Time-Critical Influence Maximization in Social Networks with Time-Delayed Diffusion Process

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Abstract
Influence maximization is a problem of finding a small set of highly influential users, also known as seeds, in a social network such that the spread of influence under certain propagation models is maximized. In this paper, we consider time-critical influence maximization, in which one wants to maximize influence spread within a given deadline. Since timing is considered in the optimization, we also extend the Independent Cascade (IC) model and the Linear Threshold (LT) model to incorporate the time delay aspect of influence diffusion among individuals in social networks. We show that time-critical influence maximization under the time-delayed IC and LT models maintains desired properties such as submodularity, which allows a greedy approximation algorithm to achieve an approximation ratio of $1 - 1/e$. To overcome the inefficiency of the greedy algorithm, we design two heuristic algorithms: the first one is based on a dynamic programming procedure that computes exact influence in tree structures and directed acyclic subgraphs, while the second one converts the problem to one in the original models and then applies existing fast heuristic algorithms to it. Our simulation results demonstrate that our algorithms achieve the same level of influence spread as the greedy algorithm while running a few orders of magnitude faster, and they also outperform existing fast heuristics that disregard the deadline constraint and delays in diffusion.

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1 Introduction

Recently, the rapidly increasing popularity of online social networking sites such as Facebook, Twitter, and Google+ opens up great opportunities for large-scale viral marketing campaigns. Viral marketing, first introduced to the data mining community by Domingos and Richardson [5], is a cost-effective marketing strategy that promotes products by giving free or discounted items to a selected group of highly influential individuals (seeds), in the hope that through the word-of-mouth effects, a large number of product adoption will occur.

Motivated by viral marketing, influence maximization emerges as a fundamental data mining problem concerning the propagation of ideas, opinions, and innovations through social networks. In their seminal paper, Kempe et al. [10] formulated influence maximization as a problem in discrete optimization: Given a network graph \( G \) with pairwise user influence probabilities on edges, and a positive number \( k \), find \( k \) users, such that by activating them initially, the expected spread of influence is maximized under certain propagation models. Two classical propagation models studied in the literature are the Independent Cascade (IC) and the Linear Threshold (LT) model.

The family of models considered in Kempe et al. and its follow-ups, including IC and LT, do not fully incorporate important temporal aspects that have been well observed in the dynamics of influence diffusion. First, the propagation of influence from one person to another may incur a certain amount of time delay, which is evident from recent studies by statistical physicists on empirical social networks. Iribarren and Moro [8] observed that the spread of influence in social networks slows down due to heterogeneity in human activities. Karsai et al. [9] reported similar observations and attributed such slow-down to the bursty nature of human interactions and the topological correlations in networks with the small-world property.

Second, the spread of influence may be time-critical in practice. In a certain viral marketing campaign, it might be the case that the company wishes to trigger a large volume of product adoption in a fairly short time frame, e.g., a three-day sale. As a motivating example, let us suppose that Alice has bought an Xbox 360 console and Kinect with a good discount, but the deal would only last for three days. Alice wanted to recommend this deal to Bob, but whether her recommendation would be effective depends on whether Alice and Bob can be in touch (e.g., meeting in person, or Bob seeing the message left by Alice on Facebook) before the discount expires. Therefore, when we try to maximize the spread of influence for a viral marketing campaign facing this kind of scenarios, we need to take both the time delay aspect of influence diffusion and the time-critical constraint of the campaign into consideration.

To this end, we extend the influence maximization problem to have a deadline constraint to reflect the time-critical effect. We also propose two new propagation models, the Independent Cascade model with Meeting events (IC-M) and the Linear Threshold model with Meeting events (LT-M) to capture the delay of propagation in time. We show that both the IC-M and LT-M models maintain desired properties, namely monotonicity and submodularity, which implies a greedy \((1 - 1/e)\)-approximation algorithm in spite of the NP-hardness of the problem.

For the IC-M model, we design two efficient and effective heuristic algorithms, MIA-M and MIA-C, based on the notion of Maximum Influence Arborescence (MIA) [2] to tackle time-critical influence maximization. On the other hand, similarly for the LT-M model, we adapt the notion Local Directed Acyclic Graph (LDAG) proposed in [4] to obtain the LDAG-M heuristic algorithm. Our experiments evaluate performance of various algorithms for the IC-M model, including the greedy approximation algorithm, MIA-M, and MIA-C heuristics. The empirical results demonstrate that our heuristic algorithms produce seed sets with equally good quality as those mined by approximation algorithm, while being two to three orders of magnitude faster. Moreover, we show that only using standard heuristics such as MIA and disregarding time delays and deadline constraint could result in poor influence spread compared to our heuristics that are specifically designed for this context.

1.1 Related Work

Domingos and Richardson [5, 14] first posed influence maximization as an algorithmic problem. They modeled the problem using Markov random fields and proposed heuristic solutions. Kempe et al. [10] studied
influence probability $p$ of activating neighbors $v$ with independent success probability $p(u,v)$. Once a node is activated, it stays active. The process continues until no new nodes can be activated. The influence maximization problem under the IC model is to find a seed set $S$ with at most $k$ nodes such that the expected number of activated nodes after the diffusion terminates, called influence spread and denoted by $\sigma(S)$, is maximized.

We now describe our extension to the IC model to incorporate time-delayed influence diffusion, which we denote by IC-M (for Independent Cascade with Meeting events). In the IC-M model, each edge $(u,v) \in E$ is also associated with a meeting probability $m(u,v)$ defined by function $m : E \rightarrow [0,1]$ (if $(u,v) \notin E$, $m(u,v) = 0$). As in IC, a seed set $S$ is targeted and activated at step 0. At any step $t \geq 1$, an active node $u$ meets any of its currently inactive neighbors $v$ independently with probability $m(u,v)$. If a meeting event occurs between $u$ and $v$ for the first time, $u$ is given a single chance to try activating $v$, with an independent success probability $p(u,v)$. If the attempt succeeds, $v$ becomes active at step $t$ and will start propagating
influence at \( t + 1 \). The diffusion process quiesces when all active nodes have met with all their neighbors and no new nodes can be activated.

Several possibilities can be considered in mapping the meeting events in the IC-M model to real actions in online social networks. For instance, a user \( u \) on Facebook posting a message on her friend \( v \)’s wall can be considered as a meeting event. In the IC-M model, the meeting probabilities are not necessarily the same for different pair of users. Different pairs of friends may have different frequencies of exchanging messages on each other’s walls, which is reflected by the meeting probability.

Note that the original IC model is a special case of IC-M with \( m(u, v) = 1 \) for all edges \((u, v) \in E\). More importantly, for the original influence maximization problem, the meeting probability is not essential, because as long as \( m(u, v) > 0 \), eventually \( u \) will meet with \( v \) and try to influence \( v \) once. Thus, if we only consider the overall influence in the entire run, there would be no need to introduce meeting probabilities. However, if we consider influence within a \textit{deadline constraint}, then meeting probability is an important factor in determining the optimal seed set.

Formally, for a deadline \( \tau \in \mathbb{Z}_+ \), we define \( \sigma_\tau : 2^V \to \mathbb{R} \) to be the set function such that \( \sigma_\tau(S) \) with \( S \subseteq V \) is the expected number of activated nodes by the end of time step \( \tau \) under the IC-M model, with \( S \) as the seed set. The \textit{time-critical influence maximization with a deadline constraint} \( \tau \) is the problem of finding the seed set \( S \) with at most \( k \) seeds such that the expected number of activated nodes by step \( \tau \) is maximized, i.e., finding \( S^* = \arg \max_{S \subseteq V, |S| \leq k} \sigma_\tau(S) \).

Note that the original influence maximization problem is NP-hard for the IC model \cite{ic} and that problem is a special case of time-critical influence maximization for the IC-M model with all \( m(u, v) = 1 \) and deadline constraint \( \tau = |V| \). This leads to the following hardness result.

\textbf{Theorem 1.} \textit{The time-critical influence maximization problem is NP-hard for the IC-M model.}

\subsection{2.2 Properties of the IC-M Model}

Although to find the optimal solution for time-critical influence maximization with deadline \( \tau \) under IC-M is \textit{NP}-hard (Theorem 1), we show that the influence function \( \sigma_\tau(\cdot) \) is monotone and submodular, which allows a hill-climbing-style greedy algorithm to achieve a \((1 - 1/e)\)-approximation to the optimal.

Given a ground set \( U \), a set function \( f : 2^U \to \mathbb{R} \) is \textit{monotone} if \( f(S_1) \leq f(S_2) \) whenever \( S_1 \subseteq S_2 \). Also, the function is \textit{submodular} if \( f(S_1 \cup \{w\}) - f(S_1) \geq f(S_2 \cup \{w\}) - f(S_2), \forall S_1 \subseteq S_2, \forall w \in U \setminus S_2 \). Submodularity captures the law of diminishing marginal returns, a well-known principle in economics.

\textbf{Theorem 2.} \textit{The influence function} \( \sigma_\tau(\cdot) \) \textit{is monotone and submodular for an arbitrary instance of the IC-M model, given any deadline constraint} \( \tau \geq 1 \).

To prove the theorem, we can view the random cascade process under IC-M using the “possible world” semantics and the principle of deferred decisions. That is, we can suppose that before the cascade starts, a set of outcomes for all meeting events, as well as the “live-or-blocked” identity for all edges are already determined but not yet revealed.

More specifically, for each meeting event (a \((u, v)\) pair and a time step \( t \in [1, \tau]\)), we flip a coin with bias \( m(u, v) \) to determine if \( u \) will meet \( v \) at \( t \). Similarly, for each edge \((u, v) \in E\), we flip once with bias \( p(u, v) \), and we declare the edge “live” with probability \( p(u, v) \), or “blocked” with probability \( 1 - p(u, v) \). All coin-flips are independent. The identity of the edge \((u, v)\) is revealed \textit{in the event} that \( u \) is active and is meeting the inactive \( v \) for the first time. Therefore, a certain set of outcomes of all coin flips corresponds to one \textit{possible world}, denoted by \( X \), which is a deterministic graph (with all blocked edges removed) obtained by conditioning on that particular set of outcomes.

Now we prove Theorem 2.

\textit{Proof of Theorem 2.} Fix a set \( X_M \) of outcomes of all meeting events \((\forall (u, v) \in E, \forall t \in [0, \tau])\), and also a set \( X_E \) of live-or-blocked identities for all edges. Since the coin-flips for meeting events and those for live-edge selections are orthogonal, and all flips are independent, any \( X_E \) on top of an \( X_M \) leads to a possible world \( X \).
Next, we define the notion of “reachability” in $X$. Consider a live edge $(u, v)$ in $X$. Traditionally, without meeting events, $v$ is reachable from $u$ via just one hop. Now with pre-determined meeting sequences, $v$ is reachable from $u$ via $t_u - t_v$ hops, where $t_u$ is the step in which $u$ itself is reached, and $t_v$ is the first step when $u$ meets $v$, after $t_u$. Hence, we say that $v$ is reachable from a seed set $S$ if and only if (1) there exists at least one path consisting entirely of live edges (called live-path) from some node in $S$ to $v$, and (2) the collective number of hops along the shortest live-path from $S$ to $v$ is no greater than $\tau$.

Then, let $\sigma^X(S)$ be the number of nodes reachable from $S$ in $X$ (by the reachability definition above). Let $S_1$ and $S_2$ be two arbitrary sets such that $S_1 \subseteq S_2 \subseteq V$, and let node $w \in V \setminus S_2$ be arbitrary. The monotonicity of $\sigma^X(S)$ holds, since if some node $u$ can be reached by $S_1$, the source of the live-path to $u$ must be also in $S_2$. As for submodularity, consider a certain node $u$ which is reachable from $S_2 \cup \{w\}$ but not from $S_2$. This implies (1) $u$ is not reachable from $S_1$ either, and (2) the source of the live-path to $u$ must be $w$. Hence, $u$ is reachable from $S_1 \cup \{w\}$ but not from $S_1$. This gives $\sigma^X(S_1 \cup \{w\}) - \sigma^X(S_1) \leq \sigma^X(S_2 \cup \{w\}) - \sigma^X(S_2)$.

Let $E_I$ denote the event that $I$ is the true realization (virtually) of the corresponding random process. Taking the expectation over all possible worlds, we have $\sigma_r(S) = \sum_{X} \Pr[E_X] \cdot \sigma^X_r(S), \forall S \subseteq V$, where $X$ is any combination of $X_E$ and $X_M$, and $\Pr[E_X] = \Pr[E_{X_E}] \cdot \Pr[E_{X_M}]$. Therefore, $\sigma(\cdot)$ is a nonnegative linear combination of monotone and submodular functions, which is also monotone and submodular. This was to be shown.

3 Time-Critical Influence Maximization under Time-Delayed Linear Threshold Model

3.1 Model and Problem Definition

In the LT model, a social network is modeled as a directed graph $G = (V, E)$, where $V$ is the set of nodes representing individuals and $E$ is the set of directed edges representing links (relationships, ties, etc.) between individuals. Each edge $(u, v) \in E$ is associated with an influence weight $b(u, v)$ defined by function $b: E \rightarrow [0, 1]$. We require that $\sum_{u} b(u, v) \leq 1, \forall v \in V$. If $(u, v) \notin E$, define $b(u, v) = 0$. Each node $v$ chooses a threshold $\theta_v$ uniformly at random from the interval $[0, 1]$, which represents the weighted fraction of $v$’s in-neighbors that must be active so as to let $v$ become active.

Given the random choices of node thresholds, and a seed set $S \subseteq V$, the dynamics of the diffusion process under the LT model proceed in discrete time steps $0, 1, 2, \ldots$. Initially, at step $0$, nodes in $S$ are activated. Then at any step $t \geq 1$, nodes who have been active in previous steps remain active, and we activate any node $v$ such that its threshold $\theta_v$ is surpassed by the total weights of its currently active in-neighbors. That is, $\sum_{u \in \mathcal{N}^{in}(v)} b(u, v) \geq \theta_v$. The process continues until no new nodes can be activated. The influence maximization problem under the LT model is to find a seed set $S$ with $|S| \leq k$ such that the expected number of activated nodes after the diffusion process terminates, called influence spread and denoted by $\sigma(S)$, is maximized.

We now describe our extension to the LT model that incorporates time-delayed diffusion processes, which we call LT-M (Linear Threshold model with Meeting events). In the LT-M model, each edge $(u, v) \in E$ is also associated with a meeting probability $m(u, v)$ defined by function $m: E \rightarrow [0, 1]$. Note that $m(u, v) = 0$ if $(u, v) \notin E$. Same as in LT, nodes choose a uniform random number out of $[0, 1]$ as threshold, and a seed set $S$ is targeted and activated at step 0.

At any step $t \geq 1$, each active node $u$ remains active and it meets any of its currently inactive out-neighbors $v$ with probability $m(u, v)$, independently. If since $u$’s activation, $u$ and $v$ meet for the first time at $t$, then we say $u$’s influence weight to $v$ is effective. An inactive $v$ becomes active if the total effective weight from its active in-neighbors is at least $\theta_v$. That is,

$$\sum_{u \in \mathcal{N}^{out}(v)} b(u, v) \geq \theta_v,$$
where $\tilde{N}^m(v) \subseteq N^m(v)$ denotes the set of effective in-neighbor of $v$. After $v$ becomes active, it starts to meet her neighbors from the next step. The process quiesses when all active nodes have met with their out-neighbors and no new nodes can be activated.

Note that the original influence maximization problem is NP-hard for the LT model [10] and that is a special case of time-critical influence maximization under LT-M with all $m(u, v) = 1$ and deadline $\tau = |V|$. This leads us to the following hardness result.

**Theorem 3.** The time-critical influence maximization problem is NP-hard for the LT-M model.

3.2 Properties of the LT-M Model

**Theorem 4.** The influence function $\sigma_\tau(\cdot)$ is monotone and submodular for an arbitrary instance of the LT-M model, given any deadline constraint $\tau \geq 1$.

To prove Theorem 4, let us first give an alternative form of the model definition for LT-M. The main idea is to show that the diffusion process guided by LT-M is equivalent to one guided by a random “live-edge” selection process. Recall that in LT-M, each edge $(u, v)$ has an weight $b(u, v)$, and $\sum_u b(u, v) \leq 1$ for all $v$. The random edge selection protocol lets $v$ pick at most one incoming edge (and the corresponding in-neighbor) independently at random, selecting a particular $u$ with probability $b(u, v)$, or selecting no one with probability $1 - \sum_u b(u, v)$. If $v$ selects $u$, then we declare edge $(u, v)$ “live”; otherwise declare it “blocked”. Kempe, Kleinberg and Tardos [10] showed that the distribution over the final active node sets obtained by running the Linear Threshold process is equivalent to that by running the above random live-edge selection process.

In our case, it is also necessary to incorporate the random meeting events in LT-M into the “live-edge” (LE) process and obtain the “LE-M” model. Specifically, now, at any step $t$, we activate any inactive $v$ provided that its selected neighbor $u$ was activated at some earlier step $t' < t$, and since $t' + 1$, they meet for the first time here at $t$.

**Lemma 1.** The Linear Threshold model incorporated with random meeting events is equivalent to the live-edge model incorporated with random meeting events. In other worlds, the distribution over the final active sets under the LT-M model is the same as the one under the LE-M model.

**Proof.** Let $A_t(v)$ be the set of nodes that are already active and have met $v$ at least once by the end of step $t$. For the linear threshold process, if some $v$ is not yet active by the end of step $t$, the chance that $v$ will become active at the next step, $t + 1$, is the probability that the incremental weight contributed by $A_t(v) \setminus A_{t-1}(v)$ manages to push the total effective weight as of $t + 1$ over $\theta_v$. Denote this probability by $P_1(v, t + 1)$.

For the live-edge process, we analyze the probability of the same event, that is, an inactive $v$ will be activated at $t + 1$, given that it has not been active yet by the end of $t$. Let $E_1$ be the event that the corresponding node $u$ of the live-edge $v$ selected becomes active at $t$, and $u$ meets $v$ right away at $t - 1$. Let $E_2$ be the event that this selected $u$ has become active before $t$, and $u$ and $v$ have not met until $t + 1$. The probability that we want equals to $\Pr[E_1 \cup E_2]$. Notice that since $v$ selects at most one live-edge, $E_1$ and $E_2$ are mutually exclusive. Let this probability be $P_2(v, t + 1)$.

What remains to be shown is that $P_1(v, t + 1) = P_2(v, t + 1)$. Notice that the meeting events are all independent and orthogonal to the live-edge selection or the linear threshold process. Thus, by the principle of deferred decision, we can treat these meeting events as if their outcomes were determined before the diffusion starts, but were only going to get revealed as the process proceeds. Without loss of generality, we fixed a set $M$ of outcomes, by independently flipping a coin with bias $m(u, v)$, $\forall (u, v) \in E$ in all time steps.

Conditioning on the fixed $M$, for any $v \in V$ and $t \in \{1, \ldots, \tau - 1\}$, we have

$$P_1^M(v, t + 1) = P_2^M(v, t + 1) = \frac{\sum_{u \in (A_t(v) \setminus A_{t-1}(v))} b(u, v)}{1 - \sum_{u \in A_{t-1}(v)} b(u, v)}.$$
Then, by un-conditioning, i.e., taking the expectation over all possible outcomes of meeting events, we have 
\[ P_1(v, t + 1) = P_2(v, t + 1) \]. This completes the proof.

With Lemma 1, we can apply the same argument used in the submodularity proof for the IC-M model, to prove Theorem 4. The flow of the proof and the techniques used in it is similar to the proof of Theorem 2. We first run the live-edge selection random process and flip coins for all meeting events. Conditioning on a fixed set of meeting events outcomes, and removing all edges but the live ones, we obtain a deterministic graph (possible world). Then following the same arguments used in the proof of Theorem 2 leads us to the submodularity of the influence function \( \sigma_T(\cdot) \) for the LT-M model.

**Approximation Guarantees.** Thus far, we have shown that the influence function \( \sigma_T(\cdot) \) is monotone and submodular under both IC-M and LT-M models, then our time-critical influence maximization problem is a special case of monotone submodular function maximization subject to a cardinality (uniform matroid) constraint. Therefore, we can apply the celebrated result in Nemhauser et al. [13] to obtain a greedy \((1 - 1/e)\)-approximation algorithm. The greedy algorithm repeatedly grows \( S \) by adding \( u \) with the largest marginal influence w.r.t \( S \) in each iteration until \( |S| = k \).

**Generalizing to the Triggering Set Model.** So far we have obtained a constant factor approximation algorithm for the time-critical influence maximization under both IC-M and LT-M models (Theorem 2 and Theorem 4). In fact, this result can be applied to a more general time-delayed propagation model called the Triggering Set model with Meeting events (TS-M).

In the original Triggering Set (TS) model [10], each node \( v \in V \) independently chooses a random triggering set \( T(v) \subseteq N^{in}(v) \), according to some distribution over all subsets of \( N^{in}(v) \). During the influence diffusion process guided by the TS model, a node \( v \) becomes active at step \( t \) if there is some \( u \in T(v) \) that is active at step \( t - 1 \). Viewing the process using the live-edge model, we declare the edge \((u,v)\) live if \( u \) is selected into the triggering set of \( v \); otherwise it is declared blocked.

The Triggering Set model generalizes IC and LT for the following reasons. Recall that for IC, each edge \((u,v)\) in the graph is live with an independent probability \( p(u,v) \). Thus, for any \( v \), we can view the triggering set selection process as \( v \) adds each in-neighbor \( u \) independently. Meanwhile, for LT, recall that it is equivalent to the live-edge selection process, which amounts to saying that \( v \) picks at most one in-neighbor \( u \) into its triggering set with probability \( b(u,v) \), and picks an empty set with probability \( 1 - \sum_u b(u,v) \).

The meeting events are orthogonal and independent from the triggering set selection process, and thus the TS-M model still generalizes the IC-M and LT-M models. Using the same arguments in the proofs for Theorem 2 and Theorem 4, the influence function \( \sigma_T(\cdot) \) is monotone and submodular for every instance of the TS-M model as well, and thus this general model also enjoys the approximation guarantees provided by the greedy algorithm.

**Inefficiency of the Greedy Approximation Algorithm.** Although the greedy approximation algorithm, it is \#P-hard to compute the exact influence in general graphs for the IC and LT models [2, 4]. The hardness applies to IC-M and LT-M, since each of them subsumes corresponding original model. A common practice is to estimate influence spread using Monte-Carlo (MC) simulations, in which case the approximation ratio of Greedy drops to \( 1 - 1/e - \epsilon \), where \( \epsilon \) is small if the number of simulations is sufficiently large. Due to expensive simulations, the greedy algorithm is not scalable to large data, even the implementation can be accelerated by the CELF optimization [12].

### 4 Computing Influence in Arborescences in the IC-M model

In this section, we derive an dynamic programming algorithm that computes exact influence spread in tree structures, which will be used in Sec. 5 to develop MIA-M. The algorithmic problem of efficient computation of exact influence spread in trees in the IC-M model with deadline constraint is also of independent interest.
Algorithm 1: Greedy \((G = (V, E), k, \sigma_\tau)\)

1. \(S \leftarrow \emptyset;\)
2. \(\text{for } i = 1 \rightarrow k \text{ do}\)
3. \(\quad u \leftarrow \arg\max_{v \in V \setminus S} [\sigma_\tau(S \cup \{v\}) - \sigma_\tau(S)];\)
4. \(\quad S \leftarrow S \cup \{u\};\)
5. \(\text{Output } S;\)

An in-arborescence is a directed tree where all edges point into the root. Given a graph \(G = (V, E)\) with influence probability function \(p\) and meeting probability function \(m\), consider an in-arborescence \(A = (V_A, E_A)\) rooted at \(v\) where \(V_A \subseteq V\) and \(E_A \subseteq E\). We assume that influence propagates to \(v\) only from nodes in \(A\). We also assume that there exists at least one \(s \in S\) such that \(s \in V_A\); otherwise no nodes can be activated in \(A\). Given a seed set \(S\) and deadline \(\tau\), we show how to compute \(\sigma_\tau(S)\) in \(A\) in time linear to the size of the graph.

Let \(ap(u, t)\) be the activation probability of \(u\) at step \(t\), i.e., the probability that \(u\) is activated at step \(t\) after the cascade ends in \(A\). Since the events that \(u\) gets activated at different steps are mutually exclusive, the probability that \(u\) ever becomes active by the end of step \(\tau\) is \(\sum_{t=0}^{\tau} ap(u, t)\). By linearity of expectation, \(\sigma_\tau(S) = \sum_{u \in V} \sum_{t=0}^{\tau} ap(u, t)\). Hence, the focus is to compute \(ap(u, t)\), for which we have the following theorem.

**Theorem 5.** Given any \(u \in A\) and any \(t \in [0, \tau]\), the activation probability \(ap(u, t)\) can be recursively computed as follows.

For base cases when \(u \in S\) or \(t = 0\),

\[
    ap(u, t) = \begin{cases} 
        1 & (u \in S \land t = 0) \\
        0 & (u \notin S \land t = 0) \\
        0 & (u \in S \land t \in \{1, \ldots, \tau\})
    \end{cases}
\]  

(1)

For \(u \notin S \land t \in \{1, \ldots, \tau\}\),

\[
    ap(u, t) = \prod_{w \in N^\text{in}(u)} \left(1 - \sum_{t' = 0}^{t-2} ap(w, t')p(w, u)[1 - (1 - m(w, u))^{t-t'-1}]\right)
    - \prod_{w \in N^\text{in}(u)} \left(1 - \sum_{t' = 0}^{t-1} ap(w, t')p(w, u)[1 - (1 - m(w, u))^{t-t'}]\right),
\]  

(2)

where \(N^\text{in}(u) \subseteq V_A\) is the set of in-neighbors of \(u\) in \(A\).

**Proof.** The base cases \((u \in S\) or \(t = 0)\) are trivial. When \(u \notin S\) and \(t \in \{1, \ldots, \tau\}\), for any in-neighbor \(w \in V_A\) of \(u\) and \(t' < t\), \(p(w, u)(1 - (1 - m(w, u))^{t-t'-1})\) is the probability that \(w\) meets \(u\) at least once from \(t' + 1\) to \(t - 1\) and that \((w, u)\) is live. Since the events that \(w\) gets activated at different \(t'\) are mutually exclusive, \(1 - \sum_{t' = 0}^{t-2} ap(w, t')p(w, u)(1 - (1 - m(w, u))^{t-t'-1})\) is the probability that \(u\) has not been activated by \(w\) before or at \(t - 1\). Note that \(\sum_{t' = 0}^{t-1} ap(w, t')p(w, u)(1 - (1 - m(w, u))^{t-t'-1}) = 0\), so the above still holds for \(t = 1\). Similarly, \(\prod_{w \in N^\text{in}(u)} \left(1 - \sum_{t' = 0}^{t-1} ap(w, t')p(w, u)[1 - (1 - m(w, u))^{t-t'}]\right)\) is the probability that \(u\) has not become active before or at \(t\). Hence, Formula 2 is exactly the probability that \(u\) is activated at \(t\), which is \(ap(u, t)\).

The recursion given by Formula 2 can be carried out by dynamic programming, traversing from leaves to the root. In a general in-arborescence, given as input a node \(u\) and a deadline constraint \(\tau\), the time complexity of calculating \(\sum_{t=0}^{\tau} ap(u, t)\) by Formula 2 is polynomial to \(\tau\), which is exponential to the size.
of the input: \( \Theta(\log \tau) \) bits. In principle, this does not affect efficiency much as \( \tau \) is small (5 or 10), and in general much smaller than the size of the graph.

To reduce the amount of computations, a few optimizations can be applied in implementation. Let \( path(u) \) be the path from some \( s \in S \) in \( A \) to \( u \) that has the minimum length among all such paths. Note that we only need to compute \( ap(u, t) \) for \( t \in \{ |path(u)|, \ldots, \tau \} \), as \( u \) cannot be reached earlier than step \( |path(u)| \). That is, \( ap(u, t) = 0 \) when \( t < |path(u)| \). Also, if \( path(u) = \emptyset \) (i.e., does not exist), \( ap(u, t) = 0, \forall t \).

For computing \( ap(u, t) \) on a chain of nodes within an in-arborescence, we derive a more efficient method that reduces the computation to polynomial to \( \log \tau \), as shown in the next section.

### 4.1 Fast Influence Computation on Chain Graphs

Let \( r \in \{1, \ldots, |V|\} \). We consider a length-\( r \) (directed) chain graph \( L = (V_L, E_L) \), where \( V_L = \{u_0, u_1, \ldots, u_r\} \) and \( E_L = \{(u_i, u_{i+1}) : i \in \{0, \ldots, r-1\}\} \):

\[
\begin{align*}
    u_0 &\rightarrow u_1 \rightarrow \ldots \rightarrow u_{r-1} \rightarrow u_r.
\end{align*}
\]

Here, \( L \) can be thought of as a “sub-arborescence” of an in-arborescence \( A \). The problem is to compute \( ap(u, t) \), given a step \( t \in \{0, \ldots, \tau\} \), for any node \( u \) on this chain. Notice that for any particular node \( u \), what really matters in our analysis is the distance, i.e., the length of the path from the closest effective seed to \( u \). Suppose that there is another seed \( u_s \neq u_0 \) on the chain, where \( s < r \). Nodes \( u_1, \ldots, u_{s-1} \) will only be possibly influenced by \( u_0 \) (which is the effective seed for them), due to the structure of the chain, while nodes \( u_{s+1}, \ldots, u_r \) will only be possibly influenced by \( u_s \) (the effective seed), since the influence from \( u_0 \) and any node before \( u_s \) will be blocked by \( u_s \). Therefore, without loss of generality, we assume that the seed set \( S \) is a singleton set \( \{u_0\} \) and the sole seed \( u_0 \) is activated at step 0, i.e., \( ap(u_0, 0) = 1 \) and \( ap(u, t) = 0 \) for any \( t \geq 1 \).

Denote by \( m_i \overset{\text{def}}{=} m(u_{i-1}, u_i) \) the meeting probability and by \( p_i \overset{\text{def}}{=} p(u_{i-1}, u_i) \) the influence probability between \( u_{i-1} \) and \( u_i \), respectively, for all \( i \in \{1, \ldots, r\} \). The activation of node \( u \) at step \( t \) can be characterized by a probability distribution over all possible \( t \), taking all relevant meeting probabilities and influence probabilities into consideration.

For all \( i \in \{1, \ldots, r\} \), let \( X_i \) be the random variable indicating the number of steps needed for node \( u_{i-1} \) to meet \( u_i \) for the first time, given meeting probability \( m_i \). Note that \( X_i \) is a geometric random variable with parameter \( m_i \), and taking values from \( \{1, 2, 3, \ldots\} \). Suppose that the path from \( u_0 \) to \( u \) is of length \( \ell \). Let \( X = \sum_{i=1}^{\ell} X_i \). The following lemma links the activation probability \( ap(u, t) \) with the probability distribution of \( X \).

**Lemma 2.** The activation probability of node \( u \) at time \( t \) is given as

\[
ap(u, t) = \left( \prod_{i=1}^{\ell} p_i \right) \cdot \Pr[X = t].
\]

**Proof.** The event that \( u \) is activated at time \( t \) is equivalent to that for all \( i \in \{1, \ldots, \ell\} \), node \( u_{i-1} \) meets \( u_i \) and activates \( u_i \) upon their first meeting, and the first meeting of \( u_{\ell-1} \) and \( u_{\ell} \) after \( u_{\ell-1} \) is activated occurs at time \( t \). Since \( X = \sum_{i=1}^{\ell} X_i \), \( \Pr[X = t] \) is the probability that \( u_0 \) meets \( u_1 \), and then \( u_1 \) meets \( u_2 \), and so on, and \( u_{\ell-1} \) meets \( u_{\ell} \), and the total number of steps taken until \( u_{\ell-1} \) meets \( u_{\ell} \) is \( t \). \( \prod_{i=1}^{\ell} p_i \) is the probability that all activation attempts are successful upon first meetings, conditioned on the event that meetings of \( u_{i-1} \) and \( u_i \) for all \( i \in \{1, \ldots, \ell\} \) occur. Therefore, it is clear that \( \left( \prod_{i=1}^{\ell} p_i \right) \cdot \Pr[X = t] \) is the probability that \( u = u_{\ell} \) is activated at time \( t \).

With Lemma 2, the key to compute activation probability \( ap(u, t) \) is to compute the probability distribution of \( X \), the sum of \( \ell \) geometric random variables. When all geometric random variables have the same parameter, \( X \) is the well-known negative binomial random variable. We restate the result on the distribution of negative binomial random variable below. For completeness, a proof is given in the appendix.
Let \( \text{Theorem 6.} \) \linebreak \text{theorem for the computation of activation probabilities for the chain graphs.} \linebreak \text{Since the size of the seed set is typically much smaller than the size of the original graph, for any node} \ \tau \ \text{polynomial to log} \ \tau \ \text{variable can be computed via the regularized incomplete beta function, which can also be done in time} \ \tau \ \text{to log} \ \tau \ \text{it is well known that the cumulative distribution of a negative binomial random\text{variable with parameter} \ m \ \text{is distinct, as shown below.} \linebreak \text{Lemma 4.} \ \text{Lemma 3}\) \linebreak \text{that all parameters of geometric random variables are distinct. Then we have} \ \text{Pr}[X = t] = 0 \ \text{for} \ t < \ell, \text{and for all} \ t \geq \ell, \linebreak \text{Pr}[X = t] = m^\ell \cdot (1 - m)^{t - \ell} \cdot \binom{t - 1}{\ell - 1}. \linebreak \text{For the summation of geometric random variables with different parameters, the result is more complex.} \linebreak \text{We cannot find the result from literature for the general case, so we provide our own analysis for the case} \ \text{of node} \ \tau \ \text{We defer the proof of Lemma 4 to the appendix. With the above lemmas, we can derive the following theorem for the computation of activation probabilities for the chain graphs.} \linebreak \text{Theorem 6.} \ \text{Let} \ L = (V_L, E_L) \ \text{be a directed length-} \ r \ \text{chain and let} \ \{u_0\} \ \text{be the seed set. Let} \ u \ \text{be a node in the graph with distance} \ \ell \ \text{from node} \ u_0 \ \text{For the activation probability} \ ap(u, t) \ \text{of node} \ u \ \text{at time} \ t, \text{we have} \ ap(u, t) = 0 \ \text{if} \ t < \ell, \ \text{and (a) if all meeting probabilities} \ m_i \ \text{’s of the edges are distinct, then} \ \linebreak \text{Computing activation probabilities by Theorem 6 has time complexity polynomial to log} \ \tau \ \text{for} \ t \leq \tau. \ \text{Moreover, if we want to compute the cumulative probability} \ \sum_{t=0}^{\tau} ap(u, t), \ \text{for Equation (3) it is easy to see that the key computation is} \ \sum_{t=0}^{\tau} (1 - m_i) t - 1 \ \text{which can be done in time polynomial to log} \ \tau; \ \text{for Equation (4), it is well known that the cumulative distribution of a negative binomial random variable can be computed via the regularized incomplete beta function, which can also be done in time polynomial to log} \ \tau. \linebreak \text{Although chain graphs seem to be a rather restricted version of arborescences, in actual computations, since the size of the seed set is typically much smaller than the size of the original graph, for any node} \ \nu, \ \text{the number of seeds in this particular} \ \nu \ \text{’s in-arborescence is usually quite small, and hence the chain cases will be common. In view of the above, this can help reduce the running time of our dynamic programming algorithm. An interesting open problem is to design an algorithm that computes influence spread in general in-arborescences with running time polynomial in log} \ \tau. \linebreak \text{5 MIA Algorithms for IC-M} \linebreak \text{The aforementioned greedy approximation algorithm is too inefficient to use in practice as it lacks of a way to efficiently compute influence spread in general graphs (Sec. 2). To circumvent such inefficiency, we propose two MIA-based heuristic algorithms. The first algorithm is MIA-M (Maximum Influence Arborescence for IC-M) which uses the dynamic programming in Theorem 5 to compute exact influence of seeds. The second one is MIA-C (Maximum Influence Arborescence with Converted propagation probabilities) which first estimates propagation probabilities for pairwise users by combining meeting events, influence events, and the deadline} \ \tau, \ \text{and then uses MIA for IC to select seeds.} \ \text{Both algorithms first construct a maximum influence in-arborescence (MIA) for each node in the graph, we calculate influence propagated through these MIAs to approximate the influence in the original network.}
5.1 The MIA-M Algorithm

Before describing the algorithm, we first introduce some necessary notations. For a pair of nodes $u, v$, let $\mathcal{P}(u, v)$ be the set of all paths from $u$ to $v$ in $G$. Given a path $P = (u = u_1, \ldots, u_l = v) \in \mathcal{P}(u, v)$, its propagation probability

$$pp(P) = \prod_{i=1}^{l-1} p(u_i, u_{i+1}).$$

Next, we define the maximum influence path from $u$ to $v$ to be

$$\text{MIP}(u, v) = \arg\max_{P \in \mathcal{P}(u, v)} pp(P).$$

Note that $\text{MIP}(u, v) = \emptyset$ if $u = v$ or $\mathcal{P}(u, v) = \emptyset$. In addition, we require at most one MIP($u, v$) for each $u, v$ pair, with ties broken in a consistent way. To compute MIPs, notice that if we transfer influence probability $p(u, v)$ into edge weight $-\log p(u, v)$, computing MIP($u, v$) is equivalent to finding the shortest path from $u$ to $v$ in $G$, and this can be done efficiently by Dijkstra’s algorithm.

For MIA-M, we also introduce the “augmented” length $\ell_A(P)$ of a path $P$ to take meeting events and the deadline constraint into account. Consider an edge $(u_i, u_j) \in P$. Due to random meeting events, after $u_i$ activates at step $t$, its influence will not propagate to $u_j$ exactly at $t + 1$. Instead, the propagation may take multiple steps and the number of such steps is a random variable $X_{i,j}$, which can also be interpreted as the number of Bernoulli trials needed to get the first meeting between $u_i$ and $u_j$ after $u_i$’s activation (See also Sec 4.1). Clearly, $X_{i,j}$ follows the geometric distribution, with success probability $m(u_i, u_j)$, expectation $\frac{1}{m(u_i, u_j)}$, and standard deviation $\sqrt{\frac{1-m(u_i, u_j)}{m(u_i, u_j)}}$. Here we propose to estimate the value of $X_{i,j}$ by

$$\frac{1}{m(u_i, u_j)} - \sqrt{\frac{1-m(u_i, u_j)}{m(u_i, u_j)}},$$

and define the augmented path length $\ell_A(P)$ of $P$ to be the sum of all estimated values of the random variables (one per edge) along $P$:

$$\ell_A(P) = \sum_{(u_i, u_j) \in P} \left( \frac{1}{m(u_i, u_j)} - \sqrt{\frac{1-m(u_i, u_j)}{m(u_i, u_j)}} \right).$$

We empirically verify that this is a good choice for $\ell_A(P)$.

**Constructing Arborescences**

For any node $v$ in $G$, we approximate the influence to $v$ from all $u \in V \setminus \{v\}$ using the maximum influence in-arborescences (MIIA) of $v$. To construct the MIIA rooted at $v$, we first take the union over the maximum influence paths to $v$ over all $u \in V \setminus \{v\}$. After that, two pruning steps will be done. First, we remove paths whose propagation probability is below a pre-defined influence threshold $\theta \in (0, 1)$, which controls the size of the local influence region and is a trade-off between efficiency and seed set quality. Second, to take the effect of deadline into account, we eliminate paths whose augmented length is greater than $\tau$.

**Definition 1** (Maximum Influence In-Arborescence). Given an influence threshold $\theta \in (0, 1)$ and a deadline constraint $\tau \in \mathbb{Z}_+$, the maximum influence in-arborescence of any node $v \in V$ is

$$\text{MIIA}_\tau(v, \theta) = \bigcup_{u \in V, pp(\text{MIP}(u, v)) \geq \theta, \ell_A(\text{MIP}(u, v)) \leq \tau} \text{MIP}(u, v)$$

The full MIA-M is described in Algorithm 2, where $MG(u) = \sigma_\tau(S \cup \{u\}) - \sigma_\tau(S)$ is the marginal influence of $u$ w.r.t. to seed set $S$, $MG(u, v)$ is the marginal influence of $u$ on a specific $v$, and realized($v$) is the cumulative influence realized on $v$ by $S$. Also, for each $u \in V$, $\text{InfSet}(u) = \{v \in V : u \in \text{MIIA}_\tau(v, \theta)\}$.

After constructing MIIA$_\tau(v, \theta)$ and using Theorem 5 to obtain $\sigma_\tau(\{v\})$ for all $v \in V$ (lines 4-10), the algorithm selects $k$ seeds iteratively in a greedy manner, and uses Theorem 5 to update the marginal gain of
Algorithm 2: MIA-M \((G = (V, E), k, \theta, \tau)\)

1. \(S \leftarrow \emptyset\);
2. \(\forall v \in V, MG(v) \leftarrow 0\) and realized\((v) \leftarrow 0\);
3. \(\forall v \in V, \text{MIA}_v(v, \theta) \leftarrow \emptyset\) and \(\text{InfSet}(v) \leftarrow \emptyset\);
4. \(\text{foreach } v \in V \text{ do}\)
   
   | Compute \(\text{MIA}_v(v, \theta)\) (Definition 1);
   | \(\text{foreach } u \in \text{MIA}_v(v, \theta) \text{ do}\)
   | \(\text{InfSet}(u) \leftarrow \text{InfSet}(u) \cup \{v\}\);
   | Compute \(\text{ap}(v, t, \{u\}, \text{MIA}_v(v, \theta)), \forall t \leq \tau\) (Theorem 5);
   | \(MG(u, v) \leftarrow \sum_{t=0}^{\tau} \text{ap}(v, t, \{u\}, \text{MIA}_v(v))\);
   | \(MG(u) \leftarrow MG(u) + MG(u, v)\);
5. \(\text{for } i = 1 \rightarrow k \text{ do}\)
   
   | Computes \(u \leftarrow \argmax_{v \in V \setminus S} MG(v)\);
   | \(S \leftarrow S \cup \{u\}\);
   | \(\text{foreach } v \in \text{InfSet}(u) \text{ do}\)
   | realized\((v) += MG(u, v)\);
   | \(\text{foreach } w \in \text{MIA}_v(v, \theta) \text{ do}\)
   | Compute \(\text{ap}(v, t, S \cup \{w\}, \text{MIA}_v(v, \theta)), \forall t \leq \tau\) (Theorem 5);
   | \(MG_{\text{new}}(w, v) \leftarrow \left[\sum_{t=0}^{\tau} \text{ap}(v, t, S \cup \{w\}, \text{MIA}_v(v, \theta))\right] - \text{realized}(v)\);
   | \(MG(w) \leftarrow MG(w) + MG_{\text{new}}(w, v) - MG(w, v)\);
   | \(MG(w, v) \leftarrow MG_{\text{new}}(w, v)\);

5.2 The MIA-C Algorithm

We now discuss our second algorithm, MIA with Converted propagation probability (MIA-C). It consists of two steps. First, for each \((u, v), \in E\), we estimate a converted propagation probability \(p_c(u, v)\) that incorporates meeting probability \(m(u, v), influence probability p(u, v), and deadline \(\tau, with the intention to simulate the influence spread under the IC-M model in the original IC model. Second, after obtaining all \(p_c(u, v)\), we treat these converted probabilities as parameters for the IC model and run the MIA algorithm proposed for IC to select \(k\) seeds.

In the IC-M model with deadline \(\tau\), the value of \(p_c(u, v)\) depends on \(p(u, v), m(u, v), \text{and } \tau\). We use the following conversion function to obtain \(p_c(u, v)\):

\[
p_c(u, v) = p(u, v) \cdot \left(1 - (1 - m(u, v))^{\beta}\right),
\]

where \(\beta \in [1, \tau]\) is the parameter used to estimate the number of meeting attempts. If \(\beta = 1\), \(p_c(u, v) = p(u, v) \cdot m(u, v)\), in which case we are pessimistic that \(u\) has only one chance to meet \(v\) (the minimum possible, assuming \(u\) itself activates before \(\tau\)). On the other hand, if \(\beta = \tau\), \(p_c(u, v) = p(u, v) \cdot \left[1 - (1 - m(u, v))^{\tau}\right]\), for which we are optimistic that \(u\) has \(\tau\) chances to meet \(v\) (the maximum possible). To achieve a balanced heuristic, we let \(\beta = \frac{\tau}{2}\) for all pairs of \(u, v\), and experiments show that this estimation turns out to be more effective than other choices in most cases.

After the probability conversion step, we utilize MIA (Algorithm 4, [2]) to find the seed set, making MIA-C take the advantage of updating marginal gains of nodes in an extremely efficient manner.

The time complexity of converting probabilities is \(O(|E|)\), and second part of MIA-C has the same time complexity as MIA, which is \(O(|V|t_{m\theta} + kn_{m\theta}n_{s\theta}(t_{m\theta} + \log |V|))\).
6 LDAG Algorithms for LT-M

In this section, we present a dynamic programming algorithm that computes exact influence spread in directed acyclic graphs (DAGs), and use it to develop our heuristic solution based on DAGs. Chen et al. [4] proved that computing exact influence spread in general graphs for any node set is \#P-hard. Now we show that in directed acyclic graphs, computing influence can be done in time linear to the size of the graph.

6.1 Fast Influence Computation in DAGs

Consider an acyclic subgraph \( D = (V, E) \). Let \( S \subseteq V \) be the seed set. For any \( v \in V \), let \( ap_D(u, t \mid S) \) be the activation probability of \( u \) and step \( t \), that is, the probability that \( u \) is activated right at step \( t \) in DAG \( D \) under the LT-M model, given the seed set \( S \). When the notations are clear from the context, we write \( ap(v, t) \) for short. By definition, \( ap(v, t) = 1 \) if \( v \in S \wedge t = 0 \). Similarly, \( ap(v, t) = 0 \) if \( v \in S \wedge t > 0 \), or \( v \not\in S \wedge t = 0 \). These cases form the basis for the recursion that we will develop for the dynamic programming algorithm, which computes \( ap(v, t) \) when \( v \not\in S \wedge t > 0 \).

The following theorem shows the important linear property of activation probability in a DAG. The proof for this theorem also requires Lemma 1.

**Theorem 7.** For any \( v \in V \setminus S \), and any \( t \in [1, \tau] \), the activation probability of \( v \) at \( t \) is

\[
ap(v, t) = \sum_{u \in \mathcal{N}^n(v)} b(u, v) \sum_{t' = 0}^{t-1} ap(u, t') \cdot m(u, v) \cdot (1 - m(u, v))^{t-t'-1}. \tag{6}
\]

**Proof.** By Lemma 1, the event that a certain node \( v \) becomes activate at a certain step \( t \) has the same probability to happen under the LT-M model and the LE-M model. Let \( E_{u,v} \) be the event that \( v \) selects edge \((u, v)\) as a live edge. By the protocol of the live-edge selection process, we have \( \Pr[E_{u,v}] = b(u, v) \). Let \( R(v, t) \) be the event that \( v \) is reached by \( S \) at step \( t \). Then, for all \( v \in V \setminus S \),

\[
ap(v, t) = \sum_{u \in V \setminus \{v\}} \Pr[E_{u,v}] \cdot \Pr[R(v, t) \mid E_{u,v}]. \tag{7}
\]

In order to activate \( v \) at \( t \), the selected \( u \) must be already active before or at \( t - 1 \). Furthermore, the events that \( u \) activates at possible steps \( 0, 1, \ldots \) are mutually exclusive. Hence, the probability that event \( R(v, t) \) happens conditioned on \( E_{u,v} \) is

\[
\Pr[R(v, t) \mid E_{u,v}] = \sum_{t' = 0}^{t-1} ap(u, t') \cdot m(u, v) \cdot (1 - m(u, v))^{t-t'-1}. \tag{8}
\]

Putting Eq. (7) and (8) together, we obtain Eq. (6). This completes the proof.

A directed application of Theorem 7 gives us a dynamic programming method to compute activation probabilities.

6.2 The LDAG-M Heuristic Algorithm

In this subsection, we propose a DAG-based heuristic algorithm, called LDAG-M, which leverages the proposed dynamic programming approach to compute influence efficiently. The algorithm first constructs a local directed acyclic graph (LDAG) for each node \( v \) in the graph. These LDAGs are small subgraphs of the original network. Then, LDAG-M uses influence propagated through these LDAGs to approximate the influence propagated in the original network.
Then it adds an empty edge set \( F \) to obtain transfer the meeting probability \( m_{u,w} \) when no new node has influence value of at least \( \lambda \). There are possibly more than one DAGs satisfying the above conditions, but ideally, we want to find an optimal DAG \( D \). We construct LDAGs heuristically in a greedy fashion.

InfSet structure called

The full LDAG-M algorithm first uses the approach described above to find out a suitable local DAG for all nodes in the graph (lines 3-4), then it greedily select at most \( k \) seeds, given the input \( G = (V,E) \) and the budget \( k \). The pseudo-code of LDAG-M is given in Algorithm 4. For each node \( u \), we also maintain a data structure called \( InfSet(u) := \{ v \in V : u \in LDAG(v, \lambda) \} \), a value \( MG(u) \) which denotes the incremental influence by adding \( u \) to the current seed set \( S \), and a value \( realized(v) \) denotes the cumulative influence realized on \( v \) by the seed set \( S \). After constructing LDAGs and InfSets, we use Theorem 7 to compute obtain \( \sigma_+(\{ u \}) \) for all \( u \) in the graph (lines 7-9). Line 10-19 iteratively pick \( k \) seeds in a greedy manner. After selecting a new seed \( u \), we need to update the incremental influence of all \( w \) in \( LDAG(v, \lambda), \forall v \in InfSet(u) \).
Algorithm 4: LDAG-M \((G = (V, E), k, \lambda)\)

1. \(S \leftarrow \emptyset; \forall v \in V : MG(v) \leftarrow 0; realized(v) \leftarrow 0;\)
2. foreach \(v \in V\) do
   3. Compute \(LDAG(v, \lambda)\) (Algorithm 3);
   4. Post-process (prune) \(LDAG(v, \lambda)\);
   5. foreach \(u \in LDAG(v, \lambda)\) do
      6. \(InfSet(u) \leftarrow v;\)
      7. Compute \(ap(v, t|\{u\}), \forall t \leq \tau\) (Theorem 7);
      8. \(MG(u, v) \leftarrow \sum_{t=0}^{\tau} ap(v, t|\{u\});\)
      9. \(MG(u) += MG(u, v);\)
   10. for \(i = 1 \rightarrow k\) do
        11. \(u \leftarrow \arg\max_{v \in V\setminus S} MG(v);\)
        12. \(S \leftarrow S \cup \{x\};\)
        13. foreach \(v \in InfSet(u)\) do
            14. \(realized(v) += MG(u, v);\)
        15. foreach \(w \in LDAG(v)\) do
            16. Compute \(ap(v, t|S \cup \{w\}), \forall t \leq \tau\) (Theorem 7);
            17. \(MG_{new}(w, v) \leftarrow \sum_{t=0}^{\tau} ap(v, t|S \cup \{w\}) - realized(v);\)
            18. \(MG(w) += MG_{new}(w, v) - MG(w, v);\)
            19. \(MG(w, v) \leftarrow MG_{new}(w, v);\)

| Dataset       | NetHEPT | WikiVote | Epinions | DBLP  |
|---------------|---------|----------|----------|-------|
| Number of nodes | 15K     | 7.1K     | 75K      | 655K  |
| Number of edges | 62K     | 101K     | 509K     | 2.0M  |
| Average degree | 4.12    | 26.6     | 13.4     | 6.1   |
| Maximum degree | 64      | 1065     | 3079     | 588   |
| #Connected components | 1781 | 24        | 11       | 73K   |
| Largest component size | 6794 | 7066     | 76K      | 517K  |
| Average component size | 8.55 | 296.5    | 6.9K     | 9.0   |

Table 1: Statistics of Real-world Networks.

7 Empirical Evaluations

We conduct experiments on four real-world datasets to evaluate MIA-M and MIA-C, and compare them to a few other algorithms in terms of seed set quality and running time. All experiments are conducted on a server running Microsoft Windows Server 2008 R2 with 2.33GHz Quad-Core Intel Xeon E5410 CPU and 32G memory.

7.1 Experiment Setup

Dataset Preparation. The statistics of the datasets are summarized in Table 1. NetHEPT is a standard dataset in this area: It is a collaboration network extracted from the High Energy Physics Theory section (1991 to 2003) of the arXiv e-print repository (http://www.arxiv.org/). The network data is publicly available at http://research.microsoft.com/en-us/people/weic/projects.aspx. DBLP (http://www.informatik.uni-trier.de/~ley/db/) is a much larger collaboration network from the DBLP computer science bibliography server maintained by Michael Ley. Nodes in both datasets represent authors, and if \(u\) and \(v\) collaborated at least once, we draw direct arcs \((u, v)\) and \((v, u)\). Note that edges in the NetHEPT and DBLP graphs may carry multiplicity greater than 1, because two authors might co-author more than one papers.
It outputs the top-k Degree is a heuristic based on the notion of degree centrality that considers high degree nodes influential.

Graph Parameters (Models for Assigning Influence and Meeting Probabilities). Influence probabilities are assigned using the Weighted Cascade (WC) model proposed in Kempe et al. [10]: For WikiVote and Epinions, \( p(u,v) = 1/d^u(v) \) where \( d^u(v) \) is the in-degree of \( v \). For NetHEPT and DBLP, \( p(u,v) = A(u,v)/A(v) \) where \( A(u,v) \) is the number of papers in which \( u \) and \( v \) were co-authors, and \( A(v) \) is the number of papers that \( v \) published in total. We also do experiments on the Trivalency (TV) model proposed in Chen et al. [2]: On every edge \( (u,v) \), we choose its edge probability uniformly at random from the set \{0.001, 0.01, 0.1\}.

For meeting probabilities, it is reasonable to deem that the more friends an individual \( u \) has, the smaller the chance that \( u \) could meet a certain friend is. Therefore, we assign each edge \( (u,v) \) its meeting probability \( m(u,v) = \frac{d^u(v)}{\text{out}(u)c(d^u(v))} \), where \( d^u \) is the out-degree of \( u \) and \( c \) is a constant chosen to be 5 here. In addition, we test on cases where for every edge \( (u,v) \), \( m(u,v) \) is chosen uniformly at random from the set \{0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8\}.

Algorithms Compared. We evaluate MIA-M, MIA-C, the greedy algorithm (Greedy) and the other two: Degree and MIA. For Greedy, we apply CELF and run Monte Carlo for 10000 times as in Kempe et al. [10]. Degree is a heuristic based on the notion of degree centrality that considers high degree nodes influential. It outputs the top-k highest out-degree nodes as seeds (Kempe et al. [10]). We then test MIA, one of the state-of-the-art heuristic algorithms for the standard IC model. For the purpose of comparisons, we let MIA select seeds disregarding meeting probabilities and the deadline constraint entirely, i.e., treating \( m(u,v) = 1 \) for all edges and \( \tau = |V| \). We also test on the Prefix-excluding MIA (PMIA) algorithm, which is a variant of MIA [2]. Since the results are similar, we omit it here. MIA-M, MIA-C, and MIA all use 1/320 as the influence threshold \( \theta \), as recommended by Chen et al. [2]. For MIA-C, we choose \( \beta = \frac{2}{5} \) since it gives more stable performance (compared to 1 and \( \tau \)) in most cases.

7.2 Results and Analysis

We compare the five algorithms on quality of seeds sets and running time. The deadline \( \tau \) is set to 5 (relatively short time horizon) and 15 (relatively long time horizon) in all results reported. Greedy is too slow to finish on Epinions and DBLP within a reasonable amount of time (3 days).

Quality of Seed Sets. The quality of seed sets is evaluated based on the expected influence spread achieved. To ensure fair and accurate comparisons, we run MC simulations 10000 times to get the “ground truth” influence spread of all seed sets obtained by various algorithms. Fig. 1 and 2 illustrate influence spread achieved on datasets with weighted and uniform random meeting probabilities, respectively.

On graphs with weighted meeting probabilities, except for Greedy, MIA-M has the highest seed set quality, while MIA-C is the second best in most test cases. MIA-M performs consistently better than Degree and MIA, e.g., on Epinions, the influence of 50 seeds by MIA-M is 99.4% (\( \tau = 5 \)) and 53.6% (\( \tau = 15 \)) higher than those by MIA. On NetHEPT and WikiVote, MIA-M produces seed sets with equally good quality as Greedy does, e.g., on WikiVote, when \( \tau = 5 \) they both achieve influence spread of 101; when \( \tau = 15 \), MIA-M (181) even achieves 3% higher than Greedy (175).

When meeting probabilities are assigned uniformly at random, seed sets by MIA-M, MIA-C, and MIA tend to have matching influence, all being close to Greedy and better than Degree. Most often, MIA-M is marginally better than MIA-C and MIA. The reason why MIA catches up is that it picks seeds assuming all \( m(u,v) = 1 \) and \( \tau = |V| \), and in expectation those seeds will still have high influence under uniform random
Figure 1: Influence spread (#nodes, Y-axis) against seed set size (X-axis) on graphs with weighted meeting probabilities.

(a) NetHEPT  
(b) WikiVote  
(c) Epinions  
(d) DBLP

Figure 2: Influence spread (#nodes, Y-axis) against seed set size (X-axis) on graphs with uniform random meeting probabilities.

(a) NetHEPT  
(b) WikiVote  
(c) Epinions  
(d) DBLP
Table 2: Running Time (Weighted Meeting Probability)

| Algorithm | NetHEPT | WikiVote | Epinions | DBLP |
|-----------|---------|----------|----------|------|
| Greedy    | 5       | 15       | 5        | 15   |
|           | 40m     | 1.3h     | 22m      | 28m  |
| MIA-M     | 1.6s    | 15s      | 7.9s     | 43s  |
|           | 47s     | 5.1m     | 6.6m     | 10m  |
| MIA-C     | 0.3s    | 0.3s     | 0.4s     | 0.5s |
|           | 2.7s    | 3.3s     | 24s      | 33s  |
| MIA       | 0.3s    | 0.3s     | 1.4s     | 1.4s |
|           | 12s     | 13s      | 40s      | 41s  |

Table 3: Running Time for Random Meeting Probabilities

| Algorithm | NetHEPT | WikiVote | Epinions | DBLP |
|-----------|---------|----------|----------|------|
| Greedy    | 5       | 15       | 5        | 15   |
|           | 44m     | 1.5h     | 1.1h     | 3.2h |
| MIA-M     | 3.8s    | 21.4s    | 28.7s    | 2.5m |
|           | 3.3m    | 12.4m    | 7.3m     | 14.3m|
| MIA-C     | 0.2s    | 0.2s     | 0.57s    | 1.23s|
|           | 4.9s    | 10.2s    | 32.5s    | 45.6s|
| MIA       | 0.4s    | 0.5s     | 6.5s     | 6.5s |
|           | 37.9s   | 39.7s    | 38.9s    | 43.1s|

Running Time. We demonstrate the running time results on weighted meeting probability datasets in Table 2 and the results on the uniform random cases in Table 3. Greedy takes 0.5 to 1.3 hours to finish on NetHEPT and WikiVote, and fails to complete in a reasonable amount of time (three days) on Epinions and DBLP with $\tau = 5$. Degree finishes almost instantly in all test cases so it is not included in the table.

MIA-C and MIA are three orders of magnitude faster than Greedy, since both benefit from the linearity rule of activation probabilities when updating marginal gains [2]. MIA-C is more efficient because its converted probabilities are smaller than the original influence probabilities used in MIA, and hence arborescences are smaller for MIA-C under the same influence threshold ($1/320$). MIA-M is two orders of magnitude faster than Greedy, and is scalable to large graphs like Epinions and DBLP. It is slower than MIA-C and MIA because its dynamic programming procedure computes activation probabilities associated with steps, and hence is not compatible with the linearity rule of activation probabilities.

Figure 3: Influence spread vs. meeting probabilities on NetHEPT.
Effects of Deadline Constraints and Meeting Probabilities. It can be seen from both Fig. 1 and 2 that as $\tau$ increases from 5 to 15, seed sets by all algorithms obtain higher influence spread, which is intuitive to see. We also test other values of $\tau$, such as 10 and 20, and since the trend is the same, to avoid densely clustered figures we do not include them here. For meeting probabilities, we conduct five test cases on NetHEPT, running Greedy with meeting probability $0.2, 0.4, 0.5, 0.6, 0.8$ for each edge in the graph. The results in Fig. 3 show that as meeting probabilities increase, the influence spread of the seed set also go up.

8 Conclusion and Discussions

In this paper, we extend the IC and LT models, and their generalization, the Triggering Set model, to include time-delayed influence diffusion and we consider the time-critical influence maximization problem. We prove the submodularity of the influence function under these time-delayed models, and propose fast heuristics to solve the problem. There are a number of extensions and future directions on time-critical influence maximization.

One extension is to use login probabilities to model time-delayed influence diffusion, which could fit better into online social networks. Specifically, each user has a probability of entering the system, and only after this action, the user could be influenced by her friends who are already activated. Incorporating these login probabilities into the current models turns out to be more challenging than incorporating meeting probabilities, because it introduces dependency in activation events. We have obtained partial results using more complicated dynamic programming methods to deal with this case, which we include in Appendix B.

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Appendix

A Analysis on the summation of geometric random variables

In this appendix, we provide analysis of the distribution of summation of geometric random variables. We first provide a proof for the negative binomial distribution for completeness.

**Lemma 3 (Negative Binomial Distribution, re-stated).** Let $X = \sum_{i=1}^{\ell} X_i$, where each $X_i$ is a geometric random variable with parameter $m$ and range $\{1, 2, 3, \ldots\}$. Then we have $\Pr[X = t] = 0$ for $t < \ell$, and for all $t \geq \ell$,

$$
\Pr[X = t] = m^\ell \cdot (1 - m)^{t - \ell} \cdot \binom{t - 1}{\ell - 1}.
$$

**Proof.** We prove the lemma by an induction on $\ell$. For the base case when $\ell = 1$, $X$ is just a geometric random variable with parameter $m$, and thus $\Pr[X = t] = (1 - m)^{t - 1} m$. For the induction step, assume that the lemma holds when $\ell = z$ for some $z$. Let $X' = \sum_{i=1}^{z} X_i$ and $X = \sum_{i=1}^{z+1} X_i$. It is clear that when $t < z + 1$, $\Pr[X = t] = 0$. Then for the case of $\ell = z + 1$ and $t \geq z + 1$, we have

$$
\Pr[X = t] = \sum_{t'=z}^{t-1} \Pr[X' = t'] \cdot (1 - m)^{t-t'-1} m
$$

$$
= \sum_{t'=z}^{t-1} \left[ m^z \cdot (1 - m)^{t'-z} \cdot \binom{t' - 1}{z - 1} \right] \cdot (1 - m)^{t-t'-1} m
$$

$$
= m^{z+1} \cdot (1 - m)^{t-(z+1)} \cdot \sum_{t'=z}^{t-1} \binom{t' - 1}{z - 1}
$$

$$
= m^{z+1} \cdot (1 - m)^{t-(z+1)} \cdot \binom{t - 1}{z},
$$

where for the second equation we have applied the induction hypothesis, and for the last one we have applied the property of binomial coefficients: $\sum_{j=k}^{n} \binom{j}{k} = \binom{n+1}{k+1}$. This completes the proof.\qed
We now study the case where all geometric random variables $X_i$'s have distinct parameters $m_i$. Before proving Lemma 4, we first show the following technical lemma.

**Lemma 5.** Suppose that $m_i \neq m_j$ whenever $i \neq j$. Then,

$$\sum_{i=1}^{\ell} \frac{(1-m_i)^{\ell-1}}{(m_i - m_{\ell+1}) \cdot \prod_{j=1,j \neq i}^{\ell}(m_j - m_i)} = \frac{(1-m_{\ell+1})^{\ell-1}}{\prod_{j=1}^{\ell}(m_j - m_{\ell+1})}.$$  \hspace{1cm} (9)

**Proof.** Let $t_i \overset{\text{def}}{=} 1 - m_i$, then Formula (9) (with $\ell$ switched to $z$) becomes

$$\sum_{i=1}^{z} t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_{z+1}) = \frac{t_i^{z-1}}{t_i^{z+1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_i)}.$$  \hspace{1cm} (10)

Equivalently, we need to show the following holds:

$$\sum_{i=1}^{z} t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_{z+1}) = t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_i) = 1.$$  \hspace{1cm} (11)

For the base case of $z = 1$, it is clear that (10) holds. Suppose Formula (10) holds for some $z > 1$, now we show that it also holds for the case of $z + 1$. We first conduct the following manipulation:

$$\begin{align*}
\sum_{i=1}^{z} t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_{z+2}) &= \sum_{i=1}^{z} t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_i) - \sum_{i=1}^{z} t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z+1}(t_j - t_{z+2}) \\
&= t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_{z+1}) - t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z+1}(t_j - t_{z+2}) \\
&= t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_{z+1}) - t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z+1}(t_j - t_{z+1}) \\
&= t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_{z+1}) - t_i^{z-1} \cdot \prod_{j=1,j \neq i}^{z}(t_j - t_{z+1}) = 0.
\end{align*}$$  \hspace{1cm} (12)
where (12) is obtained by applying the induction hypothesis. Also notice that in (11),
\[ \sum_{i=1}^{Z} t_i^{z-1} \cdot \frac{\Pi_{j=1,j\neq i}(t_j - t_{z+2})}{t_{z+2} \cdot \Pi_{j=1,j\neq i}(t_j - t_i)} = 1, \]
based again on the induction hypothesis (with \( t_{z+1} \) replaced by \( t_{z+2} \)).

Hence, we have
\[ 1 - \sum_{i=1}^{Z} t_i^{z+1} \cdot \frac{\Pi_{j=1,j\neq i}(t_j - t_{z+2})}{t_{z+2} \cdot \Pi_{j=1,j\neq i}(t_j - t_i)} = 0 \]
This implies that equation (10) holds for all \( z \geq 1 \), which completes the proof. \( \blacksquare \)

We are now ready to prove Lemma 4.

**Lemma 4 (re-stated).** Let \( X = \sum_{i=1}^{\ell} X_i \), where each \( X_i \) is a geometric random variable with parameter \( m_i \) and range \( \{1, 2, 3, \ldots\} \). Suppose that all \( m_i \)'s are distinct. Then we have \( \Pr[X = t] = 0 \) for \( t < \ell \), and for all \( t \geq \ell \),
\[ \Pr[X = t] = \left( \prod_{i=1}^{\ell} m_i \right) \cdot \sum_{i=1}^{\ell} \frac{(1 - m_i)^{t-1}}{\prod_{j=1,j\neq i}(m_j - m_i)}. \]

**Proof.** We prove the lemma by an induction on the path length \( \ell \). For the base case when \( \ell = 1 \), \( X = X_1 \), and thus \( \Pr[X = t] = (1 - m_1)^{t-1}m_1 \) for all \( t \geq 1 \). For the induction step, suppose that the lemma is true for \( \ell = z \) for some \( z \in \mathbb{Z}_+ \). Let \( X' = \sum_{i=1}^{z} X_i \) and \( X = \sum_{i=1}^{z+1} X_i \). By the induction hypothesis, we have that for all \( t \geq z \),
\[ \Pr[X' = t] = \left( \prod_{i=1}^{z} m_i \right) \cdot \sum_{i=1}^{z} \frac{(1 - m_i)^{t-1}}{\prod_{j=1,j\neq i}(m_j - m_i)}. \]

Now consider the case of \( \ell = z + 1 \). It is clear that for \( t < z + 1 \), \( \Pr[X = t] = 0 \). For \( t \geq z + 1 \), the event \( \{X = t\} \) is the union of mutually exclusive events of \( \{X' = t', X_{z+1} = t - t'\} \) for all \( t' = z, z + 1, \ldots, t - 1 \). Thus we have
\[ \Pr[X = t] = \sum_{t'=z}^{t-1} \Pr[X' = t'] \cdot (1 - m_{z+1})^{t-t'+1} \cdot m_{z+1} \]
\[ = \left( \prod_{i=1}^{z+1} m_i \right) \cdot \sum_{t'=z}^{t-1} \sum_{i=1}^{z} \frac{(1 - m_i)^{t'-1}}{\prod_{j=1,j\neq i}(m_j - m_i)} \cdot (1 - m_{z+1})^{t-t'+1}, \]
where we have applied the induction hypothesis for the last equality.

Next, we switch the order of the two summations and get
\[ \Pr[X = t] = \left( \prod_{i=1}^{z+1} m_i \right) \cdot \sum_{i=1}^{z} \sum_{t'=z}^{t-1} \frac{(1 - m_i)^{t'-1}}{\prod_{j=1,j\neq i}(m_j - m_i)} \cdot (1 - m_{z+1})^{t-t'+1} \]
\[ = \left( \prod_{i=1}^{z+1} m_i \right) \cdot \left[ \sum_{i=1}^{z} \frac{(1 - m_{z+1})^{t-2}}{\prod_{j=1,j\neq i}(m_j - m_i)} \cdot \sum_{t'=z}^{t-1} \frac{1 - m_i}{1 - m_{z+1}} \cdot \left( \frac{1 - m_{z+1}}{1 - m_{z+1}} \right)^{t'-1} \right] \]
\[ = \left( \prod_{i=1}^{z+1} m_i \right) \cdot \left[ \sum_{i=1}^{z} (1 - m_{z+1})^{t-2} \cdot \frac{1 - m_i}{1 - m_{z+1}} \cdot \left( \frac{1 - m_{z+1}}{1 - m_{z+1}} \right)^{t-1} \right] \]
In online social networks, users usually will not stay online interacting with friends all the time. For example, on Twitter or Facebook, users may respond to posts generated by friends perhaps hours or even days ago. Processes.

How to incorporate the login events into both IC and LT models to reflect time-delayed influence diffusion becomes active when it first logs into the system. In every subsequent time step \( t \geq 0 \), a node \( u \) becomes active in step \( t \) by time \( t \), meaning that \( u \) can pass its influence \( b(u, v) \) to \( v \). An inactive \( v \)

\[
\begin{align*}
&= \left( \prod_{i=1}^{z+1} m_i \right) \cdot \sum_{i=1}^{z} \frac{(1 - m_i)^{z-1}(1 - m_{z+1})^{t-z} - (1 - m_i)^{t-1}}{(m_i - m_{z+1}) \cdot \prod_{j=1,j\neq i}^{z} (m_j - m_i)} \\
&= \left( \prod_{i=1}^{z+1} m_i \right) \cdot \left[ \sum_{i=1}^{z} \frac{(1 - m_i)^{t-1}}{\prod_{j=1,j\neq i}^{z} (m_j - m_i)} + \sum_{i=1}^{z+1} \frac{(1 - m_i)^{z-1}(1 - m_{z+1})^{t-z}}{(m_i - m_{z+1}) \cdot \prod_{j=1,j\neq i}^{z} (m_j - m_i)} \right] \tag{13}
\end{align*}
\]

For the second summation term in (13), we need to prove the following equation:

\[
\sum_{i=1}^{z} \frac{(1 - m_i)^{z-1}(1 - m_{z+1})^{t-z}}{(m_i - m_{z+1}) \cdot \prod_{j=1,j\neq i}^{z} (m_j - m_i)} = \frac{(1 - m_{z+1})^{t-1}}{\prod_{i=1}^{z+1} (m_i - m_{z+1})}. \tag{14}
\]

This can be done by dividing both sides of (14) by \( (1 - m_{z+1})^{t-1} \) and applying Lemma 5. Then, we substitute (14) back into (13) and get

\[
\Pr[X = t] = \left( \prod_{i=1}^{z+1} m_i \right) \cdot \sum_{i=1}^{z+1} \frac{(1 - m_i)^{t-1}}{\prod_{j=1,j\neq i}^{z+1} (m_j - m_i)}.
\]

Thus, the lemma holds for \( \ell = z + 1 \), and this completes the proof. \( \square \)

### B Time-Critical Influence Maximization with Login Events

In online social networks, users usually will not stay online interacting with friends all the time. For example, on Twitter or Facebook, users may respond to posts generated by friends perhaps hours or even days ago. This time-delayed behavior can be modeled using the probabilities of logging into the social systems. Let \( \ell_u \in [0, 1] \) denote the login probability of user \( u \in V \). In any time step \( t \), each user \( u \in U \) independently logs into the social networking site with probability \( \ell_u \), or stays offline with probability \( 1 - \ell_u \). Next, we describe how to incorporate the login events into both IC and LT models to reflect time-delayed influence diffusion processes.

**Independent Cascade with Login Events (IC-L)** In the IC-L model, we start with a seed set \( S \) at time step 0. In every time step \( t \geq 0 \), a node \( u \) has an independent online probability \( \ell_u \). For \( s \in S \), it becomes active when logging into the system for the first time.

If a node \( u \) becomes active in step \( t \), then \( u \) will have a single chance to influence each of its inactive neighbor \( v \) at step \( t' \geq t + 1 \), when \( v \) logs in for the first time after \( t \). This attempt has a success probability of \( p(u, v) \). If the attempt succeeds, \( v \) will become active at \( t' \); otherwise, \( u \) cannot attempt to influence \( v \) even if \( v \) logs in again in the future. The diffusion process terminates either naturally, i.e., when no more nodes can be activated, or by a specific deadline, i.e., the end of time step \( \tau \).

It can be easily shown that the influence maximization problem is also NP-hard under the IC-L model, as we can restrict all login probabilities to be 1, making IC-L equivalent to IC.

**Linear Thresholds with Login Events (LT-L)** Similar to the traditional LT model, in the LT-L model, each node \( v \in V \) chooses a threshold \( \theta_v \) uniformly at random from \([0, 1]\), and it is influenced by its neighbors \( u \) based on edge weight \( b(u, v) \).

The diffusion dynamics unfold as follows. First, a seed set \( S \) is targeted at time step 0, and for any \( s \in S \), \( s \) becomes active when it first logs into the system. In every subsequent time step \( t \geq 0 \), each node \( v \) logs in with probability \( \ell_v \). If a node \( u \) becomes active in step \( t \), we say \( u \) is an effective active in-neighbor of its currently inactive out-neighbor \( v \) by time \( t \), meaning that \( u \) can pass its influence \( b(u, v) \) to \( v \). An inactive \( v \)
would get activated at step $t'$ if $v$ logs in and the total weight of its effective active neighbors by time $t' - 1$ is at least $\theta_v$:
\[ \sum_{u \in E(A_v')} b(u, v) \geq \theta_v. \]

The propagation of influence stops either naturally or by the end of deadline $\tau$. Similarly, influence maximization under the LT-L model is also NP-hard, due to that the LT-L model subsumes LT when all login probabilities are 1.

### B.1 Submodularity and Approximation Guarantees

Kempe et al. [10] shows that both IC and LT are special cases of the Triggering Set (TS) model, in which each node $v$ randomly picks a Triggering Set $T(v)$, a subset of its in-neighbors $\mathcal{N}_\text{in}(v)$, according to some distribution over subsets of $\mathcal{N}_\text{in}(v)$. An inactive $v$ becomes active at time step $t$ if there exists some $u \in T(v)$ that are active by $t - 1$.

Combining the TS model with deadline constraint and login probability, we propose the TS-L model. In this model, an inactive $v$ becomes active at time step $t$ if it logs in at $t$ and notices for the first time that there exists $u \in T_v$ such that $u$ is already active (i.e., before $t$). Note that TS-L generalizes IC-L and LT-L:

- For the IC-L model, the triggering set $T(v)$ of each user $v$ is to include every in-neighbor $u \in \mathcal{N}_\text{in}(v)$ independently with probability $p(u, v)$.
- For the LT-L model, the triggering set $T(v)$ consists of at most one in-neighbor of $v$: a particular $u \in \mathcal{N}_\text{in}(v)$ is chosen with probability $b(u, v)$. And with probability $1 - \sum_{u \in \mathcal{N}_\text{in}(v)} b(u, v)$, $T(v) = \emptyset$.

In all three models, the login events happen independently for all users at all time steps. Thus, TS-L indeed includes IC-L and LT-L as special cases.

Next, we show that the influence spread function is submodular for the TS-L model, which then implies that submodularity also holds for IC-L and LT-L.

**Theorem 8.** The influence function $\sigma(\cdot)$ is monotone and submodular under the TS-L model.

**Proof.** First, we fix a set $X_T$ of outcomes of triggering set selections for all nodes. In this fixed $X_T$, if $u \in T(v)$, then we declare $(u, v)$ to be live; otherwise we declare it blocked. Next, for each $u$ at each time step $t \in [0, \tau]$, we independently flip a coin with bias $\ell_u$ to determine whether $u$ will log in in $t$. Eventually, we obtain a sequence of log-in events for $u$. Let $X_L$ be the set of such sequences of all pairs.

Any fixed $X_L$, on top of a fixed $X_T$, forms a possible world $X$ where influence propagates deterministically. First, consider a live-edge path $P = \{u_0, u_1, \ldots, u_z\}$ in possible world $X$, where $z$ is the length of $P$. Suppose, without loss of generality, that $u_0 \in S$ and $u_i \notin S$, for all $1 \leq i \leq z$. Note that if none of the nodes in $P$ is a seed, such a path can be ignored in influence propagation.

Let $t(P, u_0)$ be the time step at which $u_0$ becomes active (since $u_0 \in S$, technically the activation time of $u_0$ does not depend on $P$, and we use this notation simply for technical convenience). For all $1 \leq i \leq z$, let $t(P, u_i)$ be the first time step at which $u_i$ logs in after the activation of $u_{i-1}$, its predecessor on $P$. Hence, by model definition, $u_i$ will become active at $t(P, u_i)$ if we ignore other paths along which influence may propagate to $u_i$. Clearly, if $t(P, u_z) \leq \tau$, then the end node $z$ becomes active by the deadline and should count toward influence spread.

We now define the notion of reachability in a possible world $X$, which is slightly different from the traditional reachability in graphs due to log-in events. We say $v$ is reachable from seed set $S$ iff (1) there exists a live-edge path $P_{S,v}$ from some $s \in S$ to $v$, and (2) $t(P_{S,v}, v) \leq \tau$. Note that if there are multiple live-edge paths from $S$ to $v$ in this possible world, we take the shortest one in terms of the activation time of $v$.

Let $\sigma_X(S)$ be the number of nodes reachable from $S$ by the reachability definition above. Now consider two seed set $S_1$ and $S_2 \supseteq S_1$, and a node $x \in V \setminus S_2$: $\sigma_X(\cdot)$ is clearly monotone as if $u$ can be reached by $S_1$, then the origin of the live-edge path to $u \in S_1$ must also belong to $S_2$, thus we have $\sigma_X(S_1) \leq \sigma_X(S_2)$. 24
For submodularity, consider a node $u$ is reachable from $S_2 \cup \{x\}$ but not $S_2$, then we conclude immediately that (1) $u$ is not reachable from $S_1$ either, and (2) the origin of the live-path to $u$ must be $x$. Hence, $u$ is reachable from $S_1 \cup \{x\}$ but not $S_1$, and we have $\sigma_X(S_1 \cup \{x\}) - \sigma_X(S_1) \geq \sigma_X(S_2 \cup \{x\}) - \sigma_X(S_2)$.

The influence function $\sigma(\cdot)$ can be written as a nonnegative linear combination of $\sigma_X(\cdot)$ functions: for any $S \subseteq V$

$$\sigma(S) = \sum_X \Pr[X] \cdot \sigma_X(S)$$

where $X$ is any combination of $X_T$ and $X_M$, and $\Pr[X] = \Pr[X_T] \cdot \Pr[X_M]$. Hence, $\sigma(\cdot)$ is also monotone and submodular, which completes the proof.

\[\square\]

**B.2 Influence Computation under IC-L Model and LT-L Model**

We now consider the problem of computing influence spread under these two models. Since IC-L (LT-L) subsumes the classical IC (resp. LT) model as a special case (by setting all login probabilities to be 1), computing the exact value of $\sigma(S)$ for any seed set $S \subseteq V$ remains $\#P$-hard [2, 4]. Therefore, we focus on the computation of influence spread in local structures, i.e., Maximum Influence Arborescence (MIA) for IC-L and Local Directed Acyclic Graphs (LDAG) for LT-L. In what follows, we give formulas for computing the activation probability of a node, given its local influence structure. The construction of such local influence structures can be done in a similar fashion to MIA-M (Section 5) and LDAG-M (Section 6), and we omit details here.

**B.2.1 IC-L Model: Partial Results for Computations in an In-Arborescence**

For the IC-L model, since the login probability is the property of node instead of edge, the events of users' activated by different in-neighbors are no longer independent. For example, suppose node $v$ has two in-neighbors $u_1$ and $u_2$, and suppose that both $u_1$ and $u_2$ are seeds. Then the event that $u_1$ activates $v$ by time $\tau$ is the joint event of (a) $u_1$ logged in at some time $t < \tau$ and get activated; (b) $v$ logged in at some time $t'$ with $t < t' \leq \tau$; and (c) $u_1$ successfully influenced $v$ at time $t'$ when $v$ logged in. Similarly we have the event that $u_2$ activates $v$ by time $\tau$ as the three parallel joint events. When comparing these events, we can see that (a) and (c) for $u_1$ and $u_2$ are independent, but not (b), since they are both for the login event of $v$. This is different from the meeting probability model IC-M we provide before, in which case we would replace (b) above with $u_1$ meeting $v$ at time $t'$, which is indeed independent of $u_2$ meeting $v$ at time $t'$. As the result, we need a new dynamic programming method to compute the activation probabilities and influence spread, even in local influence regions.

Consider an in-arborescence $H = (V_H, E_H)$ and a node $v \in V_H$. Let $A^{in}(v,t) = \{u_1, u_2, \ldots , u_m\} \subseteq N'_H(v)$ denote the set of $v$’s active in-neighbors (in $H$) at the beginning of time step $t$ and let $m = |A^{in}(v,t)|$. We order these nodes by their activation time (ascending order, with ties broken arbitrarily). Also, let $p_i$ be the influence probability $p(u_i,v)$. Let $T_{[1,m]} = (t_1, t_2, \ldots , t_m)$ be the ordered sequence of activation time steps of nodes in $A^{in}(v,t)$. Let $P_{[1,m]} = (p_1, p_2, \ldots , p_m)$ be the corresponding sequence of influence probabilities.

**Theorem 9.** Consider a node $v \in V_H \setminus S$. Given $T_{[1,m]}$ and $P_{[1,m]}$ (that correspond to a particular sequence of active in-neighbors), $v$’s activation probability $ap(v,t,T_{[1,m]}, P_{[1,m]})$, $\forall t \geq t_m$, can be computed as follows:

$$ap(v,t,T_{[1,m]}, P_{[1,m]}) = (1-(1-\ell_v)^{t_2-t_1}) \cdot (1-p_1) \cdot ap(v,t,T_{[2,m]}, P_{[2,m]}) + (1-\ell_v)^{t_2-t_1} \cdot ap(v,t,T_{[2,m]}, P'_{[2,m]}),$$

(15)

where $m \geq 3$ and $P'_{[2,m]} = 1-(1-p_1)(1-p_2) \oplus P_{[3,m]}$, with $\oplus$ denoting the operation of sequence concatenation. There are two base cases.

- If $m = 1$, we have $ap(v,t,(t_1), (p_1)) = (1-\ell_v)^{t-t_1-1} \cdot \ell_v \cdot p_1$.
- If $m = 2$, apply Equation (15) with $P_{[3,m]}$ being an empty sequence.
Proof. It is straightforward to verify the correctness of the two base cases. For \( m \geq 3 \), two cases arise as sub-problems:

(i). If \( v \) has logged in at least once during this period with probability \( 1 - (1 - \ell_v)^{t_2-t_1} \), then in order for \( v \) to be active at time \( t \), \( u_1 \) must have tried but failed to activate \( v \), which happens with probability \( 1 - p_1 \). Hence, \( u_1 \) can be disregarded and we only need to consider the subproblem on the remaining in-neighbor sequence \( \{u_2, u_3, \ldots, u_m\} \). This gives the first summation term in Equation (15).

(ii). If \( v \) never logged in during \( (t_1, t_2] \), then, when it first logs in at some time step \( t' \geq t_2 + 1 \), \( u_1 \) and \( u_2 \) each has a single chance to independently activate \( v \). Their “collective” influence probability is \( 1 - (1 - p_1)(1 - p_2) \). This leads to the second summation term in Equation (15).

Since (i) and (ii) are mutually exclusive, the recursive formula correctly computes the activation probability. Note that if there are \( k \geq 2 \) in-neighbors whose activation time steps are the same, we can “collapse” them into a single node, influence probability \( 1 - \prod_{i=1}^{k}(1 - p_i) \), similar to case (ii) above.

Computing Equation (15) takes \( O(m) \) time, but it only works for a fixed sequence of active in-neighbors. Given a seed set \( S \), there may well be multiple possible sequences of in-neighbors to be considered, and the final activation probability of \( v \) at time step \( t \) is a linear combination of \( ap(v, t) \) w.r.t. all applicable sequences. Thus, Theorem 9 should only be regarded as a partial result, and further analysis is needed to obtain the final dynamic programming formula for computing activation probability in arborescences for the IC-L model.

Also, note that Theorem 9 is applicable to all non-seed nodes. For seeds, dynamic programming is not required: Consider any \( s \in S \), the probability that \( s \) becomes active at time step \( t \) is simply \( (1 - \ell_s)^t \cdot \ell_s \).

B.2.2 LT-L Model: Computations in Directed Acyclic Graphs

For the LT-L model, activation probabilities can be similarly computed as in the LT-M model (Theorem 7).

**Theorem 10.** Consider any directed acyclic graph \( H = (V_H, E_H) \), and a node \( v \in V_H \setminus S \). For any time step \( t \in [1, \tau] \), the activation probability of \( v \) at \( t \) is

\[
ap(v, t) = \sum_{u \in N_{\text{in}}^H(v)} b(u,v) \sum_{t'=0}^{t-1} ap(u, t') \cdot \ell_v \cdot (1 - \ell_v)^{t-t'-1},
\]

where \( N_{\text{in}}^H(v) \) is the set of in-neighbors of \( v \) in \( H \).

**Proof (Sketch).** The arguments in the proof of Theorem 7 also apply to the LT-L model. The main observation is that in the live-edge graph model equivalent to the LT model, each node \( v \) only randomly select one in-neighbor \( u \) and make edge \((u, v)\) live. With only one in-coming live edge \((u, v)\), whether we consider the event of \( v \) meeting \( u \) after \( u \) is activated as in the LT-M model or the event \( v \) logging in after \( u \) is activated at in the LT-L model is essentially the same.

Again, for seeds, the probability that a seed \( s \in S \) becomes active at time step \( t \) is simply \( (1 - \ell_s)^t \cdot \ell_s \).