On the Role of Central Individuals in Influence Propagation

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Abstract: Recently, the influence of individuals in complex networks received the attention of several fields of science. In the context of influence spreading, the understanding of the role and importance of each individual can be used to control the spread of memes. By considering centrality measures as defining factors of individual importance, this paper investigates the relationship between the importance of an individual and its role in the propagation of influence within and over a network. In order to do so, we used degree measures, betweenness centrality, closeness centrality, eigenvector centrality and clustering coefficient over four different real graphs. The Min-SEIS-Cluster model was employed in order to simulate the spread of memes, which involve cutting connections to minimize an epidemic. The results revealed a high correlation between individual importance and prominence on influence propagation, and the potential to utilize centrality measures to identify which connections should be cut off in specific application scenarios.

1 INTRODUCTION

Complex networks have been subject to extensive investigation in several domains. They are typically modeled using the concepts from graph theory, which pervades computer science and mathematics. However, many advances in the field have been influenced other branches of science, mainly the social and natural sciences. Complex networks can be employed in the analyses of a wide array of network-like structures such as electrical power grids, the Internet, and social networks as well as in the analyses of phenomena occurring within them, such as blackouts, computer viruses and the spread of ideas in groups of individuals (Newman, 2004; Strogatz, 2001).

Many complex networks exhibit interesting patterns. While some systems (mostly theoretical ones) display elevated levels of regularity or randomness, (Watts and Strogatz, 1998) demonstrated that a multitude of real networks manifests the *small-world property*, characterized by a low average shortest path length and high clusterization. To measure how clustered together the network is, Watts and Strogatz developed the *clustering coefficient*, which determines how many neighbors of a node are also neighbors of each other.

Other measures that evaluate the structure of networks have been developed and applied in multiple studies. Examples include *modularity*, which evaluates the division of the network in groups or communities (Newman, 2004); *assortativity*, which quantifies the likelihood of similar or different individuals to be connected to each other (Newman, 2003); and *centrality*, which attempts to describe how important or influential a (central) individual is.

Centrality has been studied in the context of human communications (Bavelas, 1948), trade routes, and communication in city urban development planning (Pitts, 1965), organizations design (Beauchamp, 1965) and many other fields such as medicine, to analyze and mitigate the spread of contagious diseases, and psychology and sociology, to understand leadership and influence, and also to comprehend the diffusion of ideas and behavior between individuals, known as memes (Dawkins, 1976).

Many different methods for measuring centrality have been proposed in the literature. One of the simplest and earliest methods is known as *degree*, which represents the number of connections an individual has with others. An individual that has an elevated number of connections can be viewed as someone with a high communication activity (Freeman, 1978). Another measure, proposed by (Bavelas, 1948), determines how strongly an individual acts as a “control

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point" or "bridge" among others, i.e. how many paths connecting two individuals pass through that individual; appropriately, it was named *betweenness* (Freeman, 1978). An additional measure, described by (Bavelas, 1948) and formally defined by (Sabidussi, 1966), calculates the sum of distances from each individual to every other. This measure was named *closeness*, and represents how independent an individual is (Freeman, 1978).

There are several works that analyze the social relationship among individuals in complex networks (Baldoni et al., 2015; Dhamal et al., 2015; Duarte et al., 2015; Pathania and Karlapalem, 2015; Tsang and Doucette, 2015). This work proposes to apply metrics of centrality in the examination of the dynamics of the spread of memes in complex networks, modeled as undirected and unweighted graphs, specifically in the context of minimizing the spread of memes. Here, we aim at understanding the correlation between the centrality of an individual and her role in the propagation of influences, as well as applying centrality measures to develop techniques that improve the process of contagion mitigation.

This remainder of the paper is organized as follows. Section 2 describes the epidemic model used in this work and the measures used to evaluate the importance of the individuals. Section 3 presents the methods employed to analyze the spread of memes in networks and the examination of the collected data. Section 4 concludes this paper, offering a summary of our results and directions for further investigation.

2 RELATED WORK

In the context of disease transmission networks, (Bell et al., 1999) examined the applicability of centrality measures using the following methods. In the analysis of HIV infection probability, they applied a network of 22 cocaine injectors and sexual partners who were at risk of being infected with HIV. Their work compared values of vulnerability and infectivity, which determined the probability of being infected and infecting others, to the centrality of the individuals, and through simulations, detected that the correlation varied significantly between measures and also as the number of cycles of the simulation increased.

(Kimura et al., 2009) explored the problem of influence maximization. They used two models: Independent Cascade and Linear Threshold, which simulated the propagation of influences in discrete steps with a specific number of individuals initially active (infected). In the Independent Cascade model, each connection between individuals is given a weight, and for each step, every active individual tries to spread the infection to their neighborhood with a chance given by the weight of each connection. In the Linear Threshold model, the parents of every individual are given weight. At each step, every inactive individual has the sum of the weights of their active parents computed, and if the value exceeds a specific threshold, the individual becomes active. They proposed an approximate algorithm based on bond percolation, which obtained results very similar in quality to a conventional hill-climbing algorithm in significantly less time.

(Weng et al., 2013) studied how the structure of a network affects the diffusion of memes, using data collected from the microblogging Twitter. Their findings suggest the capability to predict the virality of memes is much higher when the community structure of a network is taken into account, and that viral memes spread to multiple communities with relative ease, like simple contagions.

(Noble et al., 2015) investigated the relationship between centrality and the performance of individuals in problem-solving systems through computational simulations. Their work used the agent-based models Particle Swarm Optimization, Fully Informed Particle Swarm, Memetic Networks and Dynamic Search Range, and represented the problem as thirty-dimensional real-valued functions. They identified a high linear correlation between the centrality of an individual and its contribution to the resolution of the problem, particularly when the agent can exploit her position in the network.

2.1 The Min-SEIS-Cluster Epidemic Model

The Min-SEIS-Cluster problem uses the infection model SEIS (Susceptible, Exposed, Infected, Susceptible) that is based on the states of SEIR, but instead of removing the infected individuals, the individuals become susceptible again (de Santiago et al., 2016). This problem considers that each individual belongs to one cluster. These clusters are used to represent the infection and exposition for each social group within the network. In groups of friends, the infection could be spread more often than in groups composed of coworkers.

The problem also uses a parameter k to define the limit of relationships that must be cut off to lead to minimal infection over the execution time. Therefore, search methods can find the set of k edges that minimize the infection when they are cut off.

The problem Min-SEIS-Cluster is defined as a tuple $(G, C, T, \chi, \phi, k, \varepsilon, \lambda)$, where $G = (V, E)$ is the network composed of a set of individuals V and the set of edges between them E; C is the set of all clusters of the network, composed of disjoint subsets of V; the total time of spreading T, which is a natural number; $\chi = \{P_c \mid c \in C\}$ is the set of probability functions of an individual infecting an adjacent when both are inside the same cluster i, where $P_i : t \to [0,1]$ for each $P_i \in \chi$, where $t \in [0,T]$; $\phi : t \to [0,1]$ is the probability function of an individual infecting an adjacent when they are not within the same cluster, where $t \in [0,T]$; k is the maximal number of edges that could be cut from G; the exposition time function $\varepsilon : t \to \mathbb{Z}^+$ calculates the Exposition state duration for each period, where $t \in [0,T]$; the infection time function $\lambda : t \to \mathbb{Z}^+$ calculates the duration of the infection, where $t \in [0,T]$.

2.2 Measures and Centrality

The centrality of an individual in a network expresses how important, powerful and influential they are concerning others. Many different methods to determine the centrality of an individual have been proposed in the literature, but to the best of our knowledge, there is no consensus about their quality and the relationship between them (Noble et al., 2015). For this paper, we selected five well-established techniques to evaluate the centrality of the network's individuals; their characteristics and formal definitions are specified in the next subsections.

2.2.1 Degree

Degree is a ubiquitous concept in graph theory. It is defined for each vertex as the amount of vertices that have edges incident with it (Bondy, 1976). Formally, the degree of an individual α_i is defined as follows:

$$DEG(\alpha_i) = \sum_{j=1}^{n} \varphi(\alpha_i, \alpha_j), \tag{1}$$

where $\varphi(\alpha_i, \alpha_j) = 1$ if the two individuals are connected with each other and $\varphi(\alpha_i, \alpha_j) = 0$ otherwise.

2.2.2 Betweenness Centrality

The betweenness centrality of a node is defined by (Freeman, 1978) as the frequency of shortest paths (geodesics) between every node which pass through the node being measured currently. It is defined for an individual α_i as:

$$BET(\alpha_i) = \sum_{\alpha_i \neq \alpha_j \neq \alpha_k} \frac{\sigma_{\alpha_j \alpha_k(\alpha_i)}}{\sigma_{\alpha_j \alpha_k}}, \tag{2}$$

where $\sigma_{\alpha_j \alpha_k}$ is the number of shortest paths between α_j and α_k and $\sigma_{\alpha_j \alpha_k(\alpha_i)}$ is the amount of such paths that pass through α_i.

2.2.3 Closeness Centrality

Closeness indicates whether or not an individual depends on others to receive or transmit messages, a measure that is given by how small the distances (shortest paths) between them and other individuals are (Freeman, 1978). Mathematically, it is defined for an individual α_i as:

$$CLO(\alpha_i) = \frac{1}{\sum_{j=1}^{n} d(\alpha_i, \alpha_j)}, \tag{3}$$

where $d(\alpha_i, \alpha_j)$ is the distance of the shortest path between α_i and α_j.

2.2.4 Eigenvector Centrality

(Bonacich, 1972) proposed a measure of centrality based on the adjacency matrix A of a graph, whose values are $a_{ij} = 1$ if the individuals α_i and α_j are connected and $a_{ij} = 0$ if they are not. The centrality of an individual α_i is given by λx_i, where λ is the largest eigenvalue of the adjacency matrix A and x is its corresponding eigenvector. Formally, eigenvector centrality is defined for an individual α_i as:

$$EIG(\alpha_i) = x_i, \qquad Ax = \lambda x. \tag{4}$$

The author argues that eigenvector centrality might offer a better assessment of the importance of an individual, since unlike other measures, it takes into account the importance of other individuals as well (Bonacich, 2007).

2.2.5 Clustering Coefficient

Proposed by (Watts and Strogatz, 1998), the clustering coefficient is not strictly defined as a measure of centrality. However, they have shown that infectious diseases spread more rapidly in small-world networks; due to that result, we have chosen to include clustering coefficient as a metric of the importance of an individual. For simplicity, it is also referred to as a centrality measure.

Clustering coefficient is defined as the fraction of the number of connections existent in the neighborhood of an individual α_i over the total amount of such connections that could exist, which is equal to $k_{\alpha_i}(k_{\alpha_i} - 1)/2$ for undirected graphs, where k_{α_i} is the degree of the individual. Mathematically, this metric can be defined as:

$$CCF(\alpha_i) = \frac{2\,\delta(\alpha_i)}{k_{\alpha_i}(k_{\alpha_i} - 1)}, \tag{5}$$

where $\delta(\alpha_i)$ denotes the number of neighbors of α_i that are connected with each other.

3 EXPERIMENTS AND RESULTS

This section presents the methodology used in the experiments. We carried out two main experiments. The first one identified correlations between centrality measures of section 2.2 and the number of infections suffered or caused. In the second, we identified methods to select connections in the network for removal based on the centrality of the individuals and examined the distinctions between these methods and the original Min-SEIS-Cluster heuristic.

All our experiments used the real graphs of Table 1. The column "Id" shows the reference id used in this paper. The column "Graph" shows the instance name (Batagelj and Mrvar, 2006), the column "#Clusters" shows the number of clusters found in the instance, and "#Nodes" and "#Edges" show the number of nodes and edges of the instance, respectively. The clusters used in the tests were obtained by the Louvain method heuristic for Modularity Maximization community detection problem (Blondel et al., 2008).

Table 1: Instances used in the experiments.

Id	**Graph**	**#Clusters**	**#Nodes**	**#Edges**
1	Karate	2	34	78
2	Dolphins	7	62	159
3	Celegansneural	6	297	3592
4	Email	43	1113	5451

3.1 Correlation of Centralities

In the first experiment, the Min-SEIS cluster heuristic (de Santiago et al., 2016) was tested with the parameter $k \in \{0.1|E|, 0.5|E|\}$ and $T = 100$. The data was collected from 400 solutions. The results can be divided into two different correlations. The first was about the correlation between the centrality measure and the number of infections received; and the second investigated the correlation between the centrality score and the number of caused infections.

The results of the first are shown in Table 2 and Figure 1. Mainly in the largest instance, Table 2 shows positive correlations between the number of infections suffered and the centrality measures. In contrast, the clustering coefficient measure displays a very strong negative correlation in the Celegans Neural instance. The scatter plots of Figure 1 shows each individual, its centrality score, and the number of infection suffered. For the two largest instances, it is to corroborate the results from Pearson correlation of Table 2. Except by the clustering coefficient, all measures presented a positive correlation between the number of suffered infections and the centrality score.

The results of the second kind of experiment are shown in Table 3 and Figure 2. Table and Figure show a similar result. For almost all measures, there is a positive correlation between the number of infections caused and the centrality score. However, the clustering coefficient once again displayed a negative correlation.

These results show that individuals with a high centrality score have a larger chance to be infected by a meme, or pass an infection for their neighbors. So, if we used this information in a network of individuals, what kind of behavior will the infection present? Some experiments to find answers to this question are described in the following subsection.

Table 2: Pearson's r score between the centrality score and the number of infections suffered by individuals.

	$^k/_{\|E\|}$	**1**	**2**	**3**	**4**
BET	(10%)	0.656	0.478	0.196	0.489
	(50%)	0.585	0.422	0.226	0.527
CCF	(10%)	-0.415	0.337	-0.800	0.053
	(50%)	-0.373	0.265	-0.831	0.033
CLO	(10%)	0.368	0.453	0.445	0.750
	(50%)	0.297	0.458	0.489	0.792
DEG	(10%)	0.662	0.648	0.465	0.714
	(50%)	0.482	0.634	0.517	0.751
EIG	(10%)	0.272	0.396	0.579	0.671
	(50%)	0.077	0.499	0.635	0.735

Table 3: Pearson's r score between the centrality score and the number of infections caused by individuals.

	$^k/_{\|E\|}$	**1**	**2**	**3**	**4**
BET	(10%)	0.806	0.481	0.884	0.766
	(50%)	0.796	0.440	0.902	0.774
CCF	(10%)	-0.270	0.324	-0.568	-0.061
	(50%)	-0.272	0.214	-0.582	-0.063
CLO	(10%)	0.523	0.494	0.957	0.681
	(50%)	0.559	0.610	0.969	0.689
DEG	(10%)	0.922	0.737	0.977	0.865
	(50%)	0.933	0.738	0.989	0.872
EIG	(10%)	0.682	0.381	0.924	0.739
	(50%)	0.713	0.619	0.938	0.748

3.2 Identifying which Connections to Cut

In the original presentation of the Min-SEIS-Cluster model, Santiago et al. (de Santiago et al., 2016) proposed a heuristic to minimize the spread of infections based on the Monte Carlo concept, which generated random solutions (connections to be cut) of size k until the terminating condition was reached. Although

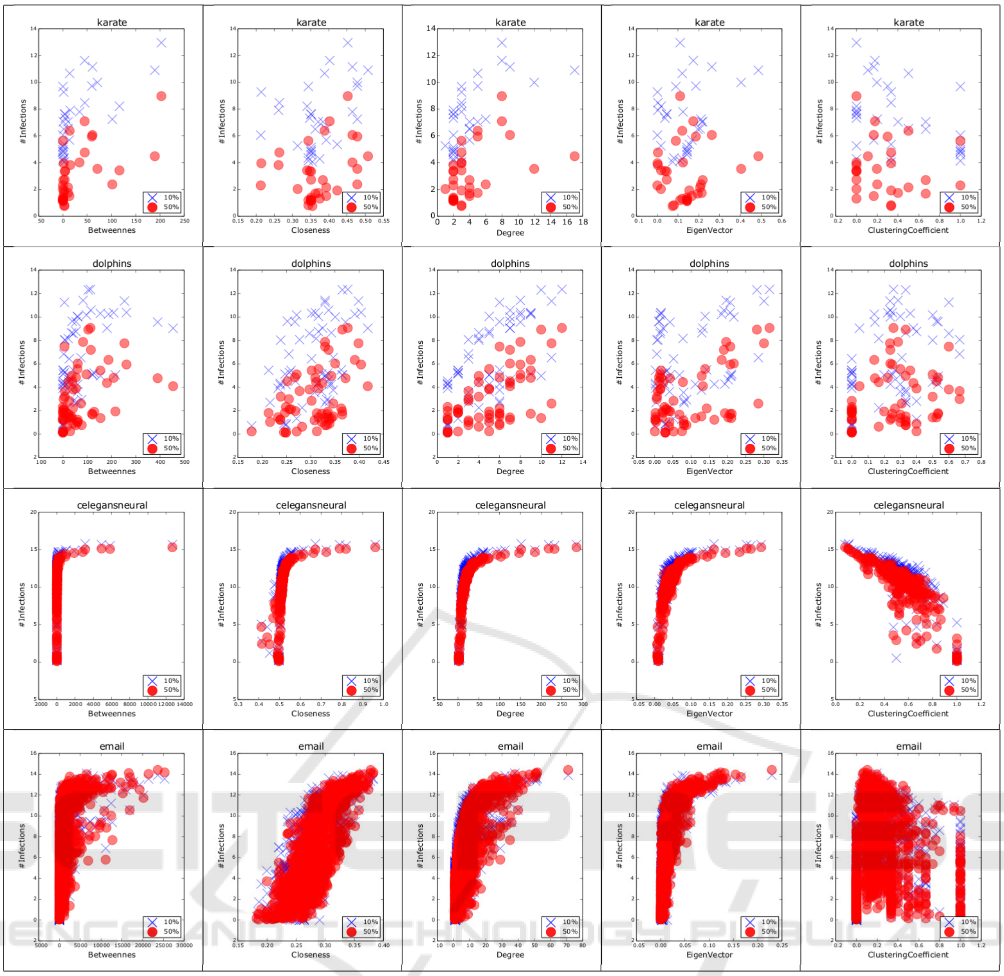

Figure 1: Correlation between centrality measures and the number of infections that each node suffered. The blue and red marks are assigned to experiments with 10% and 50% of edges removed respectively.

that method produced interesting results, it was rather unreliable, due to the following reasons: *i)* the complete randomness of the search, which does not employ any criterion to determine which region of the search space will be explored, an aspect that is especially harmful due to the large number of possible solutions, which is given by $\binom{|V|}{k}$; and *ii)* the running time of the algorithm, which needed to execute multiple simulations of the infection model for each randomly chosen solution and did not offer any guarantee of a minimum amount of iterations needed to improve a solution.

Examining the notion of the centrality of individuals in a network, we have come to hypothesize that centrality measures could be utilized to determine which connections should be cut to minimize the propagation of influence. Individuals with elevated centrality values tend to be very prominent in the network, either because they know many other individuals, are situated in strategic positions or have very dense neighborhoods; all of these properties might be significant in the spread of an epidemic. We also chose to investigate to what extent an individual is involved in the spread of memes if it is *not* central.

Taking these observations into account, we propose an algorithm to select connections for removal based on the centrality of each individual in the network, defined formally in Algorithm 1. As inputs, the algorithm takes the network, k (the number of connections to be selected), $measure \in \{DEG, BET, CLO, CCF, EIG\}$ and $ordering \in \{ascending, descending\}$. Its output is the set of selected connections to be cut from the network. First, the set of connections $solution$ is declared as an empty set. Then, k connections are selected through the procedure detailed in the following.

The centrality of every individual in the network is calculated according to the *measure* parameter and stored in the set C, composed by the individuals of

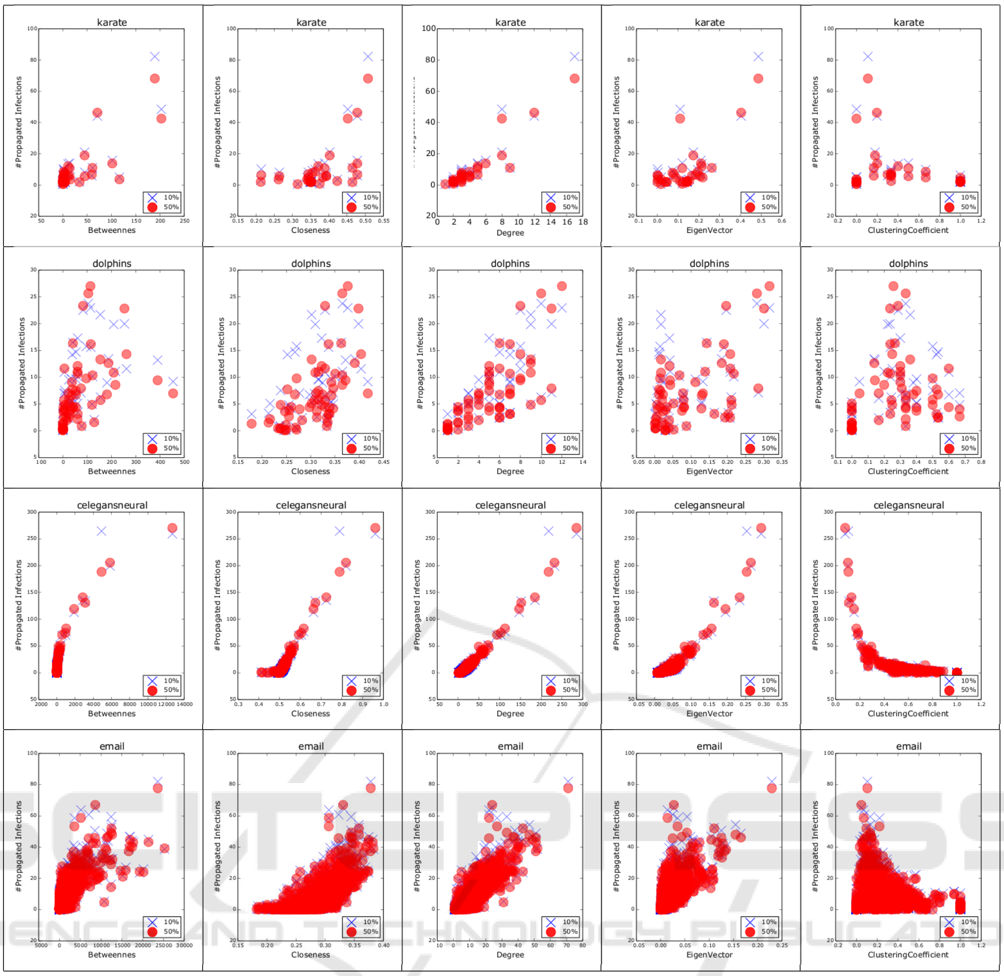

Figure 2: Correlation between centrality measures and the number of infections that each node caused. The blue and red marks are assigned to experiments with 10% and 50% of edges removed respectively.

the network and their corresponding centrality. Then, the set C is sorted in order of the centrality of the individuals, conforming to the parameter *ordering*: if ascending order is chosen, then C_1 is the least central individual of the network; otherwise, C_1 is the most central individual. Afterward, we choose the first individual of C whose degree is greater than zero and store it under the symbol α. This is the first extremity of the connection selected for removal.

Next, the neighbors of individual α are assembled into the set N, with the same structure as the set C. Then, the set N is ordered in the same manner C was. The second extremity of the connection is then established as N_1, the least or most central individual in the neighborhood of α, depending on the parameter *ordering*. This connection is thus inserted into the set *solution* to be later removed from the network.

Algorithm 1: Solution generation based on centrality.

```
procedure GEN($network, measure, ordering, k$)
    $solution \leftarrow \emptyset$
    while $k > 0$ do
        $C \leftarrow calcCentrality(network, measure)$
        $sort(C, ordering)$
        $\alpha \leftarrow$ first element of $C$ with degree $> 0$
        $N \leftarrow neighbors(\alpha)$
        $sort(N, ordering)$
        $connection \leftarrow (\alpha, N_1)$
        $solution \leftarrow solution \cup \{connection\}$
        $k \leftarrow k - 1$
    end while
    return $solution$
end procedure
```

3.3 Analysis of the Algorithm

To validate the proposed method of generating solutions based on the centrality of individuals, extensive simulations were performed on the real networks presented in table 1 using the Min-SEIS-Cluster model. Six sets of experiments were carried out utilizing the five centrality measures described in subsection 2.2 and the conventional random method presented in the original paper (de Santiago et al., 2016). Each experiment was run with $k \in \{0.2\,|E|,\ 0.5\,|E|\}$ and $\mathit{ordering} \in \{\mathit{ascending},\ \mathit{descending}\}$ and was repeated 60 times for every method and value of k, and for each experiment, 100 different sets of initially infected individuals ($n = 5$) were randomly chosen, totalizing 6000 simulations per experiment. Since our proposed method is deterministic and always generates the same solution given a network and a centrality measure, the same solution was tested in all 60 runs; in the original version of the algorithm, 60 randomly generated solutions were tested. Every test consisted of removing connections in the network as determined by the solution and simulating the epidemic for 100 steps. The results obtained through these experiments, described by the mean amount of infections observed over the 60 runs together with its standard error, are demonstrated in Figure 3 for both values of k. The rightmost column displays the result obtained through the original random method; as such, the distinction between ascending and descending order should be ignored.

3.3.1 Descending Order

We observed a rather unexpected outcome: in the majority of experiments, removing connections between the most central individuals did not reduce the number of infection events; rather, even more infections occurred in comparison with the original method. This behavior is particularly noticeable when the experiments were executed with $k = 0.2\,|E|$, where for three of the four networks, every measure employed with the exception of clustering coefficient (CCF) displayed the aforementioned behavior. The only instance where the distinction was less sharp was on the "Dolphins" network, in which the usage of the measures of clustering coefficient and closeness centrality (CLO) offered slightly better results, while betweenness centrality (BET) presented an equivalent amount of infections. In the instances "Email" and "Celegansneural", however, generating solutions based on the clustering coefficient of the individuals offered rather positive results, with approximately 21% less infection events occurring along the simulations.

When k was set to $0.5\,|E|$, slightly different results could be noted: in the "Email" network, solutions generated through betweenness centrality (BET) offered a much better reduction in the number of infection events, surpassing the random method by approximately 22%; an even greater reduction was noticed when using the measure of clustering coefficient (CCF), with 33% less infections than the random method. On the other hand, for the "Celegansneural" network, betweenness centrality continued to produce worse results than the random method, but clustering coefficient was exceptionally efficient, producing approximately 46% less infection events than the original method. This result is likely related to the density of the "Celegansneural" network, which is significantly higher than the other three networks. A similar distinction was also observed in the results obtained in the experiments involving the correlation between centrality and the suffering and causing of infections (Section 3.1), where a sharply negative correlation was observed. The effectiveness of betweenness centrality (BET) could also be noted in the "Dolphins" network, where a reduction of approximately 34% in comparison with the random method was observed. In the "Karate" network, the usage of the clustering coefficient (CCF) also produced a significant reduction of approximately 33%, while the other measures were not very useful.

3.3.2 Ascending Order

Perhaps the most surprising result was the performance of the removal of connections between the *least* central individuals. Except when using the measure of clustering coefficient (CCF), every single experiment using measures of centrality presented better results than the original, random method. In the smaller networks ("Karate" and "Dolphins"), the improvement was not very pronounced when $k = 0.2\,|E|$, with an average of approximately 13% less infection events. However, when $k = 0.5\,|E|$, the usage of closeness centrality (CLO) in the "Karate" network offered 38% less infections than the random method, slightly outperforming clustering coefficient in descending order; however, clustering coefficient in ascending order produced unsatisfactory results, causing more infections than the random method. In the "Dolphins" network, every measure performed reasonably well, including the clustering coefficient, with an average of approximately 25% less infections.

For the larger networks ("Email" and "Celegansneural"), the improvement obtained from removing connections between peripheral individuals was even more accentuated. An interesting behavior present in the "Celegansneural" network is that every measure was very similar to each other in terms of performance: for $k = 0.2\,|E|$, every measure except clustering coefficient offered approximately 19% less infections than the random method, while $k = 0.5\,|E|$ produced a remarkable reduction of 48%. Also, these values are very similar to the usage of the clustering coefficient in *descending* order in this network. In the “Email” network, when k was set to $0.2\,|E|$, every measure produced approximately 21% less infections, with the exception of clustering coefficient, which offered only 8% less infection events. Once again, using the clustering coefficient in *descending* order provided a reduction equivalent to the other measures in *ascending* order. When $k = 0.5\,|E|$, the usage of clustering coefficient provided a moderate reduction of about 22%, while other measures produced a profound reduction of 46% in comparison with the random method.

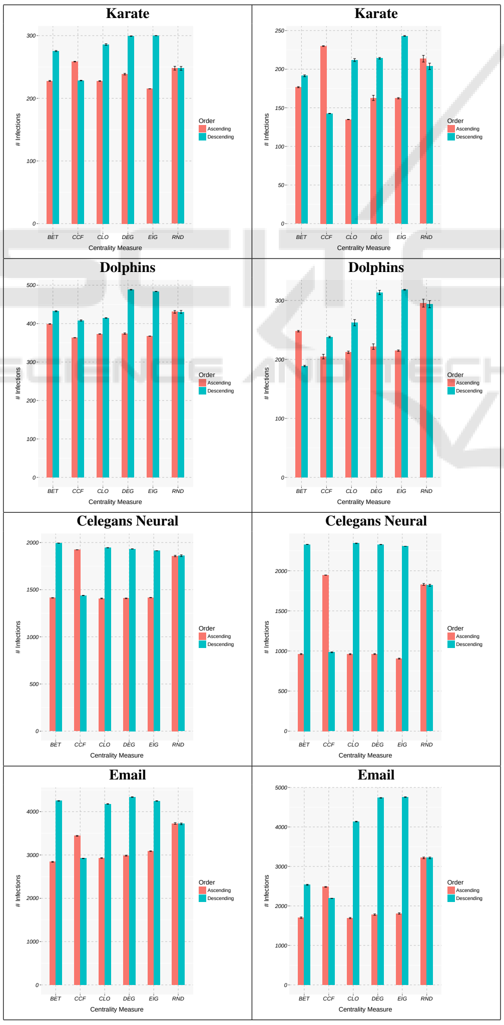

Figure 3: Number of infections by cutting 20% (left) and 50% (right) of edges from central (descending) and peripheral (ascending) individuals.

4 CONCLUSIONS

Centrality is an important structural attribute within social network studies. In this paper, we investigated the relationship between the centrality of an individual and its role in the diffusion of a meme through a network and explored methods to mitigate diffusion.

In our experiments, we used real complex networks of individuals and the Min-SEIS-Cluster model (de Santiago et al., 2016). We first investigated the correlations between the centrality score and the number of infections suffered and caused. These results showed that central individuals have an important role in spreading of memes, with the highest correlation values being observed in the largest networks when the number of infections caused was analyzed. When examining the clustering coefficient metric, we noticed inconsistent correlation values, with some networks presenting negative results, others positive, and even no correlation at all.

In the main experiments, we explored an improvement to the Min-SEIS-Cluster algorithm by cutting connections of individuals that were scored with more and less centrality. The experiments showed that removing the connections between the most central individuals did not result in less infection events, with the exception of the usage of the clustering coefficient measure, which offered a significant improvement over the original, random method, especially in the larger networks. We suggest exploring the relationship between the effectiveness of this measure and the correlations explored in Section 3.1, since a similar distinction was observed. When removing the connection between peripheral individuals, however, we noticed a significant reduction of infection events when employing every measure, except the clustering coefficient, which offered little to no improvement. This method produced astounding results, ranging from 13% to 21% less infections when 20% of the connections were removed, and 17% to an impressive 48% reduction when 50% of the connections were removed. The improvement became more noticeable as the size of the network increased.

These surprising results raised some interesting questions and interpretations. At first, we hypothesized that removing connections between central individuals would provide a significant reduction in the number of memes being transmitted (referred to as *infections*), as the conceptual descriptions of the centrality measures suggested that these individuals are connected with many others and have control over the communication paths of the network. However, this hypothesis was proved incorrect within the Min-SEIS-Cluster model, as the epidemic did not depend on the connections between central individuals to affect the whole network.

However, the epidemic was less successful when the connections between peripheral individuals were removed. To our understanding, this outcome was observed due to the fact that there will be several individuals who are completely segregated from the rest of the network, as individuals with few connections tend to possess low centrality scores. Although the number of infections was reduced, we introduced isolation in the network, which could be very problematic in a real-world context.

As further work, one could aim at designing experiments to explore additional relationships between central and peripheral individuals in the spread of memes, investigate the role of communities in the propagation of influences and examine how central and non-central individuals can better find a solution for an optimization problem by spreading memes to their neighbors.

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