Top-K Entity Resolution with Adaptive Locality-Sensitive Hashing

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ABSTRACT

Given a set of records, entity resolution algorithms find all the records referring to each entity. In this paper, we study the problem of top-k entity resolution: finding all the records referring to the k largest (in terms of number of records) entities. Top-k entity resolution is driven by many modern applications that operate over just the few most popular entities in a dataset. We propose a novel approach, based on locality-sensitive hashing, that can very rapidly and accurately process massive datasets. Our key insight is to adaptively decide how much processing each record requires to ascertain if it refers to a top-k entity or not: the less likely a record is to refer to a top-k entity, the less it is processed. The heavily reduced amount of processing for the vast majority of records that do *not* refer to top-k entities, leads to significant speedups. Our experiments with images, web articles, and scientific publications show a 2x to 25x speedup compared to the traditional approach for high-dimensional data.

ACM Reference format:
Vasilis Verroios and Hector Garcia-Molina. 2018. Top-K Entity Resolution with Adaptive Locality-Sensitive Hashing. In *Proceedings of Infolab, CA, Stanford (Technical Report),* 20 pages.
https://doi.org/10.1145/nnnnnnn.nnnnnnn

1 INTRODUCTION

Given a set of records, the objective in entity resolution (ER) is to find clusters of records such that each cluster collects all the records referring to the same entity. For example, if the records are restaurant entries on Google Maps, the objective of ER is to find all entries referring to the same restaurant, for every restaurant.

In many applications the *size* of a resolved entity (i.e., the number of records) reflects the *importance* or *populatity* of the entity. For example, if the records are bug reports and the entities are code bugs, the larger the entity, the more users have encountered the bug, and the more important it is to fix the bug. If we only have resources to fix say three bugs this week, then we only need to identify the top three bugs, i.e., we do not need to resolve all entities (which may be very time consuming), just the three largest. It also so happens that in most of these applications where importance matters, entity sizes follow a Zipfian distribution, so the top few entities are way more important or popular than the rest. As we will see, this fact makes it easier to find the top-k entities without computing all entities. We call the problem of finding the k entities with the largest number of records, top-k entity resolution (top-k ER).

We next illustrate two additional applications where one typically only needs top-k entities. Incidentally, two of the datasets we use for our experiments are from these applications. First, consider news articles: in many cases, the same story (or a large portion of it) is copied/reproduced in different articles. In this case a resolved entity represents a single story or news event, and its records are the articles that refer to that story. The larger an entity, the more web sites or newspapers decided to present that story, so the more popular (arguably important) that story is. If we are preparing a news summary for readers with limited time, it makes sense to include the top-k stories. (Of course, the summary may also include other hand-picked stories.) Again, for the summary of the popular stories one does not need to resolve all entities. Note that computing all entities in this application can be prohibitive: there can be hundreds of thousands of articles, resolution is quadratic in the number of articles, and we want to produce our summary in a very timely manner.

Second, consider viral images in social media: images that are being copied (possibly transformed) and shared, sometimes without a direct connection to the original post. Large entities represent images that have been shared a lot and can be much more interesting than other images for a number of reasons, e.g., copyright issues or they indicate what images are being shared the most. In all those cases, finding the top-k entities can be sufficient. For instance, serious copyright violations may require an expert's attention and intervention and since experts' time is limited, it can be better allocated in content that is being extensively shared (i.e., one of the top-k entities).

Overall, we can find a motivating example for any application where the user experience drastically improves by awareness of the popular entities. Other interesting examples include: popular questions in search engine query logs, suspicious individuals appearing very often in specific areas of an airport, and viral videos in video streaming engines.

The naive approach for finding the largest entities is to first apply an ER method on the whole dataset to find all entities, and then output only the largest entities. However, for applications where finding the largest entities is important, we can expect the datasets to be large and change rapidly over

Technical Report, Stanford, CA

ACM ISBN 978-x-xxxx-xxxx-x/YY/MM.
https://doi.org/10.1145/nnnnnnn.nnnnnnn

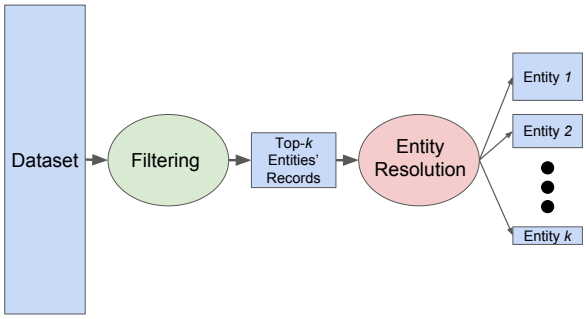


Figure 1: Overview of the workflow for top-k ER.

time. Hence, it is quite wasteful and inefficient to apply ER on the entire dataset. For instance, a traditional ER algorithm may require the computation of pairwise similarities for every two records in the dataset. (For example, a dataset of 100 thousand records would require the computation of almost 5 billion pairwise similarities.) Note also that computing each pairwise similarity may be an expensive operation for many applications, e.g., records containing images.

To deal with the prohibitive cost of applying ER on the whole dataset, blocking [7, 9, 13, 15, 21, 29, 30] can be applied, before ER takes place. A traditional blocking mechanism will partition a dataset into blocks so that records referring to the same entity fall in the same block. Then, an ER method is independently applied on each block to further group the records of the block into specific entities. For example, consider a set of product records, each containing a *type* field that can be used to partition the records. For instance, all "smartphone" devices will end up in one block, while all "cameras" will be in another. Then the ER algorithm will partition the cameras into the particular models, the smartphones into the individual products, and so on. Note that false negatives can occur; for example, a given product can have type "camera" in some of its records, and type smartphone in others. These records will not be resolved as the same product.

In addition to the false negatives issue, there are two other limitations of traditional blocking. First, for high-dimensional data, like images, video, or natural language, there may be no dimension or set of dimensions (like product *type*) that can be used to easily partition the records into buckets. Second, some or many blocks may contain many records, so performing ER on those blocks is still quite expensive. In our products example, we would expect a very large number of records to fall in the "book" or the "smartphone" blocks.

Locality-Sensitive Hashing (LSH) [24] can also be used to partition records. LSH does not require a field (or fields) that easily partition the records by value. Furthermore, LSH can "control" the number of false positives and negatives (e.g., by using more hash functions and/or more hash tables). Thus, it is possible to obtain smaller buckets where it is unlikely to find records from more than one entity (very low false positives). However, to achieve low false positives/negatives LSH may require a prohibitive number of hash functions to be applied to each record.

In this paper we use LSH to partition the records with very low false potitives/negatives. But we take advantage of our top-k goal (*not* general ER) to dramatically reduce the per-record hashing cost. In particular, the adaptive LSH approach we propose, requires a very low hashing cost for the vast majority of records that do *not* refer to a top-k entity and shows a speedup of up to 25x, compared to traditional LSH blocking, for top-k ER.

Even though LSH false positive/negative errors are small, we still need to run the full ER algorithm on the resulting blocks, since there may be application-dependent issues not captured by value hashing. (For example, LSH may be using a distance function like the bigram jaccard distance, which may not capture that records "Bob Schmidt" and "Robert Smith" are referring to the same person.) This ER cost is low, since our blocks are approximately one-entity blocks. And again, because of our top-k application, we can use specialized techniques (see Section 6.1.2) to compensate for any errors that occurred during partitioning. Overall, our approach can be seen as a lightweight preprocessing stage that receives the whole dataset as an input and tries to *filter out* all the records that do *not* belong to the k largest entities (Figure 1). The output of this *filtering* stage is then fed to an ER algorithm that produces one cluster of records for each of the top-k entities.

1.1 Contributions

(1) We give an overview of our novel adaptive LSH approach (Adaptive LSH), in Section 2.
(2) We present the LSH clustering functions, a key component of Adaptive LSH, in Section 3.
(3) We discuss the algorithm and details of Adaptive LSH, in Sections 4 and 5.
(4) We prove that the Adaptive LSH algorithm is optimal, under specific assumptions, in Section 4.2.
(5) We discuss our experimental results with datasets of web articles, images, and scientific publications, in Sections 6 and 7.

2 APPROACH OVERVIEW

2.1 Problem Definition

Let us denote the set of records in the dataset by

$$R = \{r_1, \ldots, r_{|R|}\}$$

Each record r_i refers to a single entity. In the ground truth clustering

$$\mathcal{C}^* = \{C_1^*, \ldots, C_{|\mathcal{C}^*|}^*\}$$

cluster C_j^* contains all the records referring to entity j.

Assume a descending order on cluster size in our notation, i.e., $|C_i^*| \geq |C_j^*|$ for $i < j$. The objective of the filtering stage, in Figure 1, is to, very efficiently, find the set of records $\mathcal{O}^*$ that belong to the k largest clusters in $\mathcal{C}^*$:

$$\mathcal{O}^* = \{r_j : r_j \in C_i^*, i \leq k\}$$

The filtering methods we study in this paper output a set of records $\mathcal{O}$ and their main objective is to maximize the:

$$precision = \frac{|\mathcal{O} \cap \mathcal{O}^*|}{|\mathcal{O}|}, \quad recall = \frac{|\mathcal{O} \cap \mathcal{O}^*|}{|\mathcal{O}^*|}$$

and

$$F1\ score = \frac{2 * precision * recall}{precision + recall}$$

2.2 Clustering Functions

To achieve a high precision and recall with a very low execution time, Adaptive LSH relies on a sequence of L clustering functions $(g_j : S \rightarrow \{C_i\})_{j=1}^{L}$. Each function g_j receives as input a set of records $S \subseteq R$ and clusters those records into a set of non-overlapping clusters $\{C_i\}$. The input set S can be the whole dataset R, or a single cluster produced by a previous function in the sequence.

The functions in the sequence are probabilistic and have the following four properties:

(1) *conservative evaluation*: the functions attempt to cluster the records of any ground truth cluster C_i^* under the same cluster in the output. That is, a cluster in the output of any function g_j may contain two or more ground truth clusters, but a ground truth cluster should very rarely split into two (or more) of the output clusters.

(2) *increasing accuracy*: the further a function is in the sequence, the higher the chances of outputting the ground truth clustering $\mathcal{C}^*$ when applied on R; or the ground truth clusters in a subset S, for any subset S.

(3) *increasing cost*: the further a function is in the sequence, the higher the cost of applying the function on any subset of records S.

(4) *incremental computation*: the computation of the functions in the sequence can be performed incrementally. That is, the computation required by a function g_i consists of the computation required by g_{i-1} plus some additional computation.

2.3 Sequential Function Application

Our approach starts by applying the most lightweight function in the sequence, g_1, on the whole dataset R, and continues by applying subsequent functions on the "most-promising" (for being a top-k entity) clusters.

Let us illustrate the concept of sequential function application via the example in Figure 2. The most "light-weight" function g_1 is applied on the whole dataset R and splits it into the first round clusters $C_1^{(1)}, C_2^{(1)}, C_3^{(1)}$; the superscript denotes the round. In the second round, we select cluster $C_1^{(1)}$ which is the largest, in terms of number of records, of the three clusters. Since cluster $C_1^{(1)}$ is an outcome of function g_1, the next sequence function g_2 is applied to it. Function g_2 splits $C_1^{(1)}$ into two clusters $C_1^{(2)}, C_2^{(2)}$. The other two clusters $C_2^{(1)}, C_3^{(1)}$ from the first round, are also added, unchanged, to the list of clusters after Round 2. In the third round, cluster $C_3^{(2)}$ is the largest one in the list and, since it is the outcome of a g_1 function, the next function to be applied to it is g_2. In the fourth round, $C_1^{(3)}$ is the largest cluster and function g_3 is applied to it, since it is an outcome of function g_2.

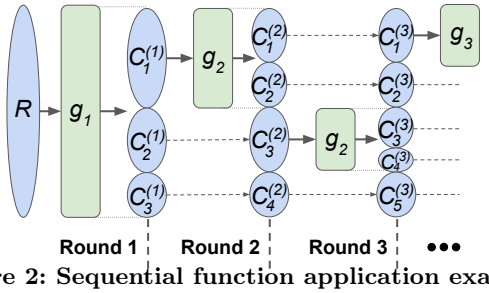


Figure 2: Sequential function application example.

In general, in each round, our approach processes the largest cluster that is *not* an outcome of the last function in the sequence. The intuition for this choice is that a large cluster has to be processed sooner or later, to find out if it contains a top-k entity or not. On the other hand, consider a small cluster C_1 that is an outcome of one of the first few functions in the sequence and a larger cluster C_2 that is an outcome of the last function in the sequence. If we would be looking for, say, the top-1 entity, any further processing of C_1 would be redundant: there is already one cluster (C_2) that will still be larger than C_1 after all functions are applied to both clusters. We prove that the largest-cluster selection rule is actually optimal, in Section 4.

The sequential function application stops when the k largest clusters, at the end of a round, are an outcome of the last function in the sequence: the union of records in the k clusters are returned as the output of the filtering stage. In this case, based on Properties 1 and 2, each of the k clusters is very likely to refer to exactly one of the ground truth clusters in $\mathcal{C}^*$. In addition, based on Property 1, all other ground truth clusters are very likely to be smaller than the k clusters and, thus, it is "safe" to conclude that the k clusters after the last round are the top-k clusters in $\mathcal{C}^*$. Of course, our approach may introduce errors and the output may not be identical to the ground truth output $\mathcal{O}^*$, as the objective is a fast filtering process that significantly reduces the size of the initial dataset. Nonetheless, even when those errors are non-negligible, we can trade precision for recall and control the output's quality with a small cost in performance, as we discuss in the experimental section.

When the sequential function application terminates, we expect that for the vast majority of records only the first few functions in the sequence will have been applied. Note also that because of Property 4, the sequential function application is performed incrementally. For instance, part of the computation required for applying g_2 on $C_1^{(1)}$, is already performed by g_1 and does not need to be repeated.

2.4 Locality-Sensitive Hashing

The third key concept in our approach is using LSH [24] as the main component of the clustering function sequence. We give an overview of LSH and discuss how to build clustering functions with Properties 1 to 4 in the next section.

3 CLUSTERING FUNCTIONS

In this section, we present the clustering functions used in our approach. Our goal is to provide an overview without

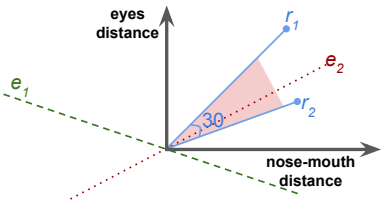


Figure 3: Random hyperplanes example.

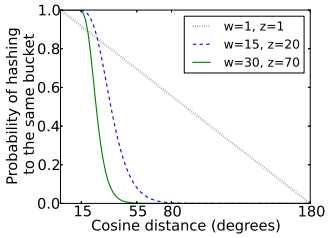


Figure 4: Probability of hashing to the same bucket

going into the technical details that involve LSH. All details can be found in Appendix A.

The clustering functions rely on distance metrics: the smaller the distance between two records, the more likely the two records are to refer to the same entity. Note that while the filtering stage uses a specific set of distance metrics, the subsequent ER stage (Figure 1) may use different metrics/rules to decide when two records refer to the same entity or even involve human curation. To illustrate the use of distance metrics, we use the following example:

`EXAMPLE 1` *Consider a set of records where each record consists of a person's photo, processed so that the eyes distance and the distance of nose tip to mouth are computed. The two distances form a vector. Consider the cosine distance, i.e., the angle between the vectors of two records. If two photos show the same person we can expect the ratio of eyes distance to nose-mouth distance to be roughly the same in the two photos and, hence, the angle between the vectors to be small.*

In addition, the clustering functions assume that a *matching rule* is used to decide if two records refer to the same entity. To keep the discussion in the next sections concise, we focus on matching rules that involve a single distance threshold d_{thr}. The single-threshold rules apply to two cases: A) the distance on a single field (e.g., cosine distance for face images) or B) the average distance from multiple fields (e.g., cosine distance on photo and hamming distance on fingerprints) must be within the threshold d_{thr}. We discuss how to extend the mechanisms in our approach for AND, OR, and weighted average rules, in Appendix B.

Two records can also be considered a *match*, via transitivity. That is, if two records a and b are within the distance threshold, and b is also within the threshold with a record c, records a and c are also considered a match.

To find the matches without having to compute the $\binom{|R|}{2}$ distances, the clustering functions use LSH. LSH is based on hash functions that are applied individually on each record. The smaller the distance between two records, the more likely a hash function is to give the same value when applied to each of the two records. One example of such hash functions is the random hyperplanes for the cosine distance:

`EXAMPLE 2` *Consider again the dataset of photos, in Example 1. Consider two random hyperplanes (lines) through the origin, in the two dimensional space representing the photos. Figure 3 depicts two such lines, e_1 and e_2. In addition, consider the vectors, r_1 and r_2, for two photos in the dataset. The cosine distance between r_1 and r_2 is 30 degrees. Note that the difference between e_1 and e_2, is that r_1 and r_2 are on the same side for line e_1, but on different sides for line e_2. A hash function in this case is a random line and the hash value is 1 or -1, depending on which side of the line the input record lies. In general, the smaller the angle between two records, the higher the likelihood of selecting a random line where the two records lie on the same side of the selected line: note that the likelihood for records r_1 and r_2 is $1 - \frac{30}{180}$, while, in general, the likelihood is $1 - \frac{\theta}{180}$, if θ is the angle between the two records.*

LSH applies a large number of such hash functions on each record. The outcome of those functions is used to build hash tables: the index of each bucket, in each table, is formed by concatenating the outcome from a number of hash functions. The following example illustrates the tables built by LSH:

`EXAMPLE 3` *Consider again the hash functions and dataset, from Example 2. Assume LSH uses two hash tables: for each table, three hash functions (random lines through the origin) are selected. Since the outcome of each function is binary, there are $2^3 = 8$ buckets in each table. Now consider the event of two records hashing to the same bucket in at least one of the two tables. If the angle between the two records is θ, the probability of this event is: $1 - \left(1 - (1 - \frac{\theta}{180})^3\right)^2$.*

When averaging the distance for multiple fields (case B), in order to select each hash function for a table, one of the fields is first selected, uniformly at random. Then, a hash function from the selected field's hash function family is selected, again, uniformly at random (e.g., random hyperplane).

The number of hash tables z, and the number of hash functions per table w, are selected so that: (a) if two records are within the distance threshold d_{thr}, the probability of the two records hashing to the same bucket in at least one table, must be very close to 1.0 and (b) if the distance between two records is greater than d_{thr}, the probability of the two records hashing to the same bucket in at least one table, must be as close to 0.0 as possible (details in Section 5.1).

Figure 4 illustrates the probability of two records hashing to the same bucket, in at least one table, for the setting of Examples 1 to 3. The x-axis shows the cosine distance and the y-axis the probability for three w, z value pairs.

Consider a threshold d_{thr} of 15 degrees. As Figure 4 shows, the more hash functions used, the more sharply the probability of hashing to the same bucket drops, after the threshold. On the other hand, applying more functions on each record, incurs a higher cost.

Each clustering function in the sequence relies on an LSH scheme with z tables and w hash functions per table, or (w, z)-*scheme* for short: the further a function is in the sequence,

the larger the values of w and z are. We call these clustering functions *transitive hashing* functions:

`DEFINITION 1 (Transitive Hashing)` *A transitive hashing function H, based on a (w, z)-scheme, receives as input a set of records S, and splits S into a set of clusters $\{C_i\}$ as follows: consider the graph $G = (S, E)$, where $(r_1, r_2) \in E$ iff records r_1 and r_2 hash to same bucket of at least one of the z hash tables. Function H outputs one cluster C_i for each of the connected components of G.*

In Appendix D, we present an efficient implementation for transitive hashing functions.

Note how transitive hashing functions satisfy the four properties stated in Section 2.2:

(1) *conservative evaluation*: even when w and z are small, pairs of records within the threshold are very likely to be placed in the same bucket, in at least one of the tables; based on point (a) above.
(2) *increasing accuracy*: the further a function is in the sequence, the larger the values of w and z are, and the less the false matches are.
(3) *increasing cost*: the further a function in the sequence, the larger the values of w and z, and the higher the cost of applying that function on any subset of records S.
(4) *incremental computation*: function computation is performed incrementally, as the hash values from previous sequence functions are re-used by functions that follow.

4 ADAPTIVE LSH

4.1 Algorithm

INPUT
parameter k, records R, distance metric d, threshold d_{thr}, sequence of transitive hashing functions $H_1, \ldots, H_L$
OUTPUT
k largest connected components in graph $G = (R, E)$, where $(r_1, r_2) \in E$ iff $d(r_1, r_2) \leq d_{thr}$.

The sequence of clustering functions used by Adaptive LSH is a sequence of transitive hashing functions $H_1, \ldots, H_L$, where function H_i is based on a (w_i, z_i)-scheme, with $w_i \leq w_{i+1}, z_i \leq z_{i+1}$, $i \in [1, L)$. Sequence $H_1, \ldots, H_L$ is given as input (two integers w_i, z_i, for each function H_i) and in Section 5 we discuss how to decide all the function parameters.

Besides the sequence of transitive hashing functions, Adaptive LSH also uses an additional function that computes the matches in a cluster of records given as input, using the exact record pair distances:

`DEFINITION 2 (Pairwise Computation)` *The pairwise computation function P receives as input a set of records S and splits S into a set of clusters $\{C_i\}$ as follows: consider the graph $G = (S, E)$, where $(r_1, r_2) \in E$ iff $d(r_1, r_2) \leq d_{thr}$. Function P computes the distances between pairs of records and outputs one cluster C_i for each of the connected components of graph G.*

When a cluster C is the outcome of a function H_i and the application of the next function in the sequence, H_{i+1}, has a cost greater than the cost of applying function P on C, Adaptive LSH applies P instead of H_{i+1} on cluster C. This is usually the case when cluster C is small and computing the distances for, potentially, all pairs in C, is preferable to computing a large number of hashes for each record in C. Thus, the termination rule for Adaptive LSH (as discussed in Section 2.3) is extended as follows: terminate once the k largest clusters, in the list of clusters at the end of a round, are an outcome of an H_L or P function.

Algorithm 1 *Adaptive LSH*

Input: R - Set of all records
Input: k - top-k parameter
Input: d - distance metric
Input: d_{thr} - distance threshold
Input: $H_1, \ldots, H_L$ - sequence of functions
Input: $cost_P, cost_1, \ldots, cost_L$ - cost model parameters
Output: top-k entities

1: $\{C_i^{(1)}\} := H_1(R)$
2: **for** each Round j **do**
3: $C :=$ largest cluster in $\{C_i^{(j)}\}$; $\{C_i^{(j)}\} := \{C_i^{(j)}\} \setminus C$
4: $t :=$ sequence number of function H_t that produced C
5: **if** $(cost_{t+1} - cost_t) * |C| \geq cost_P * \binom{|C|}{2}$ **then**
6: $\{C_i\} := P(C)$
7: **else**
8: $\{C_i\} := H_{t+1}(C)$
9: **end if**
10: $\{C_i^{(j+1)}\} := \{C_i\} \cup \{C_i^{(j)}\}$
11: **if** largest k clusters in $\{C_i^{(j+1)}\}$ are all an outcome of function H_L or P **then**
12: **return** largest k clusters in $\{C_i^{(j+1)}\}$
13: **end if**
14: **end for**

To decide when to apply the pairwise computation function P, the algorithm relies on a simple cost model:

`DEFINITION 3 (Cost Model)` *The cost of applying function P, on a set of records S, is $cost_P * \binom{|S|}{2}$. The cost of applying function H_i in the sequence, on a set S, is $cost_i * |S|$. Moreover, the cost of applying function H_i on a record r, when function H_j, $j < i$, is already applied on r, is $cost_i - cost_j$. After the completion of the algorithm, the overall cost is $\sum_{i=0}^{L} n_i * cost_i + n_P * cost_P$, when function H_i is the last sequence function applied on n_i records and n_P is the overall number of similarities computed by function P.*

In Appendix E.2, we run experiments to evaluate how sensitive adaptive LSH is to the cost model: we manually add noise to the model's cost estimations and measure how the execution time changes. Algorithm 1 gives the detailed description of the process in Section 2.3.

4.2 Largest-First Optimality

`THEOREM 1` *Consider the family of algorithms that:*
(1) *do* not *"jump ahead" to function P, i.e., if a cluster C is an outcome of a function H_i, the algorithm can only apply function P on C, when $(cost_{i+1} - cost_i) * |C| \geq cost_P * \binom{|C|}{2}$ (Line 5 on Algorithm 1).*
(2) *do* not *"terminate early", i.e., terminate only when the k largest clusters are an outcome of either an H_L or P function.*

Algorithm 1 gives the minimum overall cost compared to any other algorithm of this family.

PROOF: The proof can be found in Appendix C. □

The rationale for the two conditions of Theorem 1 is simple. Condition 2 states that we consider algorithms that try to minimize the errors by only returning clusters "thoroughly checked" by an H_L or P function. For Condition 1, accurately predicting if "jumping ahead" to function P will eventually give a lower cost for a cluster C, is quite challenging, may not necessarily show significant gains (even if predicting right), and requires a significant overhead of keeping estimates for the structure (e.g., subclusters) of C, as we discuss in Appendix C.1.

Algorithm 1 can also be applied in an incremental mode, where it directly outputs each cluster of records generated by an H_L or P function; instead of waiting for the condition in Line 11 to be satisfied. The incremental mode is useful when a user wants to observe the results during the execution of the filtering stage or when an active learning approach [14, 22] is applied for ER. For instance, human curators could start working on the top-1 entity, before the filtering stage is completed. This way, human curation and machine processing can overlap and the overall time to resolve an entity can be minimized. Moreover, the larger (and arguably more important or difficult to resolve) an entity is, the fastest it will be resolved/curated. As we prove in Theorem 4 in Appendix C, the incremental mode of Algorithm 1 also provides optimality guarantees; similar to the ones of Theorem 1.

5 FUNCTION SEQUENCE DESIGN

5.1 Selecting the (w,z)-scheme

Given a budget b_i, the objective is to select the parameters w_i and z_i of a (w_i, z_i)-scheme, for function H_i in the sequence. (We discuss how to decide b_i for each function H_i in the next section.) To simplify the discussion, we assume that the cost of applying function H_i is proportional to the overall number of hash functions, and that w_i and z_i are factors of b_i, i.e., $w_i * z_i = b_i$. An extension for the cases where these two assumptions do not hold is straightforward as we discuss in the end of the section. To decide parameters w_i and z_i, for function H_i, we solve the following optimization program:

$$\min_{w,z} \quad \int_0^1 \Big[1 - \big[1 - p^w(x)\big]^z\Big] dx \tag{1}$$

$$s.t. \quad w * z = b_i \tag{2}$$

$$1 - \big[1 - p^w(x)\big]^z \geq 1 - \epsilon, \quad x \leq d_{thr} \tag{3}$$

Function $p(x)$ is the probability of selecting a hash function that gives the same hash value for two records at a distance x, where $0 \leq x \leq 1$, and depends on the distance metric. Parameter ϵ is the initial LSH guarantee for false negatives, i.e., the probability that pairs of records within distance d_{thr} do not end up in the same bucket, in any of the tables. Both $p(x)$ and ϵ are given as input. As illustrated in Example 3 (and analyzed in Appendix A) the probability of hashing to the same bucket in at least one table, in a (w, z)-scheme, is given by: $1 - \big[1 - p^w(x)\big]^z$. Hence, constraint 3 states that the probability of a false negative should be less than ϵ, thereby satisfying the *conservative evaluation* property.

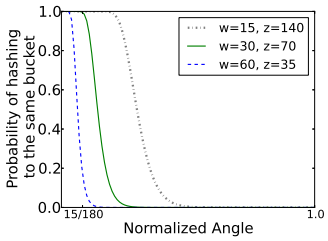


Figure 5: Example (w, z) values for Program 1 to 3.

The objective in Equation 1 states that the probability of a false positive should be minimized, under the budget constraint 2 and the false negative constraint 3.

EXAMPLE 4 *Consider the cosine distance as a distance metric, function $p(x) = 1 - x$ (where x is the normalized angle, i.e., for an angle θ, $x = \frac{\theta}{180}$), a distance threshold of $d_{thr} = \frac{15}{180}$, a parameter $\epsilon = 0.001$, and a budget of 2100 hash functions. Let us examine three pairs of (w, z) values: $(15, 140)$, $(30, 70)$, and $(60, 35)$. The plot in Figure 5 is equivalent to the one in Figure 4 (angle distance between two records on the x-axis, probability of the two records hashing to the same bucket, given their distance, on the y-axis). Pair $(15, 140)$ minimizes the objective function value in Equation 1 (area under the curve), but violates the distance threshold constraint in Equation 3. Both pairs $(30, 70)$ and $(60, 35)$ satisfy the two constraints, with pair $(30, 70)$ giving a lower objective function value.*

To find the optimal (w, z) values for Program 1 to 3, we can perform a binary search over w values such that $\frac{budget}{w}$ is an integer. Note that the greater the value of w, the lower the value of the objective function (see Figure 5). Moreover, if the distance threshold constraint is not satisfied for a value of w, it will also not be satisfied for any greater values.

In practice, we may also want to examine (w, z) values, where $\frac{budget}{w}$ is not an integer. In this case, we would have to adjust the probability expression in Equations 1 and 3: expression $\big[1 - p^w(x)\big]^z$ becomes $\big[1 - p^w(x)\big]^z * \big[1 - p^{w'}(x)\big]$, where $z = \lfloor \frac{budget}{w} \rfloor$ and $w' = budget - w * z$. In addition, we would have to exhaustively search over all possible values for w, z that satisfy the budget constraint. That is, for $w \in [1, budget]$, we would examine if the distance threshold constraint is also satisfied, and keep the (w, z) value pair minimizing the objective function.

Furthermore, we may also want to take into account a cost model, in the Program 1 to 3. For instance, consider two value pairs (w_1, z_1) and (w_2, z_2), such that $w_1 * z_1 = w_2 * z_2 = budget$. There are cases where the actual cost of applying a function based on a (w_1, z_1)-scheme is different compared to the cost for a function based on a (w_2, z_2)-scheme. (For example, when matrix multiplication is involved, the scheme (w_1, z_1) may be more cost effective if $w_1 > w_2$.) In those cases, Equation 2 needs to include a cost function that reflects the actual cost based on a specific (w, z) value pair.

5.2 Budget and Sequence Length

We use two simple strategies to select the budget b_i for each transitive hashing function H_i, in the sequence:

- **Exponential:** The budget for function H_{i+1} is twice the budget for function H_i, i.e., $b_{i+1} = 2 * b_i$.
- **Linear:** The budget for function H_i is a multiple of a constant, i.e., $b_i = i * const$.

In Appendix E, we discuss experiments with different parameter values for the two strategies and we draw conclusions regarding which strategy and values work better in each case.

When the i-th function in the sequence satisfies:

$$1 - \left[1 - p^{w_i}(x)\right]^{z_i} \leq \epsilon', \quad x \geq d_{thr} + \delta \tag{4}$$

the i-th function becomes the last one in the sequence. Equation 4 states that record pairs with distance greater than $d_{thr} + \delta$, end up in the same bucket, with probability less than ϵ'. Parameters ϵ' and δ express the LSH false positive guarantee and are given as input. Note, however, that when a strict false positive guarantee is used, the full sequence of functions usually does not apply to any of the records, since the computation even for large clusters often ends up by applying the pairwise function P.

6 EXPERIMENTAL SETTING

6.1 Methods

The methods we explore extend across two orthogonal dimensions, as we discuss next.

6.1.1 adaLSH vs Alternatives. We compare adaptive LSH with LSH-based blocking approaches, a traditional blocking algorithm (Canopies), and a traditional transitive closure algorithm (Pairs).

adaLSH: The adaptive LSH approach we propose in this paper. The default mode is the Exponential (Section 5.2) with $b_1 = 20$ hash functions.

LSH-X: Different blocking variations that rely on LSH, adjusted for the problem studied in this paper. LSH starts by applying the same number X of hash functions on every single record in the dataset. Given the number of hash functions X and a distance threshold, LSH selects the number of hash tables z and the number of hash functions per table w, by solving the same optimization problems with adaptive LSH (see Section 5.1 and Appendix B). (By solving such a problem we find the "optimal" w, z values that satisfy $w*z \leq X$.) After the first stage of applying X hash functions on all records, LSH uses the pairwise computation function P (Definition 2) to verify if pairs of records in the same bucket are indeed within the distance threshold. To make the comparison fair, we use three additional optimizations for LSH methods: (1) LSH terminates early when there are k clusters that have been "verified" using function P that are larger than any other cluster not yet verified, (2) when applying function P we skip checking pairs of records that are already "transitively closed" by other pairs and, hence, belong to the same cluster, and (3) we use the same efficient implementation and data structures with adaptive LSH (see Appendix D). In Appendix E.1, we also study a variation of LSH that only applies the first stage and does not apply function P at all. This variation, assumes that all pairs of records within each hash table bucket are within the distance threshold, and applies transitive closure on those pairs to find the k largest clusters. In the plots, we just use LSH if only one LSH variation is used in the experiment. If more than one LSH variations are used, we use LSHX (e.g., LSH640 applies 640 hash functions on each record) if function P is applied after the first stage and LSHXnP otherwise.

Pairs: Essentially, Pairs is the application of the pairwise computation function P on the whole dataset. Again, we use the above optimizations (2) and (3), i.e., we skip pairs already "transitively closed" and use the efficient implementation described in Appendix D.

Canopies: Canopy-based blocking [29], uses two thresholds T_1 and T_2, with $T_1 < T_2$. The first canopy is generated by randomly selecting a record r_1, copying r_1 to the canopy, and comparing r_1 with all the other records: records with a similarity to r_1 greater than T_1, are also copied to the first canopy. Moreover, record r_1 and records with a similarity to r_1 greater than T_2, are removed from the dataset. The same process is repeated, with the reduced dataset, until there are no records left. After the canopies are generated, the actual clustering algorithm (transitive closure, in our case) takes place: only the distance between pairs in the same canopy is computed. In large datasets, Canopies can give large times savings compared to Pairs, by significantly reducing the overall number of pairwise comparisons computed.

6.1.2 Improving Accuracy.

Return more clusters than the needed k: One way to include more records from the top-k entities in the filtering output, is to return more than the k largest clusters found during filtering, i.e., return the $\widehat{k}$ largest clusters, for a $\widehat{k} > k$. However, note that by returning more than k clusters the filtering output increases. In Section 7.2, we study the trade-offs between accuracy and performance as we increase $\widehat{k}$.

Recovery process: After applying an ER algorithm on the filtering output (Figure 1), we can apply an additional recovery process to retrieve additional records for top-k entities that were *not* included in the filtering output. In particular, after applying an ER algorithm on the filtering output, we have k clusters of records. We can then apply cleansing and aggregation on each cluster to create an summary for the information on the entity represented by each cluster. For instance, for a customer we could collect all the first and last names, email accounts, and telephone numbers she uses. The recovery process compares all the records from the initial dataset that were not included in the filtering output, with each of the k clusters, after applying ER (and possibly cleansing/aggregation) on the filtering output. The goal is to find records that refer to the same entities with the entities in the k clusters, that were mistakenly left out from the filtering output. Note that if all the records for a top-k entity are left out from the filtering output, there is no way for this

recovery process to retrieve the records for that entity and include the entity in the extended top-k result.

6.2 Metrics

6.2.1 Accuracy. We use two types of metrics:

Treating filtering output as a single set of records: in this case we compare the set of records in the filtering output with the set of records that refer to the top-k entities as determined by the ground truth. In the experiments presented here, we use the precision, recall, and F1 score, as defined in Section 2.1. (We will be referring to these three metrics as Precision/Recall/F1 Gold, throughout the section.)

Treating filtering output as a set of clusters: To weigh the accuracy of higher ranked clusters higher, we can consider the filtered records, not a set, but a set of clusters. That is, we consider a filtering output clustering $\mathcal{C} = \{C_1, \ldots, C_{|\mathcal{C}|}\}$, such that all records in each cluster C_i of $\mathcal{C}$ refer to the same entity and each cluster in $\mathcal{C}$ refers to a different entity. We compare $\mathcal{C}$ to the ground truth clustering $\mathcal{C}^*$ (Section 2.1) and we compute the *mean Average Precision (mAP)* and *mean Average Recall (mAR)*. For example, assume we are looking for the top-2 entities and consider a clustering $\mathcal{C} = \big\{\{a, b, c, f\}, \{e\}\big\}$ and a ground truth clustering $\mathcal{C}^* = \big\{\{a, b, c\}, \{e, g\}\big\}$. The precision on the top-1 cluster is $\frac{3}{4}$ and the precision on the top-2 clusters is $\frac{|a,b,c,e|}{|a,b,c,f,e|} = \frac{4}{5}$. Hence, the mAP in this case is $\frac{0.75+0.8}{2} = 0.775$; in similar fashion, the mAR is $\frac{1.0+0.8}{2} = 0.9$.

Note that we do *not* consider the accuracy of the final result after applying an actual ER algorithm on the filtering output. If the ER algorithm is "perfect" the output will be exactly the same with clustering $\mathcal{C}$. Of course an actual ER algorithm would, most likely, introduce more errors, however, we can expect that the better the ER algorithm is, the closer the final result would be to clustering $\mathcal{C}$. Hence, the accuracy metrics we obtain for the filtered set should closely approximate the accuracy of the final result. (To get the actual accuracy of the final result would require knowing precisely the ER algorithm used, so the results would be specific to a single ER algorithm. We believe that an approximate accuracy value is more useful in our context.)

We also compute the Precision Gold, Recall Gold, F1 Gold, mAP, and mAR, after the recovery process of Section 6.1.2 is applied. (We call those metrics *Precision/Recall/F1/mAP/mAR with Recovery*.) For the same reasons as before, we consider a "perfect" recovery process that outputs a set of clusters $\mathcal{C} = \{C_1, \ldots, C_{|\mathcal{C}|}\}$ when applied on the output $\mathcal{O}$ of a filtering approach: for each entity referenced by a record in $\mathcal{O}$, we collect all the records for that entity on the whole dataset, in a single cluster in $\mathcal{C}$. For mAP/mAR, we compare $\mathcal{C}$ to the ground truth clustering $\mathcal{C}^*$, while for Precision/Recall/F1, we compare the union of all records in $\mathcal{C}$ to the union of all records in $\mathcal{C}^*$.

6.2.2 Performance. We use the following four metrics:

Execution Time: the time it takes for a filtering method to compute the output.

Dataset Reduction: we compute the reduction percentage from the filtering stage, e.g., if the filleting output consists of 100 records while the whole dataset is 1000 records, the reduction percentage is 10%.

Speedup w/o Recovery: we compare the time it takes to apply ER on the whole dataset ($WholeTime$) to the time it takes to apply ER on the reduced dataset ($ReducedTime$), after the filtering stage, taking into account the time spent on filtering ($FilteringTime$). Hence, the speedup is the ratio $\frac{WholeTime}{FilteringTime+ReducedTime}$. Since we are not considering particular ER algorithms, we assume a "benchmark ER algorithm" is applied to compute $WholeTime$ and $ReducedTime$. This benchmark ER algorithm applies the matching rule on all pairs in the whole or reduced dataset. On one hand, our speedup numbers are conservative, because we expect the run time of a real ER algorithm to be higher, as the benchmark ER algorithm does not take into account the actual clustering time. On the other hand, a real ER algorithm many not apply a rule on all pairs, so it would perform better than our benchmark algorithm. But without an extensive evaluation of multiple real ER algorithms in different domains, which is beyond the paper's scope, we believe the use of a benchmark ER algorithm yields valuable insights.

Speedup with Recovery: The speedup in this case is the ratio $\frac{WholeTime}{FilteringTime+ReducedTime+RecoveryTime}$, where $RecoveryTime$ is the run time for the recovery process. To compute the $RecoveryTime$, we consider a "benchmark recovery algorithm", that applies the matching rule between each record in the filtering output with each record that was *not* included in the filtering output. For instance, if the filtering output consisted of a single record, we would compare that record with every other record in the dataset. (Again, we believe that a simple benchmark recovery algorithm is sufficient for our purpose and yields valuable insights.)

6.3 Datasets

We used 3 datasets in our experiments. (The ground truth entities are available in each dataset's material.)

***Cora* [1]**: a dataset of around 2000 scientific publications, extensively used in the entity resolution literature. Each record consists of the title, authors, venue, and other publication information (e.g., volume, pages, year). Together with the original dataset, we used 2x, 4x, and 8x versions. For example, the 2x version contains twice as many records as the original dataset. To extend the original dataset, we uniformly at random select an entity a and uniformly at random pick a record r_a referring to the selected entity a, for each record added to the dataset. For each record, three sets of shingles are created: one for the title, one for the authors, and one for the rest of the fields. The matching rule is an AND rule (see Appendix B.1) with two distance thresholds: two records match when (i) the average jaccard similarity for the title and author sets are at least 0.7 AND (ii) the jaccard similarity for the rest of the information is at least 0.2.

***SpotSigs* [3]**: a dataset of around 2200 web articles: each article is based on an original article and, thus, all articles having the same origin are considered the same entity (e.g.,

news articles discussing the same story with slight adjustments for different web sites). The main body of each article is transformed to a set of spot signatures (see the original paper [36]). The matching rule uses a d_{thr} of 0.4 for the spot-signatures jaccard similarity. (We also tried thresholds of 0.3 and 0.5 in some experiments.) We also used a 2x, a 4x, and an 8x version of the dataset in the experiments; using the same sampling process with Cora.

***PopularImages* [4]**: three datasets of 10000 images each. The images that are transformations (random cropping, scaling, re-centering) of the same original image, are considered the same entity. The main difference between the three datasets is the distribution for the number of records per entity. They all follow a zipfian distribution, however, the exponent is different in each dataset (e.g., the top-1 entity consists of around 500, 1000, and 1700, in each dataset, respectively). To compute the similarity between images, we extract for each image an RGB histogram: for each histogram bucket, we count the number of pixels with an RGB value that is within the bucket RGB limits. The RGB histogram forms a vector and the matching rules we tried use the vector cosine distance and angle thresholds of $2, 3$, and 5 degrees.

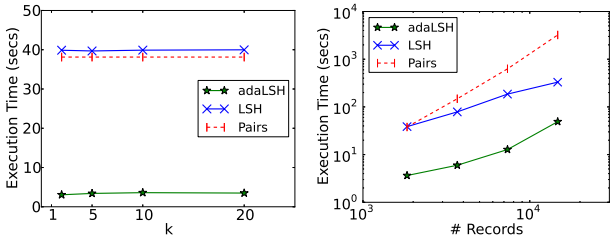
***DAS* [2]**: a dataset of 72000 scientific publication records from DBLP, the ACM digital library, and Google Scholar, also used extensively in the entity resolution literature. Each record contains four fields: title, authors, venue, and year. We discuss our experiments with DAS in Section 7.3.

7 EXPERIMENTAL RESULTS

7.1 adaLSH vs Alternatives

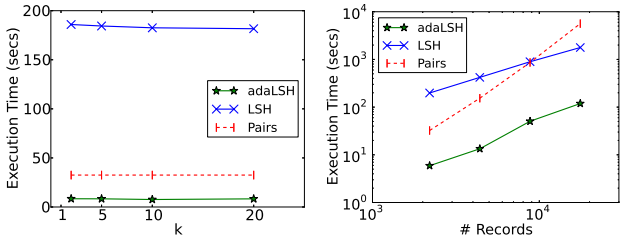
We compare adaLSH, LSH1280, and Pairs, for different values of k (number of top entities) and for different dataset sizes. (For LSH-X methods we tried X values that are a power of two and since a typical number of hash functions for LSH is 1000, we use LSH1280 in the experiments of this section. In Appendix E and Section 7.4, we compare adaLSH to other LSH blocking variations and as we find out the optimal value of X for LSH-X varies from 80 to 2560, in the settings we tried.) The second baseline, Canopies, is used in Section 7.3, where we use a much larger dataset and the performance gains compared to Pairs are more evident.

7.1.1 Performance. We start by examining the execution time of adaLSH, LSH1280, and Pairs, on Cora, for different k values. Our objective here is to assess the execution time, as we increase the number of entities that must be retrieved. We run experiments for $k = 2, 5, 10$, and 20. In the plot of Figure 6(a), the x-axis shows the k value, and the y-axis the execution time. adaLSH gives a 10x speedup compared to LSH1280, for any k value: while LSH needs to apply 1280 hash functions on all records, adaLSH starts by applying only 20 hash functions on all records and then adaptively decides which records to process further. Pairs needs almost the same time with LSH1280 and, hence, the speedup of adaLSH is also approximately 10x compared to Pairs. Furthermore, the execution time for adaLSH just slightly increases as



(a) different k values (b) different dataset sizes

Figure 6: Execution time on Cora.



(a) different k values (b) different dataset sizes

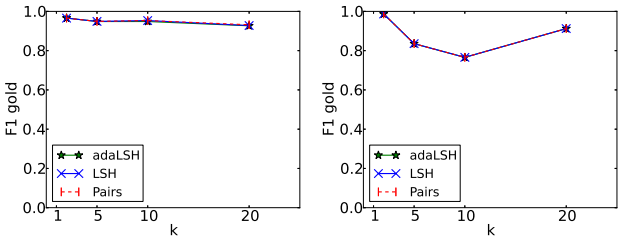
Figure 7: Execution time on SpotSigs.

k increases. This means that the amount of computation adaLSH performs to find the top-2 entities comprises a large percentage of the overall computation for the top-20 entities.

Next, we study how the execution time increases for each approach as we increase the dataset size. The log-log plot in Figure 6(b) depicts the results on experiments for Cora, Cora2x, Cora4x, and Cora8x (dataset size on x-axis). We use $k = 10$ here; same results hold for other k values. We observe that there is always a very large speedup (9x to 20x) for adaLSH compared to LSH1280. Note also that the speedup from Cora4x to Cora8x decreases. Nevertheless, we have observed that, in general, the adaLSH speedup compared to LSH remains large (and can even increase) as we increase the dataset size. The only case where we found the speedup to be limited is when the records of the top-1 entity comprise a very large percentage of the dataset: in this case, the run time of applying function P on the top-1 entity dominates the execution time of both approaches (more in Section 7.4).

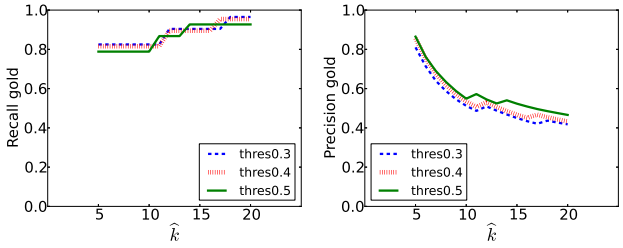
Let us now switch to the SpotSigs dataset, which is a higher dimensional dataset compared to Cora. We will compare the results on Cora from Figure 6(a) to the results for the same experiment on SpotSigs, in Figure 7(a). The main difference is that the cost of applying a hash function on SpotSigs is much higher compared to Cora, so the execution time for both adaLSH and LSH increases. Still, adaLSH is not affected as much as LSH: the execution time for LSH increases to around 180 seconds while for adaLSH it goes to around 7 seconds, thus, we get an impressive speedup of 25x by applying adaLSH.

The log-log plot in Figure 7(b) is analogous to the plot of Figure 6(b), for SpotSigs1x, 2x, 4x, and 8x, when $k = 10$. The speedup of adaLSH compared to Pairs increases from 5x on SpotSigs to 50x on SpotSigs8x, while the speedup compared



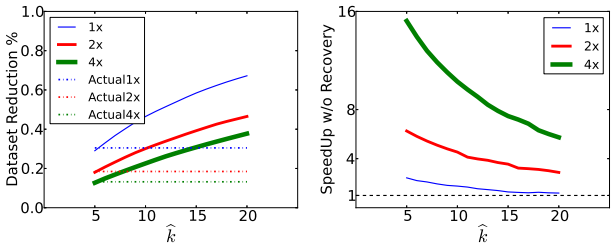
(a) Cora (b) SpotSigs

Figure 8: F1 Gold for different k values.



(a) Recall (b) Precision

Figure 9: Precision/Recall on SpotSigs, for $k = 5$.



(a) Dataset Reduction (b) Speedup w/o Recovery

Figure 10: Reduction % and Speedup on SpotSigs.

to LSH ranges from 15x to 25x. LSH is slower than Pairs on small datasets and shows a better performance than Pairs, only when the dataset is larger than 9000 records.

7.1.2 Accuracy. The last part in this section focuses on accuracy: we compare the outcome of the different filtering approaches to the set of records for the top-k entities and we compute the F1 Gold. The plots in Figures 8(a) and 8(b) give the F1 Gold (y-axis) for the same experiments of Figures 6(a) and 7(a), on Cora and SpotSigs, respectively.

All three approaches give an almost identical F1 score, as they produce very similar clusters. Thus, the probabilistic nature of adaLSH and LSH1280 does not introduce errors. (However, there are other LSH methods that do introduce errors, as we discuss in Appendix E.1.) In Cora, the filtering output is very close to the ground truth, i.e., we get a very high F1 score on all k values. Nevertheless, the F1 score in case of SpotSigs (Figure 8(b)) is low (around 0.8) for $k = 5$ and 10: as the filtering stage relies on simple record matching rules to boost performance, we can expect that the accuracy will not always be high, on all datasets.

7.2 Improving Accuracy

As discussed in Section 6.1.2, we can handle situations where the filtering outcome may not be sufficiently accurate, by increasing the number of clusters $\widehat{k}$ that a filtering method must return. Remember that the main goal of the filtering stage is to reduce the size of the initial dataset. Therefore, by increasing $\widehat{k}$, we can get a recall that is very close to 1.0, while still significantly reducing the size of the original dataset, as we discuss in this section.

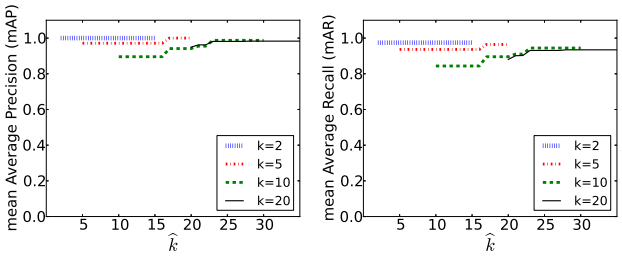
7.2.1 Precision and Recall Gold. To illustrate the trade-off between precision and recall, we focus on a k value of 5 for SpotSigs, where the F1 score is just above 0.8, as we saw in Figure 8(b). In the experiment of Figure 9(a), the x-axis shows $\widehat{k}$, i.e., the number of clusters we ask a method to return. Then, we compute the precision and recall of this set against the set of records in the ground truth top-5 entities. Figure 9(a) shows the Recall Gold on the y-axis. Since adaLSH and LSH give practically the same output with Pairs, we plot just one curve for all methods. Moreover, we include the results for three different d_{thr} thresholds, 0.3, 0.5, and the default 0.4 (one curve per threshold), in Figure 9(a).

The recall for all thresholds is almost the same and, more importantly, follows the same trend: recall keeps going up as $\widehat{k}$ increases, to reach very close to 1.0 for 20 clusters.

By increasing the output's size, the precision inevitably drops. Figure 9(b) shows the Precision Gold for the same setting with Figure 9(a). As we increase $\widehat{k}$ from 5 to 20, the precision drops from 80% to almost 40%. A lower precision means that a lower percentage of the original dataset will be filtered out, which in turn means that the Speedup w/o (with) Recovery will be lower. We quantify the trade-off between accuracy and reduction in Sections 7.2.2 to 7.2.4.

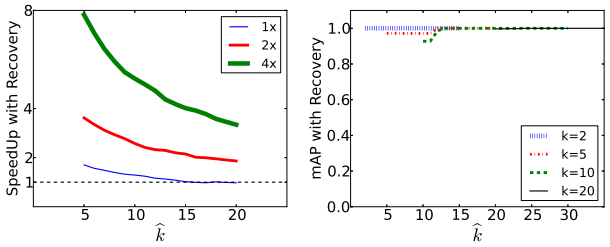
It is important to note here that we would not necessarily increase the recall by relaxing threshold d_{thr}, instead of including more clusters in the output. Consider, for example, trying to find the top-1 entity in a dataset. Let us assume that for a similarity threshold of 0.9, the largest cluster a method finds, contains only 80% of all the records in the ground truth top-1 entity. If we relax the threshold to 0.8, the method may merge the second largest cluster with a smaller one, which would now form the largest cluster. However, the new largest cluster may be actually referring to the ground truth top-2 entity and contain all the records for that entity, but none of the top-1 entity records. Hence, the recall would drop from 80% to 0% by relaxing the threshold.

7.2.2 Reduction and Speedup. Figure 10(a) depicts the Dataset Reduction percentage (y-axis), for different $\widehat{k}$ values, on different dataset sizes (SpotSigs1x-4x), for $k = 5$. In addition to the three curves, we plot one horizontal dashed line for each dataset size, indicating the actual percentage of records for the ground truth top-k entities (Actual1x-4x). As $\widehat{k}$ increases, a filtering method ends up returning a larger portion of the dataset. However, for larger datasets this



(a) mean Average Precision (b) mean Average Recall

Figure 11: mAP and mAR on SpotSigs.



(a) Speedup with Recovery (b) mAP with Recovery

Figure 12: Applying recovery on SpotSigs.

portion is still rather small even for a large number of clusters returned; e.g., less than 40% on SpotSigs4x, for $\widehat{k} = 20$.

To see how those percentages translate to speedups, we plot the Speedup w/o Recovery (y-axis) in Figure 10(b), where we use adaLSH for the filtering stage. We see that the speedup increases as the dataset size increases, and even for a reduction percentage of 40% (SpotSigs4x at $\widehat{k} = 20$), we get a significant speedup of 6x.

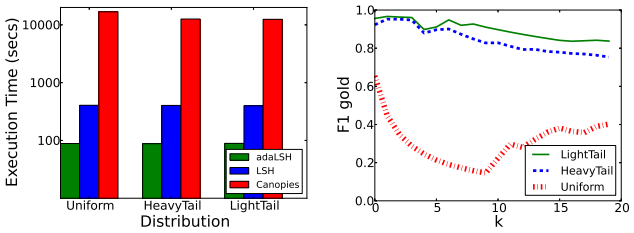
7.2.3 mean Average Precision and Recall. Next, we study how accuracy, in terms of mAP and mAR, increases, as $\widehat{k}$ increases. The goal is to understand how easily we can reconstruct the ground truth outcome, when we apply a "perfect" ER algorithm (see Section 6.2) on the reduced dataset. Figures 11(a) and 11(b) show the mAP and mAR, respectively, on the y-axis, while the x-axis shows $\widehat{k}$. We plot results for different k values; one curve per k value. We see that for all values of k, the mAP eventually reaches 1.0 as we increase $\widehat{k}$; results for mAR are slightly worse.

The comparison between the mAP/mAR metrics in Figures 11(a), 11(b) with the precision and recall in Figures 9(a), 9(b), points out a beneficial fact: accuracy for higher-ranked entities is higher. For instance, for $k = \widehat{k} = 5$, the set-based precision and recall are around 0.8, while the ranked-cluster precision and recall are higher than 0.9.

7.2.4 Recovery. Figure 12(a) corresponds to Figure 10(b) and depicts the Speedup with Recovery with adaLSH used for filtering, while Figure 12(b) corresponds to Figures 11(a) and 11(b) and depicts the mAP with Recovery; the results for the mAR with Recovery are almost identical to the ones for mAP with Recovery.

Distribution	top1	top2	top3	top4	top5	top10	top20	top40
LightTail	461	335	228	160	91	28	16	13
HeavyTail	274	180	140	98	59	21	16	13
Uniform	41	24	20	20	20	17	15	12

Table 1: Record-per-entity distributions, in DAS.



(a) Performance (b) Accuracy

Figure 13: Performance and Accuracy on DAS.

In Figure 12(a), we see that the speedup decreases as $\widehat{k}$ increases. As expected, the speedup is lower compared to the Speedup w/o Recovery since we also include the run time for recovery, here. However, as the dataset size increases the speedup increases: in SpotSigs4x, even for a large $\widehat{k}$ value of 20, we get an almost 4x speedup. With respect to accuracy, we observe that the mAP with Recovery, in Figure 12(b), very quickly reaches 1.0 for all k values, as we increase $\widehat{k}$.

Whether it is useful to increase $\widehat{k}$ and/or use recovery depends on the desired accuracy level and performance. But our results do suggest that both techniques are useful tools: they can noticeably increase accuracy while still retaining significant speedups over a non-filtered approach.

7.3 DAS dataset

In this section, we compare adaLSH to LSH1280 and Canopies, in a much larger dataset compared to Cora and SpotSigs. Since Canopies requires two thresholds, we decided to use a simpler matching rule compared to Cora: we tokenize the title and authors fields of each record and we consider two records a match when both the jaccard similarity for the title and authors are greater than the same d_{thr} threshold; i.e., we use an AND rule with the same threshold on both parts. The threshold d_{thr} used in the experiments presented here is 0.5, but the same general conclusions hold for other values of d_{thr} and for more complicated matching rules.

Moreover, we use three different versions of DAS: the original dataset that has an almost uniform distribution for the number of records per entity, and two slightly altered versions, created using a preferential attachment process, that have lightly and heavily skewed distributions. The preferential attachment process first selects, uniformly at random, a record from the set of existing records. Assume the selected record refers to an entity E. For each field of the selected record, we collect all the values for that field, from records that also refer to entity E. A new record is constructed, by selecting uniformly at random a value from the set of all the collected values, for each field. The new record is added to the set of existing records and can be selected in the next

steps of the process. This preferential attachment process increases the frequency of errors happening often in specific fields, for a given entity. All versions have 72000 records and their distributions appear on Table 1.

The execution time on the three different versions of DAS appears in Figure 13(a). adaLSH gives a 5x speedup compared to LSH and a 140x speedup compared to Canopies. Canopies uses thresholds $T_1 = d_{thr} = 0.5$ and $T_2 = 0.7$ here: we also tried other thresholds to find out that the time savings were negligible compared to the penalty in accuracy. (For instance, for $T_2 = 0.7$ in the LightTail distribution, Canopies saves 34% of the pairwise comparisons that Pairs would perform, while setting T_2 to 0.6 and 0.55 saves 36% and 37% of the comparisons, respectively. Moreover, the F1 gold in the LightTail distribution, for $k = 5$, is around 0.91 on average for $T_2 = 0.7$ and drops to 0.88 for $T_2 = 0.6$ and 0.84 for $T_2 = 0.55$.) Note also that only Canopies execution time is affected by the distribution type, while adaLSH and LSH1280 have the same performance in all three cases; however, as we will see in the next section this is not always the case.

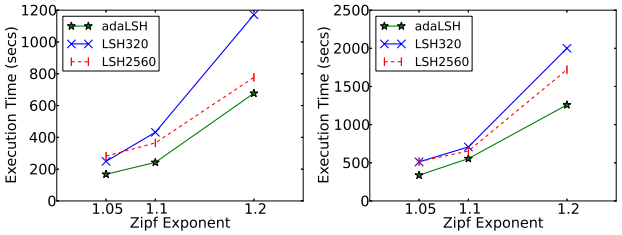
Figure 13(b) depicts the F1 gold for adaLSH on the three record-per-entity distributions: On all three distributions, LSH gives an almost identical accuracy with adaLSH, while Canopies with $T_1 = d_{thr} = 0.5$ and $T_2 = 0.7$ has a slightly lower accuracy on average than adaLSH. Hence, we only plot one curve per distribution in the figure. For the Uniform distribution, the F1 gold is above 0.4 only for $k = 1$: since there are no clearly popular entities, missing a few matches can significantly degrade accuracy. For example, consider the following toy example of a dataset with two entities: one with 10 records and one with 9 records. A clustering where only 8 of the 10 records for the first entity are clustered together, while all 9 records from the second entity are clustered together, would have a zero precision and recall for the top-1 entity.

In Figure 13(b), as we change the distribution to add skewness and popular entities appear, the F1 gold becomes greater than 0.95 for the first few most popular entities, and stays above 0.8 for the LightTail distribution and above 0.75 for the HeavyTail distribution. Note that as k increases the F1 gold drops; slightly in the LightTail distribution and more heavily in the HeavyTail distribution. The reason for the drop is that after the top-10 entities the two distributions start to become more "uniform", as Table 1 indicates.

7.4 PopularImages dataset

Our objective in this section is to study a more challenging scenario for adaLSH: when using the cosine distance for RGB histograms, for almost every image in the dataset, there are images that refer to a different entity but have a similar histogram with that image. (Clearly, there are better features we can extract for each image, still, the cosine distance for RGB histograms serves our propose well, here.)

In addition, we want to illustrate how the distribution of records per entity cannot only affect accuracy, as in the DAS dataset, but performance as well. The three datasets in PopularImages, follow zipfian distributions, with exponents



(a) $d_{thr} = 3$ degrees, $k = 10$ (b) $d_{thr} = 5$ degrees, $k = 10$

Figure 14: Execution time on PopularImages.

of 1.05, 1.1, and 1.2, respectively. For instance, in the 1.05-exponent dataset, the top-3 entities consist of around 500, 250, and 150 records, while in the 1.2-exponent dataset, the top-3 entities consist of around 1700, 800, and 500 records.

Even in this far from ideal, scenario, adaLSH gives a 1.5 to 1.7 speedup for $d_{thr} = 3°$, in Figure 14(a), and a 1.3 to 1.6 speedup for $d_{thr} = 5°$, in Figure 14(b), compared to LSH320. (The speedup compared to LSH2560 is similar in most cases.)

Note that the execution time for both thresholds increases as the exponent increases. The main reason for this increase is the sizes of the top entities, that, as discussed above, increase as the exponent increases. For example, applying the pairwise computation function P on the top-1 entity often takes more than 50% of the execution time. LSH320 that applies less hash functions than LSH2560 in the first stage, ends up applying function P on clusters even larger than the top-1 entity, and the increase in execution time, as the exponent increases, is even more evident.

Finally note that while LSH320 underperforms compared to LSH2560 in this scenario, it can be much more efficient than LSH2560 in other scenarios. (For instance, see Figures 17(a) and 17(b), in Appendix E.) On the other hand, adaLSH always gives a better performance without requiring tuning, i.e., selecting the number of hash functions to use.

8 RELATED WORK

Blocking: To enable ER on large datasets, many blocking approaches have been suggested for different settings [7, 9, 13, 29, 30, 33]. Paper [15] proposes a mechanism that automatically learns hash functions for blocking and is applicable on heterogeneous data expressed in multiple schemas without requiring predefined blocking rules. Blocking over heterogeneous data is also the topic in paper [32]. The framework in paper [21] is able to produce blocks that satisfy size constraints, i.e., blocks are not larger than an upper threshold (e.g., for performance) and/or blocks are not smaller than a lower threshold (e.g., for privacy). Blocking using LSH is applied in Helix [17], a large scale data exploration system.

Entity Resolution: A good overview of traditional ER approaches can be found in surveys [19] and [44]. Here, we cover a few recent studies with a connection to this paper's setting. Paper [42] uses a set of positive (matches) and negative examples (non-matches) to find the best similarity functions and thresholds to use in a dataset; note that our approach could be combined with such a method that computes the "right" threshold for each function. Examples can also be

provided in an active manner as research in crowd entity resolution suggests [8, 14, 16, 20, 22, 38–41, 45]. An alternative of using examples, is defining constraints for matching records, through declarative/interactive frameworks [11, 18]. Entity resolution is also studied in settings where the data is distributed across multiple nodes [6], and the goal is to reduce the bandwidth usage while maintaining a low execution time. Incremental ER is the focus in paper [23], where data updates can be handled efficiently and can also provide evidence to fix previous errors.

Progressive ER: While in traditional and top-k ER only the quality of the final outcome matters, in progressive ER [5, 20, 34, 43], the goal is to maximize the quality of any intermediate outcome, as well. Progressive ER is motivated by scenarios where the consumer of the ER outcome has limited time to process the outcome, or processes the outcome in a pipelined fashion (see also the discussion in the end of Section 4.2). In many cases, progressive ER algorithms try to resolve large entities first, before handling smaller entities (e.g., by first resolving large entities, a large number of matches are found with a few pairwise comparisons). Therefore, progressive ER is a topic closely related to the top-k ER setting we study in this paper. In fact, most of the ideas and mechanisms proposed in progressive ER can work in conjunction with our adaLSH approach, by using adaLSH (or a properly adjusted version of it) in the blocking stage before progressive ER takes place. For example, adaLSH provides a very efficient way to construct a *hierarchy of record partitions*, a concept used in paper [43]: in a hierarchy constructed with adaLSH, the bottom level partition contains all the clusters produced by function P, and one cluster for each record not processed by function P, the second level partition also includes clusters produced by function H_L, the third level partition includes clusters produced by function H_{L-1}, and so on. Besides efficiency, using adaLSH in conjunction with progressive ER mechanisms enables progressive ER on high-dimensional data; many progressive ER mechanisms can be efficient only for the relational model.

Locality-Sensitive Hashing: The LSH variations discussed here are related to our approach because they involve some notion of adaptivity. The entropy-based LSH [26, 31], trades time for space for Nearest-Neighbor (NN) queries on Euclidean spaces. Multi-Probe LSH [28] reduces the number of hash tables it uses, by probing multiple buckets at query time. Bayesian [35] and sequential hypothesis testing LSH [12] use the hash values generated in the first stage of LSH, to efficiently verify if each two records in the same hash bucket are indeed within the threshold. Paper [27] focuses on a specific LSH family of functions, the minwise hashing functions [10] for jaccard similarity: based on a theoretical framework, only a few bits are kept for each hash value, in order to reduce space and computational overhead. Paper [37] also focuses on a specific function family, random projections for cosine similarity, and proposes a mechanism that trades accuracy for space, in an online setting for LSH. In the LSH variation in [25], a notion of accuracy, with respect to NN queries, is defined for each hash function and, at query time, the most appropriate hash functions are selected.

9 CONCLUSION

We proposed adaptive LSH, a novel approach for finding the records referring to the top-k entities in large datasets. The main component of our approach is a sequence of clustering functions that adaptively apply LSH. The large cost savings come from applying only the few first lightweight functions in the sequence on the vast majority of records and detecting with a very low cost that those records do *not* refer to the top-k entities. The filtering output is a drastically reduced dataset that can be used to very accurately and efficiently find the top-k entities using the full ER algorithm.

Our experiments involved different types of data: multi-field publication records, web articles, and images. We compared adaptive LSH to the common, for high dimensional data, LSH-blocking approach. The speedup ranges from 2x to 25x compared to traditional LSH blocking, while introducing only negligible errors due to the approach's probabilistic nature. Furthermore, our adaLSH approach does *not* require knowing in advance the right number of hash functions to apply and may apply a different number of hash functions on different records. We also presented two schemes for improving accuracy further, with modest performance overhead.

In the future, we plan to explore a couple of interesting directions for adaLSH. First, we believe that adaLSH can offer large performance gains in online settings, where we do not have a fixed dataset and input records arrive dynamically. Second, we plan to study a weighted setting for top-k ER, where different records have different weights (e.g., each news article record includes the number of times it has been viewed) and the goal is to find the k entities with the largest sum of weights. Finally, we plan to study how we can pipeline the execution of the filtering stage with ER algorithms.

A LOCALITY-SENSITIVE HASHING

The clustering functions of the approach proposed in this paper use LSH, as discussed in Section 3. In this appendix, we present the details for LSH.

LSH uses a set of hash tables and applies a number of hash functions on each record, such that two records that are "close" to each other, based on the given distance metric and distance threshold, hash to the same bucket, in at least one of the tables.

In particular, LSH is based on the notion of $(d_t, \rho d_t, p_1, p_2)$-sensitive functions:

`DEFINITION 4 (Locality-Sensitive Family)` *For a given distance metric d, a $(d_t, \rho d_t, p_1, p_2)$-sensitive family $\mathcal{F}$ consists of hash functions, where each function $h : R \rightarrow B$ maps a record $r \in R$ to a bucket $b \in B$ and has the following two properties for records r_1 and r_2:*

- *if $d(r_1, r_2) \leq d_t$, then $h(r_1) = h(r_2)$ with probability* at least p_1.
- *if $d(r_1, r_2) \geq \rho d_t$, then $h(r_1) = h(r_2)$ with probability* at most p_2.

That is, when selecting a hash function $h \in \mathcal{F}$ uniformly at random, for two records r_1 and r_2 with $d(r_1, r_2) \leq d_t$, the probability of selecting a function h with $h(r_1) = h(r_2)$ is at least p_1. If $d(r_1, r_2) \geq \rho d_t$ the probability of selecting a function h with $h(r_1) = h(r_2)$ is at most p_2. Note that ρ needs to be greater than one and p_1 greater than p_2, for $\mathcal{F}$ to be useful. Intuitively, when picking a hash function from a $(d_t, \rho d_t, p_1, p_2)$-sensitive family $\mathcal{F}$, we will pick with high probability a function that hashes to the same bucket two records that are very similar, and we will pick with high probability a function that hashes to different buckets two records that are not very similar.

EXAMPLE 5 *Consider again Example 2. When selecting uniformly at random a hyperplane through the origin, the likelihood of picking a hyperplane like e_2 (where r_1 and r_2 lie on different sides) is $\frac{30}{180}$; while the likelihood of picking a hyperplane like e_1 is $\frac{180-30}{180}$. As discussed in Example 2, we consider each random hyperplane as a hash function, $h : R \rightarrow \{b_1, b_2\}$, that hashes each vector/record, $r \in R$, to two buckets, b_1 or b_2, depending on which side of the hyperplane vector r lies. In general, the family of hash functions defined by the random hyperplanes, is $(\theta_1, \theta_2, \frac{180-\theta_1}{180}, \frac{180-\theta_2}{180})$-sensitive, for $\theta_1, \theta_2 \in [0, 180]$ and $\theta_1 < \theta_2$. That is, if the distance between two vectors/records is θ, the likelihood of picking a hash function that hashes the two vectors to the same bucket is exactly $\frac{180-\theta}{180}$.*

Although in Example 5 the space is two dimensional, it is not hard to see that the family of hash functions defined by random hyperplanes, is $(\theta_1, \theta_2, \frac{180-\theta_1}{180}, \frac{180-\theta_2}{180})$-sensitive for any number of dimensions, for the cosine distance.

A $(d_t, \rho d_t, p_1, p_2)$-sensitive family can be "amplified" using an *AND-construction* or an *OR-construction*:

DEFINITION 5 (AND-construction) *Given a $(d_t, \rho d_t, p_1, p_2)$-sensitive family $\mathcal{F}$, a $(d_t, \rho d_t, p_1^w, p_2^w)$-sensitive family $\mathcal{F}'$ is constructed by selecting w functions, $h_1, h_2, \ldots h_w \in \mathcal{F}$, to define a function $h' \in \mathcal{F}'$ such that $h'(r_1) = h'(r_2)$ iff $h_i(r_1) = h_i(r_2)$ for all $i \in [1, w]$, for two records r_1, r_2.*

DEFINITION 6 (OR-construction) *Given a $(d_t, \rho d_t, p_1, p_2)$-sensitive family $\mathcal{F}$, a $(d_t, \rho d_t, 1-(1-p_1)^z, 1-(1-p_2)^z)$-sensitive family $\mathcal{F}'$ is constructed by selecting z functions, $h_1, h_2, \ldots h_z \in \mathcal{F}$, to define a function $h' \in \mathcal{F}'$ such that $h'(r_1) = h'(r_2)$ iff $h_i(r_1) = h_i(r_2)$ for at least one $i \in [1, z]$, for two records r_1, r_2.*

For the AND-construction, if the probability of selecting a hash function $h \in \mathcal{F}$ with $h(r_1) = h(r_2)$ is p_1 (or p_2), it follows that the probability of selecting w functions $h_1, h_2, \ldots h_w \in \mathcal{F}$, with all of them having $h_i(r_1) = h_i(r_2)$ ($i \in [1, w]$), is p_1^w (or p_2^w).

For the OR-construction, if the probability of selecting a hash function $h \in \mathcal{F}$ with $h(r_1) = h(r_2)$ is p_1 (or p_2), it follows that the probability of selecting z functions $h_1, h_2, \ldots h_z \in \mathcal{F}$, with none of them having $h_i(r_1) = h_i(r_2)$ ($i \in [1, z]$), is $(1-p_1)^z$ (or $(1-p_2)^z$). Hence, the probability of at least one having $h_i(r_1) = h_i(r_2)$ is $1-(1-p_1)^z$ (or $1-(1-p_2)^z$).

The two constructions can be combined together to form an AND-OR construction. In particular, a $(d_t, \rho d_t, p_1, p_2)$-sensitive family $\mathcal{F}$ is first transformed to a $(d_t, \rho d_t, p_1^w, p_2^w)$-sensitive family $\mathcal{F}'$ using an AND-construction, and then $\mathcal{F}'$ is transformed to a $(d_t, \rho d_t, 1-(1-p_1^w)^z, 1-(1-p_2^w)^z)$-sensitive family $\mathcal{F}''$ using an OR-construction.

As discussed in Section 3, the AND-OR construction can be thought of as a hashing scheme of z hash tables: in each of the z tables two records r_1 and r_2 hash to the same bucket if $h_i(r_1) = h_i(r_2)$ for all of the w hash functions h_i, for that table. (For each table there is an independent selection of w functions $h_i \in \mathcal{F}$.)

B COMPLEX DISTANCE RULES

When records have multiple fields, distance rules may involve more than one field, as discussed in Section 3. The main workflow of Adaptive LSH, summarized in Algorithm 1, remains the same in that case, however, some of the details of transitive hashing functions and the design of the function sequence change.

We focus on distance rules that consist of: AND rules, OR rules, and weighted average rules. Next, we discuss how to design the sequence of transitive hashing functions for each type of rules and conclude this section with a brief discussion on the case of more complicated rules that combine several AND, OR, and weighted average rules.

B.1 AND rules

To keep the discussion simple, we assume the AND rule involves only two record fields: given a distance metric and threshold for each field, two records $r_1 = \{f_1^{(1)}, f_1^{(2)}\}$ and $r_2 = \{f_2^{(1)}, f_2^{(2)}\}$ refer to the same entity if

$$d(f_1^{(1)}, f_2^{(1)}) \leq d_{thr}^{(1)} \;\; AND \;\; d(f_1^{(2)}, f_2^{(2)}) \leq d_{thr}^{(2)}$$

In the AND-OR hashing scheme used by function H_i in the sequence, the hash value for each of the hash tables will be formed using both fields $f^{(1)}$ and $f^{(2)}$. In particular, given a Locality-Sensitive family of hash functions for each field, for each hash table used by function H_i, we pick w hash functions from the family of field $f^{(1)}$ and u hash functions from the family of field $f^{(2)}$. The hash value for each hash table is a concatenation of the w and u hash values.

Consider functions $p_1(x_1)$ and $p_2(x_2)$ that give the probability of selecting a hash function that gives the same hash value for two records at a distance x_1 (x_2) on field $f^{(1)}$ ($f^{(2)}$); $0 \leq x_1, x_2 \leq 1$. Assuming z tables are used, the probability of two records at a distance x_1 on field $f^{(1)}$ and x_2 on field $f^{(2)}$, hashing to the same bucket in any of the z tables, is:

$$1 - \left[1 - p_1^w(x_1) p_2^u(x_2)\right]^z$$

To decide the values w, u, z, for a given *budget* of hash functions, we use a generalization of Program 1 to 3:

$$\min_{w,u,z} \quad \int_0^1 \int_0^1 \Big[1 - \big[1 - p_1^w(x_1) p_2^u(x_2)\big]^z\Big] dx_1 dx_2 \qquad (5)$$

$$s.t. \quad (w+u) * z = budget \qquad (6)$$

$$1 - \big[1 - p_1^w(x_1) p_2^u(x_2)\big]^z \geq 1 - \epsilon,\ x_1 \leq d_{thr}^{(1)}, x_2 \leq d_{thr}^{(2)} \qquad (7)$$

Just as in Program 1 to 3, we can also search over w, u, z values, where $\frac{budget}{w+u}$ is not an integer, by adjusting the probability expression, or take into account cost functions that reflect the actual cost of computing each hash value.

Note one more important detail here: we may have to add some constraints in Program 5 to 7 that reflect the solutions obtained for previous functions in the sequence. That is, if the previous function in the sequence is using w' functions from the family of field $f^{(1)}$ and u' hash functions from the family of field $f^{(2)}$, on each table, we need to add the constraints $w \geq w'$ and $u \geq u'$. Those constraints are related to the incremental computation property of the sequence of clustering functions: there are already w' plus u' hash values computed for each table, so, ideally, we want to use all of them for the next function in the sequence.

B.2 OR rules

An OR rule for records of two fields states that two records $r_1 = \{f_1^{(1)}, f_1^{(2)}\}$ and $r_2 = \{f_2^{(1)}, f_2^{(2)}\}$ refer to the same entity if

$$d(f_1^{(1)}, f_2^{(1)}) \leq d_{thr}^{(1)} \quad OR \quad d(f_1^{(2)}, f_2^{(2)}) \leq d_{thr}^{(2)}$$

For an OR rule, the AND-OR hashing scheme used by function H_i in the sequence, has hash tables that involve only field $f^{(1)}$ and tables that involve only field $f^{(2)}$. Assuming a (w, z)-scheme is used for field $f^{(1)}$ and a (u, v)-scheme is used for field $f^{(2)}$, the probability of two records at a distance x_1 on field $f^{(1)}$ and x_2 on field $f^{(2)}$, hashing to the same bucket in any of the $z + v$ tables, is:

$$1 - \big[1 - p_1^w(x_1)\big]^z \big[1 - p_2^u(x_2)\big]^v$$

To decide the values w, z, u, v, for a given *budget* of hash functions, we use the following program:

$$\min_{w,z,u,v} \quad \int_0^1 \int_0^1 \Big[1 - \big[1 - p_1^w(x_1)\big]^z \big[1 - p_2^u(x_2)\big]^v\Big] dx_1 dx_2 \qquad (8)$$

$$s.t. \quad w * z + u * v = budget \qquad (9)$$

$$1 - \big[1 - p_1^w(x_1)\big]^z \geq 1 - \epsilon,\ x_1 \leq d_{thr}^{(1)} \qquad (10)$$

$$1 - \big[1 - p_2^u(x_2)\big]^v \geq 1 - \epsilon,\ x_2 \leq d_{thr}^{(2)} \qquad (11)$$

B.3 Weighted average rules

Handling weighted average rules requires a slightly different approach compared to the AND and OR rules.

A weighted average rule uses a list of weights $\alpha_1, \ldots, \alpha_F$ ($\sum_i \alpha_i = 1$), for records of F fields, and a single distance threshold d_{thr}. Two records $r_1 = \{f_1^{(1)}, \ldots, f_1^{(F)}\}$ and $r_2 = \{f_2^{(1)}, \ldots, f_2^{(F)}\}$ refer to the same entity if

$$\bar{d}(r_1, r_2) = \sum_{i=0}^{F} \alpha_i d(f_1^{(i)}, f_2^{(i)}) \leq d_{thr}$$

For a weighted average rule a (w, z)-scheme is used for function H_i in the sequence, just like in the case of a single field: the values for parameters w and z are chosen based on the process described in Section 5.1. Nevertheless, there is one important difference compared to the single field case. In order to select each of the w hash functions, for each of the z hash tables, the following process is used:

`DEFINITION 7 (Weighted-Average Function Selection)` *(a) randomly select one of the F fields based on the distribution defined by the field weights $\alpha_1, \ldots, \alpha_F$, i.e., the probability of picking field i is α_i, and (b) select uniformly at random one of the hash functions from the locality-sensitive family for the selected field i.*

The process of Definition 7 has the theoretical properties summarized in the following two theorems.

`THEOREM 2` *For each field i, consider a locality sensitive family $\mathcal{F}^{(i)}$, such that the probability of selecting a hash function $h_j \in \mathcal{F}^{(i)}$ with $h_j(r_a) = h_j(r_b)$, for any two records r_a and r_b, is:* $Pr[h_j(r_a) \equiv h_j(r_b)] = 1 - d(f_a^{(i)}, f_b^{(i)})$ *where* $0 \leq d(f_a^{(i)}, f_b^{(i)}) \leq 1$

If h'_j is a hash function selected using the process of Definition 7, then:

$$Pr[h'_j(r_a) \equiv h'_j(r_b)] = 1 - \bar{d}(r_a, r_b)$$

`PROOF`: The probability of selecting a field i in step (a) of the process is $Pr[\textit{field } i \textit{ picked}] = \alpha_i$. Moreover, if field i is picked then $Pr[h'_j(r_a) \equiv h'_j(r_b)] = [1 - d(f_a^{(i)}, f_b^{(i)})]$.

$$\begin{aligned} Pr[h'_j(r_a) \equiv h'_j(r_b)] &= \sum_{i=0}^{F} Pr[\textit{field } i \textit{ picked}][1 - d(f_a^{(i)}, f_b^{(i)})] \\ &= \sum_{i=0}^{F} \alpha_i [1 - d(f_a^{(i)}, f_b^{(i)})] \\ &= \sum_{i=0}^{F} \alpha_i - \sum_i \alpha_i d(f_a^{(i)}, f_b^{(i)}) \\ &= 1 - \bar{d}(r_a, r_b) \end{aligned}$$

□

An example where Theorem 2 applies is the family of minhash functions for the Jaccard distance. A more general version of Theorem 2 is stated in Theorem 3 (see Appendix A for the definition of locality-sensitive function families):

`THEOREM 3` *For each field i, consider a $(d_{thr}, \rho d_{thr}, p_1^{(i)}, p_2^{(i)})$-sensitive family. In this case, the family of functions $\mathcal{F}'$, where each function $h'_j \in \mathcal{F}'$ is selected using the process of Definition 7, is $(d_{thr}, \rho d_{thr}, \sum_{i=0}^{F} \alpha_i p_1^{(i)}, \sum_{i=0}^{F} \alpha_i p_2^{(i)})$-sensitive.*

`PROOF`: The proof is similar to the one of Theorem 2. □

B.4 Combining rules

In the last part of this appendix, we briefly discuss the case of ER rules that combine AND, OR, and weighted average rules. In this case, we need to form more general optimization programs that are based on the same principles as the ones

discussed above: the probability of hashing to the same bucket should be very close to 1.0 for pairs of records that satisfy the combined ER rule (e.g., Equation 7) and the overall volume under the probability curve should be minimized (e.g., Equation 5). For instance, to form a program for rule $title < d_{thr}^{(1)}$ AND $\left[venue < d_{thr}^{(2)} \text{ OR } authors < d_{thr}^{(3)}\right]$, we can first apply the distributive property, and then form a program with a) three constraints, one for the budget and one for each of the two OR terms after the distributive property is applied, and b) the objective function, by combining Equations 5 and 8.

Note also that the process of solving the optimization programs can be performed offline for a large set of distance functions, thresholds, and rules. Hence, the execution time for the filtering stage can stay unaffected by programs that are computationally expensive to solve. Moreover, depending on the program, there may be optimizations in order to avoid an exhaustive search over all parameter values (e.g., binary search for Program 1 to 3).

C LARGEST-FIRST OPTIMALITY

In this appendix, we give the full proofs for Theorems 1 and 4 (Section 4.2) and discuss when it could make sense for an algorithm *not* to follow the largest-first optimality assumptions.

THEOREM 1 *Consider the family of algorithms that:*

(1) *do* not *"jump ahead" to function P, i.e., if a cluster C is an outcome of a function H_i, the algorithm can only apply function P on C, when $(cost_{i+1} - cost_i) * |C| \geq cost_P * \binom{|C|}{2}$ (Line 5 on Algorithm 1).*

(2) *do* not *"terminate early", i.e., terminate only when the k largest clusters are an outcome of either an H_L or P function.*

Algorithm 1 gives the minimum overall cost compared to any other algorithm of this family.

PROOF: We will prove that Algorithm 1 gives the minimum overall cost compared to any other algorithm, for any *execution instance*. In an execution instance, the outcome of applying a function H_i or P on a set of records S, is the same across all algorithms. In other words, all algorithms would observe the exact same clusters during their execution if they would select the same cluster to process in each step. Assume that another algorithm $\mathcal{B}$ in this family, gives a lower overall cost than Algorithm 1, for a given execution instance. Based on the cost model (Definition 3), for algorithm $\mathcal{B}$ to have a lower overall cost than Algorithm 1, there are three possibilities:

(1) there must be a set of records S_1 such that: both Algorithms 1 and $\mathcal{B}$ apply P on S_1, but the last function Algorithm 1 applies on S_1, before P, is H_i, and the last function applied on S_1 by $\mathcal{B}$, before P, is H_j for $j < i$.

(2) there must be a set of records S_2 such that: algorithm $\mathcal{B}$ applies P on S_2 and the last function Algorithm 1 applies on S_2, is H_i, while the last function algorithm $\mathcal{B}$ applies on S_2, before P, is H_j for $j < i$.

(3) there must be a set of records S_3 such that: the last function Algorithm 1 applies on S_3 is either P or H_i, and the last function $\mathcal{B}$ applies on S_3 is H_j for $j < i$.

The first two possibilities violate Condition 1, in the definition of the family of algorithms, since they would require algorithm $\mathcal{B}$ to "jump ahead" to function P; otherwise, Algorithm 1 would apply the exact same functions on sets S_1 or S_2. Hence, we focus on the third possibility. Consider step l, where Algorithm 1 selects set S_3 (or a cluster that is a subset of S_3), to apply function H_{j+1} (where H_j is the last function algorithm $\mathcal{B}$ applies on S_3). At step l, set S_3 is the largest cluster for Algorithm 1 to select it. Since clusters always split in subsequent steps, S_3 will also be larger than the top-k clusters after the final step of Algorithm 1. Hence, since we are focusing on the same execution instance, Condition 2 in the algorithms' family definition is violated, as the largest cluster after the final step of algorithm $\mathcal{B}$ will *not* be an outcome of an H_L or P function. □

THEOREM 4 *For an input k, Algorithm 1 reaches to a state where the k' largest clusters are an outcome of either an H_L or P function, for any $k' < k$, with a lower cost compared to any other algorithm in the family defined in Theorem 1.*

PROOF: For a $k' < k$, consider applying Algorithm 1 with input k' and with input k. Assume the same execution instance in both cases. Note that Algorithm 1 will execute in the exact same way for both inputs, until it terminates when applied with input k'. That is, Algorithm 1 will process the same clusters using the same functions and in the same order, in both cases, before the k' largest clusters are an outcome of either an H_L or P function. We know from Theorem 1 that Algorithm 1 finds the k' largest clusters with a minimum cost when applied with input k'. Since Algorithm 1 executes in the same way when applied with input k, we conclude that Algorithm 1 reaches to a state where the k' largest clusters are an outcome of either an H_L or P function, with a minimum cost. □

C.1 Assumptions

Let us start with the second assumption and consider algorithms that *do* "terminate early". (That is, algorithms that may terminate even when the k largest clusters are not all an outcome of either an H_L or P function.) In that case, the algorithm would either: (a) output a cluster which is not an outcome of an H_L or P function, or (b) would *not* output one of the k largest clusters. In case (a), the algorithm should be fairly certain that this cluster would not split into smaller clusters if function P (or H_L) was applied on it. In case (b), the algorithm should be fairly certain that the cluster not contained in the output, would split into small (smaller than the k largest clusters that are an outcome of an H_L or P function) clusters. Thus, an algorithm should have a good estimation of how likely it is for clusters to split, if more functions in the sequence were to be applied on them, and how large the new clusters would be.

A good estimation of how likely are clusters to split and how large the new clusters would be, is also the key condition

for an algorithm to potentially benefit from breaking the first assumption. Seeing how it could be beneficial to break the first assumption, is a bit more complicated. Let us illustrate with a simple example. Consider two clusters, C_1 of 10 records and C_2 of 12 clusters, and assume we are looking for the top-1 entity. Moreover, assume that: (a) C_1 either does not split at all, with 50% probability, or splits into two clusters of 5 records, with 50% probability, (b) C_2 either does not split at all, with 5% probability, or splits into two clusters of 9 and 3 records, with 50% probability, or splits into four clusters of 3 records each, with 45% probability, and (c) to find out if C_1 splits, we need to apply function P on it, while for C_2, we can apply the next sequence-function, to find out if it splits, but we need to apply function P to find out if it splits to four clusters or two clusters. In this example, it can be beneficial to first apply function P on the smaller cluster C_1 first. If cluster C_1 splits into two clusters of 5 clusters each, then it only makes sense to directly apply P on C_2 to find out if the largest cluster in C_2 consists of 9 or 3 records. (Note that the largest-first strategy would first apply the next sequence-function on C_2, so we would not be able to avoid the cost of that function on C_2.) Potentially, such a strategy could lead to a lower execution time compared to largest-first.

The bottom line is that an algorithm could benefit from breaking the two assumptions, only when it keeps estimates of the sizes of sub-clusters inside each cluster. Computing accurately such estimates may not always be possible, or may be so costly, in terms of execution time, that the overhead outweighs the benefits. We plan to investigate in future research if this could be a direction giving a non-trivial improvement.

D IMPLEMENTATION DETAILS

In this appendix, we discuss how to efficiently implement all the key components of Algorithm 1, in Section 4. In particular, we discuss the implementation for transitive hashing functions (Line 8) and the pairwise computation function (Line 6), finding the largest cluster (Line 3), and the termination condition (Line 11). We start with the description of two data structures, and then we focus on how the two structures are used in the lower level operations in Algorithm 1.

D.1 Data Structures

The data structures used in the implementation are a parent-pointer tree structure (to efficiently support union-find operations) and a bin-based structure. The parent-pointer tree structure is used by transitive hashing functions and the pairwise computation function, while the bin-based structure is used for finding the largest cluster and in the termination condition.

The parent-pointer tree structure is depicted in Figure 15. Each node has a pointer to the parent, leaf nodes have a pointer to the first leaf on the right, and the root has a pointer to the first and last leaves. Each parent-pointer tree represents a cluster: the leaves of the tree refer to the records

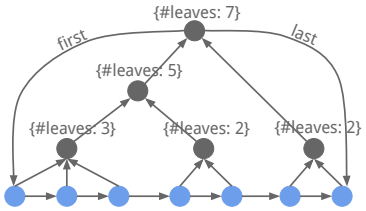


Figure 15: Parent-pointer tree.

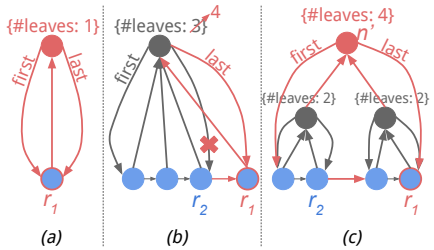


Figure 16: Tree updates when adding a record r_1 to a hash table.

that belong to the cluster. In addition, each node stores the number of leaves that are successors of that node.

The bin-based structure is an array of $log(|R|)$ bins; where $|R|$ is the number of all records in the dataset. In each bin, the roots of different parent-pointer trees are stored. The root of a parent-pointer tree with x leaves, is stored on the $log(\lfloor x \rfloor)$-th bin of the array. For example, an array for $|R| = 10$ records would have four bins: the first bin would store trees with 1 leaf, the second bin trees with 2 or 3 leaves, the third bin trees with 4 to 7 leaves, and the fourth bin trees with 8 to 10 leaves.

D.2 Transitive Hashing Functions

A transitive hashing function H_i based on a (w_i, z_i)-scheme, uses z_i hash tables. For each record r of an input set S, z_i bucket indices (consisting of w_i hashes each) are computed. Based on those hashes, record r is added to each of the z_i tables. (Note that the computation of hashes is incremental and uses the hashes computed from the previous function in the sequence H_{i-1}, on record r.) Hashing function H_i uses a number of parent-pointer trees: each cluster in the output (see Definition 1) refers to one parent-pointer tree. When a function H_i is invoked, it starts with an empty set of trees and none of the input records belongs to a tree. Moreover, the z_i hash tables are empty, i.e., each invocation of a function H_i uses a different set of tables; to avoid a possible merge of clusters from different invocations. To process a cluster of records stored in a parent-pointer tree, a function H_i uses the "first" pointer in the root to reach the first leaf, processes that record, then uses the "right" pointer of the first leaf to access the next record in the cluster, and so on. When a record r_1 is added to a hash table there are four cases:

(1) the bucket in the table is empty and record r_1 has *not* been added yet to a parent-pointer tree: a new tree is created with record r_1 being the single leaf of that tree, as depicted in Figure 16a.

(2) the bucket in the table is empty and record r_1 has already been added to a parent-pointer tree: just add r_1 in the bucket.
(3) the bucket in the table is *not* empty and record r_1 has *not* been added yet to a parent-pointer tree: find the root of the tree of the record r_2 that was last added in the bucket and add record r_1 to this tree, by updating all tree pointers (updates appear in red on Figure 16b).
(4) the bucket in the table is *not* empty and record r_1 has already been added to a parent-pointer tree: find the root of the tree of the record r_2 that was last added in the bucket. If the root for r_2 is the same with the root of the tree of r_1 (i.e., the two records belong to the same tree), just add r_1 to the bucket. Otherwise, merge the two trees into one: use a new node n' as a root and update all pointers, as depicted in Figure 16c.

Note that all records of a bucket in a hash table are under the same tree. To find the root of a bucket's tree, the process starts from the record that was last added in the bucket, in cases 3 and 4, because it is more likely that the path to the root is shorter, compared to when starting from the, say, first record added in the bucket. The complexity of adding a record r to a hash table is $O(log(|C_r|))$, where C_r is the cluster where record r belongs in the output of function H_i.

D.3 Pairwise Computation Function

The pairwise computation function P also uses parent-pointer trees. When the distance between two records is less than the threshold, the trees of the two records are merged; the process is similar to the one discussed in the previous section. In addition, for two records that belong to the same tree, P can safely skip the distance computation for those two records. Nevertheless, note that in our cost model (Definition 3) we are being conservative and assume that the cost of function P involves the computation of all pairwise distances.

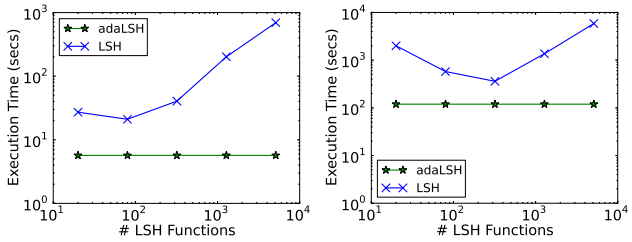
D.4 Finding the Largest Cluster

Upon completion of a function H_i or P, the output clusters(trees) are added to the bin-based array. When the largest cluster must be found for the next iteration, the search starts from the last *non-empty* bin in the array and the largest cluster in that bin is returned and removed from the bin.

Adding a cluster to the bin-based array is a constant-time operation and we expect that the clusters in the last *non-empty* bin to always be much fewer than all the clusters stored in the array.

D.5 Termination Condition

To efficiently compute when the loop of Algorithm 1 must terminate, we use an array of "final" clusters. When the largest cluster selected in an iteration, is an outcome of a function H_L or a function P, the cluster is not processed but it is added instead to the array of final clusters. Once k clusters are added in the final clusters array, Algorithm 1 terminates and the clusters in the final clusters array are returned as the output. Note that this condition is equivalent to the condition in Line 11 of Algorithm 1.



(a) SpotSigs (b) SpotSigs8x

Figure 17: adaLSH vs different LSH variations.

E ADDITIONAL EXPERIMENTS

E.1 LSH blocking variations

In this appendix, we start by exploring different LSH blocking variations, in a couple of scenarios. Clearly, knowing in advance which LSH variation is better in each case is not possible. Our goal here is to examine how much better adaLSH is, compared to the best LSH variation, if we knew in advance the best LSH variation to use in each case.

The log-log plot in Figure 17(a) shows the execution time on SpotSigs and $k = 10$, for five LSH variations: LSH20 to LSH5120. That is, the x-axis shows the number of hash functions used by LSH and the y-axis the execution time. (For adaLSH we plot the same execution time for all x-axis values.) We see that adaLSH gives a 4x speedup even when compared to the best LSH variation; LSH80 in this case.

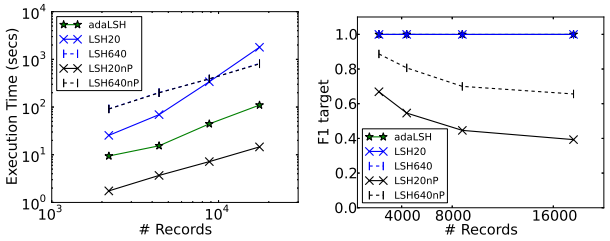
When the size of the dataset increases we expect that some other LSH variation will perform better. Indeed, as we see in Figure 17(b), for SpotSigs8x and $k = 10$, LSH320 is now the lowest execution time variation. Still, adaLSH gives a 3x speedup compared to LSH320.

Hence, as the experiments in this section point out, a big advantage of adaLSH compared to LSH variations is that adaLSH does not need tuning with respect to the number of hash functions to apply. In addition, adaLSH can apply a different number of hash functions on different records and manages to achieve 3-4x speedups compared to the optimally tuned LSH version.

Next, we focus on a setting that illustrates the tradeoff between accuracy and performance when we run only the first stage of LSH. To measure accuracy in this case we use a metric called F1 target: we consider as ground truth the outcome of function P on the whole dataset and we compute the harmonic mean of precision and recall, just like we do for F1 Gold. The purpose of this metric is to quantify the errors introduced by the probabilistic nature of the LSH approaches.

We use four LSH variations: LSH20, LSH20nP, LSH640, and LSH640nP. (As discussed in Section 6.1, the nP variations do *not* apply function P after the first stage.) Figure 18(a) depicts the results, for $k = 10$ on SpotSigs, SpotSigs2x,

SpotSigs4x, and SpotSigs8x. We see that adaLSH gives an, at least, 4x speedup against all variations of LSH, besides LSH20nP.



(a) Execution time (b) F1 target

Figure 18: LSH vs adaLSH, performance/accuracy

Of course, the nP variations, and especially LSH20nP, are much less accurate than the other methods as Figure 18(b) shows: the F1 Target is just 0.7 for LSH20nP on SpotSigs and drops to 0.4 on SpotSigs8x, while for LSH640nP the F1 Target drops from 0.9 to below 0.7. On the other hand, all other methods give an F1 Target very close to 1.0.

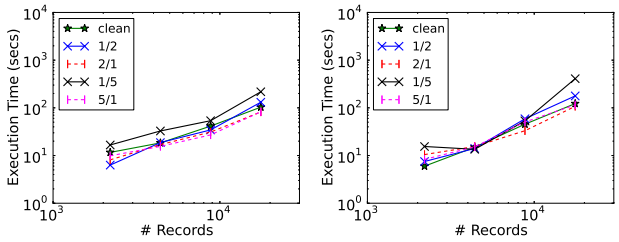
There is another interesting perspective on the results from Figure 17(a). Note that the computation performed by LSH20nP is actually the computation that adaLSH performs in the first round; as discussed in Section 6.1, in the adaLSH used in the experimental evaluation, the first function in the sequence applies 20 hash functions on all the records. As Figure 17(a) shows, the overall computation adaLSH performs takes just 5 to 10 times more than the computation it performs on the first round.

E.2 Adaptive LSH Tuning

Here, we discuss a couple of experiments regarding the fine tuning of adaptive LSH. First, we add noise to the simple cost model used by Algorithm 1 in Line 5. In particular, we multiply by a noise factor nf, the cost of applying the pairwise computation function P on a cluster C: $cost_P * \binom{|C|}{2}$. That is, when factor nf is less than one, the cost of applying P is under-estimated and P is applied sooner (and on larger clusters) compared to when no noise is added. On the other hand, when factor nf is greater than one, the cost of applying P is over-estimated and the application of P is deferred until clusters are small enough.

We tried four values for factor nf: $\frac{1}{2}$, $\frac{1}{5}$, $\frac{2}{1}$, and $\frac{5}{1}$. In Figure 19(a), the y-axis shows the execution time for $k = 2$, on SpotSigs, SpotSigs2x, SpotSigs4x, and SpotSigs8x (x-axis). In Figure 19(b), we run the same experiment for $k = 10$. Each curve refers to a different value for factor nf. We also plot the execution time for adaptive LSH without any noise added ("clean" curve). (Note that parameters $cost_P$ and $cost_i, 1 \leq i \leq L$, are estimated using 100 samples each.)

We draw one main conclusion from the plots of Figures 19(a) and 19(b): adaptive LSH is not sensitive to cost-model noise and the execution time may only be significantly affected for



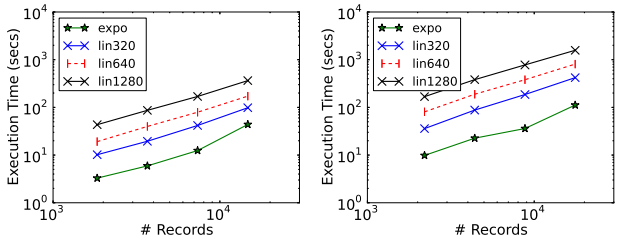
(a) $k = 2$ (b) $k = 10$

Figure 19: Adding noise to the cost model.

a very small nf of $\frac{1}{5}$. That is, there is a considerable increase in the execution time for adaptive LSH, only when the cost of applying P is heavily under-estimated and P ends up being applied early and on larger clusters compared to when no (or a little bit of) noise is added.

The second experiment in this appendix, studies the different modes for budget selection, discussed in Section 5.2. We try:

- expo: the default Exponential mode, where the budget is doubled for every function in the sequence, starting from 20 hash functions for the first function.
- lin320, lin640, lin1280: the Linear mode, where the budget starts from 320, 640, or 1280 hash functions, for the first function, and is increased by 320, 640, or 1280 hash functions, for every function in the sequence.



(a) Cora (b) SpotSigs

Figure 20: Different budget selection modes.

Figure 20(a) shows the execution time for the four modes in the y-axis, on Cora, Cora2x, Cora4x, Cora8x (x-axis), for $k = 10$. Figure 20(b) refers to the same experiment for SpotSigs.

Clearly, the Exponential mode is the best option requiring a far lower execution time compared to other modes. Note that, in the Exponential mode (when the budget is doubled for every function in the sequence), the "amount" of processing performed on the selected cluster in each step, is almost the same with the amount of processing performed in all previous steps, on the records of the selected cluster. Hence, the Exponential mode is able to find the sweet spot in the trade-off between running fewer hash functions, overall, in many steps and running more hash functions in fewer steps.

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