MatchCatcher: A Debugger for Blocking in Entity Matching

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ABSTRACT

Blocking is a fundamental step in entity matching (EM). Much work has examined the design and runtime of blockers. However, very little if any work has examined the problem of debugging blocking accuracy. In practice, blockers' accuracy can vary drastically, and using an accurate blocker is critical for many EM applications. To address this problem, we describe the MatchCatcher solution. Given two tables to be matched and a blocker, MatchCatcher finds matches killed off by the blocker, so that the user can examine these matches to understand how well the blocker does accuracy-wise and what can be done to improve its accuracy. We show how to quickly find such matches using string similarity joins, iterative user engagement, rank aggregation, and active/online learning. Extensive experiments show that MatchCatcher is highly effective in helping users develop blockers, can help improve accuracy of even the best blockers manually created or automatically learned. MatchCatcher has been open sourced and used by 300+ students in data science class projects and 7 teams at 6 organizations.

1 INTRODUCTION

Entity matching (EM) finds data instances referring to the same real-world entity [6, 13], such as tuples (Dave Smith, San Francisco, CA) and (David Smith, S.F., CA). This problem is critical for many Big Data and data science applications.

When doing EM, we often must perform blocking. Consider for example matching two tables A and B. Real-world tables often have hundreds of thousands, or millions, of tuples. Trying to match all tuple pairs in $A \times B$ is practically infeasible. So we often perform a step called *blocking* which uses domain heuristics to quickly drop many pairs judged obviously non-matched (e.g., person tuples that do not have the same state). The next step, called *matching*, matches the remaining pairs, using rule- or learning-based techniques. Blocking can greatly reduce the number of pairs considered in the matching step, drastically reducing the total EM time. As a result, virtually all real-world EM applications use blocking.

Numerous blocking methods have been developed [6]. For example, *hash blocking* drops all tuple pairs that do not have the same hash value, using a predefined hash function. This method is popular because it is easy to understand and fast. Other methods include sorted neighborhood, overlap, phonetic, rule-based, etc. (see Section 2).

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Given two tables A and B to match, we often want a blocker Q that is *fast*, *selective*, and *accurate*. "Fastness" is measured by the time to apply Q to A and B to produce a set of tuple pairs C. "Selectivity" is typically measured as the ratio $|C|/|A \times B|$. "Accuracy" is typically measured as the fraction of *true matches* surviving blocker Q, i.e., $|M \cap C|/|M|$, where M is the set of (unknown) true matches in $A \times B$. As such, it is also referred to as *recall*.

In practice, blockers can vary drastically in recall, and using a blocker with high recall is critical for many EM applications (see Section 2). Yet today there is still no good way to develop such blockers. For example, given the popularity of hash blockers, suppose we have decided to use a hash blocker Q on two tables. While fast, Q may have low recall if the attribute values to be hashed are dirty, misspelt, missing, or have many natural variations (e.g., "New York", "NY", "NYC"). A common way to address this problem is to use multiple hash blockers and take the union of their outputs, to maximize recall. However, even in this case, the recall can still be quite low. For instance, a recent work [8] describes two real-world datasets where extensive effort at combining hash blockers achieves only 38.8% and 72.6% recall. Such low recalls are simply unacceptable for many EM applications. To improve recall, we can revise the current hash blockers, replace some of them, or adding more blockers (of the non-hash types). *To do any of these, however, we need a way to understand whether the current blocker has low recall, and if so, then what the possible problems are, so that we can improve it.*

The MatchCatcher Solution: In this paper we take the first step toward solving the above problems. We describe MatchCatcher, a solution to debug blocker accuracy. Given two tables A and B to be matched and a blocker Q, MatchCatcher attempts to find matches that are "killed off" by Q, i.e., those that do not survive the blocking step. We can examine these matches to see if they are indeed true matches, and if so, then why they get killed off by Q. This tells us whether Q has low recall, and if so, then how to improve it. The following example illustrates our solution:

Example 1.1. Consider matching tables A and B in Figure 1.a. Suppose a user U begins by creating a blocker Q_1 that keeps only tuple pairs sharing the same value for "City". Figure 1.b shows this blocker as Q_1: $a.City = b.City$. (This is attribute-equivalence blocking, a special type of hash blocking.) Applying Q_1 to A and B produces a set of tuple pairs C_1 (see Figure 1.b).

User U wants to know if blocker Q_1 kills off too many true matches. To answer this, U applies MatchCatcher*, which operates in iterations. In the first iteration,* MatchCatcher *shows the user n tuple pairs judged most likely to be matches killed off by Q_1. These pairs are listed on Figure 1.b, under "Debugger Output, Iter 1" (here $n = 3$).*

User U finds that the first two pairs, (a_1, b_1) and (a_3, b_2), are indeed true matches (shown in red color on the figure). A closer examination reveals that they do not survive blocking because their "City" values

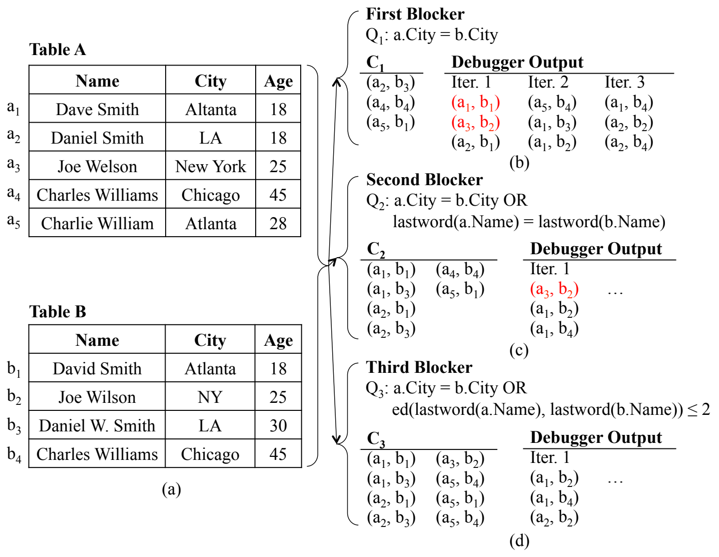


Table A

	Name	City	Age
a_1	Dave Smith	Altanta	18
a_2	Daniel Smith	LA	18
a_3	Joe Welson	New York	25
a_4	Charles Williams	Chicago	45
a_5	Charlie William	Atlanta	28

Table B

	Name	City	Age
b_1	David Smith	Atlanta	18
b_2	Joe Wilson	NY	25
b_3	Daniel W. Smith	LA	30
b_4	Charles Williams	Chicago	45

(a)

First Blocker
Q_1: a.City = b.City
C_1: (a_2, b_3), (a_4, b_4), (a_5, b_1)
Debugger Output
Iter. 1: (a_1, b_1), (a_3, b_2), (a_2, b_1)
Iter. 2: (a_5, b_4), (a_1, b_3), (a_1, b_2)
Iter. 3: (a_1, b_4), (a_2, b_2), (a_2, b_4)
(b)
Second Blocker
Q_2: a.City = b.City OR lastword(a.Name) = lastword(b.Name)
C_2: (a_1, b_1), (a_1, b_3), (a_2, b_1), (a_2, b_3), (a_4, b_4), (a_5, b_1)
Debugger Output
Iter. 1: (a_3, b_2), (a_1, b_2), (a_1, b_4) …
(c)
Third Blocker
Q_3: a.City = b.City OR ed(lastword(a.Name), lastword(b.Name)) ≤ 2
C_3: (a_1, b_1), (a_1, b_3), (a_2, b_1), (a_2, b_3), (a_3, b_2), (a_5, b_4), (a_5, b_1), (a_5, b_4)
Debugger Output
Iter. 1: (a_1, b_2), (a_1, b_4), (a_2, b_2) …
(d)

Figure 1: An example to illustrate MatchCatcher

do not match due to misspellings and abbreviation, e.g., "Altanta" vs. "Atlanta", "New York" vs. "NY".

Next, U wants to know if there are any more true matches. Toward this goal, U flags the true matches in the first iteration (i.e., the above two pairs). MatchCatcher *uses this feedback to find the next n pairs judged most likely to be killed-off matches, then shows those pairs in the second iteration (see Figure 1.b, under "Iter 2"). U finds no true matches in this iteration, as well as in the third iteration.*

At this point, U decides to stop looking for more killed-off matches, to focus on revising blocker Q_1 to improve its recall. U observes that the problem with pair (a_1, b_1), which disagree on "City", can be fixed by adding a new hash blocker that blocks on the last word of "Name", i.e., keeps a tuple pair if they agree on this word (which is typically the last name). Figure 1.c shows Q_2, the revised blocker, which is the union of two hash blockers.

Invoking MatchCatcher *for Q_2 produces the list shown under "Debugger Output, Iter 1" in Figure 1.c. This list shows that while the new blocker Q_2 successfully keeps (a_1, b_1), it still kills off (a_3, b_2), a true match. A closer examination reveals that this is due to a mispelt last word: "Welson" vs. "Wilson".*

To fix such misspelling problems, U decides to keep a tuple pair if the last words of "Name" are very similar, e.g., within an edit distance of 2. This produces blocker Q_3 in Figure 1.d. Here, the hash blocker $lastword(a.Name) = lastword(b.Name)$ has been replaced by the more general blocker $ed(lastword(a.Name), lastword(b.Name) \leq 2$, where ed computes the edit distance (Section 2 shows how to execute this blocker efficiently). Invoking MatchCatcher *for Q_3 brings back no true matches, even after several iterations. Thus, user U stops, deciding to use Q_3 as the final blocker for A and B.*

It is important to emphasize that MatchCatcher works with any of the current blocker types. Indeed, it requires as input only the two tables A and B and the set C resulting from applying the target blocker to the tables. Further, MatchCatcher does not estimate the *actual* recall, i.e., the fraction of matches surviving blocking. Doing so would require it to know the set of true matches in $A \times B$, which would be solving the EM problem itself! Indeed, MatchCatcher does *not* attempt to match A and B. Instead, *its goal is to quickly find a large set of plausible matches killed off by the blocker and bring them to the user's attention*, so that the user can examine them to find true matches, get a sense about whether the blocker kills off too many such matches, and if so, what the problems are, so that he/she can fix them. Section 6 shows that real-world users indeed find MatchCatcher very helpful in answering these questions.

Challenges: While promising, developing MatchCatcher raises difficult challenges. First, we must quickly search the vast space $D = A \times B - C$ (where C is the blocker's output) to find plausible matches killed off by the blocker, and we must do so without materializing D. This search is further complicated by the fact that at this point MatchCatcher does not even know what it means to be a match (only the user knows). To address these problems, we observe that matching tuples tend to have similar values for certain attributes (e.g., Name, City). So we convert each tuple into a string that concatenates these attributes, e.g., converting tuple a_1 of Table A in Figure 1.a into "Dave Smith Altanta". We then perform a *top-k string similarity join (SSJ)* to find the k tuple pairs with the highest score with respect to these strings, and output these pairs as plausible matches. The state-of-the-art solution for top-k SSJs [28] proves too slow for our interactive setting. So we develop a new solution that is significantly faster.

Second, to find as many plausible matches as possible, we need to repeat the above procedure, but for different sets of attributes (e.g., find tuple pairs that are similar with respect to Name only, City only, both Name and City, etc.). We cannot consider all such sets, called *configs*, as there are too many. So we develop a solution to find a good set of configs.

Third, we must perform multiple related top-k SSJs, one for each config. This raises the challenge of how to perform them *jointly* across the configs. We develop an efficient solution that perform them in parallel on multiple cores yet reuse computations across the joins.

Finally, top-k SSJs over the configs produce a large set E of plausible matches (e.g., in the thousands). We cannot realistically expect the user to examine all of these matches. So we develop a solution that uses rank aggregation and active/online learning to rank the pairs in E, show the top n pairs to the user, ask him/her to identify the true matches, use this feedback to rerank the pairs, and so on, until the user has been satisfied or a stopping condition is reached. In summary, we make the following contributions:

- We show that debugging blocker accuracy is critical for EM.
- We describe MatchCatcher. As far as we know, this is the first in-depth solution to address the above problem. Our solution advances the state of the art in top-k string similarity joins, and exploits active/online learning to effectively engage with the user.
- Over the past two years, MatchCatcher has been successfully used by 300+ students in data science projects and by 7 teams at 6 organizations. We briefly report on this experience. We also describe extensive experiments showing that MatchCatcher is highly effective in helping users develop blockers, and that it can help improve the accuracy of even the best blockers manually created or automatically learned.

2 DEBUGGING BLOCKER ACCURACY

In this section we show that debugging blocker accuracy is critical for EM, discuss the limitations of current solutions, then provide an overview of the MatchCatcher solution.

Entity Matching (EM): This problem has received significant attention (see [6, 13] for recent books and surveys). Many EM scenarios exist, e.g., matching two tables, matching within a table, matching a table with a knowledge base, etc. [6]. In this paper, as a first step, we will consider the common EM scenario that matches two tables A and B, i.e., finds all tuple pairs ($a \in A, b \in B$) that refer to the same real-world entity.

Types of Blockers: As discussed in the introduction, for large tables A and B we typically perform EM by creating a blocker Q, apply Q to A and B to produce a relatively small set of tuple pairs C, then apply a matcher to pairs in C. Over the past few decades blocking has received much attention. The focus has been on developing different blocker types and scaling up blockers, e.g., [11, 17, 20, 23, 27] (see [7] for a survey).

Many blocker types have been developed. MatchCatcher works with all of them. In what follows we briefly discuss the most important types, as Section 6 experiments with many of them.

Well-known blocker types are attribute equivalence, hash, and sorted neighborhood. *Attribute equivalence (AE)* outputs a pair of tuples if they share the same values of a set of attributes (e.g., blocker Q_1: $a.City = b.City$ in Figure 1.b). *Hash blocking* (also called *key-based blocking*) is a generalization of AE, which outputs a pair of tuples if they share the same hash value, using a pre-specified hash function. For example, blocker Q_2 in Figure 1.c combines the hash blocker $lastword(a.Name) = lastword(b.Name)$ and the AE blocker Q_1. *Sorted neighborhood* outputs a pair of tuples if their hash values (also called *key values*) are within a pre-defined distance.

More complex types of blockers include similarity-based and rule-based [6, 8, 17]. *Similarity-based blocking (SIM)* is similar to AE, except that it accounts for dirty values, mispellings, abbreviations, and natural variations by using a predicate involving string similarity measures, such as edit distance, Jaccard, overlap, etc. [30]. Examples include blocker $ed(lastword(a.Name), lastword(b.Name) \leq 2$, which outputs tuple pairs where the last words of their names have an edit distance of at most 2, and blocker $jaccard(a.title, b.title) \geq 0.4$, which outputs pairs of books whose titles have a Jaccard similarity score of at least 0.4. *Rule-based blocking* is perhaps most general. It outputs a tuple pair satisfying a rule or a set of rules encoding domain heuristics, e.g., blocker Q_3 in Figure 1.d consists of two rules. Such blockers can be viewed as the union of multiple blockers, one per rule.

Other types of blockers include phonetic (e.g., soundex), suffix-array, canopy, etc. (see [6, 13] for an extensive discussion).

Efficient Execution of Blockers: Efficient techniques have been developed to execute the above blocker types, both on a single machine and a cluster of machines (e.g., [8, 11, 17, 20, 23]). To execute hash/AE blocking, we partition the tuples in A and B into *blocks*, such that all tuples in each block share the same hash value, then output only pairs of tuples that are in the same block.

To execute a SIM blocker, such as $ed(lastword(a.Name), lastword (b.Name) \leq 2$, we build an index I (e.g., prefix filtering index [30]) on the tuples in A, say. Next, for each tuple $b \in B$, we consult I to identify all tuples $a \in A$ such that the pair (a, b) can possibly satisfy $ed(lastword(a.Name), lastword(b.Name) \leq 2$. We check if (a, b) indeed satisfies this predicate, and if yes, then output the pair. Many efficient string indexing techniques [30] can be used to implement SIM blockers. Recent work [8] has also discussed efficient techniques (e.g., using indexing and MapReduce) to execute rule-based blockers.

Accuracy of Blockers: Blocker accuracy is typically measured using recall, defined as follows:

Definition 2.1. [Blocker recall] Suppose applying blocker Q to two tables A and B produces the output C. Let $M \subseteq A \times B$ be the (unknown) set of true matches between A and B, then $recall(Q) = |M \cap C|/|M|$.

Due to dirty data, misspellings, natural variations, synonyms, missing values, etc., no single blocker type produces the highest recall on all datasets. In fact, on any particular dataset, blockers can vary drastically in recalls (e.g., 2.5-98.2% in our experiments).

Finding a blocker with high recall (ideally 100%), however, is critical for many EM applications. Counter-terrorism EM applications often need very high coverage., i.e., finding *all* person descriptions that match, and thus want 100% blocking recall. Similar high-coverage examples arise in fraud detection, e-commerce, law, medicine, insurance, and pharmaceutical industry, among others. EM applications with inherently small numbers of matches naturally do not want the blocker to kill off many of these. Finally, EM applications often compute statistics over the matches (e.g., the percentage of patients attending both hospitals), which can be seriously distorted by blockers with low recall.

Limitations of Current Work: As a result, the topic of blocker accuracy has received growing attention. Proposed solutions include combining multiple blockers to maximize recall (e.g., [12, 18, 20]), and using a sample of tuple pairs labeled as match/no-match to learn blockers with high recall [2, 8, 17, 21].

While promising, these solutions can still produce blockers with varying recalls, oftentimes falling short of 100%. For example, a recent work [8] shows that extensive manual effort to combine hash blockers achieves only 38.8% and 72.6% recall on two datasets. (Obviously we cannot combine *all* possible blockers as there are too many of them.) Another recent work [17] learns blockers using samples labeled by crowdsourcing, but achieves only 92% recall on a data set. In general, due to the difficulties in obtaining a good sample, sampling flukes, etc., today there is still no guarantee that a blocker learned on a *sample* provably achieves high recall when applied to the original tables.

Since there is still no “fool-proof” method to develop a blocker with high recall, it follows that given a blocker Q (either created manually or learned), it is still highly desirable to know how well Q does recall-wise, and what the possible problems are, so that we can improve it. MatchCatcher helps answer these questions, and thus can be considered *complementary* to the above solutions. For example, Section 6 describes a scenario where after the solution in [8] had been used to learn a blocker, we applied MatchCatcher to this blocker and uncovered multiple problems, which can be addressed to further improve the blocker recall.

Overview of MatchCatcher: As discussed, MatchCatcher addresses the following problem:

Definition 2.2. [Finding killed-off matches] Let C be the output of applying blocker Q to tables A and B. Then $D = A \times B - C$ is the set of all pairs killed off by Q. Quickly find as many true matches as possible in D (without materializing it). This helps the user understand how well Q does recall-wise, and what can be done to improve its recall.

Figure 2 shows the architecture of MatchCatcher. Given two tables A and B, the Config Generator examines the two tables to generate a set of configs, each of which is a set of attributes (e.g., $\{Name, City\}$). For each config g, the Top-k SSJs module performs a top-k string similarity join to find the k tuple pairs that (a) have the highest score with respect to the attributes in g, and (b) are killed off by blocker Q. Note that to check Condition (b), this module does not need to know Q. It only needs to know C, the output of applying Q to A and B. Hence MatchCatcher works independently of the blocker type.

The Top-k SSJs module sends all top-k lists (one per config) to the Match Verifier. This module uses a rank aggregator to combine the lists into a single global list, shows the top n pairs to user U, asks U to identify true matches, uses this feedback together with active and online learning to rerank the pairs, and so on, until U is satisfied or a stopping condition is met. U can examine the true matches to understand how well blocker Q does recall-wise, and to obtain explanations for why these matches are killed off. This helps U decide if Q should be revised, and if so, then how. The next few sections describe MatchCatcher in detail.

3 GENERATION OF CONFIGURATIONS

We now describe the Config Generator, which outputs a set of configs, each being a set of attributes. We cannot consider all possible configs, so the key challenge is to select a good subset of configs. We show how to do so, by carefully managing attributes with many missing values, few unique values, or long string values.

3.1 How Configurations Are Used

We first motivate the notion of configurations (or "configs" for short) and explain how they are being used. Later we build on this to discuss how to select a good set of configs.

Recall that we want to quickly search $D = A \times B - C$, the set of tuple pairs killed off by blocker Q, to find pairs that can be matches. This raises three problems. First, D is not materialized, we only have A, B, and C. Second, even if D is materialized, it would be too large to search quickly. Finally, we do not even know what to search for, since at this point MatchCatcher does not know what a match is (only the user knows).

To address these problems, we begin by assuming that tables A and B share the same schema S (MatchCatcher can be trivially extended to the case of different schemas). We observe that matching tuples tend to share similar values in a set of attributes, say g (e.g., $\{Name, City\}$). So we want to quickly find tuple pairs in D that share similar values for g and return those as possible matches.

To do so, we convert each tuple a in A into a string $str_g(a)$ that concatenates the values of all attributes in g. For example, if a is (David Smith, Atlanta, 43) and $g = \{Name, City\}$, then $str_g(a)$ is "David Smith Atlanta". This converts Table A into a set A_g of such strings. We convert Table B into a set B_g of strings similarly.

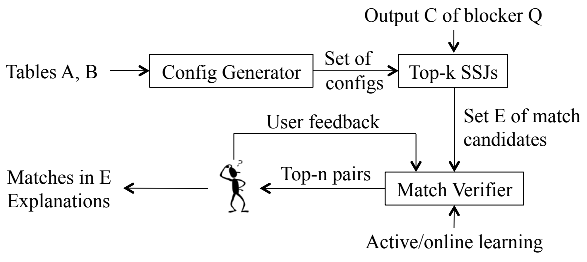


Figure 2: The MatchCatcher architecture

Let $h(x, y)$ be a string similarity measure which computes a score in $[0, 1]$ between two strings x and y. Examples of such measures are Jaccard, cosine, overlap, edit distance, etc. [30]. Then next we perform a top-k string similarity join (SSJ) between A_g and B_g to find the k tuple pairs in $A \times B$ with the highest $h(x, y)$ score. Techniques have been developed to quickly perform top-k SSJs [28, 31]. Of course, our goal is not to find pairs in $A \times B$, but rather in $D = A \times B - C$. We can modify the above techniques slightly to ensure this, by dropping a found pair if it is in C. We then return the k pairs in D with the highest $h(x, y)$ score as possible matches.

The above procedure does not require a materialized D, only tables A, B, and C (the output of blocker Q). It can quickly search D using a modified version of top-k SSJs to return possible matches. Of course, at this point we still do not know if these are indeed matches. But later we can work with the Match Verifier to quickly shift through them to find true matches, if any. We now discuss several important aspects of the above procedure.

Why Concatenating the Attributes? We can use a variety of methods to find tuples that share similar values for attributes in g, e.g., finding pairs that share similar values for *each* attribute in g, then taking their intersection, say. However, given the interactive nature of debugging, we want this step to be as fast as possible. Hence we decide not to treat the attributes in g separately, but concatenate all of them into a single string, then compare them using SSJs. Section 4 shows that this method can quickly search a very large set D. But a drawback is that we can return *false positives* such as tuple pair (Jim Madison, Smithville, 32) and (Jim Smith, Madison, 32), because their concatenated strings are very similar given certain similarity measures. Such false positives, however, can be "weeded out" in the Match Verifier, using user feedback and active/online learning (see Section 5).

Which String Similarity Measure to Use? Given that similar attribute values can still vary significantly (e.g., "Dave Smith" vs "David Frederic Smith"), we believe that measures that treat strings as sets (e.g., Jaccard, cosine, etc.) work better than those that treat strings as sequences of characters (e.g., edit distance). So for MatchCatcher, we use the well-known Jaccard measure that tokenizes two strings x and y into two sets of words P_x and P_y, then returns $|P_x \cap P_y|/|P_x \cup P_y|$ [28]. However, Theorem 4.2 shows that our solution can also work with other set-based similarity measures, namely overlap, cosine, and Dice [28].

Why Multiple Configurations? So far we have used just one config g to find match candidates. Using multiple configs, however, can produce more matches. For example, config $\{Name, City\}$ may not return the pair (David Smith, Seattle) and (Dave Smith,

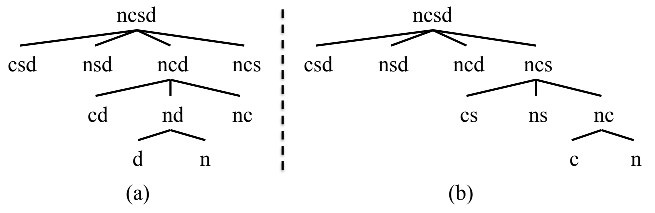


Figure 3: An example of generating config trees.

Redmond) because the cities are different. Config $\{Name\}$ however can. Conversely, config $\{Name\}$ may not return the pair (Chuck Smith, San Francisco) and (Charles F. Smith, San Francisco) because the names are too different, but config $\{Name, City\}$ can. Together, these two configs can return more matches than either of them in isolation. Generating a good set of configs however is a major challenge, which we address next.

3.2 Generating Multiple Configurations

As a baseline, we can use all subsets of attributes in S (the schema of A and B) as configs. But this generates too many configs even for a moderate size (e.g., $|S| = 10$ produces $2^{|S|} - 1 = 1023$ configs). We cannot use all of them because the total SSJ time would be too high. So we must select a smaller set of configs.

To do so, we select a set of promising attributes in S, then use them to generate configs, in a top-down fashion. In each step of the process, we select which configs to generate next by carefully considering the impact of attributes with many missing values, few unique values, or long string values. The end result is a *config tree* consisting of multiple configs. Later the Top-k SSJs module will traverse this tree to perform top-k SSJs on the configs in a joint fashion. We now elaborate on these steps.

Selecting the Most Promising Attributes: We first classify attributes in S as string, numeric, categorical, and boolean, using a rule-based classifier. Next, we drop numeric attributes (e.g., Salary, Price) because matching tuples still often differ in their values (e.g., the same product having different prices). Finally, we drop categorical and boolean attributes whose appearances in tables A and B are different. For example, if Gender has values $\{Male, Female\}$ in A but $\{M, F, U\}$ in B, then we drop it as these two sets share no value (in general if the Jaccard score of these two sets is less than a pre-specified threshold then we drop the attribute). The remaining attributes are string, or categorical/boolean but with similar sets of values. We return these as T, the set of the most promising attributes to be used for config generation. (Of course, the user can also manually curate schema S to generate T. The experiments in Section 6 however do not involve any manual curation.)

Generating a Config Tree: Given the set T of promising attributes, we generate a *config tree* in a top-down fashion, then return all configs in the tree. Specifically, we start with T as the config at the root of the tree. Next, we "expand" this node by removing each attribute from T to obtain a smaller config of size $|T| - 1$. This produces $|T|$ new configs, which form the nodes at the *next level* of the tree. We then select just one node at this level to "expand" further, and so on (we will discuss how to select shortly). This continues until we have reached configs of just one node. Figure 3.a shows an example config tree, assuming $T = \{n, c, s, d\}$ (which stand for Name, City, State, and Description, respectively).

Intuitively, this strategy ensures that we generate a diverse set of $|T|(|T| + 1)/2$ configs of varying size $|T|, |T| - 1, \ldots, 1$. The config tree will also be used to guide the joint execution of top-k SSJs on the configs (see Section 4.2). We now turn to the challenge of how to select a node to expand in the config tree.

Managing Many Missing Values and Few Unique Values: Consider again the config tree in Figure 3.a. Suppose we are currently at the second level of the tree, and need to select one node among the four nodes *csd*, *nsd*, *ncd*, and *ncs*, to expand. This selection is equivalent to *selecting an attribute to exclude from subsequent config generation.* Indeed, if we exclude attribute s, then we select node *ncd* to expand (as shown in the figure). Otherwise if we exclude d, then we select the rightmost node *ncs* to expand, and so on.

So which attribute should we exclude? We observe that if an attribute has many missing values, then keeping it for subsequent config generation is not desirable, because we will end up with configs that produce similar top-k lists. For example, suppose we have selected config *ncd* to expand (as shown in Figure 3.a), and suppose that d has many missing values, then many strings for config *ncd* and config *nc* will be identical, potentially leading to similar top-k lists. In the extreme case, if all values for d are missing, then these two top-k lists are identical. Clearly, we want different configs to produce substantially different top-k lists, to avoid redundant work and to maximize the number of matches we can retrieve.

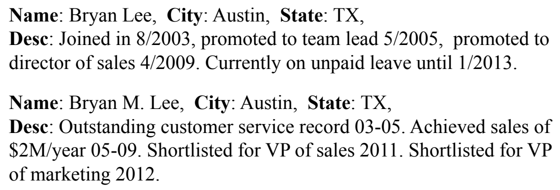
Another observation is that if an attribute has more unique values than another, e.g., c vs s (which stand for City and State, respectively), then it is better to exclude s, the one with fewer unique values, because intuitively, if two tuples agree on c, they are more likely to match than if they agree on s, all else being equal. Thus, to maximize the number of matches we can retrieve, we should strive to keep the "more specific" attributes, i.e., the ones with more unique values.

Combining the above two observations, we define the e-score (shorthand for "expected benefit") of an attribute as follows:

Definition 3.1. [E-score of an attribute] Let $n_A(f)$ be the ratio of the number of non-missing values of attribute f in A over the number of tuples in A, and $u_A(f)$ be the ratio of number of unique values of f in A over the number of non-missing values of f in A. We define $n_B(f)$ and $u_B(f)$ similarly. Define $e_A(f) = 2n_A(f)u_A(f)/[n_A(f)+u_A(f)]$ and define $e_B(f)$ similarly. Then we define the e-score of attribute f as $e(f) = e_A(f)e_B(f)$.

We then select the attribute with the lowest e-score to exclude at each level of the config tree. For example, suppose $e(n) > e(d) > e(c) > e(s)$. Then at the second level of the tree in Figure 3.a, we exclude attribute s, which means selecting node *ncd* to expand. At the third level of the tree, we exclude c, which means selecting node *nd* to expand.

Managing Long String Attributes: Many datasets contain attributes with long string values, e.g., Comment, Desc, etc. Figure 4 shows two tuples where attribute Desc has such long values. Such long attributes can cause two problems. First, they can cause multiple configs to generate very similar top-k lists.



Name: Bryan Lee, **City**: Austin, **State**: TX,
Desc: Joined in 8/2003, promoted to team lead 5/2005, promoted to director of sales 4/2009. Currently on unpaid leave until 1/2013.

Name: Bryan M. Lee, **City**: Austin, **State**: TX,
Desc: Outstanding customer service record 03-05. Achieved sales of \$2M/year 05-09. Shortlisted for VP of sales 2011. Shortlisted for VP of marketing 2012.

Figure 4: Examples of tuples with long string attributes.

Example 3.2. Consider again the config tree in Figure 3.a. Suppose attribute d has long string values (such as those shown in Figure 4). Then all seven configs involving d can generate similar top-k lists because the long values of d "overwhelm" the short values of the remaining attributes. So when moving from a config involving d to another (e.g., from ncd to nd), the strings do not change much, and therefore their similarity scores also do not change much (we formalize this notion below), leading to similar top-k lists.

The second problem is that if the long string values are different for matching tuples, then a config involving this long attribute will fail to return the match. For example, the two tuples in Figure 4 match, but any config involving attribute Desc will not return this match, because the values for Desc here are very different, and so the score between the two tuples will be low.

To address this, we modify our config-tree generation procedure as follows. Suppose we need to select a config node in the tree to expand. Before, we select $g_{default}$, the one without the attribute with the smallest e-score. Now, we first run a procedure FindLongAttr to see if there is any attribute that is "too long" (i.e., likely to adversely affect selecting good configs). If such an attribute f_{long} exists, then we select the config without f_{long} to expand. Otherwise we select $g_{default}$, as usual.

Example 3.3. Consider again Figure 3.a, which shows the "default" config tree with root ncsd. To handle long attributes, once we are at the second level, we do not automatically select ncd (the config without s, the attribute with the smallest e-score) for expansion. Instead, we run FindLongAttr *at this level. Suppose it returns d (thus judging d to be too long). Then we select ncs, the config without d, for expansion. This produces new configs cs, ns, and nc (see Figure 3.b). Suppose running* FindLongAttr *at the level of these new configs returns no attribute. Then we select config nc (the config without s, the attribute with the smallest e-score) for expansion (see Figure 3.b).*

We now explain procedure FindLongAttr. The key challenge is to formalize what it means to be "too long". Let p be a node in the config tree. Suppose that when running the default config generation procedure (the one that does not consider long attributes), we end up selecting q, a child node of p, for expansion, and that we eventually generate a subtree T_q rooted at q (see Figure 5.a).

We say that an attribute f is too long if it "overwhelms" many config nodes in subtree T_q, specifically if it overwhelms at least half of the configs in $F(T_q)$, the set of configs in T_q that contain f. In turn, we say that f overwhelms a config $r \in F(T_q)$ (see Figure 5.a) *if the top-k list obtained from config r is "roughly the same" as the top-k list obtained from config q (we formalize this below).* Intuitively, we want to avoid such cases, because we want each config to return a different top-k list, to maximize the number of true matches that we will find. So if we find that f overwhelms at least half of the

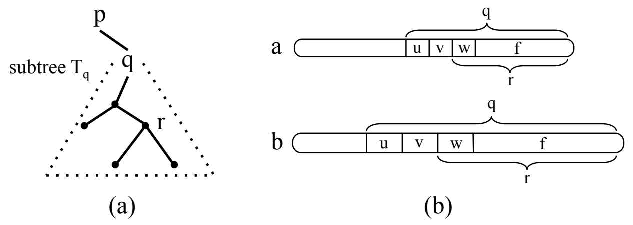


Figure 5: Finding attributes judged too long.

configs in $F(T_q)$, then we judge f to be too long and should be removed. That is, instead of selecting q for expansion, we will select the config (in the same tree level as q) that does not contain f.

Of course, we do not have access to the top-k lists of r and q. So we develop a condition which if true would suggest that the two lists are "roughly the same". Specifically, let $sim_g(a,b) = h(str_g(a), str_g(b))$ be the string similarity function between the string values of two tuples a and b, for config g. Suppose that for all tuple pairs (a,b) in $D = A \times B - C$ we have

$$\textit{Condition } 1: |sim_q(a,b) - sim_r(a,b)|/sim_q(a,b) \leq \alpha,$$

for a small pre-specified α value, say 0.2. Then we can say that when we switch config from q to r, the score of each tuple pair does not change much, so the top-k list for r will stay roughly the same as that of q.

Checking Condition 1 for all pairs (a,b) in D is not feasible. Hence we perform a theoretical analysis for an idealized scenario (described below). Of course, this idealized scenario rarely happens in practice. But understanding it helps us come up with an efficient heuristic to check Condition 1.

Let $L_f(a)$ be the length (i.e., the total number of words) of attribute f in tuple a, $L_q(a)$ be the sum of the lengths of all attributes in q, for tuple a, and so on. The idealized scenario assumes that (a) attribute f takes the same proportion of the total length of q in both a and b, i.e., $L_f(a)/L_q(a) = L_f(b)/L_q(b) = \beta$, and (b) the remaining length of q is equally distributed among the remaining attributes of q, i.e., $L_k(a) = [(1-\beta)L_q(a)]/(|q|-1)$ for all attribute k in $q - \{f\}$, and the same condition applies to tuple b.

Example 3.4. Consider the two tuples a and b in Figure 5.b, where $q = \{u, v, w, f\}$ and $r = \{w, f\}$. We assume that $L_f(a)/L_q(a) = L_f(b)/L_q(b) = \beta$, and $L_u(a)/L_q(a) = L_v(a)/L_q(a)$ and $L_u(b)/L_q(b) = L_v(b)/L_q(b)$.

Then we can show that (see Appendix H for a proof sketch):

Theorem 3.5. *Let $a \in A$ and $b \in B$ be two tuples that satisfy the above assumptions. If*

- (R_1) $sim_q(a,b) \geq [\sqrt{(1+\alpha)^2 + 8} - (1+\alpha)]/4$, *and*
- (R_2) $\beta \geq 1 - \frac{(|q|-1)}{|q \backslash r|} \cdot \frac{\alpha}{(1+\alpha)} \cdot \frac{max\{L_q(a), L_q(b)\}}{L_q(a)+L_q(b)}$,

then pair (a,b) satisfies Condition 1.

Intuitively, this theorem says that if $sim_q(a,b)$ is sufficiently high (Requirement R_1), and attribute f is sufficiently long (Requirement R_2), then $sim_r(a,b)$ will be close to $sim_q(a,b)$. It is not difficult to show that the quantity on the right-hand side of R_1 is upper bounded by 0.5. In practice, we observe that users typically examine only the *top few tens of pairs* in each top-k list (see Section 5), and that if these pairs are true matches, their scores often exceed 0.5, making R_1 true. As a result, if R_2 is also true, then attribute f is long enough to "overwhelm" these pairs. That is, these pairs will change little score-wise when switching from config q to r, thus typically will still show up in the top few tens of pairs of the top-k list for r, an undesirable situation.

To avoid such situations, we will focus on checking R_2. Checking R_2 for many pairs (a, b) is not practical. So we approximate this checking using average lengths, i.e., we (a) replace the quantity β in the left-hand side of R_2 with $min\{AL_f(A)/AL_q(A), AL_f(B)/AL_q(B)\}$, where $AL_f(A)$ for example is the average length of attribute f in Table A, and (b) replace $L_q(a)$ and $L_q(b)$ in the right-hand side of R_2 with $AL_q(A)$ and $AL_q(B)$, respectively.

Procedure FindLongAttr then works as follows. Suppose we have selected config q for expansion (because it does not contain s, the attribute with the least e-score). Then for each attribute f (other than s), we (a) identify $F(T_q)$, the set of configs in T_q that contain f, (b) declare f "too long" if the above approximate checking is true for at least half of the configs $r \in F(T_q)$. It is not difficult to prove that at most one attribute f will be found too long. If so, we do not select q, but select instead the config that does not contain f for expansion. Otherwise, we select q, as usual. This procedure takes less than a second in our experiments.

Discussion: Note that we do not completely remove attributes with many missing values, few unique values, or long values from config generation. Instead, each such attribute f may be removed *only at some point* during the generation process. Configs generated earlier still contain f.

Further, our work here is related to, but very different from work such as [3, 9, 15]. Those works find attributes that are discriminative for classification, often using a labeled sample (as many works in learning do). Here we do not look for discriminative attributes. Instead, we look for attributes such that if two tuples agree on their values, then they are likely to match. For example, suppose all tuples in table A have the same value "US" for "Country", and all tuples in table B have the same value "Canada". Then "Country" is a discriminative attribute because if two tuples disagree on it, they definitely do not match. For our purpose, however, "Country" has little expected benefits, because if two tuples agree on it, it is still not likely that they match (not as much as if they agree on "State" and "City" say).

In fact, the work [25] also treats attributes with missing values and few unique values in a way similar to ours (for blocking and matching). However, it does not handle long attributes, and uses only one config, and thus is significantly outperformed by MatchCatcher (see Section 6).

4 TOP-K STRING SIMILARITY JOINS

So far we have discussed generating a set of configs. We now discuss performing top-k SSJs over these configs (one per config). Previous work has discussed top-k SSJs for a single config [28]. Here we significantly improve that work (and our solution can be applied to top-k SSJ situations beyond this paper). We then discuss executing multiple top-k SSJs jointly, by reusing results across the configs, in a parallel fashion.

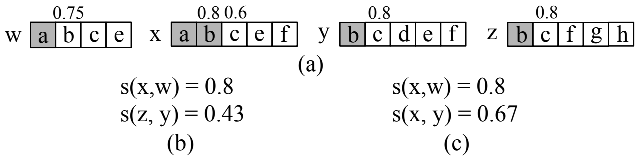


Figure 6: An illustration of top-k computation.

It is important to note that all SSJ algorithms discussed below (including ours) work with the set-based similarity measures Jaccard, cosine, overlap, and Dice [28]. For ease of exposition, however, we will explain them using the Jaccard measure.

4.1 Improving Top-k Join for a Single Config

As far as we can tell, the state of the art in top-k SSJs is TopKJoin [28]. Given a set J of strings, TopKJoin finds the k string pairs with the highest similarity scores, for a pre-specified k, in a branch-and-bound fashion. Specifically, it maintains a prefix for each string in J, incrementally extends these prefixes, finds string pairs whose prefixes overlap, computes their similarity scores, use these scores to maintain a top-k list, then extends the prefixes again, and so on.

Example 4.1. Suppose J consists of the four strings w, x, y, z in Figure 6.a. We begin by creating a prefix $p(w)$ = "a" for w, then a prefix $p(x)$ = "a" for x. At this point the prefixes of the pair (x, w) overlap. Hence we compute the Jaccard score 0.8 for this pair, then initializes the top-k list K to be containing just this pair. (Here we assume $k = 2$.)

Next, we create prefix $p(y)$ = "b". This does not produce any new pair whose prefixes overlap. So we continue by creating prefix $p(z)$ = "b". This produces a <u>new</u> pair whose prefixes overlap: (z, y) with score 0.43. Figure 6.b shows the updated top-k list K.

Next, we select one prefix to extend (we will discuss shortly how). Suppose we select $p(x)$ and extend it by one token. Then $p(x)$ = "ab" (see Figure 6.a). This produces two new pairs whose prefixes overlap: (x, y) with score 0.67 and (x, z) with score 0.43. Figure 6.c shows the updated top-k list K. We then select another prefix to extend, and so on. Finding new pairs with overlapping prefix can be done efficiently using an inverted index from token to the prefixes of the strings [28].

We now discuss how to select a prefix to extend. Suppose we have imposed a global ordering on all tokens, and sorted the tokens in each string w, x, y, z in that order (see Figure 6.a). Suppose also that we have created prefixes of size 1, namely $p(w)$ = "a", $p(x)$ = "a", $p(y)$ = "b", $p(z)$ = "b", and are now deciding which prefix to extend. Suppose we select $p(w)$ and extend it by one token, to be "ab". Then it is easy to show that the scores of all *new* pairs generated by this extension are capped by 0.75. Indeed, any *new* pair must involve w. Let such a pair be (w, v). Then the first common token that they share should be "b" (the token just being added to $p(w)$). So they can share at most this token b and the remaining "unseen" tokens of w. Thus $|w \cap v| \leq 3$. Since $|w \cup v| \leq |w| = 4$, it follows that the Jaccard score of (w, v) is capped by 3/4=0.75. We write 0.75 on top of token "b" in w to indicate that when we extend $p(w)$ to include this token, the score of any *new* pair generated by TopKJoin will be *capped* by 0.75. Similarly, we can write 0.8 for the second tokens of x, y, z (see Figure 6.a).

We then select the prefix that when extended will include the token with the highest "cap" number (in the hope that it will generate new pairs with the highest possible scores). In this case, we select $p(x)$ (but $p(y)$ and $p(z)$ also work).

We now discuss how to stop. Observe that the "cap" number for "c" in x is 0.6. By the time we have to consider whether to extend $p(x)$ to include "c", the top-k list already has a lower-bound score of 0.67 (see Figure 6.c), greater than 0.6. As a result, we do not have to extend $p(x)$ to include "c", and in fact, prefix extension on x can be stopped at this point. TopKJoin terminates when all prefix extensions have stopped, either early (as described above) or because the prefix has covered the entire string. The paper [28] describes TopKJoin in detail, including optimizations to avoid redundant computations.

The QJoin Algorithm: TopKJoin has a major limitation. Every time it generates a new pair (u, v), it immediately computes the similarity score of (u, v) (then updates the top-k list). Computing this score turns out to be very expensive, especially if u and v are long strings. In a sense, it is also "premature", because it can be shown that when we generate (u, v) (as a new pair), we only know that they share a *single* token. There is no evidence yet that they share more tokens and thus are likely to have high similarity score. If they indeed share only one or few tokens, and yet we still compute their score, then that score is likely to be low. So the pair will not make it into the top-k list, yet we have wasted time computing it score.

To address this problem, when generating new pairs, we do not immediately compute their scores. Instead, we keep track of the number of common tokens each pair has, and update this number whenever a prefix is extended. We then compute the score of a pair only if it has q common tokens, and thus is likely to have a high score. It is difficult to select q analytically, so we select it empirically as follows. Assuming at least four CPU cores, we begin by running the modified TopKJoin for $q = 1$, $q = 2$, etc., on all cores, one q value for each core, for $k = 50$. (Note that TopKJoin always does $q = 1$.) Then whichever core finishes first, we keep the process on that core running to produce the rest of the top-k list (effectively selecting the q value associated with that core), and kill the processes on the other cores.

It is straightforward to adapt the above algorithm to work with two tables (instead of just one), and to remove a pair from the top-k list (during the top-k computation) if it happens to be in the candidate set C. Henceforth we refer to this new algorithm as QJoin.

4.2 Joint Top-k Joins Across All Configs

TopKJoin can only be applied to a single config [28]. Our setting however involves multiple related configs. We now describe a solution to find top-k lists *jointly across the configs*. To do so, we use QJoin, but modify it to reuse similarity score computations and top-k lists across the configs, and process the configs in parallel.

Reusing Similarity Score Computations: As discussed in Section 4.1, computing the similarity score of a pair (a, b) is very expensive, especially for long strings. Hence, we want to reuse such computations across the configs. To do so, we process the configs in the config tree in a breadth-first order, e.g., processing the root

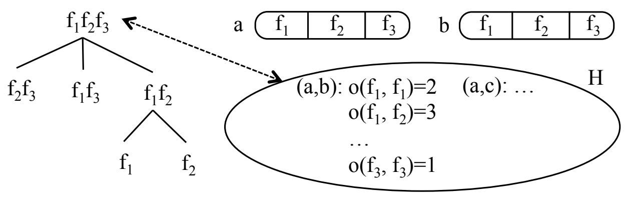


Figure 7: Reusing across top-k computations.

config $f_1 f_2 f_3$ of the config tree in Figure 7 (where the f_i-s are attributes), then the next-level configs, $f_2 f_3, f_1 f_3, f_1 f_2$, and so on.

When processing a config g (i.e., finding its top-k list), we keep track of certain information, then reuse it when processing configs in the subtree of g. For example, consider again the config tree in Figure 7. We start by tokenizing the strings wrt the root config $f_1 f_2 f_3$ into multisets of word-level tokens. Next, we process the config $f_1 f_2 f_3$. This process computes the Jaccard score of multiple tuple pairs. When computing the score of such a pair, say (a, b), we compute and store the number of overlapping tokens between any two attributes f_i of a and f_j of b in an in-memory database H. Figure 7 illustrates this step. Here, $o(f_1, f_1) = 2$ means attributes f_1 of a and f_1 of b share two tokens. (We only store in H attribute pairs that share tokens.)

Then we can reuse H to drastically speed up processing configs in the subtree rooted at $f_1 f_2 f_3$. For example, consider processing config $f_1 f_2$. If during this process we need to re-compute the score of (a, b) (now with respect to only f_1 and f_2), then we can use H to compute $Overlap_{f_1 f_2}(a, b) = o(f_1, f_1) + o(f_1, f_2) + o(f_2, f_1) + o(f_2, f_2)$, then compute the above score as

$$Overlap_{f_1 f_2}(a, b)/(L_{f_1 f_2}(a) + L_{f_1 f_2}(b) - Overlap_{f_1 f_2}(a, b)),$$

where $L_{f_1 f_2}(a)$ for instance is the length in tokens of the concatenation of f_1 and f_2 for a. Computing the score of (a, b) this way is far faster than computing from scratch.

Note that while processing config $f_1 f_2$, if we have to compute the score of a new pair (c, d) not yet in H, then we will store similar overlap information for (c, d) in H, to enable reuse when processing configs in the subtree rooted at $f_1 f_2$, and so on.

Reusing Top-k Lists: When applying to a config g, algorithm QJoin starts with an empty top-k list K, then gradually grows K as it iteratively expands the prefixes. In our setting, however, since we process multiple configs, a promising idea is to use the top-k list of a previous config to initialize the top-k list of the current config.

For example, after processing config $g = f_1 f_2 f_3$ (Figure 7), we store its top-k list K_g. Then when processing config $h = f_1 f_2$, we use the database H described earlier (which stores overlap information) to re-adjust all scores in K_g. This is necessary because these scores are computed wrt $f_1 f_2 f_3$, but now we want them to be adjusted to consider only $f_1 f_2$. This re-adjustment is fairly straightforward (and inexpensive) because the overlap information for all pairs in K_g should already be in H. Next, we run the algorithm QJoin as usual to process config $h = f_1 f_2$, but using the K_g list with the adjusted scores as the initial top-k list K_h (instead of using an empty list).

Observe that the above procedure enables reusing top-k lists from a parent to a direct child (e.g., from $f_1 f_2 f_3$ to $f_1 f_2$). Reusing across the "siblings" appears much more difficult. For example, given the top-k list for $f_1 f_3$, there is no obvious way to quickly adjust its scores for f_1f_2, using database H. Hence, currently we do not yet consider such sibling reuse.

Finally, reuse does not come for free. It helps avoid computing certain similarity scores from scratch, but incurs an overhead of storing and looking up the overlap information. If the tuples are short, then the overhead can easily overwhelm the savings. As a result, we trigger reuse only if the average tuple length is at least t tokens (currently set to 20).

Parallel Processing of the Configs: Finally we explore parallel processing on multiple cores. (We consider multicore single machines for now because many data analyst users do not know how to use a machine cluster.) An obvious idea is to process each config across multiple cores. For example, we can split Table A into two halves A_1 and A_2 and Table B into B_1 and B_2, find the top-k list for A_1 and B_1 on the first core, the top-k list for A_1 and B_2 on the second core, etc., then merge the top-k lists. In practice, this approach suffers from severe skew: one core finishes quickly while another runs forever. While it is possible to split the tables intelligently to mitigate skew, this adds considerable overhead and implementation complexity.

As a result, we opted for processing one config per core. Specifically, we traverse the config tree breadth-first, and assign configs to cores in that order (when a core finishes, it gets the next config "in queue"). This solution *continuously utilizes all cores.* But it raises two problems. First, two configs (e.g., $f_1f_2f_3$ and f_1f_2) may concurrently write, or one reads and the other writes, into database H, causing concurrency control issues. To address concurrent writes, observe that only configs with non-empty subtrees (e.g., $f_1f_2f_3$ and f_1f_2 in Figure 7) will write. For each such config g, we require it to write into a separate in-memory database H_g.

To address dirty reads (e.g., $f_1f_2f_3$ writes into a database while f_2f_3 reads from it), we note that here each "write" just *inserts* a value; it never modifies or deletes. For such cases there are atomic hashmaps that perform *atomic inserts*, thus avoiding dirty reads. So we implement each database H_g as one such hashmap (using the Atomic Unordered Hashmap in Facebook's C++ Folly package).

Finally, if a parent config, e.g., $g = f_1f_2f_3$, has not yet finished, then a direct-child config, $h = f_1f_2$, cannot reuse g's top-k list. In such situations, we start config h with an initial empty top-k list. When config g finishes, it sends its top-k list to h. Config h merges its current top-k list with the new top-k list from g, to obtain a potentially better top-k list, then continues. Appendix A shows the pseudo code of the complete algorithm, and the following theorem shows its correctness (see Appendix I for a proof sketch):

THEOREM 4.2. *Given two tables A and B, the output C of a blocker on A and B, a set of configs G, a string similarity measure which is Jaccard, consine, overlap, or Dice, and a value k, the algorithm described in Appendix A returns a set of top-k lists, where each top-k list is the output of applying Algorithm* QJoin *to A, B, and C, using a config g ∈ G and the given similarity measure and k value.*

5 INTERACTIVE VERIFICATION

So far we have discussed processing configs to obtain a set of tuple pairs. We now discuss identifying true matches in this set, via user engagement, rank aggregation, and active/online learning.

L_1	L_2	L_3	$L*$
a: 1.0 (1)	a: 0.9 (1)	b: 0.8 (1)	a (1)
b: 0.8 (2)	c: 0.7 (2)	a: 0.5 (2)	b (2)
c: 0.8 (2)	d: 0.6 (3)	c: 0.3 (3)	c (2)
d: 0.6 (4)		d: 0.2 (4)	d (4)

Figure 8: Combining top-k lists using MedRank.

Engaging the User: Let E be the union of the top-k lists obtained from processing all configs. Typically E is large (e.g., 3,011-7,089 in our experiments) and the true matches make up just a small portion of E. Thus expecting a user U to be able to examine the entire set E to find true matches is unrealistic.

A reasonable solution is to rank the pairs in E such that the true matches "bubble" to the top, then present the ranked list to U. However, our experiments with a variety of ranking methods (see below) suggest it is very difficult to do so. Typically, the top of the ranked list indeed contains multiple matches. But then the remaining matches tend to be scattered far and wide in the list.

As a result, we decided to engage user U: we rank the pairs in E, present the top-n pairs to U (currently $n = 20$), ask U to identify the true matches, use this feedback to rerank the list, then present the next top-n pairs to U, and so on. As such, we help U iteratively identify true matches, but use this identification to help "bubble" the remaining matches to the top of the ranking.

Using Rank Aggregation: Let m be the number of configs and $L_1, \ldots, L_m$ be the top-k lists obtained from these configs. To engage user U, we first need to aggregate these lists into a single list. Many aggregation methods exist, e.g., [4, 14]. Here we use MedRank [14], a popular method. To use MedRank, we first sort each list L_i in decreasing order of score, then associate each item in the list with a rank, i.e., an integer, such that the higher the score, the lower the rank and items with the same score receive the same rank. Next, we compute for each item a global rank which is the median of its ranks in the lists. Finally, we sort the items in increasing order of global rank, breaking ties randomly, to obtain a list $L*$ which is the aggregation of all top-k lists L_i-s.

Example 5.1. Figure 8 shows three top-k lists L_1, L_2, L_3 and the global list $L*$. A line such as "a: 1.0 (1)" under L_1 means that item "a" in list L_1 has score 1.0 and has been assigned rank 1. The ranks for "a" is 1, 1, 2 (see Figure 8). So its global rank is 1. The ranks for "b" is 2, 4, 1 (here "b" is missing from L_2, which has ranks 1-3; so we assign to it rank 4). Thus "b"'s global rank is 2. And so on.

Once we have obtained the global list $L*$, we can present the top-n items of $L*$ to user U. But how do we incorporate the user feedback for the next iteration? A reasonable solution is to use weighted median ranking (WMR): we first assign an equal weight $w_i = 1/m$ to each top-k list L_i ($i \in [1, m]$). At the end of the first iteration, we adjust $w_i = w_i \cdot [1 + log(1 + r_i)]$, where r_i is the number of true matches user U has identified that appear in L_i, then normalize all weights w_i. At the start of the next iteration, we merge the lists $L_1, \ldots, L_m$ again, using WMR to compute the global rank of each item. Next, we present the top-n pairs in this merged list to the user, and so on. Intuitively, the top-k lists in which more true matches appear will become more important, and the weighted global ranking will be "leaning toward" those lists.

Using Learning: WMR does not perform well in our experiments (see Section 6). It uses a very limited combination model which fails to fully utilize user feedback. To address this, we explored active learning. Specifically, we iteratively show the next n items of $L*$ to user U, until we have obtained at least one match and one non-match. Suppose we have carried out t iterations, then this produces a set T of nt labeled items. We use T to train a random forest classifier F, use F to find n most informative items in $L*$, show them to the user to label, add the newly labeled items to T, then retrain F, and so on.

Active learning alone however is not quite suited for our purpose. Its goal is to learn a good classifier as soon as possible. Hence it typically shows user U controversial items that it finds difficult to classify. But many or most of these items can be non-match. User U, however, wants to find many *true matches* as soon as possible (so that U can examine them to quickly understand the problems with the blocker).

The above two goals conflict. To address this problem, we adopt a hybrid solution. After we have obtained the training set T and trained a classifier F, as described above, for the next iteration, we show user U n items where $n/4$ items are the top controversial items chosen by F, as described above. The remaining $3n/4$ items however are those with the *highest positive prediction confidence*, where the confidence is computed as the fraction of decision trees in F that predict the item as a match. Intuitively, the first $n/4$ items are intended to help the active learner, whereas the remaining $3n/4$ items can contain many true matches, and are intended to help the user quickly find many true matches in the first few iterations.

After three such iterations, we stop active learning completely (judging that classifier F has received enough labeled controversial examples in order to do well), but continue the online-learning process with F. Specifically, in each subsequent iteration, we show user U the top n items with the highest positive prediction confidence, produced by F. Once these items have been labeled by U, we add them to the existing training set, retrain F, and so on.

When to Stop? A natural stopping point is when user U finds no new matches in 2 consecutive iterations. Of course, U can stop earlier or continue. If the required blocker recall is very high, U can continue for many iterations. Otherwise, U can stops after the first few iterations (because if these iterations contain many matches, then examining them often already reveals problems with the blocker, which U can then fix).

6 EMPIRICAL EVALUATION

We evaluated MatchCatcher in three ways. First, we asked volunteers to provide blockers for several datasets. These blockers vary in recall, types, and complexity, representing blockers that users may write *at various points* during the blocker development process. We show that MatchCatcher works well with these blockers, thus can effectively support the users in the development process.

Second, we performed best-effort blocking on several datasets, by asking volunteers to manually develop the best hash-based blockers, or applying a state-of-the-art solution to learn the best blockers. We show that even in this case MatchCatcher can help uncover problems and improve the blockers.

Dataset	Tuple type	Table A	Table B	# of matches	# of attrs	Average length
Amazon-Google	software product	1363	3226	1300	5	205, 38
Walmart-Amazon	electronic product	2554	22074	1154	7	76, 179
ACM-DBLP	paper	2294	2616	2224	5	16, 19
Fodors-Zagats	restaurant	533	331	112	7	11, 10
$Music_1$	song	100000	100000	2978	8	9, 9
$Music_2$	song	500000	500000	73646	8	9, 9
Papers	paper	455996	628231	unknown	7	17, 18

Table 1: Datasets for our experiments.

Dataset	Blocker Q
A-G	**(OL)** title_overlap_word<3 **(HASH)** attr_equal_manuf **(SIM)** title_cos_word<0.4 **(R)** title_jac_word<0.2 AND manuf_jac_3gram<0.4
W-A	**(OL)** title_overlap_word<3 **(HASH)** attr_equal_brand **(SIM)** title_cos_word<0.4 **(R)** price_absdiff>20 OR title_jac_word<0.5
A-D	**(OL)** authors_overlap_word<2 **(SIM)** title_jac_3gram<0.7 **(R_1)** title_cos_word<0.8 AND authors_jac_3gram<0.8 **(R_2)** year_abs_diff>0.5 OR title_jac_word<0.7
F-Z	**(OL)** name_overlap_word<2 **(HASH)** attr_equal_city **(SIM)** addr_jac_3gram<0.3 **(R)** (name_cos_word<0.5 AND type_jac_3gram<0.7) OR addr_jac_3gram<0.3
M_1	**(OL)** artist_name_overlap_word<2 **(HASH)** attr_equal_artist_name **(SIM)** title_cos_word<0.5 **(R)** year_absdiff>0.5 OR title_cos_word<0.7
M_2	**($HASH_1$)** attr_equal_artist_name **($HASH_2$)** attr_equal_release_OR_attr_equal_artist_name **(SIM_1)** title_cos_word<0.6 **(SIM_2)** title_cos_word<0.7 **(SIM_3)** title_cos_word<0.8

Table 2: Blockers for the first set of experiments.

Finally, we asked real-world users in several data science classes, domain science projects, and at several organizations to use MatchCatcher. We show that MatchCatcher has proven highly effective in helping these users develop blockers.

6.1 Supporting Users in Developing Blockers

For this experiment we need "gold" matches, so we use the six datasets shown in the first six rows of Table 1. As far as we can tell, these datasets are the largest ones used in previous EM work for which "gold" matches are available. Here we created two versions of the Music dataset, Music1 and Music2, to ensure a diversity of size (from 331 to 100K to 500K of tuples per table). Appendix B describes these datasets in more details.

For each dataset we asked volunteers to create multiple blockers (see Table 2). They are of the types described in Section 2: overlap (OL), hash (HASH), similarity-based (SIM), and rule-based (R). For example, the first row of Table 2 describes 4 blockers for dataset A-G. These include a hash blocker on attribute "manufacturer" and a rule-based blocker that combines two SIM blockers. See Appendix C for more details on these blockers. (The next subsection describes experiments with the best hash blockers manually created for these datasets.)

Developing a blocker is typically *a long process* in which users often start with a simple blocker, then gradually revise it into a more complex one with higher recall. The above blockers differ in type, recall, and complexity, representing blockers that users may write *at various points* during the above process. We now show that MatchCatcher can help debug these blockers, suggesting that it can support the user during the entire development process.

Overall Accuracy: First we examine the top-k SSJs module. The first two columns of Table 3 list datasets and blockers. Column C lists the size of C, the output of the blocker on Tables A and B. Column M_D lists the number of true matches in $D = A \times B - C$. This number varies drastically, e.g., 137-1,267 for A-G, 87-566 for W-A, etc., suggesting that blocker recall often varies widely and that it is important to debug to improve recall.

	Q	C	M_D	E	M_E	F	I
A-G	OL	8,388	291	4,063	190 (65.3)	166 (87.4)	40
	HASH	1,835	1,267	3,337	820 (64.7)	803 (97.9)	97
	SIM	7,406	192	4,341	104 (54.2)	73 (70.2)	29
	R	27,650	137	4,362	76 (55.5)	65 (85.5)	24
W-A	OL	210,782	87	6,570	48 (55.2)	37 (77.1)	7
	HASH	256,341	201	5,089	168 (83.6)	147 (87.5)	26
	SIM	46,900	135	7,089	56 (41.5)	46 (82.1)	7
	R	4,265	566	5,027	256 (45.2)	233 (91.0)	33
A-D	OL	56,869	41	4,270	41 (100.0)	37 (90.2)	8
	SIM	2,487	61	3,335	59 (96.7)	56 (94.9)	11
	R_1	3,764	41	3,843	41 (100.0)	38 (92.7)	10
	R_2	2,173	107	3,011	104 (97.2)	101 (97.1)	16
F-Z	OL	115	47	5,079	46 (97.9)	46 (100.0)	5
	HASH	10,165	52	4,653	51 (98.1)	51 (100.0)	5
	SIM	2,146	13	5,908	12 (92.3)	12 (100.0)	5
	R	124	33	5,239	32 (97.0)	32 (100.0)	5
M_1	OL	253,286	778	5,045	673 (86.5)	671 (99.7)	38
	HASH	212,296	188	4,948	100 (53.2)	100 (100.0)	13
	SIM	2,601,349	78	5,050	38 (48.7)	36 (94.7)	7
	R	89,344	202	5,213	113 (55.9)	109 (96.5)	11
M_2	$HASH_1$	11,115,136	4,530	5,428	661 (14.6)	648 (98.0)	47
	$HASH_2$	14,632,318	3,844	5,735	450 (11.7)	432 (96.0)	35
	SIM_1	27,461,378	2,220	5,420	1,012 (45.6)	1,012 (100.0)	54
	SIM_2	14,924,148	3,238	5,533	1,087 (33.6)	1,087 (100.0)	58
	SIM_3	8,512,446	4,228	5,587	1,151 (27.2)	1,151 (100.0)	61

Table 3: Accuracy in retrieving the killed-off matches.

Column E lists the size of E, the union of all top-k lists over the configs (for $k = 1000$). Column M_E lists the number of true matches in E (the numbers outside parentheses), and shows that set E contains a substantial fraction of true matches in D, e.g., 54-65% for A-G, 41-83% for W-A, 96-100% for A-D, etc. (see the numbers in parentheses). This suggests that the top-k module can effectively find the true matches in D.

Next we examine the Match Verifier. We want to know its accuracy if run until its natural stopping point (see Section 5). It is difficult to recruit enough real users for this large-scale experiment involving 25 blockers. So we use synthetic users, whom we assume can identify the true matches accurately (we describe multiple experiments with real users below).

Column F of Table 3 show that this module can retrieve a large number of matches in E, e.g., 65-803 for A-G (see the numbers outside parentheses), and that the retrieval rate is very high, e.g., 70-98% for A-G, 77-91% for W-A, etc. (see the numbers inside parentheses). Finally, Column I shows that the total number of iterations is 5-13 in 12 cases, 16-40 in 8 cases, 47-61 in 4 cases, and 97 in 1 case. The higher number of iterations is often due to the larger number of matches that have to be retrieved from E, e.g., for blocker HASH of dataset A-G, the module needed 97 iterations to retrieve 803 matches, a reasonable number of iterations given that each iteration shows only 20 tuple pairs to the user.

Thus, if the user runs the Match Verifier until its natural stopping point, he/she can retrieve a large number of matches. This is good news for applications in which blocker recall is critical, thus the user may want to examine *all* matches that the module can retrieve.

Accuracy & Explanations for the First Few Iterations: To examine if users can quickly find many matches and explanations, we asked volunteers to *manually work with the Match Verifier for the first three iterations.* Table 4 shows the results (for space reasons we only list five blockers for five datasets, the results for other blockers are similar). The table shows that the user needed only 7-10 mins to examine the first three iterations, was able to identify a large number of matches (28-43), and was able to identify multiple reasons for why they are killed off (a reason such as "large threshold (18)" means that tuple pair #18 was killed off due to the blocker using a large threshold, and this was the first pair where the user observed this problem). Overall, the results suggest that after examining the first few iterations, the user can already identify multiple problems with the blocker (which he/she can then fix).

6.2 Debugging State-of-the-Art Blockers

Suppose a user has manually developed a good standard blocker, or has used state-of-the-art techniques to learn a blocker, we want to know if MatchCatcher can still help improve the blocker's accuracy. Toward this goal, we performed two experiments.

Hash Blockers: First, we asked a user well-trained in EM to develop the best possible hash blockers for five datasets (the first five in Table 1). For example, for dataset A-G, this user created the blocker Q_1 which keeps a pair of tuples if they agree on "manufacturer" *or* on a hash of "price" *or* on a hash of "title". Thus, Q_1 combines three hash blockers. (Appendix D describes all five blockers in details.) We selected hash blocking because it is well-known, easy to understand, and fast. Hence it is considered a standard blocking method commonly used in practice. On the five datasets A-G, W-A, A-D, F-Z, and Music1, the best hash blockers achieve 75.6, 95.1, 100, 97.3, and 100% recall, respectively.

We then asked the same user to use MatchCatcher to try improving the above hash blockers. For A-D and Music1, which already have 100% recall, using MatchCatcher the user did not find any killed-off matches (as expected), so debugging terminated early. For A-G, W-A, and F-Z, however, debugging significantly improved recall from 75.6 to 99.7, 95.1 to 99.6, and 97.3 to 100%, respectively. Appendix D describes one such debugging scenario in details.

Learned Blockers: From a group of researchers we obtained Papers, the dataset described in the last row of Table 1. For this dataset, they have applied the method in [8] to learn blockers using a sample labeled by crowdsourcing, and we were able to obtain three such blockers (learned on three separate samples). Appendix D describes these blockers, which are the best blockers that the learning method has found in a very large space of blockers, including hash ones. Unfortunately, we do not have the entire set of "gold" matches for Papers (we do have some "gold" matches, but not all of them). Hence, we are unable to report recalls for these blockers.

We then asked a user to apply MatchCatcher to these blockers. After 5 iterations, the user found 76, 61, and 65 matches for the three blockers, respectively. More importantly, the user was able to identify a set of reasons for why these matches were killed off and suggestions for improving the blockers (see Appendix D). Given the lack of "gold" matches, we were not able to improve the blockers then compare their recalls. Nevertheless, the above experiments suggest that blockers learned using state-of-the-art solutions can still have many problems and MatchCatcher can help pinpoint these, to help the user improve recall.

Blocker	# iteration	Label time	Blocker problems
OL (A-G)	3 iterations 31 matches	8 mins	large threshold (18); attribute “manuf" is sprinkled in the attribute “title" (18)
HASH (W-A)	3 iterations 43 matches	10 mins	different words for the same brand (6); missing values in attribute “brand" (13)
SIM (A-D)	3 iterations 28 matches	7 mins	large threshold (16); attribute “title" contains subtitle in one table (22)
R (F-Z)	3 iterations 32 matches	7 mins	different descriptions for attribute “type" (11); unnormalized attribute “address" (33); attribute “city" is sprinkled in “name" (47)
R (M_1)	3 iterations 41 matches	10 mins	input tables are not lower-cased (5); missing values in attribute “year" (12)

Table 4: Accuracy in the first 3 iterations and explanations.

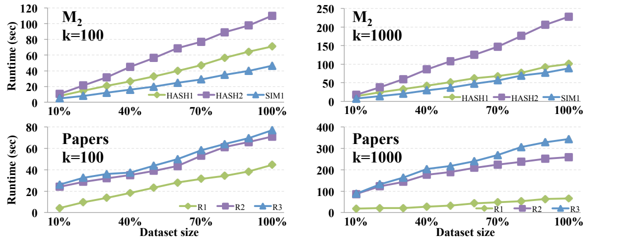


Figure 9: Runtime of top-k module for varying table sizes.

6.3 MatchCatcher “in the Wild”

Over the past two years variations of MatchCatcher have been used by 300+ students in 4 data science classes and 7 EM teams at 6 organizations. The feedback has been overwhelmingly positive. For example, 18 teams used MatchCatcher in a class project, and reported that it helped (a) discovering data that should be cleaned, (b) finding the correct blocker types and attributes, (c) tuning blocker parameters, and (d) knowing when to stop. We have reported on some of this experience in a separate paper (not cited for anonymity reasons). Overall, we found that many real-world users have used MatchCatcher as *an integral part of an end-to-end blocker development process:* start with a simple blocker, use MatchCatcher to identify problems, improve the blocker, and so on, until MatchCatcher no longer reports substantial problems with the blocker.

6.4 Runtime & Scalability

MatchCatcher was implemented in Cython, and all experiments used a RedHat 7.2 Linux machine with Intel E5-1650 CPU. The top-k module took 6.6-9.4 secs (for dataset A-G), 97-310 (W-A), 2.8-3.2 (A-D), 0.2 (F-Z), 12.1-24.4 (M_1), 57-230 (M_2), and 65-344 (Papers), respectively. For the first five datasets, these times are quite small except 97-310 secs for W-A. On W-A, the k-th pair on the top-k list (recall that $k = 1000$) often has a very low score, e.g., 0.21-0.225. Thus the top-k module took more time. The last two datasets (M_2 and Papers) are much larger (500K tuples per table), and so took longer to run. In all cases, however, the total time is still under 5.8 minutes.

To examine how the top-k module scales, we measure its time as we vary the size of the two largest datasets, M_2 and Papers, at various percentages of the original datasets (which have 500-600K tuples per table). Figure 9 shows the results for the first three blockers in Table 3 for M_2 and all three blockers for Papers, for $k = 100$ (the left two plots) and $k = 1000$. The results show that the top-k module scales linearly or sublinearly as the table size grows. Finally, on all datasets the Match Verifier took under 0.1 sec to aggregate the top-k lists, and 0.14-0.18 secs to process user feedback in each iteration.

6.5 Additional Experiments

Appendixes E-G describe extensive experiments on the performance of the MatchCatcher components, sensitivity analysis, and comparison with a recent related work. For space reasons we only briefly summarize those experiments here.

Performance of the Components: We show that using multiple configs instead of just one config significantly increases the number of retrieved matches, by 10-74%. Handling long attributes increases the recall of E (the fraction of matches in D that are in E) by up to 11%, compared to not handling them in config generation. Our experiments also show that the joint top-k processing strategy over multiple configs significantly outperforms the baseline of executing each config individually, by as much as 3.5 times. Finally, we found that active/online learning significantly outperforms weighted median ranking in the Match Verifier.

Sensitivity Analysis: We found that increasing k (the number of pairs retrieved per config) does increase the number of true matches retrieved, but only up to a certain k, and comes at the cost of higher runtime, and that using 3 active learning iterations (as we currently do) provides a good balance between increasing the classifier accuracy and increasing recall in the Match Verifier.

Comparison with Recent Work: We found MatchCatcher significantly outperforms the work in [25], which uses a single config, e.g., improving the recall of E by 26-47% on the A-G dataset.

7 ADDITIONAL RELATED WORK

We have discussed related work throughout the paper. We now discuss additional related work. As far as we can tell, a recent work (citation removed for anonymity reasons) is the first to raise the need for debugging for blocking. But it does not discuss any debugging solution in depth, as we do here. Other related works include debugging for data cleaning [16], schema mapping [5], and data errors in spreadsheets [1]. They do not address EM and their solutions do not apply to our context. But they do underscore the importance of debugging for data integration and cleaning.

SSJs have received much attention, e.g., [19, 29] (see [30] for a survey). Top-k SSJs are studied in [28, 31]. [31] proposes a B+ tree based index to scale top-K SSJs on edit distance. It does not work well for datasets with large textual difference [30], however, a common occurrence in our case. The work [28], which uses prefix filtering to find the top-k pairs, is better suited to our case. But it does not handle long strings well [30]. Here we have significantly improved this work and extended it to work over multiple configs.

Rank aggregation has been studied extensively in the database/IR communities, e.g., [4, 10, 14]. Active learning (AL) for EM has been studied in [17, 22, 24]. But they perform extensive AL to learn an accurate matcher. In contrast, we use only a few AL iterations to learn a classifier with reasonable accuracy, then use it to surface matches for debugging purposes. The above work also does not combine AL with online learning as we do. Finally, the work [26] uses a learning-based UI model similar to ours, but for IR tasks.

8 CONCLUSIONS & FUTURE WORK

We have shown that debugging blocker accuracy is critical for EM, and have described MatchCatcher, a solution to this problem. As for future work, in certain cases the user may find a large number of killed-off matches. So we plan to develop a method to automatically explain why each match is killed off by the blocker, summarize these explanations, then present the summary to the user. When fixing a problem affecting a killed-off match, the user may want to know how pervasive this problem is (and focus on fixing the most pervasive ones first). For this purpose, given a killed-off match, we plan to develop a method to find all tuple pairs that are similar to that match (from a blocking point of view).

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Algorithm 1 Joint Top-k String Similarity Join

```
Procedure JointTopkSimJoin($T_A$, $T_B$, $C$, $\mathcal{G}$, $k_1$, $k_2$, $n$)
Input:    tokenized set table $T_A$ on $A$, $T_B$ on $B$, blocking candidate set $C$, config tree $\mathcal{G}$, $k_1$ for
          top-k size, $k_2$ for selecting $q$, $n$ for the number of cores
Output:   a set $\mathcal{K}$ of top-k lists
 1:  $\mathcal{K} \leftarrow \emptyset$, $\mathcal{H} \leftarrow \emptyset$
 2:  $\mathcal{Q} \leftarrow$ queue by breadth-first traverse of $\mathcal{G}$
 3:  $g \leftarrow \mathcal{Q}$.pop()                    // get the root config of the config tree
 4:  $q \leftarrow 1$
 5:  RunInitialQJoinThreads($T_A$, $T_B$, $C$, $g$, $k_1$, $k_2$, $n$, $q$, $\mathcal{K}$, $\mathcal{H}$)
 6:  RunParallelQJoinThreads($T_A$, $T_B$, $C$, $\mathcal{G}$, $k_1$, $q$, $\mathcal{K}$, $\mathcal{H}$)
 7:  return $\mathcal{K}$

Procedure RunInitialQJoinThreads($T_A$, $T_B$, $C$, $g$, $k_1$, $k_2$, $n$, $q$, $\mathcal{K}$, $\mathcal{H}$)
 1:  for $i$ = 1 to $n$ do in parallel
 2:      Run QJoin($T_A$, $T_B$, $C$, $g$, $k_2$, $i$) on core $i$ with $q = i$, record $H_i$
 3:      if core $i$ first finishes QJoin do
 4:          $q \leftarrow i$ and stop QJoin on other cores
 5:          $\mathcal{H} \leftarrow \mathcal{H} \cup \{H_q\}$
 6:          Continue QJoin($T_A$, $T_B$, $C$, $g$, $k_1$, $q$) on core $q$ and update $H_q$
 7:  $K_g \leftarrow$ top-$k_1$ list by QJoin on core $q$
 8:  $\mathcal{K} \leftarrow \mathcal{K} \cup \{K_g\}$
 9:  return

Procedure RunParallelQJoinThreads($T_A$, $T_B$, $C$, $\mathcal{G}$, $k_1$, $q$, $\mathcal{K}$, $\mathcal{H}$)
 1:  while $\mathcal{Q}$.size() > 0 and has idle cores do
 2:      $c \leftarrow \mathcal{Q}$.pop()
 3:      $K_c \leftarrow$ []                    // a list that will store the top-k pairs for $c$
 4:      $p \leftarrow$ parent of $c$ in $\mathcal{G}$
 5:      $A \leftarrow$ ancestors of $c$ in $\mathcal{G}$
 6:      $H_A \leftarrow \{H_a \in \mathcal{H} \mid a \in A\}$
 7:      if $c$ has children in $\mathcal{G}$ do
 8:          $H_c \leftarrow \emptyset$
 9:          $\mathcal{H} \leftarrow \mathcal{H} \cup \{H_c\}$
10:      Run QJoin($T_A$, $T_B$, $C$, $c$, $k_1$, $q$) to update $K_c$ by reusing $H_A$ on a new core; update
11:                  $K_c$ by reusing top-k list $K_p$ of $p$ when QJoin on $p$ is finished; record
12:                  new pairs in $H_c$ if $c$ has children in $\mathcal{G}$
13:      $\mathcal{K} \leftarrow \mathcal{K} \cup \{K_c\}$
14:  return
```

A PSEUDO CODE FOR JOINT TOP-K SSJ

Algorithm 1 shows the pseudo code for the joint top-k SSJ algorithm described in Section 4.2.

B DATASETS

Table 5 shows the schema for the datasets in Table 1. The first six datasets in Table 5 have been used in prior EM work and are publicly available. The datasets Music$_1$ and Music$_2$ have just one table (this is a case of deduplication within a single table), so we use it as both tables A and B to develop blockers. The Papers dataset is obtained from a group of EM researchers. We omit further description of these datasets for anonymity reasons.

Dataset	Schema
Amazon-Google	id, title, description, manufacturer, price
Walmart-Amazon	id, title, category, brand, modelno, price, proddescrlong
ACM-DBLP	id, title, authors, venue, year
Fodors-Zagats	id, name, addr, city, phone, type, class
Music$_1$	id, title, release, artist_name, duration, artist_familiarity, artist_hotness, year
Music$_2$	the same as for Music$_1$
Papers	id, title, authors, journal, month, year, publication_type

Table 5: Schemas of the datasets in our experiments.

Dataset	Blocker Q
A-G	**(OL)** title_overlap_word<3 **(HASH)** attr_equal_manuf **(SIM)** title_cos_word<0.4 **(R)** title_jac_word<0.2 AND manuf_jac_3gram<0.4
W-A	**(OL)** title_overlap_word<3 **(HASH)** attr_equal_brand **(SIM)** title_cos_word<0.4 **(R)** price_absdiff>20 OR title_jac_word<0.5
A-D	**(OL)** authors_overlap_word<2 **(SIM)** title_jac_3gram<0.7 **(R$_1$)** title_cos_word<0.8 AND authors_jac_3gram<0.8 **(R$_2$)** year_abs_diff>0.5 OR title_jac_word<0.7
F-Z	**(OL)** name_overlap_word<2 **(HASH)** attr_equal_city **(SIM)** addr_jac_3gram<0.3 **(R)** (name_cos_word<0.5 AND type_jac_3gram<0.7) OR addr_jac_3gram<0.3
M$_1$	**(OL)** artist_name_overlap_word<2 **(HASH)** attr_equal_artist_name **(SIM)** title_cos_word<0.5 **(R)** year_absdiff>0.5 OR title_cos_word<0.7
M$_2$	**(HASH$_1$)** attr_equal_artist_name **(HASH$_2$)** attr_equal_release_OR_attr_equal_artist_name **(SIM$_1$)** title_cos_word<0.6 **(SIM$_2$)** title_cos_word<0.7 **(SIM$_3$)** title_cos_word<0.8

Table 6: Blockers for the first set of experiments.

C MATERIALS FOR SECTION 6.1

We now provide more details for the blockers in Table 2 and used in Section 6.1. For ease of exposition, we have replicated that table as Table 6 shown above. The volunteers have created four types of blocker for the datasets: OL, HASH, SIM, and R.

OL: The basic OL blocker format is *attr_overlap_tok<t*, meaning that a tuple pair with values (v_1, v_2) on the attribute *attr* is tokenized by the tokenizer *tok* to get two token sets (s_1, s_2), and if the overlap of (s_1, s_2) is less than the threshold *t*, the blocker will drop the pair. Here *attr* is one of the string attributes in Table 2, and the tokenizer *tok* can be word-based, k-gram based, etc. For example, the OL blocker of A-G "title_overlap_word<3" means that if the overlap of the titles of a tuple pair, tokenized by the word-based tokenizer, is less than 3, then drop the pair.

HASH: A HASH blocker such as *attr_equal_manuf* outputs a pair of tuples if they agree on the value of "manufacturer". Such a blocker may combine multiple HASH blockers. For example, blocker HASH$_2$ of dataset M$_2$ is the union of two HASH blockers on "release" and "artist_name", respectively.

SIM: A SIM blocker has the format *attr_sim_tok<t*. Here *sim* is a similarity measure (e.g., Jaccard, cosine, etc.), *tok* is a tokenizer, and *t* is a threshold. For example, the SIM blocker "title_jac_3gram<0.7" states that if the Jaccard similarity on titles of a tuple pair, tokenized by the 3gram-based tokenizer, is less than 0.7, then drop the pair. Note that if distance-based measures are used (e.g., edit distance and its variants), we should reverse the *less than* sign to *greater than*, and the format to be used is *attr_dist>t*.

R: A rule-based blocker is the union of a set of rules, where each rule is a conjunction of blockers as described above. Rules can also contain blockers of new types, e.g., a blocker that checks for the absolute difference in the values of "year". For example, blocker R of M$_1$ states that a tuple pair will be dropped if the absolute difference on attribute "year" is greater than 0.5, or the word-based cosine similarity on "title" is less than 0.7.

D MATERIALS FOR SECTION 6.2

We now provide additional materials for Section 6.2.

Experiments with Hash Blockers: Table 7.a describes the five hash blockers that were manually created for five datasets. Each blocker is a disjunction of hash keys on attributes. For example, the blocker of A-G is a union of three hash keys: attribute "manufacturer", truncated value of attribute "title" (only select the longest word in "title" as the hash key), and truncated "price" (only keep the first digit of "price" and set all others to 0, e.g., price 599.99 will be 500.00 after truncation). Other hash blockers are created similarly.

Dataset	Best hash blocker
A-G	manuf OR trunc_title OR trunc_price
W-A	brand OR modelno OR category OR trunc_title OR trunc_price
A-D	year
F-Z	name OR addr OR city OR type
M_1	title OR release OR artist_name

(a)

R_1	(title_dice<0.61 AND title_jac<0.5) OR title_jac<0.32 OR (authors_dice<0.49 AND authors_jac<0.14) OR (authors_dice<0.13 AND title_overlap<5.5)
R_2	(title_dice<0.73 AND title_jac<0.36) OR authors_jac<0.14
R_3	authors_dice<0.2 OR (title_dice<0.7 AND title_jac<0.35)

(b)

Table 7: Blockers for the second set of experiments.

We now describe a real-world debugging scenario in which a user U used MatchCatcher to debug and revised the blocker for A-G shown in Table 7.a (we will refer to this blocker as Q_0). After invoking MatchCatcher and manually labeling the first 5 iterations, U retrieves 70 true matches (out of the 100 pairs proposed by MatchCatcher).

U examines these matches and finds the following problems. First, two tuples of a match does not agree on the hash key *trunc_title* due to "manufacturer" being sprinkled into "title". For example, a match (a, b) with $a.title$ = "boomerang web designer" and $b.title$ = "webpage designer" does not agree on *trunc_title* which are "boomerang" and "designer". However, "boomerang" is the manufacturer which should not appear in the title. Second, two tuples do not match due to missing values in the attributes used for $manuf$ and *trunc_price*.

At this point, U realizes that there are dirty data issues and that hash blockers might not work well. U observes that the titles of (a, b) shares common tokens even if they do not agree on the hash key, and thinks that this problem can be fixed using an OL blocker. So U revises Q_0 to a rule-based blocker Q_1 = "title_overlap_word<3 OR manuf OR trunc_price". U then redoes blocking using Q_1.

To see if Q_1 is accurate, U invokes MatchCatcher again, labels 5 iterations, and retrieves 27 matches. Examining the matches, U finds that the threshold 3 of the OL blocker in Q_1 is too high. For example, a match (a, b) with $a.title$ = "bryce 6" and $b.title$ = "re:launch bryce 6" is killed off by Q_1 as the overlap value is only 2. Thus, U revises Q_1 by decreasing the threshold to 2. The new blocker Q_2 is "title_overlap_word<2 OR manuf OR trunc_price".

U debugs Q_2 using MatchCatcher and retrieves 9 true matches after labeling 5 iterations. Examining the matches, U finds that the threshold for the OL blocker is still too high, e.g., a match (a, b) with $a.title$ = "prey" and $b.title$ = "aspyr media inc prey" is killed off as the overlap value is only 1. So U further revises Q_2 to Q_3 = "title_overlap_word<1 OR manuf OR trunc_price". Invoking MatchCatcher for Q_3 brings back no true matches in 5 iterations. So U uses Q_3 as the final blocker (which has 99.7% recall).

Experiments with Learned Blockers: Table 7.b describes the three rule-based blockers automatically learned using a state-of-the-art solution (as described in Section 6.2). Each blocker is a disjunction of rules where each rule is a conjunction of SIM blockers (described in Appendix B). Note that all blockers use the word-based tokenizer. For example, blocker R_3 drops a tuple pair if (1) the word-based Dice similarity on "authors" is less than 0.2, or (2) the word-based Dice and Jaccard similarity on "title" are less than 0.7 and 0.35 respectively.

We now describe a case in our experiments showing that a real user U can use MatchCatcher to debug and revise blocker R_1. After invoking MatchCatcher for this blocker and manually labeling 5 iterations, U retrieves 76 matches out of 100 candidates.

Examining these matches, U finds the following four problems. First, "title" contains many other random text (perhaps from other attributes). For example, a match (a, b) with $a.title$ = "LETTER Communicated by Gal Chechik Parametric Embedding for Class Visualization" and $b.title$ = "Parametric Embedding for Class Visualization." is killed off by R_1 due to low word-based Jaccard and Dice similarity. Here the prefix "LETTER ... Chechik" should not be in the title.

Second, "title" also contains redundant prefix/suffix. For example, a match (a, b) with $a.title$ = "Abstract Matching Nuts and Bolts (Extended Abstract Version)" and $b.title$ = "Matching Nuts and Bolts Abs." is killed off by the blocker. Third, "authors" contains incomplete values. For example, a match (a, b) with $a.authors$ = "Jieh-Sheng Lee" and $b.authors$ = "Jieh-Sheng Lee, Jieh Hsiang, Po-Hao Tsang" is killed off by the blocker. Finally, the tokenization may cause problems, e.g., R_1 uses a white space as the tokenization delimiter, but U finds that for authors the delimiter should be either a white space or a comma.

U can then revise R_1 in several ways. First, due to dirty data problems, Jaccard or Dice similarity measures could be too strict in some rules in R_1. Therefore, U can replace the last rule in R_1 which is "authors_dice<0.13 AND title_overlap<5.5" with a new rule "authors_overlap< 2 AND title_overlap<4". Second, in the word-based tokenizer for attribute "authors", U can use as the delimiters a comma or a white space, rather than always a single white space.

E PERFORMANCE OF THE COMPONENTS

Multiple Configurations: We show that multiple configs are necessary to help the system achieve higher recall. For space reasons, we only discuss the results for five blockers: OL, HASH, SIM, R, and R, for datasets A-G, W-A, A-D, F-Z, and M_1, respectively (the results for the other blockers are similar). For these blockers, the number of matches that the string similarity detector can retrieve (in set E), for the best single config vs. using multiple configs is 109 vs 190, 139 vs 168, 53 vs 59, 29 vs 32, and 90 vs 113, respectively. Thus, clearly using multiple configs significantly increases the number of retrieved matches, by 10-74%.

Handling Long Attributes: On the two datasets A-G and W-A, if we do not remove attributes judged too long, then the recall of E (i.e., the fraction of matches in D that are in E) drops by 4-8% and 1-11%, respectively, as shown in Table 8. Similarly the recall of F drops by 4-8% and 0-10%, respectively. (On the remaining five datasets MatchCatcher does not detect any attributes that are too long.) These results suggest that handling long attributes can substantially increase the recall, by up to 11%.

Effects of Different Top-k Strategies: We compare four strategies to generate top-k lists: ori (run topk-join for each config), ori+para (run topk-join in parallel), new+para (run QJoin, our improved version of topk-join, in parallel; see Section 4.1 for a description of both topk-join and QJoin), and new+para+reuse (the previous strategy with reuse, see Section 4.2).

Figure 10 shows the runtime of these four strategies for four datasets, as we vary k (F-Z is too small, so all strategies took negligible time to run; and we omit results for M_2 and Papers for space

	Q	Recall by RLH	Recall by KLH	# of iter. by RLH	# of iter. by KLH
A-G	OL	57.0 (65.3)	53.3 (59.5)	40	38
	HASH	63.4 (64.7)	59.3 (60.1)	97	91
	SIM	38.0 (54.2)	29.7 (46.4)	29	25
	R	47.5 (55.5)	40.2 (47.5)	24	21
W-A	OL	42.5 (55.2)	36.8 (50.6)	7	7
	HASH	73.1 (83.6)	73.6 (82.6)	26	31
	SIM	34.1 (41.5)	29.6 (36.3)	7	8
	R	41.2 (45.2)	31.6 (34.3)	33	31

Table 8: Performance comparison of Remove-Long-Early Heuristic (RLH) and Keep-Long Heuristic (KLH) on the two datasets with long attribute, with $K = 1000$.

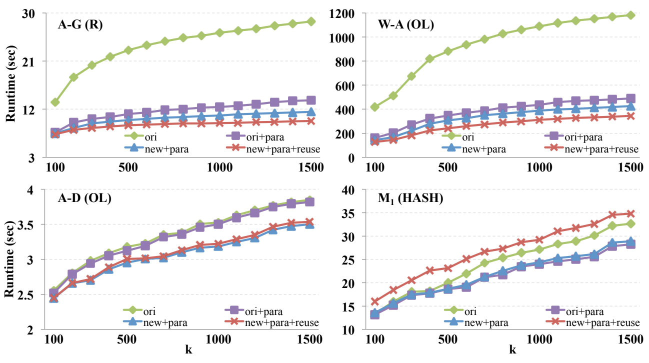

Figure 10: Effects of different top-k generation strategies.

reasons). Also for space reasons, we only show the result for one blocker per dataset (the results are similar for other blockers). The figure shows that new+para, the new top-k algorithm and parallel processing combined (the blue line), significantly reduces runtime on all four datasets. This reduction is especially large on the two datasets with long average tuple length (A-G and W-A). On these two datasets, adding reuse also significantly reduces runtime (the red line). On the other two datasets, however, their average tuple lengths are small and reuse is ineffective (as its overhead overwhelms the savings).

In all four cases, MatchCatcher selects the correct strategy (the red lines for A-G and W-A and the blue line for A-D and M_1), which outperforms ori (the green line), often by a large margin, e.g., 2.8 times and 3.5 times better at $k = 1000$ for A-G and W-A, respectively.

Effects of Learning for Interactive Verification: Finally, we found that active/online learning-based ranking (AOR) significantly outperforms weighted median ranking (WMR) for interactive verification (see Section 5). For example, on two datasets A-G and W-A, for blockers OL, HASH, SIM, R, strategy AOR retrieves 30-167 more matches than WMR in 7 cases, and 17 fewer matches in 1 case (blocker HASH of dataset A-G). For the first 5 iterations, AOR also outperforms WMR, achieving 1-57% higher precision in 7 cases, and -14% lower precision in 1 case (again blocker HASH of A-G). Table 9 shows the comparison on the datasets in detail. Note that the "N/A" in the last column means the result is unknown as the interactive verification using WMV terminates earlier before the fifth iteration.

	Q	F by AOR	F by WMV	P@3N by AOR	P@5N by AOR	P@3N by WMV	P@5N by WMV
A-G	OL	166	57	47.3	50.2	41.6	40.0
	HASH	803	820	42.6	55.2	56.7	69.0
	SIM	73	28	27.6	24.4	25.0	22.0
	R	65	23	23.0	20.6	23.3	19.0
W-A	OL	37	7	53.0	35.8	11.7	7.0
	HASH	147	99	73.3	78.2	61.7	50.0
	SIM	46	4	50.3	45.4	6.7	N/A
	R	233	66	65.6	75.8	20.0	18.0
A-D	OL	37	36	53.8	35.5	51.7	36.0
	SIM	56	35	52.5	46.3	20.0	24.0
	R_1	38	25	40.7	33.9	25.0	18.0
	R_2	101	82	23.3	41.1	20.0	15.0
F-Z	OL	46	40	76.7	46.0	60.0	40.0
	HASH	51	49	85.0	51.0	68.3	43.0
	SIM	12	10	20.0	12.0	11.7	10.0
	R	32	19	53.3	32.0	30.0	19.0
M_1	OL	671	339	100.0	100.0	100.0	100.0
	HASH	100	10	64.3	71.4	16.7	N/A
	SIM	36	7	53.0	36.0	11.7	N/A
	R	109	27	60.0	71.2	33.3	21.0
M_2	$HASH_1$	648	188	35.0	54.0	10.0	9.0
	$HASH_2$	432	88	33.0	55.0	5.0	12.0
	SIM_1	1,012	1,012	65.0	74.0	97.0	97.0
	SIM_2	1,087	1,087	75.0	76.0	98.0	99.0
	SIM_3	1,151	1,151	100.0	99.0	100.0	99.0

Table 9: Performance comparison of the active/online learning-based ranking (AOR) and weighted-median-based verification (WMV) on six datasets with $K = 1000$.

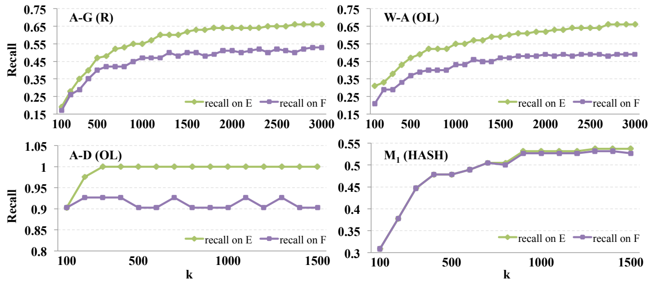

Figure 11: The effects of varying k.

F SENSITIVITY ANALYSIS

We now examine how MatchCatcher performs as we vary major parameters.

The Number k of Pairs Retrieved Per Config: Recall that E is the union of the top-k lists (produced by the detector), and that F is the set of matches returned by the interactive verifier. As we vary k, we observe that the recalls of E and F increase steeply, up to $k =$ 1500, 1500, 300, 1000 for datasets A-G, W-A, A-D, M_1, respectively, then plateau after that, as shown in Figure 11. This suggests that increasing k does increase recall, but only up to a certain k, and comes at the cost of higher runtime. As a result, the current $k =$ 1000 appears to provide a reasonable balance between achieving high recall while keeping the runtime low.

The Number of Active Learning Iterations: Recall from Section 5 that the interactive verifier uses active learning (AL) in the first 3 iterations (then it stops AL and uses only online learning). When we vary the number of AL iterations from 0 to 10 (for $k = 1000, 600, 200$), we observed that the recall of set F increases, maxing out at 2-4 iterations, then decreases. As discussed in Section

	Q	M_E by CTL	M_E by CKL	Δ_{relative}	Δ_{absolute}
A-G	OL	190 (65.3)	87 (29.9)	118.4	35.4
	HASH	820 (64.7)	494 (39.0)	66.0	25.7
	SIM	104 (54.2)	16 (8.3)	550.0	45.8
	R	76 (55.5)	11 (8.0)	590.9	47.5
W-A	OL	48 (55.2)	9 (10.3)	433.3	44.9
	HASH	168 (83.6)	116 (57.7)	44.8	25.9
	SIM	56 (41.5)	1 (0.7)	5500.0	40.8
	R	256 (45.2)	97 (17.1)	163.9	28.1
A-D	OL	41 (100.0)	38 (92.7)	7.9	7.3
	SIM	59 (96.7)	41 (67.2)	43.9	29.5
	R_1	41 (100.0)	33 (80.5)	24.2	19.5
	R_2	104 (97.2)	83 (77.6)	25.3	19.6
F-Z	OL	46 (97.9)	36 (76.6)	27.8	21.3
	HASH	51 (98.1)	46 (88.5)	10.9	9.6
	SIM	12 (92.3)	12 (92.3)	0.0	0.0
	R	32 (97.0)	19 (57.6)	68.4	39.4
M_1	OL	673 (86.5)	330 (42.4)	103.9	44.1
	HASH	100 (53.2)	34 (18.1)	194.1	35.1
	SIM	38 (48.7)	9 (11.5)	322.2	37.2
	R	113 (55.9)	22 (10.9)	413.5	45.0

Table 10: Performance comparison of Configuration Tree Learning (CTL) and Candidate Key Learning (CKL) on five dataset with $K = 1000$.

5, this is because more AL iterations can improve the accuracy of the classifier, but does not necessarily show more matches to the user. As a result, using 3 AL iterations appears to provide a good balance between increasing the classifier accuracy and increasing recall.

G COMPARISON WITH A RELATED WORK

Finally, we compare our configuration generation method (named Configuration Tree Learning, CTL) with [25]. We denote the solution in that paper as CKL (for Candidate Key Learning). After applying CKL, for each of our datasets it generates only one configuration (i.e., one candidate key).

Table 10 shows the results of the two methods. Δ_{relative} is the relative recall improvement of CTL over CKL in percentage (i.e., (M_E by CTL - M_E by CKL) / M_E by CKL), and Δ_{absolute} is the absolute recall improvement of CTL over CKL. From the table we can see that CTL significantly outperforms CKL in all cases except for the SIM blocker of F-Z, for which they achieve the same performance. For example, for datasets A-G, CTL achieves 66.0-590.9 relative recall improvement in percentage and 25.7-47.5 absolute recall improvement in percentage.

H PROOF FOR THEOREM 3.5

We show the proof sketch of Theorem 3.5. Without loss of generality, suppose $L_q(a) \le L_q(b)$. Denote $sim_q(a,b) = \frac{k_q}{L_q(a)+L_q(b)-k_q}$ and $sim_r(a,b) = \frac{k_r}{L_r(a)+L_r(b)-k_r}$, where k_q, k_r are the overlaps of (a,b) on q and r respectively with $k_r \le k_q$. Then we can rewrite Condition 1 as $\left|\frac{k_q}{L_q(a)+L_q(b)-k_q} - \frac{k_r}{L_r(a)+L_r(b)-k_r}\right| \le \alpha$. Based on the assumptions of the theorem, we have $L_r(a) = (1 - \frac{1-\beta}{|q|-1} \cdot |q \setminus r|) \cdot L_q(a)$, and similar for $L_r(b)$. Let $c = 1 - \frac{1-\beta}{|q|-1} \cdot |q \setminus r|$, Condition 1 $\Leftrightarrow \left|\frac{k_q}{L_q(a)+L_q(b)-k_q} - \frac{k_r}{cL_q(a)+cL_q(b)-k_r}\right| \le \alpha$. Notice that $\frac{k_r}{cL_q(a)+cL_q(b)-k_r}$ is an increasing function of k_r and $[k_q - (1-c)L_q(b)] \le k_r \le k_q$, we have $\frac{[k_q-(1-c)L_q(b)]}{cL_q(a)+cL_q(b)-[k_q-(1-c)L_q(b)]} \le \frac{k_r}{cL_q(a)+cL_q(b)-k_r} \le \frac{k_q}{cL_q(a)+cL_q(b)-k_q}$. Therefore to get Condition 1 satisfied, we only need to bound the following two inequalities,

$$\frac{k_q}{cL_q(a)+cL_q(b)-k_q} - \frac{k_q}{L_q(a)+L_q(b)-k_q} \le \alpha \cdot \frac{k_q}{L_q(a)+L_q(b)-k_q} \quad (1)$$

$$\frac{k_q}{L_q(a)+L_q(b)-k_q} - \frac{[k_q-(1-c)L_q(b)]}{cL_q(a)+cL_q(b)-[k_q-(1-c)L_q(b)]} \le \alpha \cdot \frac{k_q}{L_q(a)+L_q(b)-k_q} \quad (2)$$

Bounding Inequality 1: Ineq. 1 $\Leftrightarrow \frac{k_q}{cL_q(a)+cL_q(b)-k_q} \le (1+\alpha) \cdot \frac{k_q}{L_q(a)+L_q(b)-k_q} \Leftrightarrow c \ge \frac{L_q(a)+L_q(b)+\alpha k_q}{L_q(a)+L_q(b)} \cdot \frac{1}{1+\alpha}$. Plugin $c = 1 - \frac{1-\beta}{|q|-1} \cdot |q \setminus r|$, we have

$$\begin{aligned} & c \ge \frac{L_q(a)+L_q(b)+\alpha k_q}{L_q(a)+L_q(b)} \cdot \frac{1}{1+\alpha} \\ \Leftrightarrow & 1 - \frac{1-\beta}{|q|-1} \cdot |q \setminus r| \ge \frac{L_q(a)+L_q(b)+\alpha k_q}{L_q(a)+L_q(b)} \cdot \frac{1}{1+\alpha} \\ \Leftrightarrow & \beta \ge 1 - \frac{|q|-1}{|q \setminus r|} \cdot \frac{\alpha}{1+\alpha} \cdot \frac{L_q(a)+L_q(b)-k_q}{L_q(a)+L_q(b)}. \end{aligned}$$

Since $k_q \le \min\{L_q(a), L_q(b)\} = L_q(a)$, if we put harder constraint on β by requiring $\beta \ge 1 - \min_{k_q} \frac{|q|-1}{|q \setminus r|} \cdot \frac{\alpha}{1+\alpha} \cdot \frac{L_q(a)+L_q(b)-k_q}{L_q(a)+L_q(b)} = 1 - \frac{|q|-1}{|q \setminus r|} \cdot \frac{\alpha}{1+\alpha} \cdot \frac{L_q(b)}{L_q(a)+L_q(b)} = 1 - \frac{|q|-1}{|q \setminus r|} \cdot \frac{\alpha}{1+\alpha} \cdot \frac{\max\{L_q(a),L_q(b)\}}{L_q(a)+L_q(b)}$. Thus, we get the second requirement R_2 in the theorem that if $\beta \ge 1 - \frac{|q|-1}{|q \setminus r|} \cdot \frac{\alpha}{1+\alpha} \cdot \frac{\max\{L_q(a),L_q(b)\}}{L_q(a)+L_q(b)}$ is satisfied, Ineq. 1 can be bounded.

Bounding Inequality 2: Now we find the requirements for bounding Ineq. 2 based on R_2 derived above. Let $d = 1 - c = \frac{1-\beta}{|q|-1} \cdot |q \setminus r|$. Then Ineq. 2 can be rewritten as

$$\begin{aligned} & \frac{k_q}{L_q(a)+L_q(b)-k_q} - \frac{k_q - dL_q(b)}{(1-d)(L_q(a)+L_q(b)) - (k_q - dL_q(b))} \le \alpha \frac{k_q}{L_q(a)+L_q(b)-k_q} \\ \Leftrightarrow & \frac{k_q - dL_q(b)}{(1-d)(L_q(a)+L_q(b)) - (k_q - dL_q(b))} \ge (1-\alpha) \cdot \frac{k_q}{L_q(a)+L_q(b)-k_q} \\ \Leftrightarrow & \alpha \ge \frac{d \cdot (L_q(b)-k_q)[L_q(a)+L_q(b)]}{k_q \cdot [(L_q(a)+L_q(b)-k_q) - dL_q(a)]} \end{aligned} \quad (3)$$

Let $f(k_q) = \frac{d(L_q(b)-k_q)[L_q(a)+L_q(b)]}{k_q \cdot [(L_q(a)+L_q(b)-k_q)-dL_q(a)]}$ be a function of k_q, then the first derivative of $f(k_q)$ is

$$f'(k_q) = \frac{d[L_q(a)+L_q(b)][(d-1)L_q(a)L_q(b) - (k_q - L_q(b))^2]}{\{k_q \cdot [(L_q(a)+L_q(b)-k_q) - dL_q(a)]\}^2} < 0$$

Therefore $f(k_q)$ is monotonically decreasing as k_q grows. So if Ineq. 3 is satisfied for small k_q, we can bound Ineq. 2 generally. Notice that k_q cannot be too small (e.g., when $k_q = dL_q(a)$, the maximum possible value of $\frac{sim_q(a,b)-sim_r(a,b)}{sim_q(a,b)}$ is 1, which is impossible to bound by α), hence we need to set a lower bound requirement on k_q. Assume $sim_q(a,b) = \frac{k_q}{L_q(a)+L_q(b)-k_q} \ge \theta \Rightarrow k_q \ge \frac{\theta}{1+\theta}(L_q(a) + L_q(b))$. Notice that the right-hand-side of Ineq. 3 is an increasing function of d, if we put harder constraint on α by requiring

$$\alpha \ge \max_{k_q,d} \frac{d \cdot (L_q(b)-k_q)[L_q(a)+L_q(b)]}{k_q \cdot [(L_q(a)+L_q(b)-k_q) - dL_q(a)]}$$

, Ineq. 2 can be bounded. From R_2 derived about, we know $d = 1 - c \leq \frac{\alpha}{1+\alpha} \frac{L_q(b)}{L_q(a)+L_q(b)}$. Thus, we plugin $d = \frac{\alpha}{1+\alpha} \frac{L_q(b)}{L_q(a)+L_q(b)}$ and $k_q = \frac{\theta}{1+\theta}(L_q(a) + L_q(b))$, and we have

$$\begin{aligned} \alpha &\geq \max_{k_q, d} \frac{d \cdot (L_q(b) - k_q)[L_q(a) + L_q(b)]}{k_q \cdot [(L_q(a) + L_q(b) - k_q) - dL_q(a)]} \\ &= \frac{\frac{\alpha}{1+\alpha} L_q(b) \left[L_q(b) - \frac{\theta}{1+\theta}(L_q(a) + L_q(b))\right]}{\frac{\theta}{1+\theta}\left[\frac{1}{1+\theta}(L_q(a) + L_q(b))^2 - \frac{\alpha}{1+\alpha} L_q(a) L_q(b)\right]} \end{aligned} \tag{4}$$

Let $g(L_q(a))$ be the right-hand-side of Ineq. 4 as a function of $L_q(a)$, we can get $g'(L_q(a)) < 0 \Leftrightarrow C_1 L_q(a)^2 + 2(C_1 - 1)L_q(b)L_q(a) + (C_1 + C_2 - 2)L_q(b)^2 < 0 \Leftrightarrow \frac{1-C_1-\sqrt{1-C_1C_2}}{C_1} L_q(b) < L_q(a) < \frac{1-C_1+\sqrt{1-C_1C_2}}{C_1} L_q(b)$, where $C_1 = \frac{\theta}{1+\theta}$ and $C_2 = \frac{\alpha}{1+\alpha}$. As we can easily see $C_1 \leq 0.5$ and $C_2 \leq 0.5$, we have $\frac{1-C_1-\sqrt{1-C_1C_2}}{C_1} L_q(b) < 0$ and $\frac{1-C_1+\sqrt{1-C_1C_2}}{C_1} L_q(b) > L_q(b)$. Then we get $g'(L_q(a)) < 0$ when $L_q(a) \in [0, L_q(b)]$ and $g(L_q(a))$ is monotonically decreasing. Since we assume $sim_q(a, b) \geq \theta$, we have $L_q(a) \geq \theta L_q(b)$, therefore $g(L_q(a)) \leq g(\theta L_q(b)) = \frac{\frac{\alpha}{1+\alpha}(1-\theta)}{\theta - \frac{\theta}{1+\theta} \frac{\alpha}{1+\alpha} \theta}$. Let $g(\theta L_q(b)) \leq \alpha$, we can finally have $\frac{\frac{\alpha}{1+\alpha}(1-\theta)}{\theta - \frac{\theta}{1+\theta} \frac{\alpha}{1+\alpha} \theta} \leq \alpha \Leftrightarrow \theta \geq \frac{\sqrt{(1+\alpha)^2+8}-(1+\alpha)}{4}$, which is R_1 described in the theorem. This means if R_1 is satisfied, we can bound Ineq. 2.

In all, if R_1 and R_2 are both satisfied under the theorem assumptions, Condition 1 can be satisfied. □

I PROOF FOR THEOREM 4.2

We show the proof sketch for Theorem 4.2. Basically we need to prove the following two parts. First, the correctness of QJoin. That is, given a similarity measure $m \in \mathcal{M}_{set} = \{Jaccard, cosine, overlap, Dice\}$, for each config $g \in G$ QJoin will return the correct top-k list. Second, the correctness of the joint top-k similarity join (JTSJ) with reusing. Without loss of generality, we use Jaccard as the similarity measure for the proof, and we show how to extend it to all measures in $\mathcal{M}_{set}$ in Appendix I.3.

I.1 Correctness of QJoin

We show the correctness of QJoin on a config g. For ease of mathematical exposition, we follow the same notations and terminology in [28].

Lemma I.1. *Let r be a tuple in table A or B sorted by a global order, the probing similarity upper bound for the t-th token is $u_t = 1 - \frac{\max\{0, t-q\}}{L_g(r)}$ with parameter q in* QJoin.

Proof. If the token overlap is $\min\{t, q\}$ in the prefix of t tokens of r with any other tuple s, the maximum possible overlap of (r, s) is $\min\{t, q\} + (L_g(r) - t) = L_g(r) + \min\{0, q - t\}$. Therefore the similarity score $sim_g(r, s) \leq \frac{L_g(r)+\min\{0,q-t\}}{L_g(r)+L_g(s)-(L_g(r)+\min\{0,q-t\})} \leq \frac{L_g(r)+\min\{0,q-t\}}{L_g(r)} = 1 - \frac{\max\{0,t-q\}}{L_g(r)}$. The equality can be achieved when s has length of $L_g(s) = L_g(r) + \min\{0, q - t\}$ with all tokens appearing in r. □

Lemma I.1 shows the new probing similarity upper bound for prefix event generation in QJoin. When QJoin terminates, we can classify all tuple pairs of $A \times B$ into 4 parts.

(1) the verified set, denoted as V. All tuple pairs in this set will have q common tokens in the prefix and the similarity scores will be actually calculated (verified as a top-k candidate).
(2) the active set, denoted as K, contains all pairs with common tokens in the prefix but the number is less than q. We can further decompose this set into K_1 and K_2. For each tuple pair (a, b) in K_1, all prefix events generated by tokens in a and b have been visited, meaning (a, b) has been verified in fact but the overlap is less than q. All pairs in this set will be traversed before the termination of QJoin to update T (the traverse is cheap since we have the number of common tokens for each pair). For each pair (a, b) in K_2, at least one token in a or b hasn't been visited in the prefix event queue.
(3) the filtered set, denoted as F. All tuple pairs in this set have no common token in the prefix and therefore are filtered from considering as a top-k candidate.
(4) the candidate set C. Pairs in this set should not appear in the top-k list.

Let T be the top-k list returned by QJoin, and t_{lb} be the largest value of the unvisited prefix events at the termination of QJoin. We know for any (a, b) in T, the similarity score $sim_g(a, b) \geq t_{lb}$. Since T contains the top-k pairs in V and K_1. We only need to prove all similarity scores in $K_2 \cup F$ are less than or equal to t_{lb}.

Lemma I.2. *The similarity scores of all pairs in $K_2 \cup F$ are less than or equal to t_{lb}.*

Proof. We first consider F. Pairs in F can be split into two parts F_0 and F_1. F_0 contains all pairs with no token can be added into the prefix event queue, meaning the pairs are actually verified with similarity score 0 which is less than t_{lb}. $F_1 = F \setminus F_0$ contains all pairs with at least one unseen token that can be extended into the prefix. Specifically, for each $(a, b) \in F_1$, suppose a has unseen tokens and the first index is i. Clearly $sim_g(a, b) \leq 1 - \frac{i}{L_g(a)} < u_{p,i} = 1 - \frac{\max\{0,i-q\}}{L_g(a)} \leq t_{lb}$.

For each $(a, b) \in K_2$, suppose a has unseen tokens and the first index is i. Because a and b share at most q tokens in the prefix, we have $sim_g(a, b) \leq 1 - \frac{\max\{0,i-q\}}{L_g(a)} = u_{p,i} \leq t_{lb}$.

Thus, for each pair $(a, b) \in K_2 \cup F$, we have $sim_g(a, b) \leq t_{lb}$. □

Lemma I.2 shows that all pairs in $K_2 \cup F$ have similarity scores less than or equal to t_{lb}. As we mentioned above, T contains the top-k pairs in $V \cup K_1$ with similarity scores no less than t_{lb}, therefore T contains the top-k pairs in $A \times B \setminus C$. This proves the correctness of QJoin.

I.2 Correctness of JTSJ

Based on the correctness of QJoin, it's obvious that the parallel processing of configs without reusing will be correct as each QJoin on a config will run independently on a single thread. So we only need to prove that concurrent execution of multiple configs with reusing will produce correct top-k lists for all of them. The following proof will be based on the condition of concurrent execution of the configs as describe in Algorithm 1. Two reusing strategies have been utilized which are *reusing similarity score computations* and *reusing top-k lists*, as described in Section 4.2. Since they are unrelated to each other, we prove the correctness of each.

Reusing Similarity Score Computations: Recall we reuse similarity score computations across configs described in Section 4.2. Specifically, for each $g \in G$, if g has a subtree, we will maintain a database H_g for it.

Lemma I.3. *Let $G_s \in G$ be the set of configs having a subtree. For each $g \in G_s$, H_g will record the correct reusing information for all tuple pairs that have been verified in* QJoin *on g.*

Proof. Since we maintain a separate H_g for each $g \in G_s$, during the execution of Algorithm 1, there will be one and only one thread updating H_g which is the one executing QJoin on g. Hence there are no writing conflicts to each H_g. So we only need to prove for each descendant $r \subset g$, if a tuple pair (a, b) having reuse information in H_g, we can get the correct similarity score for it on r. Let $g = \{f_{g_1}, f_{g_2}, \ldots, f_{g_k}\}$ with k attributes. By definition the reuse information $I_g(a, b) = \{o(f_i, f_j) \mid (f_i, f_j) \in g \times g\}$. As $r \subset g$, it's easy to get $Overlap_r(a, b) = \sum_{(f_i, f_j) \in r \times r} o(f_i, f_j)$ from $I_g(a, b)$. Then we have $sim_r(a, b) = \frac{Overlap_r(a,b)}{L_r(a)+L_r(b)-Overlap_r(a,b)}$. This proves the lemma. □

Lemma I.3 proves that each database will maintain the correct information for reusing. The next lemma will show that no dirty read happens.

Lemma I.4. *Let g be a config with a database H_g and $r \subset g$ is a descendant. If g and r are executed concurrently, for any pair (a, b) that will be verified in* QJoin *on r, we can get the correct similarity score $sim_r(a, b)$ by only using $I_g(a, b)$ if we have the reuse information $I_g(a, b)$ in H_g.*

Proof. When QJoins on g and r are running concurrently, H_g is updated while QJoin on r is consulting it. So we only need to prove there is no dirty read when H_g is consulted for reusing. That is, for any pair (a, b) that is verified for QJoin on r, we will have either $I_g(a, b)$ in H_g with complete reuse information, or $I_g(a, b)$ not in H_g, but not some intermediate state in between (e.g., $I_g(a, b)$ in H_g with incomplete reuse information). This requires the insertion operation to H_g to be atomic. As mentioned in Section 4.2, we use the Atomic Unordered Hashmap in Facebook's C++ Folly package which guarantees atomic insertion to H_g, no dirty read will happen. This proves the lemma. □

Based on Lemma I.3 and I.4, we show for any config $g \in G$, we can get the correct top-k list by reusing similarity computation. Let $N = \{n \mid \text{ancestors of } g \text{ in } G\}$, and $H_N = \{H_n \mid n \in N\}$ be the corresponding reuse databases. For any pair (a, b) that will be verified by the QJoin on g, by Lemma I.3 if we have the reuse information $I_n(a, b)$ for some $n \in N$, $I_n(a, b)$ will record correct reuse information. According to Lemma I.4, for any $n \in N$ that is concurrently executed with g, if $I_n(a, b)$ exists, we can get the correct $sim_g(a, b)$ by using $I_n(a, b)$. This proves the correctness of reusing similarity computations in JSTJ.

Reusing Top-k lists: The correctness of reusing top-k lists is obvious. Let T_g be the actual top-k list for config g, and $\hat{T}_g$ be the top-k list right after merging its parent's top-k list. Denote $T_g[i]$ be the similarity score of i-th pair of T_g sorted from high to low (similar for $\hat{T}_g[i]$). Clearly we have $\hat{T}_g[k] \leq T_g[k]$. According to QJoin, all pairs with similarity scores greater than $\hat{T}_g[k]$ will be found and inserted into $\hat{T}_g[k]$. This means at the termination of QJoin, $\hat{T}_g$ will be identical to T_g or $\hat{T}_g[k] = T_g[k]$. As we will only merge the top-k list after QJoin on g's parent is finished, there is no concurrency issue for the merging procedure. All of these prove the correctness of reusing top-k lists in JSTJ.

I.3 Extending to All Measures in $\mathcal{M}_{set}$

To generalize QJoin to all measures in $\mathcal{M}_{set}$, we need to modify the probing similarity upper bound. It's not hard to prove the following upper bound for each measure which is similar to the deduction in Lemma I.1: Jaccard similarity measure with $u_{Jaccard,t} = 1 - \frac{\max\{0,t-q\}}{L_g(s)}$, cosine similarity with $u_{cosine,t} = \sqrt{1 - \frac{\max\{0,t-q\}}{L_g(s)}}$, Overlap similarity with $u_{Overlap,t} = L_g(s) - \max\{0, t - q\}$, and Dice similarity with $u_{Dice,t} = \frac{2(L_g(s)-\max\{0,t-q\})}{2L_g(s)-\max\{0,t-q\}}$.

It's easy to extend reusing similarity score computations to all measures in $\mathcal{M}_{set}$, since the calculation of similarity scores in $\mathcal{M}_{set}$ only requires the number of common token overlap of a tuple pair and the information is stored in the reusing databases.