Influential Node Ranking in Complex Networks Using A Randomized Dynamics-Sensitive Approach

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Abstract—Identifying the most influential nodes in information networks has been the focus of many research studies. This problem has crucial applications in various contexts including biology, medicine, and social science, such as controlling the propagation of virus or rumours in real-world networks. While existing methods mostly employ local neighbourhood features which heavily rely on the network structure and disregard the underlying diffusion dynamics, in this work we present a randomized sampling algorithm that not only takes into account the local and global structural features of the network, but also considers the underlying diffusion dynamics and its parameters. The main idea is to compute the influence of a node through reachability from that node in a set of random graphs. We use a hyper-graph to capture the reachability from nodes in the original network, and theoretically argue that the hyper-graph can be used to approximate the theoretical influence of nodes in the original graph with a factor of \( (1 - \epsilon) \). The performance of the proposed model is also evaluated empirically by measuring the correlation between the ranking generated by the proposed method and the ground-truth ranking. Our results show that the proposed method substantially outperforms state-of-the-art methods and achieves the highest correlation with the ground-truth ranking. While the generated ranking has a high level of uniqueness and uniformity, theoretical and practical analysis of the running time of the algorithm also confirm that the proposed method maintains a competitive running time in comparison to the state-of-the-art methods.

Index Terms—Influential Node Ranking, Complex Networks, Vital Node Identification, Influence Maximization, Randomized Sampling, Epidemic Analysis

1 INTRODUCTION

In recent years, much research has focused on studying the spreading process in complex networks [1-3][51], mainly because it can model the spreading phenomena in the real-world [4][54, 55]. Complex systems in general are difficult to model or control, due to inherent nonlinearity, coupling, chaotic behaviour, uncertainty, embedded stochastic patterns and parameter sensitivities, under multi-scale responses [56]. Identifying the influential nodes in a complex network is the first question when studying the spreading process [5], such as disease propagation [6], rumours diffusion [1], cascading failure [3, 7], and viral advertising [2]. When vital nodes act in a network, the impact quickly propagates to the whole network. Therefore, developing an accurate method for quantifying the importance of nodes in complex networks is of high theoretical and practical significance [8, 9]. For instance, development of such method is crucial for controlling a pandemic through restricting and treating the key nodes in a disease network [10, 11], stopping the diffusion of rumours through controlling the most important nodes in social networks [12], avoiding cascade failure by taking protective measures for the key circuits of the power network [13], accelerating information diffusion, or promoting new products.

When it comes to ranking nodes based on importance in a complex network, degree is the most straightforward and simplest indicator [14]. Although ranking nodes based on their degree has low computational cost and appears to be an efficient method for large-scale graphs, it suffers from low accuracy. To address the shortcomings of the degree centrality, other centrality measures have been proposed, such as betweenness centrality [15], and closeness [16]. However, not all of these methods are scalable to large-scale networks due to high computational complexity. Furthermore, they neither provide accurate results for many real-world networks. The idea of decomposing the network has been developed in methods such as K-Shell [17]. Following K-Shell, other methods including gravity centrality [18] and extended K-Shell sum [19] adopted the decomposition idea to rank nodes based on importance.

Kitsak et al., [17] showed that nodes in the core part of the network are more likely to be influential. Inspired by that, Chen et al. [20] proposed the coreness centrality measure. Using the k-Shell decomposition, the coreness method assigns many nodes to the same shell. However, nodes of the same shell may have different influence.
Furthermore, k-Shell may fail to identify influential nodes in core-less networks [21]. Often, methods based on k-coreness does not provide satisfactory performance. Recently, improved centrality measures, such as mixed degree centrality (MMD) [22], local structure centrality [23], neighbourhood coreness centrality [24], and H-index [25], have been proposed in which multiple measures were combined to derive a new measure.

In addition to the structural centrality measures that mainly focus on the neighbourhood information of the nodes to quantify influentiality, there are iterative refinement centrality measures, such as eigenvector centrality [26], cumulative nomination [27], PageRank [28], HITS [29] and their variants that take the influentiality of the neighbours of a node into account for computing the influentiality of nodes. Often, these methods assign a uniform start score to all nodes in the network and then refine the score through an iterative process to get to a steady state.

One major disadvantage of the centrality-based measures is that they do not take the properties of the underlying dynamical process into account. In other words, if the underlying dynamics change, ranking of the nodes based on centrality measures will stay the same. However, it has been shown that even for the same dynamics, under different dynamics parameters, no single centrality measure can always give the most accurate ranking of the nodes [30]. For example, in the Susceptible-Infected-Removed (SIR) dynamics where the spreading rate, $\beta$, is small, the degree centrality can better identify the influentiality of nodes, while the eigenvector centrality performs better when the spreading rate is close to the epidemic threshold $\beta_c$ [31]. To address this issue, alternative methods should also take into account the properties and parameters of the target dynamics. We refer to such methods as dynamics-sensitive methods. In this regard, Klemm et al. [31] proposed the dynamical influence measure which is the left eigen vector of the largest eigenvalue of the dynamics matrix, assuming a linear approximation of non-linear dynamics like SIR. On the same subject, Ide et al. [32] proposed similar dynamic-sensitive approach for the Susceptible-Infected- Susceptible (SIS) model, which is argued to be equal to a typical path counting method. In another work, Bauer and Lizier [33] proposed a method that directly counts the number of possible walks of various length in the SIR and SIS model where the dynamics properties are used to design the decaying faction of path weight.

In this manuscript, we propose a novel dynamics-sensitive method that employs a randomized sampling algorithm to generate influence paths. We treat each influence path as a hyper-edge of a hyper-graph that has the same nodes as the original network. We theoretically prove and empirically show that the degree of nodes in the hyper-graph is a good indicator of their influentiality. Our results show that the proposed randomized sampling approach yields state-of-the-art results, while the computational complexity is still comparable with the existing methods. We also show that the proposed method achieves an unseen stability in performance for different values of parameters of the underlying diffusion dynamics, a behaviour that is absent in the results of the existing dynamics-insensitive models.

2 RELATED WROKS

In this section, we review some of the most notable existing works about influential node ranking in more details. There are many factors that can affect the ability of a node to propagate its influence throughout the network such as the structure of its neighbourhood, its location in the network, the content and context of the message and many more [34]. Since obtaining contextual information is challenging in many cases, the structural and topology-based features of a network are primarily used for determining the influentiality of nodes in many of the existing methods, making these approaches independent of the underlying dynamical processes. The notion of centrality that assigns a real value to the nodes in a network is proposed for providing a measure for quantifying the vitality of the nodes [35, 36].

The most intuitive centrality measure is the degree centrality, where the importance of the nodes is quantified by the number of their neighbours. Although this measure appears to be very simplistic, but it can achieve surprisingly good performance, especially when the propagation rate is very small. In fact in the latter case, degree centrality outperforms some of the more sophisticated centralities such as the eigenvector centrality [31]. Later, an improved version of degree centrality, called LocalRank, was proposed by Chen et al. [20] that extends the idea behind the degree centrality and takes the information of the forth-order neighbours of the nodes into account. LocalRank algorithm has a lower computational complexity compared to the path-based centralities, yet outperforms path-based methods in special occasions [20]. Inspired by the fact that local interconnectedness has a negative correlation with the size of the propagation [37, 38], Chen et al. [39] proposed ClusterRank which takes into account the clustering coefficient of a node [40], as well as the number of neighbours. The clustering coefficient is used to incorporate the interconnectedness effect into the new centrality, as a large clustering coefficient is an indicator of the high interconnectedness and low influence. We use $CR(i)$ to denote the ClusterRank of node $i$. We have:

$$CR(i) = f(c_i) \sum_{j=1}^{k_{out}} (k_{j}^{out} + 1)$$

In the above formulation, $c_i$ is the clustering coefficient of node $i$, $f$ is a function of the cluster coefficient, and $k_{j}^{out}$ is the out degree of node $j$.

Recently, Kitsak et al. [17] introduced a new family of centrality measures where the focus is more on the location of the node in the graph rather than its degree and neighbourhood structure. They argue that if a node is located in the core part of the network, its influence is higher compared to other nodes that are located in the outer parts of the network. The new measure is referred to as coreness and is obtained by applying k-core decomposition in networks [41]. The k-core decomposition process is
as follows: given an input graph G, every isolated node with a degree of zero receive a coreness score of 0 and are then removed from the network. Next, all the nodes with a degree of one are removed from the network and will receive a coreness score of 1. Following the removal of nodes with degree of 1, the degree of other nodes will decrease by 1. Therefore, nodes with a residual degree less than equal to 1 should also be removed from the network. These nodes will receive a coreness score of 1 too. The process will continue by removing nodes with a residual degree of 2, and then removing all the nodes with a residual degree less than equal to 2 and so on. The coreness score of nodes is equal to the degree threshold by which nodes are selected for removal. Due to its low computational complexity, the k-shell decomposition method also known as the KS or the k-core method can be used for large-scale networks and in fact has many applications in real networks [22, 42].

The k-core method, however, only focuses on the residual degrees of the nodes and drops all the information about the removed nodes. In contrast, Zeng et al. [22] proposed a new decomposition method called mixed degree decomposition (MMD), in which both the residual degree of the nodes along with the exhausted degree of the nodes are considered when picking the nodes for removal. In fact, in each step, nodes are removed based on the mixed degree which is calculated through the following formulation:

\[ k^m = k^r + \lambda k^e \]

where \( k^m \) is the mixed degree, \( k^r \) is the residual degree, \( k^e \) is the exhausted degree, and \( \lambda \) is a tenable parameter between 0 and 1.

Another drawback of the k-core method is that it assigns the same coreness score to many nodes with different degree, which results in a ranking list where many nodes have the same rank. To address this issue, Bae and Kim [24] proposed a new measure that considers both the degree and coreness score of a node to calculate a new score. The main idea behind this centrality measure is the assumption that nodes which reside in the central part of the network and have a large number of neighbours are more vital. Based on this idea, the neighbourhood coreness is defined as follows.

\[ C_{nc}(v) = \sum_{w \in \Gamma(v)} ks(w) \]

where \( \Gamma(v) \) is used to denote the set of neighbours of node \( v \), and \( ks(w) \) shows the k-shell score of node \( w \). By adding the \( C_{nc} \) scores of all the neighbours of a node, the \( C_{nc+} \) score is defined recursively. We have:

\[ C_{nc+}(v) = \sum_{w \in \Gamma(v)} C_{nc}(w) \]

The \( C_{nc} \) method improves the traditional KS algorithm, but still shares some disadvantages with the main algorithm. Both of the KS method and the method proposed by Bae and Kim [24] disregard the iteration information. In fact, in these algorithms, some nodes may end up having the same coreness score with the coreness score assigned to them at different iterations. To address this issue, Wang et al. [43] proposed a method that also incorporates the iteration information by defining a k-shell iteration factor. For each node, the k-shell iteration factor is calculated using the following formula, where \( k \) is the coreness score of the node, \( n \) is the iteration in which the score is assigned to the node, and \( m \) is the total number of iterations for processing all nodes with coreness score \( k \).

\[ \delta_u = k(1 + \frac{n}{m}) \]

Using the k-shell iteration factor, the influence capability of a node \( u \) is defined as follows:

\[ IC_u = \delta_u.d_u + \sum_{v \in \Gamma(u)} \delta_v.d_v \]

where \( d_u \) is the degree of node \( u \), and \( \Gamma(u) \) is the set of all neighbours of node \( u \).

In a similar approach, Zareie et al. [44] changed the notion of k-shell iteration factor, and introduced shell clustering coefficient where for each node, the Pearson correlation between the shell vector of the target node and all of its neighbours are added together. For this new measure we have:

\[ SCC_u = \sum_{v \in \Gamma(u)} (2 - C_{uv}) + (2 \cdot \frac{\text{deg}(u)}{\text{max deg}(k)} + 1) \]

where \( C_{uv} \) is the correlation between the nodes \( u \) and \( v \). The cluster coefficient ranking measure for a node \( u \) is then defined as the sum of the the shell clustering coefficient for all of its neighbours.

Although many improvements have been made to the original KS algorithm, all of the KS-based methods still require global topological information of the network, which is not always available in real-world scenarios. We refer to such centrality measures as global centrality measures. In contrast, local centrality measures only require partial information of the network to be computed. H-index [45] is a local centrality measure that only requires the degrees of neighbours of a node. H-index was originally proposed for quantifying the impact of researches based on the number of citations that they received but was later extended to measure the influentiality of nodes in social networks [46]. In the extended version of H-index, a node \( v_i \) has an h-index of \( h \), if it has \( h \) neighbours all of which with a degree not less than \( h \) [46]. There are also a number of works that put together the notion of coreness along with other concepts to derive new ranking measures. The MCDE [47] method adds up a factor of coreness with a factor of degree, and a factor of entropy for ranking nodes based on their vitality. In a similar work, Zareie et al. [34] proposed the diversity-strength ranking where entropy of the KS score of nodes over the KS score of their neighbours is the main component of the new centrality.

There are many more centrality measures out there, but we have only limited the focus of this section to the state-of-the-art methods that have achieved outstanding ranking performance on a number of real and synthetic datasets. In the results section, we have compared the performance of our proposed model with some of the models that we briefly introduced in this section.
3 PROPOSED METHOD

Let us denote a network by graph $G = (V, E)$, where $V$ represent the nodes and $E \subseteq V \times V$ is the set of undirected edges between nodes. In this graph, if there is an edge $e = (u, v)$ connecting two nodes $u$ and $v$, we refer to $u$ and $v$ as neighbours. The notation $\Gamma(v)$ is used to represent the set of neighbours of a given node $v$. The number of neighbours of a node shows the degree of that node or, $\text{deg}_G(v) = |\Gamma(v)|$.

In this work we study the Susceptible-Infected-Removed (SIR) model [48], as the underlying dynamics that models the spreading process in the network. Given graph $G$ and a node $v$ as the infected node (known as the seed node), the SIR process is as follows.

- At round 1, only node $v$ is in the infected state, and the rest of the nodes are in susceptible state. At this round, node $v$ infects (influences) each of its neighbours with infection probability $\beta$, the influence probability. Influence probability is a parameter of the SIR model that is uniform for all nodes in this work.
- At round $t > 1$, all nodes that were at the infective state at the previous round move to the removed state. Nodes at the removed state will no longer influence other nodes or get influenced by others. Moreover, nodes that were at the susceptible state and become infected at round $t - 1$ will move to the infected state at round $t$. These newly infected nodes will now infect each of their neighbours with probability $\beta$.
- The influence propagation stops when no more nodes become infected at the last round.
- At the end of the propagation, the total number of nodes that are in removed state divided by the network size marks the influence of $v$.

Since influence propagation is a stochastic process, we use $I(v)$ to show the expected number of infected nodes in a propagation process. In fact, if we use $\text{Dist}(v, G, D)$ to show the distribution of the influence-spread of node $v$ in graph $G$ under dynamics $D$, $I(v)$ is a random sample from this distribution. Influential Node Ranking (INR) is to sort nodes of a network based on their influence [34]. The main drawback of the existing approaches for INR is the sensibility of the influence-spread (influentiality) estimation to the underlying dynamics. Most of the existing approaches disregard the distribution of the influence-spread under a given dynamics and only rely on structural properties of $G$ to estimate $I(v)$.

In this work, we introduce a novel dynamics-sensitive algorithm that efficiently estimates the influence of nodes and considers the underlying dynamics. To do so, we first show that the influence of a node in each graph $G$ under the SIR model is equivalent to reachability from that node in random sub-graphs of $G$. By learning from this lemma, we aim to estimate influence of nodes in $G$ through computing reachable nodes from them in sub-graphs of $G$. We build a hyper-graph on the nodes of $G$, with hyper-edges that model reachability between nodes in $G$. The hyper-edges are sampled using a randomized algorithm. We show that if enough random graphs are sampled, then a factor of degree of nodes in the hyper-graph well approximates the influence of nodes in $G$. We then conclude the theoretical section of the paper by giving a lower bound for the number of random sub-graphs to sample.

Definition 1 (Random Sub-graphs of $G$: $\beta$-graphs) Given $G = (V, E)$ as the original graph, a $\beta$-graph is a random graph with a subset of nodes of $G$ as $V_G$. Let $E_\beta$ denote edges of the $\beta$-graph where $\beta < 1$, then each edge $e \in E$ will be added to $E_\beta$ with probability $\beta$, and $V_\beta$ only includes nodes that have an active edge in $E_\beta$.

Lemma 1. The influence of a node $v \in V_\beta$ is equal to the number of nodes reachable from $v$ on $G_\beta$.

Proof. Each edge in $g_\beta$ is picked with a probability $\beta$ from the edges of the original graph $G = (V, E)$. Therefore, we can assume that each connected component, $CC_v$, on $g_\beta$ is an influence path under the SIR dynamics started from one of the nodes of that connected component, let’s say $v$. In other words, $|CC_v| - 1$ shows the number of nodes influenced by $v$. This is also equal to the number of nodes reachable from $v$ on $g_\beta$ as the connected components are mutually disconnected, and each node appears in at most one connected component.

Definition 2 ($G_\beta^v$): Let’s define $G_\beta^v$ as the set of all connected distinct $\beta$-graphs defined on a directed graph $G = (V, E)$, where $\text{deg}_{in}^v(v) = 0$, and $\text{deg}_{out}^v(v) = 1$ for all $g_\beta \in G_\beta^v$.

Lemma 2. Define $I_{SIR}(v, u, m)$ as the probability of influence of node $v$ on node $u$ under SIR dynamics over all paths of length $m$ in a Directed Acyclic Graph (DAG) $G$. Let us also define $r_{G_\beta^v}^v(v, u, m)$ as the probability of reachability of $u$ with paths of length $m$ in $G_\beta^v$. Then we have $I_{SIR}(v, u, m) = r_{G_\beta^v}^v(v, u, m)$.

Proof. We employ an inductive approach to prove this lemma. It is clear that the lemma holds for paths of length one, and $I_{SIR}(v, u, 1) = r_{G_\beta^v}^v(v, u, 1)$ is equal to the probability of existence of a link between $v, u$. Let us assume that the lemma holds for paths of length $m - 1$. To show that it generally holds, we assume that the $m + 1^{st}$ node $(v_{m+1})$ is the node with the highest rank ($h$) in the topological sorting of $G$. This assumption implies that $v_{m+1}$ does not appear neither in any propagation paths starting from $v_1$ to other nodes, nor in any reachability path starting from $v_1$ and ending in nodes other than $v_{m+1}$. In other words, it means that the reachability and influence probabilities of other nodes is independent from $v_{m+1}$. Given this, the influence probability of node $v_{m+1}$ is the probability that $v_{m+1}$ becomes influenced by any of its neighbours that have rank $h - 1$ in the topological sort order. This probability is equal to $I_{SIR}(v_1, v_{m+1}, m) = \sum_{u \in \Gamma^v(v_{m+1})} r_{G_\beta^v}^v(v_1, u, m - 1)$, where $G^T$ shows the
transpose of the graph $G$. Similarly, the probability for reachability of $v_{m+1}$ is equal to the probability that an edge exists between $v_{m+1}$ and one of its neighbours at rank $h-1$ that is already reachable from $v_1$. We can write $r^G_{\beta}(v_1, v_{m+1}, m) = \sum_{\gamma \in \Gamma(v_{m+1})} \beta^G_{\gamma}(v_1, u, m-1)$. According to the step assumption, we already know that the equality $I^{SIR}(v_1, u, m-1) = r^G_{\beta}(v_1, u, m-1)$ holds for any node $u$ on paths of length $m-1$. We see that the equality also holds for $m$, if we substitute $I^{SIR}$ with $r^G_{\beta}$ for paths of length $m-1$ in the equation for paths of length $m$, and the proof is complete.

Theorem 1. Let us take $I^{SIR}(v, G)$ as the theoretical influ-
entiality of node $v$ in a directed acyclic graph (DAG) $G$ over
the set of all paths generated by the underlying dy-
namics, SIR. Let us also use $R^G_{\beta}(v, G)$ to denote the theo-
retical reachability of $v$ in all connected distinct $\beta$-graphs, $G^\beta$.
Then, we have:

$$I^{SIR}(v, G) = R^G_{\beta}(v, G)$$

We prove this theorem by two different methods.

Proof 1. In the first method, we define theoretical influ-
entiality of a node as the sum of the influence of that node on each individual node in the original network. Since influence-spread under SIR dynamics is a stochastic pro-
cess, we sum over the expected influence of the spreader
node ($v$) on target node. We define the expected influence to be the probability of influence times the size of nodes
becoming influenced. For a target node $u$ (size of the nodes is $1$), this value is equal to the probability of influ-
ence of $v$ on $u$ over paths of different lengths, or:

$$I^{SIR}(v, u) = \sum_m I^{SIR}(v, u, m) \times 1$$

By summing over all target nodes, we can define the theo-
retical influence-spread of $v$ as follows:

$$I^{SIR}(v, G) = \sum_u I^{SIR}(v, u) = \sum_u \sum_m I^{SIR}(v, u, m)$$

According to Lemma 2, $I^{SIR}(v, u, m) = r^G_{\beta}(v, u, m) \forall u, m$, therefore we can rewrite the above equation as:

$$I^{SIR}(v, G) = \sum_u \sum_m r^G_{\beta}(v, u, m)$$

According to the definition, $R^G_{\beta}(v, G)$ is the theoretical
reachability from $v$ that is equal to the aggregated ex-
pected reachability for all nodes from $v$ over all random
graphs. $r^G_{\beta}(v, u, m)$ is defined as the reachability proba-
ability of $u$ from $v$ through paths of length $m$ over all ran-
dom graphs in $G^\beta$. To express $R^G_{\beta}(v, G)$ using
$r^G_{\beta}(v, u, m)$, we need to aggregate over all nodes and
paths of all lengths. We can write $R^G_{\beta}(v, G) = \sum_u \sum_m r^G_{\beta}(v, u, m)$, making $R^G_{\beta}(v, G)$ and $I^{SIR}(v, G)$ equal and the proof is complete.

Proof 2. In the second method, we start from $R^G_{\beta}(v, G)$. We define the theoretical reachability on $G^\beta$ as the ex-
pected reachability on all $g_{\beta} \in G^\beta$, we can write:

$$R^G_{\beta}(v, G) = \sum_{g_{\beta} \in G^\beta} P(g_{\beta}) |R(v, g_{\beta})|$$

where $|R(v, g_{\beta})|$ shows the number of nodes reachable
from $v$ on $g_{\beta}$, and $P(g_{\beta})$ shows the probability of $g_{\beta}$. Ac-

According to Lemma 1, $|R(v, g_{\beta})| = |I^{SIR}(v, g_{\beta})|$, therefore, we can write:

$$R^G_{\beta}(v, G) = \sum_{g_{\beta} \in G^\beta} P(g_{\beta}) I^{SIR}(v, g_{\beta})$$

Since the input graph is a DAG, each $g_{\beta} \in G^\beta$ corresponds
to an influence path under the SIR dynamics starting from
$v$. Therefore, we can substitute $g_{\beta} \in G^\beta$ with an SIR path
starting from $v$, denoted by $\pi^{SIR}_v$, and $G^\beta$ with the set
of all paths under SIR starting from $v$, denoted by $\Pi^SIR_v$. We can then rewrite the above equation as follows:

$$R^G_{\beta}(v, G) = \sum_{\pi \in \Pi^SIR_v} P(\pi^{SIR}_v) I^{SIR}(v, \pi^{SIR}_v)$$

In the above equation, the right-hand side is the theoreti-
cal influence-spread of node $v$ in the given graph $G$ under
the SIR dynamics and the proof is complete.

Theorem 1 suggests that computing reachability over $\beta$-
graphs is an alternative for computing influentiality un-
der SIR dynamics. One advantage for computing reacha-
bility over influence-spread is that it can be done in a non-

iterative way, as the edges of the $\beta$-graph are independent
and can be generated simultaneously. We use this insight
to design a randomized algorithm that estimates influen-
ciality through random generation of $\beta$-graphs.

To capture the aggregated reachability of nodes on a set of $\beta$-graphs ($G^\beta$) and accurately approximate the theoretical
reachability, inspired by the Reverse-Influence-Sampling (RIS) framework [49], we build a hyper-graph with hyper-edges
that represent reachability relation between nodes in the original graph. We then provide a theo-
retical guarantee that shows a factor of the degree of the
nodes in the hyper-graph is a $(1 - \epsilon)$ approximation
of the theoretical influentiality of the nodes in the original
network if enough $\beta$-graphs are sampled. Since Theorem 1
is stated for a special set of $\beta$-graphs that are connected
and distinct ($G^\beta$), we make some changes to the straight-
forward way of generating $\beta$-graphs to keep everything
close to the theory to the best extent possible. In this re-
gard, we define a threshold ($T$) for size of the connected
components generated in a $\beta$-graph, and only keep the
connected components that have a size greater than or
equal to this threshold. This threshold directly depends
on the underlying dynamics and its parameters and helps
the $\beta$-graph sampling method to generate connected
components that represent influence paths under the giv-
en dynamics. To illustrate, a random $\beta$-graph might have
many connected components of size one or two, while under a certain dynamic with a high influence probability, influence paths of length zero or one are very rare. In such cases, the threshold can help keeping only the connected components that have an equivalent influence path under the given dynamics. After applying the threshold, each \( -\text{graph} \) includes several connected components (Figure 1). In fact, a collection of random \( -\text{graphs} \) approximately generate the union of \( F \) for all nodes. We use the notation \( F \) for this collection, which is defined as \( F = \bigcup_{g \in G} F_g \). Algorithm 1, which we call it Randomized Influence Paths Selection (RIPS), shows the pseudo code of our proposed method. Figure 1 illustrates the steps of the algorithm on a toy network.

Algorithm 1. Randomized Influence Paths Selection (RIPS)

\textbf{Input}: A directed graph \( G = (V, E) \), a threshold \( T \) that depends on \( G \) and \( \beta \).

\textbf{Output}: A ranking of nodes in \( G \) based on their influenti-

\# Sampling \( -\text{graphs} 

1:  For \( \theta \) rounds:
2:  Build a \( -\text{graph} \) \( g \) by selecting \( m \) edges each with probability \( \beta \) from \( E \).
3:  \( G_\beta = \bigcup \{ |CC| > T : \forall CC \in g \} \)

\# Creating a hyper-graph from the sampled \( -\text{graphs} 

4:  \forall \text{cc in } G_\beta: \# \text{ adding one hyper-edge per connected component}
5:  \text{if uniform-weight:}
6:  \( W_H(u) = W_H(u) + 1 \quad \forall u \in \text{cc} \)
7:  \text{else:}
8:  \( W_H(u) = W_H(u) + |cc| \beta \deg_G(u) \quad \forall u \in \text{cc} \)
9:  Return \( \{u_1, u_2, ..., u_n\}: \forall i < j \}

The RIPS algorithm has two major steps. In the first step, a number of \( -\text{graphs} \) are randomly sampled from the input graph \( G \) and stored in \( G_\beta \). In the next step, the creation of a hyper-graph is simulated by creating a hyper-edge between the nodes that appear in the same connected component. There are two version of the RIPS al-

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Lemma 4. The expected influentiality of a spreader node \( v \) in a random beta-graph \( g_{\beta} \), can be calculated through the probability that a random node \( u \) belongs to the hyper-edge that includes \( v \), or

\[
E_{g_{\beta}^c} (I_{g_{\beta}}(v)) = \frac{n}{n} \Pr_{g_{\beta}^c} (u \in \epsilon_{\beta}(v))
\]

Proof. We use \( E_{g_{\beta}^c} (I_{g_{\beta}}(v)) \) to denote the expected influentiality which is the expected number of nodes that will become influenced if we start the propagation process from node \( v \). By dividing this number by \( n \) we have the probability of influence of \( v \) on a random node \( u \) in \( G \). According to lemma 2, the probability of influence of \( v \) on \( u \) is equal to the probability of reachability of \( v \) to \( u \). Therefore, we can write:

\[
\frac{E_{g_{\beta}^c} (I_{g_{\beta}}(v))}{n} = \frac{\Pr_{g_{\beta}^c} (u \in R(v, g_{\beta}))}{n}
\]

All the nodes that are reachable from \( v \) on \( g_{\beta} \) constitute a connected component that is also represented by a hyper-edge in RIPS. Therefore, we can substitute \( R(v, g_{\beta}) \) with \( \epsilon_{\beta}(v) \) in the above equality. We have:

\[
\frac{E_{g_{\beta}^c} (I_{g_{\beta}}(v))}{n} = \frac{\Pr_{g_{\beta}^c} (u \in \epsilon_{\beta}(v))}{n}
\]

Corollary 1. \( E(I(v)) = n \Pr (\epsilon_{\beta} \subseteq \epsilon_{H}(v)) \).

Proof. This corollary is a generalization to lemma 4. Assuming that the hyper-graph \( H \) is built by a sampling a number of \( \beta \)-graphs, the corollary is yielded by marginalizing over the sampled \( \beta \)-graphs. Let’s denote the set of sampled \( \beta \)-graphs by \( G_{\beta} \). Lemma 4 holds for every \( g_{\beta} \) in \( G_{\beta} \). If we take a sum over all \( g_{\beta} \) in \( G_{\beta} \) from both sides of the equation, the equality should still hold. According to lemma 4, we have:

\[
\frac{\sum_{g_{\beta} \in G_{\beta}} E_{g_{\beta}^c} (I_{g_{\beta}}(v))}{n} = \frac{\sum_{g_{\beta} \in G_{\beta}} \Pr_{g_{\beta}^c} (u \in R(v, g_{\beta}))}{n}
\]

By summing over \( g_{\beta} \), we can write:

\[
\frac{\sum_{g_{\beta} \in G_{\beta}} E_{g_{\beta}^c} (I_{g_{\beta}}(v))}{n} = \frac{\sum_{g_{\beta} \in G_{\beta}} \Pr_{g_{\beta}^c} (u \in \epsilon_{\beta}(v))}{n}
\]

The right-hand side of the above equation can also be expressed by \( \Pr (\epsilon_{\beta} \subseteq \epsilon_{H}(v)) \), where \( \epsilon_{H}(v) \) refers to the set of hyper-edges that include \( v \). By using \( E(I(v)) \) to represent the sum of the expected influentiality over all \( \beta \)-graphs, the corollary holds, and the proof is complete.

Corollary 2. \( E(I(v)) = n \frac{\deg_{\beta}(v)}{m_{\beta}} \), with \( m_{\beta} \) being the number of hyper-edges in the hyper-graph.

Proof. This corollary is yielded by expressing the right-hand side of Corollary 1 in terms of the parameters of the hyper-graph \( H \). The probability that a random node \( u \) belongs to \( \epsilon_{\beta}(v) \), the set of all hyper-edges that include \( v \), is equal to the number of hyper-edges that have \( v \), or \( \deg_{\beta}(v) \), over the total number of hyper-edges that exist in the hyper-graph. Since the hyper-graph \( H \) is built through random sampling of \( \beta \)-graphs, we use the expected value of \( \frac{\deg_{\beta}(v)}{m_{\beta}} \) to show the probability of a random node \( u \) belonging to \( \epsilon_{H} \).

Theorem 2. By using \( I_{\text{STR}}(v, G) \) to denote the theoretical influentiality of \( v \), the following inequality holds with probability \( 1 - n^{-k} \) for every node \( v \in G \) that satisfies \( E(I(v)) \leq I_{\text{STR}}(v, G) \) when \( \theta \geq \frac{\log 2 + \log n}{I_{\text{STR}}(v, G) c^2} (8 + 2\epsilon)n \).

Proof. Let’s use \( \phi \) to denote the probability that node \( v \) influences a random node \( u \). According to corollary 2 we have:

\[
\phi = \frac{E(I(v))}{n} = \frac{\deg_{\beta}(v)}{m_{\beta}}
\]

Let’s use the Chernoff bounds for the reverse inequality. We have:

\[
\Pr \left[ \left| \frac{\deg_{\beta}(v)}{m_{\beta}} - \frac{E(I(v))}{n} \right| \geq \frac{\epsilon}{1 - I_{\text{STR}}(v, G)} \right] \leq 2 \exp \left( -\frac{\epsilon^2 E(I(v))^2}{8n^2 \phi^2 + 2n \phi e I_{\text{STR}}(v, G)} \right)
\]

As discussed earlier, \( \frac{\deg_{\beta}(v)}{m_{\beta}} \) shows the number of hyper-edges that contain node \( v \) over the total number hyper-edges that \( v \) could participate in. Therefore, we can say that \( \frac{\deg_{\beta}(v)}{m_{\beta}} \) is the sum of \( \theta \) i.i.d. Bernoulli variables with a mean of \( \phi \). According to the assumption we know \( \phi \leq \frac{E(I(v))}{n} \). We also set \( \delta = \frac{\epsilon I_{\text{STR}}(v, G)}{2n\phi} \). According to the Chernoff bounds we have:

\[
\Pr \left[ \left| \theta \frac{\deg_{\beta}(v)}{m_{\beta}} - \phi \right| \geq \delta \phi \right] \leq \exp \left( -\frac{\delta^2 \phi \phi}{2 + 2\delta} \right) \leq \exp \left( -\frac{\epsilon^2 \theta E(I(v))^2}{8n^2 \phi^2 + 2n \phi \theta I_{\text{STR}}(v, G)} \right) \leq \exp \left( -\frac{\epsilon^2 \theta E(I(v))^2}{8n I_{\text{STR}}(v, G) + 2n \epsilon I_{\text{STR}}(v, G) \theta} \right) \leq \exp \left( -\frac{\epsilon^2 \theta E(I(v))^2}{8n I_{\text{STR}}(v, G) + 2n \epsilon \theta} \right) \leq \frac{1}{n^R}
\]

The right-hand side of the last inequality holds for any \( \theta \geq \frac{\log 2 + \log n}{I_{\text{STR}}(v, G) c^2} (8 + 2\epsilon)n \) and the proof is complete.
Theorem 3. Given an input graph \( G = (V, E) \), the RIPS algorithm approximates the theoretical influentiality of a given node \( v \) with a factor of \((1 - \frac{2}{m})\) with a probability of at most \((1 - n^k)\left(\frac{|E|_{\text{max}}(\deg(v))}{|E|}\right)^{d_{\text{p}}}/m\), where \( d_{\text{p}} \) is the minimum degree for node \( v \) in a random hyper-graph \( H \) that satisfy the inequality \( n \frac{d_{\text{p}}}{m} > E(I(v)) \), where \( |E|_{\text{max}} \) is the maximum size of a connected component in graph \( G \), \(|E|\) is the size of edges in \( G \), and \( \theta \geq \frac{\log k + \log n}{\log |E|} \left( |E| - 2e \right) n \).

Proof. Corollary 2 states that \( E(I(v)) = n E\left(\frac{\deg_H(v)}{m_H}\right) \). Given a finite number of \( m_H \) (for simplicity shown with \( m \)), there exist a finite number of hyper-graphs, \( \mathcal{H} \), with the same number of hyper-edges but different graph topology. By expanding the righthand side of corollary 2, we can write:

\[
E\left(\frac{\deg_H(v)}{m_H}\right) = \sum_{H_{E} \in \mathcal{H}_{m}} \Pr(H_{E}) \frac{\deg_{H_{E}}(v)}{m}
\]

We assume that \( d_{\text{p}} \) is the minimum degree for node \( v \) in a random hyper-graph \( H \) that satisfy the inequality \( n \frac{d_{\text{p}}}{m} > E(I(v)) \). For every degree \( \deg_H(v) \geq d_{\text{p}} \), where the inequality \( n \frac{\deg_H(v)}{m} < I^{\text{STR}}(v, G) \) does not hold, we can use Theorem 2 in the following way:

\[
E(I(v)) \geq n \frac{\deg_H(v)}{m} - \frac{\epsilon}{2} I^{\text{STR}}(v, G) \\
\geq I^{\text{STR}}(v, G) - \frac{\epsilon}{2} I^{\text{STR}}(v, G) \\
\geq \left(1 - \frac{\epsilon}{2}\right) I^{\text{STR}}(v, G)
\]

According to Theorem 2, the main inequality holds with probability \( 1 - n^k \), when \( \theta \geq \frac{\log k + \log n}{\log |E|} \left( |E| - 2e \right) n \). The probability for \( n \frac{\deg_H(v)}{m} \geq I^{\text{STR}}(v, G) \) is at most

\[
\left(\frac{|E|_{\text{max}}(\deg(v))}{|E|}\right)^{d_{\text{p}}}
\]

because \( v \) requires at least a degree of \( d_{\text{p}} \) in the hyper-graph \( H \), which means it should participate in at least \( d_{\text{p}} \) connected component, where the probability for participating in a connected component is \( \left(\frac{|E|_{\text{max}}(\deg(v))}{|E|}\right)^{d_{\text{p}}} \). Therefore, the theorem is held with a probability of at most \((1 - n^k)\left(\frac{|E|_{\text{max}}(\deg(v))}{|E|}\right)^{d_{\text{p}}}/m \), and the proof is complete.

The important takw-away from Theorem 3 is that RIPS approximates the theoretical influentiality of nodes with higher degrees with a higher probability. Moreover, the choice of the cut-off threshold \( T \) also affect the real possibility of having a node in \( H \) with a degree of at least \( d_{\text{p}} \), where a higher threshold leads to a higher probability. Practical experiments confirm that both of these insights are aligned with the empirical results. However, calculating the exact value for a few parameters like \( \theta, d_{\text{p}} \) or \( T \) is challenging as they require information such as theoretical influence-spread for every node, which is unknown. \( \theta \) in Theorems 2 and 3 is referring to the number of required hyper-edges (equivalently the overall number of connected components). We can use \( \theta \) to derive the theoretical number of required \( \beta \)-graphs by dividing that number to the number of connected components in each \( \beta \)-graph. Instead, we employ an empirical approach to find the right value for \( \theta \). Although Theorems 2 and 3 are stated for the unweighted version of the RIPS algorithm, our empirical results show that the weighted version of RIPS has a better performance, therefore we only report the results of the weighted version. We have tested the RIPS algorithm on 8 undirected graphs that are widely used in the literature and compared the results with the results of 10 existing methods. The results show that our model achieves the state-of-art performance on 6 graphs and gets a comparable performance on the other two graphs. A detailed discussion of the experimental results is included in the next section.

4 EXPERIMENTAL RESULTS

We have selected 8 graph datasets widely used in the literature to evaluate the performance of influential node ranking methods. We have included graph datasets of different sizes and internal structures to ensure that this selection covers a wide range of graph datasets with different types. Table 1 details the specifications of the datasets used in the experiments. In this table, \( \beta_{\text{est}} \) is the epidemic threshold reported for each dataset [24], and \( \beta \) is the influence probability that we used in our experiments. According to [24], the influence probability \( \beta \) should be greater than the epidemic threshold, \( \beta_{\text{est}} \), to end up having a reasonable size for the set of influenced people. That is why we have set \( \beta \) to be slightly bigger than \( \beta_{\text{est}} \) in Table 1.

Table 1. Details of the datasets used for the experimentation. Datasets with different size of nodes and different number of internal connections are selected.

| Dataset     | Number of Nodes | Number of Edges | Max Degree | Average Degree | \( \beta_{\text{est}} \) | \( \beta \) |
|-------------|-----------------|----------------|------------|----------------|------------------------|----------|
| Dolphins    | 379             | 914            | 49         | 4.823          | 0.025                  | 0.01     |
| Copertiled  | 453             | 4963           | 6.599      | 20.291         | 0.086                  | 0.001    |
| NetScience  | 356             | 1417           | 10         | 2.414          | 0.035                  | 0.003    |
| Euroroad    | 26,246          | 16,631         | 273        | 13.711         | 0.024                  | 0.003    |
| PowerGrid   | 14,941          | 6,594          | 19         | 2.669          | 0.028                  | 0.003    |
| PGP         | 10,680          | 24,316         | 205        | 4.554          | 0.053                  | 0.01     |

To highlight the pros and cons of our proposed model, we compare its results with the results of the state-of-the-art models reported in the literature. The baseline models include k-shell decomposition centrality (KS) [17], mixed degree decomposition (MDD) [22], semi-local degree and weighted entropy (CDE) [47], mixed core and semi-local degree and weighted entropy (MCDE) [47], extended neighbourhood coreness centrality (CNC) [24], k-shell iteration factor (Ks-IF) [24], diversity-strength ranking (DSR) [34], extended diversity-strength ranking (EDSR) [34], entropy based ranking measure (CRM) [44], and extended cluster coefficient ranking measure (ECRM) [44].
which we briefly introduced in section 2. We use three criteria for evaluation of our proposed method, namely, the correlation of the generated ranking with the ground-truth ranking, the uniqueness of ranking, and the computational complexity of the method, each of which are elaborated hereunder.

### 4.1 Ranking Correlation with Ground-Truth

The main criterion that we use for evaluation is the correlation of the ranking generated by the algorithms ($R$) with the ground-truth ranking obtained by numerical simulations. Since the real influentiality of the nodes are unknown, to obtain an approximation of a node’s influentiality, we simulate the underlying dynamics (in this case SIR) starting from that node. The number of iterations that we run the SIR simulation varies from dataset to dataset. For each dataset, we set this to be the smallest number that can get a unique ranking, where nodes with different influential capabilities have different ranks. The approximate influentiality obtained by simulating SIR is used to build the ground-truth ranking list ($GTR$). In this list, the node with the highest influentiality is ranked at the top, and the influentiality of each node is measured by the number of nodes that become influenced if the propagation starts from that node. We then use Kendall’s tau correlation coefficient (KT-correlation) [50] to measure the extent to which the generated ranking ($R$) matches with the ground-truth ranking ($GTR$). Kendall’s tau correlation coefficient takes a value between -1 and +1, where a bigger number shows a higher degree of correlation. For two lists of size $n$ we have:

\[
(GTR, R) = \frac{1}{n(n-1)} \sum_{i<j} sign((gtr_i - gtr_j)(r_i - r_j))
\]

In the above formula, $sign(x)$ is the sign function that takes 1 if $x > 0$, takes $-1$ if $x < 0$, and takes 0 if $x = 0$.

Table 2 shows the KT-correlation of rankings generated by each of the algorithms, including our proposed model, with the ground-truth ranking. For each dataset, the influence probability is set according to Table 1.

The results confirm that for a $\beta$ close to the epidemic threshold, our proposed model outperforms other algorithms for most of the datasets. For two datasets (Netscience and Hamster), the proposed model shows very close results to the top-performer. The major advantage of the proposed model is its dynamics sensitivity that enables $RIPS$ to generate a different ranking if the underlying dynamics or its parameters change. This characteristics of $RIPS$ is in contrast with the static nature of the other methods, as they generate the ranking only based on the structural properties of the input network and disregard the underlying dynamics.

Figure 2 shows the KT-correlation between the ranking generated by different models and the ground-truth for different values of $\beta$. Due to space limit, we have only included the results for one small-scale and one large-scale network, but the results for other datasets is very similar to the reported cases. We see that the KT-correlation for $RIPS$ stays in a small neighbourhood around its KT-correlation reported in Table 2, while the performance of other state-of-the-art models, including EDSR and ECRM significantly drops for low values of $\beta$.

| Dataset | KS   | MMD  | CNC+ | KS-IF | MCDE | DSR | EDSR | CRM | ECRM | RIPS |
|---------|------|------|------|-------|------|-----|------|-----|------|------|
| Dolphins| 0.7957 | 0.7812 | 0.8619 | 0.8410 | 0.8321 | 0.8884 | 0.8754 | 0.8584 | 0.9325 | 0.9426 |
| Copperfiled | 0.8691 | 0.8206 | 0.9125 | 0.8725 | 0.8604 | 0.8525 | 0.8742 | 0.8301 | 0.9328 | 0.9330 |
| Netscience | 0.5797 | 0.5606 | 0.6966 | 0.8364 | 0.6183 | 0.6804 | 0.8167 | 0.8458 | **0.9083** | 0.8971 |
| Elegansa | 0.7683 | 0.7301 | 0.8109 | 0.6962 | 0.7564 | 0.7681 | 0.7121 | 0.6595 | 0.7989 | **0.8614** |
| Euroroad | 0.602 | 0.5998 | 0.7188 | 0.8071 | 0.6385 | 0.7473 | 0.839 | 0.7886 | 0.8694 | **0.8818** |
| Hamster | 0.7165 | 0.702 | 0.8193 | 0.8787 | 0.725 | 0.814 | 0.8819 | 0.8669 | 0.9 | **0.8574** |
| PowerGrid | 0.5456 | 0.5494 | 0.6564 | 0.7668 | 0.5841 | 0.6826 | 0.7722 | 0.7453 | 0.839 | **0.8395** |
| PGP | 0.4893 | 0.4776 | 0.6733 | 0.6913 | 0.489 | 0.5964 | 0.6991 | 0.6554 | 0.7264 | **0.7303** |

Table 2. The Kendall-Tau correlation with the ground-truth ranking for the rankings generated by baseline methods and the proposed method.
This behaviour suggests that these models are tuned to only work for a certain range of $\beta$. As it can be seen, MMD and MCDE are among the top performing models for low values of $\beta$. This is because when $\beta$ is low, the length of the influence path is short and the first-order neighbours play an important role in the diffusion process. Therefore, methods that only consider the first-order neighbours, such as MDD and MCDE, achieve good performance. However, as the $\beta$ increases, we can see that the performance of MDD and MCDE declines significantly. The results also imply that as the size of the network increases, the correlation score of all of the methods drop. This is probably due to the fact that ranking nodes of a larger network is more challenging, as there is a higher chance of having nodes with similar properties that should be assigned with the same rank, while it is difficult for the algorithms to identify these similar nodes and give them equal ranks. The top performing models among the baselines such as DSR, EDSR, CRM and ECRM are showing good performance around the epidemic threshold while their performance drop at both ends of the graph. This behaviour suggests that these models are tuned to only work for a certain range of $\beta$, and using them other values of $\beta$ requires significant changes in the model.

### 4.2 Uniqueness of Ranking

Uniqueness of ranking is the second criterion that we use for the evaluation of the models. An ideal ranking should assign unique ranks to each of the nodes in the network, when the influentiality of the nodes are different. Monotonicity relation ($M(R)$) [24] is a metric that is widely used in the literature for measuring the uniqueness of ranking. Monotonicity relation for ranking list ($R$) is defined as follows:

$$M(R) = 1 - \left( \frac{\sum_{r \in R} n_r \times (n_r - 1)}{n \times (n - 1)} \right)^2$$

with $n$ being the number of unique ranks in $R$, and $n_r$ being the number of nodes with the same rank $r$. $M(R)$ gets a value between 0 and 1, where a bigger value indicates greater uniqueness and uniformity for the ranking.

Table 3 shows the monotonicity relation values for ranking lists generated by different models. The results show that the RIPS algorithm achieves the best performance across all datasets.

Moreover, the ranking generated by RIPS achieves absolute uniqueness for three of the small and medium scale networks, while achieving an almost unique ranking for three other datasets. Its lowest performance in terms of ranking uniqueness is on Euroroad dataset, which is a not so dense, medium scale network. The reason is that there are many nodes in Euroroad with the same degree and potentially similar structural properties that are hard to distinguish between.

To show the distribution of nodes at different ranks, we also plot the fraction of nodes that have the same rank.

| Datasets | KS | MMD | CNC+$^*$ | KS-IF | MCDE | DSR | EDSR | CRM | ECRM | RIPS |
|----------|----|-----|---------|-------|------|-----|------|-----|------|------|
| Dolphins| 0.6538 | 0.8584 | 0.9409 | 0.9842 | 0.9365 | 0.9979 | 0.9968 | 0.9895 | 0.9968 | 1.0  |
| Copperfield| 0.7338 | 0.8888 | 0.9792 | 0.9977 | 0.9555 | 0.9997 | 0.9994 | 0.9981 | 0.9994 | 1.0  |
| NetScience| 0.6643 | 0.7925 | 0.943 | 0.9895 | 0.9034 | 0.995 | 0.994 | 0.9864 | 0.9941 | 1.0  |
| Eleganza| 0.715 | 0.8117 | 0.9765 | 0.9988 | 0.9486 | 0.9987 | 0.9985 | 0.9968 | 0.9984 | 0.9999 |
| Euroroad| 0.243 | 0.4442 | 0.6954 | 0.9099 | 0.6852 | 0.968 | 0.9919 | 0.9331 | 0.9792 | 0.9986 |
| Hamster| 0.8779 | 0.8895 | 0.9756 | 0.9851 | 0.9544 | 0.9857 | 0.9856 | 0.9845 | 0.9855 | 0.9993 |
| PowerGrid| 0.3614 | 0.5927 | 0.7997 | 0.9517 | 0.7566 | 0.9996 | 0.9932 | 0.9529 | 0.9876 | 0.9999 |
| PGCP| 0.5093 | 0.6193 | 0.9032 | 0.981 | 0.6856 | 0.9996 | 0.9999 | 0.9786 | 0.9971 | 0.9998 |

Table 3. The $M(R)$ measure for rankings generated by different methods for various datasets. The proposed method outperforms every other model.

The ECRM that has the best correlation with ground-truth among the baselines is being outperformed by the DSR and EDSR methods.
over the total number of nodes. Figure 3 shows the ranking distribution of different models. We have plotted the ranking distribution for two medium and large scale networks that had low \(M(R)\) reported in Table 3, but the results for other networks is also very similar. According to the two plots, our proposed method achieves a uniform distribution of nodes at different ranks with assigning a slightly larger number of nodes to the highest ranks. However, the distribution of ranking for other methods is far from being uniform; most of them assign too many nodes to low ranks and have no nodes with ranks greater than a certain number. In fact, networks that have lower average degree for nodes are divided into less shells when performing a shell-decomposition over the graph. Therefore, methods such as KS, MMD and CNC+, which only rely on shell-index have difficulties assigning nodes to unique ranks. For a graph with around 1100 nodes, the highest rank that these methods assign to the nodes is 80, which means a majority of the nodes share the same rank somewhere between rank 10\(^{th}\) and 50\(^{th}\). KS-IF is performing much better than KS, MMD and CNC+ as it uses iterations over the k-shell algorithm. MCDE is also performing good, and at points even better than KS-IF, mainly because it also takes local information into account. Although ECRM was the top-performer among the baselines in achieving a high correlation with the ground-truth, it achieves the baselines in achieving a high correlation with the ground-truth, in terms of uniqueness of ranking, it achieves into account. Although ECRM was the top-performer among the baselines in achieving a high correlation with the ground-truth, it achieves the baselines in achieving a high correlation with the ground-truth, in terms of uniqueness of ranking, it achieves into account. Although ECRM was the top-performer among the baselines in achieving a high correlation with the ground-truth, it achieves the baselines in achieving a high correlation with the ground-truth, in terms of uniqueness of ranking, it achieves into account. Although ECRM was the top-performer among the baselines in achieving a high correlation with the ground-truth, it achieves the baselines in achieving a high correlation with the ground-truth, in terms of uniqueness of ranking, it achieves into account. Although ECRM was the top-performer among the baselines in achieving a high correlation with the ground-truth, it achieves the baselines in achieving a high correlation with the ground-truth, in terms of uniqueness of ranking, it achieves.

4.2 Computational Complexity and Run-Time Analysis

Computational complexity accounts for the order of processing time required for running an algorithm and is usually expressed as a function of the input size to the algorithm. In this study, if we assume an input network of \(|V|\) nodes and \(|E|\) connections, Table 4 shows the computational complexity of each of the baseline methods along with the proposed method.

| Method | Computational Complexity |
|--------|-------------------------|
| KS     | \(O(|V|^2)\)            |
| MMD    | \(O(|V|^2)\)            |
| CNC+   | \(O(|V|^2 + |E|)\)     |
| KS-IF  | \(O(|V|^2 + |E|)\)     |
| CDE    | \(O(|V|^2 + |E|)\)     |
| MCDE   | \(O(|V|^2 + |E|)\)     |
| DSR    | \(O(|V|^2 + 6|E|)\)    |
| EDSR   | \(O(|V|^2 + 7|E|)\)    |
| CRM    | \(O(|V|^2 + 2V + |E|)\) |
| ECRM   | \(O(|V|^2 + 2V + 2|E|)\) |
| RIPS   | \(O(|V| \log|V| + 2|E|)\) |

Table 4. Computational complexity of different methods stated in terms of the size, \(|V|\), and density, \(|E|\), of the input network.

As it can be seen, a majority of the models have a component of \(|V|^2\) in their computational complexity. This factor of \(|V|^2\) originates from the k-core decomposition algorithm that is used in these methods. The term \(|E|\) in the computational complexity of some of the methods denotes that there is a traversal over all the connections. Such methods use the information of all the neighbours of a node when computing the score for that node. For examples, the KS-IF method adds the KS-score of all the neighbours of a node to compute the KS-IF score. A similar idea is employed in other methods with a factor of \(|E|\) in their computational complexity. Our algorithm has three major steps. In the first step which is \(\beta\)-graph sampling, a Bernoulli trial with success rate of \(\beta\) is accomplished for each edge. The computational complexity of this step is \(O(|E|)\). Then the connected components in the resulting \(\beta\)-graph are identified and hyper-edges corresponding to the connected components are added to the hyper-graph. The computational complexity of this step is \(O(V + |E|)\). Finally, nodes are
The computational complexity of the latter step is $O(|V| \log |V|)$, with all the steps adding up to an overall computational complexity of $O(|V| \log |V| + 2|E|)$. Our proposed method achieves a comparable computational complexity compared to the baselines and state-of-the-art methods. It is because that all the other methods except k-core decomposition assume all of their algorithm, while our algorithm uses a randomized sampling approach. Although $RIPS$ has a competitive computational complexity, its practical run time depends on the choice of $\theta'$, or the number of $\beta$-graphs. A bigger number of sampled $\beta$-graphs helps a better approximation of the theoretical in 1 atity at the cost of a higher computation time.

Figure 4 shows the impact of changing the number of sampled $\beta$-graphs on the running time and correlation with the ground truth for the $RIPS$ algorithm. As it can be seen, the running time of $RIPS$ elevates as the number of nodes in the network, or the number of sampled $\beta$-graphs increase. The change to the correlation with the ground-truth is however slight after the first few iteration, namely from 200 $\beta$-graphs onwards. This fact suggests that a small number of randomized $\beta$-graphs is sufficient to include every node in the final hyper-graph. By comparing the rank correlations of the $RIPS$ as shown in Figure 4-b with the rank correlations of the baselines as in Table 2, we see that a $RIPS$ model 7 with 200 sampled $\beta$-graphs outperform all baseline methods except $ECRM$, while maintains a very competitive practical running time in comparison to the running time of the baseline methods (see Table 4). With 200 sampled $\beta$-graphs, the $RIPS$ algorithm achieves a running time of 1.69 seconds on Elegansa dataset while the $DSR$, $EDSR$ and $CRM$ methods have a running time of 1.39, 1.30, and 0.58 on this dataset respectively. The results of the practical running time confirm the theoretical analysis of the computational complexity of the models, and also shows that only for a small number of $\beta$-graphs, the $RIPS$ algorithm can achieve state-of-the-art performance in terms of correlation with the ground-truth in a reasonable time, while the uniqueness of ranking is also maintained.

Table 5. Practical running time of baselines on various datasets. $DSR$ and $EDSR$ methods are the top performers among the baselines in terms of uniqueness of ranking have the highest running time.

| Datasets | KS | MMD | CNC+ | KS-IF | MCDE | DSR | EDSR | CRM | ECRM |
|----------|----|-----|------|-------|------|-----|------|-----|------|
| Dolphins | 0.02139 | 0.07239 | 0.002942 | 0.003684 | 0.011502 | 0.056571 | 0.062266 | 0.047088 | 0.049503 |
| Copperfield | 0.003829 | 0.01627 | 0.006884 | 0.008379 | 0.021543 | 0.141674 | 0.149331 | 0.120207 | 0.123724 |
| NetScience | 0.00861 | 0.041476 | 0.015917 | 0.020446 | 0.064821 | 0.454396 | 0.478023 | 0.277087 | 0.281722 |
| Elegansa | 0.016111 | 0.083277 | 0.033338 | 0.038469 | 0.117644 | 1.390531 | 1.30345 | 0.581637 | 0.595031 |
| Euroroad | 0.016798 | 0.062323 | 0.03033 | 0.043149 | 0.139569 | 1.965506 | 1.991379 | 0.473582 | 0.486616 |



7 CONCLUSIONS

With the ever-increasing growth of the online social networks, addressing the key questions of the complex networks, such as vital node identification, has attracted much attention. Most of the existing methods for influential node identification and ranking rely only on the structural properties of the network and disregard the underlying diffusion model. One may customize the diffusion models to capture the real-life dynamics in a given complex network, but with the existing structural-based vital node identification methods, the impact of changing the diffusion model will not be seen in the generated rankings. In this research, we proposed a randomized dynamics sensitive method, called $RIPS$, for influential node ranking under the $SIR$ dynamics. To the best of our knowledge, we are the first to provide a theoretical guarantee for the quality of the solution to the influential node ranking problem. Our results confirm that the ranking of the proposed model changes as the parameters of the underlying dynamics, $\beta$, changes. While the performance of state-of-the-art models drop for low values of $\beta$, the performance of our proposed algorithm stays within a small neighbourhood of its performance on low and high values of $\beta$. Moreover, the proposed model also achieves the best performance in terms of uniqueness of ranking, outperforming the state-of-the-art model, $ECRM$, by far while maintaining a competitive running time. Future works can study the applicability of a dynamics sensitive model on other dynamics such as linear threshold, independent cascade or $SIS$. Moreover, more theoretical study can be accomplished on finding the number of rounds, $\theta'$, required for the $RIPS$ to obtain an approximate solution, or on the cut off threshold, $T$, that is used to prune some of the connected components of a $\beta$-graph.

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