DAW2: Duplicate-AWare Federated Query Processing over the Web of DAta

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Abstract. Over the last years, the Web of Data has developed into a large compendium of interlinked data sets from multiple domains. Due to the decentralised architecture of the Linked Open Data Web, several of these data sets contain duplicated data. Several federated querying approaches have been proposed to retrieve information from these data sources. Still, only little attention has been paid to the effect of duplicated data on the processing of federated queries. This work presents a novel duplicate-aware approach to federated SPARQL querying based on Min-Wise Independent Permutations (MIPs) applied to RDF predicates. Our approach DAW2 allows taking into account the overlap among the available data sources and thus avoid submitting sub-queries that produces overlapping results. DAW2 can be combined with the existing federated query engines and enables them to achieve the same recall while submitting fewer queries. Therewith, it can reduce both the overall runtime of and the amount of network traffic generated by federated query engines. We combine our approach with DARQ, and SPLENDID and compare it with the original implementation of these frameworks on four datasets of different sizes by using 79 queries of various shapes. Our evaluation shows that our approach achieves significantly smaller mean squared errors than the state of the art with respect to the approximation of result set sizes as well as in the ranking of data sources. Moreover, it requires less sub-queries federation to achieve the same recall with smaller execution time.

Keywords: Federated queries, SPARQL, Min-wise independent permutations

1 Introduction

Over the last years, the Data Web has developed into a large compendium of interlinked data sets from multiple domains [2]. One of the central principles underlying the architecture of these data sets is the reuse of URIs and vocabularies as well as the linking of knowledge bases [3]. One of the results of this architectural choice is that certain queries can only be answered by retrieving

information from several knowledge bases. This type of queries, called *federated queries*, is of central importance for manifold applications such as question answering [34] and knowledge retrieval [30]. Due to the reuse of URIs and the independence of the data sources, certain pieces of information (i.e., triples) can be found in several knowledge bases. For example, the name of movie directors can be found both in DBpedia and LinkedMDB. Authors of papers can be found in both the ACM and DBLP libraries. Similarly, we have noticed that the *DrugBank*[3] and *Neurocommons* [4] datasets are duplicated at *DERI health Care and Life Sciences Knowledge Base* [5]. A list of the mirrored SPARQL endpoints is given in the url [6]. These duplicates are common in life sciences domain as well. Examples of data sets which might contain the same triples across the life science domain is shown in Figure 1. We call triples that can be found in several knowledge bases across the Web of Data *duplicates*.

Avoiding the retrieval of duplicate records is a crucial issue in large scale distributed datasets. As the SPARQL endpoints are autonomous, there is always the possibility of high mutual overlap between different datasets residing in different endpoints. It is thus likely that an optimized query execution plan contains a sub-query that retrieves records which are already retrieved by another sub-query from a different SPARQL endpoint. In this case it is not necessary to execute the later sub-query, as it would not only result in duplicate records being retrieved but also increase the total processing time.

While the importance of federated queries over the Web of Data has been stressed in previous work, the impact of duplicates has not received much attention. Yet, as we will show in the remainder of this paper, a duplicate-aware approach to query processing can lead to more time-efficient and effective algorithms for federated queries. In this paper, we address this drawback by presenting a duplicate-aware approach for query processing based on Min-Wise Independent Permutations (MIPs). Our query federator makes use of MIPs to estimate the possible overlap between the results of different sub-queries in order to avoid the retrieval of redundant information.

Our approach begins by parsing each input query for triple patterns. Then, for each of these triple patterns, it uses MIPs to approximate the amount of non-duplicate triples contained in each of the available data sources. This approximation is used to select and rank relevant data sources. Finally, the selected data sources are queried by means of the sub-queries contained in the user input.

The use of statistical synopsis such as MIPs for overlap estimation is very common in the literature (as discussed in the next section), however these synopsis cannot be use all alone in semantic web domain due to the diverse nature of SPARQL queries. For example, the synopsis result set estimation for a triple pattern needs to be completely changed if any of the subject or object becomes bound in the query triple. To address such issues, we combine MIPs synopsis

[3] http://datahub.io/dataset/fu-berlin-drugbank
[4] http://neurocommons.org/page/RDF_distribution
[5] http://hcls.deri.org:8080/openrdf-sesame/repositories/hclskb
[6] http://hcls.deri.org/RoadMapEvaluation/#Sparql_Endpoints

with the data summaries statistics for more accurate overlap estimation. Thus by creating small summaries of the data found in the available knowledge bases, our approach is able to estimate the amount of new information contained in a knowledge base with a high accuracy, leading to a better performance with respect to source ranking, estimation of result set sizes, execution time and network traffic.

The main contributions of this paper are as follows:

1. We propose the (to the best of our knowledge) first duplicate-aware approach for federated SPARQL querying.
2. We combine data summaries statistics with MIPs to address the diversity in SPARQL queries.
3. We evaluate our approach against the state of the art on 79 queries and four datasets and show that we achieve better estimations of result set sizes and therewith a better ranking of data sources, lower execution times and consequently less network traffic.

The rest of this paper is organized as follows: We begin by giving a brief overview of the state of the art in federated query processing. In addition, we present different statistical synopsis approaches that can be used for the approximation of duplicate-free result set sizes. Thereafter, we elaborate on our novel duplicate-aware federated query processing approach and present the components of our approach in detail. Subsequently, we present a thorough evaluation of our approach against state of the art approaches. We finally conclude the paper with a discussion of our findings and an overview of future work.

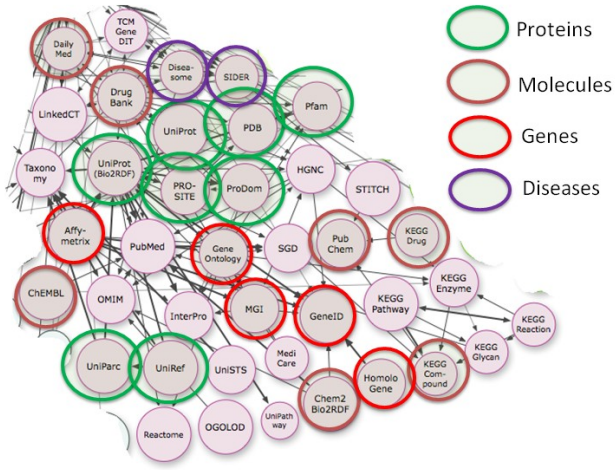


Fig. 1: Possible duplicates in life sciences domain

2 Related Work

2.1 Federated SPARQL Queries

The research work on federated query processing over the Data Web can be categorized into three main directions:

- Service description/index-assisted approaches, which make use of the dataset summaries that have been collected in a pre-processing stage. These approaches may lead to a more efficient query federation. However, the index needs to be constantly updated to ensure up-to-date results. Also, the index size should not be large to ensure that it does not increase the overall query processing cost.
- Index-free approaches, in which the query federation is performed without using any stored data summaries. The data source statistics can be collected on-the-fly before the query federation. This approach promises the up-to-date records retrieval however; it may increase the query execution time, depending on the extra processing required in collecting, processing on-the-fly statistics.
- Hybrid approaches, in which some of the data source statistics are pre-stored while some are collected on-the-fly.

All of the above approaches can be further divided into two categories (a) Query federation with complete result retrieval (100% recall), and (b) Query federation with partial (sufficient) record retrieval. In our work, we focus on index-assisted query federation which can be used both for complete and partial record retrieval .

Heiner et al. [32] describe how to extend the Sesame RDF repository to support distributed SeRQL queries over multiple Sesame RDF repositories. They use a special index structure to determine the relevant sources for a query. Quilitz and Leser [28] use the theoretical knowledge of [32] to develop the first federated query engine (named DARQ) for remote RDF data sources. DARQ uses service descriptions for relevant data source selection. A service description describes the capabilities of a SPARQL endpoint. They use a query rewriting mechanism based on [26] and a cost-based optimization algorithm to reduce the query processing time with the minimum bandwidth usage. DARQ is compatible with any SPARQL endpoint that implements the SPARQL standard. Their experimental results show that the optimization algorithm can greatly reduce the query processing time.

Andreas et al. [18] propose a solution similar to DARQ using a mediator approach. The SPARQL endpoints need to register first with the mediator using HTTP POST requests with an RDF document attached. The mediator continuously monitors the SPAQL endpoints for any dataset changes and updates the service descriptions automatically. Unlike DARQ, the service descriptions remain up-to-date all time.

Olaf et al. [14] present a new approach for federated query processing over the Web of Data. Their approach discovers data that might be relevant for answering

a query during the query execution itself. The discovery of relevant data is accomplished by traversing RDF links. They use an iterator-based pipeline and a URI prefetching approach for efficient query execution. Both DARQ and [18] are not able to discover relevant data sources by the query itself.

The previous techniques cannot answer all types of queries due to index or service description limitations. Umbrich et al. [12, 33], propose a Qtree-based index structure which summarizes the content of data source for query execution over the Web of Data. Their approach is able to handle more expressive queries however; because of the complete-query based source ranking, it may skip querying many sources which are capable of answering a sub-set of the query triples. Schwarte et al. [29] propose an index-free query federation for the Web of Data. Their approach gives a reasonably fast data retrieval as compared to all the previous techniques. However, since they do not keep any statistics, it works only for limited data sources.

Li and Heflin [19] build a tree structure which supports federated query processing over multiple heterogeneous sources. They make use of an OWL reasoner to answer queries over the selected sources and their corresponding ontologies. Kaoudi et al. [15] propose a federated query technique on top of distributed hash tables (DHT). The overall goal is to minimize the query execution time and the bandwidth consumption by reducing the cardinality of intermediate results. The DHT-based optimizer make use of three greedy optimization algorithms for best plan selection.

Ludwig and Tran [16] propose a mixed query engine that assumes some incomplete knowledge about the sources to select and discover new sources at run time. A Symmetric Hash Join is implemented to incrementally produce answers. This approach is extended to query both remote and local linked data [17].

Maribel et al. [1] present ANAPSID, an adaptive query engine that adapts query execution schedulers to SPARQL endpoints data availability and run-time conditions. ANAPSID provides physical SPARQL operators that detect when a source becomes blocked or data traffic is bursty. The operators produce results as quickly as data arrives from the sources. Amol et al. [10] present a survey of the adaptive query processing techniques, common issues, and the settings in which each piece of work is most appropriate. Avalanche [4] gathers endpoints dataset statistics and bandwidth availability on-the-fly before the query federation. The advantage of this technique is the live query execution over the Web of Data. However, on-the-fly statistics calculation can increase the overall query execution time. Olaf [13] propose a heuristics-based technique to minimize query intermediate results.

Few other contributions address the problem of SPARQL query federation [8], [31] but none, to the best of our knowledge has taken into account the possibility of mutual overlap between different RDF datasets before query execution. Similar to DARQ engine, we use service descriptions for query federation. In addition, we store MIPs vector statistics for each of the indexed data source. Our query federator makes use of this special statistic information to estimate the possible

overlap between the results of different sub-queries in order to avoid the retrieval of redundant information.

2.2 Dataset Overlap Estimation

Avoiding the retrieval of duplicate records is a crucial issue in large scale distributed datasets. As the SPARQL endpoints are autonomous, there is always the possibility of high mutual overlap between different datasets residing in different endpoints. It is thus likely that an optimized query execution plan contains a sub-query that retrieves records which are already retrieved by another sub-query from a different SPARQL endpoint. In this case it is not necessary to execute the later sub-query, as it would not only result in duplicate records being retrieved but also increase the total processing time.

Statistical synopsis like min-wise independent permutations [7], bloom filters [6], hash sketches [24], XSKETCH [27], fractional XSKETCH [11], and compressed bloom filters [21] have been extensively used in the literature to provide a compacted representation of data sets. Statistical synopsis allow to estimate a number os set operations such as overlap and union without having to compare the original sets directly. For example, Bender et al. [5] propose a technique for predicting the query-specific mutual overlap datasets in a peer to peer network. MIPs have proved to be the more accurate overlap estimation with small bandwidth consumption[7] therefore we have chosen them in our approach.

3 Notation

In this section, we present the core of the notation that will be used throughout this paper. We denote data sources with S and the total number of data sources with n. The set of all data sets is dubbed $\mathfrak{S}$. The set of all possible result sets is denoted R while the set of all possible SPARQL queries is labeled with Q. A data source ranking function $rank : S \times Q \rightarrow \{1 \dots n\}$ is a function that assigns a ranking to each data source given a particular query $q \in Q$. Note that for any source ranking function $rank$, we assume that $\forall S, S' \forall q \in Q : S \neq S' \iff rank(S, q) \neq rank(S', q)$. A result set estimation function $est : S \times Q \rightarrow \mathbb{N}$ aims at approximating the size of the result set that will be returned by a given query. Note that this function plays a crucial role in the processing of federated queries as it is most commonly used to decide upon the ranking of data sources for a given query. The aim of a federated query system such as the one described in this work is thus to optimize its estimation function est so as to ensure a ranking of the source close to the optimal ranking.

4 Duplicate-aware Federated Query Processing

4.1 Overview

Given a query, it is first parsed, then sent to federator which makes use of the services descriptions directory/index to decompose the query into duplicate free

multiple sub-queries. Each sub-query is optimized to generate an optimized execution plan. The optimized sub-queries are forwarded to the relevant SPARQL endpoints. The results of each sub-query execution are integrated and the final query result set is generated. This architecture for duplicate-aware federated query processing is shown in Figure 2. While this architecture is similar to other

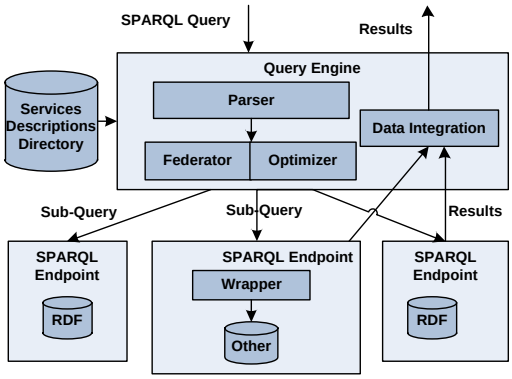


Fig. 2: Duplicate-aware federated query processing architecture

federated query systems, the federator in our system differ significantly from those of other approaches as it makes use of MIPs statistical information to generate duplicate-free query execution plans. The generation of MIPs statistical information is explained in the next section.

4.2 Service Description Directory

To find the set of relevant servers and generate the appropriate sub-queries, the federator needs information about the different data sets available at the different servers. We call the catalog containing such information the *service description directory*. Each service description provides a declarative description of the data available from a server along with statistical information.

For each server our *service description directory* stores *server url, graph name*, and for each distinct predicate p we record *predicate name, MIPs vector, subject selectivity, object selectivity*, and *total number of triples* having predicate p. The MIPs vectors are used to estimate the dataset overlap among the capable datasets before the sub-query distribution and it will be explained in detail in section 4.3. The *subject* and *object selectivity* are used to estimate the sub-query result set when *subject, object* are bound, respectively. We call the set $C_i = \{(p_i, mipsv_i, sbjsel_i, objsel_i, totTrpl_i)\}$ as a *capability* of the data source. The total number of capabilities of a data source is equal to the number of distinct predicate in that data source. A sample service description is given in the Listing 1.

Listing 1.1: A Service Description Example

```
[] a sd:Service ;
     sd:url    <http://localhost:8890/sparql> ;
     sd:graph ''diseasome/DS1'';
     sd:capability
     [
      sd:predicate  diseasome:name ;
      sd:MIPv  ''-6908232 -7090543 -6892373 -7064247 ...'';
      sd:subjectSelectivity  ''0.0068'' ;
      sd:objectSelectivity  ''0.0069'' ;
      sd:triples    147  ;
      ] ;
     sd:capability
     [
      sd:predicate  diseasome:chromosomalLocation ;
      sd:MIPv  ''-7056448 -7056410 -6845713 -6966021 ...'';
      sd:subjectSelectivity  ''0.0062'' ;
      sd:objectSelectivity  ''0.0072'' ;
      sd:triples    160  ;
      ] ;
```

It is very crucial to keep the directory size small to minimize the pre-query federation time. However,this directory must contain sufficient information to enable the generation of sub-query, the optimization, and the pre-processing dataset overlap estimation. Our index size is mostly depended upon the size of the MIPs vectors which can be adjusted to any length. In general MIPs can provide a good estimation of the overlap between sets with a few integer in length. Min-Wise Independent Permutations have been in the peer to peer networks literature [25, 20, 9].

4.3 Min-Wise Independent Permutations

MIPs assumes that the set elements can be ordered and computes N random permutations of the elements. Each permutation uses a linear hash function of the form $h_i(x) := a_i * x + b_i \ mod \ U$ where U is a big prime number and a_i, b_i are fixed random numbers [25]. By ordering the resulting hash values, we obtain a random permutation. For each of the N permutations, the MIPs technique determines the minimum hash value, and stores it in an N-dimensional vector, thus capturing the minimum set element under each of these random permutations. The technique is illustrated with an example in Figure 3. Its fundamental rationale is that each element has the same probability of becoming the minimum element under a random permutation. By using sufficiently many different permutations, we can approximate the set cardinality.

Let S_A and S_B be the two MIPs set, the cardinality of the intersection is defined as the overlap between these two sets. The overlap and union of the two sets is given in Equation 1 and Equation 2, respectively.

$$Overlap(S_A, S_B) = |S_A \cap S_B| \tag{1}$$

$$Union(S_A, S_B) = |S_A \cup S_B| \tag{2}$$

An unbiased estimate of the pair-wise resemblance of the sets can be obtained by counting the number of positions in which the two MIPs vectors have the

same number and dividing this by the number of permutations N. Essentially, this holds as the matched numbers are guaranteed to belong to the intersection of the sets. The resemblance formula is given in Equation 3.

$$Resemblance(S_A, S_B) = \frac{Overlap(S_A, S_B)}{Union(S_A, S_B)} \tag{3}$$

In our service descriptions the MIPs are used as follow: for a predicate $p \in S$, we create a MIPs vector representing all triples $T \in S$ having predicate p. We concatenate the *subject* and *object* of each triple in T and apply a hash function to get the *ID set*. Finally, we computes N random permutations of the *ID set*. The resulting MIPs vector is stored against each capability of the service description. Note that we are not applying hash function to the complete triple because the predicate is already stored with each service capability and source selection is bound by query predicate.

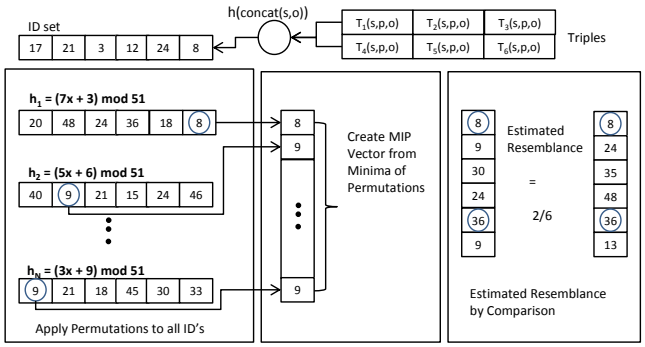


Fig. 3: Min-Wise Independent Permutations

4.4 Source Selection

A SPARQL query contains one or more basic graph patterns. Similar to DARQ, our query planning step is performed separately for each basic graph pattern. The source selection algorithm used in DARQ for a query simply matches all triple patterns against the capabilities of the data sources. The matching compares the predicate in a triple pattern with the predicate defined for a capability.

Let $S = \{(s_1, C_1), .., (s_n, C_n)\}$ be a set of all indexed data sources $s_1..s_n$ and their capabilities $C_1..C_n$, where $C_i = \{(p_i, mipsv_i, sbjsel_i, objsel_i, totTrpl_i)\}$. Let BGP be a set of triple patterns in a filtered basic graph pattern. The result of the source selection is a set of data sources D_j for each triple pattern $t_j = (s_j, p_j, o_j) \in BGP$ such that

$$D_j = \{\text{s}|(\text{s,C}) \in \text{ S} \wedge \exists \ p_j \in \text{ C }\}$$

We extend the DARQ source selection algorithm by comparing MIPs vectors for duplicates. For a triple pattern, we compare the MIPs vectors of all the relevant data sources for possible duplicates. A specific source s is only added to the set of capable sources D_j, if it is able to produce a number of new results above a specific threshold value pre-defined for final source selection. For a triple $t \in BGP$ and a dataset $s \in S$, if the value of new results generated is less than the threshold, s is ignored from set D_j. For 100% recall the threshold value should be 1. Which means if a source is able to produce a single triple, it will be added to the set of capable sources. For sufficient (not complete) record retrieval the threshold can be fixed to any number greater than 1. For all of the 79 queries in this work, our threshold value is 1.

4.5 Source Ranking

To show the importance of the duplicate-aware data source ranking (based on the amount of duplicate-free records retrieved), suppose we have a triple pattern query$q$ shown in Listing 2 and ds_1, ds_2, ds_3 are the data sources capable of answering that query. If we apply DARQ source selection algorithm we will get all 3 datasets as the list of capable sources. Let us assume that ds_1 has a total of 50 triples satisfying q, ds_2 and ds_3 each have 40 triples satisfying the query. Further suppose that 25 of the ds_3 triples are duplicated at ds_1 while remaining 15 are duplicated at ds_2. The DARQ sub-query generator would forward the query to all 3 data sources. Thus, it would generate unnecessary network traffic to retrieve the data contained in ds_3. The integration time would also be suboptimal as the ds_3 records would have to be joined to the results of the two other data sets during the final result set compilation. Now if we apply duplicate-aware source ranking approach, which would select ds_1 as first, ds_2 as second and would skip ds_3, we would only send two sub-queries (one to $ds_1$and one to ds_2) and thus improve both network traffic and integration time.

Similar to DARQ, our system make use of the triple-by-triple sub-query federation, therefore it is important to have a duplicate-aware triple pattern source ranking algorithm for sub-query escaping. We present this triple pattern source ranking algorithm in the next section.

Listing 1.2: A single triple pattern query

```
SELECT ?o
  WHERE
   {
       ?s  <p1> ?o  .
   }
```

Triple Pattern Source Ranking Algorithm 1 shows the single triple pattern source ranking. For a triple *t(s,p,o)* $\in T$ the set of capable data sources D is obtained using the source selection algorithm explained in previous section. The source $d \in D$ which has the highest *totTrpl* value in the matched capability *C(p, mipsv, sbjsel, objsel, totTrpl)* is selected as first in the rank. The union and intersection of *MIPs Vectors* is explained in section 4.3. In order to get the

accurate result set estimate, we multiply *sbjsel, objsel* $\in C$ to the *orignal size* of the *MIPs Vectors* if *subject* or *object* of the triple pattern is bound respectively. The same is true for rank 1 dataset selection. However, the multiplication is performed with *totTrpl* of mached capability instead of *orignal size*.

It is important to note that the number of elements in the MIPs vector may be different from its *orignal size*. The *orignal size* is the number of elements in the *ID set* over which we applied N random permutations to get the MIPs Vector as explained in MIPs section. In the line 24 we set the threshold value to 1 in order to get 100% recall. For each triple pattern $t_j = (s_j, p_j, o_j)$ in the query $q \in Q$, we apply the Algorithm 1 to get a set of selected capable data sources D_{s_j} which is used in sub-query generating algorithm explained in Section 4.6.

Join Source Ranking As mentioned earlier, we perform individual triple based sub-query federation. Consequently, triple pattern source ranking is most important for sub-query escaping. The advantage of this approach is that if a data source is not capable of answering the complete query, it may produce enough results for a specific sub-set of query triples. For the comparison purpose we propose a complete query source ranking which works as follow: For a star shape queries like the query given in Listing 4, the overall result set is bound by the triple with lowest number of estimated records. Therefore, we perform the source ranking for that triple (using Algorithm 1) and use this as complete query ranking. The lowest records query triple can be estimated using the rank 1 source selection explained in previous section. However, this time we are looking for a source which has the lowest estimated value of all. For path shaped queries the total records are bound by the triple which has *subject* variable equal to the *object* of the previous query triple. For example the result set in the query given in Listing 3, is bound by the second triple in which the *object* variable in the first triple is used as *subject* in the second triple. Therefore, we perform the triple pattern ranking for second triple and use this as ranking for complete query.

Listing 1.3: A P-1 query example

```
SELECT ?o1
  WHERE
   {
        ?s  <p1> ?o .
        ?o  <p2> ?o1
   }
```

4.6 Sub-query generation

The sub-query generation algorithm is similar to the one presented in DARQ. However, instead of using all capable sources, we use selected data sources (obtained from Algorithm 1) for the sub-query generation. Let *(T,s)* be a sub-query, where T is a set of triple patterns, and s is the data source that can answer this sub-query. The sub-query generation is shown in Algorithm 2. If a triple pattern t_j matches exactly one data source *(*$D_{s_j} = \{s\}$*)* then the triple will be added to the set of sub-queries for this data source. All triples in this set will be sent to

the data source in one sub-query. If a triple matches more than one data sources then the triple will be sent individually to all matching data sources in separate sub-queries. After the sub-queries are generated, the federator sends all of them to the optimizer for further optimization, before the federation. Our optimizer and data integrator module is similar to DARQ.

5 Experiments and Results

The goal of our experiments was to assess how well our duplicate-aware solution performs in terms of result set recall, ranking of data sources and runtime. We compared our approach with DARQ, a well-known, publicly available and widely used federated query execution engine.[7] We also compared our approach with a simulation of the optimal duplicate-unaware (DU) approach, where (1) the result set estimation of carried is carried out regardless of the overlap between data source and each source containing at one relevant triple is queried. In the following, we describe our experimental setup in detail and contrast the results achieved by each of the approaches. All data used in this evaluation is either publicly available or can be found at the project webpage.[8]

5.1 Experimental Setup

Datasets Within our experiments, we used the four datasets described in Table 1. The first data set, Diseasome, contains diseases and disease genes linked by disease-gene associations. The Publication data set is the Semantic Web Dog Food data set[9] and contains information on publications, venues and authors of publications. The Geo data set resulted from retrieving the portion of triples from DBpedia that maps resources to their geo-coordinates[10]. Finally, LinkedMDB [11] is the RDF version of IMDB and contains amongst others a large number of actors, movies and directors. We chose data sets of different data sizes to assess the scalability of our approach. The size of the MIPS vectors was set to achieve a compression ratio between 96% and 98%, which is similar to that used in previous work [12].

Given that we wanted to emulate fragmented data sets distributed across several sources, we distributed each of the data sets D across $n = 10$ data sources (which we also call "slices"). The first step of this process consisted of deciding on the size of the slices. We controlled the maximal size difference between the different slices by setting the *discrepancy factor* d, which is given by

$$d = \max_{1 \leq i \leq n} |S_i| - \min_{1 \leq j \leq n} |S_j|, \tag{4}$$

[7] We refrained from comparing with the approach presented in [12] because it connot deal with the partly fragmented data which is generated in our experiments.
[8] https://sites.google.com/site/dupawarefedqueries/
[9] http://data.semanticweb.org/
[10] http://wiki.dbpedia.org/Downloads38#geographic-coordinates.
[11] http://queens.db.toronto.edu/ oktie/linkedmdb

where S_i stands for the ith slice. Given a value of d, we computed the sizes of the slices by assigning them random sizes such that $\sum_i |S_i| = D$ and $\forall i \forall j \, i \neq j \rightarrow ||S_i| - |S_j|| \leq d$. The data was then distributed across the 10 data sources by partitioning the input according to the pre-computed sizes of the slices. Finally, we picked m out of the n data sources randomly ($m < n$) and redistributed their content across all $n - m$ remaining data sources . We set d to values between ca 1.6% and 2.8% of the triples. Note that the value of d was increased with increasingly larger data sets.

Dataset	Size (MB)	Summary Size (MB)	CR (%)	Slices	Discrepancy	Duplicate Slices	Duplicate Datasets	Total Triples	Sum. Gen. Time (sec)
Diseasome	18.6	0.64	96	10	1,500	1	10	91,122	9
Publication	39.0	1.15	97	10	2,500	1	10	234,405	16
Geo	274.1	4.66	98	10	50,000	2	5,8	1,900,006	1302
LinkedMDB	448.9	7.9	97	10	100,000	1	2	3,579,616	1837

Table 1: Overview of datasets. Size gives the magnitude of the data sets in MB. Summary size is the size of the correspoding MIPS. Slices is the number of data sources used during the experiments. Discrepancy gives the absolute value of the discrepancy used for the given experiment. CR stands for Compression Ratio.

Queries We used three main types of queries in our experiments: basic graph patterns (BGP), star-shaped and path-shaped queries. *Basic graph pattern* (BGP) queries consist of exactly one triple pattern in the query. Star-shaped and path-shaped queries are defined as in [12]: *star-shaped queries* (denoted by S-k) have one variable as subject and contained k joins, i.e., (k+1) triple patterns. An example of a S-1 star-shaped query is given in the listing below.

Listing 1.4: A S-1 query example

```
SELECT ?s
  WHERE
   {
        ?s  <p1> ?o1  .
        ?s  <p2> ?o2
    }
```

Path-shaped queries (denoted by P-k) were generated by using a random walk approach to generate a path of length k (see Listing 2 for an example of a P-1 query). Note that previous work has shown that these query shapes are the most common shapes found in real-world RDF queries [22]. Overall, our benchmark data consisted of 79 queries as shown in Table 2. Some query shapes could not be used on certain datasets due to the topology of the ontology underlying the datasets not being permissive for such queries. For example, P-1 queries could not be sent to the Geo datasets because it only contained object properties.

Dataset	BGP	S-1	S-2	P-1	P-2	P-3	Total
Diseasome	5	5	5	4	5	2	26
Geo	5	5	5	0	0	0	15
LinkedMDB	5	0	0	0	0	0	5
Publication	5	5	5	7	7	4	33
Total	20	15	15	11	12	6	79

Table 2: Distribution of query types across datasets

Metrics We used two metrics to compare our approach with the state of the art. First, we measured the mean squared error of each approach tested with respect to their result set evaluation as follows: For each query q_i, each source S_i contained a number $R_i(q_i)$ of non-duplicate results. Each of the approaches generated an approximation $\tilde{R}_i(q_i)$ of $R_i(q_i)$. The mean squared error with respect to the result set size (short $RSMSE$) was then computed as follows:

$$RSMSE = \frac{1}{|Q|} \sum_{q_i \in Q} |R_i(q_i) - \tilde{R}_i(q_i)|^2. \tag{5}$$

In addition to the RSMSE, we also computed how well the approaches were able to rank the data sources with respect to the unseen triples they would return for a given query. Given the ideal ranking $rank(S_i, q_j)$ of each data source S_i for each query q_j and the ranking $\tilde{r}(S_i, q_j)$ achieved by a given approach, we computed the mean squared ranking error (short $RankMSE$) as follows:

$$RankMSE(q_j) = \frac{1}{|\mathfrak{S}|} \sum_{S_i} |rank(S_i, q_j) - \tilde{r}(S_i, q_j)|^2. \tag{6}$$

$$RankMSE = \frac{1}{|Q|} \sum_{q_j \in Q} RankMSE(q_j). \tag{7}$$

For both measures, the higher values the worse the performance of the federated query approach.

5.2 Results

Result Set Estimation and Ranking The RSMSE results are shown in Figures 4 while the ranking results are shown in Figure 5. In each figure, we compared the results of the approaches w.r.t. both the whole input query and to each of the triples patterns contained in the input queries. Our results clearly show that we outperform the state of the art w.r.t. both result set estimation and ranking. In particular, our estimation of the result set sizes is approximately 4 orders of magnitude better than DARQ's and DU's. This is due to our approach being able to capture the existence of duplicates in the data sets and thus to better approximate the number of new results that can be expected from an endpoint. As expected, the ranking error for datasets decreases when carrying

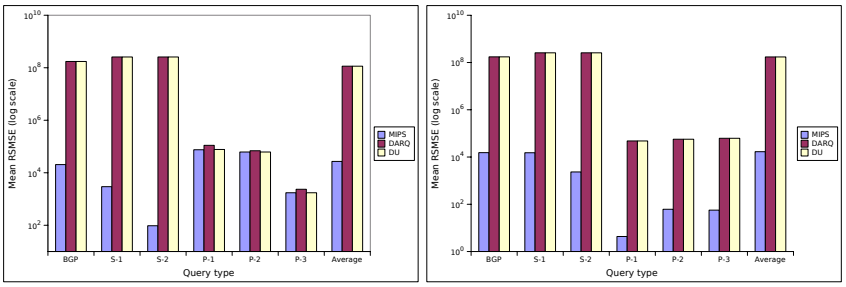
the ranking of data sources at triple pattern level instead of query level (see Figures 4). This is simply due to the overall error increasing when combining the several triple patterns to a query. The same overall behavior is also displayed when considering the result set estimation error (see Figures 5).

As stated before, we used a compression ratios between 96% and 98% across all experiments. The main advantage of such a high compression ratio is the small size of the index generated by our approach. Yet, higher compression ratios also lead to cruder approximations and thus to larger error margins of the number of duplicate-free triples in each data source. Consequently, the $RSMSE$ and $RankMSE$ of our approach can be high for queries whose sub-queries lead to result sets of similar magnitude. We wanted to know whether a decrease of the reduction ratio leads to our approach being able to capture even small differences across the sizes of the sub-query result sets. We thus studied the effect of decreasing the compression ratio on the $RSMSE$ and $RankMSE$ for such a query (which one)?. Our results in Table 3 suggest that MIPS vectors can successfully detect even small differences in the sizes of the result sets when given a sufficiently small compression ratio.

Recall and Runtime Table 5 shows the recall achieved by MIPS and DARQ in relation to the number of slices taken into consideration. Our results display the superiority of our ranking function, which is always able to achieve full recall of 1 by querying 9 from the 10 available data sources. In contrast, DARQ always has to visit all data sources to achieve a comparable recall. We measured the number of sub-query executions that could be escaped by our approach without any loss in recall. The results shown in Table 4 clearly demonstrate that our approach can effectively reduce the total number of queries executed overall. Especially, on BGP queries, we were able to escape up to 10 sub-queries. Our approach was most successful on star-shaped queries, where up to 21 sub-queries could be escaped. The better ranking function also leads to a superior overall runtime as shown in Figure 6. In average, our approach requires solely between 79.85% (S-2 queries) and 93.46% (P-1 queries) of the runtime of DARQ to retrieve the complete result set to each query.

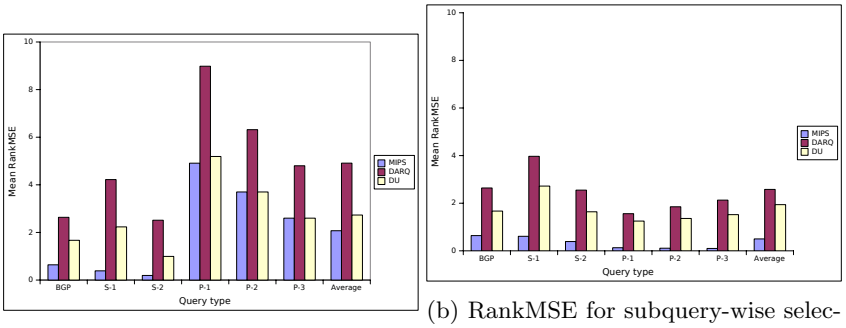
Compression Ratio	$RSMSE$	$RankMSE$
97%	253.9×10^6	3.4
94%	33.3×10^6	0.6
91%	0	0

Table 3: Effect of compression ratio



(a) RSMSE for query-wise selection (b) RSMSE for subquery-wise selection

Fig. 4: Mean squared errors with respect to result set evaluation across six query types



(a) RankMSE for query-wise selection (b) RankMSE for subquery-wise selection

Fig. 5: Mean squared errors with respect to ranking across six query types

Dataset	BGP	S-1	S-2	P-1	P-2	P-3	Total
Diseasome	7	21	21	8	20	12	89
Geo	10	15	23	0	0	0	48
LinkedMDB	5	0	0	0	0	0	5
Publication	1	2	5	0	0	0	8
Total	23	38	49	8	20	12	150

Table 4: Distribution of sub-query escaped by our approach

6 Conclusion and Future Work

In this paper, we presented an approach for duplicate-aware federated SPARQL querying. Our approach combines object and subject selectivity with MIPs to estimate the number of duplicate-free result subsets. Based on this estimation, it can select relevant data sources for a given query, rank these data sources according to the magnitude of relevant triples they contain and finally query them so as to maximize its recall. We compared our approach with DARQ and a simulation of an perfect duplicate-unaware SPARQL federated query engine and showed that we achieve lower mean squared errors with respect to both the estimation of the result set sizes and the ranking of data sources. Our results suggest that our approach can be easily adapted to scenarios where accurate approximations of result set sizes are required. Moreover, the execution time of our approach was shown to be superior to that of the state of art's. Our approach is also able to generate less network traffic by escaping sub-queries that would not lead to non-duplicate result sets. In future work, we will extend our approach by combining it with tiem-efficient duplicate detection systems such as LIMES [23]. By these means, we will enable our engine to merge facts which are expressed in different vocabularies or by using different URIs for the same real-world entity.

Rank	BGP		S1		S2		P1		P2		P3	
	MIPS	DARQ	MIPS	DARQ	MIPS	DARQ	MIPS	DARQ	MIPS	DARQ	MIPS	DARQ
1	29,22	19,22	26,53	24,42	30,69	30,69	18,12	15,67	24,60	21,99	31,60	29,30
2	49,61	39,50	46,20	39,67	52,15	49,70	34,04	31,49	38,84	38,56	43,78	45,02
3	67,48	61,78	60,90	54,78	66,48	59,96	50,28	49,23	55,74	53,16	61,86	56,76
4	78,44	72,68	70,75	63,86	76,60	71,49	65,71	64,04	72,25	69,11	80,17	73,72
5	85,65	79,26	79,76	74,32	83,64	80,54	77,24	79,87	83,04	86,11	90,45	91,74
6	90,54	84,00	86,67	79,59	89,90	86,76	82,28	83,75	87,69	89,95	94,48	95,70
7	94,68	87,25	92,94	85,61	94,88	90,22	85,56	87,17	89,99	92,08	95,59	96,73
8	99,40	89,38	98,62	89,98	99,35	93,43	87,71	89,29	91,47	93,31	95,70	97,53
9	100,00	97,95	100,00	96,52	100,00	97,06	100,00	94,97	100,00	97,15	100,00	99,26
10	100,00	100,00	100,00	100,00	100,00	100,00	100,00	100,00	100,00	100,00	100,00	100,00

Table 5: Comparison of recall on top-k data sources (in %).

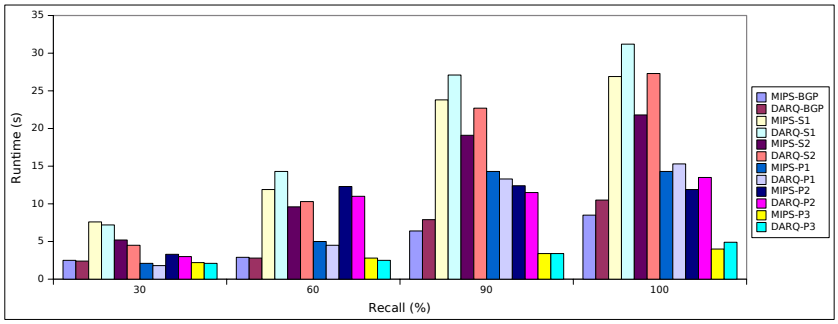


Fig. 6: Comparison of runtimes for different recall values. The x-axis shows the recall (%) achieved by our approach and DARQ on each of the six query types in our benchmark.

Algorithm 1 triple pattern source ranking

Require: t(s,p,o) ∈ T //triple pattern
D = getCapableSources(t) //all sources capable of answering triple t
$rank_1Source$ = getMaxSizeSource(D,t)
rnkNo = 1
unionMipv = $rank_1Source$.getMIPv(t)
D_s[rnkNo] = selectedSource
D = D - {selectedSource}
rnkNo = rnkNo+1
while $D \neq \emptyset$ **do**
  selectedSource = null
  maxDistinctRecords =0
  for each $d_i \in$ D **do**
    mipv = d_i.getMipv(t)
    if s is bound in t **then**
      mipv.orignalSize =mipv.orignalSize*d_i.getSbjSel(t)
    else if o is bound in t **then**
      mipv.orignalSize =mipv.orignalSize*d_i.getObjSel(t)
    end if
    overlap = unionMipv.intersectionSize(mipv)
    distinctRecords = mipv.getOrignalSize()-overlap
    if distinctRecords ¿ maxDistinctRecords **then**
      selectedSource = d_i
      maxDistinctRecords = distinctRecords
    end if
  end for
  if maxDistinctRecords $\geqslant$ 1 **then**
    D_s[rnkNo] = selectedSource
    selectedMipv = selectedSource.getMipv(t)
    unionMipv = unionMipv.union(selectedMipv)
    rnkNo = rnkNo+1
  end if
  D = D - {selectedSource}
end while
return D_s //rank wise selected sources

Algorithm 2 sub-query generation

Require: T = { $t_1, .., t_n$}
S = {D_{s_1},..,D_{s_n}} // sets of data sources obtained from algorithm 1
sub-queries = $\emptyset$, *seperateSub-queries* = $\emptyset$
for each $t_i \in$ T **do**
  if D_{s_j} = {s} **then**
    q = *queries.getQuery(s)*
    if q not null **then**
      q.T = q.T + t_i
    else
      sub-queries = *sub-queries* + ({t_i},s)
    end if
  else
    for each $s_j \in D_{s_j}$ **do**
      seperateSub-queries = *seperateSub-queries* + ({t_i},s)
    end for
  end if
end for
return *sub-queries* $\cup$ *seperateSub-queries* //Return all sub-queries

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