Timed Influence: Computation and Maximization

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ABSTRACT

We consider a cost model for diffusion in a network that captures both the scope of infection and its propagation time: The edges of the network have associated lengths which model transmission times, and influence scores are higher for faster propagation. We propose an intuitive measure of timed influence, which extends and unifies several classic measures, including the well-studied “binary” influence [Richardson and Domingos 2002; Kempe et al. 2003] (which only measures scope), a recently-studied threshold model of timed influence [Gomez-Rodriguez et al. 2011] (which considers a node influenced only within a fixed time horizon), and closeness centrality (which is extended from being defined for a single node to multiple seed nodes and from a fixed network to distributions). Finally, we provide the first highly scalable algorithms for timed influence computation and maximization. In particular, we improve by orders of magnitude the scalability of state-of-the-art threshold timed influence computation. Moreover, our design provides robust guarantees and is novel also as a theoretical contribution.

1. INTRODUCTION

Most models of information diffusion [24, 28, 35] focus on what we refer to here as binary influence. The network is modeled by a set of instances (directed graphs over the same set of nodes) or by a probabilistic model that defines a distribution over such instances. A node is considered infected by a set of seed nodes \( S \) (in an instance) if it is reachable from \( S \). The influence of \( S \) is then defined as the average (or expected) number of nodes reachable from \( S \).

More recently, a notion of continuous-time or timed influence was proposed by Gomez-Rodriguez et al. [25], which more finely captures the potency of an information cascade by also considering the speed in which infection is propagated. In a timed influence model, elapsed time is modeled by associating nonnegative edge lengths with the edges in each instance. As with binary influence, we can work with a fixed set of instances (directed graphs over the same set of nodes) or with a probabilistic model (distribution over such instances). In particular, the binary Independent Cascade (IC) model of Kempe et al. [28] naturally extends to permit live edges to have nonnegative randomized edge lengths (REL) [11, 22, 25]. The propagation time of the infection from a seed set \( S \) of nodes to a node \( v \) is modeled by the shortest path distance to \( v \) [25].

A node can then be considered influenced if it is reached within a certain elapsed time threshold \( T \) [22, 25]. A smoother and more general way to model the potency of a set of seed nodes, which we propose here, applies decay models to capture the decrease in the value of getting influenced as a function of elapsed time or distance [15, 19]. A slower propagation means a weaker impact. Smooth decay with time or distance naturally occurs in physical systems and is extensively used in averaging or aggregating data points across space or time [36].

More precisely, we define the timed influence of a seed set \( S \) with respect to an non-increasing (decay/kernel) function \( \alpha \) as the expectation \( E[\sum v \alpha(t_v)] \), where \( t_v \) is the distance of node \( v \) from the seed set. When our model is a fixed set of instances, we use the average over instances instead of the expectation. Natural and commonly used decay functions include exponential decay \( \alpha(x) = \exp(-\lambda x) \), polynomial decay \( \alpha(x) = 1/poly(x) \), Gaussian \( \alpha(x) = \exp(-\lambda x^2) \), and threshold, obtained using \( \alpha(x) = 1 \) when \( x \leq T \) and \( \alpha(x) = 0 \) otherwise. The range of different functions used in practice demonstrates the value of this flexibility in modeling.

Binary and threshold influence are special cases of our timed influence model, where binary influence is captured using \( \alpha(x) = 1 \) for finite \( x \) and \( \alpha(+\infty) = 0 \). Timed influence also generalizes the distance-decaying variant [11, 15, 20, 34] of closeness centrality [3], which was studied with exponential, harmonic, threshold, and general decay functions. In this context, closeness centrality is timed influence when there is a single seed node and a single instance (a graph with fixed edge lengths). Either one of the extensions to multiple seed nodes and to randomized edge lengths is natural and powerful. In particular, the randomization of edge lengths means that distances depend both on the length and on the multiplicity of paths from the seed set, and thus better capture the exposure of a node to the seed set than possible by deterministic lengths [13].

Two fundamental problems in the study of diffusion are influence computation and influence maximization (IM).

Influence computation is the problem of computing the influence of a specified seed set \( S \) of nodes. This can be done using multiple single-source shortest-paths computations from the seed set, but the computation does not scale well when there are many queries on very large networks. Cohen et al. for binary influence [14] and Du et al. for threshold timed influence [22] designed influence oracles which preprocess the input so that influence queries Inf(\( \mathcal{G}, S \)) for a specified seed set \( S \) can be approximated quickly. In both cases, a sketch, based on [10], is computed for each node so that the influence of a seed set \( S \) can be estimated from the sketches of the nodes in \( S \). For general timed influence, we consider an oracle designed for a pre-specified function \( \alpha \) (say binary or threshold), or a more powerful oracle which allows \( \alpha \) to be specified at query time.

Influence maximization is the problem of finding a seed set \( S \subset V \) with maximum influence, where \( |S| = s \) is given. Since binary influence [28] and threshold timed influence [25] are special cases, we know that timed influence maximization with general \( \alpha \) is \( \text{NP} \)-complete and hard to approximate [23] to anything better than \( 1 - (1-1/s)^s \) of the optimum for a seed set of size \( s \) (the hardness result is asymptotic in \( s \)). For binary influence and timed influence with a threshold function, the influence objective is mono-
tone and submodular \[25, 28\] and therefore the greedy algorithm (GREEDY), which iteratively adds to the seed set the node with maximum marginal influence, is guaranteed to provide a solution that is at least \(1 - (1 - 1/s)^2 > 1 - 1/e\) of the optimum \[32\]. This (worst-case) guarantee holds for every prefix size of the sequence of seeds reported, which means GREEDY actually approximates the Pareto front of the trade-off of seed set size versus its influence. This property, in particular, allows us to find a sweet spot of the tradeoff and to characterize the influence coverage of the network.

In terms of solution quality, GREEDY had been the gold standard for influence maximization but unfortunately it does not scale well, even with various optimizations \[8, 30\]. As a result, extensive research work on binary influence maximization proposes scalable heuristics \[27\], alternative approaches that provide guarantees but lose other properties of GREEDY \[6, 39\], and, more recently, an approximation of GREEDY \[14\] that uses sketches. For threshold timed-influence, the only existing scalable maximization algorithm is by Du et al. \[22\] and based on sketches \[10\].

We make the following contributions. We present and motivate a general model of timed influence, with respect to arbitrary decay/kernel functions, precisely defined in Section 2. Our model naturally unifies and generalizes binary influence, threshold timed influence, and distance-decaying closeness centrality.

In Section 2 we also state the basic GREEDY influence maximization algorithm for timed influence. Similarly to the well-studied special cases of binary influence and timed influence with a threshold function, our general influence objective is monotone and submodular, and thus GREEDY has the same approximation ratio guarantees.

In Section 3 we consider the threshold timed influence model \[22, 25\]. We extend the state-of-the-art (approximate) influence oracles and the SKIM influence maximization algorithm, designed for binary influence \[14\], to obtain T-SKIM for threshold timed influence. T-SKIM provides strong guarantees of estimates with a small relative error with very high probability. Our algorithms scale much better than the state-of-the-art threshold timed influence algorithms of Du et al. \[22\]. In particular, a much smaller storage (sketch size) is needed for obtaining an oracle with the same accuracy guarantees and IM is orders of magnitude faster.

The influence oracles of Section 3 are computed with respect to a fixed threshold \(T\). In Section 4, we present general timed influence oracles, which take as input a seed set \(S\) and (any) decay function \(\alpha\), which can be specified at query time. As explained earlier, many different decay/kernel functions are used extensively in practice, which makes the flexibility of the oracle handle arbitrary \(\alpha\) valuable.

Our oracle computes a novel sketch for each node: we call it the combined All-Distances sketch (cADS). The cADS generalizes All-Distances Sketches (ADS) \[10, 11, 16\] to multiple instances or probabilistic models. These per-node sketches have expected size at most \(k \ln(n \min \{n, \ell\})\) (with good concentration), where \(n\) is the number of nodes, \(\ell\) is the number of instances, and \(k\) is a sketch parameter that determines a trade-off between information and the amounts of computation and space required. We estimate the timed influence of a seed set \(S\) from the sketches of the nodes in \(S\). Our estimator uses HIP probabilities \[11\] with the L* estimator \[12\], which optimally uses the information in the sketches, and has worst-case coefficient of variation (CV) \(\leq 1/\sqrt{2k-2}\).

In Section 5 we present \(\alpha\)-SKIM, the first influence maximization algorithm that works for a general specified decay function \(\alpha\). Our design is a contribution both from theoretical and practical perspectives, providing novel worst-case asymptotic bounds, performance guarantees, and a scalable implementation that runs on large networks.

Section 6 presents a comprehensive experimental evaluation of the techniques we propose. For threshold timed influence oracles and maximization, we obtain three order(s) of magnitude speedups over the algorithms of Du et al. \[22\] with no loss in quality. Even though both approaches apply the sketches of Cohen \[10\], we are able to obtain improvements by working with combined sketches, applying better estimators, and in our IM algorithm, only computing sketches to the point needed to determine the next node. We also show that the generalization to arbitrary decay functions \(\alpha\) is only slightly slower, and can easily handle graphs with hundreds of millions of edges.

In Section 7 we discuss related prior work and we conclude in Section 8.

2. TIMED INFLUENCE MODEL

A propagation instance \(G = (V, E, w)\) is an edge-weighted directed graph \(G\) specified by a set of nodes \(V\) and an edge set \(E\) with weights \(w(e) > 0\). For a set of nodes \(S \subseteq V\), its influence in instance \(G\) with respect to a non-increasing function \(\alpha\) is defined as

\[
\text{Inf}(G, S) = \sum_{u \in V} \alpha(d_{su}),
\]

where \(d_{su} = \min_{v \in S} d_{uv}\) is the shortest-path distance in \(G\) from \(S\) to \(u\), and \(d_{uv}\) is the shortest-path distance in \(G\) from \(v\) to \(u\). When there is no path from \(v\) to \(u\) in \(G\) we define \(d_{uv} \equiv \infty\) and \(\alpha(\infty) = 0\).

We interpret edge length as propagation time and accordingly refer to such instances as timed. The well-studied special case of binary influence is obtained when using uniform edge lengths \(w(e) \equiv 1\) and \(\alpha(x) \equiv I \iff x < \infty\); recall that the binary influence of \(S\) is the cardinality of its reachability set, that is, the number of nodes reachable from at least one node in \(S\).

Our input is specified as a set \(\mathcal{G} = \{G^{(i)}\}\) of \(\ell \geq 1\) propagation instances \(G^{(i)} = (V, E^{(i)}, w^{(i)})\), in which case, the influence of \(S\) over all instances \(\{G^{(i)}\}\) is the average single-instance influence:

\[
\text{Inf}(\mathcal{G}, S) = \frac{1}{\ell} \sum_{i \in [\ell]} \text{Inf}(G^{(i)}, S). \tag{1}
\]

The set of propagation instances can be derived from cascade traces or generated by a probabilistic model.

Our input can also be specified directly as a probabilistic model and provided as a distribution \(\mathcal{G}\) over instances \(G \sim \mathcal{G}\) which share a set \(V\) of nodes. In this case, we define the influence of \(\mathcal{G}\) as the expectation

\[
\text{Inf}(\mathcal{G}, S) = \mathbb{E}_{G \sim \mathcal{G}} \text{Inf}(G, S). \tag{2}
\]

In particular, an Independent Cascade (IC) model \(\mathcal{G}\) is specified by associating an independent random length \(w(e) \in \{+\infty\} \cup R_{>0}\) with each edge \(e\) according to a distribution that is associated with the edge. The probability that \(e\) is live is \(p_e = \Pr[w(e) < \infty]\) and its length if it is live is \(w(e)\). We use the convention that an edge \(e\) that is not explicitly specified has \(w(e) \equiv \infty\) (is never live). Random edge lengths (REL) from an exponential \([1, 13, 25]\) or Weibull \([22]\) distribution have natural interpretations.

2.1 Greedy Timed Influence Maximization

We present the exact greedy algorithm for the timed influence objective \(\text{Inf}(\{G^{(i)}\}, S)\), as defined in Equation 1. GREEDY starts with an empty seed set \(S = \emptyset\). In each iteration, it adds the node with maximum marginal gain, that is, the node \(u\) that maximizes the influence of \(S \cup \{u\}\). GREEDY thus produces a sequence of nodes, providing an approximation guarantee for the seed set defined by each prefix.
We now elaborate on the computation of the marginal gain of \( u \) given \( S \). To do so efficiently as \( S \) grows, we work with a residual problem. We denote the residual problem of \( G \) with respect to seed set \( S \) as \( \mathcal{G}/S \). The influence of a set of nodes \( U \) in the residual problem is equal to the marginal influence in the original problem:

\[
\text{Inf}(\mathcal{G}/S, U) = \text{Inf}(\mathcal{G}, S\cup U) - \text{Inf}(\mathcal{G}, S).
\]

A residual problem has a slightly more general specification. The input has the form \((G, \delta)\), where \( \delta^{(i)} \geq 0 \) maps node-instance pairs \((v, i)\) to nonnegative numbers. The \( \delta \) values we use for the residual problem \( \mathcal{G}/S \) are the respective distances from the seed set: (but can be truncated without violating correctness at any distance \( x \) in which \( \alpha(x) = 0 \)).

\[
\delta^{(i)}_v = \min_{\alpha \in S} \delta^{(i)}_{uv}.
\]

When the seed set is empty or the node \( v \) is either not reachable from \( S \) in instance \( i \) or has distance \( d^{(i)}_{sv} > \sup_{x} \{\alpha(x) > 0\} \), we can use \( \delta^{(i)}_v = \infty \) or, equivalently, any \( \delta^{(i)}_v > \sup_{x} \{\alpha(x) > 0\} \).

We now extend the influence definition for inputs of the form \((\mathcal{G}, \delta)\). For a node \( u \), we consider the contribution of each node-instance pair \((v, i)\) to the influence of \( u \):

\[
\Delta^{(i)}_u \equiv \max \left(0, \alpha(d^{(i)}_{uv}) - \alpha(\delta^{(i)}_v)\right) \quad (3)
\]

The influence of \( u \) in the residual problem is the (normalized) sum of these contributions over all instances in all instances:

\[
\text{Inf}(\mathcal{G}/S, U) \equiv \frac{1}{k} \sum_{i} \sum_{\Delta^{(i)}_u}. \quad (4)
\]

It is not hard to verify the following.

**Lemma 2.1.** For any set of nodes \( U \), the influence of \( U \) in \( \mathcal{G}/S \) is the same as marginal influence of \( U \) with respect to \( S \) in \( \mathcal{G} \).

Given a residual input \((\mathcal{G}, \delta)\), the influence of a node \( u \) (which is the same as its marginal influence in the original input \( G \)) can be computed using a pruned application of Dijkstra's algorithm from \( u \). A pseudocode is provided as the function MargGain\((u)\) in Appendix D.7. The pruning is performed for efficiency reasons by avoiding expanding the search in futile directions. In particular, we can always prune at distance \( d \) when \( \alpha(d) = 0 \) or when \( d \geq \delta^{(i)}_v \). The correctness of the pruning follows by observing that all nodes \( v \) Dijkstra could reach from the pruned node have \( d^{(i)}_{uv} = 0 \).

At each step, GREEDY selects a node with maximum influence in the residual input. It then updates the distances \( \delta \) so that they capture the residual problem \( \mathcal{G}/S \cup \{u\} \). A pseudocode for updating \( \delta \) is provided as the function AddSeed\((u)\) in Appendix D.1. To update, we perform a pruned single-source shortest-paths computation in each instance \( i \) from \( u \), as in MargGain\((u)\).

GREEDY can be implemented by recomputing MargGain\((u)\) for all nodes after each iteration. A common acceleration is instead to perform lazy evaluations: one keeps older values of marginal gains, which are upper bounds on the current values, and updates the current values only for the candidates at the top of the queue as needed to determine the maximum one. Lazy evaluations for binary influence were used by Leskovec et al. [20] in their CELF algorithm. The correctness of lazy evaluations follows from the submodularity and monotonicity of the objective, which imply that the marginal gain of a node can only decrease as the seed set grows. Even with lazy evaluations, however, exact GREEDY does not scale well for large networks.

Following SKIM for binary IM [14], we propose here algorithms for timed IM which approximate GREEDY. In each iteration, we select a seed node with estimated marginal contribution that is close to maximum, within a small relative error with high probability. In the following sections we first propose T-SKIM for threshold timed influence and then extend it to \( \alpha \)-SKIM for timed IM with respect to an arbitrary decay function \( \alpha \).

### 3. THRESHOLD TIMED INFLUENCE

We present both an oracle and an IM algorithm for timed-influence with a threshold \( T \).\[22,25\]. In this model, a node is considered influenced by \( S \) in an instance if it is within distance at most \( T \) from the seed set. Formally, \( \alpha(x) = 1 \) when \( x \leq T \) and \( \alpha(x) = 0 \) otherwise. The threshold model has a simpler structure than timed influence with general decay; intuitively, this is because the contributions to influence \( \Delta^{(i)}_u \) are in \([0, 1]\), similar to binary influence. Our algorithms generalize state-of-the-art algorithms for binary influence [14].

#### 3.1 Influence Oracle

Our influence oracle for a prespecified threshold \( T \) generalizes the binary influence oracle of Cohen et al. [14]. The binary influence oracle preprocesses the input to compute a combined reachability sketch for each node. Each node-instance pair is assigned a random permutation rank (a number in \([n]!\)) and the combined reachability sketch of a node \( u \) is a set consisting of the \( k \) smallest ranks amongst node-instance pairs \((v, i)\) such that \( v \) is reachable from \( u \) in instance \( i \). This is also called a bottom-\( k \) sketch of reachable pairs. The oracle uses the sketches of the nodes in \( S \) to estimate their influence by applying the union size estimator for bottom-\( k \) sketches [17]. The combined reachability sketches are built by first computing a set of reachability sketches (one for each node) [10] in each instance and then combining, for each node, the sketches obtained in different instances to obtain one size-\( k \) sketch. Inc. the computation for each instance uses reverse (backward) reachability computations. The algorithm of Cohen [10] initiates these reversed reachability searches from all nodes in a random permutation order. These searches are pruned at nodes already visited \( k \) times.

For threshold timed influence, we instead consider a pair \((v, i)\) reachable from \( u \) if \( d^{(i)}_{uv} \leq T \). We then compute for each node the bottom-\( k \) sketch of these “reachable” pairs under the modified definition. The oracle estimator [17] is the same one used for the binary case; the estimate has (worst-case) CV that is at most \( 1/\sqrt{2k-2} \) with good concentration. The computation of the sketches is nearly as efficient as for the binary case. Instead of using reverse reachability searches, for threshold timed influence we use reverse Dijkstra computations (single-source shortest-path searches on the graph with reversed edges). These computations are pruned both at distance \( T \) and (as with reachability sketches) at nodes already visited \( k \) times. The sets of sketches obtained for the different instances are combined as in [14] to obtain a set of combined sketches (one combined sketch with \( k \) entries for each node).

The running time is dominated by the computation of the sketches. It is similar to the binary case, except that we use single-source shortest paths computations instead of generic graph searches. The preprocessing takes \( O(k\sum_{i=1}^{k} |E^{(i)}| \log n) \) computation and each influence query for a set \( S \) can be implemented in \( O(|S|k \log |S|) \) time.

#### 3.2 Influence Maximization

Our algorithm for threshold timed influence maximization, which we call T-SKIM, generalizes SKIM [14], which was designed for binary influence. A pseudocode for T-SKIM is provided as Algorithm 2 in Appendix D.2. Intuitively, both SKIM and T-SKIM build sketches, but only to the point of determining the node with maximum estimated influence. We then compute a residual problem
which updates the sketches.

Our algorithm, $T$-SKIM, uses reverse single-source shortest path computations that are pruned at distance $T$ (depth-$T$ Dijkstra) to build the sketches. As with exact greedy for timed influence (Section 3), $T$-SKIM maintains a residual problem. This requires updating the distances $d(v, i) = d_v^i$ from the current seed set $S$, as in AddSeed$(u)$, and also updating the sketches to remove the contributions of pairs that are already covered by the seed set.

The (worst-case) estimation quality guarantee of $T$-SKIM is similar to that of SKIM. When using $k = O(e^{-2} \log n)$ we obtain that, with high probability ($\geq 1 - 1/(\text{poly}(n))$), for all $s \geq 1$, the influence of the first $s$ selected nodes is at least $1 - (1 - 1/s)^s - \varepsilon$ of the maximum influence of a seed set of size $s$. The computation time analysis of $T$-SKIM is deferred to Appendix A.

4. ORACLE FOR TIMED INFLUENCE

We now present our oracle for timed influence, as defined in Equation 4. We preprocess the input $G$ to compute a sketch $X_i$ for each node $v$. Influence queries, which are specified by a seed set $S$ and a function $\alpha$, can be approximated from the sketches of the query seed nodes.

Note that the same set of sketches can be used to estimate timed influence with respect to any non-increasing function $\alpha$. That is, $\alpha$ can be specified on the fly, after the sketches are computed. When we are only interested in a specific $\alpha$, such as a threshold function with a given $T$ (Section 3) or binary influence [14], the sketch size and construction time can be reduced.

In the following subsections we present in detail the three components of our oracle: the definition of the sketches, estimation of influence from sketches (queries), and building the sketches (preprocessing). Before providing details, we state the properties of our oracle, in terms of storage, estimation quality, query time, and preprocessing time.

The sketches are defined in Section 4.1 and we show that for an input specified as either a set of instances or as a timed IC model, each sketch $X_i$ has a (well concentrated) expected size that is at most $k \ln(nk)$. The total storage of our oracle is therefore $O(nk \log(nk))$.

The sketch-based influence estimator is presented in Section 4.2.

We establish the following worst-case bounds on estimation quality.

**Theorem 4.1.** Influence queries $\ln_{G, S}$, specified by a set $S$ of seed nodes and a function $\alpha$, can be estimated in $O(|S| \log n)$ time from the sketches $X_i$, $i \in S$. The estimate is nonnegative and unbiased, has $CV \leq 1/\sqrt{2k - 2}$, and is well concentrated (the probability that the relative error exceeds $a/\sqrt{k}$ decreases exponentially with $a > 1$).

We also show that our estimators are designed to fully exploit the information in the sketches in an instance-optimal manner.

The preprocessing is discussed in Section 4.3. We show that for a set of $\mathcal{L}$ instances $G = \{G^\ell\}$, the preprocessing is performed in expected time $O(k \sum_{\ell=1}^{\mathcal{L}} |E(\ell)| \log n)$.

4.1 Combined ADS

We present the combined All-Distances Sketches (cADS), which are multi-instance generalizations of All-Distances Sketches (ADS) [10, 11, 16] and build on the related combined reachability sketches [14] used for binary influence.

Our cADS sketches are randomized structures defined with respect to random rank values $r_{uv}^i \sim U[0, 1]$ associated with each node-instance pair $(u, i)$. To improve estimation quality in practice, we restrict ourselves to a particular form of structured permutation ranks [14]. For a set of instances, the ranks are a permutation of $1, \ldots, n \min\{\ell, k\}$, where each block of positions of the form $in, (i + 1)n - 1$ (for integral $i$) corresponds to an independent random permutation of the nodes. For each node $\gamma$, the instances $i_j$ in $r_{uv}^i$, when ordered by increasing rank, are a uniform random selection (without replacement).

For each node $v$, cADS$(v)$ is a set of rank-distance pairs of the form $(r_{uv}^i, d_{uv}^i)$ which includes $\min\{\ell, k\}$ pairs of distance 0, that is, all such pairs if $\ell \leq k$ and the $k$ smallest rank values otherwise. It also includes pairs with positive distance when the rank value is at most the $k$th smallest amongst closer nodes (across all instances).

Formally, cADS$(v)$ = \begin{cases} \{(r_{uv}^i, d_{uv}^i) | r_{uv}^i < k_u h_s(d_{uv}^i) \} & \text{if } (v, i) \notin A, \\ \{(r_{uv}^i, d_{uv}^i) | r_{uv}^i < k_u h_s(d_{uv}^i) \} \cup \{(r_{uv}^i, d_{uv}^i) | r_{uv}^i = s_u \} & \text{if } (v, i) \in A, \end{cases} \quad (5)

Here bottom-$k$ refers to the smallest $k$ elements in the set and $k_u$ denotes the $k$th smallest element in the set. When there are fewer than $k$ elements, we define $k_u$ as the domain maximum. For the purpose of sketch definition, we treat all positive distances across instances as unique; we apply some arbitrary tie-breaking, for example according to node-instance index, when this is not the case.

The size of cADS sketches is a random variable, but we can bound its expectation. Moreover, $|\text{cADS}(u)|$ is well concentrated around the expectation. The proof resembles that for the basic ADS [10].

**Lemma 4.1.** $\forall u, E[|\text{cADS}(u)|] \leq k \ln(n \min\{\ell, k\})$.

**Proof.** We consider all node-instance pairs $(v, i)$ such that $r_{uv}^i \in \text{bottom-}k\{r_{uv}^j | j \in \ell\}$ by increasing distance from $u$. The probability that the $j$th item contributes to cADS$(u)$ is the probability that its rank is amongst the $k$ smallest in the first $j$ nodes, which is $\min\{1, j/k\}$. Summing over $i \leq |R_u|$ we obtain the bound. \hfill $\square$

Note that we can also define cADS sketches with respect to a probabilistic model. The definition emulates working with an infinite set of instances generated according to the model. Since there are at most $nk$ distinct rank values in the sketches, and they are all from the first $nk$ structured permutation ranks, the entries in the sketches are integers in $[nk]$.

4.2 Estimating Influence

Our estimators use the HIP threshold, $\tau_i(x)$, defined with respect to a node $v$ and a positive distance value $x > 0$:

$$\tau_i(x) = \begin{cases} k_u h_s(d_{uv}^i) & \text{if } u \neq v, \\ k_u h_s(x) & \text{if } u = v. \end{cases}$$

The HIP threshold for basic ADS was introduced by Cohen [11], and we extend it here to combined sketches. The value $\tau_i(x)$ is the $k$th smallest rank value amongst pairs $(y, j)$ whose distance $d_{uv}^i$ is smaller than $x$. If there are fewer than $k$ pairs with distance smaller than $x$, then the threshold is defined to be the maximum value in the rank domain. Note that, since the cADS contains the $k$ smallest ranks within each distance, $\tau_i(x)$ is also the $k$th smallest amongst such pairs that are in cADS$(v)$. Therefore, the threshold values $\tau_i(x)$ can be computed from cADS$(v)$ for all $x$.

The HIP threshold has the following interpretation. For a node-instance pair $(u, i)$, $\tau_i(d_{uv}^i)$ is the largest rank value $r_{uv}^i$ that would allow the (rank of the) pair to be included in cADS$(v)$, conditioned on fixing the ranks of all other pairs. We now consider the probability that the pair $(y, j)$ is included in cADS$(v)$, fixing the
ranks of all pairs other than \((y, j)\). This is exactly the probability that a random rank value is smaller than the HIP threshold \(\tau(r)\). In particular, if \(\tau(r)\) is the domain maximum, the inclusion probability is 1. We refer to this probability as the HIP inclusion probability.

When ranks are uniformly drawn from \([0, 1]\) the HIP probability is equal to the HIP threshold \(\tau(r)\) and we use the same notation. When we work with integral structured ranks, we divide them by \(n\ell\) to obtain values in \([0, 1]\).

We now present the estimator for the influence

\[
\Inf((G(i)), S) = \frac{1}{\ell} \sum_{(y, i) \in S} \max \alpha(d_{uv}^{(i)})
\]

\[
= \frac{1}{\ell} \sum_{y \in S} \alpha(\min_{d \in cADS(y)} d_{uv}^{(i)}) = \frac{1}{\ell} \sum_{y \in S} \alpha(d_{uv}^{(i)})
\]

(7)

from \(cADS(u) \mid u \in S\). We first discuss \(|S| = 1\). We use the HIP estimator

\[
\Inf((G(i)), u) = \alpha(0) + \frac{1}{\ell} \sum_{(r, d) \in cADS(u), d > 0} \alpha(d) / \tau_r(d)
\]

(8)

which is the sum over “sampled” pairs \((r, d)\) (those included in \(cADS(u)\)) of the contribution \(\alpha(d)/\ell\) of the pair to the influence of \(u\), divided by the HIP inclusion probability of the pair.

**Lemma 4.2.** The estimator \([11]\) is unbiased and has CV that is at most \(1/\sqrt{2k-2}\).

**Proof.** A node always influences itself (the only node of distance 0 from it), and the estimate for that contribution is \(\alpha(0)\). We apply the HIP estimator of \([11]\) to estimate the contribution of nodes with positive distance from \(u\). For a pair \((v, i)\), the HIP estimate is 0 for pairs not in \(cADS(u)\). When the pair is in \(cADS(u)\), we can compute the HIP probability \(\tau_r(d_{uv}^{(i)})\) and obtain the estimate \(\alpha(d_{uv}^{(i)}) / \tau_r(d_{uv}^{(i)})\). Since we are considering node-instance pairs, we divide by the number of instances \(\ell\). The variance analysis is very similar to \([11]\). □

We now consider a seed set \(S\) with multiple nodes. The simplest way to handle such a set is to generate the union \(cADS\), which is a \(cADS\) computed with respect to the minimum distances from any node in \(S\). The union \(cADS\) can be computed by merging the \(cADS\) of the seed nodes using a similar procedure to Algorithm\[5\] (in Appendix D.3) which will be presented in Section 4.3. We then estimate the contribution of the nodes in \(S\) by \(|S|\alpha(0)\) and estimate the contribution of all nodes that have a positive distance from \(S\) by applying the HIP estimator to the entries in the union \(cADS\). This estimator has the worst-case bounds on estimation quality claimed in Theorem\[4,11\] but discards a lot of information in the union of the sketches which could be used to tighten the estimate.

**4.2.1 Optimal Oracle Estimator**

The estimator we propose and implement uses the information in the sketches of nodes in \(S\) in an optimal way. This means the variance can be smaller, up to a factor of \(|S|\), than that of the union estimator. A pseudocode is provided as Algorithm\[3\] in Appendix D.3. The estimator first computes the set \(Z\) of rank values \(r\) that appear with distance 0 in at least one sketch. These ranks correspond to node-instance pairs involving a seed node. For each rank value \(r\) that appears in at least one sketch in \(S\) and is not in \(Z\) (has positive distance in all sketches), we build the set \(T_r\) of threshold-contribution pairs that correspond to occurrences of \(r\) in sketches of \(S\). We then compute from \(T_r\) the sorted skyline (Pareto set) skylines\([r]\) of \(T_r\). The skyline skylines\([r]\) includes a pair \((r, \alpha)\) in \(T_r\) if and only if the pair

is not dominated by any other pair. That is, any pair with a larger \(\tau\) value must have a smaller \(\alpha\) value. We compute skylines\([r]\) from \(T_r\) as follows. We first sort \(T_r\) lexicographically, first by decreasing \(\tau\), and then if there are multiple entries with same \(\tau\), by decreasing \(\alpha\). We then obtain skylines\([r]\) by a linear scan of the sorted \(T_r\) which removes pairs with a lower \(\alpha\) value than the maximum \(\alpha\) value seen so far. The entries of the computed skylines\([r]\) are sorted by decreasing \(\tau_j\) (and increasing \(\alpha\)).

For each \(r\) for which we computed a skyline (appears in at least one sketch of a node in \(S\) and is not in \(Z\)), we apply the \(L^*\) estimator\[12\] to the sorted skylines\((r) = \{(\tau_j, \alpha_j)\}\). The pseudocode for \(L^*\) tailored to our application is in Algorithm\[4\] in Section 4.3 and details on the derivation and applicability of the estimator are provided in Appendix B.

Finally, the influence estimate \(\hat{\Inf}((G(i)), S)\) returned by Algorithm\[3\] has two components. The first summand \(|S|\alpha(0)\) is the contribution of the seed nodes themselves. The second component is the sum, over all node-instance pairs of positive distance from \(S\), of their estimated contribution to the influence (normalized by the number of instances \(\ell\)). We estimate this by the sum of the \(L^*\) estimates applied to skylines\((r)\).

**4.3 Computing the Set of cADS**

We compute a set of \(cADS\) sketches by computing a set of ADS sketches \(ADS(i)(v)\) for each instance \(i\) \([10, 11]\). The computation of sketches for all nodes \(v\) in a single instance can be done using PRUNED DIJKSTRA’S \([10, 16]\) or the node-centric LOCAL UPDATES \([11]\).

An ADS is a \(cADS\) of a single instance and has the same basic form: a list of rank-distance pairs sorted by increasing distance. It can have, however, at most one entry of distance 0.

For each node \(v\), we compute \(cADS(v)\) by combining \(ADS(i)(v)\) for all instances \(i\). A pseudocode for combining two rank-distance lists to a \(cADS\) format list is provided as Algorithm\[5\]. The algorithm can be applied repeatedly to \(ADS(i)(v)\) and the current \(cADS(v)\), or in any combination order of rank-distance lists to obtain the same end result.

The computation of the set of \(cADS\) sketches is dominated by computing a set of All-Distances Sketches \([10, 11, 16]\) in each instance. The computation for instance \(i\) takes \(O(k|E(v)|\log n)\) time.

**5. TIMED INFLUENCE MAXIMIZATION**

We present \(\alpha\)-SKIM (pseudocode in Algorithm\[4\]) which performs approximate greedy timed influence maximization with respect to an arbitrary non-increasing \(\alpha\). The input to \(\alpha\)-SKIM is a set of instances \(\mathcal{I}\) and a decay function \(\alpha\). The output is a sequence of nodes, so that each prefix approximates the maximum influence seed set of the same size.

Like exact greedy (Section\[2\]) and \(T\)-SKIM (Section\[3\]), \(\alpha\)-SKIM maintains a residual problem, specified by the original input \(\mathcal{I}\) and distances \(d_r^{(i)}\). It also maintains, for each node, a sample of its influence set, weighted by the respective contribution of each element. The sampling is governed by a global sampling threshold \(\tau\), which inversely determines the inclusion probability in the sample (the lower \(\tau\) is, the larger is the sample). The weighted sample has the same role as the partial sketches maintained in \(T\)-SKIM, as it allows us to estimate the influence of nodes.

At a high level, \(\alpha\)-SKIM alternates between two subroutines. The first subroutine examines the influence estimates of nodes. We pause if we have sufficient confidence that the node with the maximum estimated influence (in the current residual problem) has actual influence that is sufficiently close to the maximum influence.
Otherwise, we decrease $\tau$, by multiplying it by a (fixed) $\lambda < 1$ (we used $\lambda = 0.5$ in our implementation), extend the samples, and update the estimates on the influence of nodes to be with respect to the new threshold $\tau$. We pause only when we are happy with the node with maximum estimated influence.

The second subroutine is invoked when a new node $s$ is selected to be added to the seed set; $\alpha$-SKIM updates the residual problem, that is, the distances $\delta$ and the samples.

We provide an overview of our presentation of the components of $\alpha$-SKIM. In Section 5.1, we precisely define the weighted samples we use. In Section 5.2, we present our main data structure, index, which stores the (inverted) samples. The building of index, which dominates the computation, is done using applications of pruned reverse Dijkstra, discussed in Section 5.3. The selection of the next seed node is detailed in Section 5.4. The samples are defined with respect to the current residual problem and the sampling threshold $\tau$. Therefore, they need to be updated when $\tau$ is decreased or when a new seed node is selected. While the new estimates can always be computed by simply scanning index, this is inefficient. In Section 5.5, we present additional structures which support efficient updates of samples and estimates. Finally, Section 5.6 includes a worst-case analysis.

### 5.1 PPS Samples of Influence Sets

We start by specifying the sampling scheme, which is the core of our approach. The sample we maintain for each node $u$ is a Probability Proportional to Size (PPS) sample of all node-instance pairs $(v,i)$, where the weighting is with respect to the contribution values $\Delta_{uv}^{(i)}$, as defined in Equation (5). Recall from Equation (4) that the influence, which we are estimating from the sample, is the sum of these contributions. PPS sampling can be equivalently defined with respect to a threshold $\tau$ (17): Each entry $(v,i)$ has an independent $r_{v,i} \sim U[0,1]$ and it is included in the sample of $u$ if

$$\frac{\Delta_{uv}^{(i)}}{r_{v,i}} \geq \tau. \quad (9)$$

From the PPS sample we can unbiasedly estimate the influence of $u$, using the classic inverse-probability estimator [26]. We denote by $H_u$ the set of all pairs $(v,i)$ such that $\Delta_{uv}^{(i)} \geq \tau$ and by $M_u$ the set of all other sampled pairs, that is, those where $\Delta_{uv}^{(i)} \in (0, \tau]$. Note that pairs in $H_u$ are sampled with probability 1, whereas pairs in $M_u$ are sampled with probability $\frac{\Delta_{uv}^{(i)}}{r_{v,i}}$ (this is the probability of having a rank value so that (9) is satisfied). The estimate is the sum of the ratio of contribution to inclusion probability:

$$\widehat{\text{Inf}}((\mathcal{G}, \delta), u) = \frac{1}{|H_u|} \sum_{(v,i) \in M_u} \Delta_{uv}^{(i)} \left(1 - \frac{1}{|H_u|} \sum_{(v,i) \in M_u} \Delta_{uv}^{(i)} \right). \quad (10)$$

With PPS sampling, when $\tau$ is low enough so that the estimate is at least $k\tau$, which always happens when we have $k$ samples, the CV is at most $1/\sqrt{k}$. The estimate is also well concentrated according to the Chernoff bound.

We note that our use of PPS sampling, rather than uniform sampling, is critical to performance with general $\alpha$. When using say exponential or polynomial decay, the positive contributions of different pairs to the influence of a node can vary by orders of magnitude. Therefore, we must use weighted sampling, where heavier contributions are more likely to be sampled, to obtain good accuracy with a small sample size. With threshold timed influence, in contrast, contributions were either 0 or 1, which meant that we could get good performance with uniform sampling.

---

**Algorithm 1: Timed-Influence Maximization ($\alpha$-SKIM)**

**Input:** Directed graphs $\{G^{(i)}(V,E^{(i)},w^{(i)})\}$. $\alpha$

**Output:** Sequence of node and marginal influence pairs

```
// Initialization
rank ← map node-instance pairs $(v,i)$ to $j/|n_l|$ where $j \in |n_l|$;
forall the node-instance pairs $(v,i)$ do index[$v,i$] ← ⊥;
// List of $(u,d^{(i)}_u)$ scanned by reverse Dijkstra
for all the pairs $(u,i,d)$ do $\delta[u,i] \leftarrow \infty$; // Distance from $S$
forall the nodes $v$ do $\text{Est}H[v] \leftarrow 0; \text{Est}M[v] \leftarrow 0$
seedlist ← ⊥ // List of seeds & marg. influences
forall the node-instance pairs $(v,i)$ do Insert $(v,i)$ to Qpairs with priority $\alpha(0)/\text{rank}[v,i]$;
// Initialize Qpairs
s ← 0; $\tau \leftarrow \alpha(0)n_l/2k$; coverage ← 0 // coverage of current seed set
while coverage < $\alpha(0)$ do
  // Build PPS samples of marginal influence sets until confidence in next seed
  while $(s, s_i) \leftarrow \text{NextSeed}()$ do
    $\tau \leftarrow \lambda \tau$; MoveUp() // Update est. components
    forall the pairs $(v,i)$ in Qpairs with priority $\geq \tau$ do
      Remove $(v,i)$ from Qpairs
      Resume reverse Dijkstra from $(v,i)$.
      foreach scanned node $u$ of distance $d$ do
        $c \leftarrow \alpha(d) - \alpha(\hat{\delta}[v,i])$;
        if $c \leq 0$ then Terminate rev. Dijkstra from $(v,i)$
        if $c/\text{rank}[v,i] < \tau$ then
          place $(v,i)$ with priority $c/\text{rank}[v,i]$ in Qpairs; Pause reverse Dijkstra from $(v,i)$
          else // $c/\text{rank}[v,i] \geq \tau$
            $\text{Est}H[u] \leftarrow c$; // H entry
            $\text{Est}M[u] \leftarrow c$; // M entry
        if $c \geq \tau$ then $\text{Est}H[u] \leftarrow \max(c, \text{Est}H[u])$
        $\text{Est}.M[u] \leftarrow \max(c, \text{Est}.M[u])$
        if $\text{H}[v] = 1$ then
          $\text{H}[v] \leftarrow \text{index}[v,i]$; Insert $(v,i)$ with priority $c$ to Qhml
          Update the priority of $u$ in Qcands to $\text{Est}H[u] + \tau \text{Est}.M[u]$
      // Process new seed node $x$
      $I_s \leftarrow 0$ // Exact marginal influence
      foreach instance $i$ do
        Perform a forward Dijkstra from $x$ in $G^{(i)}$;
        foreach visited node $v$ at distance $d$ do
          if $d \geq \delta[v,i]$ then Pruncelse
            priority $(v,i)$ in Qpairs ← $\alpha(d) - \alpha(\hat{\delta}[v,i])$;
            if priority of $(v,i)$ in Qpairs ≤ 0 then
              terminate rev. Dijkstra $(v,i)$ and remove $(v,i)$ from Qpairs
              MoveDown $(v,i)$, $\delta[v,i], d$;
            $c \leftarrow \alpha(d) - \alpha(\hat{\delta}[v,i])$;
          $\delta[v,i] \leftarrow d - s$
        $s \leftarrow 1$; coverage ← $I_s/|I_s|$; seedlist.append $(s, s_i)/\ell, s_i/\ell$
      return seedlist
```
The PPS samples we will maintain for different nodes are computed with respect to the same threshold \( \tau \). The samples are also coordinated, meaning that the same values \( r_u^{(i)} \) are used in the samples of all nodes. Coordination also helps us to maintain the samples when the contribution values \( \Delta \) are modified, since the sample itself minimally changes to reflect the new values. In our implementation, node-instance pairs are assigned structured random permutation ranks, which are integers in \([n\ell]\), and we use for permutation rank \( i \), \( \text{rank}[u,i] \equiv r_u^{(i)} = i/(n\ell) \).

5.2 The Index Structure

The main structure we maintain is index, which can be viewed as an inverted index of the PPS samples (but technically can include entries that used to be included in the PPS sample and may still be relevant). For each node-instance pair \((v,i)\), \( \text{index}[v,i] \) is an ordered list of node-distance pairs \((u,d_u^{(i)})\). Note that typically the lists are empty or very small for most pairs \((v,i)\). The list is ordered by increasing \( d_u^{(i)} \), which is the order in which a reverse Dijkstra algorithm performed from \( v \) on the graph \( G^{(i)} \) (with all edges reversed) scans new nodes. \( \text{index}[v,i] \) always stores a (prefix) of the scanned nodes, in scanning order. It always includes all nodes \( u \) for which the pair \((v,i)\) is included in the PPS sample of \( u \), that is, nodes \( u \) that satisfy (9). Each list \( \text{index}[v,i] \) is trimmed from its tail so that it only contains entries \((u,d_u^{(i)})\) where \( \Delta_u^{(i)} > 0 \), that is, \( \alpha(d) - \alpha(\delta_u^{(i)}) > 0 \). This is because other entries have no contribution to the marginal influence of \( u \). Note that the lists are always a prefix of the Dijkstra scan order, and once they are trimmed (from the end), they do not grow, and the respective reverse Dijkstra computation never resumed, even if \( \tau \) decreases.

Each list \( \text{index}[v,i] \) is logically viewed as having three consecutive parts (that could be empty). The H part of the list are all entries \((u,d_u^{(i)})\) with \( \alpha(d) - \alpha(\delta_u^{(i)}) \geq \tau \). These are the nodes \( u \) for which the pair \((v,i)\) contributes to the \( H_u \) part of the PPS sample. The M part of the list are all entries with \( \alpha(d) - \alpha(\delta_u^{(i)}) \in [r_u^{(i)} \tau, \tau) \), which include nodes \( u \) for which \((v,i)\) contributes to \( M_u \). Finally, the L part of the list includes nodes for which \( 0 < \alpha(d) - \alpha(\delta_u^{(i)}) < r_u^{(i)} \tau \). The L nodes do not currently include \((v,i)\) in the PPS sample of their influence sets, but are still relevant, since this may change when \( \tau \) decreases.

To support efficient updates of this classification, we maintain \( \text{HM}[v,i] \) and \( \text{ML}[v,i] \), which contain the positions in the list \( \text{index}[v,i] \) of the first \( M \) and the first \( L \) items (and are empty if there are no \( M \) or \( L \) items, respectively).

To efficiently compute the influence estimates, we maintain for each node \( u \) the values

\[
\text{Est}.H[u] = \sum_{(v,i) : \Delta_u^{(i)} \geq \tau} \Delta_u^{(i)}
\]

\[
\text{Est}.M[u] = |\{(v,i) : \Delta_u^{(i)} \in [r_u^{(i)} \tau, \tau)\}|
\]

The PPS estimate (10) on the influence of \( u \) is

\[
\frac{1}{\ell} \left( \text{Est}.H[u] + \tau \text{Est}.M[u] \right).
\]

5.3 Reverse Dijkstra Computations

We build the samples using reverse Dijkstra computations starting at node-instance pairs \((v,i)\). The computation is from source \( v \) in the transpose graph of \( G^{(i)} \) and reveals all nodes \( u \) for which the pair \((v,i)\) is included in the PPS sample for \( u \) as defined in (9). The nodes scanned by the reverse Dijkstra on \([v,i]\) are maintained as index\([v,i]\), in the same order. The computation for \((v,i)\) is paused once the distance \( d \) from the source satisfies

\[
\alpha(d) - \alpha(\delta_u^{(i)}) < r_u^{(i)} \tau.
\]

The computation may resume when \( \tau \) is decreased and the pause rule (12) no longer holds. It is not hard to verify that this pause rule suffices to obtain all entries of \((v,i)\) in the PPS samples of nodes. When the depth \( d \) satisfies \( \alpha(d) - \alpha(\delta_u^{(i)}) < 0 \), the computation of the reverse Dijkstra \((v,i)\) is (permanently) terminated, releasing all auxiliary data structures.

Note that the reverse Dijkstra computations for different pairs are paused and resumed according to the global threshold \( \tau \), and can be performed concurrently.

The algorithm maintains “state” for all active Dijkstras. We use the notation \( \mu(v,i) = d \) for the next distance the reverse Dijkstra from \((v,i)\) would process when resumed. Initially, \( \mu(v,i) = 0 \). In order to efficiently determine the pairs \((v,i)\) for which reverse Dijkstra needs to be resumed, we maintain a max priority queue \( Q_{\text{pairs}} \) over node-instance pairs \((v,i)\), prioritized by

\[
\frac{\alpha(\mu(v,i)) - \alpha(\delta_u^{(i)})}{r_u^{(i)}(v)}.
\]

This priority is the sampling threshold that is required to get \((v,i)\) into the PPS sample of the next node to be scanned by the reverse Dijkstra \((v,i)\). We only need to resume the reverse Dijkstra \((v,i)\) when its priority (13) is at least \( \tau \). Note that the priority of a pair \((v,i)\) can only decrease over time, when \( \delta_u^{(i)} \) decreases or when the reverse Dijkstra progresses and \( \mu(v,i) \) increases. This allows us to maintain \( Q_{\text{pairs}} \) with lazy updates.

In order to determine, after we decrease \( \tau \), all the pairs for which the reverse Dijkstra computation should resume (or start), we simply extract all the top elements of the queue \( Q_{\text{pairs}} \) which have priority at least \( \tau \). These top elements are removed from \( Q_{\text{pairs}} \). The reverse Dijkstra is resumed on each removed pair \((v,i)\) until the pause rule holds again, that is, we reach a distance \( d \) such that \( \alpha(d) - \alpha(\delta_u^{(i)}) < r_u^{(i)} \tau \). At this point the reverse Dijkstra is terminated or paused. If it is paused, we set \( \mu(v,i) \leftarrow d \), and the pair \((v,i)\) is placed in \( Q_{\text{pairs}} \) with the new priority (13).

Note that the resume and pause rules of the reverse Dijkstras are consistent with identifying all sampled pairs according to (9), ensuring correctness.

5.4 Selecting the Next Seed Node

The algorithm decreases \( \tau \) until we have sufficient confidence in the node with maximum estimated marginal influence. The selection of the next node into the seed set is given in the pseudocode NextSeed in Appendix D.4.

We first discuss how we determine when we are happy with the maximum estimate. When looking at a particular node, and the value of the estimate is at least \( \tau \xi \), we know that the value is well concentrated with CV that is \( 1/\sqrt{\xi} \). We are, however, looking at the maximum estimate among \( n \) nodes. To ensure an expected relative error of \( \varepsilon \) in the worst case, we need to apply a union bound and use \( k = O(\varepsilon^{-2} \log n) \). The union bound ensures that the estimates for all nodes have a well concentrated maximum error of \( \varepsilon \) times the maximum influence. In particular, the estimated maximum has a relative error of \( \varepsilon \) with good concentration.

In practice, however, the influence distribution is skewed and therefore the union bound is too pessimistic (14). Instead, we propose the following adaptive approach which yields tighter bounds for realistic instances. Consider the node \( u \) with maximum estimated
marginal influence $I_u$ and let $I_u^*$ be its exact marginal influence $I_u$. The exact marginal influence can be computed, using $\text{MargGain}(u)$ (Section 2), and is also computed anyway when $u$ is added to the seed set.

The key to the adaptive approach is the following observation. When working with a parameter $k$, always selecting the node with maximum estimate when the estimate exceeds $k\tau$ we obtain with good probability for a prefix ratio we obtain with good probability for a prefix of reclassified entries $\delta(u)$. When $\delta(u)$ decreases, entries can “move down.” In addition, entries at the tail of index[v,i], those with $\alpha(d) \leq \alpha(\delta(u))$, get removed.

When an entry $(u,d)$ changes its classification, or when a new entry is generated by a reverse Dijkstra, we may need to update the estimate components $\text{Est}.H[u]$ and $\text{Est}.M[u]$. This is enabled by the pointers $\text{HM}[v,i]$ and $\text{ML}[v,i]$.

### 5.5 Updating PPS Estimate Components

The positions $\text{HM}[v,i]$ and $\text{ML}[v,i]$, and accordingly the classification of entries $(u,d)$ as H,M, or L, can be updated both when $\tau$ or $\delta(u)$ decreases. When $\tau$ decreases, entries can only “move up.” L entries can become M or H entries and M entries can become H entries. New entries can also be generated by a reverse Dijkstra on $(v,i)$. Newly generated entries are always H or M entries. When $\delta(u)$ decreases, entries can “move down.” In addition, entries at the tail of index[v,i], those with $\alpha(d) \leq \alpha(\delta(u))$, get removed.

To efficiently identify the index lists that have entries that change their classification, we maintain a max priority queues $\text{Qhm}$. It contains node-instance pairs with priority equal to the reclassification threshold, the highest $\tau$ that would require reclassification of at least one entry in the list. The procedure $\text{UpdateReclassThreshold}$ computes the reclassification threshold for a pair $(v,i)$ and places the pair with this priority in $\text{Qhm}$. When $\tau$ is decreased, we only need to process lists of pairs that are at the top of the queue $\text{Qhm}$.

Lastly, we discuss the processing of a list $(v,i)$ which requires reclassification. The reclassification, the updates of the estimation components $\text{Est}$, and the update of the reclassification threshold using $\text{UpdateReclassThreshold}(v,i)$, are all performed in computation that is proportional to the number of reclassified entries. In particular, processing does not require scanning the full list index[v,i]. This is enabled by the pointers $\text{HM}[v,i]$ and $\text{ML}[v,i]$.

### 5.5.1 Initial Updates When $\tau$ Decreases

When $\tau$ decreases, we first (before resuming the reverse Dijkstra’s) need to update the classification of existing entries and the implied changes on $\text{Est}$. The pseudocode for this update is provided as the function $\text{MoveUp}()$ in Appendix D.4.

To efficiently identify the index lists that have entries that change their classification, we maintain a max priority queues $\text{Qhm}$. It contains node-instance pairs with priority equal to the reclassification threshold, the highest $\tau$ that would require reclassification of at least one entry in the list. The procedure $\text{UpdateReclassThreshold}$ computes the reclassification threshold for a pair $(v,i)$ and places the pair with this priority in $\text{Qhm}$. When $\tau$ is decreased, we only need to process lists of pairs that are at the top of the queue $\text{Qhm}$.

Lastly, we discuss the processing of a list $(v,i)$ which requires reclassification. The reclassification, the updates of the estimation components $\text{Est}$, and the update of the reclassification threshold using $\text{UpdateReclassThreshold}(v,i)$, are all performed in computation that is proportional to the number of reclassified entries. In particular, processing does not require scanning the full list index[v,i]. This is enabled by the pointers $\text{HM}[v,i]$ and $\text{ML}[v,i]$.

### 5.5.2 New Scanned Node

The estimation components also need to be updated when a new entry is appended to the index[v,i] list when running a reverse Dijkstra for $(v,i)$. The pseudocode for this update is included in Algorithm 1. The new scanned node $u$ with distance $d$ creates a new entry $(u,d)$ which is appended to the end of index[v,i]. A new entry is always an H or M entry (otherwise the pause rule applies). If $\text{HM}[v,i] \neq \perp$, that is, there is at least one M entry in index[v,i], the new entry must also be an M entry. In this case, we increase $\text{Est}.M[u]$ by 1. If $\text{HM}[v,i] = \perp$, we check if $(c \leftarrow \alpha(d) - \alpha(\delta(u))) \geq \tau$. If so, the new entry is an H entry and we increase $\text{Est}.H[u]$ by 1. Otherwise, it is the first M entry. We set $\text{HM}[v,i] \leftarrow \text{index[v,i]} - 1$, $\text{Est}.M[u] = 1$, and insert the pair $(v,i)$ to the queue Qhm with priority $c$. After updates are completed, we recompute the estimated influence $\text{Est}.H[u] + \text{Est}.M[u]$ of the node $u$ and update accordingly the priority of $u$ in $\text{Qhm}$.

### 5.5.3 New Seed Node

When a new seed node $u$ is selected, we perform a forward Dijkstra from the seed in each instance $i$. We update $\delta(i)$ at visited nodes $v$ and compute the exact marginal influence of the new seed. The forward Dijkstra is pruned at nodes $v$ with $\delta(i)$ that is smaller or equal to their distance from $u$. When we update $\delta(i)$, we also may need to reclassify entries in index[v,i], update the positions $\text{HM}[v,i]$ and $\text{ML}[v,i]$ and update estimation components $\text{Est}.H[u]$ and $\text{Est}.M[u]$ of reclassified entries $(u,d)$. A pseudocode for this update is provided as the function $\text{MoveDown}()$ in Appendix D.4...
We also update the priority of the pair \( (v, i) \) in \( Q_{\text{hrm}} \) and decrease its priority in \( Q_{\text{pairs}} \) to \( \alpha(\mu(v, i)) - \alpha(\delta(i)) / r(v) \) (since we do not track \( \mu(v, i) \) explicitly in the pseudocode, we instead decrease the priority to reflect the decrease in \( \delta(i) \)). If the updated priority in \( Q_{\text{pairs}} \) is \( \leq 0 \), the reverse Dijkstra of \( (v, i) \) is terminated and it is removed from \( Q_{\text{pairs}} \). Note that in this update, entries can only be reclassified “down.” E.g. an entry \( (a, d) \) that was in \( H \) can move to \( M, L \), or be purged, if \( \alpha(d) \leq \alpha(\delta(i)) \).

5.6 Analysis

When we run the algorithm with fixed \( k = O(e^{-2} \log n) \) or use the adaptive approach in seed selection (as detailed in Section 5.5), we obtain the following guarantee on the approximation quality:

**Theorem 5.1.** \( \alpha \)-SKIM returns a sequence of seeds so that for each prefix \( S \) of size \( s \), with high probability,

\[
\inf(\mathcal{S}, S) \geq (1 - (1 - 1/s)^s - \epsilon) \max_{U \cup \mathcal{S} = s} \inf(\mathcal{S}, U).
\]

**Proof.** The algorithm, with very high probability, selects a node with marginal influence that is at least \( 1 - \epsilon \) of the maximum one. This follows from a union bound over all steps and nodes of the quality of the estimate obtained from a PPS sample. We then apply an approximate variant (e.g., [14]) of the classic proof [22] of the approximation ratio of GREEDY for monotone submodular problems.

We provide a worst-case bound on the (expected) running time for (i) the important cases of polynomial or exponential decay (both are instances of \( \alpha \) with nonpositive relative rate of change) and (ii) general decay functions when we consider approximation with respect to relaxed influence computed with small relative perturbations in distances. The proof is provided in Appendix C. We note that our design exploits properties of real instances and exhibits a much better performance in practice also with general decay functions.

**Theorem 5.2.** A modified Algorithm \( \alpha \)-SKIM runs in expected time

\[
O \left( \frac{\log^2 n}{\epsilon} \sum_{i=1}^{\ell} |E_i| + \frac{\log^2 n}{\epsilon^2} n + \frac{\log n}{\epsilon} \sum_{i=1}^{\ell} |E_i| \right) = O\left(e^{-\epsilon} \sum_{i=1}^{\ell} |E_i| \log^2 n \right)
\]

providing the guarantee [14], when \( (\ln \alpha(x))^2 \leq 0 \) (\( \alpha \) has nonpositive relative rate of change). For a general decay function \( \alpha \), we obtain with high probability approximation with respect to max\(U \cup \mathcal{S} \), \( \inf(\mathcal{S}, U) \), where \( \inf(\mathcal{S}, S) = \sum_{v \in V} \alpha((1 + \epsilon)d_{Sv}) \).

6. EXPERIMENTS

Our algorithms were implemented in C++ and compiled using Visual Studio 2013 with full optimization. Our test machine runs Windows 2008R2 Server and has two Intel Xeon E5-2690 CPUs and 384 GiB of DDR3-1066 RAM. Each CPU has 8 cores (2.90 GHz, 8 × 64 kIB L1, 8 × 256 kIB, and 20 MiB L3 cache). For consistency, however, all runs are sequential.

The inputs in our experiments are obtained from the SNAP [38] project and represent social (Epinions, Slashdot [37], Gowalla [6], TwitterFollowers [21]), LiveJournal [2], Orkut [40] and collaboration (AstroPh) networks. All inputs are unweighted.

Unless otherwise mentioned, we follow Cohen et al. [14] and test our algorithms using \( \ell = 64 \) instances and use \( k = 64 \) during ADS construction. Each instance is obtained by assigning a random length to every edge according to an exponential distribution with expected value 1 [13],[25]. To do so, we sample a value \( x \) uniformly at random from the range \( (0, 1] \), then set the edge length to \(-\ln x\).

6.1 Timed Influence Maximization

We start with the Influence Maximization problem. Recall that we consider two variants of this problem: threshold timed influence and general timed influence. We discuss each in turn.

6.1.1 Threshold Influence

For threshold timed influence and some threshold \( T \), we set \( \alpha(x) = 1 \) for \( x \leq T \) and \( \alpha(x) = 0 \) otherwise. We consider \( T = 0.01 \) and \( T = 0.1 \) in our experiments.

Our first experiment considers the performance of \( T \)-SKIM (Algorithm 2 Section 3), which finds a sequence of seed nodes such that each prefix of the sequence approximately maximizes the influence. Our results are summarized in Table 1. For each instance, we first report its total numbers of nodes and edges. This is followed by the total influence (as a percentage of the total number of nodes of the graph) of the seed set found by our algorithm. We report figures for 50 and 1000 seeds (for both thresholds \( T \) we consider). Finally, we show the total running time of our algorithm, including the time for finding a permutation of all \( n \) nodes such that the influence of each prefix is within a constant factor of that of any other set of the same size. Note that we omit the influence of the entire set, since it is 100% by definition.

The table shows that, unsurprisingly, higher thresholds lead to higher influence values. The running time of our algorithm depends on that influence (since its graph searches must run for longer), but is still practical even for fairly large thresholds and even if we compute the entire permutation. For the largest graph we test (Orkut), with hundreds of millions of edges, we can compute the top 50 seeds in less than 15 minutes, and order all nodes in a few hours using a single CPU core.

Figure 1 presents a more detailed perspective on the same experiment. It shows, for \( T = 0.01 \) and \( T = 0.1 \), how total influence and the running times depend on the size of the seed set. We note that the first few seeds contribute with a disproportionate fraction of the total influence, particularly with \( T = 0.1 \), and an even higher percentage of the total running time. The overall shape of the curves is quite similar, with Orkut as a noticeable outlier: its first few seeds contribute relatively more to the overall influence than in other instances. Note that Orkut is also the densest instance in our testbed.

Figure 2 compares \( T \)-SKIM to the algorithm by Du et al. [22], ConTinEst. We generated the same instances as they used in their evaluation: core-periphery Kronecker networks [38] (parameter matrix: [0.9 0.5; 0.5 0.3]) of varying size, using the Weibull distribution \( f(x, \alpha, \beta) = \beta / \alpha (x / \alpha) ^ {\beta - 1} e^{- (x / \alpha)^\beta} \) for the edge lengths [29]. (Note that \( \alpha \) controls scale and \( \beta \) shape.) For each edge we choose \( \alpha \) and \( \beta \) uniformly at random from \( (0, 1) \).

We ran the same experiment as they did, setting \( |S| = 10 \), and \( T = 10 \). We observe that our approach is consistently about 3 orders of magnitude faster than their algorithm.

6.1.2 General Timed Influence

We now evaluate \( \alpha \)-SKIM, a more general version of our IM algorithm that can handle arbitrary decay functions. For this experiment, we consider both harmonic and exponential decay functions, the
Table 1: Performance of TSKIM using \( k = 64, \ell = 64 \), and exponentially distributed edge weights. We evaluate the influence on 512 (different) sampled instances for thresholds 0.1 and 0.01.

| instance   | # nodes | # edges | 50 seeds | 1000 seeds | Running Time [sec] |
|------------|---------|---------|----------|------------|-------------------|
|            |         |         | 0.01     | 0.1        | 0.01  | 0.1 | 0.01  | 0.1 | 0.01  | 0.1 |
| AstroPh    | 14,845  | 239,304 | 1.02     | 19.17      | 9.96  | 39.25 | 0.9     | 2.0     | 2.0  | 4.0  | 3.7  | 6.6  |
| Epinions   | 75,888  | 508,837 | 0.53     | 8.52       | 2.88  | 12.68 | 2.0     | 5.2     | 6.3  | 11.1 | 14.1 | 21.3 |
| Slashdot   | 77,360  | 828,161 | 0.72     | 19.97      | 3.90  | 25.04 | 1.9     | 14.6    | 7.6  | 27.9 | 18.9 | 40.5 |
| Gowalla    | 196,591 | 1,900,654 | 0.62 | 14.13 | 1.93 | 17.61 | 4.4 | 21.8 | 14.8 | 36.9 | 47.6 | 81.7 |
| TwitterF's | 456,631 | 14,855,852 | 0.20 | 19.38 | 1.64 | 24.26 | 9.9 | 133.4 | 36.4 | 269.6 | 269.9 | 648.4 |
| LiveJournal| 4,847,571 | 68,475,391 | 0.07 | 9.16 | 0.33 | 13.81 | 34.6 | 606.0 | 117.5 | 1,244.4 | 1,983.4 | 4,553.9 |
| Orkut      | 3,072,627 | 234,370,166 | 2.82 | 74.44 | 4.61 | 77.47 | 779.7 | 5,490.5 | 1,788.7 | 11,060.7 | 7,360.9 | 24,520.3 |

Table 2: Performance of \( \alpha \)-SKIM using \( k = 64, \ell = 64 \), and exponentially distributed edge weights for 50 and 1000 seeds. We use exponential (exp.: \( \alpha \cdot x \rightarrow e^{-10x} \)) and harmonic (harm.: \( \alpha \cdot x \rightarrow 1/(10x+1) \)) decay functions.

| instance    | 50 seeds | 1000 seeds | Running Time [sec] |
|-------------|----------|------------|-------------------|
|             | exp. harm. | exp. harm. | 50 seeds | 1000 seeds | exp. harm. | exp. harm. |
| AstroPh    | 17.6    | 31.4      | 33.5 | 44.9 | 15 | 15 | 43 | 40 |
| Epinions   | 7.6     | 14.9      | 11.2 | 18.2 | 35 | 40 | 93 | 99 |
| Slashdot   | 16.9    | 29.1      | 21.3 | 32.8 | 104 | 88 | 238 | 224 |
| Gowalla    | 13.1    | 25.9      | 15.9 | 28.2 | 166 | 213 | 323 | 455 |
| TwitterF's | 16.0    | 26.3      | 19.7 | 29.2 | 1,500 | 1,367 | 2,459 | 2,816 |
| LiveJournal| 10.6    | 23.5      | 13.4 | 25.8 | 5,637 | 5,765 | 11,906 | 13,016 |

Figure 1: Evaluating influence permutations (left) and running times (right) on several instances for threshold decays 0.01 and 0.1. The legend applies to all plots.

most commonly used in the literature. To test harmonic decay, we use \( \alpha(x) = 1/(10x + 1) \); for exponential decay, we use \( \alpha = e^{-10x} \). These functions turn out to give interesting influence profiles. In \( \alpha \)-SKIM we initialize \( \tau \) to \( n/k \) and set \( \lambda \) to 0.5.

Table 2 shows, for both functions, the influence values (in percent) obtained by \( \alpha \)-SKIM for 50 and 1000 seeds, as well as the corresponding running times.

The table shows that \( \alpha \)-SKIM is slower than T-SKIM by up to an order of magnitude for comparable influence. In fact, if we ran \( \alpha \)-SKIM with a threshold function (not shown in the table), it would be about three times as slow as T-SKIM, while producing the exact same results. However, this is to be expected, since \( \alpha \)-SKIM is a much more sophisticated (and flexible) algorithm, which, unlike T-SKIM, can handle smooth decay functions with guarantees.

Even though \( \alpha \)-SKIM is slower, it is still practical. It scales well with the number of seeds (increasing from 50 to 1000 barely doubles the total running time) and can still handle very large graphs.

Figure 2 presents a more detailed view of the same experiment (for a few graphs), with up to \( n \) seeds. It shows that computing a full permutation (with \( n \) seeds) is not much more expensive than computing \( n/1000 \) (a few dozen) seeds. An interesting difference between these results and those for T-SKIM (reported in Figure 1) is that for \( \alpha \)-SKIM the running time grows less smoothly with the number of seeds. The discontinuities correspond to decreases in the sampling threshold \( \tau \), causing additional sampling.

6.1.3 Solution Quality

The quality of the solutions provided by the algorithm depend on the number of instances (simulations) \( \ell \). Our experiments so far have used \( \ell = 64 \). We now compare this with other choices of \( \ell \).

Figure 3 compares the quality of the seed sets found by Greedy for AstroPh for \( \ell = 1, 4, 16, 64, 128 \) with those found by \( \ell = 256 \). We consider sets of size 1 to 50 and three different decay functions: exponential, harmonic, and threshold (with \( T = 0.01 \)). Each point in the curve represents the error (in percent) relative to the solution with \( \ell = 256 \). Although the error is consistently high for the threshold IM when \( \ell \) is very small, it becomes negligible for \( \ell \geq 64 \), justifying our choice of parameters. For smoother (exponential or harmonic) decay, all errors are significantly smaller, and even smaller values of \( \ell \) would be acceptable.

Figure 4 compares the quality of the seed sets found by T-SKIM (for threshold decay) and \( \alpha \)-SKIM (for exponential and harmonic decays) with those found by Greedy on AstroPh. We consider sets of size 1 to \( 10^2 \) and the same decay functions as above. Each point of the curve represents the error (in percent) of our algorithm when compared to Greedy. We observe that the error is very low in general (less than 1 % for exponential and harmonic decay, and less than 4 % for threshold). Considering the fact that
SKIM is many orders of magnitude faster than GREEDY (while still providing strong guarantees), these errors are acceptable. Note that the error of the first seed vertex is very low in all cases (close to 0%), indicating that SKIM does very well in finding the most influential node.

6.2 Timed Influence Oracle

We now evaluate our influence oracles. Recall that this setting has two stages. The preprocessing stage takes as input only the graph and computes sketches. The query stage takes a set $S$ of seeds and a function $\alpha$ and uses the sketches to estimate the influence of $S$ with respect to $\alpha$. Note that same preprocessing stage can be used to answer queries for any decay function $\alpha$. For this experiment, we consider three such functions: exponential ($\alpha(x) = e^{-10x}$), harmonic ($\alpha(x) = 1/(10x + 1)$), and threshold (with $T = 0.01$).

Table 3 summarizes our results in this setting. For each instance tested, it first shows the preprocessing time and the total space required to store all sketches. Then, for each decay function, we report the query time (in microseconds) and the estimation error for random sets $S$ of sizes 1, 50, and 1000. (Note that measuring the error requires computing exact influence of each seed set with multiple Dijkstra searches; this time is not included in the table.) Each entry in the table is the average of 100 random seed sets.

The table shows that, as predicted, query times are almost independent of the $\alpha$ function, the size of the influenced set, and the size of the graph. Moreover, they have a slightly superlinear dependence on the number of seeds Queries are somewhat slower than for binary IC (as reported in [14]), since sketches are bigger and the estimator is more involved. Our oracles are much more flexible, however, and still practical. For 50 seeds, one can answer queries in a few milliseconds, whereas an exact computation could take minutes or more on large graphs. Moreover, its error is consistently low, regardless of the number of seeds.

7. RELATION TO PRIOR WORK

Our approach builds on and generalizes a recent sketch-based influence oracle and IM algorithm (SKIM) [13]. SKIM, however, only applies to binary influence. IM in the timed model and in particular timed IM with smooth decay functions (such as exponential and polynomial decay) requires many additional insights and novel techniques.

The special case of the threshold timed influence model was introduced in [25]. More recently, new algorithms for influence oracle and IM were developed [22], also based on All-Distances Sketches [10]. We obtain orders of magnitude improvements in scalability for these problems. Our improved oracle is made possible by generalizing the sketches themselves to apply to multiple instances, without paying storage overhead for the number of instances and also by careful applications of state-of-the-art estimators. We also provide a leaner oracle, with smaller storage and faster preprocessing when the threshold is fixed. Our threshold timed IM algorithm $T$-SKIM only computes sketches to the point needed to approximate the greedy selection, and is thus much more efficient.

Our timed influence model generalizes distance-decaying closeness centrality [3, 11, 15, 20, 34] to be with respect to multiple seed nodes and multiple instances (or a probabilistic model). Oracles for closeness, also based on the sketching techniques of Cohen [10], were developed for general decay function [11, 15] and for un-weighted graphs [4]. Our timed influence oracle generalizes the state-of-the-art design [11] from centrality to timed influence. As far as we know, IM has not previously been considered in the context of centrality (single static graph). Our timed IM algorithm, $\alpha$-SKIM, is the first scalable solution also for a static network, both from theoretical and practical perspectives.

8. CONCLUSION

We introduce a new model of timed influence, which reflects real-world phenomenon of decay of relevance with elapsed time. We provide the first scalable algorithms for timed influence queries and influence maximization. Our approach is the first to work with natural smooth decay functions including exponential and polynomial decay. For the threshold model, which was previously studied, we design much more scalable algorithms. Our algorithms provide theoretical guarantees and demonstrated to work well on large networks.

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Table 3: Evaluating the timed influence oracle with $\ell = 64$.

| Instance   | Time [h:m] | Space [MiB] | Time Err. (%) | Time Err. (%) | Time Err. (%) | Time Err. (%) | Time Err. (%) | Time Err. (%) |
|------------|------------|-------------|---------------|---------------|---------------|---------------|---------------|---------------|
| AstroPh    | 0:10       | 149.2       | 38            | 7.2           | 9,695         | 1.2           | 229,340       | 0.5           |
| Epinions   | 0:46       | 674.0       | 32            | 3.2           | 8,552         | 1.1           | 222,470       | 1.0           |
| Slashdot   | 1:10       | 851.4       | 46            | 5.6           | 11,884        | 1.5           | 310,170       | 0.4           |
| Gowalla    | 3:55       | 2,558.6     | 52            | 3.8           | 17,109        | 1.0           | 356,818       | 0.4           |
| TwitterF’s | 19:33      | 6,165.1     | 51            | 3.8           | 13,816        | 1.4           | 345,366       | 0.7           |

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Figure 5: Evaluating influence permutations (left) and running time (right) on several instances for exponential (exp.: $\alpha \propto e^{-10x}$) and harmonic (harm.: $\alpha \propto 1/(10x + 1)$) decays. The legend applies to all plots.
APPENDIX

A. RUNNING TIME ANALYSIS FOR T-SKIM

The computation is dominated by two components. The first is the reversed pruned Dijkstra searches which build the inverted sketches. The second is the forward pruned Dijkstra searches that we use to compute and update the residual problem after a new seed node is selected. In both components we use pruned shortest-paths computations (whereas SKIM for binary influence uses generic searches). The bound on the number of reversed edge traversals performed for sketch building and the analysis deriving this bound are essentially the same as with binary SKIM [14]. We bound the total number of increments to the entries in the array size. Each entry in that array corresponds to a node and the size (number of entries) in the partial sketch. Recall that the sketches themselves are maintained in an inverted structure.

The number of forward traversals used to update the residual problem is linear in binary SKIM; this is because there can be at most one search which proceeds through a node in each instance: once a node is reachable from the seed set in that instance, it is influenced, and everything reachable from the node in the same instance is reachable as well. So these nodes never need to be visited again (in reversed or in forward traversals).

With T-SKIM, however, a search can progress through node $v$ in instance $i$ multiple times. The residual problem uses the distances $\delta[v,i]$ of node $v$ in instance $i$ from the seed set. When a seed node is added, distances may decrease. When a distance is decreased, the node and its relevant outgoing edges are visited and $\delta[v,i]$ is updated to the new distance.

The total number of visits depends on the number of times the distance $\delta[v,i]$ for each pair $(v,i)$ is decreased as seed nodes are added. It is possible to construct pathological inputs, even with exact Greedy, where the number of updates per node-instance pair is proportional to the number of seed nodes selected. On realistic inputs, however, we expect the number of updates to be no more than $\ln n$ per node. This is because even if seed nodes are added in random order, the expected number of times the distance to the seed set decreases is well concentrated around $\ln n$. Therefore, since selected seeds should typically be closer than other nodes, we would expect a small number of updates. Our experiments verify this behavior, as T-SKIM is very efficient, and the overall computation was typically dominated by the reversed searches.

We next propose a solution which provides worst-case robustness of the number of forward traversals on any input at the cost of a slight softening of the sharp threshold. This design was not implemented, as we did not encounter pathological inputs when running with the sharp threshold on benchmark networks. The design, however, can be used if the need arises and is also of theoretical interest.

We first formalize the notion of a softened threshold $T$ in the influence function: For a parameter $v \in (0,1)$, we only require approximation with respect to the maximum influence of a seed set of size $s$ when the threshold is $(1-v)T$. Since we expect the value of the threshold used in an application not be precise anyway, this relaxation approximates the intended semantics of using a threshold of $T$.

We next outline a slight modification of T-SKIM which provides a bound on the running time and approximation quality with respect to the soft threshold.

**Theorem A.1.** Our modified T-SKIM, guarantees with high probability, for all $s$ that the first $s$ selected seeds have influence for threshold function $\alpha(x) = x \leq T \iff: 0$ that is at least $1 - (1 - 1/s)^s - \epsilon$ times the maximum influence of a seed set of size $s$ with respect to a threshold function $\alpha(x) = x \leq (1 - v)T ? 1 : 0$. The algorithm runs in time

$$O(v^{-1} \sum_{i} |E^{(i)}| \log n + m e^{-2} \log^3 n),$$

where $m \leq |\cup_i E^{(i)}|$ is the sum over nodes of the maximum in-degree over instances.

**Proof.** We outline the modifications needed to support the soft threshold.

In the forward searches, we only propagate updates to $\delta[v,i]$ when the decrease in distance is at least $vT$. In particular, the reversed Dijkstras are always pruned at distance $T(1-v)$ and the forward Dijkstras are pruned when $d \leq T$ or $d > \delta[v,i] - vT$. This means that at any given time, if $d^{(i)}_{S^v} \leq (1-vT)$ then $\delta[v,i] \in [d^{(i)}_{S^v}, d^{(i)}_{S^v} + vT]$. That is, node-instance pairs of distance at most $(1-v)T$ are counted as influenced and pairs of distance greater than $T$ are not influenced, but other pairs can be counted either way and our estimation guarantee is with respect to a threshold of $(1-v)T$.

When discretizing to $vT$, we obtain a worst-case guarantee of $1/v$ on the number of updates of $\delta[v,i]$ in each node-instance pair. In total, we obtain the claimed worst-case bound on the running time. $\square$

B. OPTIMAL ORACLE ESTIMATOR

We show that the timed influence estimator presented in Algorithm 3 is an instance of the $L^v$ estimator of [12].

We first explain the derivation of the estimator. Similarly to the single node, this is a sum estimator applied to each summand $(v,i)$ in Equation (7) to obtain an unbiased estimate of $\alpha(\min_{u \in S} d^{(i)}_{u,v})$. Rank values $r$ that belong to pairs $(v,i)$ where $v \in S$ can be identified because they must appear as $(r,0)$ in cADS$(v)$ when we use structured permutation ranks. For these pairs, we do not compute an estimate but simply add an exact contribution of $|S|\alpha(0)$ to the estimated influence.

The remaining rank values are those associated with pairs that have a positive distance from $S$. That is, a pair $(v,i)$ so that $d^{(i)}_{S^v} > 0$. We would like to estimate $\alpha(\min_{u \in S} d^{(i)}_{u,v})$ for each such pair $(v,i)$. We apply the $L^v$ estimator of Cohen [12], which is applicable to any monotone estimation problem (MEP) and is the unique admissible (nonnegative unbiased) monotone estimator. We first show that our estimation problem is a MEP. To represent the problem as a MEP, we fix the rank values of all pairs, and consider the outcome (presence in cADS$(u)$ for $u \in S$) as a function of the "random seed" $r^{(i)}_v$. Clearly, the lower bound $r^{(i)}_v$ is, the more information we have (a tighter upper bound) on $\alpha(d^{(i)}_{S^v})$. Therefore, the problem is a MEP.

The information in the outcome is actually contained in the skyline of occurrences of the rank $r^{(i)}_v$. When the skyline for a pair $(v,i)$ is empty ($r^{(i)}_v$ is not included in any of the sketches of nodes in $S$), the $L^v$ estimate is 0 and is not explicitly computed.

Note that the estimator is applied to each rank value $r^{(i)}_v \notin Z$ (and does not require explicit knowledge of the corresponding pair $(v,i)$).

Since the $L^v$ estimator is admissible, it dominates the union estimator and in particular has CV at most $1/\sqrt{2(k-1)}$. Note that this is an upper bound on the CV; the worst case is $|S| = 1$ or when sketches are very similar. As with reachability sketches, we can expect the estimate quality to be up to a factor of $\sqrt{|N|}$ smaller when the “coverage” of different seed nodes are sufficiently different. Similarly, Chernoff concentration bounds apply here: If we use $k = e^{-2c \ln n}$, the relative error exceeds $\epsilon$ with probability...
we obtain on the computation of each one, and pointers to the proofs
that exceeds $k$ bound on the total number of times
s lower bound on the total influence of any seed set of size $\leq t$
ional seed nodes, the relative contribution of these nodes is at most
Now observe that at this point, for all $\epsilon \alpha$
over all nodes, is less than $\tau$
is decreased only when the maximum estimated marginal influence,
changes (Lemma C.2) expected sample sizes remain
This involves $O(\log n)$ operations in updating priority queues in the
state of the Dijkstra run, structures maintaining the samples, and
looking at all outgoing edges of the node in the transposed instance $G_i^0$.
Each such scan can be charged to an entry inserted into a PPS sample. From Lemma C.1, we obtain that each node, in expectation, can have $O(\log n)$ such entries. Therefore, the node is scanned $O(\log n)$ times. □

C. Running time of $\alpha$-SKIM

This section provides the proof of Theorem 5.2.

We first list the main components of the computation, the bounds we obtain on the computation of each one, and pointers to the proofs in the sequel. The analysis assumes that $\lambda = 0.5$.

- The reversed Dijkstra runs when building the sketches, including updating the sample and estimation data structures as new entries are inserted. Since we use efficient structures to identify which runs need to be resumed and to update estimates and samples, this component is dominated by the Dijkstra computations. We obtain a bound of $O(k\log^2 n \sum_{i} \max_{|i|} degrees^{(i)}(v))$ on the number of operations (see Lemma C.5).
- The forward Dijkstra runs which update the residual problem after a seed node is selected. We express the bound in terms of the maximum number of times, which we denote by $X$, that $\delta_v^{(i)}$ is decreased for a pair $(i,v)$. The forward Dijkstra runs in this case take $O(X \sum_{i} |E^{(i)}| \log n)$ operations (see Lemma C.6). In Section C.3, we obtain a bound of $X = O(\log n)$ for a slightly modified algorithm. The modified algorithm has the same approximation guarantee (as in Theorem 5.1) when $\alpha$ has nonpositive relative rate of change. For general $\alpha$, the guarantee is with respect to a relaxed condition. In practice on realistic inputs, however, we expect $X$ to be small and we observe good running times even without the modifications.
- Updating the sample and estimation structures when entries are reclassified up. This happens after a seed is removed from the forward Dijkstra run from the seed in instance $i$ updates $\delta_v^{(i)}$. This means all samples which include a $(v,i)$ entry need to be updated. Expressed in terms of $X$, this cost is $O(Xnk\log n)$ (see Lemma C.7).
- Updating the sampling and estimation structures when entries are reclassified down. This can happen after $\tau$ is decreased. We obtain a bound of $O(nk\log^2 n)$ (in Section C.1).

C.1 The threshold $\tau$

An immediate upper bound on the maximum influence of a node is $n\alpha(0)$. This means that we can safely initialize our algorithm with $\tau = (n\alpha(0)/\epsilon) / k$ and have an expected initial sample sizes $O(k)$ for each node.

Next observe that we can safely terminate the algorithm when $\tau$ decreases to below $\epsilon \alpha(0)/\epsilon / k$ and incur at most $O(\epsilon)$ contribution to the error. To establish that, first observe that the threshold $\tau$ is decreased only when the maximum estimated marginal influence, over all nodes, is less than $\tau k$. Therefore, when $\tau \leq \epsilon \alpha(0)/\epsilon / k l$, the maximum marginal influence of all nodes is at most $\epsilon \alpha(0)$. Now observe that at this point, for all $s' \geq 0$, if we add $s'$ additional seed nodes, the relative contribution of these nodes is at most $\leq (s' \alpha(0)) / (s + s') \alpha(0) \leq \epsilon$ (The denominator $(s + s') \alpha(0)$ is a lower bound on the total influence of any seed set of size $s + s'$). Combining the start and end values of $\tau$, we obtain the following bound on the total number of times $\tau$ is decreased:

\textbf{Lemma C.1.} $\tau$ can decrease at most $\log_{1/\lambda} (n/\epsilon) = O(\log n)$ times.

When $\tau$ decreases, we have the property that the PPS samples of all nodes are of size smaller than $k$ (otherwise we have an estimate that exceeds $k \tau$).

After $\tau$ is decreased, we extend the samples to be with respect to the new $\tau$. We show that the expected sample size remains $O(k)$:

\textbf{Lemma C.2.} For every node, the expected number of entries after a threshold decrease $\tau \leftarrow \lambda \tau$ is at most $k/\lambda$, with good concentration.

\textbf{Proof.} Equivalently, we consider the size of a PPS sample with threshold $\lambda \tau$ when the total weight of the set is at most $k \tau$. □

We are now ready to bound the total number of reclassification of sample entries.

\textbf{Lemma C.3.} The total number of reclassifications of entries in the sample is $O(nk\log n)$.

\textbf{Proof.} An entry in index $[v,i]$ can only be reclassified down 3 times before it is removed from the sample (from H to M, M to L, or L to removal), unless it is reclassified up. An entry can be reclassified up only when $\tau$ decreases, which happens at most $O(\log n)$ times. Each decrease “resets” at most $kn$ entries to class $H$: Either existing entries reclassified up or at most new entries (since by Lemma C.2, expected sample sizes remain $O(k)$). These entries can then be reclassified down at most 3 times before they are eliminated from the sample. So the total number is $O(nk\log n)$. □

We are now ready to bound the total work performed by updating the sample and estimation components by entries being reclassified up as a result of a $\tau$ decrease (hereUp calls). The cost of each such call is proportional to the number of reclassified entries. It also requires a call to the priority queue to efficiently find all inverted samples with at least one reclassified element. In the worst case, the cost is $O(\log(nl) \times \log n)$ times the number of reclassifications. In total using Lemma C.3, we obtain a worst case bound of $O(nk\log^2 n)$ on the reclassification-component of the computation.

C.2 Bounding the reversed Dijkstra computations

We bound the expected total number of distinct entries (pairs $(v,i)$) that were included in the PPS sample of a node $u$ at any point during the execution of the algorithm.

\textbf{Lemma C.4.} For a node $v$, the number of distinct entries in the sample of $v$ during the execution of the algorithm is $O(k\log n)$ with good concentration (of the upper bound).

\textbf{Proof.} Each decrease of $\tau$ introduces in expectation $O(k)$ new entries, and there are $O(\log n)$ such decreases (Lemma C.1). □

We can now bound the work of the reverse Dijkstra runs used to construct the sketches.

\textbf{Lemma C.5.} The number of operations performed by the reverse Dijkstra runs is $O(k\log^2 n \sum_{i} \max_{|i|} degrees^{(i)}(v))$.

\textbf{Proof.} Each productive scan of a node $v$ by a reverse Dijkstra sourced at $(v,i)$ (productive means that the node was next on the Dijkstra state priority queue) means that the entry $(v,i)$ is inserted into a PPS sample of $u$, updating the estimation structure accordingly. This involves $O(\log n)$ operations in updating priority queues in the state of the Dijkstra run, structures maintaining the samples, and looking at all outgoing edges of the node in the transposed instance $G_i^0$.

Each such scan can be charged to an entry inserted into a PPS sample. From Lemma C.4, we obtain that each node, in expectation, can have $O(k\log n)$ such entries. Therefore, the node is scanned $O(k\log n)$ times. □
We remark that if the instances are generated by an IC model, we can replace \( \max_{v \in [n]} \deg(v) \) by the expected degree \( E[\deg(v)] \) and accordingly obtain the bound \( O(k \log^2 n E[|E|]) \).

### C.3 Bounding the expected number of times \( \delta_{vk}^{(i)} \) decreases for a certain pair \((v,i)\)

We now bound the number of updates of \( \delta_{vk}^{(i)} \) performed as seed are added when maintaining the residual problem.

If we have a bound of \( X \) on the number of updates per node-instance pair, then

**Lemma C.6.** The computation of the forward Dijkstra runs is \( O(X \sum_{i \in [n]} |E(i)| \log n) \).

**Proof.** Each node-instance scan can be charged to a decrease of \( \delta_{vk}^{(i)} \).

We also can express the total cost of the \texttt{MoveDown()} calls by \( X \).

**Lemma C.7.** The total computation of all \texttt{MoveDown} calls is \( O(Xnk\log n) \).

**Proof.** Each call to \texttt{MoveDown} for \((v,i)\) updates a value for \((v,i)\) in a priority queue (at \( O(\log n) \) cost), which is of the order of the forward Dijkstra computation that generated the update of \( \delta_{vk}^{(i)} \). Otherwise, the \texttt{MoveDown} call performs a number of operations that is linear in the number of active entries in \texttt{index}[v,i] (entries that are in a sample of some node). In addition, \texttt{MoveDown} may also permanently discard entries at the tail of the \texttt{index}[v,i], but the removal of these entries is charged to their insertion.

It remains to bound the computation of \texttt{MoveDown} when processing active entries of \texttt{index}[v,i]. Using Lemma C.4, there is a total of \( O(nk \log n) \) entries that were active in a sample at any point during the execution. Each such entry can be affected at most \( X \) times.

We now bound \( X \). As argued in Section 3, we expect \( X = O(\log n) \) on realistic instances, but it is possible to construct inputs with a a number of updates that is proportional to the number of seeds.

Here we propose modifications of the algorithm that allow us to bound \( X \) in interesting cases. The first case covers all smooth decay functions that are exponential or slower.

**Lemma C.8.** We can modify \( \alpha \)-SKIM so that when \( \alpha(x) \) has a nonpositive relative rate of change, that is, \( (\ln \alpha(x))' \geq 0 \), then \( X = O(\varepsilon^{-1} \log n) \).

**Theorem C.7.**

**Proof.** The requirement \( (\ln \alpha(x))' \geq 0 \) implies that for all \( x \geq 0 \), \( d \geq 0 \), and \( \Delta \geq 0 \),

\[
\frac{\alpha(d - \Delta) - \alpha(d)}{\alpha(d)} \geq \frac{\alpha(x + d - \Delta) - \alpha(d)}{\alpha(x + d)}.
\]

This means that when we apply the following prune rules on forward updates of \( \delta_{vk}^{(i)} \): We prune at nodes where

\[
\frac{\alpha(d - \Delta) - \alpha(d)}{\alpha(d)} \leq \varepsilon,
\]

where \( d \) is the current value of \( \delta_{vk}^{(i)} \) and \( d - \Delta \) is the updated value, the condition (16) would actually hold for all nodes in instance \( i \) reachable from \( v \) via the Dijkstra search (since all these nodes have larger \( \delta_{vk}^{(i)} \)).

The prune condition implies that for \((v,i)\) and all nodes Dijkstra would have reached from the pruned one, the updated influence contribution by the better (closer) coverage is at most \( \varepsilon \) times the previous value. So with this pruning, the influence of the seed set is captured with relative error of at most \( \varepsilon \).

We also observe that we can also always prune the Dijkstra computations when the distance satisfies \( \alpha(d) \leq \alpha(0)/n^2 \leq \varepsilon \alpha(0)/n \).

Combining, it means that with the prune rules, the total number of updates of \( \delta_{vk}^{(i)} \) per node-instance pair is \( O(\varepsilon^{-1} \log n) \).

**Lemma C.9.** We can modify the algorithm so that for any general decay function \( \alpha \), \( X = O(\varepsilon^{-1} \log n) \). With the modification, we obtain that with high probability,

\[
\inf(\mathcal{G}, S) \geq (1 - (1 - 1/s^2 - \varepsilon)) \max_{U \subseteq [s]} \inf(\mathcal{G}, U),
\]

where \( \inf(\mathcal{G}, S) \equiv \sum_{v \in V} \alpha((1 + \varepsilon)d_{Su}) \).

**Proof.** We can apply a similar prune rule in the forward Dijkstra runs which updates only when the decrease to distance is at least \( \varepsilon \) times the current distance. This would give us a bound on the number of updates, but a weaker approximation guarantee that holds with respect to a softened influence function \( \sum_{v \in V} \alpha((1 + \varepsilon)d_{Su}) \).

### C.4 Discussion

An interesting theoretical question that we leave open is the existence of an \( \tilde{O}(m) \) time algorithm that tightly approximates greedy timed influence maximization for general decay functions (where \( m = \sum_{i=1}^{l} |E(i)| \) is the combined sizes of the edge sets).

We argued and observed experimentally that our algorithm behaves well on realistic instances (does not update the residual distances \( \delta_{vk}^{(i)} \) too many times). We also proved that we can obtain \( \tilde{O}(m) \) running time when the decay function is polynomial or exponential (nonpositive relative rate of change). We also showed that we can also guarantee \( \tilde{O}(m) \) time if we slightly soften the approximation ratio requirement to allow small perturbations of distances.

The hardest case seems to be embodied in the sharp threshold, even on a single instance (a single deterministic graph). Interestingly, even in other settings such as time-decay on streams, the sharp threshold (aka, sliding window) seems to be the hardest case [19].

### D. PSEU**CO**CODE

### D.1 Functions for Timed GREEDY

This appendix contains the pseudocode of functions for our timed version of GREEDY from Section 2.

**Function MargGain(u): Marginal influence of u**

**Input:** Residual instance \((\mathcal{G}, \delta)\) and node \( u \)

**Output:** \( \inf(\mathcal{G} \setminus \{u\}, \delta) \)

\( I_u \leftarrow 0; \) // sum of marginal contributions

**foreach instance i do**

**Run Dijkstra from u in G(i), during which**

**foreach visited node v at distance d do**

\[
\text{if } \alpha(d) = 0 \text{ or } d \geq \delta_{vk}[i] \text{ then Prune else }
\]

\[
I_u \leftarrow \alpha(d) - \alpha(\delta_{vk}[i])
\]

```
return \( I_u / \ell \)
```
D.2 Algorithms for Threshold Model

This appendix contains the pseudocode for algorithms for threshold timed influence maximization (Section 3).

**Algorithm 2: Threshold Timed IM (T-SKIM)**

**Input:** Directed graphs \( \{G^{(i)}\} \), threshold \( T \), parameter \( k \)

**Output:** Sequence of node and marginal influence pairs

```plaintext
// Initialization

forall the node-instance pairs \((u,i)\) do
  if \( \delta(u,i) < \infty \) then skip; // Pair \((u,i)\) is covered
run Dijkstra from \( u \) in reverse graph \( G^{(i)} \), during which
foreach scanned node \( v \) do
  size[v] \leftarrow 0
index[v,i] \leftarrow hash map of node-instance pairs to nodes
seedlist \leftarrow \perp // List of seeds & marg. influences
rank \leftarrow 0
shuffle the \( n \) node-instance pairs \((u,i)\)

// Compute seed nodes
while \(|\text{seedlist}| < n \) do
  while rank < \( n \) do // Build sketches
    rank \leftarrow rank + 1
    \((u,i)\) \leftarrow rank-th pair in shuffled sequence
    if \( \delta(u,i) < \infty \) then skip; // Pair \((u,i)\) is covered
    run Dijkstra from \( u \) in reverse graph \( G^{(i)} \), during which
    foreach scanned node \( v \) do
      if \( d > T \) then prune; // Prune at depth \( T \)
      size[v] \leftarrow size[v] + 1
      index[u,i] \leftarrow index[u,i] \cup \{v\}
      if size[v] = \( k \) then
        \( x \leftarrow v \) // Next seed node
        // Prune by decreasing \( \alpha \)
      // abort sketch building
    if all nodes \( u \) have size[\( u \)] < \( k \) then
      \( x \leftarrow \arg \max_{u \in V} \text{size}[u]\)
    \( I_x \leftarrow 0 \) // The coverage of \( x \)
  foreach the instances \( i \) do // Residual Problem
    run Dijkstra from \( x \) in forward graph \( G^{(i)} \), during which
    foreach scanned node \( v \) do // Prune by decreasing \( \alpha \)
      if \( \delta[v,i] \leq d \) or \( d > T \) then prune if \( \delta[v,i] = \infty \)
      then \( I_x \leftarrow I_x + 1 \)
      \( \delta[v,i] \leftarrow d \)
    foreach the nodes \( w \) in index[v,i] do
      size[w] \leftarrow size[w] - 1
      index[v,i] \leftarrow \perp // Erase \((v,i)\) from index
    seedlist.append(\( x, I_x/\ell \))

return seedlist
```

D.3 Algorithms for Timed Influence Oracle

This appendix contains the pseudocode for our timed influence oracle (Section 4).

**Algorithm 3: Timed Influence Oracle**

**Input:** Seed set \( S \), function \( \alpha \), sketches \( \text{cADS}(u) \) for \( u \in S \)

**Output:** Estimated influence for \( S \)

// Remember ranks who have distance zero in at least one sketch with respect to \( S \)
\( Z \leftarrow \) empty set (e.g. hash map) of ranks

forall the nodes \( u \in S \) do
  foreach entry \((r,d)\) in \( \text{cADS}(u) \) with \( d = 0 \) do
    \( Z.insert(r) \)

// Build for each appearing rank a set of threshold rank/influence pairs
skylines \( \leftarrow \) new max heap of \( k \) smallest rank values

forall the ranks \( r \) \in skylines do
  if \( |Q| < k \) then
    if \( r \notin Z \) then skylines[r].append((1.0, \( \alpha(d) \))
    Q.insert(r)
  else
    if \( r \notin Z \) then skylines[r].append((Q.max_element(), \( \alpha(d) \))
    Q.insert(r)
  Q.delete_max(r)

// Eliminate dominated entries
forall the ranks \( r \) \in skylines do
  // Sort by threshold rank in decreasing order. Break ties by decreasing \( \alpha \)
  sort(skylines[r])
  \( \alpha^* \leftarrow 0 \)
  forall the thresholds \((\tau, \alpha) \in \text{skylines}[r] \) do
    if \( \alpha < \alpha^* \) then skylines[r].erase((\( \tau, \alpha \)) else
      \( \alpha^* \leftarrow \alpha \)

// This calls the \( L^* \) estimator for each skyline
return \(|S| \cdot \alpha(0) + (1/\ell) \cdot \sum_{r \in \text{skylines}} L^*(\text{skylines}[r]) \)
**Algorithm 4:** L∗estimator applied to a sorted skyline

**Input:** A sorted skyline $\text{skylines}[r] = \{(\tau_j, \alpha_j)\}$

**Output:** $L^*(\text{skylines}[r])$

$S \leftarrow 0; \ x \leftarrow 0$

for $i = 1, \ldots, |\text{skylines}[r]|$ do

$x \leftarrow (\alpha_i - S) / \tau_i$ // Note that $x$ is overwritten

if $i < |\text{skylines}[r]|$ then $S \leftarrow S + x \cdot (\tau_i - \tau_{i+1})$

return $x$

---

**Algorithm 5:** Combine rank-distance lists

**Input:** Two rank-distance lists $A_1$ and $A_2$

**Output:** Combined all-distance sketch $\text{ADS}_c$

$\text{ADS}_c \leftarrow \text{new (empty) ADS}$

// Merge sketches by increasing distance, breaking ties by increasing rank

$\text{tempsketch} \leftarrow \text{merge}(A_1, A_2)$

$numzero \leftarrow 0$

$Q \leftarrow \text{new max-heap of } k \text{ smallest rank values}$

// Handle entries with distance 0

foreach entry $(r, d) \in \text{tempsketch with } d = 0$ do

if numzero $< k$ then $\text{ADS}_c(u).\text{append}((r, d))$

$Q.\text{insert}(r)$

if $|Q| > k$ then $Q.\text{delete\_max()}$

$numzero \leftarrow \text{numzero} + 1$

// Handle the rest of the entries

foreach entry $(r, d) \in \text{tempsketch with } d > 0$ do

if $|Q| < k \text{ or } r < Q.\text{max\_element()}$ then

$\text{ADS}_c(u).\text{append}((r, d))$

$Q.\text{insert}(r)$

if $|Q| > k$ then $Q.\text{delete\_max()}$

return $\text{ADS}_c$
D.4 Functions for $\alpha$-SKIM

This appendix contains the subroutines of Algorithm $\Pi(\alpha$-SKIM), our fast algorithm for timed influence maximization.

Function NextSeed
Output: The node $u$ which maximizes $\text{Est}.H[u] + \tau \text{Est}.M[u]$, if happy with estimate. Otherwise ⊥.

while true do
   if max priority in Qcands $< k\tau$ then return ⊥ else
      Remove maximum priority $u$ from Qcands;
      $I_u \gets \text{Est}.H[u] + \tau \text{Est}.M[u]$;
      if $I_u \geq k\tau$ and $I_u \geq$ max in Qcands then
         $I_u \gets \text{MargGain}(u)$;
         if $I_u \geq (1 - 1/\sqrt{k}) f_u$ then return $(u, I_u)$ else
            Place $u$ with priority $I_u$ in Qcands;
      return ⊥
   else
      Place $u$ with priority $I_u$ in Qcands

Function MoveUp Update estimates after decreasing $\tau$

foreach $(v,i)$ in Qhml with priority $\geq \tau$ do
   delete $(v,i)$ from Qhml
   // Process index[v,i]
   if HM[v,i] $\neq \bot$ then // move entries from H/L to H
      while HM[v,i] $< \text{index}[v,i]$ and
         $(u,d) \leftarrow \text{index}[v,i][\text{HM}[v,i]]$ satisfies
         $(\alpha(d) - \alpha(\delta^{(i)})) \geq \tau$ do
         $\text{Est}.H[u] \leftarrow c$ if ML[v,i] $= \bot$ or ML[v,i] $> \text{HM}[v,i]$ then
            // Entry was H
            $\text{Est}.M[u] \leftarrow 1$
            $\text{HM}[v,i] \leftarrow 1$
         if ML[v,i] $\neq \bot$ and ML[v,i] $< \text{HM}[v,i]$ then
            $\text{ML}[v,i] \leftarrow \text{HM}[v,i]$
         if HM[v,i] $\geq |\text{index}[v,i]|$ then
            $\text{HM}[v,i] \leftarrow \bot$; $\text{ML}[v,i] \leftarrow \bot$
         if ML[v,i] $\neq \bot$ then // Move from L to M
            while ML[v,i] $< |\text{index}[v,i]|$ and
               $(u,d) \leftarrow \text{index}[v,i][\text{ML}[v,i]]$ satisfies
               $(\alpha(d) - \alpha(\delta^{(i)})) \geq r^{(i)}_v \tau$ do
               $\text{ML}[v,i] \leftarrow 1$; $\text{Est}.M[u] \leftarrow 1$
               if ML[v,i] $\geq |\text{index}[v,i]|$ then $\text{ML}[v,i] \leftarrow \bot$
      UpdateReclassThresh(v,i) // update Qhml
   end

Function UpdateReclassThresh(v,i)
Output: Update priority of $(v,i)$ in Qhml
$c \leftarrow 0$;
if HM[v,i] $\neq \bot$ then
   $(u,d) \leftarrow \text{index}[v,i][\text{HM}[v,i]]$; $c \leftarrow \alpha(d) - \alpha(\delta^{(i)})$
else
   if ML[v,i] $\neq \bot$ then
      $(u,d) \leftarrow \text{index}[v,i][\text{ML}[v,i]]$;
      $c \leftarrow \max \{c, (\alpha(d) - \alpha(\delta^{(i)}))/r^{(i)}_v\}$
   if $c > 0$ then
      update priority of $(v,i)$ in Qhml to $c$
   end
end

Function MoveDown ($(v,i), \delta_0, \delta_1$)
Output: Update estimation components for $(v,i)$ when $\delta^{(i)}$ decreases from $\delta_0$ to $\delta_1$
$j \leftarrow 0$; $t \leftarrow \bot$; $\text{HM}[v,i] \leftarrow \bot$;
$z \leftarrow |\text{index}[v,i]| - 1$; if ML[v,i] $\neq \bot$ then $z \leftarrow \text{ML}[v,i]$
ML[v,i] $\leftarrow \bot$
while $j \leq z$ do
   $(u,d) \leftarrow \text{index}[v,i][j]$;
   if $(\alpha(d) - \alpha(\delta_1)) \geq \tau$ then // entry was H
      $\text{Est}.H[u] \leftarrow \alpha(d) - \alpha(\delta_1)$;
      if $(\alpha(d) - \alpha(\delta_1)) \geq \tau$ then // is H
         $\text{Est}.H[u] \leftarrow \alpha(d) - \alpha(\delta_1)$
      else if $(\alpha(d) - \alpha(\delta_1)) \geq r^{(i)}_v \tau$ then // is M
         $\text{Est}.M[u] \leftarrow 1$; if $\text{HM}[v,i] = \bot$ then $\text{HM}[v,i] = j$
      else if $(\alpha(d) - \alpha(\delta_1))$ then // truncate
         if $t = \bot$ then $t = j$
      else // is L
         if $\text{ML}[v,i] = \bot$ then $\text{ML}[v,i] \leftarrow j$
      end
   else if $(\alpha(d) - \alpha(\delta_1)) \geq r^{(i)}_v \tau$ then // entry was M
      $\text{Est}.M[u] \leftarrow 1$; if $\text{HM}[v,i] = \bot$ then $\text{HM}[v,i] = j$
      else // is M
         $\text{Est}.M[u] \leftarrow 1$; $\text{HM}[v,i] \leftarrow j$
   else // is not M
      $\text{Est}.M[u] \leftarrow 1$;
      if $(\alpha(d) - \alpha(\delta_1))$ then // truncate
         if $t = \bot$ then $t = j$
      else // is L
         if $\text{ML}[v,i] = \bot$ then $\text{ML}[v,i] \leftarrow j$
      end
   end
   $j \leftarrow j + 1$
end
if $t \neq \bot$ then truncate index[v,i] from $t$ on.
else // clean tail
   $t \leftarrow |\text{index}[v,i]| - 1$;
   while $t \geq 0$ and $(u,d) \leftarrow \text{index}[v,i][t]$ has $\alpha(d) \leq \alpha(\delta_1)$ do
      $t \leftarrow t - 1$
   truncate index[v,i] at position $t + 1$ on
Remove pair $(v,i)$ from Qhml
UpdateReclassThresh(v,i) // update Qhml

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