

# Diffusion of Innovations in Social Networks

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**Abstract**—While social networks do affect diffusion of innovations, the exact nature of these effects are far from clear, and, in many cases, there exist conflicting hypotheses among researchers. In this paper, we focus on the linear threshold model where each individual requires exposure to (potentially) multiple sources of adoption in her neighborhood before adopting the innovation herself. In contrast with the conclusions in the literature, our bounds suggest that innovations might spread further across networks with a smaller degree of clustering. We provide both analytical evidence and simulations for our claims. Finally, we propose an extension for the linear threshold model to better capture the notion of path dependence, *i.e.*, a few minor shocks along the way could alter the course of diffusion significantly.

## I. INTRODUCTION

Existing evidence suggests that diffusion of innovations is a social process and an individual's adoption behavior is highly correlated with the behavior of her contacts [1]. However, the complex structure of the social networks and heterogeneity of individuals make it far from obvious how these local correlations affect the final outcome of the diffusion process. These considerations have been modeled in the literature using the *linear threshold model*, originally proposed by Granovetter [2]. This model is defined over a *graph* representing a (social) network of potential adopters. There exists a subset of individuals (*seed set*) who have already adopted the innovation. Each member is assumed to adopt the innovation if the fraction of her neighbors that have adopted is above a certain (potentially heterogeneous) threshold. In this paper, we use the linear threshold model to analyze the effects of network structure, threshold values and the seed set on the dynamics of the diffusion. Our analysis is novel in three fronts: First, we study the dynamics of the linear threshold model under *deterministic* networks, threshold values and the seed set rather than randomizing over all these quantities, and characterize the final adopter set. Our characterization is based on *cohesion of social groups*, where cohesion is measured comparing the relative frequency of ties among group members to ties with non-members. We generalize the definition of *cohesive set* by Morris [3], and show that the final adopter set is related to the largest cohesive subset of the complement of the seed set.

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Second, by only randomizing over the seed set (keeping network structure and threshold values fixed), we capture the effect of clusters and long links on the expected number of final adopters. Our upper bound (on the expected number of final adopters) suggests that networks with highly clustered sub-communities and short range links only might be less effective than networks with a smaller degree of clustering and with long links. We observe such behavior even when *threshold values are large, i.e.*, when each individual requires multiple adoption in her neighborhood before adopting the innovation. Our upper bound is also linear in the cardinality of the seed set  $k$ , for small  $k$ .

Finally, we propose an extension for the linear threshold model to capture the idea of path dependence, *i.e.*, a few minor shocks along the way could alter the course of diffusion significantly [4]. In the proposed model, an individual *actively considers* adoption if the fraction of her neighbors that have adopted is above a certain threshold. The active consideration is a stochastic process and it can lead to either adoption or rejection of the innovation. We argue that this simple extension can capture the notion of path dependence. Our paper is related to the growing literature on diffusion over social networks (*e.g.*, [3], [5]–[8]). Our study is most relevant to the literature which measure the effect of clustering on innovation diffusion [5]–[7], [9]. In particular, in [7], [9], the authors discuss that the effect of clustering on *complex contagions* (the case where individuals have high threshold values) differs significantly from the one on *epidemics* (the case where individuals have low threshold values). They argue that complex contagions might diffuse further on networks with highly clustered sub-communities and short range links only, while epidemics diffuse further on networks with long links. Despite the positive reinforcement effects of clusters on complex contagions, our results show that highly clustered sub-communities are also difficult to penetrate unless there exists a seed node inside the communities themselves. Therefore, especially when the number of seed nodes is small, complex contagions might diffuse further on networks with a smaller degree of clustering and with long links, contrary to the intuition provided by above studies. Our result holds on both complex contagions and epidemics.

Our study is also related to the literature on the linear threshold model (*e.g.* [10]–[12]). Unlike these studies, we

focus on deterministic networks, threshold values and seed sets. In return, our results are not limited to the degree distribution of the social graph, and we can infer the effects the seed set location and the network clustering on the set of final adopters.

Due to the space limitations, proofs will be omitted, and can be found in [13].

## II. LINEAR THRESHOLD MODEL

We consider a set of agents  $\mathcal{V} = \{1, \dots, N\}$  situated in a social network represented by a directed graph  $\mathcal{G}(\mathcal{V}, \mathcal{E})$ , where  $\mathcal{E}$  is the set of edges representing the connectivity among these individuals.<sup>1</sup> We do not allow self-loops. An edge  $(i, j) \in \mathcal{E}$  is directed from  $i$  to  $j$ . We define the neighbor set of agent  $i \in \mathcal{V}$  as  $\mathcal{N}_i(\mathcal{G}) = \{j | (j, i) \in \mathcal{E}\}$ . In other words, the set  $\mathcal{N}_i(\mathcal{G})$  consists of individuals who can potentially influence agent  $i$  for a given graph  $\mathcal{G}$ .

We assume that at iteration  $k = 0$ , a subset of individuals  $\Phi(0) \subseteq \mathcal{V}$  is selected as the seed for the innovation. The set  $\Phi(0)$  could represent a group of innovators who have already been exposed to innovation as well as the set of promoters who have certain social, economic and/or political agenda. We assume that the seed set adopts the innovation at iteration  $k = 0$ . At the next iteration, an individual  $i \in \mathcal{V} \setminus \Phi(0)$  will adopt the innovation if at least  $\phi_i \in (0, 1]$  fraction of her neighbors are in the seed set, *i.e.*,

$$\frac{|\Phi(0) \cap \mathcal{N}_i(\mathcal{G})|}{|\mathcal{N}_i(\mathcal{G})|} \geq \phi_i \Rightarrow i \in \Phi(1). \quad (1)$$

In other words, the set  $\Phi(1)$  consists of individuals who have been exposed to the innovation, are persuaded by their neighbors that adoption is worth considering, and then adopt the innovation. For a given  $k \geq 0$ , the above discussion can be generalized as follows: a node  $i \in \mathcal{V} \setminus \bigcup_{l=0}^{k-1} \Phi(l)$  will adopt the innovation at  $k$  if

$$\frac{|\{\bigcup_{l=0}^{k-1} \Phi(l)\} \cap \mathcal{N}_i(\mathcal{G})|}{|\mathcal{N}_i(\mathcal{G})|} \geq \phi_i \Rightarrow i \in \Phi(k). \quad (2)$$

## III. CHARACTERIZATION OF THE SET OF FINAL ADOPTERS

In this section, we will characterize the final adopter set in terms of the underlying network, the seed set and the threshold values.

Before introducing our results, we first introduce a measure of *cohesion* of a social group.

*Definition 1:* A subset  $\mathcal{M} \subseteq \mathcal{V}$  is called a cohesive set if;

$$\frac{|\mathcal{M} \cap \mathcal{N}_i(\mathcal{G})|}{|\mathcal{N}_i(\mathcal{G})|} > 1 - \phi_i \text{ for all } i \in \mathcal{M}. \quad (3)$$

Definition 1 states that a group of agents form a cohesive set if for each member of the set the fraction of neighbors residing in the set is strictly greater than the individual specific threshold. This definition is due to Morris [3], and it measures the cohesion of a group by comparing the relative

<sup>1</sup>Throughout the paper, we will use the terms agent, individual, and node interchangeably. Similarly, the terms network and graph will be used interchangeably.

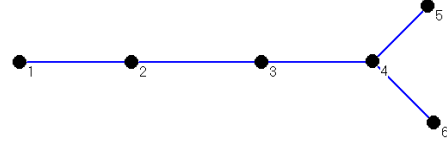


Fig. 1. A sample network.

frequency of ties among group members to ties with non-members.<sup>2</sup> For the sake of completeness, we will assume that the empty set  $\emptyset$  is cohesive.

Fig. 1 introduces a sample network with six individuals. We assume that threshold values are equal to  $0.5 - \epsilon$  for the first two agents, and are equal to  $0.5 + \epsilon$  for the last four agents, where  $0 < \epsilon \ll 1$ . The sample network has multiple cohesive subsets, *e.g.*,  $\{3, 4, 5, 6\}$ ,  $\{4, 5, 6\}$ ,  $\{1, 2, 3, 4, 5\}$ . For instance, for  $\mathcal{M} = \{4, 5, 6\}$ , the ratio in Eq. (3) is equal to  $\{2/3, 1, 1\}$ , respectively. Since each of these values are strictly greater than  $1 - \phi_i = 0.5 - \epsilon$ ,  $i \in \mathcal{M}$ , the set  $\mathcal{M}$  is a cohesive set.

*Definition 2:* For a given graph and threshold values, a nonempty set  $\Phi^*$  is a fixed point of the deterministic threshold model if

$$\Phi(0) = \Phi^* \Rightarrow \Phi(k) = \emptyset, \text{ for all } k > 0. \quad (4)$$

Definition 2 states that a nonempty set is a fixed point if an innovation initiated at that particular set can not diffuse through the rest of the society. The following lemma introduces a characterization of the fixed points of the deterministic threshold model in terms of cohesive sets.

*Lemma 1:* For a given graph  $\mathcal{G}$  and threshold values  $\{\phi_i\}_{i \in \mathcal{V}}$ ; an adopter set  $\Phi^*$  is a fixed point if and only if  $(\Phi^*)^c = \mathcal{V} \setminus \Phi^*$  is a cohesive set.

Lemma 1 characterizes the set of possible fixed points for a given graph  $\mathcal{G}$  and threshold values  $\{\phi_i\}_{i \in \mathcal{V}}$ . The proof is based on the following discussion by Morris [3, Proposition 1]: Members of a cohesive set  $\mathcal{M}$  can not satisfy Eq. (2) unless there exists an individual inside the set  $\mathcal{M}$  who has previously adopted the innovation. In other words, the members of a cohesive set can not adopt the innovation unless there exists at least one adopter inside the set itself. Therefore, if one initializes an innovation from a set  $\Phi^*$  whose complement is a cohesive set, the innovation will not be adopted by the members of the complement set.

The society given in Fig. 1 has several fixed points, *e.g.*,  $\{1, 2\}$ ,  $\{1, 2, 3\}$ ,  $\{5\}$ ,  $\{1, 2, 3, 4, 5, 6\}$ . We note that the universal set  $\{1, 2, 3, 4, 5, 6\}$  is also a fixed point.

In the following, we introduce the main result of the section which characterizes the set of final adopters for a given graph, seed set and threshold values.

*Lemma 2:* For a given graph  $\mathcal{G}$ , threshold values  $\{\phi_i\}_{i \in \mathcal{V}}$  and seed set  $\Phi(0)$ , denote  $\{\Phi_s^*\}_{s=1}^K$ ,  $K \geq 1$  as the set of fixed points for which  $\Phi(0) \subseteq \Phi_s^*$  holds. Then,

$$\Phi^* = \bigcap_{s=1}^K \Phi_s^*, \quad (5)$$

<sup>2</sup>As noted by Morris, relative frequency of ties is not the only way to capture cohesion of a social group [3].

is the set of final adopters.

Each  $\Phi_s^*$  is a fixed point and a non-empty subset of  $\mathcal{V}$ . Therefore,  $\{\Phi_s^*\}_{s=1}^K$ ,  $K \geq 1$ , is a set of subsets whose intersection identify the set of final adopters, *i.e.*,  $\Phi^*$ . We note that  $K > 0$ , since  $\mathcal{V}$  is a fixed point and  $\Phi(0) \subseteq \mathcal{V}$  for any given seed set  $\Phi(0)$ . Moreover, the intersection in Eq. 5 is nonempty since each  $\Phi_s^*$  is a superset of the seed set  $\Phi(0)$ .

According to Lemma 2, the network structure, threshold values and the seed set uniquely identifies the final adopter set. For instance, if we choose the seed set as  $\Phi(0) = \{1\}$  in Fig. 1, there exists four fixed points which are also supersets of  $\Phi(0)$ , *i.e.*,  $\Phi(0) = \{1\} \subset \{1, 2\}, \{1, 2, 3\}, \{1, 2, 5\}, \{1, 2, 6\}$ . Therefore, the spread of the innovation stops once it reaches the intersection of these sets, *i.e.*,  $\{1, 2\}$ .

An immediate corollary of Lemmas 1 and 2 characterizes the final adopter set in terms of cohesive sets.

*Corollary 1:* For a given graph  $\mathcal{G}$ , threshold values  $\{\phi_i\}_{i \in \mathcal{V}}$  and seed set  $\Phi(0)$ , denote  $\{\mathcal{M}_s\}_{s=1}^K$ ,  $K \geq 1$  as the set of cohesive subsets of  $\mathcal{V}$  for which  $\Phi(0) \cap \mathcal{M}_s = \emptyset$  holds. Then,

$$\Phi^* = \left( \bigcup_{s=1}^K \mathcal{M}_s \right)^c, \quad (6)$$

is the set of final adopters.

Corollary 1 states that the final adopter set is the complement of the unions of cohesive subsets of  $\mathcal{V} \setminus \Phi(0)$ . The proof follows from the fact that  $\Phi^* = \bigcap_{s=1}^K \Phi_s^* = \left( \bigcup_{s=1}^K (\Phi_s^*)^c \right)^c$ , and, there exists a bijective mapping  $f : \{1, \dots, K\} \rightarrow \{1, \dots, K\}$  such that  $(\Phi_s^*)^c \sim \mathcal{M}_{f(s)}$ .

We note that, due to the definition of cohesiveness, finite unions of cohesive sets are also cohesive. Therefore, there exists an  $s^* \in \{1, \dots, K\}$ , such that  $\mathcal{M}_s \subseteq \mathcal{M}_{s^*}$  for all  $s$ , and  $\bigcup_{s=1}^K \mathcal{M}_s = \mathcal{M}_{s^*}$ . By Eq. (6),  $\Phi^* = (\mathcal{M}_{s^*})^c$ . In other words, the final adopter set is equal to the complement of the largest (in cardinality) cohesive subset of  $\mathcal{V} \setminus \Phi(0)$ . For instance, in Fig. 1, for  $\Phi(0) = \{1\}$ , the largest cohesive subset of  $\mathcal{V} \setminus \{1\}$  is  $\{3, 4, 5, 6\}$ , and the final adopter set is  $\{1, 2\}$ .

#### IV. AN UPPER BOUND ON THE NUMBER OF FINAL ADOPTERS

For a given graph  $\mathcal{G}$  and threshold values  $\{\phi_i\}_{i \in \mathcal{V}}$ , we can partition the graph into disjoint cohesive sets, *i.e.*, for all  $i, j \in \{1, \dots, r\}$ :

- $\mathcal{M}_i \cap \mathcal{M}_j = \emptyset$  for  $i \neq j$ ,
- $\bigcup_{i=1}^r \mathcal{M}_i = \mathcal{V}$ ,
- $\mathcal{M}_i$  cohesive for all  $i$ .

We denote the set  $\{\mathcal{M}_1, \mathcal{M}_2, \dots, \mathcal{M}_r\}$  as a *cohesive partition*. We note that cohesive partitioning is not necessarily unique for a given graph and threshold values. Therefore, we denote the set  $\mathcal{P}$  as the set of all possible cohesive partitions. Each element of the set  $\mathcal{P}$ , *i.e.*,  $\mathcal{P}_i$ , is a cohesive partition. For instance, in Fig. 1, there are two cohesive partitions  $\mathcal{P}_1 = \{\{1, 2, 3\}, \{4, 5, 6\}\}$  and  $\mathcal{P}_2 = \{\{1, 2, 3, 4, 5, 6\}\}$ . Thus,  $\mathcal{P} = \{\{\{1, 2, 3\}, \{4, 5, 6\}\}, \{1, 2, 3, 4, 5, 6\}\}$ .

In the following, we will focus on the expected number of final adopters as our metric. The expectation is taken over all possible seed sets of a given cardinality  $k \geq 1$ , where each  $k$  element subset of  $\mathcal{V}$  has equal probability.

*Lemma 3:* For a given graph  $\mathcal{G}$  and threshold values  $\{\phi_i\}_{i \in \mathcal{V}}$ , denote  $\{\mathcal{M}_s\}_{s=1}^r$ ,  $r \geq 1$  as a cohesive partition of  $\mathcal{V}$ , and assume that the sets  $\{\mathcal{M}_s\}_{s=1}^r$  are in descending order with respect to their cardinalities. Then, for a given seed set size  $k \leq r$ , the expected number of final adopters  $\mathbb{E}[\Phi^*]$  is upper bounded by:

$$\mathbb{E}[\Phi^*] \leq \sum_{s=1}^k |\mathcal{M}_s|. \quad (7)$$

The upper bound suggests that, as the cardinalities of the largest sets in a cohesive partition decrease, the expected number of final adopters might also decrease. Since  $k$  is fixed, and as the cardinalities of the  $k$  largest sets of a partition decrease, the cardinalities of the  $r - k$  smallest sets increase. Therefore, the number of non-adopters increases.

We note that the upper bound holds for any given cohesive partitions. For a given  $k$ , we can tighten the bound by minimizing it over all cohesive partitions which have at least  $k$  elements. Slightly abusing our notation, it is equivalent to:

$$\mathbb{E}[\Phi^*] \leq \min_{\mathcal{T} \in \mathcal{P}(k)} \sum_{s=1}^k |\mathcal{M}_s(\mathcal{T})|, \quad (8)$$

where  $\mathcal{P}(k)$  is the set of all cohesive partitions which have at least  $k$  elements, and  $\mathcal{M}_s(\mathcal{T})$  is the corresponding element of the partition  $\mathcal{T}$ .

The following corollary introduces the relationship between the expected number of final adopters and the number of sets  $r$  in a partition.

*Corollary 2:* For a given graph  $\mathcal{G}$  and threshold values  $\{\phi_i\}_{i \in \mathcal{V}}$ , denote  $\{\mathcal{M}_s\}_{s=1}^r$ ,  $r \geq 1$  as a partition of  $\mathcal{V}$ , and assume that the sets  $\{\mathcal{M}_s\}_{s=1}^r$  are in descending order with respect to their cardinalities. If there exists an  $\epsilon \geq 0$ , such that:

$$|\mathcal{M}_1| - \epsilon \leq |\mathcal{M}_s| \leq |\mathcal{M}_1| + \epsilon, \text{ for all } s, \quad (9)$$

then, for a given seed set of size  $k \leq r$ , the expected number of final adopters  $\mathbb{E}[\Phi^*]$  is upper bounded by:

$$\mathbb{E}[\Phi^*] \leq k \frac{N}{r} + (k + 1)\epsilon. \quad (10)$$

Corollary 2 states that if there exists a partition where the sets are uniform (in size), then the upper bound is inversely proportional to the number of sets  $r$  in the partition. Therefore, a configuration (graph and threshold values) with a partition with small numbers of sets might help the innovation to diffuse further than a configuration with a large number of sets in the partition (in expectation). Existence of a single partition with uniform set sizes is a sufficient condition for our bound to hold.

While the results are interesting, they are not easy to interpret since cohesiveness is a function of both the network structure and the threshold values. In the following, we will focus on each of them separately.

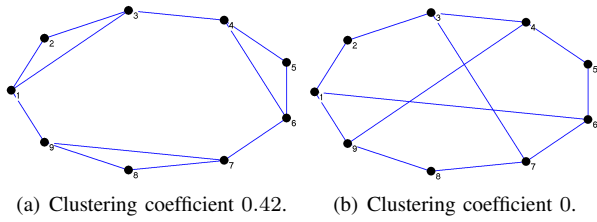


Fig. 2. Two sample networks with similar degree distributions.

**Threshold Values:** To capture the effects of threshold values on our bound, we will fix the network structure of the society. As the threshold values increase, the right side of Eq. (3) decreases. Thus, nodes can form cohesive subsets with smaller number of neighbors. This will potentially decrease the cardinalities of sets in cohesive partitions and increase  $r$ . In return, the bound on the expected number of adopters will decrease. The following proposition states our argument in a formal way.

**Proposition 1:** Given a graph  $\mathcal{G}$  and two sets of threshold values  $\{\tilde{\phi}_i\}_{i \in \mathcal{V}}$ ,  $\{\phi_i\}_{i \in \mathcal{V}}$  such that:

$$\tilde{\phi}_i \geq \phi_i \text{ for all } i \in \mathcal{V},$$

then,

$$\min_{\tilde{\mathcal{T}} \in \tilde{\mathcal{P}}(k)} \sum_{s=1}^k |\tilde{\mathcal{M}}_s(\tilde{\mathcal{T}})| \leq \min_{\mathcal{T} \in \mathcal{P}(k)} \sum_{s=1}^k |\mathcal{M}_s(\mathcal{T})|,$$

and, under the assumptions given in Corollary 2,

$$k \frac{N}{\tilde{r}} + (k+1)\epsilon \leq k \frac{N}{r} + (k+1)\epsilon$$

**Network Structure:** To capture the effects of network structure, we will use the notion of *clustering (transitivity)*, i.e., to what extent nodes tend to create tightly knit groups. There are two main reasons for utilizing clustering: First, clustering have been extensively used in the diffusion literature to capture the network structure, therefore it allows us to compare our results with the existing literature. Second, there is a direct relation between cohesiveness and clustering.

We will first illustrate the relation between cohesiveness and clustering with an example. In Fig. 2, we introduce two networks with the same number of nodes and links. Moreover, for a given node  $i$ , the number of neighbors is fixed on both graphs. The network in Fig. 2(a) has three densely connected clusters, while the network in Fig. 2(b) has a small degree of clustering. Clustering coefficients<sup>3</sup> of networks are 0.42 and 0, respectively [14]. We note that clustering coefficient is a function of network structure only and it is independent of threshold values.

We assume that each node has threshold value of 0.5 on both graphs. For the highly clustered network, the cohesive partition which minimizes the upper bound for  $k = 1, 2, 3$  is:  $\{\{1, 2, 3\}, \{4, 5, 6\}, \{7, 8, 9\}\}$ . We note that these three partitions are also distinct clusters (regardless of thresh-

old values). For the second network, the cohesive partition which minimizes the upper bound for  $k = 1, 2$  is:  $\{\{1, 2, 7, 8, 9\}, \{3, 4, 5, 6\}\}$ . In this case, the graph is less structured, clusters are not distinct, and the number of sets in the cohesive partition is smaller. Our example suggests that highly clustered networks tend to have larger numbers of sets in cohesive partitions, and cohesive partitions tend to have smaller cardinalities. When combined with Lemma 3 and Corollary 2, it suggests that highly clustered networks might to have smaller expected number of final adopters. The following proposition introduces the relationship between clustering coefficient and the bound on the expected number of adopters.

**Proposition 2:** For a given pair of graphs  $\mathcal{G}(\mathcal{V}, \mathcal{E})$ ,  $\tilde{\mathcal{G}}(\tilde{\mathcal{V}}, \tilde{\mathcal{E}})$  such that  $|\mathcal{V}| = |\tilde{\mathcal{V}}|$ , such that there exists a bijective function  $f: \mathcal{V} \rightarrow \tilde{\mathcal{V}}$ :

- $|\mathcal{N}_i| = |\tilde{\mathcal{N}}_{f(i)}|$  for all  $i \in \mathcal{V}$ ,
- $\phi_i = \tilde{\phi}_{f(i)}$  for all  $i \in \mathcal{V}$
- $\{\phi_j\}_{j \in \mathcal{N}_i} \sim \{\tilde{\phi}_{j'}\}_{j' \in \tilde{\mathcal{N}}_{f(i)}}$ , for all  $i \in \mathcal{V}$ ,

then, if the clustering coefficient of  $i$  (in all of the subsets of  $\mathcal{V}$  containing  $i$ ) is less than or equal to the clustering coefficient of  $f(i)$  (in all of the subsets of  $\tilde{\mathcal{V}}$  containing  $f(i)$ ), then:

$$\min_{\tilde{\mathcal{T}} \in \tilde{\mathcal{P}}(k)} \sum_{s=1}^k |\tilde{\mathcal{M}}_s(\tilde{\mathcal{T}})| \leq \min_{\mathcal{T} \in \mathcal{P}(k)} \sum_{s=1}^k |\mathcal{M}_s(\mathcal{T})|,$$

and, under the assumptions given in Corollary 2,

$$k \frac{N}{\tilde{r}} + (k+1)\epsilon \leq k \frac{N}{r} + (k+1)\epsilon$$

According to Proposition 2, increased local clustering decreases the bound on the expected number of final adopters (while the neighborhood properties are being held constant). We note that each cluster is indeed a strong candidate for forming a cohesive set by itself due to large number of ties among its members. Therefore, as the network clustering increases, individuals are more likely to form cohesive sets with others that are in close proximity. This, in return, will decrease the cardinalities of such sets and increase  $r$ .

As we have discussed previously, the common intuition in the literature is that highly clustered networks with short range links only might be more advantageous for complex contagions (e.g., [7], [9]), since locally dense clusters reinforce adoption, i.e., individuals in densely connected clusters are more likely to be exposed to multiple adopters (overlapping influences) through short cycles.

However, locally dense clusters will reinforce adoption if *there exists at least one adopter inside the cluster itself*. Moreover, a locally dense cluster, which does not contain any seed nodes, is highly stable and might resist the innovation. In other words, clustering might reinforce adoption once the innovation penetrates inside the cluster, however, it might also weaken adoption by making the initial penetration more difficult. Therefore, especially for small values of  $k$ , networks with a small degree of clustering and with long range links might diffuse the innovation further.

<sup>3</sup>Clustering coefficient of a node is defined as the ratio of existing triangles in the neighborhood to the number of all possible triangles in the neighborhood. Clustering coefficient of a network is defined as the ratio of existing triangles in the network to the number of all possible triangles in the network.

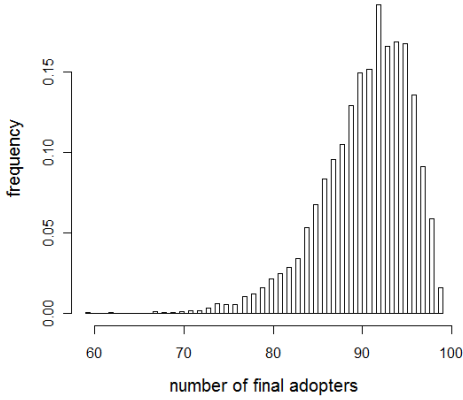


Fig. 3. Empirical distribution of the number of final adopters under stochastic linear threshold model.

In [5], [6], the authors study the effect of the network structure on the *convergence time*, and discuss that innovations diffuse faster on highly clustered networks, and much more slowly on networks with a smaller degree of clustering. While our findings might seem to contradict with the results in these studies, we note that we utilize a different metric, *i.e.*, the expected number of adopters rather than convergence time.

## V. STOCHASTIC LINEAR THRESHOLD MODEL

The linear threshold model has been powerful enough to capture the role of interpersonal influence in adoption behavior, and it has provided crucial insights about the complex relationship between innovation diffusion and network connectivity (threshold values, seed set). However, the model fails to capture a very important aspect of innovation diffusion, *i.e.*, *path dependence*. Path dependence is based on the idea that a *few minor shocks* or *insignificant events* along the way could alter the course of history [4]. It has been argued that diffusion of innovations is extremely fragile with respect to these small shocks, *i.e.*, diffusion of innovations is highly path dependent<sup>4</sup> [16]. For instance, two similar products (similar attributes, pricing and seeding strategies, perceived qualities) might diffuse differently on the same network due to different realizations of minor shocks.

To be able to capture the notion of path dependence, we will modify the linear threshold model as follows: We use  $x_i(k)$  to denote the state of agent  $i$  at iteration  $k$ . For a given  $i$ ,  $x_i(k)$  can take one of the three possible values,  $\{0, 1, -1\}$ , *i.e.*, not-yet-adopted, adopted or rejected. We assume that at iteration  $k = 0$ , a subset of individuals  $\hat{\Phi}(0) \subseteq \mathcal{V}$  is selected as the seed for the innovation. At the next iteration, an individual  $i \in \mathcal{V} \setminus \hat{\Phi}(0)$  will *actively consider* adoption if at least  $\phi_i \in (0, 1]$  fraction of her neighbors are in the seed

set, *i.e.*,

$$\frac{|\hat{\Phi}(0) \cap \mathcal{N}_i(\mathcal{G})|}{|\mathcal{N}_i(\mathcal{G})|} \geq \phi_i \Rightarrow i \in \hat{\Phi}(1). \quad (11)$$

In other words, the set  $\hat{\Phi}(1)$  consists of individuals who have been exposed to the innovation, and are persuaded by their neighbors that adoption is worth considering. Each agent  $i \in \hat{\Phi}(1)$  immediately engages in activities that lead to adoption or rejection of the innovation. This consideration may also correspond to a type of trial or just the potentially costly process of evaluating the pros and cons of the innovation. However, consideration does not necessarily translate into adoption. We will model the outcome of the decision process as a Bernoulli trial with a common parameter  $p \in [0, 1]$ . While the parameter is common to all individuals, the trials are independent. In other words, for each  $i \in \hat{\Phi}(1)$ ,  $x_i(1) = 1$  with probability  $p$ , and  $x_i(1) = -1$  with probability  $1 - p$ . The parameter  $p$  determines the likelihood of the adoption conditioned upon consideration, *i.e.*, the larger  $p$  is, the more likely a given individual will be adopt the innovation when she actively considers adoption.

The set of individuals who have adopted (rejected) the innovation at iteration  $k = 1$  will form the set  $\mathcal{A}(1)$  ( $\mathcal{R}(1)$ ). In other words,  $\mathcal{A}(1) = \{i \in \mathcal{V} | i \in \hat{\Phi}(1), x_i(1) = 1\}$ ,  $\mathcal{R}(1) = \{i \in \mathcal{V} | i \in \hat{\Phi}(1), x_i(1) = -1\}$ .

For a given  $k \geq 0$ , the above discussion can be generalized as follows: a node  $i \in \mathcal{V} \setminus \bigcup_{l=0}^{k-1} \hat{\Phi}(l)$  will actively consider adoption at  $k$  if

$$\frac{|\{\hat{\Phi}(0) \cup \bigcup_{l=1}^{k-1} \mathcal{A}(l)\} \cap \mathcal{N}_i(\mathcal{G})|}{|\mathcal{N}_i(\mathcal{G})|} \geq \phi_i \Rightarrow i \in \hat{\Phi}(k)$$

and node will adopt or reject at iteration  $k$  according to the Bernoulli trial with parameter  $p$ .

We denote the above model as the *stochastic linear threshold model*. The main difference between our model and the linear threshold model is that individuals do not necessarily adopt the innovation if the fraction of their neighbors that have adopted is above their threshold. For  $p < 1$ , an individual can reject the adoption with non-zero probability, possibly due to minor shocks.

In Fig. 3, we plot empirical distribution of the number of final adopters on a sample network with  $p = 0.95$ .<sup>5</sup> Even though  $p$  is close to 1, there exists significant variation in the number of final adopters. In other words, minor shocks to individuals' adoption decisions might generate significant variability in the outcome of the decision process, *i.e.*, the stochastic threshold model captures the notion of path dependence.

At this point, there are several interesting questions to be answered including the relationship between the parameters and the distribution of the number of final adopters. Due to the space limitations, we will present the formal analysis of the stochastic model in [17].

<sup>4</sup>Increasing returns to adoption, self-reinforcement, positive feedbacks and lock-in have been identified as the main causes of the fragility [15].

<sup>5</sup>A small world network with 1000 nodes, rewiring probability 0.5, seed node cardinality 5, threshold values are uniformly distributed in the interval  $[0, 1]$ , and 5000 runs.

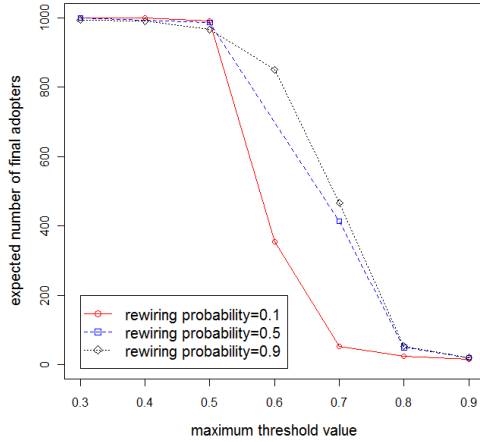


Fig. 4. Threshold values versus  $\mathbb{E}[\Phi^*]$ .

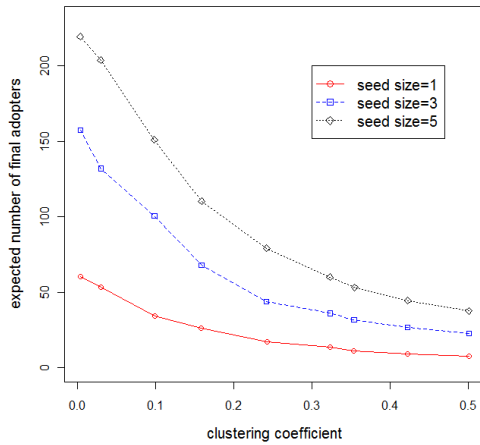


Fig. 5. Clustering coefficient versus  $\mathbb{E}[\Phi^*]$ .

## VI. SIMULATIONS

In the following, we will test our hypothesis with simulations. We plot the relationship between threshold value distribution and the expected number of final adopters in Fig. 4. For simulation purposes, for a given threshold distribution, we generate 1000 small world networks with 1000 nodes and rewiring probabilities  $\{0.1, 0.5, 0.9\}$ . For a given value  $\alpha$  in the x-axis, threshold values are uniformly distributed in the interval  $[0, \alpha]$ . As our bounds suggest, the expected number of adopters decrease, as the threshold values decrease. We note that the curves are relatively flat at both tails, and there is a sharp decrease in between. In Fig. 5, we plot the relationship between the clustering coefficient of the network and the expected number final adopters. For simulation purposes, for a given rewiring probability, we generate 1000 small world networks with 1000 nodes. Rewiring probabilities are in the range  $[0, 1]$ . We note that as the rewiring probability increases, the clustering coefficient of the graph will decrease. For each realization of the network, we draw uniformly random threshold values for

each node. Similarly, seed sets of size  $\{1, 3, 5\}$  are chosen uniformly randomly. As our results suggest, the expected number of adopters decreases as the network becomes more clustered.

## VII. CONCLUSION

In this paper, we focused on the linear threshold model on deterministic topologies and heterogeneous threshold values. By extending the definition of cohesiveness by Morris [3], we completely characterized the set of final adopters in terms of cohesive subsets of the network. We, then, focused on a random seeding scenario, where seeds are uniformly distributed over the society. By using the expected number of final adopters as our metric, we explored the relationship between our metric and clustering of the network, threshold values and the cardinality (of the seed set). Interestingly, our results suggest that highly clustered networks are not necessarily more advantageous over less structured networks with large numbers of random links. While clusters promote diffusions when there exists a seed node inside them, they are hard to penetrate when they are not targeted during initial seeding phase. Finally, we introduce an extension to the linear threshold model to capture path dependence. We discuss that, under the new model, minor shocks to the individuals' adoption decisions might alter the outcome of the diffusion process significantly.

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