{ab}\) as approximated by mean-field models in Figure S3, by applying the closure formula to the chain in the numerator.

![FIG. S3. Steady state correlation function \(C_D\) versus distance \(D\) (S30) for simulations of SIS spreading on the square lattice (lines). Colour scale indicates values of \(\beta/\gamma\) corresponding to the markers in Figure 2 and sorted such that higher correlations occur for lower values of \(\beta/\gamma\) (closer to the critical point). Markers show approximated correlations when assuming MF2 conditions hold (using (S32)) and factorising the numerator in pair fractions). Filled black markers are MF2 correlations for \(\beta/\gamma = 0.4137\) (which for simulations is the top black line). Open red markers are MF2 correlations for \(\beta/\gamma = 0.5602\) (which for simulations is the red line).](image-url)
S-V. CLOSURE EXAMPLES

Here we show 13 examples of subgraph decompositions based on the method explained in Section VII (24, 25). They are shown in table form in the accompanying pdf (./closure_examples.pdf) but we also discussed three commonly used ones (1-3 in the table) in Section VIID.

As the closures can be written independent of the particular labels, they are shown in the table for subgraphs only, with each node tagged with its index. We have also dropped the $\langle \cdot \rangle$, assuming that the law of large numbers applies, such that the counts approach their expectations almost surely for increasing network size $N$. The examples can be understood by reading the table from left to right. Comments are added in the last column. By column, it shows: 1. the example number, 2. the considered subgraph, 3. its diameter, 4. its independence map assuming independence beyond distance $diam(a-1)$, 5. whether the independence map is chordal, 6. the derived junction graph of $d$-cliques where $d = diam(a-1)$, 7. the resulting closure formula, 8. a triangulation of the independence map if the independence map is non-chordal, 9. the junction graph of $d$-cliques based on the triangulation, 10. the closure formula based on the triangulation, 11. an ad-hoc extension of the method to non-maximal cliques for some subgraphs, 12. the resulting closure formula based on this extension, 13. comments. Our Mathematica script generates these closures automatically.

S-VI. STEADY STATES OF MF1-MF2

Here, we show the expressions for the steady states and steady state correlations of MF1 and MF2.

A. MF1

The MF1 model equals SIS epidemic spreading under well-mixed conditions. Its steady states are the trivial and the endemic state,

$$[\bullet ]^*_1 = 0, [\bullet ]^*_2 = 1 - \frac{\gamma}{\kappa \beta}.$$  

B. MF2

For the MF2 model the equations and, hence, their steady states, depend on the type of network.

1. Degree-homogeneous networks

The steady states of the dynamic equations for MF2 on degree-homogeneous networks (50) are

$$([\bullet \bullet ]^*, [\bullet \bullet \bullet ]^*)_1 = (0, 0), \quad ([\bullet ]^*, [\bullet \bullet ]^*)_2 = (1 - \frac{\kappa - 1}{\kappa \beta (\kappa - 1)/\gamma - 1}, \frac{\beta (\kappa - 1) - 1}{\beta (\kappa - 1) - 1}).$$ (S33)

The non-trivial correlations, obtained by substitution of the above into (41), are

$$C_{II}^* = \frac{(\gamma - \beta \kappa)(\gamma - \beta (\kappa - 1) \kappa)}{\beta \kappa^2 (\beta (\kappa - 1) - \gamma)}, \quad C_{SI}^* = 1 - \frac{\gamma}{\beta (\kappa - 1)}, \quad C_{SS}^* = \frac{\beta (\kappa - 1) \kappa - \gamma}{\beta (\kappa - 1)^2}.$$ (S34)

2. Degree-heterogeneous networks

The steady states of the dynamic equations for MF2 on degree-heterogeneous networks (54) are

$$([\bullet \bullet ]^*, [\bullet \bullet \bullet ]^*, [\bullet \bullet \bullet ]^*)_1 = (0, 0, 0),$$

$$([\bullet ]^*, [\bullet \bullet ]^*, [\bullet \bullet \bullet ]^*)_2 = \frac{\gamma \left( \sqrt{\beta (\kappa - 1)^2 + 4 \gamma} - \sqrt{\beta (\kappa + 3)} \right)}{2 \beta^{3/2} \kappa} + 1,$$

$$\frac{\gamma \sqrt{\beta (\kappa + 1) - \gamma \sqrt{4 \gamma + \beta (\kappa - 1)^2}}}{2 \kappa \beta^{3/2}}.$$ (S35)
The non-trivial correlations, via substitution of the above into (41), are

$$C_{II} = \frac{4\beta^3/\kappa - 2\sqrt{3}\gamma(\kappa + 3) + 2\gamma \sqrt{\beta(\kappa - 1)^2 + 4\gamma}}{\sqrt{3}\kappa \left(\sqrt{\beta(\kappa - 1)^2 + 4\gamma} - \sqrt{\beta(\kappa + 1)}\right)},$$

(S36)

$$C_{SI}^* = C_{SS}^* = \frac{2\gamma}{\kappa \sqrt{\beta^2(\kappa - 1)^2 + 4\beta\gamma} - \beta(\kappa - 1)}.$$

(S37)

**S-VII. MF3 for SIS Spreading**

We only apply MF3 to the square lattice, such that we can ignore all motifs that contain triangles and set $\begin{bmatrix} \otimes \otimes \otimes \end{bmatrix} = 0$ in the remaining equations, such that we obtain

$$\begin{bmatrix} \begin{array}{cccccc}
-\gamma & \beta & 0 & -\beta & 0 & -\beta \\
-\beta - \gamma & \gamma & 0 & -\beta & 0 & -2\beta - \gamma \\
0 & 0 & 0 & 2\beta & 0 & 0 \\
0 & 0 & 0 & -2\beta - \gamma & \gamma & 0 \\
0 & 0 & 0 & 2\beta & 0 & 0 \\
0 & 0 & 0 & 2\beta & 0 & 0 \\
0 & 0 & 0 & -3\gamma & \beta & 0 \\
\end{array}\end{bmatrix} = 0.$$

The 7 conservation relations are

$$\begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix} + \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix} = N, \quad \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix} + \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix} = \kappa \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix},$$

$$\begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix} + \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix} = (\kappa - 1)\begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix},$$

and

$$\begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix} + \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix} = (\kappa - 1)\begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix},$$

We eliminate $\begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix}, \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix}, \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix}, \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix}$. Following (12-14), this means

$$\mathbf{x} = \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix}, \quad \tilde{\mathbf{x}} = \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix}, \quad \tilde{\mathbf{x}}_4 = \begin{bmatrix} \begin{array}{c}
1 \\
-\beta \\
-\beta - \gamma \\
\gamma \\
1 \\
1 \\
-3\gamma \\
\end{array}\end{bmatrix},$$

and

$$\tilde{Q}_{1\ldots,31\ldots,3} = \begin{bmatrix} \begin{array}{cccccc}
-\gamma & \beta & 0 & 0 & 0 & 0 \\
0 & -\beta - \gamma & \gamma & 0 & -\beta & 0 \\
0 & 2\beta & -2\gamma & 0 & 0 & 2\beta \\
0 & 0 & 0 & -2\beta - \gamma & 0 & 2\beta \\
0 & 0 & 0 & 0 & -\beta - \gamma & 0 \\
0 & 0 & 0 & 0 & 0 & -2\beta - \gamma \\
0 & 0 & 0 & 0 & 0 & 2\beta \\
\end{array}\end{bmatrix}, \quad \mathbf{E} = \begin{bmatrix} \begin{array}{cccccc}
1 & 0 & 0 & 0 & 0 & 0 \\
\kappa & -1 & 0 & 0 & 0 & 0 \\
-\kappa(\kappa - 1) & 2(\kappa - 1) & 0 & 1 & 0 & 0 \\
\kappa - 1 & -1 & 0 & 0 & 0 & 0 \\
0 & 1 & -1 & 0 & 0 & 0 \\
0 & 0 & 1 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 \\
\end{array}\end{bmatrix},$$

$$\mathbf{c} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}^T.$$
which results in the four remaining equations (\( \tilde{c} = 0 \) so not shown)

\[
\begin{pmatrix}
0 & -\gamma & 4\gamma & 2\beta - 2\gamma & -2\beta & 0 \\
0 & 2\beta - 2\gamma & -2\beta - 2\gamma & \gamma & 2\beta & 0 \\
0 & 2\beta & -3\gamma - 2\beta & 0 & 0 & 2\beta \\
0 & -6\beta & -2\beta - 2\gamma & \gamma & 14\beta & 0 & 4\beta & -2\beta \\
0 & 2\beta & -3\gamma - 2\beta & 0 & 0 & 2\beta & 2\beta & -\beta
\end{pmatrix},
\]

\( (S38) \)

where we have used \( \kappa = 4 \) for the square lattice. In normalised form this is

\[
\begin{pmatrix}
0 & -\gamma & 4\beta & 2\beta - 2\gamma & -6\beta & 0 \\
0 & 2\beta - 2\gamma & -6\beta - 2\gamma & \gamma & 2\beta & 0 \\
0 & 2\beta & -3\gamma - 2\beta & 0 & 0 & 2\beta \\
0 & -6\beta & -2\beta - 2\gamma & \gamma & 14\beta & 0 & 4\beta & -2\beta \\
0 & 2\beta & -3\gamma - 2\beta & 0 & 0 & 2\beta & 2\beta & -\beta
\end{pmatrix},
\]

\( (S39) \)

To close the system of equations, we apply (24) to the chains and star, and (25) to the loops (using the extension to non-maximal 2-cliques) and obtain the normalised closures (see also Section VII D, examples 3-5)

\[
\begin{align*}
\mathbf{J} \mathbf{K} \approx & \mathbf{J} \mathbf{K} \mathbf{J} = (\mathbf{J} - \mathbf{J} \mathbf{J} - \mathbf{J} \mathbf{J})^2, \\
\mathbf{J} \mathbf{K} \approx & \mathbf{J} \mathbf{K} \mathbf{J} = (\mathbf{J} - \mathbf{J} \mathbf{J} - \mathbf{J} \mathbf{J})^2, \\
\mathbf{J} \mathbf{K} \approx & \mathbf{J} \mathbf{K} \mathbf{J} \mathbf{J} \mathbf{J} = (\mathbf{J} - \mathbf{J} \mathbf{J} - \mathbf{J} \mathbf{J})^2, \\
\mathbf{J} \mathbf{K} \approx & \mathbf{J} \mathbf{K} \mathbf{J} \mathbf{J} \mathbf{J} \mathbf{J} = (\mathbf{J} - \mathbf{J} \mathbf{J} - \mathbf{J} \mathbf{J})^2,
\end{align*}
\]

\( (S40) \)

where we also used the conservation relations to substitute any previously eliminated motif. The steady state solutions of the final system are roots of a ninth-order polynomial, of which two are admissible (see Figure 2 for numerical results).

S-VIII. MF4 FOR SIS SPREADING IN MATHEMATICA

The coefficient matrix \( \mathbf{Q} \) for the (unclosed) moment equations up to fourth order is shown in the first html file below, with columns labelled by \( x_1, \ldots, x_5 \) (stored in the variable \( \text{mots} \)). In the second file, the procedure as explained in the main text is followed for MF4 on the square lattice. The algorithm can be instructed to write the resulting set of equations as MATLAB [61] functions in a format compatible with continuation software such as COCO [62] and MatCont [63].

1. General unclosed fourth-order
2. Closed fourth-order for square lattice