On the Equivalence Between High-Order Network-Influence Frameworks: General-Threshold, Hypergraph-Triggering, and Logic-Triggering Models

Wei Chen
Microsoft Research
Beijing, China
weic@microsoft.com

Shang-Hua Teng*
University of Southern California
Los Angeles, CA, USA
shanghua@usc.edu

Hanrui Zhang
Duke University
Durham, NC, USA
hrzhang@cs.duke.edu

Abstract

In this paper, we study several high-order network-influence-propagation frameworks and their connection to the classical network diffusion frameworks such as the triggering model and the general threshold model. In one framework, we use hyperedges to represent many-to-one influence — the collective influence of a group of nodes on another node — and define the hypergraph triggering model as a natural extension to the classical triggering model. In another framework, we use monotone Boolean functions to capture the diverse logic underlying many-to-one influence behaviors, and extend the triggering model to the Boolean-function triggering model. We prove that the Boolean-function triggering model, even with refined details of influence logic, is equivalent to the hypergraph triggering model, and both are equivalent to the general threshold model. Moreover, the general threshold model is optimal in the number of parameters, among all models with the same expressive power. We further extend these three equivalent models by introducing correlations among influence propagations on different nodes. Surprisingly, we discover that while the correlated hypergraph-based model is still equivalent to the correlated Boolean-function-based model, the correlated general threshold model is more restrictive than the two high-order models. Our study sheds light on high-order network-influence propagations by providing new insight into the group influence behaviors in existing models, as well as diverse modeling tools for understanding influence propagations in networks.

1 Introduction

At the heart of Network Sciences is the problem of network influence. This fundamental problem highlights the interaction between the dynamics of influence and the structures of underlying networks. In this problem, the collective influence of a group of seed nodes cascades through the network structure, step by step, following a stochastic diffusion process. Network influence has been considered in a wide range of fields, including sociology (for studying collective behaviors), medical science (for modeling the spread of infectious diseases), political science (for understanding voting behaviors and political influences), legal theory (for analyzing the impact of precedence), material science (for formulating percolation), etc. Motivated by the Internet-age application of viral

*Supported in part by the Simons Foundations’ Investigator Award and NSF CCF-1815254. Part of the work was done while the author was visiting Toyota Technological Institute at Chicago (TTIC).
marketing, Domingos and Richardson [10, 23] formulated a computational optimization problem — now known as influence maximization — for modeling the strategic selection of seed nodes aiming (under certain economic constraints) to influence maximum expected adoption of a new product or innovation. Their work introduced the problem of network influence to computer science.

1.1 Operational Network Influence Models

In their seminal paper [15] — with focus on the algorithmic study of influence maximization — Kempe, Kleinberg, and Tardos considered several classes of operational influence models, uniting many formulations proposed previously in multi-disciplinary studies of network influence. Each model specifies two basic components of network influence:

1. **The Underlying Network** — a directed graph $G = (V, E)$ which defines for each node $v \in V$, the set $N^-(v) \subseteq V \setminus \{v\}$ of all potential other nodes in the network that may directly influence $v$. In the graph, $N^-(v)$ denotes the set of all in-neighbors of $v$.

2. **The Influence Dynamics** — a set of parameters and mechanism for defining the “local rules” of the step-by-step stochastic diffusion process initiated by any selection of seed nodes.

While they use a shared formulation for the underlying network, these models differ in their characterization of the stochastic diffusion mechanisms. The following two models play important roles in studying properties of propagation dynamics and algorithmic design.

- **The General Threshold Model** is perhaps the most natural and individual-based influence model. For each node $v \in V$, (1) in the underlying network $G = (V, E)$, it determines the set $N^-(v)$ of other nodes that can directly influence it; (2) with its monotone threshold function $f_v : 2^{N^-(v)} \to [0, 1]$, it specifies how much each subset of its in-neighbors can influence $v$; and (3) with its random threshold valuable, $\theta_v \in [0, 1]$, it captures how easy it can be influenced. In the diffusion influence process, $v$ becomes active either immediately when $v$ is in the seed set, or at a later time during the process, when the $f_v$-value of its active in-neighbors rises above its threshold $\theta_v$.

- **The Triggering Model** plays an important role in the algorithm design and analysis for influence maximization [15]. In this model, instead of a threshold function over subsets of its in-neighbors, each node $v$ specifies which of its in-neighbors can directly influence it according to a distribution over subsets of its in-neighbors. The randomly chosen subset $T_v$ is called its “triggering set.” In the influence diffusion process, any member in $T_v$ can influence $v$ (no one in $N^-(v) \setminus T_v$ can influence $v$). The triggering model can also be equivalently represented as the live-edge graph model [15]. Analogous to the stochastic infrastructure in percolation theory [2], the randomly generated sub-graph, $L = \{(u, v) : v \in V, u \in T_v\}$, defines the edges that influence can cascade through.

Different models highlight different features and aspects of network influence that arise in various disciplines. For example, the general threshold model provides a framework for understanding how properties of local threshold functions impact the global influence dynamics, as highlighted by the submodular-threshold conjecture of [15], which was later settled by [21]. The triggering model provides the most direct understanding on the underlying submodularity of some network influence settings, because — as defined in [15] — it is a distribution over deterministic graph-reachability
instances. Different formulations also lead to important sub-models to further focus on various aspects of network influence. For example, important families of influence model studied in [15] such as the independent cascade model, the linear threshold model, and submodular threshold models are naturally characterized within their own respective general frameworks.

1.2 Our Contributions

In the real world, direct influences go beyond from one individual to another, and thus, the patterns of interaction are not limited to pair-wise directed graph structures. Recall that a directed graph over node set \( V \) can be viewed as a collection of directed edges. In the setting of network influence, the underlying directed graph is used to define, for each node \( v \in V \), the set \( N(v) \) of nodes, each of which potentially has direct influence on \( v \). In this paper, we study natural high-order extensions of the triggering model. We will focus on “network extension” as well as “stochastic extension.”

First, through the prism of network extension, the triggering framework can be applied to Boolean-function-based networks and hypergraph-based networks:

- On the most comprehensive spectrum, direct influences have underlying logical expressions, specifying how each individual can be potentially influence by combinations of others. This perspective suggests the use of logical networks. That is, the state of each node \( v \) is represented by a Boolean variable, \( b_v \), and the network of the potential direct influences are represented by each node’s collection \( B_v \) of Boolean functions over the Boolean variables of other nodes.

- On the relatively simplistic spectrum, direct influences potentially come from groups rather than just individuals as specified by direct graphs. This set-based perspective suggests the use of directed hypergraphs for the underlying interaction network. A directed hypergraph over \( V \) is a collection of directed hyperedges, each is a pair of a subset and a node, i.e., \((S, v)\), with \( S \subseteq V \setminus v \) as the tail set and \( v \in V \) as the head node. Intuitively, hyperedge \((S, v)\) suggests that when all tail nodes in \( S \) are activated, the head node \( v \) may be activated due to the collective influence from \( S \). Thus a directed hypergraph can be used to define, for each node \( v \in V \), the set of groups whose members together can directly influence \( v \).

In the Boolean-function triggering model and hypergraph triggering model, each node \( v \) specifies a distribution, respectively, over subsets of its collection of monotone Boolean functions or incident hyperedges. Thus, based on the underlying Boolean-function or hypergraph networks, the product distribution over Boolean functions or hyperedges then defines a live network of Boolean-functions or hyperedges, through which influences can cascade.

Our main technical result of this paper is the following model-equivalence theorem, which, through the generalization of the classical triggering model to the Boolean-function-triggering or hypergraph-triggering model, characterizes the exact power of high-order network influence.

**Theorem 1** (General Equivalence of Node-Independent Influence Models). The following three network-influence models — the Boolean-function triggering model, the hypergraph triggering model, and the general threshold model — are equivalent.\(^1\)

\(^1\)See Section 2.2 for the formal definition of *equivalence* between two influence models: Informally, the model equivalence means that influence propagations in the two models produce the same family of distributions of the node-activation sequences on networks.
The above theorem illustrates the connection and the difference between the classical triggering model and the general threshold model. The triggering model focuses on influence propagation due to pairwise influence relationship between two individuals — each node in a triggering set of a node \(v\) is able to influence/activate \(v\), and this is more restrictive than the general threshold model, which models collective behavior of the neighbors through threshold functions on subsets of neighbors of a node. Mathematically, the classical triggering model is strictly less expressive than the general threshold model in part because its influence spread is submodular, while the general threshold model can capture complementarity in influence.

Our equivalence theorem shows that once we include group influence — a basic form of “complementarity in influence” in which a group of neighbors of a node \(v\) can collectively influence or activate node \(v\) — as modeled by a hyperedge, we immediately obtain the general threshold model by extending the triggering model from graphs to high-order hypergraph-based networks: The power of modeling collective behavior through the threshold functions in the general threshold model is exactly the same as directly modeling group influence in the hypergraph triggering model. Moreover, the equivalence to the Boolean-function triggering model means that any propagation that can be modeled as a probabilistic version of the monotone Boolean-function operation is equivalent to the stochastic group influence modeled by the hypergraph triggering model.

We also study the mathematical structures of high-order network influence through the prism of stochastic extension. Note that all three models in the above theorem are node-independent models, meaning that the influence to a node \(v\) from \(v\)’s in-neighbors is independent of the influence to other nodes from their in-neighbors. We can further generalize these models to allow correlations among these influence. For the Boolean-function triggering model and the hypergraph triggering model, we can naturally extend them to their correlated versions such that Boolean-function distributions of different nodes or hyperedge subset distributions of different nodes may be correlated. We call them stochastic Boolean function diffusion (SBFD) model and stochastic hypergraph diffusion (SHD) model. For the general threshold model, we can naturally extended it to the correlated general threshold model in that the threshold distributions of nodes could be correlated.

Now a natural question is that whether the equivalence theorem still holds for these three correlated model extensions. In this paper, we show that the SBFD model is equivalent to the SHD model, but the correlated threshold model is a strict sub-class of the SBFD and SHD models. This indicates that the general threshold model and its correlated threshold model extension do have a unique way of specifying the stochastic propagation behavior, such that when this stochastic behavior is not independent across nodes, the resulting behavior is no longer equivalent to other correlated diffusion models.

In summary, our equivalence theorem connects such group influence models with the classical general threshold model, and we further understand their connection and difference when we generalize them to correlated diffusion models. We believe comparative studies of diverse high-order network influence frameworks — hypergraph diffusion, Boolean-function diffusion, and general threshold — not only allow more direct modeling of group influence behaviors but also highlight delicate difference regarding the expressiveness of these general network influence models.

### 1.3 Related Work

Kempe et al. [15] are the first summarizing and proposing several classes of influence propagation models, which are the foundation for studying the influence maximization and other optimization tasks. In particular, they summarize independent cascade and linear threshold as two basic models
from social science and statistical physics literature. Then they extend both models to the general threshold model and the general cascade model and show these two models are equivalent. They further summarize the triggering model as a generalization of the independent cascade and linear threshold model, and show that the triggering model is a strict sub-class of the general threshold model. They then study the submodularity of these models and propose the use of greedy algorithm on these models for the influence maximization task, which is to select $k$ nodes that could maximize the expected number of activated nodes, now commonly referred to as the influence spread. For the general threshold model, they conjecture that the influence spread function is submodular if every local threshold function is submodular, and this is later proved by Mossel and Roch [21].

Since their seminal work, influence diffusion modeling and influence maximization tasks have been extensively studied. One direction is scalable influence maximization, aiming at designing fast algorithms that can scalable to large graphs with millions or even billions of nodes and edges. Early studies on scalable influence maximization focuses on graph-algorithm-based heuristics [7, 29, 9, 12]. Borgs et al. propose the innovative approach of reverse influence sampling (RIS) that achieves near-linear running time and has $1 - 1/e - \varepsilon$ approximation guarantee for small $\varepsilon > 0$ [3]. RIS approach is subsequently improved by a series of studies [28, 27, 22, 25] such that it can now run on billion-edge graphs in just seconds to find 50 seed nodes. It turns out that so far the model that allows the RIS approach is exactly the triggering model.

There are many other directions in influence propagation and influence maximization, for example, competitive and complementary influence propagation [5, 14, 19], seed set minimization [11, 18, 32], profit maximization [20, 26], online influence maximization [8, 16, 31, 30], etc. In some of these studies, influence propagation models are extended and submodularity of the models are studied. But most of the studies are built on the triggering model or the general threshold model, or one of the more specific models such as the independent cascade model or the linear threshold model. We refer to the general survey work in this area for more detailed coverage on these and other related topics [6, 17].

Zhu et al. [33] has proposed an influence diffusion model incorporating hyperedges. In particular, the hyperedge is the same as modeled in this paper, which contains multiple tail nodes and one head node, with the same interpretation that all tail nodes together could activate the head node. In their model, each edge or hyperedge has an independent probability to be live, and thus it corresponds to the generalization of the independent cascade model to directed hypergraphs. This means their model is a special case of the hypergraph triggering model defined in this paper. They study the influence maximization problem under the hypergraph independent cascade model. Since the model is neither submodular nor supermodular, they use sandwich approximation technique [19] to find submodular upper and lower bounds of the original influence spread function, and then apply RIS approach to find the seed set.

Hypergraphs are used in the multimedia recommendation context [4, 24], where a heterogeneous network contains different types of nodes such as users, media contents, and tags, and hyperedges represent relationship among these nodes such as friend relationship among users, similarity relationship among media contents, and tagging relationship among user, content and tags. Amato et al. [1] apply influence maximization algorithms to such multimedia hypergraphs, but they are not really modeling influence propagation directly on the hypergraph. Instead, they simply transform the hypergraph into a bipartite regular graph and then apply influence maximization algorithms on the regular graph.
2 Preliminaries and Model Equivalence of Network Influence

In this section, we review two concrete network influence models: the general threshold model and triggering model. We then define an abstract stochastic-diffusion framework as the mathematical basis for formalizing equivalence among concrete network-influence models.

2.1 General Threshold Model and Triggering Model

The general threshold model and triggering model are two concrete network-influence models originally formulated and studied by Kempe et al. in [15]. The general threshold model is built on nodal set functions, which assign each subset of a ground set a (non-negative) real value. Recall that for a set function \( f : 2^V \rightarrow \mathbb{R} \), we say that (a) \( f \) is monotone if for all \( S \subseteq T \subseteq V \), \( f(S) \leq f(T) \); (b) \( f \) is normalized if \( f(\emptyset) = 0 \); and (c) \( f \) is submodular if for all \( S \subseteq T \subseteq V \) and all \( v \in V \setminus T \), \( f(S \cup \{v\}) - f(S) \geq f(T \cup \{v\}) - f(T) \).

**Definition 1** (General Threshold Model). A general threshold model is defined by a tuple \((V, \{f_v\}_{v \in V})\), where \( V \) is the node set and \( f_v : 2^{V \setminus \{v\}} \rightarrow [0, 1] \) is the threshold function for \( v \in V \), and all \( f_v \)'s are monotone and normalized. The diffusion process proceeds as follows. At the beginning, every node \( v \) samples a threshold \( \theta_v \) uniformly at random from \([0, 1]\) (denoted \( \theta_v \sim U[0, 1] \)). Given a seed set \( S_0 \subseteq V \), at time step \( t = 0 \), all nodes in \( S_0 \) are activated and all nodes not in \( S_0 \) are inactive. Let \( S_t \) be the set of active nodes by time \( t \). At any time step \( t > 0 \), if \( v \in S_{t-1} \), then \( v \in S_t \); if \( v \notin S_{t-1} \), then \( v \) is activated at time \( t \) (i.e. \( v \in S_t \setminus S_{t-1} \)) if \( f_v(S_{t-1}) \geq \theta_v \).

The triggering model is a subclass of the general threshold model, and it contains the well-studied independent cascade and linear threshold models as special cases.

**Definition 2** (Triggering Model). A triggering model is defined by a tuple \((V, \{T_v\}_{v \in V})\), where \( V \) is the node set and \( T_v \) is a triggering distribution over the subsets of \( V \setminus \{v\} \). The diffusion process proceeds as follows. At the beginning, every node \( v \) samples a triggering set \( T_v \sim T_v \). Given a seed set \( S_0 \), at time step \( t = 0 \), all nodes in \( S_0 \) are activated and all nodes not in \( S_0 \) are inactive. Let \( S_t \) be the set of active nodes by time \( t \). At any time step \( t > 0 \), if \( v \in S_{t-1} \), then \( v \in S_t \); if \( v \notin S_{t-1} \), then \( v \) is activated at time \( t \) (i.e. \( v \in S_t \setminus S_{t-1} \)) if \( S_{t-1} \cap T_v \neq \emptyset \).

Note that the general threshold model and triggering model can also be defined on a graph \( G = (V, E) \) with the predefined directed edge set \( E \). In this case, the threshold functions \( f_v \) is defined on the subsets of in-neighbors of \( v \), and the triggering set distribution \( T_v \) is a distribution on the subsets of in-neighbors of \( v \). However, such \( f_v \)'s and \( T_v \)'s can also be extended to \( V \setminus \{v\} \), and thus we do not need to explicitly refer to the edge set \( E \).

2.2 Model Equivalence of Network Influence: Abstract Stochastic Diffusion

Note that concrete network-influence models — such as the triggering model and the general threshold model — not only define the probabilistic time-series of node sets \( S_1, S_2, \ldots \) as the result of influence propagation/activation from each starting seed set \( S_0 \subseteq V \), but also provide details of the underlying diffusion process concerning how activated nodes influence other nodes in each time step. To comparatively study different influence models — particularly regarding their equivalence — we consider an abstract diffusion framework which only focuses on the stochastic profile of activation sequences of influence processes: We say that a sequence of sets \( S_0, S_1, S_2, \ldots \) (\( S_t \subseteq V \) for all \( t \geq 0 \)) is progressive if
(a) for all \( t \geq 0, S_t \subseteq S_{t+1}; \)

(b) for any \( t \geq 0, \) if \( S_t = S_{t+1}, \) then for all \( t' > t, S_{t'} = S_t; \) and

(c) \( S_0 \neq \emptyset. \)

In this paper, we only study influence diffusion that generates such progressive sequences, which means that — like in [15] — (a) once a node is influenced, it remains influenced forever, (b) influence propagation should occur at every step — if in one step there is no newly influenced nodes, then the influence propagation stops, and (c) influence has to be started from some nonempty seed set \( S_0 \) and cannot be generated spontaneously. Let \( n = |V|. \) For such progressive sequences, it is clear that the influence propagation stops within at most \( n - 1 \) steps, and thus we only need a sequence \( S_0, S_1, \ldots, S_{n-1} \) to represent it. The formal definition of the (abstract) stochastic diffusion model is given below (a similar definition is originally given in [6]).

**Definition 3 (Abstract Stochastic Diffusion).** Given a node set \( V \) of size \( n, \) a stochastic diffusion model \( \mathcal{D}_V \) on node set \( V \) is a mapping from every nonempty seed set \( S_0 \in 2^V \setminus \{\emptyset\} \) to a distribution \( \mathcal{D}_{V,S_0} \) over all progressive sequences \( (S_0, S_1, \ldots, S_{n-1}) \) starting from \( S_0. \) That is, for every nonempty seed set \( S_0, \) \( \mathcal{D}_{V,S_0}(S_0, S_1, \ldots, S_{n-1}) \) gives the probability that a progressive sequence \( (S_0, S_1, \ldots, S_{n-1}) \) is generated from the diffusion process starting from seed set \( S_0. \)

Comparing to concrete influence models, such as the triggering and general threshold models, the above abstract stochastic diffusion model focuses on the result of influence processes at each steps rather than the detailed logic or mechanism underlying the influence processes. It distills the influence processes into the distribution \( \mathcal{D}_{V,S_0} \) over progressive sequences for every seed set \( S_0, \) and provides a basis for reasoning about the equivalence of concrete diffusion models and network-influence frameworks:

**Definition 4 (Equivalence of Stochastic Diffusion Models).** Two stochastic network-influence models over the same node set \( V \) are equivalent if in their induced abstract stochastic diffusion models \( \mathcal{D}_V \) and \( \mathcal{D}'_V, \) the distributions over progressive sequences on every seed set are the same, i.e., for all \( S_0 \in 2^V \setminus \{\emptyset\}, \) \( \mathcal{D}_{V,S_0} = \mathcal{D}'_{V,S_0}. \)

### 3 Stochastic Hypergraph Diffusion Model

We now introduce one of the main subjects of the study in this paper, the diffusion model based on directed hypergraphs. Given a set of nodes \( V, \) a directed hyperedge \( h = (U, v) \) represents a connection from a subset \( U \subseteq V \setminus \{v\} \) to a node \( v. \) We call \( U \) as the **tail set** of hyperedge \( h \) (or simply tails), and \( v \) as the **head** of hyperedge \( h. \) A directed hypergraph is represented by \( G = (V, H), \) where \( V \) is a set of \( n \) vertices or nodes, and \( H \) is a set of directed hyperedges on \( V. \) Note that if the tail sets of all hyperedges are singletons, the hyperedge graph degenerates to a normal directed graph.

In the context of information or influence propagation, a hyperedge \( h = (U, v) \) represents a propagation step: if all nodes in \( U \) are activated in the previous step, then \( v \) is activated in the current step. Formally, given a hypergraph \( G \) and a nonempty seed set \( S_0 \subseteq V, \) the deterministic propagation on \( G \) from \( S_0 \) carries out as follows.
At time $t = 0$, all nodes in $S_0$ are activated and all nodes in $V \setminus S_0$ are inactive. Let $S_t$ denote the set of nodes that have been activated by time $t$. At any time step $t > 0$, if $v \in S_{t-1}$, then $v \in S_t$; if $v \not\in S_{t-1}$, and there exists a hyperedge $h = (U, v) \in H$ such that $U \subseteq S_{t-1}$, then $v \in S_t$; for all other $v$ not belonging to the above two cases, $v \not\in S_t$.

Thus, given $G$ and $S_0$, we generate a sequence of node sets $S_0, S_1, S_2, \ldots$, and it is easy to verify that this set sequence is progressive. Note that if $G$ degenerates to a normal directed graph, then sequence $S_0, S_1, \ldots, S_{n-1}$ corresponds to the normal breadth-first-search (BFS) sequence starting from node set $S_0$: $S_t$ is the set of nodes reached from $S_0$ in at most $t$ steps. For simplicity, we also refer to the set sequence $S_0, S_1, \ldots, S_{n-1}$ generated from the hypergraph $G$ and seed set $S_0$ as the BFS sequence of $G$ and $S_0$, and we denote $S_t = \Gamma_t(G, S_0)$ as the set of nodes $S_0$ could reach in hypergraph $G$ within $t$ steps.

The stochastic diffusion under the hypergraph model is by a probabilistic sampling of hypergraphs followed by the deterministic propagation on the sampled hypergraph. The formal definition of the model is given below:

**Definition 5 (Stochastic Hypergraph Diffusion (SHD) Model).** A stochastic hypergraph diffusion (SHD) model is defined as a tuple $(V, G_V)$, where $V$ is a set of $n$ nodes, and $G_V$ is a distribution of hypergraphs on $V$. Given a seed set $S_0 \subseteq V$, we first sample a hypergraph $G \sim G_V$, and then the propagation from $S_0$ proceeds on the hypergraph $G$ to generate the BFS sequence $S_0, S_1, \ldots, S_{n-1}$, where $S_t = \Gamma_t(G, S_0)$ for all $t = 1, 2, \ldots, n - 1$.

It is clear that the SHD model induces an abstract stochastic diffusion model as defined in Definition 3. Note that the SHD model given in Definition 5 is very general, allowing arbitrary distributions over hypergraphs. In this paper, we further investigate an important subclass of the SHD model that has the following node-independence property. We say that a hypergraph distribution $G_V$ is node-independent if $G_V = \times_{v \in V} H_v$, where $H_v$ is a distribution over subsets of hyperedges with head $v$. In other words, a sample $G \sim G_v$ can be obtained by independently sampling subsets of hyperedges pointing to $v$ according to $H_v$, for all $v \in V$, and then combining all these hyperedges together to form the hypergraph. When we restrict that $H_v$ only has supports on subsets of normal edges, not hyperedges, the node-independent SHD model degenerates to the triggering model given in Definition 2. Therefore, we refer this hypergraph version as the hypergraph triggering model.

**Definition 6 (Hypergraph Triggering Model).** A hypergraph triggering model is a stochastic hypergraph diffusion model $(V, G_V)$ where $G_V$ is node-independent, i.e. $G_v = \times_{v \in V} H_v$, where $H_v$ is a distribution over subsets of hyperedges with head $v$.

### 4 Stochastic Boolean-Function Diffusion Model and Its Equivalence to the SHD Model

To unify the study of the stochastic hypergraph diffusion model and the general threshold model, in this section, we further consider a general class of diffusion models that we will refer to as the stochastic Boolean-function diffusion (SBFD) model. Intuitively, we want to study a large class of stochastic diffusion models in which the transition from $S_{t-1}$ to $S_t$ in each propagation step $t \geq 1$ is governed by the same transition function, and this transition function is probabilistically selected.
from a distribution before the propagation starts. Both the SHD model and the general threshold model belongs to this class: In the SHD model, the transition function is given by the hypergraph and the distribution is on the hypergraph, while in the general threshold model, the transition is determined by the threshold functions \( \{ f_v \}_{v \in V} \) and the random thresholds \( \{ \theta_v \}_{v \in V} \) drawn from the uniform distribution on the thresholds. While the transition functions can be viewed as maps from subsets of \( V \) to other subsets of \( V \), they can also be defined by Boolean functions. This is because the state of whether a node is active or not can be represented as a Boolean variable. Thus, it is natural to use Boolean functions to represent the logic underlying influence propagation. We consider the Boolean-function representation also because — as it will be clear later — it is easier to connect with the hypergraph representation.

### 4.1 Stochastic Boolean Function Diffusion Model

For a Boolean vector \( \vec{x} \in \{0, 1\}^V \), we use \( x_v \) to represents its value in the dimension corresponding to \( v \). For \( \vec{x} \), we use \( S^{\vec{x}} \) to represent its corresponding set, i.e. \( S^{\vec{x}} = \{ v \in V \mid x_v = 1 \} \). Conversely, for a subset \( S \subseteq V \), we use \( \vec{x}^S \) to represent the corresponding Boolean vector, i.e. \( x_v^S = 1 \) if \( v \in S \), and \( x_v^S = 0 \) if \( v \notin S \). We use \( \vec{x}_{-v} \) to represent the projection of vector \( \vec{x} \) to \( V \setminus \{ v \} \), i.e. removing the dimension corresponding to \( v \).

For each \( v \in V \), we use Boolean variable \( x_v \in \{0, 1\} \) to represent \( v \)'s state: \( x_v = 0 \) means \( v \) is inactive and \( x_v = 1 \) means \( v \) is activated. Then for each \( v \in V \), we associate \( v \) with a Boolean activation function \( g_v : \{0, 1\}^{V \setminus \{v\}} \rightarrow \{0, 1\} \) to represent how \( v \) is influenced by other nodes in the network. We require that Boolean function \( g_v \) be monotone, meaning that for two vectors \( \vec{x}, \vec{x}' \in \{0, 1\}^{V \setminus \{v\}} \), if \( x_u \leq x'_u \) for all \( u \in V \setminus \{v\} \), then \( g_v(\vec{x}) \leq g_v(\vec{x}') \). Moreover, we require that \( g_v \) is normalized, that is, \( g_v(\vec{0}) = 0 \).

The diffusion process in \( V \) can be represented as a sequence of Boolean vectors \( \vec{x}_0, \vec{x}_1, \ldots, \vec{x}_n-1 \), where \( S^{\vec{x}_t} \) corresponds to the set of active nodes by time \( t \). The transition from \( \vec{x}_t \) to \( \vec{x}_{t+1} \) is governed by the following transition function.

**Definition 7 (Boolean Transition Function).** Given a node set \( V \) and Boolean activation functions \( \{ g_v \}_{v \in V} \), we define the Boolean transition function \( \vec{g} : \{0, 1\}^V \rightarrow \{0, 1\}^V \) as follows: for every \( v \in V \), for every \( \vec{x} \in \{0, 1\}^V \), the dimension of \( \vec{g}(\vec{x}) \) corresponding to \( v \) is defined as \( \vec{g}_v(\vec{x}) = x_v \lor g_v(\vec{x}_{-v}) \).

In the above definition, \( \vec{g}_v(\vec{x}) = x_v \lor g_v(\vec{x}_{-v}) \) means that if \( v \) is already activated, then \( v \) stays active, and if not, then we look at the states of other nodes \( \vec{x}_{-v} \), and if they could activate \( v \) according to the Boolean activation function \( g_v \), then \( v \) is activated. Given the transition function \( \vec{g} \), the diffusion is simply by repeatedly applying \( \vec{g} \), that is, \( \vec{x}_1 = \vec{g}(\vec{x}_0), \vec{x}_2 = \vec{g}(\vec{x}_1), \ldots, \vec{x}_{n-1} = \vec{g}(\vec{x}_{n-2}) \). Thus, the Boolean transition function \( \vec{g} \) is the Boolean representation of the transition function we discussed at the beginning of this section. The stochastic version is then by randomly sampling Boolean activation functions, as defined below.

**Definition 8 (Stochastic Boolean Function Diffusion Model).** A stochastic Boolean function diffusion (SBFD) model is defined as a tuple \( (V, B_V) \), where \( V \) is a set of \( n \) nodes, and \( B_V \) is a distribution on the set of Boolean activation functions \( \{ g_v \}_{v \in V} \). Given a seed set \( S_0 \subseteq V \), we first sample a set of Boolean activation functions \( \{ g_v \}_{v \in V} \sim B_V \), and then the propagation from \( S_0 \) proceeds by repeatedly applying Boolean transition function \( \vec{g} \) on \( \vec{x}^{S_0} \), i.e. \( \vec{x}_{t+1} = \vec{g}(\vec{x}_t) \) for all \( t \geq 0 \), where \( \vec{g} \) is defined in Definition 7. The equivalent set sequence is \( S_t = S_t^{\vec{x}_t} \).
Like in SHD, we say that an SBFD model \( (V, B_V) \) is node-independent if \( B_V = \times_{v \in V} B_v \), where \( B_v \) is a distribution on Boolean activation functions \( g_v \)'s for node \( v \). To be consistent with the terminology in the hypergraph model, we also call node-independent SBFD model as Boolean-function triggering model.

Illustrating that the SBFD model is indeed a general model encompassing both the SHD model and the general threshold model, we first show below that each SHD model and the general threshold model can be directly expressed by an SBFD model.

**Lemma 1** (Expressing SHD by SBFD). Any SHD model can be represented as an SBFD model.

**Proof.** Consider an SHD model \( (V, G_V) \). Let \( G = (V, H) \) be a sample hypergraph according to distribution \( G_V \). Given a seed set \( S_0 \), notice that the propagation on \( G \) from \( S_0 \) can be equivalently described as repeatedly applying function \( \Gamma_1(G, \cdot) \), i.e. \( S_t = \Gamma_1(G, S_{t-1}) \) for all \( t \geq 0 \). Then we just need to write transition function \( \Gamma_1 \) in the form of Boolean activation functions \( \{g_v\}_{v \in V} \). In fact, for every \( v \in V \), let \( (U_1, v), (U_2, v), \ldots, (U_k, v) \) be the set of hyperedges in \( H \) that point to \( v \). Then we can define the Boolean activation function \( g_v(x) = \bigvee_{j=1}^k \bigwedge_{u \in U_j} x_u \). Obviously \( g_v \) is monotone and normalized. Let \( \bar{g} \) be the Boolean transition function derived from \( \{g_v\}_{v \in V} \) according to Definition 7. For every \( S \in 2^V \setminus \{\emptyset\} \), let \( T = \Gamma_1(G, S) \), i.e. \( T \) is the set of nodes activated in \( G \) in one step from source set \( S \). It is easy to check that \( \bar{x}^T = \bar{g}(\bar{x}^S) \). Thus the propagation on hypergraph \( G \) is exactly the same as the propagation following the Boolean activation functions \( \{g_v\}_{v \in V} \). Thus, we only need to set the Boolean function distribution \( B_V \) to be corresponding to \( G_V \), then the SHD model \( (V, G_V) \) becomes the SBFD model \( (V, B_V) \). \( \square \)

**Lemma 2** (Expressing General Threshold Model by SBFD Model). Any general threshold model can be represented as a node-independent SBFD model.

**Proof.** Consider a general threshold model \( (V, \{f_v\}_{v \in V}) \). Let \( \bar{\theta} = (\theta_v)_{v \in V} \) be a sampled threshold vector, i.e. \( \theta_v \sim U[0,1] \). For each \( v \in V \), we fix its threshold \( \theta_v \in [0,1] \). Since \( \theta_v = 0 \) has zero-measure, without loss of generality we consider \( \theta_v > 0 \).

For any \( S \in 2^V \setminus \{\emptyset\} \) and any \( v \in V \), \( v \) would be activated by \( S \) in one step if either \( v \in S \) or \( v \notin S \) and \( f_v(S) \geq \theta_v \). This can be exactly represented as the Boolean activation function \( g_v^{\theta_v}(\bar{x}) = \mathbb{I}\{f_v(S^\bar{x}) \geq \theta_v\} \), where \( \mathbb{I} \) is the indicator function, and we use superscript \( \theta_v \) to explicitly denote that this Boolean activation function is determined by threshold \( \theta_v \). When \( \theta_v > 0 \), we have \( g_v^{\theta_v} \) as a monotone and normalized function, since \( f_v \) is monotone and normalized. Let \( \bar{g}^{\bar{\theta}} \) be the Boolean transition function derived from \( \{g_v^{\theta_v}\}_{v \in V} \) as in Definition 7. It is easy to check that, with the fixed \( \bar{\theta} \), for any seed set \( S_0 \), the propagation sequence generated by the general threshold model is equivalently generated by repeated applying \( \bar{g}^{\bar{\theta}} \), i.e. \( \bar{x}_0 = \bar{x}^{S_0} \), \( \bar{x}_t = \bar{g}^{\bar{\theta}}(\bar{x}_{t-1}) \), \( S_t = S^{\bar{x}_t} \), for all \( t \geq 1 \). Therefore, the general threshold model under the fixed threshold vector \( \bar{\theta} \) is the same as the SBFD model under the fixed Boolean activation functions \( \{g_v^{\theta_v}\}_{v \in V} \). Finally, we define \( B_v \) as the distribution of \( g_v^{\theta_v} \) when \( \theta_v \sim U[0,1] \). Since \( \theta_v \)'s are mutually independent, this would give us a node-independent SBFD model \( (V, \times_{v \in V} B_v) \) that exactly represents the corresponding general threshold model \( (V, \{f_v\}_{v \in V}) \). We remark that for a given \( V \), there are only a finite number of Boolean activation functions, and thus for different \( \theta_v \), we may have the same function \( g_v^{\theta_v} \), then this \( g_v^{\theta_v} \) will have a probability mass in \( B_v \). The actual probability mass value can be determined from function \( f_v \), but we omit the discussion here. \( \square \)
4.2 Equivalence of the SHD model and the SBFD model

The following theorem shows the SHD model is actually equivalent to the SBFD model, meaning that the two have exactly the same expressive power.

**Theorem 2** (Equivalence between SHD and SBFD Models). Every hypergraph $G = (V, H)$ has a corresponding set of Boolean activation functions $\{g_v\}_{v \in V}$ such that they generate the same progressive sequence for every nonempty seed set $S_0$, and vice versa. A direct consequence is that every stochastic hypergraph diffusion model $(V, G_V)$ has a corresponding equivalent stochastic Boolean function diffusion model $(V, B_V)$, and vice versa.

Proof. For the direction from a hypergraph $G = (V, H)$ to a set of Boolean activation functions $\{g_v\}_{v \in V}$, it has been shown in the proof of Lemma 1.

Conversely, suppose that we have Boolean activation function $g_v$ for every $v \in V$. It is well known (see, e.g., [13]) that the reduced disjunctive normal form of any nontrivial (i.e., not constantly 0 or 1) monotone Boolean function does not contain negations of variables. Thus, there exists $U_1, U_2, \ldots, U_k$ such that $g_v(\vec{x}) = \bigvee_{j=1}^k \bigwedge_{u \in U_j} x_u$. Then we can construct $(U_1, v), (U_2, v), \ldots, (U_k, v)$ as the set of hyperedges pointing to $v$. Again they would generate the same progressive sequence for every seed set $S_0$. Thus, the theorem holds. \qed

5 Equivalence between Hypergraph-Triggering Model and General Threshold Model

Since stochastic hypergraph diffusion model is equivalent to the stochastic Boolean-function diffusion model, for convenience, our analysis below is based on the SBFD model. Recall that Lemma 2 shows that any general threshold model can be expressed by equivalent node-independent SBFD model. To show the reverse direction, we first prove the following useful result, which shows that under the node-independent SBFD model, the progressive sequence distribution is fully determined by the set-node activation probabilities. In the following lemmas, we set $S_{-1} = \emptyset$ for convenience.

**Lemma 3.** The distribution of progressive sequences in a node-independent SBFD model $(V, \times_{v \in V} B_v)$ is fully determined by set-node activation probabilities $\{\Pr\{g_v(\vec{x}^S) = 1\}\}_{S,v}$ for all $S \subseteq V$ and $v \in V$.

More specifically, we have

$$\Pr_{g_v \sim B_v, v \in V}\{S_0, S_1, \ldots, S_{n-1} \text{ is generated}\}$$

$$= \prod_{t=1}^{n-1} \prod_{v \in S_t \setminus S_{t-1}} \left( \Pr_{g_v \sim B_v}\{g_v(\vec{x}^{S_{t-1}}) = 1\} - \Pr_{g_v \sim B_v}\{g_v(\vec{x}^{S_{t-2}}) = 1\} \right) \cdot \prod_{v \notin S_{n-1}} \left( 1 - \Pr_{g_v \sim B_v}\{g_v(\vec{x}^{S_{n-2}}) = 1\} \right).$$

(1)

**Proof.** Fix a propagation sequence $(S_0, \ldots, S_{n-1})$. Let $\vec{x}_t = \vec{x}^{S_t}$, for $t = -1, 0, 1, \ldots, n - 1$. Recall from Definition 7 that $\vec{g}$ is the Boolean transition function defined from the model $(V, \times_{v \in V} B_v)$,
with \( \bar{g}_v(\bar{x}) = x_v \lor g_v(\bar{x}_{-v}) \).

\[
\Pr_{g_v \sim B_v, v \in V} \{ S_0, S_1, \ldots, S_{n-1} \text{ is generated} \}
= \Pr_{g_v \sim B_v, v \in V} \left\{ \bigwedge_{t=1}^{n-1} \bar{x}_t = \bar{g}(\bar{x}_{t-1}) \right\}
= \Pr_{g_v \sim B_v, v \in V} \left\{ \bigwedge_{t=1}^{n-1} \left( \bigwedge_{v \in S_t \setminus S_{t-1}} g_v(\bar{x}_{t-1,v}) = 1 \right) \land \left( \bigwedge_{v \notin S_t} g_v(\bar{x}_{t-1,v}) = 0 \right) \right\}
= \Pr_{g_v \sim B_v, v \in V} \left\{ \bigwedge_{t=1}^{n-1} \left( \bigwedge_{v \in S_t \setminus S_{t-1}} (g_v(\bar{x}_{t-1,v}) = 1 \land g_v(\bar{x}_{t-2,v}) = 0) \right) \land \left( \bigwedge_{v \notin S_{n-2}} g_v(\bar{x}_{n-2,v}) = 0 \right) \right\}
= \prod_{t=1}^{n-1} \prod_{v \in S_t \setminus S_{t-1}} \Pr_{g_v \sim B_v} \left\{ g_v(\bar{x}_{t-1,v}) = 1 \land g_v(\bar{x}_{t,v}) = 0 \right\} \cdot \prod_{v \notin S_{n-1}} \Pr_{g_v \sim B_v} \left\{ g_v(\bar{x}_{n-2,v}) = 0 \right\}
= \prod_{t=1}^{n-1} \prod_{v \in S_t \setminus S_{t-1}} \left( \Pr_{g_v \sim B_v} \{ g_v(\bar{x}_{t-1,v}) = 1 \} - \Pr_{g_v \sim B_v} \{ g_v(\bar{x}_{t,v}) = 1 \} \right) \cdot \prod_{v \notin S_{n-1}} \left( 1 - \Pr_{g_v \sim B_v} \{ g_v(\bar{x}_{n-2,v}) = 1 \} \right).
\]

From the above derivation, it is clear that the probability of generating the sequence \( S_0, S_1, \ldots, S_{n-1} \) is fully determined by the set-node activation probabilities \( \Pr\{g_v(\bar{x}^s) = 1\} \)’s for all \( S \subseteq V \) and all \( v \in V \).

We are now ready to show the following theorem on the equivalence between the general threshold model and the hypergraph triggering model.

**Theorem 3** (Equivalence between General Threshold Model and Hypergraph Triggering Model). Every general threshold model \((V, \{f_v\}_{v \in V})\) has a corresponding equivalent hypergraph triggering model \((V, G_V)\), and vice versa.

**Proof.** As we have discussed before, we will use the node-independent SBFD model to show the equivalence. Lemma 2 already shows that any general threshold model has an equivalent representation as a node-independent SBFD model. Thus, we only need to show the reverse direction, that is, every node-independent SBFD model \((V, B_V) = (V, \times_{v \in V} B_v)\) has a corresponding equivalent general threshold model \((V, \{f_v\}_{v \in V})\). Given \( \times_{v \in V} B_v \), we construct the threshold functions \( \{f_v\}_{v \in V} \) such that

\[
f_v(S) = \Pr_{g_v \sim B_v} \{ g_v(\bar{x}^S) = 1 \}, \forall S \subseteq V.\tag{2}
\]

By Lemma 3, the distribution of progressive sequences in the SBFD model \((V, \times_{v \in V} B_v)\) is fully determined by \( \Pr_{g_v \sim B_v} \{ g_v(\bar{x}^S) = 1 \} \) as in Eq. (1). By Lemma 2 and its proof, we see that the general threshold model \((V, \{f_v\}_{v \in V})\) can be represented as a SBFD model \((V, \times_{v \in V} B'_v)\), where \( B'_v \) is the distribution on \( g_v^{\theta_v} \) with \( \theta_v \sim U[0,1] \). Note that \( f_v(S) \) is exactly the set-node activation probability in the model \((V, \times_{v \in V} B'_v)\), since

\[
\Pr_{g_v \sim B'_v} \{ g_v^{\theta_v}(\bar{x}^S) = 1 \} = \Pr_{\theta_v \sim U[0,1]} \{ f_v(S) \geq \theta_v \} = f_v(S).\tag{3}
\]
Then by comparing Eq. (2) with Eq. (3) and applying Lemma 3 again, we know that the distribution of progressive sequences generated by the \((V, x_v \in V B_v)\) is the same as the distribution of progressive sequences generated by \((V, x_v \in V B'_v)\), the latter of which is the same as the distribution of progressive sequences generated by the general threshold model \((V, \{f_v\}_{v \in V})\). Hence, the two models are equivalent according to Definition 4.

A follow-up of the above equivalence result is that the general threshold model is the one using the minimum number of parameters, as shown below.

**Theorem 4.** General threshold model is the one with the minimum number of parameters among all equivalent hypergraph triggering models.

**Proof.** By Theorem 2 and Lemma 3, any hypergraph triggering model (or equivalent node-independent SBFD model) is fully determined by the set-node activation probabilities \(Pr_{g_v \sim B_v} \{g_v(\bar{x}^S) = 1\}\) for all \(S \in 2^V \setminus \{\emptyset\}\) and \(v \in V\). Moreover, for every such \(S\) and \(v\), we could choose a different value for \(Pr_{g_v \sim B_v} \{g_v(\bar{x}^S) = 1\}\) (while satisfying that \(g_v\) is normalized and monotone), and thus we need at least this number of parameters to determine these set-node activation probabilities. For the general threshold model, \(f_v(S) = Pr_{\theta_v \sim U[0,1]} \{f_v(S) \geq \theta_v\}\) provide exactly these parameters. Therefore, the general threshold model uses the minimum number of parameters among the equivalent hypergraph triggering models.

By a rough counting, a general threshold model \((V, \{f_v\}_{v \in V})\) needs \(n \cdot (2^n - 1)\) number of parameters to specify \(f_v(S)\) for every \(S \in 2^V \setminus \{\emptyset\}\) and \(v \in V\). However, if we want to specify a hypergraph triggering model, we need to assign a probability to every subset of hyperedges pointing to every node \(v\). The number of hyperedges pointing to \(v\) is \(2^n - 1\), and the number of possible subsets of these hyperedges is \(2^{2n-1} - 1\). Thus roughly we need \(n \cdot 2^{2n-1} - 1\) parameters to specify a hypergraph triggering model (or an equivalent node-independent SBFD model). Thus, in terms of the number of parameters, general threshold model has exponential savings than a fully expressed hypergraph triggering model. In other words, each general threshold model may have multiple parametric representation in the SHD (or SBFD) models that are all equivalent.

**6 SHD Model and Correlated General Threshold Model**

In the previous section, we show that the node-independent SHD model, a.k.a. hypergraph triggering model, is equivalent to the general threshold model. In this section, we investigate the relationship between the general SHD model and the correlated general threshold model in which node thresholds could be correlated. The correlated general threshold model is defined below.

**Definition 9** (Correlated General Threshold Model). A correlated general threshold (CGT) model is defined as a tuple \((V, \{f_v\}_{v \in V}, \Theta_V)\), where \(V\) is a set of \(n\) nodes, \(f_v : 2^{V \setminus \{v\}} \rightarrow [0,1]\) is the threshold function for \(v \in V\) with all \(f_v\)'s being monotone and normalized, and \(\Theta_V\) is a joint threshold distribution over \([0,1]^n\). The node thresholds \(\bar{\theta} = (\theta_v)_{v \in V}\) is sampled from \(\Theta_V\) at the beginning, and the rest diffusion process follows the exactly the same way as in the general threshold model (Definition 1).

We remark that making the threshold variables \(\theta_v\)'s correlated is certainly a straightforward and natural way of generalizing the general threshold model to the correlated activation setting, but of course readers may come up with other ways of such a generalization.
One question is whether the CGT model would be equivalent to the SHD model. By a similar argument as in Lemma 2, we could show that the CGT model can be represented in the SHD (or SBFD) model. However, the reverse is not true, as shown by the following example.

**Theorem 5.** There is an SHD model instance which cannot be represented in the CGT model.

**Proof.** We show an even stronger example, a digraph “reverse triggering” instance that cannot be represented in the CGT model. Consider nodes $V = \{u_1, u_2, v_1, v_2\}$, where there are possible edges going from $u_1$ and $u_2$ to $v_1$ and $v_2$. We specify the distributions over outgoing edges from $u_1$ and $u_2$ respectively. For $u_1$, with probability 0.5, there is an edge $(u_1, v_1)$, and otherwise there is an edge $(u_1, v_2)$. For $u_2$, with probability 0.1, there are edges $(u_2, v_1)$ and $(u_2, v_2)$, and otherwise there is no outgoing edge.

Now suppose there is an equivalent CGT model instance. Consider the threshold functions of $v_1$ and $v_2$. Observe that:

- Letting $\{u_1\}$ be the seed set, we have $\Pr(\theta_{v_1} \leq f_{v_1}(\{u_1\})) = \Pr(\theta_{v_2} \leq f_{v_2}(\{u_1\})) = 0.5$.
- Letting $\{u_2\}$ be the seed set, we have $\Pr(\theta_{v_1} \leq f_{v_1}(\{u_2\})) = \Pr(\theta_{v_2} \leq f_{v_2}(\{u_2\})) = 0.1$.
- Therefore we know that $f_{v_1}(\{u_1\}) \geq f_{v_1}(\{u_2\})$, and $f_{v_2}(\{u_1\}) \geq f_{v_2}(\{u_2\})$.
- Now consider the joint activation of $v_1$ and $v_2$. When $\{u_1\}$ is the seed set, $\Pr(\theta_{v_1} \leq f_{v_1}(\{u_1\}) \land \theta_{v_2} \leq f_{v_2}(\{u_1\})) = 0$, because $u_1$ never activates $v_1$ and $v_2$ simultaneously. When $\{u_2\}$ is the seed set, $\Pr(\theta_{v_1} \leq f_{v_1}(\{u_2\}) \land \theta_{v_2} \leq f_{v_2}(\{u_2\})) = 0.1$. On the other hand, since $f_{v_1}(\{u_1\}) \geq f_{v_1}(\{u_2\})$ and $f_{v_2}(\{u_1\}) \geq f_{v_2}(\{u_2\})$, we have

\[
0 = \Pr(\theta_{v_1} \leq f_{v_1}(\{u_1\}) \land \theta_{v_2} \leq f_{v_2}(\{u_1\})) \geq \Pr(\theta_{v_1} \leq f_{v_1}(\{u_2\}) \land \theta_{v_2} \leq f_{v_2}(\{u_2\})) = 0.1,
\]

a contradiction.

Thus we conclude that the “reverse triggering” instance constructed above cannot be represented in the CGT model. \(\square\)

Note that in the above proof, we do not even use the hypergraph construction. Thus, in effect it shows that CGT is not strong enough to represent live-edge graph models where income live-edges of different nodes may be correlated. This means that the correlation only on the threshold values of different nodes is still weak in describing more complicated correlations in the general models as the SHD model.

### 7 Discussions and Future Work

In this paper, we show that the general threshold model is equivalent to hypergraph triggering model or Boolean-function triggering model. This indicates that the general threshold model exactly covers the group influence modeled by the hypergraph model. Studying the relationship among these models could help us in better understanding the characteristics of the models.

There are a number of further questions we can ask based on the results of this paper. For example, the general threshold model becomes submodular when every threshold function is submodular. What is the submodular representation under the hypergraph triggering model? The triggering model allows efficient influence maximization algorithms based on the reverse influence
sampling approach [3, 28, 27]. Can we expect that, by utilizing hypergraph triggering model, we may have some efficient algorithm for the general threshold model? Investigating these questions may help us to further enhance our knowledge on influence propagation models and their algorithmic implications.

References

[1] F. Amato, V. Moscato, A. Picariello, and G. Sperli. Influence maximization in social media networks using hypergraphs. In Green, Pervasive, and Cloud Computing (GPC), 2017.

[2] B. Bollobás and O. Riordan. Percolation. Cambridge University Press, 2006.

[3] C. Borgs, M. Brautbar, J. Chayes, and B. Lucier. Maximizing social influence in nearly optimal time. In ACM-SIAM, SODA ’14, 2014.

[4] J. Bu, S. Tan, C. Chen, C. Wang, H. Wu, L. Zhang, and X. He. Music recommendation by unified hypergraph: combining social media information and music content. In Proceedings of the 18th International Conference on Multimedia, pages 391–400, 2010.

[5] C. Budak, D. Agrawal, and A. E. Abbadi. Limiting the spread of misinformation in social networks. In WWW11, 2011.

[6] W. Chen, L. V. Lakshmanan, and C. Castillo. Information and Influence Propagation in Social Networks. Morgan & Claypool Publishers, 2013.

[7] W. Chen, Y. Wang, and S. Yang. Efficient influence maximization in social networks. In KDD, 2009.

[8] W. Chen, Y. Wang, Y. Yuan, and Q. Wang. Combinatorial multi-armed bandit and its extension to probabilistically triggered arms. Journal of Machine Learning Research, 2016.

[9] W. Chen, Y. Yuan, and L. Zhang. Scalable influence maximization in social networks under the linear threshold model. In ICDM, 2010.

[10] P. Domingos and M. Richardson. Mining the network value of customers. In KDD, 2001.

[11] A. Goyal, F. Bonchi, and L. V. Lakshmanan. On minimizing budget and time in influence propagation over social networks. Social Network Analysis and Mining, 2, 2012.

[12] A. Goyal, W. Lu, and L. V. S. Lakshmanan. SIMPATH: An Efficient Algorithm for Influence Maximization under the Linear Threshold Model. In ICDM, 2011.

[13] V. Gurvich and L. Khachiyan. On generating the irredundant conjunctive and disjunctive normal forms of monotone boolean functions. Discrete Applied Mathematics, 96:363–373, 1999.

[14] X. He, G. Song, W. Chen, and Q. Jiang. Influence Blocking Maximization in Social Networks under the Competitive Linear Threshold Model. 2012.

[15] D. Kempe, J. M. Kleinberg, and É. Tardos. Maximizing the spread of influence through a social network. Theory of Computing, 11(4):105–147, 2015. First appeared in KDD’03.
[16] S. Lei, S. Maniu, L. Mo, R. Cheng, and P. Senellart. Online influence maximization. In KDD, 2015.

[17] Y. Li, J. Fan, Y. Wang, and K. Tan. Influence maximization on social graphs: A survey. IEEE Trans. Knowl. Data Eng., 30(10):1852–1872, 2018.

[18] C. Long and R.-W. Wong. Minimizing seed set for viral marketing. In ICDM, pages 427–436. IEEE, 2011.

[19] W. Lu, W. Chen, and L. V. Lakshmanan. From competition to complementarity: comparative influence diffusion and maximization. PVLDB, 2015.

[20] W. Lu and L. V. S. Lakshmanan. Profit maximization over social networks. In ICDM, pages 479–488, 2012.

[21] E. Mossel and S. Roch. On the submodularity of influence in social networks. In STOC ’07, 2007.

[22] H. T. Nguyen, M. T. Thai, and T. N. Dinh. Stop-and-stare: Optimal sampling algorithms for viral marketing in billion-scale networks. In SIGMOD, pages 695–710, 2016.

[23] M. Richardson and P. Domingos. Mining knowledge-sharing sites for viral marketing. In KDD, 2002.

[24] G. Sperl`ı, F. Amato, V. Moscato, and A. Picariello. Multimedia social network modeling using hypergraphs. International Journal of Multimedia Data Engineering Management, 7(3):53–77, 2016.

[25] J. Tang, X. Tang, X. Xiao, and J. Yuan. Online processing algorithms for influence maximization. In SIGMOD, pages 991–1005, 2018.

[26] J. Tang, X. Tang, and J. Yuan. Profit maximization for viral marketing in online social networks. In ICNP, 2016.

[27] Y. Tang, Y. Shi, and X. Xiao. Influence maximization in near-linear time: a martingale approach. In SIGMOD, 2015.

[28] Y. Tang, X. Xiao, and Y. Shi. Influence maximization: near-optimal time complexity meets practical efficiency. In SIGMOD, 2014.

[29] C. Wang, W. Chen, and Y. Wang. Scalable influence maximization for independent cascade model in large-scale social networks. DMKD, 2012.

[30] Q. Wang and W. Chen. Improving regret bounds for combinatorial semi-bandits with probabilistically triggered arms and its applications. In NIPS, 2017.

[31] Z. Wen, B. Kveton, M. Valko, and S. Vaswani. Online influence maximization under independent cascade model with semi-bandit feedback. In NIPS, 2017.

[32] P. Zhang, W. Chen, X. Sun, Y. Wang, and J. Zhang. Minimizing seed set selection with probabilistic coverage guarantee in a social network. In KDD, pages 1306–1315, 2014.
[33] J. Zhu, J. Zhu, S. Ghosh, W. Wu, and J. Yuan. Social influence maximization in hypergraph in social networks. *IEEE Transactions on Network Science and Engineering*, 2018.