State-of-the-art in String Similarity Search and Join

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ABSTRACT

String similarity search and its variants are fundamental problems with many applications in areas such as data integration, data quality, computational linguistics, or bioinformatics. A plethora of methods have been developed over the last decades. Obtaining an overview of the state-of-the-art in this field is difficult, as results are published in various domains without much cross-talk, papers use different data sets and often study subtle variations of the core problems, and the sheer number of proposed methods exceeds the capacity of a single research group. In this paper, we report on the results of the probably largest benchmark ever performed in this field. To overcome the resource bottleneck, we organized the benchmark as an international competition; this means that various teams from different fields and from all over the world developed or tuned programs for two crisply defined problems. All algorithms were evaluated by a single group on the same machine. Altogether, we compared 14 different programs on two string matching problems (k-approximate search and k-approximate join) using data sets of increasing sizes and with different characteristics from two different domains. We compare programs primarily by wall clock time, but also provide results on memory usage, indexing time, batch query effects and scalability in terms of CPU cores. Results were averaged over several runs and confirmed on a second, different hardware platform. A particularly interesting observation is that disciplines can and should learn more from each other, with the three best teams rooting in computational linguistics, databases, and bioinformatics, respectively.

Keywords

String search, String join, Scalability, Comparison

1. INTRODUCTION AND MOTIVATION

Approximate search and join operations over large collections of strings are fundamental problems with many applications. String similarity search is used, for instance, to identify entities in natural language texts [39], to align DNA sequences produced in modern DNA sequencing with substrings of a reference genome [20,21], or to perform pattern matching in time series represented as sequences of symbols [11]. String similarity joins are building blocks in the detection of duplicate Web pages [16], in collaborative filtering [3], or in entity reconciliation [8]. Research in this field dates back to the early days of computer science and the area is still highly active today. Literally hundreds of methods have been proposed.

For similarity search and join, fundamental techniques include dynamic programming, seed-and-extend methods (turning similarity search into an exact search problem of smaller strings, e.g. All-Pairs [3], ED-Join [41], and PPJoin [42]), partitioning techniques (e.g. NGPP [39] and PartEnum [1]), prefix-filtering methods (e.g. Trie-Join [9] and PEARL [28]), and other (e.g. M-Tree [6], LSH [14], SSI [10], and FASTSS [32]). Research in the field has been carried out in various scientific disciplines, the most important ones probably being

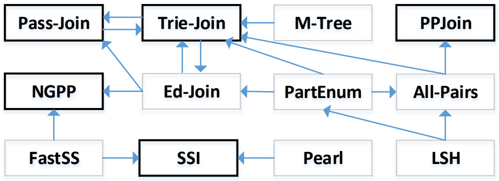

Figure 1: Recent work on string similarity search and join with edit distance constraints. An edge from method M1 to M2 visualizes that M2 was found to be superior to M1. Marked approaches are non-dominated, i.e. not reported strictly slower than any other method.

algorithms for pattern matching, computational linguistics, bioinformatics, and database / data integration. There are also subtle differences between the problems being studied, for instance varying in the concrete similarity measure (edit distance, Jaccard, Hamming etc.), the type of string comparisons (global or local alignment, approximate substring search etc.), the amount of indexing being allowed (online in the queries and/or the database). Methods often are tuned for specific ranges of allowed error thresholds or query lengths, specific hardware properties, specific alphabet sizes, or specific distributions of errors. Though newly published methods mostly compare to some prior works, selection of these works is often suboptimal and comparisons are carried out on different data sets; data sets all too often are not made publicly available, which means that results are not reproducible. In Figure 1, we show existing evaluation results for the most relevant work on string similarity search/join with edit distance constraints. As a consequence of the heterogeneity of approaches and problems, the lack of common benchmarks, and the dispersal of research in different communities, today it is hardly possible to choose the best algorithm for a given problem.

In this work, we report on the (to the best of our knowledge) most comprehensive benchmark in two specific string similarity match problems to date: k-approximate search and k-approximate join (see below for exact definition). As the number of published solutions is vast, our resources are limited, and programs are often not available for download, we organized this benchmark using a rather uncommon approach: An *International competition on Scalable String Similarity Search and Join (S4)*[1]. We made an open call for contributions and provided crisp task definitions, a loose hardware specification and example data. Nine teams from different parts of the world and stemming from different communities participated, including databases, natural language processing and bioinformatics. Thus, for the first time, we were able to evaluate different highly competitive implementations of search and join algorithms on the same evaluation platform (hardware, operating system, and datasets). In addition, organizing the benchmark as a competition, where teams developed and tuned their own programs independently, allowed us to compare original and optimized programs instead of our own, unverified and unoptimized re-implementations.

All submitted programs were tested on different datasets (DNA sequences and geographical names) of different sizes (a few KB up to a few GB) with different error thresholds (edit distance k between 0 and 16). We performed experiments in two different hardware settings: a commodity PC with 8 cores/64 GB RAM and a server with 80 cores/1 TB RAM. For the top performing programs we performed additional analyses with different number of threads to investigate the possibility to parallelize algorithms. We also performed experiments to analyze load balancing, batch-processing capabilities, and main memory usage. Furthermore, we compared submissions with a number of publicly available algorithms of groups that did not participate, showing that the best ranked programs from our competition are several orders of magnitude faster. Altogether, 14 different programs or configurations were evaluated with differences in runtime of factors of more than 1000 between the fastest and slowest program. We are confident that our results give a fairly representative picture of the state-of-the-art in string similarity search. The evaluation of all programs and datasets took more than three months of raw processing time.

The wealth of experiments we performed and the significant number of programs we compared allows us to draw several interesting conclusions. For instance, the batch processing effect is clearly visible for most implementations: while answering a single query takes up to several dozen milliseconds, for most programs the answering time per query is down to a few microseconds in batch mode (up to 200.000 queries). Two out of three top programs scale well with the number of threads, e.g. increasing the number of threads by a factor of 10 decreases the search time by a factor of 4–6. Scalability with the number of threads for the similarity join operation is not as good: only a speed up factor of 2–4 is achieved. We observed that larger data structures do not correlate with shorter search times. Indeed, the fastest program for searching our largest geographical names dataset (raw data size is 17 MB) only needs 2 GB of main memory, which is the second lowest main memory footprint among all teams. On the other hand, the second fastest search program on the same data uses 16 GB of memory.

The purpose of this paper is not only to report on efficiency of algorithms in string similarity search, but also to promote competitions as an effective, joyful, and comprehensive means to evaluate the state-of-the-art on a given problem. Actually, competitions are quite common in many related disciplines, such as information extraction, information retrieval, data analysis etc., but, to our knowledge, represent a novel approach within the database community. The only comparable effort we are aware of is the SIGMOD programming contest. However, it only addresses graduates and the focus is more on education (and probably recruitment). In contrast, the main purpose of S4 was to identify the fastest methods available.

Clearly, the most critical point for a competition like S4 is the measurement of wall clock time, which is dependent on the concrete implementation and the machine being used for measurements, instead of quality metrics independent of the concrete implementation and evaluation environment (such as precision or recall). We will expand on this issue in Section 6.

The remainder of this paper is organized as follows. We describe the concrete problems we benchmarked, the datasets, and the benchmarking methodology in Section 2. All submitted methods are briefly presented in Section 3. Evalua-

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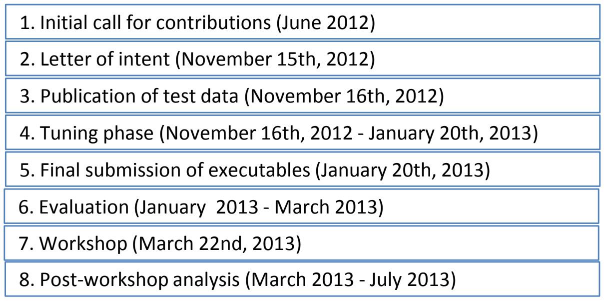
[1] `http://www2.informatik.hu-berlin.de/~wandelt/searchjoincompetition2013/`



1. Initial call for contributions (June 2012)
2. Letter of intent (November 15th, 2012)
3. Publication of test data (November 16th, 2012)
4. Tuning phase (November 16th, 2012 - January 20th, 2013)
5. Final submission of executables (January 20th, 2013)
6. Evaluation (January 2013 - March 2013)
7. Workshop (March 22nd, 2013)
8. Post-workshop analysis (March 2013 - July 2013)

Figure 2: Phases of the competition

tion results for approximate string searching are presented in Section 4 and for approximate string join in Section 5. In Section 6, we discuss the results of the competition and compare results to three external programs, Flamingo [4], Pearl [28], and SSI [10], which were evaluated after our competition was finished. The paper is concluded with Section 7.

2. BACKGROUND

We define the problems of approximate string searching and approximate string join. Our competition and evaluation methodology is introduced together with a description of datasets and evaluation environments.

2.1 Formal problem statement

Definition 1 (Strings). *A string s is a finite sequence over an alphabet Σ. The length of a string s is denoted by $|s|$ and the substring starting at position i with length n is denoted by $s(i, n)$. We write $s(i)$ as an abbreviation for $s(i, 1)$. All positions in a sequence are zero-based, i.e., the first character is accessed by $s(0)$.*

As a distance function between two strings we use unweighted edit distance for different error thresholds k.

Definition 2 (Similarity of Strings). *Given strings s and t, s will be called* k-approximately similar to t, *denoted $s \sim_k t$, if s can be transformed into t by at most k edit operations. The edit operations are: replacing one symbol in s, deleting one symbol from s, and inserting one symbol into s.*

We investigate two problems: string similarity search and string similarity join.

Definition 3 (Similarity search). *Given a collection of strings $S = \{s_1, ..., s_n\}$, a query string q, and an edit distance threshold k, the result of* string similarity search of q in S *is defined as $SEARCH(S, q, k) = \{i \mid s_i \in S \wedge s_i \sim_k q\}$.*

For instance, given a collection $S = \{ACA, TGA, AC\}$, a query string $q = ACA$, and $k = 1$, the result of string similarity search is $SEARCH(S, q, k) = \{1, 3\}$.

Definition 4 (Similarity (self) join). *Given a collection of strings $S = \{s_1, ..., s_n\}$ and an edit distance threshold k, the result of* string similarity self-join of S *is defined as $JOIN(S, k) = \{(i, j) \mid s_i \in S \wedge s_j \in S \wedge s_i \sim_k s_j\}$.*

For instance, the result of a string similarity self-join on data set S from above with $k = 1$ is $JOIN(S, 1) = \{(1, 1), (1, 3), (2, 2), (3, 1), (3, 3)\}$. Note that we explicitly include the reflexive and symmetric closure in our definition. We note that a self-join is comparable to a join between two different sets as we make no assumptions about the a priori average level of similarity of the strings in a set. In the following we will often use the term join instead of self-join.

2.2 Competition and methodology

This competition brought together researchers and practitioners from database research, natural language processing, and bioinformatics. The challenge for all participants was to perform string similarity search and join over unseen data and query sets with varying error thresholds k as fast as possible. The call for the competition was circulated by email through various lists addressing the different areas dealing with string matching, in particular databases, algorithms, computational linguistics, and bioinformatics. We also contacted directly a few dozen researchers known for their contributions to the field. The different phases of the competition are shown in Figure 2.

In total we received initial expressions of interest from 22 teams, out of which 11 teams officially submitted a program. One team failed to hand in a complete paper describing their approach on time, and another group withdrew shortly before the final deadline. Thus, we eventually compared programs from 9 teams (see Table 1).

We succeeded in reaching out to different research communities: two teams have their home in bioinformatics, two in computational linguistics, one in algorithms/computational complexity, and the remaining four are best described as database groups. Contributions came from four continents and seven countries. At least six teams published highly influential papers on string matching problems before [19, 23, 30, 33, 37, 43], while three teams can be considered as newcomers. As Table 1 shows, the techniques used cover a broad range and thus subsume a large fraction of previous research in k-approximate string matching. Note that at least one author from four out of the five non-dominated methods in Figure 1 took part in our competition.

The competition consisted of two tracks:

Track 1: Given a collection of strings S, a query string q and an error threshold k, compute $SEARCH(S, q, k)$.

Track 2: Given a collection of strings S and an error threshold k, compute $JOIN(S, k)$.

Small subsets of the final evaluation datasets (around 5%) were made available for the contestants for preparation of their submissions. It was announced that these strings are representative for the whole evaluation datasets. Furthermore, we announced a description of the evaluation hardware and provided a virtual machine mirroring the software environment used for evaluation. Thus, all teams could develop and tune their programs before submission. Each program was allowed to use any number of threads, with the restriction that the official evaluation environment System 1 (see below) has 8 cores, and a maximum of 48 GB of main memory. Details on CPU, clock rate, cache sizes, disks etc. were not provided to prevent hardware specific tuning; note that this implies that further improvements could be possible taking the specific hardware into account [24]. Programs were allowed to have two phases, one for indexing the data set, and one for evaluating a set of queries on the set (or the index).

The main evaluation criterion was measured wall clock time. In general, we ranked programs based on average runtime over three independent runs; variations in runtime were very low and are not reported here. If programs ran much longer than most of the competitors, experiments were only performed once. We also measured the indexing time and report it here, but we did not take it into account for ranking.

Team	Affiliation	General approach	Indexing?	Indexing query set?
1	Tsinghua University, China	Partitioning and pruning [18,19]	yes	no
2	Universitaet Magdeburg, Germany	Sequential search [15]	no	no
3	University of Warwick, UK	Bit-parallel LCS computation [33,34]	no	yes
4	Sofia University, Bulgaria	Symmetric compact directed acyclic word graph [13,23]	yes	no
5	FU Berlin, Germany	Approximate partitioning and bit-parallel verification [30,31]	yes/no	yes/no
6	IIT Kanpur, India	Deletion neighborhoods / hashing [2]	yes	no
7	Louisiana State University, USA	Q-gram indexing with filtering [26]	yes	no
8	University of New South Wales, Australia	Trie-index with filtering [27,43]	yes	no
9	Northeastern University, China	BWT, cache-aware implementation [38]	yes	no

Table 1: Teams which participated in the competition

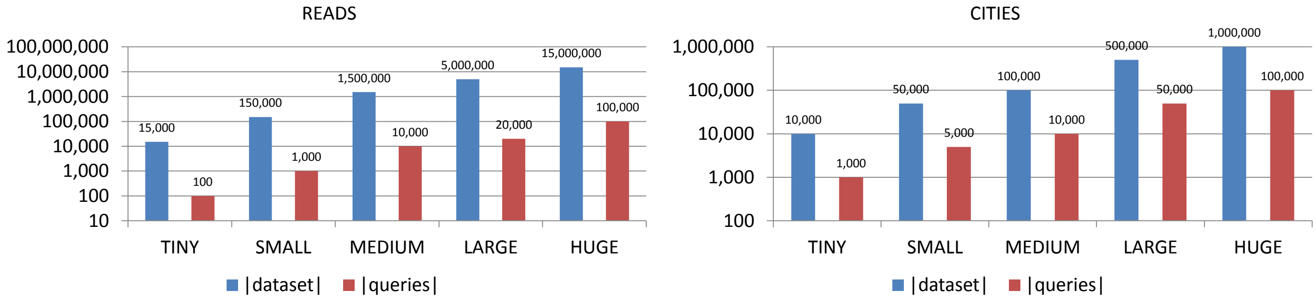


Figure 3: Size of dataset and number of queries used for evaluation (READS and CITIES)

2.3 Datasets

We used two different types of datasets for evaluation in both tracks, to cover different alphabets and string lengths.

READS: These data sets contain reads obtained from a human genome. The data is characterized by a small alphabet (5 symbols) and quite uniform length of strings (around 100 symbols per string).

CITIES: These data sets are based on geographical names taken from World Gazetteer. The data is characterized by a larger alphabet (around 200 symbols) and non-uniform length of strings (5-64).

Considered values for k depend on the dataset. For READS, we announced and used $k \in \{0, 4, 8, 12, 16\}$; for CITIES $k \in \{0, 1, 2, 3, 4\}$. The implied maximum error rate for READS is around $\frac{1}{6}$ and for CITIES around $\frac{4}{5}$. To better evaluate scalability of submissions, we created five datasets and query sets of different sizes for each type of data (READS and CITIES). The size of each dataset and the number of queries for Track 1 are shown in Figure 3. For READS, the number of reads starts with 15,000 (TINY) and ends with 15,000,000 (HUGE). For CITIES, the number of cities starts with 10,000 (TINY) and ends with 1,000,000 (HUGE). For READS and CITIES, the maximum number of queries in HUGE is 100,000.

2.4 Evaluation Environments

After the development phase of the competition, participants submitted their final programs which were evaluated on two different platforms.

System 1: A computer with 8 cores (processor: AMD FX-8320) and 64 GB RAM. The operating system (Fedora Scientific 17 x86_64) was installed on a SSD with 128 GB. The SSD contained the datasets as well as the programs. Each program serialized its results to an external USB 3.0 hard disk with 3 TB. This system was announced beforehand and results for this system were used for ranking.

System 2: A server with 80 cores (processors: Intel Xeon CPU E7 - 4870) and 1 TB RAM. The operating system was openSUSE 12.1 x86_64. All datasets, programs, and serialized results were put on a local hard disk with a total storage capacity of 10 TB. This system was introduced only during evaluation for (a) performing experiments with more cores / memories and for (b) confirming results on a separate hardware with different architecture and CPUs.

Most of the experiments were run on System 1. We have used System 2 only for an extended evaluation, investigating the scalability with the number of threads (for top performing methods on System 1). In our evaluation below, we will mention explicitly if System 2 was used. Note that the executables and configuration for both systems was exactly the same, besides the parameter for the number of threads.

3. METHODS

This section describes the methods used by each team in their submissions to the competition.

3.1 Team 1

PassJoin [18] adopts a partition-based framework for string similarity search and joins. The basic idea is that given two datasets R and S, and an edit distance threshold k,

each string in R is split into $k+1$ disjoint segments. For each string in S, PassJoin checks if it contains any substring matching the segments of R. If no, PassJoin prunes the string; otherwise the string and those strings whose segments match the substrings of the string are verified. There are two challenges in the partition-based method. The first one is how to select the substrings. A position-aware substring selection method and a multi-match-aware substring selection method have been proposed. It has been proven the multi-match-aware substring selection method selects the minimum number of substrings. And it is the only way to select the minimum number of substrings when the string length is longer than $2 * k + 1$. The second one is how to verify each candidate pair. PassJoin uses a length-based verification method, an improved early termination technique, and an extension-based verification method.
Team 1 submitted two programs: **Program 1_A** and **Program 1_B**. Both programs of Team 1 were evaluated for both tracks and both datasets.

3.2 Team 2

Team 2 tries to outperform conventional index-based searches by a sequential search algorithm, i.e., strings from the database are compared sequentially to every query string. Starting from a naive algorithm for computing edit distances, several optimizations are introduced [15]. Calculation of the edit distance is improved by using length-heuristics, i.e. if the difference in length between two strings is larger than the edit distances, then the pair is rejected and no further tests performed. If the computation of a dot matrix cannot be avoided, the program applies several heuristics to prune the search space early. Further optimizations include the use of reference-based semantics over value-based semantics and the use of simple data types. They devise simple scheduling strategies depending on the current workload.
Team 2 submitted only one program: **Program 2_A**, which was evaluated for Track 1 only.

3.3 Team 3

The Waterfall algorithm [34] solves the competition challenge without indexing or any other preprocessing of the database strings. First, a reduction of the edit distance problem to the longest common subsequence (LCS) problem between the database string and the query string, both suitably modified, is applied. The strings' LCS score is then computed by a bit-parallel algorithm, based on [7]. This technique is extended so that a database string can be tested simultaneously against multiple query strings, by a subword-parallel technique similar to that of [17], which was further developed in the waterfall algorithm. Due to the self-imposed restriction of not preprocessing the database, the algorithm runs significantly slower than other competitors, which do index the database strings before answering the queries. However, the approach chosen by Team 3 can prove useful in a situation where input preprocessing is not possible. Such a situation occurs e.g. when the string database is replaced by a continuous stream of input strings, each of which needs to be matched against a small set of query strings in real time.
Team 3 submitted only one program: **Program 3_A**, which was evaluated for both tracks and both datasets.

3.4 Team 4

The WallBreaker [13] is a new sequential algorithm for the similarity search problem in a finite set of words. It reduces and essentially overcomes the wall-effect caused by the redundantly generated false candidates. To achieve this the query is split into smaller subqueries with smaller threshold. This allows to start with an exact match and then extend these exact matches to longer candidates whereas the threshold increases slowly in a stepwise manner. In order to implement this idea in practice two kind of resources are used: (i) a linear space representation of the infixes in the finite set of words that enables a left/right extension of an infix in constant time per character; and (ii) efficient filters, universal Levenshtein automata [22, 29], sychnorised Levenshtein automata [23] and standard Ukkonen filter [35], that prune the unsuccessful candidates as soon as a clear evidence for this occurs. In the index structure information about the possible lengths of longest/shortest left/right possible extensions are encoded. This information is then used as an additional length-filter.
As a result the following breaking-the-wall-effect is achieved. In the beginning the WallBreaker considers only small neighborhoods of short words which keeps the searching space modest. Afterwards, while increasing the potential size of the neighborhoods, longer infixes are generated that are much more informative than shorter ones and suppress the searching space for their own sake. For further details the reader is refered to [12], where besides the standard Levenshtein edit-distance also the generalized Levenshtein edit-distance is handled.
Team 4 submitted two programs:
Program 4_A: It uses **16** threads, the additional length-filter, and applies universal Levenshtein automata for thresholds $\leq \mathbf{5}$, and synchronised Levenshtein automata for thresholds $\leq \mathbf{3}$.
Program 4_B: It uses **16** threads, ignores the additional length-filter, and applies universal Levenshtein automata for thresholds $\leq \mathbf{5}$, and synchronised Levenshtein automata for thresholds $\leq \mathbf{3}$.
Both programs of Team 4 were evaluated for both tracks and both datasets.

3.5 Team 5

The methods of Team 5 [31] are variations of those applied in Masai [30], a tool for mapping high-throughput DNA sequencing data. First an online solution for computing edit distances using a banded version of the Myers bit-vector algorithm [21] is proposed. Team 5 is able to check in time $O\big(\frac{(k+1)(n+|\Sigma|)}{w}\big)$, where w is the CPU word size and Σ the string alphabet, if two strings of length m and n (w.l.o.g. $m < n$) are within edit distance k. Then they propose to index multiple queries in a radix tree and backtrack them into the radix (or suffix) tree of the database. In practice, radix (and suffix) trees are replaced by simpler radix (and suffix) arrays. Multiple backtracking is parallelized with static load balancing and work queues. Finally, as proposed by Navarro and Baeza-Yates [25], a filtering method partitioning queries into approximate seeds is implemented. Such a filtering method combines the previous two methods and works well up to moderate error rates. The programs are implemented in C++ and OpenMP using the SeqAn library.
Team 5 submitted four programs:
Program 5_A: An online algorithm.

Program 5_B: Partitioning with minimum seed length (10 for READS, 4 for CITIES)
Program 5_C: Partitioning with minimum seed length (13 for READS, 5 for CITIES)
Program 5_D: Partitioning with minimum seed length (15 for READS, 6 for CITIES)

3.6 Team 6

Team 6's submission [2] uses deletion neighborhoods [32] to map strings in S into a signature space. A k-neighborhood is generated for every string $s \in S$. Every string in the k-neighborhood is referred to as a key. The underlying index structure is a hash-table which is maintains an inverted index on the keys. In order to circumvent the large space requirement, the program only indexes an L_s-length suffix for each key. Given a query string q and an edit distance threshold k, first the k-neighborhood of q, N_q, is generated. The list corresponding to every key in N_q is obtained from the index structure. A union of these lists is guaranteed to be a superset of the answer set $SEARCH(S, q, k)$. For each string s in the generated candidate list, the program uses a length-threshold aware distance computation [18] to verify s. In a multi-core environment, the program partitions the entire workload into k equal parts and each part is handled by a single, dedicated thread. Team 6's idea is that deletion neighborhoods offer a powerful, selective signature scheme to process edit distance queries. Team 6 only participated in Track 1 of the competition. Further, since deletion neighborhoods are only suited for scenarios with larger alphabet size, Team 6's submission **Program 6_A** was only evaluated on CITIES dataset.

3.7 Team 7

The index structure of Team 7 [26] consists of a generalized suffix tree (GST) and a two-level wavelet tree (WT) on its leaves. The first level WT maintains an array of starting positions of all suffixes of GST. For each leaf of this WT, another WT for the difference between the starting position of the suffix and the string length to which it belongs to is maintained. Given τ, r, Team 7 obtains $\tau + k$ disjoint partitions of r aiming to balance selectivity of count filtering and frequency of partitioned segments. Then GST and WT are used to obtain inverted list of each partition pre-filtered by "Position Restricted Alignment" that combines the well-know length and position filters. All inverted lists are then merged to retrieve the strings similar to r.
Team 7 submitted only one program: **Program 7_A**, which was evaluated for Track 1 with READS only.

3.8 Team 8

Team 8 presents [27] a solution based on tries, which have the advantages of small indexing space, freeness of verification, and computation sharing among strings with common prefixes. The method proposed is a simple adaptation of trie-based error-tolerant prefix matching [40]. Existing trie-based methods process a query by incrementally traversing the trie and maintaining a set of trie nodes (called active nodes) for each prefix of the query. One common drawback is that they have to maintain a large number of active nodes. Instead, Team 8 record only a small number of potentially feasible nodes as "active nodes" during query processing, which reduces the overhead of maintaining nodes and reporting results. In addition, Team 8 characterizes the essence of edit distance computation by a novel data structure named edit vector automaton, which substantially accelerates the state transition of active nodes, and therefore, improves the total query performance. Naive parallelization is added to exploit multi-core CPUs.
Team 8 submitted only one program: **Program 8_A**, which was evaluated for Track 1 with CITIES only.

3.9 Team 9

BWTSearcher [38] of Team 9 takes advantage of a cache-aware multicore framework using BWT (Burrows-Wheeler-Transform, see [5]). BWTSearcher segments the whole collection of database sequences to fit to the CPU cache lines. The approximate string search algorithm is based on a partition approach. The query is decomposed into $\tau + 1$ chunks. If P matches the text with at most τ errors, at least one of the parts will match a substring of the text exactly. A new data structure called BWTPA is proposed to find the matching candidates. Length filter and position filter are used to prune the candidates. Team 9 proposed a reversed segment trie to merge the identical segments, which can save much duplicated computation. In addition, a look ahead algorithm is developed to support bounded edit distance and improve the verification of the candidate strings. BWT-searcher can search on any dataset, but is not optimized on DNA data, yet.
Team 9 has only one participating program: **Program 9_A**, which was evaluated on all datasets for Track 1.

4. EVALUATING APPROXIMATE STRING SEARCH METHODS

In the following section we report results for all submissions for Track 1: approximate string search. We present results for READS datasets first and then for CITIES.

4.1 Similarity Search for READS

In Figure 4, we show the indexing and search times for the READS dataset and random values for k (for each query in the dataset we have assigned a random number out of $\{0, 4, 8, 12, 16\}$). For READS-TINY and READS-SMALL most of the programs compute the results within a few seconds, with two exceptions. 2_A, the index-less approach, needs already 185 seconds for answering READS-SMALL. For READS-MEDIUM, 2_A did not compute a result within several hours, so it was not evaluated on the larger datasets. Program 5_A, another index-less approach, needs 23.9 seconds for READS-SMALL and around 45 minutes for READS-MEDIUM. Therefore, 5_A was not tested on READS-LARGE and READS-HUGE.
The fastest programs for READS-HUGE are 4_A and 4_B, taking 232.5 and 249.0 seconds, respectively. The third program is 1_A, which needs 312.1 seconds. However, the indexing time of 1_A is around 20 times shorter than the indexing time for 4_A and 4_B. Programs 1_B, 5_B, 5_C, and 5_D need 10 to 15 minutes for READS-HUGE. Program 3_A, which does not use an index structure, already needs 8 hours to compute all solutions for READS-HUGE.
In Figure 15, we show search times for different values of k and the dataset READS-MEDIUM. Note that for all the programs the indexing time is independent of the value of k, and is shown in Figure 4. Except 3_A and 9_A, all programs can compute the results set for $k \leq 8$ within few seconds.

	TINY		SMALL		MEDIUM		LARGE		HUGE	
Prog.	I	S	I	S	I	S	I	S	I	S
1_A	0.4	0.2	1.1	0.4	10.3	**4.3**	34.0	**24.5**	108.0	312.1
1_B	0.4	0.2	1.2	0.4	10.5	9.5	33.6	64.9	100.9	924.7
2_A	0.1	2.4	1.3	185.7	-	-	-	-	-	-
3_A	0.0	1.5	0.0	4.5	0.3	289.8	0.7	1,979.8	2.0	30,898.0
4_A	2.5	0.5	29.3	**0.2**	291.0	4.6	872.5	24.6	2,251.8	**232.5**
4_B	1.7	0.3	23.0	0.5	235.2	5.4	710.3	27.8	1,754.5	249.0
5_A	0.0	0.5	0.1	23.9	0.9	2,802.1	-	-	-	-
5_B	1.4	**0.1**	2.4	0.7	15.8	8.7	55.4	51.6	192.2	580.8
5_C	1.4	**0.1**	2.4	1.7	15.7	31.4	55.3	95.8	193.9	761.2
5_D	1.4	**0.1**	2.3	2.7	15.5	52.5	55.7	138.9	193.7	900.3
7_A	0.5	0.5	1.1	0.4	168.4	13.2	567.8	62.9	2,710.9	1,587.8
9_A	0.3	0.2	2.4	9.2	26.5	532.5	85.6	3,269.4	465.6	42,866.6

Figure 4: Indexing (I) and search (S) times for different READS datasets [time in seconds].

		8 threads		24 threads		80 threads	
READS-	Prog.	I	S	I	S	I	S
MEDIUM	1_A	16.6	**4.1**	15.8	**1.8**	14.6	**1.2**
	4_A	510.6	4.9	527.2	2.0	639.4	1.5
	5_B	25.0	14.7	24.9	17.4	18.1	16.6
LARGE	1_A	47.4	**26.3**	48.3	**10.9**	47.8	**7.0**
	4_A	1,851.3	27.0	1,518.6	12.8	1,740.8	8.1
	5_B	93.7	80.0	66.1	81.8	66.0	91.2
HUGE	1_A	131.8	371.7	134.9	137.7	131.1	82.1
	4_A	4,290.4	**245.3**	3,718.7	**87.2**	4,096.2	**42.8**
	5_B	301.2	1,237.5	240.3	1,186.4	2,172.2	1,403.7

Figure 5: Search times for READS-MEDIUM, READS-LARGE, and READS-HUGE on System 2 [time in seconds].

The best program for $k = 16$ is 4_A, needing only 17.8 seconds, followed by 4_B and 1_A. For all values of k, 4_A is among the fastest programs, only clearly outperformed by 1_A for $k = 12$.

We have further analyzed the effect of batch-processing for all programs for READS-MEDIUM and $k = 4$, except 2_A. In Figure 14, the average time per query for different number of queries is shown. It can be seen that for most programs, the average query answering time per query is reduced, if the number of queries is increased. For a large number of queries, the programs of Team 1 and Team 4 have the shortest time per query.

We have further evaluated the three top-performing programs on our second evaluation environment System 2 with a different number of threads. In Figure 5, the results of the evaluation are shown. It can be seen that 1_A and 4_A scale quite well with the number of threads: if the number of threads is increased by 3 (8 to 24), the search time is reduced by a factor larger than 2. The improvement from 24 threads to 80 threads is not as big any more. For 5_B there is almost no effect when increasing the number of threads. Their multiple backtracking algorithm is not straightforward to parallelize and the static load-balancing approach doesn't scale well. In this scenario it is probably easier to abandon multiple backtracking and go back to "standard" single backtracking, to allow a query-by-query parallelization.

	TINY		SMALL		MEDIUM		LARGE		HUGE	
Prog.	I	S	I	S	I	S	I	S	I	S
1_A	0.1	0.5	0.1	**0.4**	0.2	**0.9**	0.9	18.2	1.9	59.9
1_B	0.1	0.4	0.1	**0.4**	0.2	**0.9**	0.9	17.7	1.7	**46.8**
2_A	0.0	0.5	0.0	4.0	0.1	23.6	0.2	228.3	-	-
3_A	0.0	1.5	0.0	3.0	0.0	6.1	0.1	41.2	0.2	109.6
4_A	2.3	**0.2**	3.9	0.7	7.0	1.6	25.0	28.5	39.7	69.2
4_B	1.1	0.5	3.9	0.7	7.0	1.6	24.5	28.4	39.9	67.3
5_A	0.0	2.0	0.0	39.0	0.0	176.5	0.1	3,623.9	-	-
5_B	2.4	1.1	2.4	14.6	2.5	53.8	2.7	1,018.9	3.1	4,903.0
5_C	2.4	1.1	2.4	13.6	2.4	44.7	2.7	1,088.8	3.2	4,387.4
5_D	2.4	1.6	2.4	14.6	2.5	43.2	2.7	1,062.3	3.1	3,097.0
6_A	13.0	0.5	63.2	1.3	126.3	2.8	562.4	16.0	1,206.3	248.3
8_A	0.0	0.5	0.1	1.4	0.2	5.4	1.0	107.9	2.0	445.5
9_A	0.1	0.5	0.1	0.9	0.2	2.5	1.1	**15.2**	1.6	137.5

Figure 6: Indexing (I) and search (S) times for different CITIES datasets [time in seconds].

		8 threads		24 threads		80 threads	
CITIES-	Progr.	I	S	I	S	I	S
MEDIUM	1_A	0.21	**0.57**	0.22	**0.24**	0.27	**0.19**
	4_A	10.25	0.95	10.26	0.38	10.31	0.23
	5_B	0.77	158.15	1.20	133.68	1.36	103.95
LARGE	1_A	1.123	**12.84**	1.042	**5.341**	1.143	**3.222**
	4_A	33.283	17.68	33.353	7.297	33.686	4.377
HUGE	1_A	2.225	**43.615**	2.226	**19.679**	2.247	**11.529**
	4_A	52.903	57.473	53.53	28.283	53.175	21.057

Figure 7: Search times for CITIES on System 2 [time in seconds].

4.2 Similarity Search for CITIES

In Figure 6, we show the indexing and search times for the CITIES dataset and random values for k. For CITIES-TINY and CITIES-SMALL most of the programs compute the results within a few seconds. The only exception are the programs of Team 5, which need already 13.6 -39.0 seconds for CITIES-SMALL. All programs were tested on all datasets, with two exceptions. Programs 2_A and 5_A did not return a result for CITIES-HUGE within several hours. Indexing times are quite short for all programs, except 6_A, which almost spends 20 minutes on indexing CITIES-HUGE.

The fastest program for CITIES-HUGE is 1_B, needing 46.8 seconds. It is closely followed by 1_A, 4_A, and 4_B. The programs of Team 5 are the slowest for CITIES, which probably means that their approach is better suited to deal with small-alphabets.

In Figure 17, the search times for CITIES-MEDIUM and different values of k are shown. Programs 1_A and 1_B are always among the fastest.

We have further evaluated the three top-performing programs on our second evaluation environment System 2 with a different number of threads. In Figure 7, the results are shown. The results are very similar to the results of READS: Program 1_A and 4_A scale well from 8 to 24 threads and quite good for 24 threads to 80 threads. Program 5_B does not scale as well as the other two (and was not tested for CITIES-LARGE and CITIES-HUGE).

5. EVALUATING APPROXIMATE STRING JOIN METHODS

In the following section we report on results of all submissions for Track 2: approximate string join. Again, we present results for READS datasets first and then for CITIES.

	READS-HUGE (time in minutes!)				
Prog.	**k=0**	**k=4**	**k=8**	**k=12**	**k=16**
1_A	**0.2**	1.0	**3.7**	**84.4**	**1,377.3**
1_B	**0.2**	**0.9**	8.9	231.0	-
3_A	258.8	5,760.0	-	-	-
4_A	37.6	41.3	81.2	220.8	2,489.1
4_B	29.4	31.4	75.7	214.1	-
5_A	-	-	-	-	-
5_B	0.5	12.4	126.7	2,590.4	-
5_C	0.5	12.1	111.9	-	-
5_D	0.5	12.3	74.9	-	-
9_A	5.5	1,197.5	-	-	-

Figure 8: Join times for READS-HUGE and different k [time in minutes].

	CITIES-HUGE				
Prog.	**k=0**	**k=1**	**k=2**	**k=3**	**k=4**
1_A	**1.0**	1.9	**6.1**	**50.1**	**345.5**
1_B	1.1	**1.8**	6.8	53.8	353.0
3_A	588.1	564.1	655.8	847.6	1,700.0
4_A	40.9	45.5	81.2	440.6	945.0
4_B	39.7	42.2	78.8	418.3	942.0
5_B	11.3	78.3	1,719.2	-	-
5_C	11.3	37.1	726.2	11,462.5	-
5_D	11.4	32.8	785.9	-	-
8_A	3.3	21.2	218.2	3,339.2	21,230.0
9_A	10.9	28.9	198.7	1,912.9	-

Figure 9: Join times for CITIES-HUGE and different k [time in seconds].

5.1 Similarity Join for READS

In Figure 18 and Figure 20, we show the join times for the READS dataset, for $k = 0$ (a) and $k = 16$ (b), respectively. For $k = 0$, all programs have been tested for all datasets, except from 5_A. Program 5_A already needs around 30 minutes to perform a join on READS-SMALL. The fastest programs need less than 10 seconds to perform a self-join on READS-HUGE: 1_A and 1_B. For k=16, most programs could only be tested until READS-SMALL. Two programs were evaluated in READS-HUGE: Program 1_A needed 22.9 hours and Program 4_A needed 41.5 hours.

We report the join times for READS-HUGE and different values for k in Figure 8. Programs 3_A and 9_A already need more than 20 hours to perform a 4-approximate self-join on READ-HUGE. The best performing method is implemented in Program 1_A.

We have further evaluated the three top-performing programs on our second evaluation environment System 2 with a different number of threads. In Figure 21, the results are shown. For all programs a higher number of threads reduces the runtime. It is interesting to see that with an increasing value of k, the effect is bigger than with small numbers. We conjecture that the overhead of setting up the threads and synchronization is dominating for smaller k.

5.2 Similarity Join for CITIES

Join times for the CITIES dataset and are reported in Figure 22 for $k = 0$ and in Figure 19 for $k = 4$. Apart from Program 5_A, all programs finished to compute an exact self-join on all CITIES datasets. Program 1_A is the fastest program in each case. Team 4's programs are ranked second. Program 3 _A finishes third, which is quite remarkable for an index-less approach.

The join times for CITIES-HUGE and different values of k are reported in Figure 9. Program 1_A is the best for all values of k, except for $k = 1$, where it is outperformed slightly by 1_B. We did not test the index-less approach 5_A. We have further evaluated the three top-performing programs on our second evaluation environment with a different number of threads. In Figure 23, the results are shown. For all programs a higher number of threads reduces the runtime. The results show a similar behavior as when joining READS: it seems that performing a join with a small k usually is better with a small number of threads, while for larger values of k it makes indeed sense to make use of parallelism.

6. POST-COMPETITION ANALYSIS

The main results of our competition are shown in Figure 10. For each task and dataset we list the techniques used by the three top performing teams. The partitioning and pruning techniques of Team 1 show the best performance for three out of four problems. Only for searching our READS dataset, the acyclic word graph of Team 4 slightly outperforms Team 1's techniques.

In the following we discuss our results and related it to existing work not covered by the competition.

6.1 Additional algorithms

We compare the results of the competition to existing tools for approximate string search. We only take into account non-dominated methods from Figure 1, for which no participant of our competition had a direct contribution. The only such non-dominated method is SSI [10]. In addition, we test two other methods: Flamingo [4], which is often used as baseline for evaluation, and Pearl [28], a prefix tree index. The results are shown in Figure 11, together with the comparison of the best three ranked programs from our competition.

Unfortunately, Flamingo has only implemented approximate search, no approximate join. We run Flamingo with the standard configuration (filters as set by the GettingStarted-example) and different length of q-grams. Index and search times are considerably longer than many of the competitors in our competition. However, note that Flamingo makes only use of one thread and the memory footprint seems to be very small. Possibly, performance of Flamingo can be further improved by additional filters. We have tested SSI only on the READS datasets. For each CITIES dataset, SSI stopped with a insufficient memory exception. This might be a bug affecting the handling of large alphabets.

The best programs from our competition outperform these tools by a factor of 1000 and more for READS-MEDIUM and a factor of 50 and more for CITIES-HUGE. In addition, we have evaluated Pearl for joining GEONAMES datasets: Even for GEONAMES-MEDIUM and $k = 4$, Pearl needs more than 1 hour to compute the self-join, while 1_A needs less than 2 minutes. Given the existing evaluation results from Figure 1, for each non-dominated method either one of its authors has contributed to our competition (Pass-Join, Trie-Join, PPJoin, NGPP) or the method (SSI) was shown to be way less scalable than our best programs. Therefore, we believe that our analysis represents the state-of-the-art in string similarity search and join.

	place	READS	CITIES
search	1	4_A (acyclic word graph)	1_A (partitioning and pruning)
	2	1_A (partitioning and pruning)	4_A (acyclic word graph)
	3	5_B (radix/Suffix trees)	3_A (bit-parallel LCS computation)
join	1	1_A (partitioning and pruning)	1_A (partitioning and pruning)
	2	4_A (acyclic word graph)	4_B (acyclic word graph)
	3	5_B (radix/Suffix trees)	3_A (bit-parallel LCS computation)

Figure 10: Overall ranking for search and join.

CITIES:	SMALL		MEDIUM		HUGE	
Prog.	Index	Search	Index	Search	Index	Search
Flamingo |q|=2	0.1	4.7	0.2	26.6	-	-
Flamingo |q|=3	0.2	7.6	0.4	42.8	-	-
Flamingo |q|=4	0.2	9.7	0.5	55.4	-	-
Pearl	2.9	33.5	6.4	74.9	99.4	2,541.1
SSI						
1_B	0.1	0.4	0.2	0.9	1.7	46.8
4_B	3.9	0.7	7.0	1.6	39.9	67.3
3_A	0.0	3.0	0.0	6.1	0.2	109.6

READS:	SMALL		MEDIUM		HUGE	
Prog.	Index	Search	Index	Search	Index	Search
Flamingo |q|=5	2.1	45.9	-	-	-	-
Flamingo |q|=6	2.3	44.1	36.8	6,052.2	-	-
Flamingo |q|=7	3.0	443.7	-	-	-	-
Pearl	10.1	3,567.0	-	-	-	-
SSI	0.4	27.7	1.2	5,032.1	-	-
4_A	29.3	0.2	291.0	4.6	2,251.8	232.5
1_A	1.1	0.4	10.3	4.3	108.0	312.1
5_B	2.4	0.7	15.8	8.7	192.2	580.8

Figure 11: Indexing and Search times for Flamingo, Pearl, and SSI [time in seconds].

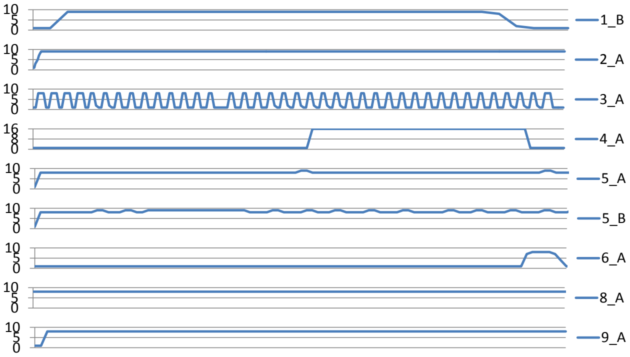


Figure 12: Searching CITIES-LARGE: number of active threads from the beginning of the program until its termination. Note that all the programs had a different run time, the x-axis has a different scale for each program.

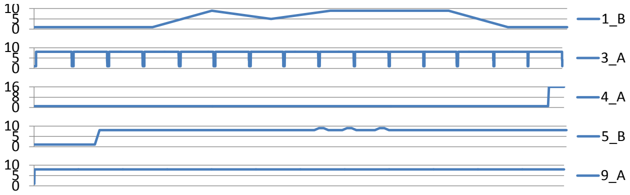


Figure 13: Joining READS-Medium with k=4: number of active threads from the beginning of the program until its termination. Note that all the programs had a different run time, the x-axis has a different scale for each program.

6.2 Memory usage

We show the peak main memory usage with respect to READS-Huge in Figure 16. Programs 5_B, 5_C, and 5_D only use around 13.6 GB of main memory, followed by 3_A with 15.6 GB. The maximum amount of main memory is used by 9_A with 40.6 GB. The average main memory is 24.2 GB, which means that all the programs make use of roughly half of the main memory available.. In Figure 24, the peak main memory usage for the dataset CITIES-HUGE is shown. Most of the programs show modest memory usage; the average is only 6 GB. The most main memory is used by Program 6_A: 24.7 GB, followed by 4_A and 4_B with 12-13 GB. Program 9_A only uses 0.6 GB of main memory. Thus, most of the main memory is left unused. We conjecture that it should be possible to further improve query answering times by pre-computation of more sophisticated index structures.

6.3 CPU utilization

In Figure 12, the number of active threads is shown over time when searching CITIES-LARGE. The graphs of 1_A, 4_B, 5_C, and 5_D are not shown since they are very similar to 1_B, 4_A, 5_B, and 5_B, respectively. Most of the programs start preprocessing with one thread and then increase the number of threads. Program 3_A is the only program which does not follow this pattern. Load scheduling of programs 1_B and 4_A can possibly be improved, since these programs do not make constant use of the full number of available cores. Program 4_A has a long single-thread preprocessing phase; queries are answered using 16 threads.

In Figure 13, the number of active threads is shown over time when joining READS-MEDIUM with $k = 4$. The graphs of 1_A, 4_B, 5_C, and 5_D are not shown since they are very similar to 1_B, 4_A, 5_B, and 5_B, respectively. The overall join time for 1_B is only few seconds, so the graph is not as stable as the other ones. For Program 4_A and 5_B the preprocessing phase can be clearly identified (with only one thread). Program 4_A makes use of 16 threads again instead of only 8. Program 9_A uses 8 threads for most of the time. (only the first few seconds are run with only one thread).

6.4 Redundancy

The official rules allowed to serialize the same answer several times: sometimes the same result is found by different components of a search algorithm independently. In Figure 25, we analyze the redundancy in the results.

7. CONCLUSION

We believe that our evaluation gives a fairly representative picture of the state-of-the-art in string similarity search and join for different data set sizes, different alphabet sizes, and different error thresholds.. Based on our datasets and competing programs, we conclude that an error rate of 20-25% pushes today's techniques to the limit. For instance, self-joining a set of 15.000.000 sequence reads of length 100 with an edit distance threshold $k = 16$ takes almost one day even for the best participant. However, the final result has more than 50.000.000 entries, which makes the usefulness of such queries in real applications questionable.

Our experiments showed that many participants used less main memory than available. The effect is perspicuous for our CITIES dataset: more than half of the competitors used less than 10 percent of the main memory. An interesting lead for future research are indexing strategies that make full use of existing main memory. Even for smaller datasets, query answering times might be further reduced by more precomputation at indexing time.
Although we have ranked programs based on search time, we have also measured indexing time separately. We found that indexing times vary a lot between implementations; in addition many programs use only one thread for indexing. Another point that could be improved as revealed by our analysis is to improve thread utilization, especially for current hardware with their quickly increasing number of cores. It is interesting to note that the three top performing teams use difference techniques for each task. Combining these techniques, e.g. the bit-parallel LCS computation from Team 3 with the pruning techniques of Team 1, could probably reduce search and join times beyond the state-of-the-art.

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	READS-MEDIUM - Number of queries				
Prog.	**1**	**100**	**10,000**	**100,000**	**200,000**
1_A	199.0000	1.9900	0.0225	0.0042	0.0031
1_B	205.0000	2.0100	0.0220	0.0048	0.0032
2_A	-	-	-	-	-
3_A	1,625.0000	18.3100	3.0682	4.2107	3.8523
4_A	83.0000	0.7800	**0.0101**	**0.0041**	0.0035
4_B	107.0000	0.8700	**0.0101**	0.0043	**0.0030**
5_A	50.0000	234.5200	-	-	-
5_B	52.0000	0.2200	0.0211	0.0160	0.0142
5_C	**38.0000**	**0.1800**	0.0228	0.0174	0.0138
5_D	44.0000	0.2100	0.0214	0.0155	0.0144
7_A	116.0000	1.5600	0.5538	0.5519	0.5423
9_A	279.0000	25.7800	24.0174	25.8930	24.8394

Figure 14: Batch effect for READS-MEDIUM: Time per query for a different number of total queries (1-200,000 queries) [time in milliseconds].

	MEDIUM				
Prog.	**k=0**	**k=4**	**k=8**	**k=12**	**k=16**
1_A	0.2	0.2	**0.3**	**1.5**	25.4
1_B	0.2	0.2	0.4	3.1	42.1
2_A	-	-	-	-	-
3_A	2.9	30.9	136.2	335.8	972.6
4_A	**0.1**	**0.1**	0.4	3.3	**17.8**
4_B	**0.1**	**0.1**	0.4	3.5	20.1
5_A	-	-	-	-	-
5_B	**0.1**	0.2	0.9	19.5	56.4
5_C	**0.1**	0.2	3.9	9.1	108.4
5_D	**0.1**	0.2	5.2	44.7	160.8
7_A	0.4	5.6	6.4	20.5	30.5
9_A	117.3	242.0	242.5	311.2	1,749.3

Figure 15: Search times for READS-MEDIUM and different values of k [time in seconds].

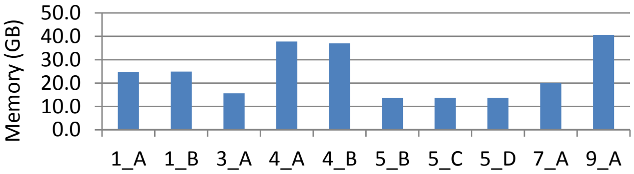

Figure 16: Peak main memory usage for READS-HUGE [memory in GB].

	MEDIUM				
Prog.	**k=0**	**k=1**	**k=2**	**k=3**	**k=4**
1_A	**0.0**	**0.0**	**0.1**	**0.5**	3.5
1_B	**0.0**	**0.0**	**0.1**	0.6	**3.0**
2_A	8.0	7.0	7.2	16.7	21.3
3_A	5.3	5.2	5.5	6.0	8.0
4_A	**0.0**	**0.0**	**0.1**	0.9	6.2
4_B	**0.0**	**0.0**	0.2	0.9	5.9
5_A	178.4	172.8	154.3	159.9	194.7
5_B	**0.0**	0.6	6.2	63.3	206.1
5_C	**0.0**	0.7	9.2	39.1	199.1
5_D	13.6	11.9	24.6	58.4	119.0
6_A	0.3	2.3	5.4	7.8	15.4
8_A	0.1	0.1	0.6	4.0	18.4
9_A	**0.0**	0.1	0.3	2.5	9.1

Figure 17: Search times for CITIES-MEDIUM [time in seconds].

	READS k=0				
Prog.	**TINY**	**SMALL**	**MEDIUM**	**LARGE**	**HUGE**
1_A	**0.5**	1.1	**1.6**	**4.4**	**9.6**
1_B	**0.5**	**0.6**	1.8	4.6	9.9
3_A	2.0	8.3	200.3	1,836.1	15,531.2
4_A	2.5	29.8	288.5	870.0	2,258.0
4_B	2.0	23.8	234.5	709.9	1,764.5
5_A	19.5	1,813.8	-	-	-
5_B	2.5	3.3	5.2	9.5	30.8
5_C	2.5	3.3	4.7	9.2	30.9
5_D	2.5	4.0	5.1	9.2	30.6
9_A	**0.5**	1.2	7.0	9.1	328.7

Figure 18: Join times for READS and $k = 0$ [time in seconds].

	CITIES k=4				
Prog.	**TINY**	**SMALL**	**MEDIUM**	**LARGE**	**HUGE**
1_A	**0.7**	**3.0**	**10.5**	**117.0**	**345.5**
1_B	0.9	**3.0**	11.0	119.5	353.0
3_A	6.5	31.0	68.5	577.0	1,700.0
4_A	2.0	17.0	54.0	807.0	945.0
4_B	2.5	17.0	57.5	810.0	942.0
5_A	10.4	205.5	982.5	-	-
5_B	13.8	241.0	920.5	-	-
5_C	15.0	226.5	926.0	-	-
5_D	22.6	266.0	838.5	2,401.0	-
8_A	6.0	141.5	532.5	3,585.0	21,230.0
9_A	16.1	193.5	578.5	-	-

Figure 19: Join times for CITIES and k=4 [time in seconds].

	READS k=16				
Prog.	**TINY**	**SMALL**	**MEDIUM**	**LARGE**	**HUGE**
1_A	**0.5**	**9.8**	**1,028.3**	**11,283.9**	**82,636.5**
1_B	**0.5**	26.0	2,941.0	33,055.5	-
3_A	26.0	1,732.3	-	-	-
4_A	33.1	362.8	4,048.4	25,823.9	149,344.1
4_B	32.5	361.7	-	-	-
5_A	19.8	2,217.3	-	-	-
5_B	4.1	50.8	4,200.9	-	-
5_C	31.0	431.0	-	-	-
5_D	40.0	625.0	-	-	-
9_A	159.7	9,327.3	-	-	-

Figure 20: Join times for READS and $k = 16$ [time in seconds].

		READS-MEDIUM				
Threads	**Progr.**	**k=0**	**k=4**	**k=8**	**k=12**	**k=16**
8	1_A	**1.22**	**8.51**	**16.22**	**87.95**	**1,000.14**
	4_A	460.37	470.45	633.01	1,724.68	6,077.06
	5_B	3.04	80.29	213.45	3,538.78	10,230.97
24	1_A	**1.23**	**6.76**	**10.76**	**33.96**	**381.07**
	4_A	460.26	462.56	576.99	869.19	2,354.78
	5_B	5.63	55.41	162.01	3,679.70	9,808.58
80	1_A	**1.22**	**6.64**	**9.57**	**23.61**	**335.73**
	4_A	469.87	460.93	486.23	645.42	1,318.72
	5_B	3.76	52.55	188.61	3,437.48	5,157.10

Figure 21: Join times for READS-MEDIUM on System 2 [time in seconds].

	CITIES k=0				
Prog.	**TINY**	**SMALL**	**MEDIUM**	**LARGE**	**HUGE**
1_A	**0.6**	**0.6**	**0.6**	**0.6**	**1.0**
1_B	0.8	0.7	0.7	**0.6**	1.1
3_A	5.8	28.4	56.7	287.2	588.1
4_A	1.9	4.2	7.0	24.9	40.9
4_B	1.7	4.3	7.2	25.0	39.7
5_A	7.7	175.1	850.1	-	-
5_B	4.7	4.6	4.5	6.7	11.3
5_C	4.6	4.7	4.8	6.3	11.3
5_D	4.9	4.8	4.8	6.2	11.4
8_A	1.0	**0.6**	0.9	1.4	3.3
9_A	0.7	1.0	**0.6**	3.4	10.9

Figure 22: Join times for CITIES and k=0 [time in seconds].

		CITIES-MEDIUM				
Threads	**Progr.**	**k=0**	**k=1**	**k=2**	**k=3**	**k=4**
8	1_A	**0.06**	**0.30**	**0.53**	**1.83**	**8.12**
	4_A	10.40	10.35	11.15	17.06	46.00
	5_B	1.45	4.17	56.12	376.39	2,513.64
24	1_A	**0.08**	**0.27**	**0.38**	**0.94**	**3.14**
	4_A	10.42	10.37	10.69	12.60	22.76
	5_B	5.76	4.07	65.28	760.71	2,353.97
80	1_A	**0.11**	**0.31**	**0.39**	**0.85**	**2.42**
	4_A	10.47	10.46	10.48	11.37	16.76
	5_B	2.38	3.92	42.47	532.91	2,051.15

Figure 23: Join times for CITIES-MEDIUM on System 2 [time in seconds].

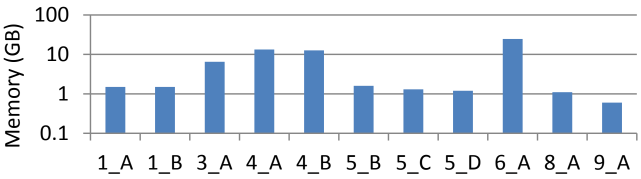

Figure 24: Peak main memory usage for CITIES-HUGE [memory in GB].

	READS-MEDIUM - Number of queries				
Prog.	**1**	**100**	**10,000**	**100,000**	**200,000**
1_A	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**
1_B	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**
2_A	-	-	-	-	-
3_A	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**
4_A	**100.0%**	200.0%	645.8%	479.2%	609.1%
4_B	**100.0%**	200.0%	645.8%	479.2%	609.1%
5_A	**100.0%**	200.0%	445.8%	479.8%	465.7%
5_B	**100.0%**	200.0%	445.8%	479.8%	465.7%
5_C	**100.0%**	200.0%	445.8%	479.8%	465.7%
5_D	**100.0%**	200.0%	445.8%	479.8%	465.7%
7_A	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**
9_A	**100.0%**	**100.0%**	**100.0%**	**100.0%**	**100.0%**

Figure 25: Result redundancy: Searching READS-MEDIUM with k=4 for different number of queries (1-200,000) [redundancy in percent; 100% stands for no redundant results; 200% means that in average each result is reported twice].