Fast Join Project Query Evaluation using Matrix Multiplication

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ABSTRACT
In the last few years, much effort has been devoted to developing join algorithms in order to achieve worst-case optimality for join queries over relational databases. Towards this end, the database community has had considerable success in developing succinct algorithms that achieve worst-case optimal runtime for full join queries, i.e. the join is over all variables present in the input database. However, not much is known about join evaluation with projections beyond some simple techniques of pushing down the projection operator in the query execution plan. Such queries have a large number of applications in entity matching, graph analytics and searching over compressed graphs. In this paper, we study how a class of join queries with projections can be evaluated faster using worst-case optimal algorithms together with matrix multiplication. Crucially, our algorithms are parameterized by the output size of the final result, allowing for choice of the best execution strategy. We implement our algorithms as a subroutine and compare the performance with state-of-the-art techniques to show they can be improved upon by as much as 50x. More importantly, our experiments indicate that matrix multiplication is a useful operation that can help speed up join processing owing to highly optimized open source libraries that are also highly parallelizable.

ACM Reference Format:
Shaleen Deep, Xiao Hu, and Paraschos Koutris. 2020. Fast Join Project Query Evaluation using Matrix Multiplication. In Proceedings of ACM Conference (Conference’17). ACM, New York, NY, USA, 16 pages. https://doi.org/10.1145/nmnnnn.nmnnnn

1 INTRODUCTION
In this paper, we study the problem of evaluating join queries where the join result does not contain all the variables in body of the query. In other words, some of the variables have been projected out of the join result. The simplest way to evaluate such a query is to first compute the full join, and then make a linear pass over the result, project each tuple and remove the duplicates. While this approach is conceptually simple, it relies on efficient worst-case optimal join algorithms for full queries, which have recently been developed in a series of papers [12, 31, 32, 34]. The main result in this line of work is a class of algorithms that run in time $O(|D|^\rho + |\text{OUT}|)$, where $D$ is the database instance and $\rho$ is the optimal fractional edge cover of the query [12]. In the worst case, there exists a database $D$ such that $|\text{OUT}| = |D|^\rho$. In practice, most query optimizers create a query plan by pushing down projections in the join tree.

Example 1. Consider relation $R(x, y)$ of size $N$ that represents a social network graph where an edge between two users $x$ and $y$ denotes that $x$ and $y$ are friends. We wish to enumerate all users pairs who have at least one friend in common [30]. This task is equivalent to the query $Q(x, z) = R(x, y), R(z, y)$, which corresponds to the following SQL query: SELECT DISTINCT $R_1.x$, $R_2.x$ FROM $R_1$ as $R$, $R_2$ as $R$ WHERE $R_1.y = R_2.y$. Suppose that the graph contains a small (constant) number of communities and the users are spread evenly across them. Each community has $O(\sqrt{N})$ users, and there exists an edge between most user pairs within the same community. In this case, the full join result is $\Theta(N^{3/2})$ but $|Q(D)| = \Theta(N)$.

As the above example demonstrates, using worst-case optimal join algorithms can lead to an intermediate output that can be much larger than the final result after projection, especially if there are many duplicate tuples. Thus, we ask whether it is possible to design faster algorithms that can skip the construction of the full result when this is large and as a result speed up the evaluation. Ideally, we would like to have algorithms that run faster than worst-case optimal join algorithms, are sensitive to the output of projected result, and do not require large main memory during execution.

In this paper, we show how to achieve the above goal for a fundamental class of join queries called star joins. Star joins are join queries where every relation is joined on the same
variable. The motivation to build faster algorithms for star joins with projection is not limited to faster query execution in DBMS systems. We present next a list of three applications that benefit from these faster algorithms.

**Set Similarity.** Set similarity is a fundamental operation in many applications such as entity matching and recommender systems. Here, the goal is to return all pairs of sets such that have contain at least \( c \) common elements. Recent work [20] gave the first output-sensitive algorithm that enumerates all similar sets in time \( O(|D|^{2-\frac{1}{c}} \cdot |\text{out}|^{\frac{1}{c}}) \). As the value of \( c \) increases, the running time tends to \( O(|D|^2) \). The algorithm also requires \( O(|D|^{2-\frac{1}{c}} \cdot |\text{out}|^{\frac{1}{c}}) \) space. We improve the running time and the space requirement of the algorithm for a large set of values that \( |\text{out}| \) can take, for all \( c \).

**Set Containment.** Efficient computation of set containment joins over set-value attributes has been extensively studied in the literature. A long line of research [26, 28, 29, 39] has developed a trie-based join method where the algorithm performs an efficient blocking step that prunes away most of the set verifications. However, the verification step is a simple set merging based method that checks if set \( t \subseteq u \), which can be expensive. We show that for certain datasets, our algorithm can identify set containment relationships much faster than state-of-the-art techniques.

**Graph Analytics.** In the context of graph analytics, the graph to be analyzed is often defined as a declarative query over a relational schema [7, 35, 37, 38]. For instance, consider the DBLP dataset, which stores which authors write which papers through a table \( R(\text{author, paper}) \). To analyze the relationships between co-authors, we can extract the co-author graph, which we can express as the view \( V(x, y) = R(x, p), R(y, p) \). Recent work [35] has proposed compression techniques where a preprocessing step generates a succinct representation of \( V(x, y) \). However, these techniques require a very expensive pre-processing step, rely on heuristics, and do not provide any formal guarantees on the running time. In the context of querying data through APIs, suppose that we want to support an API where a user checks whether authors \( a_1 \) and \( a_2 \) have co-authored a paper. This is an example of a boolean query. In this scenario, the view \( R(x, p) \) is implicit and not materialized. Since such an API may handle thousands of requests per second, it is beneficial to batch \( B \) queries together, and evaluate them at once. We show that our algorithms can lead to improved performance by minimizing user latency and resource usage.

Our contribution. In this paper, we show how to evaluate star join queries with projection using output-sensitive algorithms. We summarize our technical contribution below.

1. Our main contribution (Section 3) is an output-sensitive algorithm that evaluates star join queries with projection. We use worst-case optimal joins and matrix multiplication as two fundamental building blocks to split the join into multiple subjoin queries which are evaluated separately. This technique was initially introduced in [11], but their runtime analysis is incorrect for certain regimes of the output size. We improve and generalize the results via a more careful application of (fast) matrix multiplication.
2. We show (Section 4) how to exploit the join query algorithms for the problems of set similarity, set containment, join processing and boolean set intersection. Our algorithms also improve the best known preprocessing time bounds for creating offline data structures for set intersection problems [19] and compressing large graphs [35]. In addition, we can show that our approach is much more amenable to parallelization.
3. We develop (Section 5 and Section 6) a series of optimization techniques that address the practical challenges of incorporating matrix multiplication algorithms into join processing.
4. We implement our solution as an in-memory prototype and perform a comprehensive benchmarking to demonstrate the usefulness of our approach (Section 7). We show that our algorithms can be used to improve the running time for set similarity, set containment, join processing and boolean query answering over various datasets for both single threaded and multi-threaded settings. Our experiments indicate that matrix multiplication can achieve an order of magnitude speedup on average and upto 50x speedup over the best known baselines.

# PROBLEM SETTING

In this section we present the basic notions and terminology, and then define the problems we study in this paper.

## 2.1 Problem Definitions

In this paper, we will focus on the 2-path query, which consists of a binary join followed by a projection:

\[ \hat{Q}(x, z) = Q(x, z) = R(x, y), S(z, y) \]

and its generalization as a star join:

\[ Q^\ast(x_1, x_2, \ldots, x_k) = R_1(x_1, y), R_2(x_2, y), \ldots, R_k(x_k, y) \].

We will often use the notation \( \text{dom}(x) \) to denote the constants that the values that variable \( x \) can take. We use \( Q(D) \) to denote the result of the query \( Q \) over input database \( D \), or also \( \text{OUT} \) when it is clear from the context.

Apart from the above queries, the following closely related problems will also be of interest.
Set Similarity (SSJ). In this problem, we are given two families of sets represented by the binary relations $R(x, y)$ and $S(z, y)$. Here, $R(x, y)$ means set $x$ contains element $y$, and $S(z, y)$ means set $z$ contains element $y$. Given an integer $c \geq 1$, the set similarity join is defined as

$$\{(a, b) \mid |\pi_y(\sigma_{x=a}(R)) \cap \pi_y(\sigma_{z=b}(S))| \geq c\}$$

In other words, we want to output the pairs of sets where their intersection size is at least $c$. When $c = 1$, SSJ becomes equivalent to the 2-path query $Q$. The generalization of set similarity to more than two relations can be defined in a similar fashion. Previous work [20] only considered the un-ordered version of SSJ. The ordered version simply enumerates $\text{OUT}$ in decreasing order of similarity. This allows users to see the most similar pairs first instead of enumerating output tuples in arbitrary order.

Set Containment (SCJ). Similar to SSJ, given two families of sets represented by the relations $R, S$, we want to output

$$\{(a, b) \mid \pi_y(\sigma_{x=a}(R)) \subseteq \pi_y(\sigma_{z=b}(S))\}$$

In other words, we want to output the pairs of sets where one set is contained in the other.

Boolean Set Intersection (BSI). In this problem, we are given again two families of sets represented by the relations $R, S$. Then, for every input pair two sets $a, b$, we want to answer the following boolean CQ which asks whether the two sets have a non-empty intersection: $Q_{ab}(y) = R(a, y) \cap S(b, y)$. If we also want to output the actual intersection, we can use the slightly modified CQ $Q_{ab}(y) = \sigma_{a \subseteq b}(R(a, y) \cap S(b, y))$, which does not project the join variable. The boolean set intersection problem has been a subject of great interest in the theory community [10, 17–19, 33] given its tight connections with distance oracles and reachability problems in graphs.

In order to study the complexity of our algorithms, we will use the uniform-cost RAM model [24], where data values as well as pointers to databases are of constant size. Throughout the paper, all complexity results are with respect to data complexity where the query is assumed fixed.

2.2 Matrix Multiplication

Let $A$ be a $U \times V$ matrix and $C$ be a $V \times W$ matrix over a field $F$. We use $A_{i,j}$ to denote the entry of $A$ located in row $i$ and column $j$. The matrix product $AC$ is a $U \times W$ matrix with entries $(AC)_{i,j} = \sum_{k=1}^{V} A_{i,k}C_{k,j}$.

Join-Project as Matrix Multiplication. It will be convenient to view the 2-path query as a matrix computation. Let $A, B$ be the adjacency matrices for relations $R, S$ respectively: this means that $A_{i,j} = 1$ if and only if tuple $(i, j) \in R$ (similarly for $S$). Observe that although each relation has size at most $|D|$, the input adjacency matrix can be as large as $|D|^2$. The join output result $Q(D)$ can now be expressed as the matrix product $A \cdot B$, where matrix multiplication is performed over the boolean field.

Complexity. Multiplying two square matrices of size $n$ trivially takes time $O(n^3)$, but a long line of research on fast matrix multiplication has dropped the complexity to $O(n^\omega)$, where $2 \leq \omega < 3$. The current best known value is $\omega = 2.373$ [21], but it is believed that the actual value is $2 + o(1)$.

We will frequently use the following folklore lemma; we have added its proof for completeness.

Lemma 1. Let $\omega$ be any constant such that we can multiply two $n \times n$ matrices in time $O(n^\omega)$. Then, two matrices of size $U \times V$ and $V \times W$ can be multiplied in time $M(U, V, W) = O(UVW^{\omega/3})$, where $\beta = \min\{U, V, W\}$.

Proof. Assume w.l.o.g. that $\beta$ divides $\alpha = UVW/\beta$. Since $\beta$ is the smallest dimension we can divide the matrices into $\alpha/\beta^2$ submatrices of size $\beta \times \beta$, which can be multiplied using $O(\beta^\omega)$ operations.

For the theoretically best possible $\omega = 2 + o(1)$, rectangular fast matrix multiplication can be done in time $O(UVW/\beta)$.

2.3 Known Results

Ideally we would like to compute $Q_k^*$ in time linear to the size of the input and output. However, [13] showed that $Q$ cannot be evaluated in time $O(|\text{OUT}|)$ assuming that exponent $\omega$ in matrix multiplication is greater than two.

A straightforward way to compute any query that is a join followed by a projection is to compute the join using any worst-case optimal algorithm, and then deduplicate to find the projection. This gives the following baseline result.

Proposition 1 ([31, 32]). Any CQ $Q$ with optimal fractional edge cover $\rho^*$ can be computed in time $O(|D|^{\rho^*})$.

Proposition 1 implies that we can compute the the star query $Q_k^*$ in time $O(|D|^k)$, where $k$ is the number of joins. However, the algorithm is oblivious of the actual output $\text{OUT}$ and will have the same worst-case running time even if $\text{OUT}$ is much smaller than $|D|^k$ – as it happens often in practice. To circumvent this issue, [11] showed the following output sensitive bound that uses only combinatorial techniques:

Lemma 2 ([11]). $Q_k^*$ can be computed in time $O(|D| \cdot |\text{OUT}|^{1 - \frac{1}{k}})$.

For $k = 2$, the authors make use of fast matrix multiplication to improve the running time to $O(N^{0.862} \cdot |\text{OUT}|^{0.408} + |D|^{2/3} \cdot |\text{OUT}|^{2/3})$. In the next section, we will discuss the flaws in the proof of this result in detail.

3 COMPUTING JOIN-PROJECT

In this section, we describe our main technique and its theoretical analysis.
3.1 The 2-Path Query

Consider the query \( \mathcal{Q}(x, z) = R(x, y), S(z, y) \). Let \( N_R \) and \( N_S \) denote the cardinality of relations \( R \) and \( S \) respectively. Without loss of generality, assume that \( N_S \leq N_R \). For now, assume that we know the output size \(|\text{OUT}|\); we will show how to drop this assumption later.

We will also assume that we have removed any tuples that do not contribute to the query result, which we can do during a linear time preprocessing step.

**Algorithm.** Our algorithm follows the idea of partitioning the input tuples based on their degree as introduced in \cite{DBLP:conf/soda/ChekuriK16}, but it differs on the choice of threshold parameters. It is parametrized by two integer constants \( \Delta_1, \Delta_2 \geq 1 \). It first partitions each relation into two parts, \( R^-, R^+ \) and \( S^-, S^+ \):

\[
R^- = \{ (a, b) \mid |\sigma_{x=a,R(x, y)}| \leq \Delta_2 \text{ or } |\sigma_{y=b,S(z, y)}| \leq \Delta_1 \} \\
S^- = \{ (c, b) \mid |\sigma_{z=c,S(z, y)}| \leq \Delta_2 \text{ or } |\sigma_{y=b,S(z, y)}| \leq \Delta_1 \}
\]

In other words, \( R^-, S^- \) include the tuples that contain at least one value with low degree. \( R^+, S^+ \) contain the remaining tuples from \( R, S \) respectively. **Algorithm 1** describes the detailed steps for computing the join. It proceeds by performing a (disjoint) union of the following results:

1. Compute \( R^- \bowtie S \) and \( R \bowtie S^- \) using any worst-case optimal join algorithm, then project.
2. Materialize \( R^+, S^+ \) as two rectangular matrices and use matrix multiplication to compute their product.

Intuitively, the "light" values are handled by standard join techniques, since they will not result in a large intermediate result before the projection. On the other hand, since the "heavy" values will cause a large output, it is better to compute their result directly using (fast) matrix multiplication.

**Example 2.** Consider relation \( R \) and \( S \) as shown below.

\begin{tabular}{c|c|c}
\hline
\textbf{Relation R} & \textbf{Relation S} \\
\hline
\textbf{x} & \textbf{y} & \textbf{z} & \textbf{y} \\
1 & 1 & 1 & 1 \\
2 & 2 & 2 & 2 \\
3 & 3 & 3 & 3 \\
4 & 4 & 4 & 4 \\
5 & 5 & 5 & 5 \\
6 & 6 & 6 & 6 \\
\hline
\end{tabular}

Suppose \( \Delta_1 = \Delta_2 = 2 \). Then, all the edges marked in red (green) form relation \( R^-(S^-) \). \( R^- \bowtie S \) and \( R \bowtie S^- \) can now be evaluated using any worst-case optimal algorithm. The remaining edges consist of values that are heavy. Thus, we construct matrices \( M_1 \) and \( M_2 \) encoding all heavy tuples. The resulting matrix product \( M \) shows all the heavy output tuples with their corresponding counts.

**Algorithm 1:** Computing \( \pi_{xz}R(x, y) \bowtie S(z, y) \)

\begin{itemize}
\item[1.] \( R^- \leftarrow \{ (a, b) \mid |\sigma_{x=a,R(x, y)}| \leq \Delta_2 \text{ or } |\sigma_{y=b,S(z, y)}| \leq \Delta_1 \} \)
\item[2.] \( R^+ \leftarrow R \setminus R^- \)
\item[3.] \( S^- \leftarrow \{ (c, b) \mid |\sigma_{z=c,S(z, y)}| \leq \Delta_2 \text{ or } |\sigma_{y=b,S(z, y)}| \leq \Delta_1 \} \)
\item[4.] \( S^+ \leftarrow S \setminus S^- \)
\item[5.] \( M_1(x, y) \leftarrow R^- \bowtie S^- \text{ adj matrix, } M_2(y, z) \leftarrow S^+ \bowtie S^+ \text{ adj matrix} \)
\item[6.] \( M \leftarrow M_1 \times M_2 \text{ /* matrix multiplication */ } \)
\item[7.] \( \text{return } T \)
\end{itemize}

**Correctness.** Consider an output tuple \((a, c)\). If there exists no \( b \) such that \((a, b) \in R \) and \((c, b) \in S \), then such a pair cannot occur in the output since it will not occur in \( R^- \bowtie S, R \bowtie S^- \) or \( M \). Now suppose that \((a, c)\) has at least one witness \( b \) such that \((a, b) \in R \) and \((c, b) \in S \). If \( b \) is light in relation \( R \) or \( S \), then at least one of \((a, b) \) or \((c, b) \) will be included in \( R^- \bowtie S^- \) and the output tuples will be discovered in the join of \( R^- \bowtie S \) or \( R \bowtie S^- \). Similarly, if the degree of \( a \) or \( c \) is at most \( \Delta_2 \) in relation \( R \) or \( S \) respectively, the output tuple will be found in \( R^- \bowtie S \) or \( R \bowtie S^- \). Otherwise, \( a, b, c \) are heavy values so \( M_1 \) and \( M_2 \) matrix will contain an entry for \((a, b) \) and \((b, c) \) respectively.

**Analysis.** We now provide a runtime analysis of the above algorithm, and discuss how to optimally choose \( \Delta_1, \Delta_2 \).

We first bound the running time of the first step. To compute the full join result (before projection), a worst-case optimal algorithm needs time \( O(N_R + N_S + |\text{OUT}|) \), where \(|\text{OUT}|\) is the size of the join. The main observation is that the size of the join is bounded by \( N_S \cdot \Delta_1 + |\text{OUT}| \cdot \Delta_2 \). Hence, the running time of the first step is \( O(N_R + N_S \cdot \Delta_1 + |\text{OUT}| \cdot \Delta_2) \).

To bound the running time of the second step, we need to bound appropriately the dimensions of the two rectangular matrices that correspond to the subrelations \( R^+, S^+ \). Indeed, the heavy \( x \)-values for \( R^+ \) are at most \( N_R/\Delta_2 \), while the heavy \( y \)-values are at most \( N_S/\Delta_1 \). This is because \( \text{dom}(y) \leq N_0 \). Hence, the dimensions of the matrix for \( R^+ \) are \((N_R/\Delta_2) \times (N_S/\Delta_1) \). Similarly, the dimensions of the matrix for \( S^+ \) are \((N_S/\Delta_1) \times (N_S/\Delta_2) \). The matrices are represented as two-dimensional arrays and can be constructed in time \( C = \max \{N_R/\Delta_2, N_S/\Delta_1, N_S/\Delta_2 \} \) by simply iterating over all possible heavy pairs and checking whether they form
a tuple in the input relations. Thus, from Lemma 1 the running time of the matrix multiplication step is \(O\left(\frac{N_R}{\alpha_2} \cdot \frac{N_S}{\alpha_1} \cdot \frac{N_S}{\alpha_2}\right)\).

Summing up the two steps, the cost of the algorithm is in the order of:

\[
N_R + N_S \Delta_1 + |\text{OUT}| \Delta_2 + M\left(\frac{N_R}{\alpha_1} \cdot \frac{N_S}{\Delta_1} \cdot \frac{N_S}{\Delta_2}\right) + C
\]

Using the above formula, one can plug in the formula for the matrix multiplication cost and solve to find the optimal values for \(\Delta_1, \Delta_2\). We show how to do this in Section 5.

In the next part, we provide a theoretical analysis for the case where matrix multiplication is achievable with the theoretically optimal \(\omega = 2\) for the case where \(N_R = N_S = N\). Observe that the matrix construction cost \(C\) is of the same order as \(M\left(\frac{N_R}{\alpha_1} \cdot \frac{N_S}{\Delta_1} \cdot \frac{N_S}{\Delta_2}\right)\) even when \(\omega = 2\), since \(\beta\) is the smallest of the three terms \(N_R/\Delta_2, N_S/\Delta_1, N_S/\Delta_2\). Thus, it is sufficient to minimize the expression

\[
f(\Delta_1, \Delta_2) = N + N \cdot \Delta_1 + |\text{OUT}| \cdot \Delta_2 + \frac{N^2}{\Delta_2} \min\{\Delta_1, \Delta_2\}
\]

while ensuring \(1 \leq \Delta_1, \Delta_2 \leq N\).

The first observation is that for any feasible solution \(f(x, y) = x > y\), we can always improve the solution by decreasing the value of \(\Delta_1\) from \(x\) to \(y\). Thus, w.l.o.g. we can impose the constraint \(1 \leq \Delta_1 \leq \Delta_2 \leq N\).

**Case 1.** \(|\text{OUT}| \leq N\). Since \(\Delta_1 \leq \Delta_2\), we have \(f(\Delta_1, \Delta_2) = N \cdot \Delta_1 + |\text{OUT}| \cdot \Delta_2 + N^2/\Delta_2 \cdot \Delta_1\). To minimize the running time we equate \(\partial f/\partial \Delta_1 = N - N^2/(\Delta_2 \Delta_1^2) = 0\) and \(\partial f/\partial \Delta_2 = |\text{OUT}| - N^2/(\Delta_1 \Delta_2^2) = 0\). Solving this system of equations gives that the critical point has \(\Delta_1 = |\text{OUT}|^{1/3}, \Delta_2 = N/|\text{OUT}|^{2/3}\). Since \(|\text{OUT}| \leq N\), this solution is feasible, and it can be verified that it is the minimizer of the running time, which becomes

\[
N + N \cdot |\text{OUT}|^{1/3}
\]

**Case 2.** \(|\text{OUT}| > N\). For this case, there is no critical point inside the feasible region, so we will look for a minimizer at the border, where \(\Delta_1 = \Delta = \Delta_2\). This condition gives us \(f(\Delta) = (N + |\text{OUT}|) \cdot \Delta + N^2/\Delta^2\), with minimizer \(\Delta = (2N^2/(N + |\text{OUT}|))^{1/3}\). The runtime then becomes

\[
O(N^{2/3} \cdot |\text{OUT}|^{2/3})
\]

We can summarize the two cases with the following result.

**Lemma 3.** Assuming that the exponent in matrix multiplication is \(\omega = 2\), the query \(Q\) can be computed in time

\[
O(|D| + |D|^{2/3} \cdot |\text{OUT}|^{1/3} \cdot \max\{|D|, |\text{OUT}|\})^{1/3}
\]

**Lemma 2** implies a running time of \(O(|D| \cdot |\text{OUT}|^{1/2})\) for \(\tilde{Q}\), which is strictly worse compared to the running time of the above lemma for every output size \(|\text{OUT}|\).

**Remark.** For the currently best known value of \(\omega = 2.37\), the running time is \(O(|D|^{0.85} \cdot |\text{OUT}|^{0.59} + |D| \cdot |\text{OUT}|^{0.41})\).

**Optimality.** The algorithm is worst-case optimal (up to constant factor) for \(|\text{OUT}| = \Theta(N^2)\). The running time becomes \(O(N^2)\) which matches the lower bound \(|\text{OUT}|\), since we require at least that much time to enumerate the output.

**Comparing with previous results.** We now discuss the result in [11], which uses matrix multiplication to give a running time of \(\tilde{O}\left(|D|^{0.86} \cdot |\text{OUT}|^{0.408} + |D|^{2/3} \cdot |\text{OUT}|^{2/3}\right)\). We point out an error in their analysis that renders their claim incorrect for the regime where \(|\text{OUT}| < N\).

In order to obtain their result, the authors make a split of tuples into light and heavy, and obtain a formula for running time in the order of \(N\Delta_b + |\text{OUT}|\Delta_ac + M\left(\frac{N}{\Delta_ac}, \frac{N}{\Delta_ac}, \frac{N}{\Delta_ac}\right)\), where \(\Delta_b, \Delta_ac\) are suitable degree thresholds. Then, they use the formula from [25] for the cost of matrix multiplication, where \(M(x, y, x) = x^{1.84} \cdot y^{0.53} + x^2\). However, this result can be applied only when \(x \geq y\), while the authors apply it for regimes where \(x < y\). (Indeed, if say \(x = N^{0.3}\) and \(y = N^{0.9}\), then we would have \(M(x, y, x) = N^{1.05}\), which is smaller than the input size \(N^{1.2}\). Hence, the running time analysis is valid only when \(N/\Delta_ac \geq N/\Delta_b\), or equivalently \(\Delta_b \geq \Delta_c\). Since the thresholds are chosen such that \(N\Delta_b = |\text{OUT}|\Delta_ac\), it means that the result is correct only in the regime where \(|\text{OUT}| \geq N\). In other words, when the output size is smaller than the input size, the running time formula from [11] is not applicable.

In the case where \(\omega = 2\), the cost formula from [25] becomes \(M(x, y, x) = x^2\), and [11] gives an improved running time of \(\tilde{O}(N^{2/3} \cdot |\text{OUT}|^{2/3})\). Again, this is applicable only when \(|\text{OUT}| \leq N\), in which case it matches the bound from Lemma 3. Notice that for \(|\text{OUT}| \leq N^{1/2}\) the formula would imply a deterministic sublinear time algorithm.

### 3.2 The Star Query

We now generalize the result to the star query \(Q^*_x\). As before, we assume that all tuples that do not contribute to the join output have already been removed.

**Algorithm.** The algorithm is parametrized by two integer constants \(\Delta_1, \Delta_2 \geq 1\). We partition each relation \(R_i\) into three parts, \(R^+_i, R^-_i\) and \(R^*_i\):

\[
R^-_i = \{R_i(a, b) \mid |\sigma_{x_i=a}R_i(x_i, y) \leq \Delta_2\}
\]

\[
R^*_i = \{R_i(a, b) \mid |\sigma_{y_i=b}R_i(x_j, y) \leq \Delta_1, \text{ for each } j \in [k] \setminus i\}
\]

\[
R^+_i = R_i \setminus (R^-_i \cup R^*_i)
\]

In other words, \(R^-_i\) contains all tuples with light \(x\), \(R^*_i\) contains all tuples with \(y\) values that are light in all other relations, and \(R^+_i\) the remaining tuples. The algorithm now proceeds by computing the following result:

1. Compute \(R_1 \bowtie \ldots \bowtie R^-_1 \bowtie \ldots R^-_k\) using any worst-case optimal join algorithm, then project for each \(j \in [k]\).
(2) Compute \( R_1 \bowtie \ldots \bowtie R_j \bowtie \ldots \bowtie R_k \) using any worst-case optimal join algorithm, then project for each \( j \in [k] \).

(3) Materialize \( R_1^* \), \( \ldots \), \( R_k^* \) as rectangular matrices and use matrix multiplication to compute their product.

**Analysis.** We assume that all relation sizes are bounded by \( N \). The running time of the first step is \( O(|\text{OUT}| \cdot \Delta_2) \) since each light value of variable \( x_i \) in relation \( R_i \) contributes to at least one output result.

For the second step, the key observation is that since \( y \) is light in all relations (except possibly \( R_i \)), the worst-case join size before projection is bounded by \( O(N \cdot \Delta_1^{k-1}) \), and hence the running time is also bounded by the same quantity.

The last step is more involved than simply running matrix multiplication. This is because for each output result formed by heavy \( x_i \) values in \( R_i \) (say \( t = (a_1, a_2, \ldots, a_k) \)), we need to count the number of \( y \) values that connect with each \( a_i \) in \( t \). However, running matrix multiplication one at a time between two matrices only tells about the number of connection \( y \) values for any two pair of \( a_i \) and not all of \( t \). In order to count the \( y \) values for all of \( t \) together, we divide variables \( x_1, \ldots, x_k \) into two groups of size \( \lceil k/2 \rceil \) and \( \lfloor k/2 \rfloor \) followed by creating two adjacency matrices. Matrix \( V \) is of size \( \left( \frac{N}{\Delta_1} \right)^{\lceil k/2 \rceil} \times \frac{N}{\Delta_1} \) such that

\[
V_{(a_1, a_2, \ldots, a_{\lceil k/2 \rceil}), b} = \begin{cases} 
1, & (a_1, b) \in R_1, \ldots, (a_{\lceil k/2 \rceil}, b) \in R_{\lceil k/2 \rceil} \\
0, & \text{otherwise}
\end{cases}
\]

Similarly, matrix \( W \) is of size \( \left( \frac{N}{\Delta_1} \right)^{\lfloor k/2 \rfloor} \times \frac{N}{\Delta_1} \) such that

\[
W_{(a_{\lfloor k/2 \rfloor+1}, a_{\lfloor k/2 \rfloor+2}, \ldots, a_k), b} = \begin{cases} 
1, & (a_{\lfloor k/2 \rfloor+1}, b) \in R_{\lfloor k/2 \rfloor+1}, \ldots, (a_k, b) \in R_k \\
0, & \text{otherwise}
\end{cases}
\]

**Example 3.** Consider the relations \( R(x, y) \) and \( S(z, y) \) from previous example and consider relation \( T(p, y) \) and \( U(q, y) \) as shown below.

| Relation T | Relation U |
|------------|------------|
| p | q |
| 1 | 1 |
| 2 | 2 |
| 3 | 3 |
| 4 | 4 |
| 5 | 5 |
| 6 | 6 |

Suppose that we wish to compute the result of star query \( Q_*^* = R(a, y), S(b, y) \) parametrized by the constants \( a, b \). The queries come at a rate of \( B \) queries per time unit. In order to service these requests, we can use multiple machines. Our goal is twofold: minimize the number of machines we use, while at the same time minimizing the average latency, defined as the average time to answer each query.

**Example 4.** Let \( k = 3 \) and \( |\text{OUT}| = N^{3/2} \). The running time is minimized when

\[
N \cdot \Delta_1^3 = |\text{OUT}| \cdot \Delta_2 = M(\frac{N \cdot \Delta_1}{\Delta_2^2}, \frac{N}{\Delta_1}, \frac{N}{\Delta_2})
\]

The first equality gives us \( \Delta_1^3 = N \cdot \Delta_2 \). We will choose the thresholds such that \( \Delta_2 < \Delta_1 \). This means \( \rho = N/\Delta_1 \). From the second equality, we get \( |\text{OUT}| \cdot \Delta_2 = (\frac{N \cdot \Delta_1}{\Delta_2})^3 \). The running time is minimized when \( \Delta_2 = N^{\frac{3}{2}}, \Delta_1 = N^{\frac{1}{2}} \), in which case it is \( O(N^{\frac{3}{2}}) \) which is sub-quadratic (assuming \( \omega = 2 \)). In contrast, Lemma 2 has a worse running time \( O(N^2) \).

### 3.3 Boolean Set Intersection

In this setting, we are presented with a workload \( W \) containing boolean set intersection (BSI) queries of the form \( Q_{xy}(\cdot) = R(a, y), S(b, y) \) parametrized by the constants \( a, b \). The queries come at a rate of \( B \) queries per time unit. In order to service these requests, we can use multiple machines. Our goal is twofold: minimize the number of machines we use, while at the same time minimizing the average latency, defined as the average time to answer each query.

**Example 5.** The simplest strategy is to answer each request using a separate machine. Computing a single BSI query takes worst-case time \( O(N) \), where \( N \) is the input size. Hence, the average latency is \( O(N) \). At the same time, since queries come at a rate of \( B \) queries per time unit, we need \( \rho = B \cdot N \) machines to keep up with the workload.

Our key observation is that, instead of servicing each request separately, we can batch requests and compute them
all at once. To see why this can be beneficial, suppose that we batch together $C$ queries. Then, we can group all pairs of constants $(a, b)$ to a single binary relation $T(x, z)$ of size $C$, and compute the following conjunctive query:

$$Q_{\text{batch}}(x, z) = R(x, y), S(z, y), T(x, z).$$

Here, $R, S$ have size $N$, and $T$ has size $C$. The resulting output will give the subset of the pairs of sets that indeed intersect.

The above query can be computed by applying a worst-case optimal algorithm and then performing the projection: this will take $O(N \cdot C^{1/3})$ time. Hence, the average latency for a request will be $\frac{N}{B} + \frac{N}{C^{1/3}}$.

To get even lower latency, we can apply a variant of the AYZ algorithm [20] that uses fast matrix multiplication. The algorithm works as follows. For $x, y, z$ values with degrees less than some threshold $\Delta \geq 1$, we perform the standard join with running time $O(N \cdot \Delta)$. For the remaining values, we express relations $R, S$ as rectangular matrices of dimensions $\frac{N}{\Delta} \times \frac{N}{\Delta}$ and $\frac{N}{\Delta} \times \frac{N}{\Delta}$ respectively. We compute the matrix product, and then intersect the result with $T$ to obtain the final output. The running time for this step is $\frac{N}{\Delta} \times \frac{N}{\Delta} \times \frac{N}{\Delta}$, which for $\Delta = 2$ becomes $O(S \cdot N/\Delta^2)$. To minimize the running time for both steps, we choose $\Delta = C^{1/3}$, and thus the running time becomes $O(N \cdot C^{1/3})$.

Using the above algorithm, we can show the following.

**Proposition 2.** Let $W$ be a workload of queries of the form $Q_{\text{batch}}() = R(a, y), S(b, y)$ at the rate of $B$ access requests per second. Then, assuming the exponent of matrix multiplication is $\omega = 2$, we can achieve an average latency of $O(N^{3/5} / B^{2/5})$ using $\rho = (B \cdot N)^{3/5}$ machines.

**Proof.** Using batch size $C$, we can process $C$ queries in time $O(N \cdot C^{1/3})$. Hence, the average latency in this case is $O\left(\frac{N}{C^{1/2}} + \frac{C}{N}\right)$. To minimize the latency, we choose $C = (B \cdot N)^{3/5}$, in which case we obtain an average latency of $O(N^{3/5} / B^{2/5})$. Then, the number of machines needed to service the workload is $(B \cdot N)/C^{2/3} = (B \cdot N)^{1/5}$.

Observe that the above proposition strictly improves the number of machines compared to the baseline approach of Example 5. However, the average latency is smaller only for $B \leq N^{3/2}$, otherwise it is larger.

In our experiments, we use the requests in the batch to filter the relations $R$ and $S$, and then compute the 2-path query using Algorithm 1.

## 4 SPEEDING UP SSJ AND SCJ

In this section, we will see how to use Algorithm 1 to speed up SSJ and SCJ.

**Unordered SSJ.** We will first briefly review the state-of-the-art algorithm from [20] called SizeAware. Algorithm 2 describes the size-aware set similarity join algorithm. The key insight is to identify degree threshold $x$ and partition the input sets into light and heavy. All heavy sets that form an output pair are enumerated by a sort merge join. All light sets are processed by generating all possible $c$-sized subsets and then building an inverted index over it that allows for enumerating all light output pairs. $x$ is chosen such that the cost of processing heavy and light sets is equal to each other.

We propose three key modifications that give us the new algorithm called SizeAware++. First, observe that $f_H = R \bowtie R_h$ (line 3) is a natural join and requires $N \cdot N/\Delta$ operations (recall that $|R_h| = N/\Delta$ in the worst-case) even if the join output is smaller. Thus, Algorithm 1 is applicable here directly. This strictly improves the theoretical worst-case complexity of Algorithm 2 whenever $|f_H| < N^2/x$ for all $c$.

The second modification is to deal with high duplication when enumerating all light pairs using the inverted index $L[r_c]$. The key observation is that line 8 is also performing a brute-force operation by going over all possible pairs and generating the full join result. This step takes $|f_H| = \sum_{r_c} |L[r_c]|^2$ time. If the final output is smaller than $|f_H|$, then we can do better by using matrix multiplication based algorithm.

The final observation relates to optimizing the expansion of light nodes (line 3 in Algorithm 1). Recall that the algorithm expands all light $y$ values. Suppose we have $R(x, y)$ and $S(z, y)$ relations indexed and sorted according to variable order in the schema. Let $L[b] = \{c \mid (c, b) \in S(z, y)\}$ denote the inverted index for relation $S$. The time required to perform the deduplication for a fixed value for $x$ (say $a$) is

![Figure 1: Example instance showing inverted lists](image_url)
We illustrate the key idea with the following example.

When input sets \( A \) and \( B \) have a significant overlap, there also exists a tradeoff between space requirement and computation reuse. Storing the output and list union at every node in the prefix tree increases the materialization requirement. This is unavoidable for overlap \( c = 1 \) in the worst case. However, it is possible that for \( c > 1 \), the output size is much smaller than \( T \). In other words, deduplication step is expensive when the overlap between \( L[b] \) for different \( b \) is high. The key idea is to reuse computation across multiple \( a \) if there is a shared prefix and high overlap. We illustrate the key idea with the following example.

**Example 6.** Consider the instance shown in Figure 1 with \( \{b_1, \ldots, b_7\} \) as the possible keys for inverted index \( L[b] \) and sets \( A_1, \ldots, A_4 \) as shown in the prefix tree. We use the length of inverted list \( L[b] \) as the key for sorting the input sets descending order: Suppose overlap \( c = 2 \). After merging inverted list for \( b_1, b_2 \), we know that \( C_1, C_2, C_3 \) are present at least two times across all of the lists. At this point, we materialize two things: (i) \( O_1 = \{C_1, C_2, C_3\} \) as output and, (ii) \( U_1 = L[b_1] \cup L[b_2] \setminus O_1 \) at the node \( b_2 \) in the tree. We then continue with merging the other lists. When we start the enumeration for \( A_2 \), we know that the lists \( b_1, b_2 \) have already been processed and we can simply use the stored output. For \( b_4 \), we can go over its content and check whether the value is present in \( U_1 \). Similarly, for sets \( A_3 \) and \( A_4 \) that share \( b_1, b_2 \) as a prefix, \( U_2 \) stores the union of \( L[b_1] \) and \( L[b_2] \) after removing the sets that have appeared at least two times. For \( A_1, A_2 \), simply performing a merge step requires \( 9 + 9 = 18 \) operations in total. However, if reusing the computation, we require only 9 operations: 7 for \( A_1 \) (merging \( b_1 \) and \( b_2 \)) and 2 for merging inverted list of \( b_4 \) with stored \( U_1 \).

The global sort order for all \( b \) is the length of inverted list \( L[b] \). This encourages more computation reuse since bigger lists will give larger output and merging those repeatedly is expensive. Since a global sort order has been defined, we can construct a prefix tree and store the output and list union in the prefix tree. This technique will provide the largest gain when input sets \( A \) have a significant overlap. There also exists a tradeoff between space requirement and computation reuse. Storing the output and list union at every node in the prefix tree increases the materialization requirement. The space usage can be controlled by limiting the depth at which the output and list union is stored. This can avoid excessive materialization when space is limited. The three optimizations in SizeAware++ together can deliver speedups up to an order of magnitude over SizeAware for single threaded implementation. Next, we highlight the important aspects regarding parallelization of SSJ and why SizeAware is not as amenable to parallelization as we would it to be. Partitioning join \( J_{II} \) is straightforward since all parallel tasks require no synchronization and access the input data in a read-only manner. Parallelizing \( J_{I} \) in SizeAware is harder because of two reasons: (i) generating the \( c \)-sized subsets requires coordination since a given subset can be generated by multiple small sets; (ii) once the subsets have been generated, a given output pair \( (r, s) \) can be connected to multiple \( c \)-subsets. This means that each parallel task needs to coordinate in order to deduplicate multiple results across different \( c \)-subsets.

**Ordered SSJ.** In this part, we look at the problem of enumerating SSJ in decreasing order of set similarity. Ordered enumeration of output pairs can be done by first generating the output and then sorting it. Note that the processing of light sets in Algorithm 2 (and consequently SizeAware++) is not amenable to finding the set pair with the largest intersection. Once an output pair has been identified, we still need to enumerate over elements in the sets to identify the exact intersection size. On the other hand, our matrix multiplication and filtering the join result to find the similar set pairs is the fastest technique and also benefits the most from parallelization.

**SCJ.** SCJ algorithms [15] typically prune away most of the set pairs that are surely not contained within each other. This acts as a blocking filter. For the remaining set pairs, the verification step performs a sort-merge join to verify if containment holds for either of the sets i.e we perform a merge join for all set pairs that need to be verified. However, the verification step can be slow if the overlap between sets is high (because of multiple replicas) or the average inverted index size is large. For these cases, we can get a significant speedup by simply evaluating the join-project result. This approach is most beneficial when the set containment join result is close to the join-project result. Further, majority of SCJ algorithms do not use the power of parallel computation. PIEJoin [28] is the first and the only algorithm that addresses...
parallel SCJ. Since join processing is highly parallelizable, computing SCJ via join-project output benefits from parallel computation as well.

5 COST-BASED OPTIMIZATION

In this section, we deep dive into the challenges of making our framework practical and how we can fine tune the knobs to minimize the running time.

Estimating output size. So far, we have not discussed how to estimate for |OUT|. We derive an estimate in the following manner. First, it is simple to show that the following holds for \( R \): \(|\text{dom}(x)| \leq |\text{OUT}| \leq \min\{|\text{dom}(x)|^2, |\text{OUT}_{\text{min}}|\}\) and \(|\text{OUT}_{\text{min}}| \leq N \cdot \sqrt{|\text{OUT}|}\). Thus, a reasonable estimate for |OUT| is the geometric mean of \( \max\{|\text{dom}(x)|, (|\text{OUT}_{\text{min}}|/N)^2\} \) and \( \min\{|\text{dom}(x)|^2, |\text{OUT}_{\text{min}}|\}\). If |OUT_{\text{min}}| is not much larger than \( N \), then the full join size is also reasonable estimate. We return to this point later in the discussion of the optimizer.

Indexing relations. Join processing by applying worst-case optimal join algorithms is possible only if all relations are indexed over the variables. This means each relation will be stored once for every index order that is required. For a binary relation \( R(x, y) \), this would mean storing the relation indexed by all values of \( x \) as key and a sorted list of values for \( y \) and vice-versa. This can be accomplished in \( O(|D| \log |D|) \) time after removing all tuples that do not join. During this pass, it is also straightforward to compute the size of full join result (i.e., before the projection). Additionally, we create the following indexes:

1. For variable \( x \) and degree threshold \( \delta \), an index that tells us the deduplication effort when performing set union (i.e, \( \sum_{b \in \text{light}} (\sum_{a \in \text{heavy}} |L[b]|) \)) for all values of \( x \) with degree \( \leq \delta \). We call this index \( \text{sum}(x, \delta) \). Similarly for all values of \( y \) with degree \( \leq \delta \), \( \text{sum}(y, \delta) = \sum_{b \in \text{light}} |L[b]| \).
2. For the projected out variable \( y \) and degree threshold \( \delta \), an index that counts the number of \( x \) connected to all \( y \) values with degree \( \leq \delta \). We call this index \( \text{cdfx}(y, \delta) \).
3. For each variable (say \( w \)), an index that tells us the number of values for \( w \) with degree \( \leq \delta \). We call this index \( \text{count}(w, \delta) \).

All indexes can be built in linear time by storing the sorted vector containing the true distribution of values present in the relation. Then, given a \( \delta \), we can binary search over the vector to find the exact count (sum).

Matrix multiplication cost. A key component of all our techniques is matrix multiplication. Lemma 1 states the complexity of performing multiplication and also includes the cost of creating the matrices. However, in practice, this could be a significant overhead both in terms of memory consumption and time required. Further, the scalability of matrix multiplication implementation itself is subject to matrix size, the underlying linear algebra framework and hardware support (vectorization, SIMD instructions, multithreading support etc.) In order to minimize the running time, we need to take into consideration all system parameters in order to estimate the optimal threshold \( \Delta \) values.

![Figure 3: Matrix Multiplication Running Time](image)

| Symbol | Description |
|--------|-------------|
| \( T_s \) | avg time for sequential access in std::vector |
| \( T_m \) | avg time for allocating 32 bytes of memory |
| \( M(u, v, w, co) \) | estimate of time required to multiply matrices of dimension \( u \times v \) and \( v \times w \) using \( co \) cores |
| \( T_I \) | avg time for random access and insert in std::vector |

Table 1: Symbol definitions.

Algorithm 3 describes the cost based optimizer used to find the best degree thresholds in order to minimize the running time. To simplify the description, we describe the details for the case of \( Q \) where \( R = S \) (i.e., a self join). If the full join result is not much larger than the size of input relation, then we can simply use any worst case optimal join algorithm. For our experiments, we set the upper bound for |OUT_{\text{min}}| to be at most \( 20 \cdot N \). Beyond this point, we begin to see the benefit of using matrix multiplication for join-project computation.

To find the best possible estimates for \( \Delta_1 \), \( \Delta_2 \), we employ binary search over the value of \( \Delta_2 \). In each iteration, we increase or decrease its value by a factor of \( (1 - \epsilon) \) where \( \epsilon \) is a constant \(^1\). Once we fix the value of \( \Delta_1 \) and \( \Delta_2 \), we can query our precomputed index structure to find the exact number of operations that will be performed for all light \( y \) values and all light \( x \) values. Then, we find the number of heavy remaining values and get the estimate for time.

\(^1\) We fix \( \epsilon = 0.95 \) for our experiments.
**Algorithm 3: Cost Based Optimizer**

**Output:** degree threshold $\Delta_1, \Delta_2$

1. Estimate full join result $|\text{OUT}_{\text{prev}}|$ and $|\text{OUT}|$
2. if $|\text{OUT}_{\text{prev}}| \leq 20 \cdot N$ then
   1. use worst-case optimal join algorithm
3. $t_{\text{light}} \leftarrow |\text{OUT}_{\text{prev}}|, t_{\text{heavy}} \leftarrow 0, \text{prev}_{\text{light}} \leftarrow \infty, \text{prev}_{\text{heavy}} \leftarrow 0, \Delta_1 = N$
4. while true do
   1. $t_{\text{light}} \leftarrow \text{prev}_{\text{light}}, t_{\text{heavy}} \leftarrow \text{prev}_{\text{heavy}}$
   2. $\Delta_1 \leftarrow (1 - \epsilon)\Delta_1$
   3. $\Delta_2 \leftarrow N \cdot \Delta_1 / |\text{OUT}|$
   4. $t_{\text{light}} \leftarrow T_l \cdot \text{sum}(y_{\Delta_1}) + T_l \cdot \text{sum}(x_{\Delta_2}) +$
   5. $T_m \cdot |\text{dom}(x)| + T_s \cdot \text{cdf}(y_{\Delta_1}) \cdot |\text{dom}(x)|$
   6. $u, v, w \leftarrow \text{heavy } x, y, z$ values using $\text{count}(w_{\delta})$
   7. $t_{\text{heavy}} \leftarrow \bar{M}(u, v, w, co) + T_m \cdot (u + v + w)$
   8. if $t_{\text{light}} + \text{prev}_{\text{heavy}} \leq t_{\text{light}} + t_{\text{heavy}}$ then
      1. return $\text{prev}_{\Delta_1}, \text{prev}_{\Delta_2}$

required to compute the matrix product. At the beginning of the next iteration, we compare the new time estimates with the previous iteration. If the new total time is larger than that of the previous iteration, we stop the process and use the last computed values as the degree thresholds. The entire process terminates in worst-case $O(\log^3 N)$ steps.

So far, we have not discussed how to estimate $\bar{M}(u, v, w, co)$. Since this quantity is system dependent, we precompute a table that stores the time required for different values of $u, v, w, co$. As a brute-force computation for all possible values is very expensive to store and compute, we store the time estimate for $\bar{M}(p, p, p, co)$ for $p \in \{1000, 2000, \ldots, 2000\}, co \in [5]$. Then, given an arbitrary $u, v, w, co$, we can extrapolate from the nearest estimate available from the table. This works well since Eigen implements the naive $O(n^3)$ (with optimizations) algorithm that offers predictable running time. Figure 3a shows scalability of Eigen as the input matrix size increases. Since Eigen makes heavy use of SIMD instructions and vectorization, the running time displays a near quadratic growth rather than cubic for dimensions up to $5000 \times 5000$, beyond which the running time growth becomes cubic.

### 6 SYSTEM IMPLEMENTATION

We implement our techniques in C++ as a standalone library. To perform matrix multiplication, we use Eigen [?] with Intel MKL [?] as the underlying linear algebra framework. We choose Eigen for its ease of use and its seamless support for parallelization, even though other frameworks such as MATLAB are faster. Intel MKL offers two different functions for performing matrix operations: SGEMM and DGEMM. SGEMM allows low precision real arithmetic while DGEMM is for high precision arithmetic. This also makes DGEMM 3x slower than SGEMM for the same operation being performed. We use floating point matrices everywhere rather than double precision or integer matrices for better performance.

At this point, we also wish to draw the attention of the reader towards some low level details of the SSJ and SCJ implementation. Since the goal is to output the result in arbitrary order, both implementations enumerate the result without storing any of the output. Enumerating the result in (say) decreasing order of similarity size or containment size will require storing the output and sorting it before providing the user with a pointer to the result. We implement this in the straightforward way by sorting std::vector containing the output. Next, we describe the details of deduplication in our implementation for the case of unordered enumeration.

**Deduplication.** Since matrix multiplication deduplicates the output for all heavy values, we only need to handle deduplication for the remaining output tuples. The straightforward way to deduplicate is to use a hashmap. However, this has two disadvantages: (i) The memory for hashmap needs to be reserved upfront. This is critical to ensure that there is no resizing (and reshuffling of the keys already present) of the hashmap at any point; (ii) upfront reservation would require $|\text{OUT}|$ amount of memory for deduplication, which is expensive both in terms of time and memory.

```cpp
std::vector<int> y_light; // all light y values
std::unordered_map<int, set> R_xy; // indexed relation
std::unordered_map<int, set> R_yx; // indexed relation
std::vector<int> dedup(N); // reserving N memory

for(auto x : [N]) {
    dedup.assign(N, 0);
    for(auto y : y_light) {
        if(R_yx[x].find(y) == R_yx[x].end()) {
            for(auto z : R_yx[y]) {
                dedup.at(z) ++;
            }
        }
    }
}
```

**Deduplication.** Since matrix multiplication deduplicates the output for all heavy values, we only need to handle deduplication for the remaining output tuples. The straightforward way to deduplicate is to use a hashmap. However, this has two disadvantages: (i) The memory for hashmap needs to be reserved upfront. This is critical to ensure that there is no resizing (and reshuffling of the keys already present) of the hashmap at any point; (ii) upfront reservation would require $|\text{OUT}|$ amount of memory for deduplication, which is expensive both in terms of time and memory.
The code snippet above shows the join for all light y values, which is the estimate used in line 11 of Algorithm 3. Line 4 reuses the dedup vector to check that a given z value has already been output or not. This is possible because we have fixed an x value and then merge all the z values reachable from y that are connected to x. Since the above approach involves random access over the dedup vector, it can be easily an order of magnitude more expensive than serial access if the vector does not fit in the L1 cache. An alternative approach is to deduplicate by appending all reachable z values, followed by sorting to deduplicate. For our experiments, we choose the best of the two strategies, depending on the number of elements that need to be deduplicated and the domain size of variables.

**Parallelization.** The single-threaded execution of all algorithms easily reaches several hours when faced with gigabyte sized data sets and thus, parallel processing becomes necessary. Eigen parallelizes the matrix multiplication part in a coordination-free way, allowing both parts of our implementation to be highly parallelizable. Figure 3b shows the running time of matrix multiplication as the number of cores increases. The speedup obtained is near linear as the resources available increases. This is possible because each core calculates the matrix product of a partition of data and requires no interaction with the other tasks.

7 EXPERIMENTAL EVALUATION

In this section, we empirically evaluate the performance of our algorithms. The main goal of the section is four fold:

1. Empirically verify the speed-up obtained for the 2-path and star queries using algorithm from Section 3 compared to Postgres, MySQL, EmptyHeaded [9] and Commercial database X.
2. Evaluate the performance of the two-path query against SizeAware and SizeAware++ for unordered and ordered SSJ.
3. Evaluate the performance of the 2-path query against three state-of-the-art algorithms, namely PIEJoin [28], LIMIT+ [15], PRETTI for SCJ.
4. Validate the batching technique for boolean set intersection.

All experiments are performed on a machine with Intel Xeon CPU E5-2660@2.6GHz, 20 cores and 150 GB RAM.

### Table 2: Dataset Characteristics

| Dataset  | | No. of sets | | Avg set size | Min set size | Max set size |
|----------|------------------|--------------|--------------|--------------|--------------|--------------|
| DBLP     | 10M               | 1.5M         | 3M           | 6.6          | 1            | 500          |
| RoadNet  | 1.5M              | 1M           | 1.5          | 1            | 20           |
| Jokes    | 400M              | 70K          | 50K          | 5.7K         | 1            | 10K          |
| Words    | 500M              | 1M           | 15K          | 50           | 1            | 10K          |
| Protein  | 900M              | 60K          | 60K          | 15K          | 50           | 50K          |
| Image    | 800M              | 70K          | 50K          | 11.4K        | 10K          | 50K          |

Table 2 shows the main characteristics of the datasets. DBLP and RoadNet are examples of sparse datasets whereas the other four are dense datasets.

7.1 Datasets

We conduct experiments on six real-world datasets from different domains. DBLP [1] is a bibliography dataset from DBLP representing authors and papers. RoadNet [5] is road network of Pennsylvania. Jokes [3] is a dataset scraped from Reddit where each set is a joke and there is an edge between joke and a word if the work is present in the joke. Words [6] is a bipartite graph between documents and the lexical tokens present in them. Image [2] dataset is a graph where each image is connected to a feature attribute if the image contains the corresponding attribute and Protein [4] refers to a bipartite graph where an edge signifies interaction between two proteins. Table 2 shows the main characteristics of the datasets. DBLP and RoadNet are examples of sparse datasets whereas the other four are dense datasets.

7.2 Simple Join Processing

In this part, we evaluate the running time for the two queries: \( \bar{Q} \) and \( Q^* \). To extract the maximum performance from Postgres, we use PGTune to set the best configuration parameters. This is important to ensure that the query plan does not perform nested loop inner joins. For all datasets, we create a hash index over each variable to ensure that the optimizer can choose the best query plan. We manually verify that query plan generated by PostgreSQL (and MySQL) when running these queries chooses HashJoin or MergeJoin. For X, we allow up to 1TB of disk space and supply query hints to make sure that all of the CPU, RAM memory is available for query execution.

Figure 4a shows the run time for different algorithms on a single core. MySQL and Postgres have the slowest running time since they evaluate the full query join result and then deduplicate. DBMS X performs marginally better than MySQL and Postgres. Non-matrix multiplication (denoted
Figure 4: Join Processing for two path and star query

Figure 5: Unordered and Ordered SSJ

Non-MMJoin join based on Lemma 2 is the second best algorithm. Matrix multiplication based join (denoted MMJoin) is the fastest on all datasets except RoadNet and DBLP, where the optimizer chooses to compute the full join. A key reason for the huge performance difference between MMJoin and other algorithms is that deduplication by computing the full join result requires either sorting the data or using hash tables, both of which are expensive operations. In particular, using hash tables requires rehashing of entries every time the hash table increases. Similarly, sorting the
full join result is expensive since the full join result can be orders of magnitude larger than the projection query result. Matrix multiplication avoids this since worst-case optimal joins can efficiently process the light part of the input and matrix multiplication is space efficient due to its implicit factorization of the output formed by heavy values. Remarkably, EmptyHeaded performs comparable to MMJoin for Jokes dataset and outperforms MMJoin slightly on Image dataset. This is because Image dataset exclusively contains a dense component where every the output is close to a clique. Since EmptyHeaded is designed as a linear algebra engine like Intel MKL, the performance is very similar. Figure 4d and 4e show the performance of the combinatorial and non-combinatorial algorithm as the number of cores increases. Both algorithms show a speed-up. We omit MySQL and Postgres since they do not allow for multicore processing of single queries.

Next, we turn to the star query on three relations for this experiment, we take the largest sample of each relation so that the result can fit in main memory and the join finishes in reasonable time. Figure 4b shows the performance of the combinatorial and non-combinatorial join on a single core. All other engines (except EmptyHeaded) failed to finish in 15000 seconds except on RoadNet and DBLP. EmptyHeaded performed similarly to MMJoin on Protein and Image datasets but not on other datasets. Figure 4f and 4g show the performance in a multicore setting for Jokes and Words datasets. Once again, matrix multiplication performs better than its combinatorial version across all experiments.

7.3 Set Similarity

In this section, we look at set similarity (SSJ). For both settings below, we materialize the output at all nodes in the prefix tree. We will compare the performance of MMJoin, SizeAware and SizeAware++. We begin with the unordered setting.

Unordered SSJ. Figure 5a, 5b and 5c show the running time of MMJoin, SizeAware and SizeAware++ on a single core for DBLP, Jokes and Image dataset respectively. Since DBLP is a sparse dataset with small set sizes, MMJoin is the fastest and both SizeAware and SizeAware++ are marginally slower due to the optimizer cost. For Jokes and Image datasets, SizeAware is the slowest algorithm. This is because both the light and heavy processing have a lot of deduplication to perform. SizeAware++ is an order of magnitude faster than SizeAware since it uses matrix multiplication but is slower than MMJoin because it still needs to enumerate the c-subsets before using matrix multiplication. MMJoin is the fastest as it is output sensitive and performs the best in a setting with many duplicates. Next, we look at the parallel version of unordered SSJ. Figure 5d, 5g and 5h show the results for multi core settings. For each experiment, we fix the overlap to $c = 2$. Observe that MMJoin join and SizeAware++ are more scalable than SizeAware. This is because the light sets processing of SizeAware cannot be done in parallel while matrix multiplication based deduplication can be performed in parallel.

Ordered SSJ. Recall that for ordered SSJ, our goal is to enumerate the set pairs in descending order of set similarity. Thus, once the set pairs and their overlap is known, we need to sort the result using overlap as the key. Figure 5e and 5f show the running time for single threaded implementation of ordered set similarity. Compared to the unordered setting, the extra overhead of materializing the output and sorting the result increases the running time for all algorithms. For SizeAware, there is an additional overhead of finding the overlap for all light sets as well. Both MMJoin and SizeAware++ maintain their advantage similar to the unordered setting.

Impact of Optimizations. Recall that SizeAware++ contains three main optimizations - processing heavy sets using MMJoin, processing light sets via MMJoin and using prefix based materialization for computation sharing. Figure 8 shows the effect of switching on various optimizations. NO-OP denotes all optimizations switched off. The running time is shown as a percentage of the NO-OP running time (100%). Light denotes using two-path join on only light sets identified by SizeAware but not using the prefix optimizations. Heavy includes the Light optimizations switched on plus two-path join processing on the heavy sets but prefix based optimization is still switched off. Finally, Prefix switches on materialization of the output in prefix tree on top of Light and Heavy. As the figure shows, both Light and Heavy optimizations together improve the running time by an order of magnitude and Prefix further improves by a factor of 5x.

7.4 Set Containment

In this section, we evaluate the performance of different set containment join algorithms. Figure 4c shows the running time of PIEJoin, PRETTI and LIMIT+. For all SCJ algorithms, we use the infrequent sort order, choose a limit value of two for LIMIT+ and run the variant where the output is materialized (instead of just simply counting its size). Once again join processing yields the fastest running time since the join output is a superset of the set containment join result and except RoadNet and DBLP, the join-project result and SCJ result is close to each other. Since the average set size is large for most datasets, SCJ algorithms need to perform expensive verification operations. For the parallel setting, Figure 7a, 7b, 7c and 7d show the performance of PIEJoin vs. MMJoin. PIEJoin does not scale as well as MMJoin as it is sensitive to data distribution and choice of partitions chosen by the heuristic in the algorithm.
of $\approx 1s$ when $S = 10$. In that time, we collect a further 1000 requests, which means that there is a need for 100 parallel processing units. On the other hand, MMJoin achieves a delay of $\approx 2s$ at batch size 900. Thus, we need only 3 parallel processing units in total to keep up with the workload while sacrificing only a small penalty in latency. For the Image dataset, MMJoin can achieve average delay of 1s at $S = 1000$ queries while Non-MMJoin achieves 50s at the same batch size. This shows that matrix multiplication is useful for achieving a smaller latency using less resources, in line with the theoretical prediction. For the Words dataset, most of the sets have a small degree. Thus, the optimizer chooses to evaluate the join via the combinatorial algorithm. This explains the in sync behavior of average delay for both the algorithms. Note that MMJoin is marginally slower because of the overhead of the optimizer ($\leq 2s$).

8 RELATED WORK

Theoretically, [13] and [11] are the most closely related works to our considered setting (as discussed in Section 2.3). In practice, most of the previous work has considered join-project query evaluation by pushing down the projection operator in the query plan [14, 16, 22, 25]. LevelHeaded [8] and EmptyHeaded [9] are general linear algebra systems that use highly optimized set intersections to speed up evaluation of cyclic joins, counting queries and support projections over
We describe an algorithm based on fast matrix multiplication. Very recently, [27] made significant progress by providing algorithms that tradeoff pre-processing time and worst-case delay guarantees for hierarchical queries (star join is a subset of hierarchical queries). The main result states that for star query with $k$ relations, there exists an algorithm that pre-processes in time $T = O(N^{1+(k-1)/\epsilon})$ such that it is possible to enumerate the join-project result without duplications with worst-case delay guarantee $\delta = O(N^{1+\epsilon})$ for any $\epsilon \in [0, 1]$. This implies that the total running time is bounded by $\delta \cdot |\text{OUT}|$. For group-by aggregate queries, [36] also used worst-case optimal join algorithms to avoid evaluating binary joins at a time and materializing the intermediate results. However, the running time of their algorithm is not output sensitive with respect to the final projected result and could potentially be improved upon by using our proposed ideas.

9 CONCLUSION AND FUTURE WORK

In the paper, we study the evaluation of join queries with projections. This is useful for a wide variety of tasks including set similarity, set containment and boolean query answering. We describe an algorithm based on fast matrix multiplication that allows for theoretical speedups. Empirically, we demonstrated that the framework is also practically useful and can provide speedups of up to 50x for some datasets. There are several promising future directions that remain to be explored. The first key direction is to extend our techniques to arbitrary acyclic queries with projections. In order to do so, we need better join-project size estimation techniques and building a query plan that decomposes the join into multiple subqueries and evaluates in the optimal way. This can potentially be done by modifying estimators for set union and set intersection such as KMV and HyperLogLog. Second, it remains unclear if the same techniques can also benefit cyclic queries or not. For instance, AYZ algorithm is applicable to counting cycles in graphs using matrix multiplication. It would be interesting to extend the algorithm to enumerate join-project output where the user can choose arbitrary projection variables on a cyclic query. It will also be interesting to see if fast matrix multiplication can help in group-by aggregate queries for longer path queries.

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