fgssjoin: A GPU-based Algorithm for Set Similarity Joins

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Keywords: Advanced Query Processing, High Performance Computing, Parallel Set Similarity Join, GPU.

Abstract: Set similarity join is a core operation for text data integration, cleaning and mining. Most state-of-the-art solutions rely on inherently sequential, CPU-based algorithms. In this paper we propose a parallel algorithm for the set similarity join problem, harnessing the power of GPU systems through filtering techniques and divide-and-conquer strategies that scales well with data size. Experiments show substantial speedups over the fastest algorithms in literature.

1 INTRODUCTION

In the last few decades there have been substantial improvements in database systems, in part due to its commercial importance, usefulness and extensive testing throughout the years. And yet, managing complex data objects in these systems remains a challenge. In fact, many operations which are fine for simple objects are often ineffective for complex ones. A good example is equality tests. They are ubiquitously used in database management operations, but often cannot capture the subtle relations between complex objects, which highlights the need for similarity calculations on such data.

Set similarity join is the operation of retrieving all pairs of data objects (represented by sets of features) from some data collection, for which the result of a similarity function is not less than a given threshold. The problem has attracted growing attention over the years (Sarawagi and Kirpal, 2004; Chaudhuri et al., 2006; Bayardo et al., 2007; Vernica et al., 2010; Xiao et al., 2011; Ribeiro and Härder, 2011; Wang et al., 2012; Cruz et al., 2016), as volume and complexity of data increase in the current Big Data era. It is both an important operation by itself, and a crucial step for more advanced data processing tasks, including integration (Doan et al., 2012), cleaning (Chaudhuri et al., 2006), and data mining (Leskovec et al., 2014).

Assessing the exact similarity between complex objects, particularly for joins where all pairs of objects must be compared, is often expensive, even for state-of-the-art algorithms. In the case of textual data, the infamous *curse of dimensionality* becomes very apparent, since text data representations are often sparse and high-dimensional. Set-based similarity functions are very attractive in this context because predicates involving such functions can be equivalently expressed as a set overlap constraint. As a result, set similarity join is reduced to the problem of identifying set pairs with enough overlap.

In this scenario, it becomes clear that parallel solutions are welcome. Today, virtually all processors support parallelism through the use of multiple cores. Multi-core processing is a growing trend in the industry, and it has been followed by the so-called many-core architectures like GPUs (graphical cards used for general purpose computing). Many-core processors, also known as accelerators, have a large number of processing units — hundreds or thousands — but in the form of slower and simpler cores. Recent developments and the affordability of GPUs have made them attractive to scientists in many areas. GPUs are designed for massive multi-threaded parallelism and are inherently energy-efficient because they are optimized for throughput and performance per watt. However, GPUs have a different architecture and memory organization from traditional CPUs. Therefore, considerable parallelism (tens of thousands of threads) and an adequate use of its hardware resources are needed to fully exploit its capabilities. This fact imposes some constraints in terms of designing appropriate algorithms and new implementation approaches.

In this paper we present a fine-grained parallel algorithm for the set similarity join problem and a GPU-based implementation of this algorithm that allows the usage of state-of-the-art prefix filtering techni-

Quirino, R., Junior, S., Ribeiro, L. and Martins, W.
fgssjoin: A GPU-based Algorithm for Set Similarity Joins.
DOI: 10.5220/0006339001520161
In *Proceedings of the 19th International Conference on Enterprise Information Systems (ICEIS 2017) - Volume 1*, pages 152-161
ISBN: 978-989-758-247-9

ques. The proposed parallel algorithm is based on a divide-and-conquer strategy and partitioning of the data set in blocks in such a way that all blocks are indexed and queried against all others, following an index-filter-verify cycle. This strategy ensures that any data set can be processed regardless of the GPU memory available. It also allows the skipping of some blocks from being queried against others for which no match could be generated. The main contributions of this paper are:

- A parallel algorithm for the set similarity join problem.
- A GPU-based implementation of the proposed algorithm.
- Extensive experimental work with standard datasets.

The remainder of this paper is organized as follows. Section 2 covers related work. Section 3 defines the set similarity join problem and introduces important concepts. Section 4 presents an overview of the architecture and programming model of a GPU. Section 5 describes our solution. Section 7 presents the experimental evaluation, while Section 8 concludes the paper.

2 RELATED WORK

There have been many research on sequential set similarity joins algorithms (Sarawagi and Kirpal, 2004; Chaudhuri et al., 2006; Arasu et al., 2006; Bayardo et al., 2007; Xiao et al., 2011; Ribeiro and Härder, 2011; Wang et al., 2012). An experimental evaluation of several state-of-the-art set similarity join algorithms is presented by Mann et al. (Mann et al., 2016). The *filtering-and-verification* framework is prevalently adopted by such algorithms: first, various filtering schemes are used to prune set pairs that cannot meet the threshold; the actual similarity computation is then performed on each of the remaining set pairs and those deemed as similar are sent to the output. Popular filtering schemes are *length-based filter* (Sarawagi and Kirpal, 2004; Arasu et al., 2006), *prefix filter* (Sarawagi and Kirpal, 2004; Chaudhuri et al., 2006; Ribeiro and Härder, 2011; Wang et al., 2012), and *positional filter* (Xiao et al., 2011). Verification can be optimized by employing a merge-like procedure that stops earlier on set pairs that do not satisfy the similarity constraint. Our proposed algorithm exploits all those optimization on many-core architectures.

Approximate set similarity joins resort to data reduction techniques to speed up processing time. The most popular technique in this context is Locality Sensitive Hashing (LSH) (Indyk and Motwani, 1998), which is based on hashing functions that are approximately similarity-preserving. However, LSH-based algorithms may miss valid output pairs. In contrast, our approach always produces an exact result.

Another popular type of string similarity join employs constraints based on the edit distance, which is defined by the minimum number of character-editing operations — insertion, deletion, and substitution — to make two strings equal. As one can derive set overlap bounds from the edit distance (Gravano et al., 2001), the filtering phase of our proposal can be readily used to reduce the number of distance computations (edit distance also lends itself to efficient GPU implementation (Chacón et al., 2014)).

Lieberman et al. (Lieberman et al., 2008) presented a parallel similarity join algorithm for distance functions of the Minkowski family (e.g,. Euclidean distance). The algorithm first maps the smaller input dataset to a set of space-filling curves and then performs interval searches for each point in the other dataset in parallel. The overall performance of the algorithm drastically decreases as the number of dimensions increases (see Figure 5b in (Lieberman et al., 2008)) because every additional dimension requires the construction of a new space-filling curve. Thus, this approach can be prohibitively expensive on text data, whose representation typically involves several thousands of dimensions.

Cruz et al. (Cruz et al., 2016) proposes an approximate set similarity join algorithm designed for GPU. The Jaccard similarity between two sets is estimated using MinHash (Broder et al., 1998), an LSH scheme for Jaccard. MinHash can be orthogonally combined with our algorithm to reduce set size and, thus, obtain greater scalability.

To the best of our knowledge, the *gSSJoin* algorithm, proposed by Ribeiro-Junior et al. (Junior et al., 2016), is the only existing GPU-based algorithm for exact set similarity join. Similarly to our approach, *gSSJoin* first builds an inverted index before performing similarity computations. However, *gSSJoin* does not employ any filtering technique to reduce the comparison space. We compare our proposal with *gSSJoin* in Section 7.

Finally, recent work proposed to perform set similarity joins on the MapReduce framework (Vernica et al., 2010; Deng et al., 2014). We plan to investigate the integration of *fgssjoin* into a distributed platform to accelerate local computation in future work.

3 BACKGROUND

In this section, we provide background on set similarity join concepts and techniques.

3.1 Mapping Text Data to Sets

In order to express text data as sets of features, we use the notion of *q-grams*, which are tokens obtained by "sliding" a window of size q over the characters of a given string. For example, if we have two strings $s_1 =$ "*Computation*" and $s_2 =$ "*Compilation*", we have the following *2-gram* sets:

$$x = \{Co, om, mp, pu, ut, ta, at, ti, io, on\}$$
$$y = \{Co, om, mp, pi, il, la, at, ti, io, on\}$$

Applying the Jaccard similarity function (JS) to the strings above yields:

$$JS(x,y) = \frac{|x \cap y|}{|x \cup y|} = \frac{7}{10+10-7} \cong 0,538.$$

3.2 Problem Definition, Basic Concepts, and Optmization Techniques

Definition 1. ***(Set Similarity Join).*** *Let U be a universe of features, C be a set collection where every set consists of a number of features from U, $Sim(x,y)$ be a similarity function that maps two sets from C to a number in $[0,1]$ and γ be a number in $[0,1]$ (called threshold). Set similarity join is the operation of defining the set S of all pairs of sets from C, for which $Sim(x,y) \geq \gamma$.*

We focus on a general class of set similarity functions, for which the similarity predicate can be equivalently represented as a set overlap constraint. Specifically, we express the original similarity predicate in terms of an overlap lower bound (overlap bound, for short) (Chaudhuri et al., 2006).

Definition 2. ***(Overlap Bound).*** *Let x and y be sets of features, Sim be a set similarity function, and γ be a similarity threshold. The overlap bound between x and y relative to Sim, denoted by $overlap(x,y)$[1], is a function that maps γ and the sizes of x and y to a real value, s.t. $Sim(x,y) \geq \gamma \Leftrightarrow |x \cap y| \geq overlap(x,y)$.*

This way, the similarity join problem can be reduced to a set overlap problem, in which we need to obtain all pairs (x,y) whose overlap is not less than $overlap(x,y)$. The set overlap formulation enables the derivation of size bounds. Intuitively, observe that $|x \cap y| \leq |x|$ whenever $|y| \geq |x|$, i.e., set overlap and thus similarity are trivially bounded by $|x|$. Exploiting the similarity function definition, it is possible to derive tighter bounds allowing immediate pruning of candidate pairs whose sizes are incompatible according to the given threshold.

Definition 3. ***(Size Bounds).*** *Let x be a set of features, Sim be a set similarity function, and γ be a similarity threshold. The size bounds of x relative to Sim are functions, denoted by $minsize(x)$ and $maxsize(x)$, that maps γ and the size of x to a real value, s.t. $\forall y$, if $Sim(x,y) \geq \gamma$ then $minsize(x) \leq |y| \leq maxsize(x)$.*

Therefore, given a set x we can safely ignore all sets whose size do not fall within the interval $[minsize(x), maxsize(x)]$, because they can not match with x according to the given threshold. Table 1 shows the overlap and size bounds of three of the most widely used similarity functions: Jaccard, Dice, and Cosine (Arasu et al., 2006; Sarawagi and Kirpal, 2004; Xiao et al., 2011; Li et al., 2008; Xiao et al., 2009).

If we ensure that all sets in the collection have its features under the same total order O, we can combine overlap and size bounds to prune even more the comparison space through the *prefix filtering* technique. The idea is to derive a new overlap constraint to be applied only to subsets of the original sets. For any two sets x and y, under the order O, if $|x \cap y| \geq \alpha$ then the subsets consisting of the first $|x| - \alpha + 1$ elements of x and the first $|y| - \alpha + 1$ elements of y must share at least one element (Chaudhuri et al., 2006; Sarawagi and Kirpal, 2004). These subsets are called *prefix filtering subsets* and will be denoted by $pref(x)$. The exact prefix size is determined by $overlap(x,y)$, but it depends on each matching pair. Given a set x, the question is how to determine $|pref(x)|$ such that it suffices to identify all matches of x. Clearly, we have to take the largest prefix in relation to all y. The prefix formulation given above tell us that the prefix size is inversely proportional to $overlap(x,y)$, and the former increases monotonically with y. Therefore, $|pref(x)|$ is largest when $|y|$ is smallest. The smallest possible size of y, such that the overlap constraint can be satisfied, is $minsize(x)$.

Definition 4. ***(Max-prefix).*** *Let x be a set of features. The max-prefix of x, denoted by $maxpref(x)$, is its smallest prefix needed for identifying $\forall y$ that $|x \cap y| \geq overlap(x,y)$. $|maxpref(x)| = |x| - \lceil minsize(x) \rceil + 1$.*

We can also impose an order in the whole collection. If we sort C by its sets sizes we can guarantee that x is only matched with y if $|y| \geq |x|$. In this case the size of $pref(x)$ can be reduced. Instead of using $maxpref(x)$ we can obtain a shorter prefix by using $overlap(x,x)$ to calculate the prefix size (Bayardo et al., 2007; Xiao et al., 2011; Xiao et al., 2009).

[1]For ease of notation, the threshold γ is omitted in the definitions of this section.

Table 1: Set similarity functions.

Function	Definition	overlap(x,y)	[minsize(x),maxsize(x)]
Jaccard	$\frac{\|x \cap y\|}{\|x \cup y\|}$	$\frac{\gamma}{1+\gamma}(\|x\|+\|y\|)$	$\left[\gamma\|x\|, \frac{\|x\|}{\gamma}\right]$
Dice	$\frac{2\|x \cap y\|}{\|x\|+\|y\|}$	$\frac{\gamma(\|x\|+\|y\|)}{2}$	$\left[\frac{\gamma\|x\|}{2-\gamma}, \frac{(2-\gamma)\|x\|}{\gamma}\right]$
Cosine	$\frac{\|x \cap y\|}{\sqrt{\|x\|\|y\|}}$	$\gamma\sqrt{\|x\|\|y\|}$	$\left[\gamma^2\|x\|, \frac{\|x\|}{\gamma^2}\right]$

Definition 5. ***(Mid-prefix).*** *Let x be a set of features. The mid-prefix of x, denoted by $midpref(x)$, is its smallest prefix needed for identifying $\forall y \geq x$ that $|x \cap y| \geq overlap(x,y)$. $|midpref(x)| = |x| - \lceil overlap(x,x) \rceil + 1$.*

Further optimization is possible. We can sort each set by its features frequencies in the collection, in increasing order, which precipitates the least frequent ones to the prefixes, thus filtering out even more pairs (since less frequent ones are likely to have fewer matches). We can also exploit the positional information between common features in two sets, under the same order, to verify if the remaining features in both sets are enough to meet the given threshold (Xiao et al., 2011).

4 GPU ARCHITECTURE AND PROGRAMMING MODEL

In this section we provide a brief description of a modern GPU architecture and its corresponding programming model. We refer the reader to (Kirk and Hwu, 2010) for more details on the GPU architecture and its programming model.

Graphics processing units (GPUs) are specialized architectures originally designed as special-purpose co-processors for dedicated graphics rendering. Due to the high computation power and improved programmability, they have recently become a powerful accelerator for general purpose computing (GPGPU). GPUs can be regarded as massively parallel processors with approximately ten times the computation power and memory bandwidth of CPUs. Moreover, the computational performance of GPUs is improving at a rate higher than that of CPUs and at an exceptionally high performance-to-cost ratio.

A GPU can be considered as a Multiple SIMD (Single Instruction Multiple Data) processor, as depicted in figure 1. Each SIMD unit is known as a streaming multiprocessor (SM) and contains streaming processor (SP) cores, although different vendors and development frameworks may use different terms (in this paper we are using the terms from the CUDA development framework). At any given clock cycle, each SP executes the same instruction, but operates on different data. The GPU supports thousands of lightweight concurrent threads and, unlike the CPU threads, the overhead of creation and switching between threads is negligible. The threads on each SM are organized into thread groups (blocks) that share computation resources such as registers. A thread block is divided into multiple schedule units, called warps, that are dynamically scheduled on the SM. Because of the SIMD nature of the SP's execution units, if threads in a schedule unit must perform different operations, such as going through branches, these operations will be executed serially as opposed to in parallel. Additionally, if a thread stalls on a memory operation, the entire warp will be stalled until the memory access is done. In this case the SM scheduler selects another ready warp and switches to that one. The GPU global memory is typically measured in gigabytes of capacity. It is an off-chip memory and has both a high bandwidth and a high access latency. To hide the high latency of this memory, it is important to have more threads than the number of SPs and to have threads in a warp accessing consecutive memory addresses that can be easily coalesced. The GPU also provides a fast on-chip shared memory which is accessible by all SPs of an SM. The size of this memory is small but it has a low latency and it can be used as a software-controlled cache. Moving data from the CPU to the GPU and vice versa is done through a PCIExpress connection.

The GPU programming model requires that part of the application runs on the CPU while the computationally-intensive part is accelerated by the GPU. The programmer has to modify his application to take the compute-intensive kernels and map them

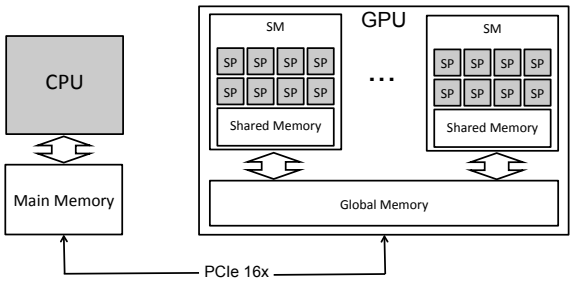


Figure 1: GPU architecture.

to the GPU. The general flow for a program consists of the following. First the program running on the CPU allocates memory on the GPU and copies data to this area. Then the GPU code (kernel function) is started on the GPU. The kernel executes its code in parallel on the GPU and then the results can be copied back to the CPU main memory. A new iteration can take place or the CPU program can deallocate memory on the GPU and terminate.

The GPU programming model exposes parallelism through the data-parallel SPMD (Single Program Multiple Data) kernel function. During implementation, the programmer can configure the number of threads to be used. Threads execute data parallel computations of the kernel and are organized in groups called thread blocks. Thread blocks are further organized into a grid structure. When a kernel is launched, the blocks within a grid are distributed on idle SMs. Threads of a block are divided into warps, the schedule unit used by the SMs, leaving for the GPU to decide in which order and when to execute each warp. Threads that belong to different blocks cannot communicate explicitly and have to rely on the global memory to share their results. Threads within a thread block are executed by the SPs of a single SM and can communicate through the SM shared memory. Furthermore, each thread inside a block has its own registers and private local memory and uses a global thread block index, and a local thread index within a thread block, to uniquely identify its data.

5 PARALLEL SIMILARITY JOIN

In this section we present our parallel algorithm to solve the set similarity join problem with prefix filtering techniques. We describe the three key phases, indexing, filtering and verification, and also our block partitioning strategy.

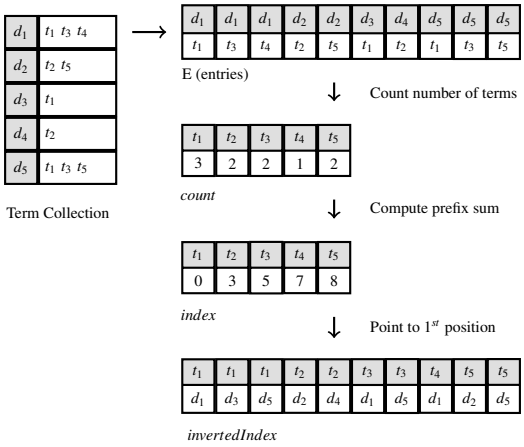


Figure 2: Creating the inverted index.

5.1 Indexing Phase

In state-of-the-art algorithms, the inverted index lists are created during the filtering process, which makes them inherently sequential algorithms: sets are sequentially probed against the index and the state of the lists in one iteration depends on their state in the previous iteration. To go around this problem we need to create the entire inverted index statically before the filtering phase, as show in figure 2. In this way we can perform probes independently, because the index is always complete. Hence, we need an efficient parallel algorithm to create the inverted index. For this purpose, we need to concatenate all features from all sets in a unique array we call E. Let $e \in E$ be an entry that contains three fields: the set it belongs to, a feature and its positional information. So, the sets are reduced to an array of tuples (s_i, f_i, p_i). This will be important in the positional filtering step of the filtering algorithm. When creating the entries for the inverted index algorithm we only add mid-prefix features to the array E. The concepts described in Section 2 allows us to use only max-prefix features from the sets to probe against mid-prefix features in the index, if we guarantee that matches will only occur between bigger probing sets and smaller indexed sets. Then, we calculate a count array, which counts the occurrence of each feature, and then perform a prefix sum on it to obtain the starting indexes of each feature list in the inverted index. Algorithm 1 shows the parallel strategy used to create the whole inverted index in memory. Note that V represents our dictionary (vocabulary).

Algorithm 1: *DataIndexing*(E).

input : Array of entries $E[0..|\mathcal{E}|-1]$.
output: *count*, *index*, *invertedIndex*.

```
1  array of integers count[0..|V|-1];
2  array of integers index[0..|V|-1];
3  invertedIndex[0..|E|-1]
4  Initialize count array with zeros;
5  Count the occurrences of each token, in parallel, on the input and
     accumulates in count.
6  Perform an exclusive parallel prefix sum on count and store the
     result in index.
7  forall t ∈ E, in parallel do
8  |   Copy t to invertedIndex, according to index and update index.
9  end
10 Return the arrays: count, index, and invertedIndex.
```

Algorithm 2: *Filtering*.

input : The collection of sets S, the inverted index I, the array of buckets b, a threshold τ
output: The candidate pairs

```
1  Initialize b with zeros;
2  for each set x in S, in parallel do
3  |   for each feature f in x's maxprefix do
4  |   |   for each set y in f's inverted list do
5  |   |   |   if x.id < y.id then
6  |   |   |   |   if |y| < minsize(x) then
7  |   |   |   |   |   b[x.id][y.id] = -∞;
8  |   |   |   |   |   break;
9  |   |   |   |   else
10 |   |   |   |   |   if b[x.id][y.id] ≥ 0 then
11 |   |   |   |   |   |   rem = min(|x| - x.fpos, |y| - y.fpos);
12 |   |   |   |   |   |   ps = b[x.id][y.id];
13 |   |   |   |   |   |   m = overlap(x,y);     /*τ omitted*/
14 |   |   |   |   |   |
15 |   |   |   |   |   |   if ps + 1 + rem < m then
16 |   |   |   |   |   |   |   b[x.id][y.id] = -∞;
17 |   |   |   |   |   |   else
18 |   |   |   |   |   |   |   b[x.id][y.id]+= 1;
19 |   |   |   |   |   |   end
20 |   |   |   |   |   end
21 |   |   |   |   end
22 |   |   |   end
23 |   |   end
24 |   end
25 end
```

5.2 Filtering Phase

With the entire inverted index stored in memory, we can set each processor to perform one probe (process one set) against the index, using only max-prefix features from the set. One problem is how to accumulate the scores (intersections) between all pairs of sets. Since we can potentially have all set pairs being candidates (specially for lower thresholds), we need "buckets" for all possible pairs of sets in the collection. So, we create an n x n matrix called b (the buckets to contain the partial scores), where n is the number of sets in our collection). It will contain the partial intersection (partial scores) between probed and indexed sets, because only parts of the sets (the prefixes) are used in the process in this stage. After performing the filtering phase, we need to compact the content of the scores table to obtain only the positive scores, i.e., the candidate pairs. So we create an additional n x n array, the *compacted_buckets* array. After the compaction, this array will contain the indexes of the scores in the table which are positive. In order to reduce memory requirements (n x n array) we partition the data collection in blocks and, thus we are be able to process collections of any size. Figure 3 illustrates the state of the memory after the filtering phase. Note that each row in the first matrix in the figure represents a set being queried against the index while each column represents an indexed set.

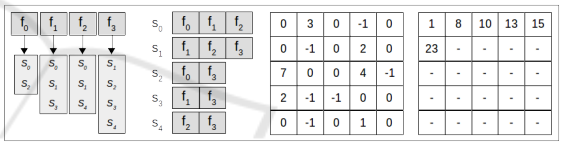


Figure 3: Memory after the filtering phase, with inverted index, sets, the array b (buckets) of partial scores and its corresponding array of compacted buckets (with the indexes to the elements in b that have positive values), respectively. Since we have five sets in this example, our tables are 5x5. The numbers in the first table are the partial scores after the filtering phase. Negative (-1) numbers represents $-\infty$. The second table is the compacted version of the first; its values (the absolute indexes of the selected elements from the first table) represent the candidate pairs and are provided to the verification phase.

Algorithm 2 is similar to state-of-the-art filtering based algorithms in literature, but here it is executed by each GPU processor (core) for one probing set. From now on we will refer to a set being probed against the index as a *query*, and to a set in the index as a *source* (because they generate the index). For each query, the filtering algorithm has two loops, one to iterate on the max-prefix features of the query, and one to consult the sources in the inverted list corresponding to each feature. Then we test if the query id is smaller than the source id, i.e., we will only match set x with set y if $x.id < y.id$. This test avoids processing the same pair twice as well as ensures that query sets are bigger than the sources, since the whole collection is sorted in decreasing set cardinality order. When we obtain a match we test if the source is smaller than the query *minsize*. If it is, we can stop iterating on the current inverted index list, because each

list is also sorted in decreasing order of set cardinality. Finally, only for pairs (buckets in *partial_scores*) not marked with $-\infty$, we test if the remaining features are enough to meet the threshold; note that $x.fpos$ is the positional information of the current feature in set x. If they are, we accumulate the score, if not we mark them with $-\infty$, so that they will not be considered anymore. In the end, array b will contain marked buckets, 0 buckets and positive ones, the former being compacted (their absolute indexes) in the array *compacted_buckets* (*cb* for short). The compacted indexes represent the pairs, since the bidimensional indexes of the matrix (which represents the ids of *query* and *source* sets) can be calculated from the absolute index. It is the resulting candidate pairs list, which will be passed to the next phase, verification.

5.3 Verification Phase

The verification phase, which ultimately produces the final result, can be trivially processed in parallel. It simply consists in performing the remaining score calculation on each candidate pair to verify if there is enough overlap to qualify them as a match. This can easily be done in parallel, by making each processor perform verification on one candidate pair. We can use the partial score to reduce a bit the overlap calculations. By comparing the last feature from the prefixes of the two sets in a candidate pair, we can start the overlap calculation in the position of the feature with the smaller id in its own set, and in the beginning with the other, with the initial value being the partial score of the candidate pair, since any match with prefix features in this set was already calculated in the filtering phase. In each step of the overlap calculation we also test if the remaining features are enough to meet the threshold, marking those which are not. Those not marked by this process form the result set, the similar pairs according to the threshold and the similarity function.

5.4 Block Partitioning and Optimization

The need for quadratic arrays in the filtering phase sets a limit for the size of the databases we can process. In order to solve this problem we need to partition our search space into blocks that fit into the memory requirements. But then we must process this blocks in such a way that all sets are matched against each other. To achieve this we proceed similarly in the filtering phase, but we index the set's prefixes of one block, and use all the others before it to query its index. In this way we create an index-filter-verify cycle with the blocks, gradually aggregating the results, which can be flushed to the disk if approaching memory limit. By using the previous blocks as queries, as shown in figure 4, we ensure that only bigger sets are queried against smaller ones in the index, since the collection is sorted in decreasing cardinality order. This fact also allows us to skip some blocks from being queried against others for which its first set's maxsize is smaller than the query block's last set. In these cases it is guaranteed that no match could be yield from the two blocks. This significantly improves performance for higher thresholds. Another consequence of block partitioning is the possibility of running in distributed memory systems, since we can process each probe/index block pair in one node in

Algorithm 3: *Verification.*

input : The array of buckets b with partial scores, the array of compacted buckets *cb* with the indexes of the candidate buckets (with positive scores), the array of features f of each set and a threshold τ

output: The similar pairs list L

```
1  Initialize a list L;
2  for each index idx in cb, in parallel do
3      x,y = calc_indexes(idx);                    /*x.id < y.id*/
4      m = overlap(x,y);
5      score = b[x.id][s.id];
6      f1 = f[x.id][|maxpref(x)|];
7      f2 = f[y.id][|midpref(y)|];
8      p1,p2 = 0;
9      if f1 < f2 then
10         p1 = |maxpref(x)|;
11     else
12         p2 = |midpref(y)|;
13     end
14     while p1 < |x| and p2 < |y| do
15         f1 = f[x][p1]; f2 = f[y][p2];
16         if (p1 == |x| − 1 and f1 < f2) or
             (p2 == |y| − 1 and f2 < f1) then
17             break;
18         end
19         if f1 == f2 then
20             score+ = 1; p1+ = 1; p2+ = 1;
21         else
22             s = f1 < f2 ? x : y; p = f1 < f2 ? p1 : p2;
23             rem = |s| − p;
24             if rem + score < m then
25                 break;
26             else
27                 p+ = 1;
28             end
29         end
30         if score ≥ m then
31             include pair (x,y) in L;
32         end
33     end
34 end
```

parallel, executing its own index-filter-verify calculations.

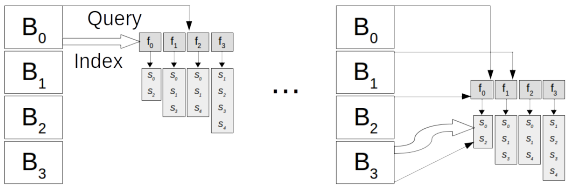


Figure 4: Illustration of the block processing scheme.

6 GPU IMPLEMENTATION

The GPU implementation consists of three main kernels (functions that executes in the GPU), plus other smaller kernels responsible for common parallel tasks used by the main ones, like parallel counting and prefix sum in the inverted index creation and compaction in the filtering phase.

The three main kernels are scheduled by the block processing function, that partitions the dataset into blocks and executes the block processing scheme, as shown in figure 4 where "Query" means filter against the index and verify the selected candidates. The block processing scheme executes the index-filter-verify cycle by calling their three associtated kernels.

The kernel responsible for the creation of the inverted index is simple, very like algorithm 1. It is composed of three smaller kernels responsible for its steps: parallel counting, parallel prefix sum and parallel building of the index according to the count and prefix sum arrays.

For the filtering algorithm, we create a single array in the GPU memory, the partial_scores array, with a number of elements equals to the square of the number of sets in one block (the number of all possible pairs for the block). We only allocate it once, and reuse it for each filtering execution, to save the allocation time. We also allocate only once a compacted_buckets array, of the same size of the partial_scores, to contain the result of the compaction. Of course these arrays must be cleaned (set to 0) at each execution of the filter-verify algorithms in the block processing scheme. The number of sets per block must be chosen in such a way that two times its squared value times the data type size used in partial_scores and compacted_buckets is less than the memory available in the GPU.

After the filtering kernel is executed, it fills the partial_scores array, and the compaction kernel can be called to fill the compacted_buckets array, as shown in figure 3. The result of the compaction is the absolute indexes of the positive elements in partial_scores. The indexes represent the pairs, since they can be derived from the absolute index. These indexes, i.e. the candidate pairs, as well as the partial_scores are passed to the verification kernel. It will calculate the intersections (the final scores) between the candidate pairs, always checking if there is still enough features in the sets to meet the minimum overlap, according to the chosen similarity function (jaccard in our implementation). The pairs that pass the verification algorithm are pushed into a list, that is periodically flushed to the output file, where the actual similarity values are calculated.

We used a fixed number of thread blocks and of threads per block, which depends on to the specific GPU used. In order to ensure maximum utilization of the device, we used a technique called persistent threads. This technique allows one thread to be reused, processing more than one data element when the number of elements to process is bigger than the number of threads sent to execution.

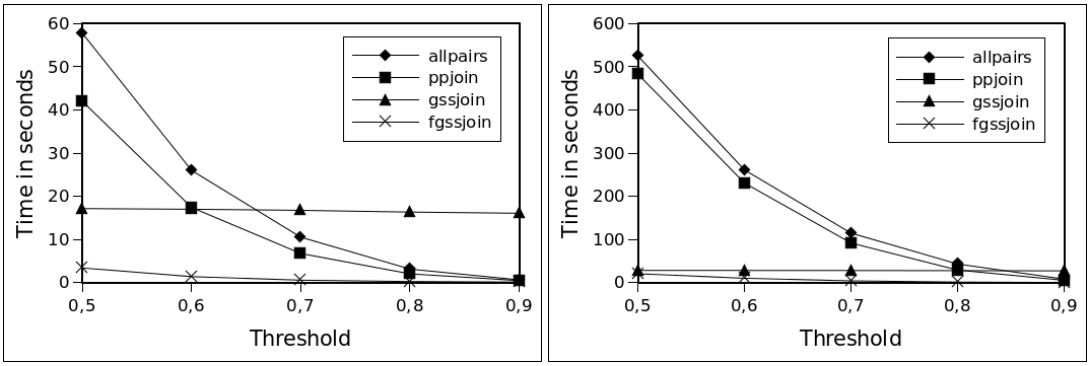
7 EXPERIMENTAL EVALUATION

7.1 Experimental Setup

We tested two reference sequential algorithms, *allpairs* (Bayardo et al., 2007) and *ppjoin* (Xiao et al., 2011), as well as a massively parallel algorithm *gssjoin* (Junior et al., 2016) and our parallel filter-based algorithm *fgssjoin*.

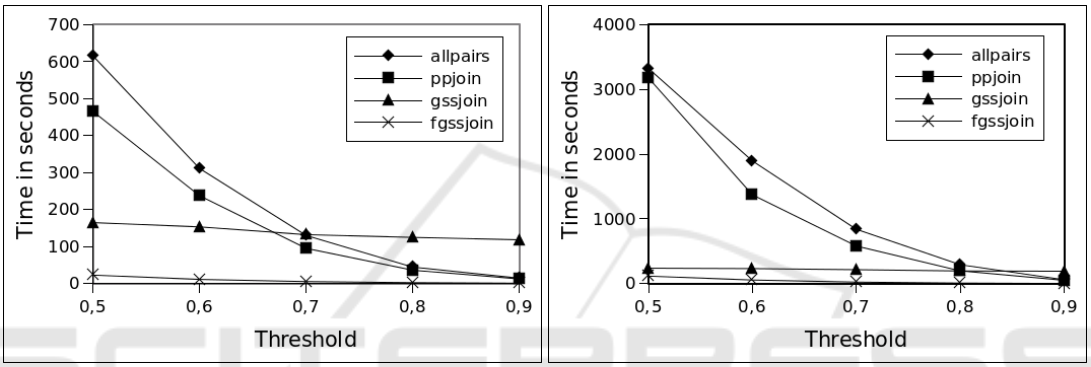
Our experiments were executed on a machine equipped with two Intel Xeon E5-2620, each with 6 processing cores (12 threads in hyper-threading) and 20MB of cache memory, 16GB of RAM memory and 4 Nvidia GTX Titan Black, each with 2880 processing cores and 6GB of memory, although we only used one GTX Titan Black for our parallel implementation.

We used two standard databases: DBLP (a collection of computer science article titles and authors), with 100k registers, and IMDB (a collection of movie titles, TV shows, etc), with 300k registers, which are popular datasets in set similarity joins related work. We pre-processed the data sets, removing accents and punctuation, and setting all characters to lowercase. Both datasets were q-tokenized with 2-grams and 3-grams. We conducted our experiments varying the threshold values from 0.5 to 0.9, in 0.1 increments. Our baseline comparison algorithms were executed on the Xeon processor, except gssjoin, which was also executed on the Gtx Titan Black.



(a) DBLP 100k, 3-gram tokens (b) DBLP 100k, 2-gram tokens

Figure 5: Execution times for DBLP dataset, 100k registers, with 2-gram and 3-gram tokens.



(a) IMDB 300k, 3-gram tokens (b) IMDB 300k, 2-gram tokens

Figure 6: Execution times for IMDB dataset, 300k registers, with 2-gram and 3-gram tokens.

7.2 Performance Analysis

We report execution runtimes with varying threshold values. Figure 5 shows the execution times obtained as we increase the threshold from 0.5 up to 0.9. As can be seen, our algorithm achieved considerable speedups of up to 25x faster than the leading sequential algorithm in literature. The best speedups were achieved when the datasets were tokenized with 2-grams. Of course the finer grained 2-grams requires more computational power, since there are fewer combinations of 2 characters and this leads to more matches and more candidate pairs in the filtering phase, consequently raising the load for the verifying phase. Also, we expect our algorithm to become even better as the size of the dataset grows. One caveat is that our algorithm relies on positional filtering, which is inherently sequential. Although it is very efficient in lowering the number of candidate pairs in the filtering phase, it imposes difficulties for some key optimization in many-core architectures. For example, it reduces memory coalescing, and hinders a higher degree of parallelism, e.g., parallelizing the tokens among processing units, instead of whole queries, in the filtering phase. Table 2 shows the best speedups achieved on each dataset over the 3 other algorithms used in experiments; the corresponding threshold value is shown in parentheses.

Table 2: Best speedups of fgssjoin over the other algorithms on each dataset, with corresponding threshold values.

Dataset	*ppjoin*	*allpairs*	*gssjoin*
DBLP, 2-gram	24.6x (0.8)	36.6x (0.8)	108.3x (0.9)
DBLP, 3-gram	12.4x (0.5)	17.1x (0.5)	132.7x (0.9)
IMDB, 2-gram	27.6x (0.6)	38.5x (0.6)	98.0x (0.9)
IMDB, 3-gram	21.0x (0.8)	27.5x (0.8)	127.1x (0.9)

8 CONCLUSIONS AND FUTURE WORK

In this paper we presented a parallel algorithm, as well as a GPU-based implementation to solve the set similarity join problem, with considerable speedups

in relation to the state-of-the-art algorithms in literature. Our experiments, with standard datasets, revealed good speedups, with a scalable behavior as we increase the size of the datasets. Besides the good results in this paper, many improvements can be done. We did not explore some specific optimization in relation to the many-core architectures, like the use of the so called shared memory in CUDA or local memory in OpenCL (both are parallel development frameworks), as well as memory coalescing. One observation in this research is the inherently sequential nature of positional filtering techniques, which hinders a higher level of parallelism. We plan, in future work, to remove the positional filtering techniques from our filtering phase, and increase the degree of parallelism by assigning one processing core to each token, instead of each set, to make possible coalesced memory accesses, hoping that the gain with the higher degree of parallelism compensates the loss in filtering capacity. We also plan to make use of shared/local memory as a way to increase locality and, hence, achieve greater speedups. Finally, we plan to implement a multi-GPU version (to run on GPU clusters) and process bigger datasets.

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