A measure of individual role in collective dynamics: spreading at criticality

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Identifying key players in collective dynamics remains a challenge affecting a great variety of research fields, from the efficient dissemination of ideas to drug target discovery in biomedical problems. The difficulty lies at several levels: how to single out the role of individual elements in such intermingled systems, or which is the best way to quantify their importance. Centrality measures aim at capturing the influence of a node from its position in a network. The key issue obviated is that the contribution of a node to the collective behavior is not uniquely determined by the structure of the system but it is a result of the interplay between dynamics and network structure. Here we show that dynamical influence measures explicitly how strongly a node’s dynamical state affects collective behavior. For diffusive processes in complex networks, dynamical influence quantifies how efficiently real systems may be driven by manipulating the state of single nodes. For critical spreading, it targets nodes with superior spreading capabilities.

Complex networks are a groundbreaking concept that is helping to understand the behaviour of many chemical, biological, social and technical systems [1] [2]. Network representations are particularly suitable for systems where heterogeneity dominates and is crucial for dynamics [3], where a few nodes are usually considered as the most important. Oftentimes, node importance is correlated with centrality measures, local [4] [5] or global [6], which are generally based on a purely topological perspective and do not explicitly account for the dynamics. However, dynamics is fundamental in assessing the impact of individual elements in global performance. Here, we show that dynamical influence is a centrality measure able to quantify how strongly a node’s dynamical state affects the collective behavior of a system, taking explicitly into account the interplay between structure and dynamics in complex networks. We prove that it applies equally well to a variety of families of dynamical models, from spreading phenomena at the critical point, for which dynamical influence targets nodes with superior spreading capabilities, to diffusive processes, for which it quantifies how efficiently real systems may be driven by manipulating the state of single nodes.

Classical centrality measures in complex networks – like the degree or number of neighbors a node interacts with [4] [5], betweenness centrality [7] counting the number of shortest paths through a certain node, eigenvector centrality [8] based on the idea that relations with more influential neighbors confer greater importance, or the k-shell decomposition [9] that correlates with the outcome of supercritical spreading originating in specific nodes [10] – rely only on topology, even if an underlying process can be indirectly associated in some cases. In contrast, the impact of individual elements in the global performance of the system inevitably depends on the specificities of the dynamics. Targeting individuals for vaccination strategies in epidemic processes is not the same as selecting electrical stimulation sites in the brain in order to suppress epileptic seizures. In this respect, a Laplacian-based centrality measure [11] [13], closely related to PageRank [14], has been proposed recently to assess the importance of complex network nodes in specific dynamical models.

In this work, we provide a remarkably general and rigorous framework where dynamical influence is defined as a centrality measure both on directed and on undirected complex networks and applies to a variety of families of dynamical models, including epidemic spreading models like the susceptible-infected-removed (SIR), the susceptible-infected-susceptible (SIS), and the contact process, and diffusive processes like the voter model or phase coupled oscillators. In all cases, dynamical influence is calculated as the left eigenvector associated to the largest eigenvalue zero of a characteristic matrix of the system, that encodes the interplay between topology and dynamics.

More specifically, we focus on systems of N time-dependent real variables $x = (x_1, \ldots, x_N)$ with coupled linear dynamics specified by a $N \times N$ real matrix $M$

$$\dot{x} = Mx. \quad (1)$$

A first classification of the dynamics is obtained by considering the largest eigenvalue $\mu_{\text{max}}$ of $M$. For $\mu_{\text{max}} < 0$, $x(t)$ converges to a null vector that represents a stable fixed point solution; for $\mu_{\text{max}} > 0$, indefinite growth from almost all initial conditions is observed. Suppose that $M$ is such that a non-degenerate $\mu_{\text{max}} = 0$ exists. Then, the scalar product $\phi_c = c \cdot x$ is a conserved quantity, where $c$ is the left eigenvector of $M$ for $\mu_{\text{max}}$.

$$\frac{d\phi_c}{dt} = c \cdot \dot{x}(t) = [cM] \cdot x(t) = 0.$$

(2)

The existence of the conserved quantity allows to calculate the final state in terms of the initial condition $x(0)$ as

$$x(t) = e^{t M} x(0).$$

The matrix exponential $e^{t M}$ of $M$ can be calculated from the eigen-decomposition $M = \sum_{i=1}^{N} \lambda_i \varphi_i \varphi_i^T$, where $\varphi_i$ are the eigenvectors of $M$ and $\lambda_i$ are the corresponding eigenvalues. This formula provides the natural time scale $\tau = \sum_{i=1}^{N} \frac{1}{\lambda_i}$ of the dynamical process, in which $x(t)$ tends to the null vector. For $\mu_{\text{max}} = 0$, $x(t)$ converges to a non-null vector that represents a limit cycle or a stable limit cycle of period $T = \sum_{i=1}^{N} \frac{1}{\lambda_i}$, such as the voter model cycle $x(t) = \varphi_{\text{max}}$.

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dynamical influence
betweenness
degree

\[ x(\infty) := \lim_{t \to \infty} x(t) = \frac{c \cdot x(0)}{c \cdot e} e_c, \quad (3) \]

where \( c \) is a right eigenvector of \( M \) for \( \mu_{\text{max}} \). Eq. (1) implies that the projection of \( x(0) \) on \( c \) is all the system remembers at large times about the initial condition \( x(0) \). Therefore, we call \( c_t \) the dynamical influence of element \( i \) in the dynamics under Eq. (1). It is easily calculated without expensive numerical simulations.

Let us first apply these insights to critical phenomena like spreading processes [15]. In the SIR model [16], each node is either susceptible, infected or removed. An infected node \( i \) transfers the epidemic along each of its outgoing arcs independently with probability \( \beta \); node \( i \) itself relaxes to the removed state at unit rate. As the spreading efficiency (details in Methods) of node \( i \) we define the expected fraction of nodes reached by an epidemic outbreak initiated with a node \( i \) infected, all others susceptible. We call \( i \) the seed node. Viewing such a configuration as a small perturbation to the stationary state with all nodes susceptible, we approximate the dynamics by the linearization

\[ \dot{x} = -x + \beta A^T x. \quad (4) \]

Here \( x_j(t) \) is the probability of node \( j \) to be infected at time \( t \). The first term is the relaxation from the infected to the removed state at unit rate. The second term quantifies the transmission of the epidemic where the network enters by the transpose of its adjacency matrix \( A \).

Equation (4) can be rewritten as Eq. (1) with \( M = \beta A^T - I \) and \( I \) the identity matrix. Matrix \( M \) has largest eigenvalue \( \mu_{\text{max}} = 0 \) when the spreading probability \( \beta \) is the inverse of the largest eigenvalue of \( A \), that is \( \beta = \beta_c = 1/\alpha_{\text{max}} \). We take again \( c \) as a left eigenvector of \( M \) at \( \mu_{\text{max}} = 0 \) or, equivalently, a right eigenvector of \( A \) at its maximum eigenvalue \( \alpha_{\text{max}} \). Then the effect of an initial infection described by the probability vector \( x(0) \) is proportional to \( c \cdot x(0) \).

Now we ask how well \( c \) may forecast the actual SIR spreading dynamics. Figure 1 shows that \( c_t \) is a good predictor of spreading efficiency at critical parameter value \( \beta = \beta_c \) in a small social network. Dynamical influence \( c_t \) outperforms the predictions made by degree, shell index and betweenness centrality. Predictive power is quantified by the rank order correlation (see Methods).

Figure 2 shows the predictive power of dynamical influence for spreading efficiency as a function of the infection probability in larger real-world networks and the Barabasi-Albert model. The results are as anticipated by the theory. Dynamical influence is a good predictor of spreading efficiency in the critical regime where \( \beta/\beta_c \approx 1 \). In this regime predictions by dynamical influence outperform those by other quantities that are supposed to provide information about expected outbreak size.

For sub- and supercritical parameter values \( \beta \), however, the degree \( d_i \) of a node \( i \) is a good predictor of spreading efficiency. In the subcritical regime, spreading is sparse and typically confined to the neighborhood of the seed node \( i \), while in the supercritical regime, the epidemics rarely fails to spread to the whole system. In the critical regime in-between these extremes, infectious seeds are perturbations that trigger relaxation dynamics at all scales. This is reflected in a dynamics dominated by a marginal linear mode and a variety of possible final states. Dynamical predictions require then a global

\[
\begin{align*}
\text{Spreading efficiency} & = 0.97 \\
\text{dynamical influence} & = 0.86 \\
\text{degree} & = 0.82 \\
\text{shell index} & = 0.79 \\
\text{betweenness} & = 0.75 \\
\end{align*}
\]
Considering the conservation law associated with the lead-

evolution, node influence deviates significantly from degree ratio.

Repeating the numerical experiments with the SIS model (see Methods) on the same networks, we obtain results (not shown) qualitatively similar to those of Figure 2. Prediction by dynamical influence may also be applied to the contact process [23]. A is replaced by the stochastic adjacency matrix, the adjacency matrix after normalization such that each row sums up to 1.

Coming back to the general framework Eq. 1 there is a class of dynamical processes in networks in which the property of $M$ having a zero maximum eigenvalue appears naturally without the need of adjusting any pa-

rameter. This is the case of diffusive processes defined by Eq. 1 with $M = -L$ and the Laplacian matrix entries

$$L_{ij} = -K_{ij} + \sum_{k=1}^{N} K_{ik}.$$  (5)

The zero eigenvalue of $L$ is non-degenerate under mild assumptions [25]. For these processes our general analysis of Eq. 1 becomes exact. A prominent example of diffusive dynamics is the voter model [26] in which node $i$ is in a spin state $s_i \in \{-1, +1\}$. For this model, $x_i$ stands for
the ensemble average of spin $i$, $x_i = \langle s_i \rangle$, and $K_{ij}$ gives
the rate at which node $i$ copies the state of node $j$. Different
definitions of the voter model dynamics provide clear
elements of how the concept of dynamical influence takes
into account the interplay between topology and dynamics:
For link update dynamics in an undirected network,
an ordered pair of nodes $(i,j)$ is chosen in each step and
node $i$ copies the state of node $j$. The rate matrix $K$
becomes then the adjacency matrix $A$. As a consequence
$c_i = 1/N$, the average magnetization $\sum_{i=1}^{N} c_i x_i$ is con-
served, and all nodes have the same dynamical influence
independently of the topological features of the network.
In the more standard node update voter dynamics, at each
step one node $i$ (having degree $d_i$) is selected at random
and copies the state of one of its neighbors $j$, also selected
at random. In this case $K_{ij} = A_{ij}/d_i$, so that $K_{ij}$ is no
longer a symmetric matrix, the conserved quantity is a
weighted magnetization and the dynamical influence
of node $i$ is proportional to its degree $d_i$.

For diffusive processes, the system is driven towards
a homogeneous final state with $x^* := x_i(\infty) = x_j(\infty)$
for all $i$ and $j$. Although $x^*$ takes continuous values,
each realization of the voter dynamics in a finite system
eventually reaches a homogeneous absorbing state with
either all nodes in the state $+1$ or all in the state $-1$. The
influence $c_i$ of a node weights the initial state of node $i$
in the probability of which of the two absorbing states is
reached. When all nodes are equivalent $x^*$ is just the
average of the initial values of the nodes, but otherwise
$x^*$ is given by the weighted average of the two absorbing
states with the probability of reaching each of them. The
value $c_i$ has an alternative interpretation as a stationary
density of a random walk.
The meaning of dynamical influence also manifests it-
self in the practical task of driving a system efficiently.
In the context of the voter model, this task might be phrased in
terms of the zealot problem. One considers a special directed
network in which a given node (the
zealot) does not copy the state of any of its neighbors.
The question is the efficiency of the zealot in driving all
other nodes to the zealot state. To show the broad applic-
ability of the dynamical influence concept, we address
this question of driving efficiency considering the problem
of phase-coupled oscillators described by the Kuramoto
model. Assuming all oscillators have the same in-
trinsic frequency $\omega$, the phase variable $x_i$ of oscillator $i$
advances as

$$\dot{x}_i = \omega + \sum_{j=1}^{N} K_{ij} \sin(x_j - x_i), \quad (6)$$

with a matrix $K$ of non-negative coupling strengths.
Around the synchronized state, phase differences are
small. Without losing generality, we choose $\omega = 0$. By
approximating each sin-term with its argument, a linear
homogeneous system as in Eq. (1) is recovered.

We study a scenario with initially all oscillators $i$ in
phase $x_i(0) = 0$. An additional node $a$ with constant
phase $x_a = \pi/2$ is added to the system and linked
through an additional edge to a chosen node $i$. We mea-
sure the time $T_i$ the system takes to reach the new
homogeneous state with $s_i = \pi/2$ for all nodes $i$. The
dynamical evolution of these systems is illustrated by
studying the motif in the inset of Fig. 3a. The global
phase $\psi(t)$ converges faster to the external forcing when
the driving is applied to the nodes with higher influence,
and the convergence of the different nodes depends on
their relative network position in relation to the driver.
In Fig. 3b, we show the results on a directed network
of phase oscillators connected as the network of regions
in the macaque cortex. The extremely high cor-
relation between dynamical influence and driving efficiency
clearly shows that influence is an excellent proxy to iden-
tify better targets for controlling global behavior, even in
non-linear dynamical systems. The extremely high
predictive power of dynamical influence for driving effi-
cy (rank order correlation of driving efficiency with
dynamical influence is 0.97, while 0.66 with degree ratio
and $-0.09$ with betweenness) clearly shows that influence
is an excellent proxy to identify better targets for
controlling global behavior, even in non-linear dynamical
systems.

To summarize, dynamical influence is a general cen-
trality measure which is not solely based on topology
but specifically designed for dynamical processes on com-
plex networks. For critical epidemic spreading, dynami-
cal influence is a good predictor of spreading capabilities.
For diffusion, dynamical influence quantifies the impact
of the dynamical states of single nodes on the asymp-
totic homogeneous state, and beyond that, it proves to
be a high-quality proxy for driving efficiency, uncover-
ing which are the best target nodes in real networks to
be forced in order to drive the system towards specific
states. In a broader context, the identification of these
targets has fundamental implications and practical ap-
lications on strategies with an interest in controlling
collective behavior, from social influence to biomedical
responses.

METHODS

Centrality measures

The degree $d_i$ of node $i$ is the number of nodes $i$ is
connected to. In directed networks, in- and out-degree
$d_i^\text{in}$ and $d_i^\text{out}$ are distinguished. For the matrix aver-
ing over all adjacency matrices of networks with fixed
node degrees, $c_i = d_i^\text{in}$ is a left eigenvector for the largest
eigenvalue. Likewise, the degree ratios $d_i^\text{out}/d_i^\text{in}$ form
a left eigenvector of the Laplacian matrix averaging over
all networks with given node degrees.

The betweenness centrality $b_i$ of a node $i$ quantifies
the fraction of shortest paths that pass through this node.

\[ b_i = \frac{1}{n(n-1)} \sum_{s\neq i \neq t} \frac{\lambda_{st}(i)}{\lambda_{st}} \]
It is defined as
\[ b_i = \sum_{(j,k)} \sigma_{jk}(i), \tag{7} \]
where the summation runs over all ordered node pairs \((j,k)\); \(\sigma_{jk}\) denotes the total number of shortest paths from node \(j\) to node \(k\); \(\sigma_{jk}(i)\) is the number of such paths running through node \(i\).

The shell-index \(k_i\) of a node \(i\) is derived from the consideration of the \(k\)-core \cite{10} for integer \(k \geq 0\). The \(k\)-core of a network is the largest induced subnetwork in which all nodes have degree at least \(k\). Starting from the full network, the \(k\)-core is obtained by deleting nodes (together with their edges) with degree strictly less than \(k\) until no such nodes are left. The shell-index \(k_i\) is the largest value \(k\) such that node \(i\) is contained in the \(k\)-core. In case of directed network, the \(k\)-core is based on the out-degree.

Epidemic models

We simulate the SIR model of epidemic spreading in the time-discrete version. Transitions between the three states (S,I,R) are as follows. If node \(i\) is in the S (susceptible) state and has \(\nu\) infected (I) neighbors at time \(t\), then node \(i\) remains susceptible with probability \((1 - \beta)^\nu\), otherwise \(i\) is infected at time \(t + 1\). If node \(i\) is in the infected state at time \(t\) then \(i\) is in the R (removed) state at time \(t + 1\). In the SIS model, at difference with SIR, a node infected at time \(t\) is susceptible again at time \(t + 1\). The probability of being removed in the SIR model does not enter in the linearized Equation \(4\) because it appears only in a second order term in the equation for \(x\). Therefore Equation \(4\) gives the same linear description for the SIR and SIS models.

The system is in an absorbing configuration if none of the nodes is infected. For both models, outbreak size is the number of nodes having been infected at least once before reaching an absorbing configuration. The spreading efficiency of node \(i\) is the average outbreak size when initiating the dynamics with node \(i\) infected and all others susceptible.

Rank order correlation

For a vector \(x \in \mathbb{R}^n\), the rank of component \(i\) is given by
\[ r_i(x) = 1 + \frac{|\{ j \neq i | x_j > x_i \}|}{n - 1} + \frac{1}{2} \frac{|\{ j \neq i | x_j = x_i \}|}{n - 1} \tag{8} \]
The rank order correlation coefficient \(\rho(x, y)\) between two such vectors \(x\) and \(y\) is the Pearson correlation coefficient between the rank vectors \(r(x)\) and \(r(y)\). Thus \(\rho(x, y)\) takes values in \([-1, 1]\) with \(\rho(x, y) = +1(-1)\) if and only if \(x\) and \(y\) are in a strictly increasing (decreasing) relation.

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