Collective Influence Algorithm to find influencers via optimal percolation in massively large social media

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We elaborate on a linear time implementation of the Collective Influence (CI) algorithm introduced by Morone, Makse, Nature 524, 65 (2015) to find the minimal set of influencers in a complex network via optimal percolation. We show that the computational complexity of CI is \(O(N \log N)\) when removing nodes one-by-one, with \(N\) the number of nodes in the network. This is made possible by using an appropriate data structure to process the CI values, and by the finite radius \(\ell\) of the CI sphere. Furthermore, we introduce a simple extension of CI when \(\ell \to \infty\), the CI propagation (CI\(_P\)) algorithm, that considers the global optimization of influence via message passing in the whole network and identifies a slightly smaller fraction of influencers than CI. Remarkably, CI\(_P\) is able to reproduce the exact analytical optimal percolation threshold obtained by Bau, Wormald, Random Struct. Alg. 21, 397 (2002) for cubic random regular graphs, leaving little improvement left for random graphs. We also introduce the Collective Immunization Belief Propagation (CI\(_B\)) algorithm, a belief-propagation (BP) variant of CI based on optimal immunization, which has the same performance as CI\(_P\). However, this small augmented performance of the order of \(1 - 2\%\) in the low influencers tail comes at the expense of increasing the computational complexity from \(O(N \log N)\) to \(O(N^2 \log N)\), rendering both, CI\(_P\) and CI\(_B\), prohibitive for finding influencers in modern-day big-data. The same nonlinear running time drawback pertains also to a Belief-Propagation-Decimation (BPD) algorithm by Mugisha, Zhou, arXiv:1603.05781. For instance, we show that for big-data social networks of typically 200 million nodes (eg. active Twitter users sending 500 million tweets per day), CI finds the influencers in less than 3 hours running on a single CPU, while the BP algorithms (CI\(_P\), CI\(_B\), and BDP) would take more than 3,000 years to accomplish the same task.

In Section II we introduce a generalized version of the CI algorithm, which we name Collective Influence Propagation (CI\(_P\)), that incorporates the information about nodes influence at the global level. Indeed, it can be seen as the limit version of CI when the radius \(\ell\) of the ball is sent to infinity. The CI\(_P\) algorithm allows one to obtain slightly better solutions to the problem, i.e., a smaller set of optimal influencers than CI. Remarkably, it is able to reach the exact optimal percolation threshold in random cubic graphs, as found analytically by Bau et al. However, this augmented performance comes at the expense of increasing the computational complexity of the algorithm from \(O(N \log N)\) to \(O(N^2 \log N)\). The same nearly quadratic running time pertains also to a Belief-Propagation-Decimation (BPD) algorithm recently suggested by Mugisha and Zhou in Ref. 6, as we show in Fig. 8. Based on this observation, CI remains the viable option for a fast and nearly-optimal influencer search engine in massively large networks. Quantitatively, a network of 200 millions nodes can be fully processed by CI (using a radius \(\ell = 2\)) in roughly 2.5 hours, while both CI\(_P\) and BPD would take a time of the order of 3,000 years to accomplish the task, as we show in Figs. 4 and 8.

In Section III we present yet another algorithm to solve the optimal influence problem, that we name Collective
I. IMPLEMENTING CI IN LINEAR TIME.

In this section we describe how to implement the CI algorithm to keep the running time $O(N \log N)$ even when the nodes are removed one-by-one.

CI is an adaptive algorithm which removes nodes progressively according to their current CI value, given by the following formula:

$$\text{CI}_I(i) = (k_i - 1) \sum_{j \in \partial B(i, \ell)} (k_j - 1), \quad \text{(1)}$$

At each step, the algorithm removes the node with the highest $\text{CI}_I(i)$ value, and keep doing so until the giant component is destroyed. A straightforward implementation of the algorithm consists in computing at each step the $\text{CI}_I(i)$ for each node $i$, sort these values, and then removing the node with the largest CI value. Despite its simplicity, this implementation is not optimal, as it takes a number of operations of the order $O(N^2 \log N)$.

However, the time complexity of the CI-algorithm can be kept at $O(N \log N)$ by using an appropriate data structure for storing and processing the CI values. The basic idea is that, after each node removal, we would like to recompute the CI of a $O(1)$ number of other nodes and we would like to avoid sorting and sorting again after each update, since we only need the largest CI value at each step, and thus is useless to have a completely sorted list of values. This idea can be realized by using a max-heap data structure.

Before to delve into the details, let us recall the definition of a "heap". A heap is a binary tree encoding a prescribed hierarchical rule between the parent node at level $h$ and its children nodes at level $h+1$, with no hierarchy among the children. In our specific case we use a heap with a max heap rule, i.e., each parent node of the heap stores a CI value greater or equal to those of the children, but there is no order between the left child and right one (see Fig. 1). The root node of the max heap stores automatically the largest CI value.

One more concept is needed, i.e., the concept of "heapification", which we shall be using often later on. Generally speaking, given a set of numbers $S = \{x_1, \ldots, x_N\}$, the heapification of the set $S$ is a permutation $\Pi$ of the elements $\{x_{\Pi(1)}, \ldots, x_{\Pi(N)}\}$ satisfying the following max-heap property:

$$x_{\Pi(i)} \geq x_{\Pi(2i)} \text{ AND } x_{\Pi(i)} \geq x_{\Pi(2i+1)} \quad \text{ (2)}$$

We call heapify($i$) the function which heapifies the CI values in the sub-tree rooted on node $i$. The aim of this function is to down-move node $i$ in the heap by swapping it with the largest of its children until it satisfies the max-heap property in the final location.

Having defined the main tools we are going to use in the implementation, we can now discuss the flow of the algorithm step by step, as schematized in Fig. 2.

**Step 1 - Computing CI.** To compute the $\text{CI}_I(i)$ value of node $i$ according to Eq. (1), we must find the nodes belonging to the frontier $\partial B(i, \ell)$ of the ball of radius $\ell$ centered on $i$ (we define the distance between two nodes as the number of edges of the shortest path connecting them). In an undirected network the nodes $j \in \partial B(i, \ell)$ can be found using a simple breadth-first-search (BFS) up to a distance $\ell$ from the central node $i$. First we visit the nearest neighbors of node $i$, which, of course, belong to $\partial B(i, 1)$. Then we visit all the neighbors of those nodes not yet visited, thus arriving to $\partial B(i, 2)$. We keep on going until we visit all the nodes in $\partial B(i, \ell)$. At this point we use the nodes $j \in \partial B(i, \ell)$ to evaluate $\text{CI}_I(i)$ using Eq. (1).

When all the CI values $\{\text{CI}_I(1), \ldots, \text{CI}_I(N)\}$ have been calculated, we arrange them in a max heap, as explained next.

**Step 2 - Building the max-heap.** We build the heap in a bottom-up fashion, from the leaves to the root. Practically, we first fill the heap with arbitrary values and then we heapify all the levels starting from the lowest one. In this way the root stores automatically the largest CI value.

**Step 3 - Removal.** We remove from the network the node having the largest CI value, and we decrement by one the degrees of its neighbors. The largest CI value is stored in the root of the max-heap. Therefore, after the removal, the root in the max heap has to be replaced by the new largest CI value. The easiest way to do this is...
FIG. 2: Flow of the CI algorithm. The first part of the algorithm, executed only once, consists of two steps: i) computing CI for each node, and ii) allocating the CI values in the max-heap. After that, it follows the main loop of the algorithm, which consists of three steps: iii) removing the node with highest CI value along with the root of the heap; iv) heapifying the heap starting from the new root (see Step3); v) updating the CI values of the perturbed nodes, and heapifying the sub-trees rooted on each updated node. The loop ends when the giant component is destroyed.

replacing the root with the rightmost leaf in the last level of the heap, decreasing the size of the heap by one, and heapifying the new root.

Step4 - Updating CI values. The removal of a node perturbs the CI values of other nodes, that must be recomputed before the next removal. The nodes perturbed by the removal are only the ones placed at distances 1, 2, ..., ℓ, ℓ + 1 from the removed one. In other words, only the nodes inside the ball B(i, ℓ + 1) change their CI values when i is removed, while the others remain the same (see Fig. [3]).

The CI values of nodes on the farthest layer at ℓ + 1 are easy to recompute. Indeed, let us consider one of this node and let us call k its degree. After the removal of the central node its CI value decreases simply by the amount k − 1. For nodes in the other layers at distance 1, 2, ..., ℓ, the shift of their CI values is, in general, not simple to assess, and we need to use the procedure explained in Step1.

When we modify the CI value stored in a node of the heap, it may happen that the new heap does not satisfy the max-heap rule. Therefore we have to restore the max heap-structure after each change of the CI values. More precisely, we proceed as follows. Let us consider one among the nodes to update. Assuming that the structure around the removed node is locally tree-like, the new CI values of the surrounding nodes can only be smaller than the old ones, and, consequently, we need to heapify only the sub-tree rooted on those nodes. We stress that the order of the update-heapification operations is important: each node update must be followed by the corresponding heapification, before updating the next node.

Step5 - Stopping the algorithm. To decide when the algorithm has to be terminated we use a very simple method, which allows one to avoid checking when the giant component G vanishes. The idea is to monitor the following quantity after each node removal:

$$\lambda(\ell; q) = \left( \frac{\sum_i \text{CI}_\ell(i)}{N\langle k \rangle} \right)^{1/(\ell+1)},$$  \hspace{1cm} (3)
where \( \langle k \rangle \) is the average degree of the network for \( q = 0 \). Equation (4) gives an approximation of the minimum of the largest eigenvalue of the non-backtracking matrix when \( Nq \) nodes are removed from the network [11]. For \( q = 0 \), it is easy to show that, for tree-like random graphs, \( \lambda(\ell; 0) = \kappa - 1 \), where \( \kappa = \langle k^2 \rangle / \langle k \rangle \). Removing nodes decreases the eigenvalue \( \lambda(\ell; q) \), and the network is destroyed when \( \lim_{\ell \to \infty} \lambda(\ell; q = q_c) = 1 \). Practically we cannot take the limit \( \ell \to \infty \), but for a reasonably large \( \ell \), the relaxed condition \( \lambda(\ell; q = q_c) = 1 \) works pretty well, as we show in Fig. 5. Therefore, we can stop the algorithm when \( \lambda(\ell; q) = 1 \). The advantage of Eq. (4) is that it can be updated on runtime at nearly no additional computational cost, and therefore does not require additional \( O(N) \) calculations needed to compute the giant component. Figure 6 shows the giant component attacked by CI and high-degree adaptive in a ER network of 100 million nodes.

### B. Reinsertion

We conclude this section by discussing a refinement of CI algorithm, which we use to minimize the giant component in the phase \( G > 0 \). This can be useful when it is not possible to reach the percolation threshold (where \( G = 0 \)), but one still wants to minimize \( G \) using the available resources, i.e., the maximum number of node removals at one’s disposal. The main idea is based on a reinsertion method, according to which nodes are reinserted in the network using the following criterion. We start from the percolation point, where the network is fragmented in many clusters. We add back in the network one of the removed node, which is chosen such that, once reinserted, it joins the smallest number of clusters. Note that we do not require that the reinserted node joins the clusters of smallest sizes, but only the minimum number of clusters, independently from their sizes. When the node is reinserted we restore also the edges with its neighbors which are in the network (but not the ones with neighbors not yet reinserted, if any). The procedure is repeated until all the nodes are back in the network. When implementing the reinsertion, we add back a finite fraction of nodes at each step. In our simulations we reinserted 0.2% of nodes at each step. Moreover we observed that even using a smaller fraction than 0.2%, we obtained the same results.

### II. CI PROPAGATION

In this section we present the CI-propagation algorithm (CI\(_P\)), which extends the CI algorithm to take into account the global information beyond the local CI sphere. However, the main idea of CI\(_P\) remains the same, i.e., minimizing the largest eigenvalue of the Non-Backtracking (NB) matrix [1]. Indeed, CI\(_P\) is obtained asymptotically from CI\(_L\) as \( \ell \to \infty \).

The NB is a non-symmetric matrix and it has different right and left eigenvectors. As we will see the right and left eigenvectors corresponding to the largest eigenvalue provides two different, yet intuitive, notions of node’s influence. The left eigenvector \( \vec{L} \) is a vector with \( 2M \)}
The interpretation of Eqs. (6) is the following. For each node $i$ the sum of all the incoming left messages $L_{k\rightarrow i}$:

$$\text{CI}_{IN}(i) = \sum_{k \in \partial i} L_{k\rightarrow i} .$$

The interpretation of this quantity comes directly from the recursive Eq. (3). Indeed, if we plug into (7) the recursion for $L_{k\rightarrow i}$ given by (1), and we keep on iterating $\ell$ times, we see that the influence of node $i$ is determined by the sum of all the messages $L_{\rightarrow \text{Ball}(i,\ell)}$ incoming into the ball of radius $\ell$ centered on $i$, which has an evident similarity with the usual CI definition.

Another possibility is to assign to node $i$ the sum of all the incoming right messages $R_{k\rightarrow i}$:

$$\text{CI}_{OUT}(i) = \sum_{k \in \partial i} R_{k\rightarrow i} .$$

This quantity is the dual of the previous one, and therefore we used the name $\text{CI}_{OUT}$. Indeed, by proceeding as before, i.e., plugging Eq. (5) into (8) and iterating $\ell$ times, we see that the influence of node $i$ is now determined by the sum of all the messages $R_{\rightarrow \text{Ball}(L,\ell)}$ outgoing from the ball of radius $\ell$ centered on $i$, which again bears a close similarity with CI. We could say that Eq. (7) measures the "IN-fluence" of node $i$, while Eq. (8) measures its "OUT-fluence". Since we believe that both measures do capture a specific aspect of the importance of a given node, we combine them in what we call the Collective Influence Propagation, which is defined as:

$$\text{CI}_P(i) = \sum_{k \in \partial i} \sqrt{L_{k\rightarrow i} R_{k\rightarrow i}} .$$

The quantity $\text{CI}_P(i)$ combines both the information received and the information propagated by node $i$. Having defined the main quantity of the $\text{CI}_P$ algorithm, we move to explain the few simple steps to implement it.

- 1) Start with all nodes present and iterate Eqs. (6) until convergence.
- 2) Use the converged messages $L_{i\rightarrow j}$ and $R_{i\rightarrow j}$ to compute the $\text{CI}_P(i)$ values for each node $i$.
- 3) Remove node $i^*$ with the highest value of $\text{CI}_P(i^*)$ and set to zero all its ingoing and outgoing messages.
• 4) Repeat from 2) until \( \lambda_{\text{max}} = 1 \).

The CI\(_P\) algorithm produces better results than CI. As we show in Fig. 7 for the case of a random cubic graph, CI\(_P\) is able to identify the optimal fraction of influencers, which is known analytically to be \( q_c = 1/4 \) \cite{4}. Unfortunately the CI\(_P\) algorithm has running time \( O(N^2 \log N) \) and thus cannot be scaled to very large networks, as we show in Fig. 8 where we also compare with the time complexity of the BPD algorithm of Mugisha, Zhou \cite{6} and with the original CI algorithm.

We close this section by noticing that CI\(_P\) is a parameter-free algorithm, i.e., it does not require any fine tuning and can be applied straight away due to its low programming complexity. The introduction of more parameters (like the temperature) may still improve the performance of the algorithm. While it may be an interesting technical problem, we did not develop further the CI\(_P\) algorithm, mainly because the introduction of external parameters would not reduce anyway the quadratic running time. Also the quasi-optimal performance of CI\(_P\) for finding minimal percolation sets in small systems in Fig. 7 leaves little improvement left, so that we do not develop the algorithm further.

![Graph showing G(q) for CI and CI\(_P\) algorithms](image)

**FIG. 7:** Giant components \( G(q) \) (red triangles and blue diamonds) computed with the CI\(_P\) and the CI\(_m\) algorithms, and the eigenvalue \( \lambda(q) \) (green crosses) computed with CI\(_P\), as a function of the removed nodes \( q \), in a Random Regular Graph of \( 10^5 \) nodes, and degree \( k = 3 \). The vertical line at \( q = 0.25 = q_c \) marks the position of the analytical exact optimal value of the percolation threshold \( \frac{1}{4} \).

### III. COLLECTIVE IMMUNIZATION

In this section we formulate the optimal percolation problem as the limit of the optimal immunization problem in the SIR –Susceptible-Infected-Recovered– disease spreading model \cite{5}, and we present the Collective Immunization (CI\(_m\)) algorithm or CI\(_{BP}\) based on Belief Propagation.

According to the SIR model, a variable \( x^t_i = \{S, I, R\} \) encodes the state of each node \( i \) at time step \( t \). A node in a state \( x_i = I \) stays infected for a finite time, and in this state, it may infect a neighboring node \( j \) if \( x_j = S \). After the infectious period, the infected node \( i \) recovers.

Nodes in state \( R \) stay in \( R \) forever, being immune to further infection. Thus in the long time limit, the disease state \( x^\infty_i \) of any node \( i \) is either \( R \) or \( S \). In this limit one can compute the marginals of \( x^\infty \) on any node, knowing the initial state \( x^0 \), in a ‘message passing’ manner. The message that node \( i \) passes to node \( j \) is the probability \( \nu_{i\rightarrow j}(x^\infty_i|x^0_i) \) that node \( i \) ends in state \( x^\infty_i \) knowing it starts in state \( x^0_i \), assuming that node \( j \) is absent.

According to the dynamic rule of SIR model, we have the following set of relations:

\[
\begin{align*}
\nu_{i\rightarrow j}(x^\infty_i = R|x^0_i = S) &= 1 - \nu_{i\rightarrow j}(x^\infty_i = S|x^0_i = S) \\
\nu_{i\rightarrow j}(x^\infty_i = S|x^0_i = R) &= 0 \\
\nu_{i\rightarrow j}(x^\infty_i = S|x^0_i = I) &= 0
\end{align*}
\] (10)

Therefore, it is clear that the knowledge of the sole \( \nu_{i\rightarrow j}(x^\infty_i = S|x^0_i = S) \) is enough to reconstruct the long time limit of the marginal of \( x^\infty_i \). Next, we assume that each node is initially infected with probability \( \gamma \), i.e., at
time 0 a randomly chosen set of $\gamma N$ sites are infected. We also introduce a binary variable $n_i$ for each node $i$, taking values $n_i = 0$ if node $i$ is immunized (i.e. removed in the language of optimal percolation), and $n_i = 1$ if it is not (i.e. present). For a locally tree-like interaction network (and when the clustering property holds), the probabilities (messages) received by node $i$ from its neighbors $j$ can be considered as uncorrelated. This allows one to calculate self-consistently the messages through the following equations:

$$
\nu_{i\rightarrow j}(x_i^\infty = S|x_i^0 \neq R) = (1 - \gamma) \prod_{k \in \partial i \setminus j} [1 - \beta (1 - \nu_{k\rightarrow i}(x_k^\infty = S|x_k^0 \neq R)) n_k],
$$

(11)

where $\beta$ is the transmission probability of the disease (or the spreading rate). In the end, we will be mainly interested in the limits $\gamma = 1/N$ and $\beta \to 1$.

The marginal probability that node $i$ is eventually susceptible given that node $i$ is not one of the immunizers is obtained through:

$$
\nu_i(x_i^\infty = S|x_i^0 \neq R) = (1 - \gamma) \prod_{k \in \partial i} [1 - \beta (1 - \nu_{k\rightarrow i}(x_k^\infty = S|x_k^0 \neq R)) n_k].
$$

(12)

From now on we drop the argument in the probabilities $\nu_{i\rightarrow j}$ and $\nu_i$, and we simply write $\nu_i(x_i^\infty = S|x_i^0 \neq R) = \nu_i$.

The best immunization problem amounts to find the minimal set of initially immunized nodes that minimizes the outbreak size $F = \sum_i n_i (1 - \nu_i)$. This problem can be equivalently solved by minimizing the following energy (or cost) function:

$$
E(\bar{\nu}) = \sum_i n_i \log [\nu_i(x_i^\infty = S|x_i^0 \neq R)].
$$

(13)

The energy function in Eq. (13) has the virtue of describing a pairwise model, and therefore is easier to treat. Indeed, substituting (12) into (13) one can rewrite the energy function as:

$$
E(\bar{\nu}) = \sum_{i<j} U_{ij}(n_i, n_j),
$$

(14)

where we drop an useless constant term. We found useful to make the following change of variables:

$$
n_i = \frac{1 - \sigma_i}{2},
$$

(15)

so that $\sigma_i = 1$ means that node $i$ is removed or immunized, and $\sigma_i = -1$ that it is present.

The minimum of the energy function (14) can be found by solving the following equations:

$$
\begin{align*}
\sigma_i &= \text{sign}(h_i), \\
h_i &= -\mu + \sum_{k \in \partial i} \max_{\sigma_k} \left\{ -U_{ik}(+1, \sigma_k) + \frac{h_{k\rightarrow i}}{2}\sigma_k \right\} - \max_{\sigma_k} \left\{ -U_{ik}(-1, \sigma_k) + \frac{h_{k\rightarrow i}}{2}\sigma_k \right\},
\end{align*}
$$

(16)

where the variable $h_i$ is the log-likelihood ratio:

$$
h_i = \log \left( \frac{\text{probability that } i \text{ is removed}}{\text{probability that } i \text{ is present}} \right),
$$

(18)

and $\mu$ is a parameter (chemical potential) that can be varied to fix the desired fraction of removed nodes $q$. The value of $\sigma_i$ is related to $h_i$ via the equation:

$$
\sigma_i = \text{sign}(h_i).
$$

(19)

Equations (11), (16), (17) and (19) constitute the full set of cavity equations of the immunization optimization problem analogous to optimal percolation since the best immunizers are those that optimally destroy the giant connected component. These equations can be solved iteratively as follows:

- Choose a value for $\mu$, $\gamma$, $\beta$, and initialize all the state variables $\sigma_i$ and $h^{i\rightarrow j}$ to random values.
- Then iterate Eqs. (11) until convergence to find the values of $\nu_{i\rightarrow j}$.
- Then iterate Eqs. (17) until convergence to find the values of $h_{i\rightarrow j}$.
- Compute the new $h^i$ using (16), and the the new state $\sigma^i$ of node $i$ via Eq. (19).
- Repeat until all the fields $\{h_i\}$ have converged.

In cases where the equations (17) do not converge, we use the reinforcement technique [3]. Once a solution to the equations have been found, the configuration $\sigma^*$ is the output of the algorithm: if $\sigma^*_i = 1$ the node is removed, and if $\sigma^*_i = -1$ it is present. The C1BP algorithm has the same performance as the C1P algorithm, as we show for the case of random cubic graphs in Fig. 7 reproducing the exact result of [4] for small system size and leaving virtually no improvement left for these systems. However, while it improves over CI, it suffers the same deficiency for large systems as CI and BDP since it is a quadratic algorithm which can be applied only to small networks.
IV. CONCLUSIONS

We have shown how to implement the CI algorithm introduced in [1] in nearly linear time when nodes are removed one by one. This is possible due to the finite radius $\ell$ of the CI sphere, which in turn allows one to process the CI values in a max-heap data structure. This trick avoids the full sorting of the CI values, thus saving exactly a factor $O(N)$.

Moreover, we have introduced $\text{CI}_P$, a slightly modified CI algorithm taking into account the global rearrangement of the CI values after each node removal, and, in this respect, it corresponds to the $\ell \to \infty$ limit of CI. We have also presented $\text{CI}_{BP}$, a new algorithm to solve the optimal percolation problem, which blends the dynamics of the SIR disease spreading model with message passing updating rules. The analysis of these algorithms (including BDP as well) reveals that the improvements over CI are small and, more importantly, they are made at the expense of increasing the computational complexity from linear (CI) to quadratic (BP) in the system size $N$, rendering BP unfit for large datasets.

Therefore, CI remains the viable option of a nearly-optimal-low-complexity influencer search engine, which is applicable to massively large networks of several hundred million of nodes, while the global $\text{CI}_P$ algorithm can still be used to find small corrections in small networks when time performance is not an issue. Furthermore, from a theoretical point of view, the simplicity of the CI analysis based on the NB eigenvalue remains as a good option for theoretical generalization of optimal percolation to more complicated topologies, as shown in [7] for brain network of networks with interdependencies and other more complex applications that are being presently developed.

[1] Morone, F. & Makse, H. Influence maximization in complex networks through optimal percolation. Nature 524, 65-68 (2015).
[2] Batagelj, V. & Brandes, U. Efficient generation of large random networks. Phys. Rev. E 71, 036113 (2005).
[3] Braunstein, A. & Zecchina, R. Learning by message passing in networks of discrete synapses. Phys. Rev. Lett. 96, 030201 (2006).
[4] Bau, S., Wormald, N. C. & Zhou, S. Decycling numbers of random regular graphs. Random Struct. Alg. 21, 397-413 (2002).
[5] Kermack, W. O. & McKendrick, A. G. A contribution to the mathematical theory of epidemics. Proc. Roy. Soc. Lo. A 115, 700-721 (1927).
[6] Mugisha, S. & Zhuo, H.J. Identifying optimal targets of network attack by belief propagation. [arXiv:1603.05781](arXiv:1603.05781)
[7] Morone, F., Roth, K., Min, B., Stanley, H. E. & Makse, H. A. A model of brain activation predicts the collective influence map of the human brain. arXiv.