Leapfrog Triejoin: A Simple, Worst-Case Optimal Join Algorithm

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ABSTRACT

Recent years have seen exciting developments in join algorithms. In 2008, Atserias, Grohe and Marx (henceforth AGM) proved a tight bound on the maximum result size of a full conjunctive query, given constraints on the input relation sizes. In 2012, Ngo, Porat, Ré and Rudra (henceforth NPRR) devised a join algorithm with worst-case running time proportional to the AGM bound [8]. Our commercial database system LogicBlox employs a novel join algorithm, *leapfrog triejoin*, which compared conspicuously well to the NPRR algorithm in preliminary benchmarks. This spurred us to analyze the complexity of leapfrog triejoin. In this paper we establish that leapfrog triejoin is also worst-case optimal, up to a log factor, in the sense of NPRR. We improve on the results of NPRR by proving that leapfrog triejoin achieves worst-case optimality for finer-grained classes of database instances, such as those defined by constraints on projection cardinalities. We show that NPRR is *not* worst-case optimal for such classes, giving a counterexample where leapfrog triejoin runs in $O(n \log n)$ time and NPRR runs in $\Theta(n^{1.375})$ time. On a practical note, leapfrog triejoin can be implemented using conventional data structures such as B-trees, and extends naturally to $\exists_1$ queries. We believe our algorithm offers a useful addition to the existing toolbox of join algorithms, being easy to absorb, simple to implement, and having a concise optimality proof.

General Terms

Algorithms,Theory

1. INTRODUCTION

Join processing is a fundamental and comprehensively-studied problem in database systems. Many useful queries can be formulated as one or more *full conjunctive queries*. A full conjunctive query is a conjunctive query with no projections, i.e., every variable in the body appears in the head [3, 1]. As a running example we use the query defined by this Datalog rule:

$$Q(a,b,c) \leftarrow R(a,b), S(b,c), T(a,c). \tag{1}$$

where a, b, c are query variables (for intuition: if $R = S = T$, then Q finds triangles.)

Given constraints on the sizes of the input relations such as $|R| \leq n$, $|S| \leq n$, $|T| \leq n$, what is the maximum possible query result size $|Q|$? This question has practical import, since a tight bound $|Q| \leq f(n)$ implies an $\Omega(f(n))$ worst-case running time for algorithms answering such queries.

Atserias, Grohe and Marx (AGM [2]) established a tight bound on the size of Q: the *fractional edge cover* bound Q^* (Section 2.2). For the case where $|R| = |S| = |T| = n$, the fractional cover bound yields $|Q| \leq Q^* = n^{3/2}$. In earlier work, Grohe and Marx [6] gave an algorithm with running time $O(|Q^*|^2 g(n))$, where $g(n)$ is a polynomial determined by the fractional cover bound. In 2012, Ngo, Porat, Ré and Rudra (NPRR [8]) devised a groundbreaking algorithm with worst-case running time $O(Q^*)$, matching the AGM bound. The algorithm is non-trivial, and its implementation and analysis depend on rather deep machinery developed in the paper.

The NPRR algorithm was brought to our attention by Dung Nguyen, who implemented it experimentally using our framework. LogicBlox uses a novel and hitherto proprietary join algorithm we call *leapfrog triejoin*. Preliminary benchmarks suggested that leapfrog triejoin performed dramatically better than NPRR on some test problems [9]. These benchmark results motivated us to analyze our algorithm, in light of the breakthroughs of NPRR.

Conventional join implementations employ a stable of join operators (see e.g. [5]) which are composed in a tree to produce the query result; this tree is prescribed by a query plan produced by the optimizer. The query plan often relies on producing intermediate results. In contrast, leapfrog triejoin joins all input relations simultaneously without producing any intermediate results.[1] Our algorithm is variable-oriented: for a join $Q(x_1, \ldots, x_k)$, leapfrog triejoin performs a backtracking search, binding each variable $x_1, x_2, \ldots$ in turn to enumerate satisfying assignments of the formula defining the query. This is in contrast to typical DBMS algorithms which are join-oriented, using a composition of algebraic joins in a specified order to produce the result.

[1] In some situations it is *desirable* to materialize intermediate results. Such materializations are compatible with leapfrog triejoin, but are not required to meet the worst-case performance bound, and are beyond the scope of this paper.

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Leapfrog triejoin is substantially different than typical join algorithms, but natural in retrospect.

In this paper we show that leapfrog triejoin achieves running time $O(Q^* \log n)$, where Q^* is the fractional cover bound, and n is the largest cardinality among relations of the join. (A variant suggested by Ken Ross eliminates the $\log n$ factor, achieving $O(Q^*)$ time (Section 6.1).)

We believe that leapfrog triejoin offers a useful addition to the existing toolbox of join algorithms. The algorithm is easy to understand and simple to implement. The optimality proof is concise, and could be taught in an advanced undergraduate course. The optimality principle strengthens and improves that of NPRR, and leapfrog triejoin is asymptotically faster than NPRR for useful classes of problems. Finally, leapfrog triejoin is a well-tested, practical algorithm, serving as the workhorse of our commercial database system.

The paper is organized as follows. In Section 2 we review the fractional edge cover bound. Section 3 presents the leapfrog triejoin algorithm. Section 4 develops the tools used in the complexity analysis, culminating in the optimality proof of Theorem 4.2. In Section 5 we consider finer-grained complexity classes for which leapfrog triejoin is optimal; in one such example we demonstrate that the NPRR algorithm has running time $\Theta(n^{1.375})$, compared to $O(n \log n)$ for leapfrog triejoin. In Section 6.2 we describe the extension of leapfrog triejoin to $\exists_1$ queries. In Section 6.1 we discuss a variant of leapfrog triejoin which eliminates the $\log n$ factor.

2. PRELIMINARIES AND BACKGROUND

2.1 Notations and conventions

All logarithms are base 2, and $[n] = \{1, \ldots, n\}$. Complexity analyses assume the RAM machine model.

Database instances are finite structures defined over universes which are subsets of $\mathbb{N}$. In algorithm descriptions we use int as a synonym for $\mathbb{N}$. (The restriction to $\mathbb{N}$ is merely to simplify the presentation; our implementation requires only that a type be totally ordered.)

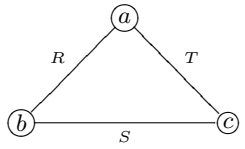
For a binary relation $R(a, b)$, we write $R(a, \_)$ for the projection $\pi_1(R)$, i.e., the set $\{a \ : \ \exists b \ . \ (a, b) \in R\}$. For a parameter a, we write $R_a(b)$ for the *curried* version of R, i.e., the relation $\{b \ : \ (a, b) \in R\}$. Similarly for relations of arity > 2, e.g., for $S(a, b, c)$ we write $S_a(b, c)$ and $S_{a,b}(c)$ for curried versions. We assume set semantics: query results are sets rather than multisets; our datalog system implements set semantics, unlike commercial SQL systems, so this is not merely a simplifying convenience.

2.2 The fractional cover bound

We begin with a review of the fractional edge cover bound for worst-case result size of full conjunctive queries. The fractional edge cover bound is not directly required by the complexity analysis for leapfrog triejoin (Theorem 4.2), which is formulated in terms of the maximum query result size Q^*. However, for families of problem instances defined by cardinality constraints on the relation sizes, Q^* can be computed using the fractional cover bound.

The fractional edge cover was proven to be an upper bound on query result size by Grohe and Marx [6] in the context of constraint solving. The bound was shown to be tight, and adapted to relational joins, by Atserias, Grohe and Marx [2].

We continue the running example of a query $Q(a, b, c)$ defined by the join $R(a, b)$, $S(b, c)$, $T(a, c)$. Suppose we know the sizes $|R|$, $|S|$, and $|T|$, and we wish to know the largest possible query result size $|Q|$. The AGM bound for $|Q|$ is obtained by constructing a hypergraph $H = (V, \mathcal{E})$ whose vertices are the variables $V = \{a, b, c\}$, and each atom such as $R(a, b)$ is interpreted as a (hyper)edge $\{a, b\}$ on the variables appearing in its argument list:



Recall that an edge cover is a subset $C \subseteq \mathcal{E}$ of edges such that each vertex appears in at least one edge $e \in C$. Edge cover can be formulated as an integer programming problem by assigning to each edge $e_i \in \mathcal{E}$ a weight λ_i, with $\lambda_i = 1$ when $e_i \in C$ and $\lambda_i = 0$ when $e_i \notin C$. The cover requirement is enacted by inequalities, one for each vertex. For the query (1) we would use edge weights λ_R, λ_S, and λ_T, and inequalities:

$$\begin{array}{lccccccc} a: & \lambda_R & + & & & \lambda_T & \geq & 1 \\ b: & \lambda_R & + & \lambda_S & & & \geq & 1 \\ c: & & & \lambda_S & + & \lambda_T & \geq & 1 \end{array} \tag{2}$$

A *fractional edge cover* is obtained by relaxing to a linear programming problem, permitting edge weights to range between 0 and 1. For example, choosing $\lambda_R = \lambda_S = \lambda_T = \frac{1}{2}$ yields a valid fractional cover. Grohe and Marx [6] established that:

$$|Q| \leq |R|^{\lambda_R} \cdot |S|^{\lambda_S} \cdot |T|^{\lambda_T} \tag{3}$$

Or equivalently:

$$\log |Q| \leq \lambda_R \log |R| + \lambda_S \log |S| + \lambda_T \log |T| \tag{4}$$

Minimizing the right-hand side of (4) yields the AGM bound on the size of $|Q|$. For example, with $|R| = |S| = |T| = n$, the bound is minimized when $\lambda_R = \lambda_S = \lambda_T = \frac{1}{2}$, yielding $|Q| \leq n^{3/2}$.

2.3 Dual formulation

The dual formulation, used by [2] to prove tightness of the bound, is more intuitive and offers a construction of worst-case instances that is instructive. We introduce the dual through an example.

Consider a scenario where the sizes of R, S, T are fixed, and $Q(a, b, c)$ has a simple cross-product structure $Q = [2^\alpha] \times [2^\beta] \times [2^\kappa]$. (The quantities α, β, κ can be interpreted as the average number of bits to represent variables a, b, c; for simplicity we assume $2^\alpha, 2^\beta, 2^\kappa$ to be integers.) From the query definition (1), it is apparent that $(a, b, c) \in Q$ implies $(a, b) \in R$; therefore $[2^\alpha] \times [2^\beta] \subseteq R$. This implies $\alpha + \beta \leq \log |R|$. Similarly for S and T. The problem of maximizing $|Q|$ can be formulated as a linear program:

$$\text{Maximize} \quad \log |Q| = \alpha + \beta + \kappa$$

$$\text{Subject to} \quad \left\{ \begin{array}{lcccccl} \alpha & + & \beta & & & \leq & \log |R| \\ & & \beta & + & \kappa & \leq & \log |S| \\ \alpha & + & & & \kappa & \leq & \log |T| \end{array} \right.$$

For example, setting $\log |R| = \log |S| = \log |T| = \log n$ yields $\log |Q| = \frac{3}{2} \log n$ at optimality, achieved by $\alpha = \beta = \kappa = \frac{1}{2} \log n$ and $Q = [n^{1/2}] \times [n^{1/2}] \times [n^{1/2}]$.

The above linear program is the dual of the fractional edge cover linear program: using $\boldsymbol{\lambda} = [\lambda_A, \lambda_B, \lambda_C]$, $\boldsymbol{\eta} = [\log|R|, \log|S|, \log|T|]$, $\boldsymbol{\alpha} = [\alpha, \beta, \kappa]$, and $\mathbf{1} = [1, 1, 1]$, the fractional edge cover program minimizes $\boldsymbol{\eta}^\top \boldsymbol{\lambda}$ subject to $\boldsymbol{A\lambda} \geq \mathbf{1}$ (each row of $\boldsymbol{A}$ yielding an inequality of Eqn. (2)) and $\boldsymbol{\lambda} \geq 0$; the dual form maximizes $\mathbf{1}^\top \boldsymbol{\alpha}$ subject to $\boldsymbol{A}^\top \boldsymbol{\alpha} \leq \boldsymbol{\eta}$ and $\boldsymbol{\alpha} \geq 0$. It follows from the duality property of linear programs that an optimal solution to the dual form yields the same upper bound on $|Q|$ as the optimal fractional edge cover.

Moreover, the dual form is constructive: let $n_a = \lfloor 2^\alpha \rfloor$, $n_b = \lfloor 2^\beta \rfloor$, and $n_c = \lfloor 2^\kappa \rfloor$, and choose

$$R \supseteq [n_a] \times [n_b]$$
$$S \supseteq [n_b] \times [n_c]$$
$$T \supseteq [n_a] \times [n_c]$$

padding with rubbish as necessary to attain the desired sizes $|R|$, $|S|$, and $|T|$. This yields a Q of maximal size.

This construction prompts the following observation: the worst cases of the AGM bound are achievable by query results which are cross-products. Since real-world queries rarely have such a structure—practical database systems avoid materializing such queries—this suggests that an algorithm achieving the AGM bound is not necessarily optimal for classes of database instances encountered in practice. This motivates our development of finer-grained classes in Section 5.

3. LEAPFROG TRIEJOIN

Leapfrog triejoin is a join algorithm for $\exists_1$ queries, that is, queries definable by first-order formulae without universal quantifiers (and, needless to say, excluding negated existential quantifiers.) In this paper we focus on the full conjunctive fragment of $\exists_1$, to which our complexity bound applies. (The additional machinery needed to go from full conjunctive queries to $\exists_1$ is described informally in Section 6.2, as a guide to implementors.)

In our datalog implementation, rule bodies are restricted to be $\exists_1$ formulas. We use leapfrog triejoin to enumerate satisfying assignments of rule bodies. We assume input relations are always provided in sorted order, consistent with the data structures used by our system. Leapfrog triejoin uses *iterator interfaces* to unify the presentation of input relations and views of (nonmaterialized) subexpressions of a join. A relation $A(x)$ is presented by a linear iterator, with familiar methods such as *next*() and *atEnd*(), which present the elements of A in order. A disjunction such as $A(x) \vee B(x)$ is likewise presented by a linear iterator whose *next*() method manipulates iterators for A, B to present a non-materialized view of the disjunction. Hence in a conjunction $C(x), D(x)$, it does not matter whether C is an input relation, or a presentation of a non-materialized view such as $A(x) \vee B(x)$. A similar approach is used for joins with multiple variables, where relations and views are presented by *trie iterators*, whose interface is described below.

We first describe the leapfrog join for unary relations (Section 3.1). This is then extended to the triejoin algorithm for full conjunctive queries (Section 3.4). With minor embellishments, leapfrog triejoin can tackle $\exists_1$ queries; we summarize these in Section 6.2, but the focus of this paper (and particularly, the complexity analysis) is on full conjunctive queries.

3.1 Leapfrog join for unary predicates

The basic building block of leapfrog triejoin is a unary join which we call *leapfrog join*. The unary leapfrog join is a variant of sort-merge join which simultaneously joins unary relations $A_1(x), \ldots, A_k(x)$. The unary join is of no particular novelty (see e.g. [7, 4]), but serves as the basic building block for leapfrog *triejoin*. Its performance bound underpins the complexity analyses which follow.

For the purposes of leapfrog join, unary relations $A_i \subseteq \mathbb{N}$ are presented in sorted order by linear iterators, one for each relation, using this interface:

int key()	Returns the key at the current iterator position
next()	Proceeds to the next key
seek(int seekKey)	Position the iterator at a least upper bound for seekKey, i.e. the least key $\geq$ seekKey, or move to end if no such key exists. The sought key must be $\geq$ the key at the current position.
bool atEnd()	True when iterator is at the end.

The key() and atEnd() methods are required to take $O(1)$ time, and the next() and seek() methods are required to take $O(\log N)$ time, where N is the cardinality of the relation. Moreover, if m keys are visited in ascending order, the amortized complexity is required to be $O(1 + \log(N/m))$, which can be accomplished using standard data structures (notably, balanced trees such as B-trees.[2])

Leapfrog join is itself implemented as an instance of the linear iterator interface: it provides an iterator for the intersection $A_1 \cap \cdots \cap A_k$. The algorithm uses an array iter$[0 \ldots k-1]$ of pointers to iterators, one for each relation. In operation, the join tracks the smallest and largest keys at which iterators are positioned, and repeatedly moves an iterator at the smallest key to a least upper bound for the largest key, 'leapfrogging' the iterators until they are all positioned at the same key. Detailed descriptions of the algorithm follow; some readers may choose to skip to the complexity analysis (Section 3.2).

When the leapfrog join iterator is constructed, the leapfrog-init method (Algorithm 1) is used to initialize state and find the first result. The leapfrog-init method is provided an array of iterators; it ensures the iterators are sorted according to the key at which they are positioned, an invariant that is maintained throughout.

The main workhorse is leapfrog-search (Algorithm 2), which finds the next key in the intersection $A_1 \cap \cdots \cap A_k$.

Immediately following leapfrog-init(), the leapfrog join iterator is positioned at the first result, if any; subsequent results are obtained by calling leapfrog-next() (Algorithm 3). To complete the linear iterator interface, we define a leapfrog-seek() function which finds the first element of $R_1 \cap \cdots \cap R_k$ which is $\geq$ seekKey (Algorithm 4).

Figure 1 illustrates a join of three relations.

3.2 Complexity of leapfrog join

In the analyses which follow, we focus on data complex-

[2]For example, if every key is visited in order then $m = N$ and the amortized complexity is $O(1)$. Rather than returning to the tree root for each seek() request, the iterator ascends just far enough to find an upper bound for the key sought.

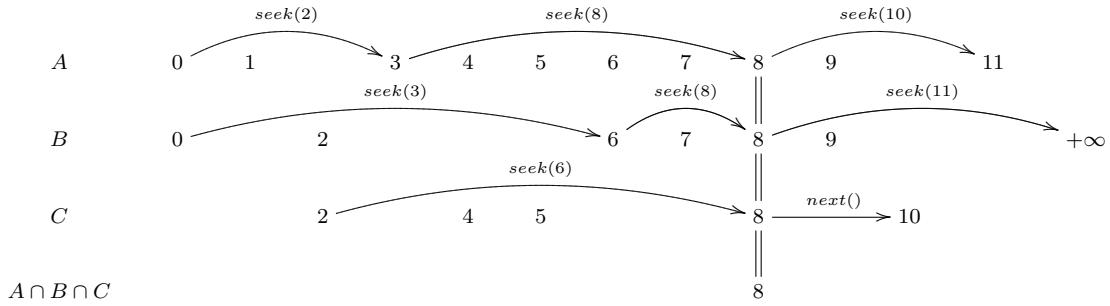


Figure 1: Example of a leapfrog join of three relations A, B, C, with $A = \{0, 1, 3, 4, 5, 6, 7, 8, 9, 11\}$ and B, C as shown in the second and third rows. Initially the iterators for A, B, C are positioned (respectively) at 0, 0, and 2. The iterator for A performs a seek(2) which lands it at 3; the iterator for B then performs a seek(3) which lands at 6; the iterator for C does seek(6) which lands at 8, etc.

Algorithm 1: leapfrog-init()

```
if any iterator has atEnd() true then
    atEnd := true ;
else
    atEnd := false ;
    sort the array Iter[0..k − 1] by keys at which the
    iterators are positioned ;
    p := 0 ;
    leapfrog-search()
```

Algorithm 2: leapfrog-search()

```
x' := Iter[(p − 1) mod k].key() ;     // Max key of any
iter
while true do
    x := Iter[p].key() ;              // Least key of any iter
    if x = x' then
        key := x ;                    // All iters at same key
        return;
    else
        Iter[p].seek(x');
        if Iter[p].atEnd() then
            atEnd := true ;
            return;
        else
            x' := Iter[p].key();
            p := p + 1 mod k;
```

Algorithm 3: leapfrog-next()

```
Iter[p].next();
if Iter[p].atEnd() then
    atEnd := true;
else
    p := p + 1 mod k;
    leapfrog-search();
```

Algorithm 4: leapfrog-seek(int seekKey)

```
Iter[p].seek(seekKey);
if Iter[p].atEnd() then
    atEnd := true;
else
    p := p + 1 mod k;
    leapfrog-search();
```

ity [11], i.e., we assume the query definition to be fixed, and omit constant factors which depend only on the structure of the query (e.g. number of atoms and variables).

Let $N_{min} = \min\{|A_1|, \ldots, |A_k|\}$ be the cardinality of the smallest relation in the join, and $N_{max} = \max\{|A_1|, \ldots, |A_k|\}$ the largest.

PROPOSITION 3.1. *The running time of leapfrog join is* $O\left(N_{min} \log\left(N_{max}/N_{min}\right)\right)$.

PROOF. The leapfrog algorithm advances the iterators in a fixed pattern: each iterator is advanced every k steps of the algorithm. An iterator for a relation with cardinality N can be advanced at most N times before reaching the end; therefore the number of steps is at most $k \cdot N_{min}$. An iterator which visits m of N values in order is stipulated to have amortized cost $O(1 + \log(N/m))$; the iterator for a largest relation will have $N = N_{max}$ and $m = N_{min}$, for total cost $N_{min} \cdot O(1 + \log(N_{max}/N_{min}))$. □

The leapfrog join is able to do substantially better than pairwise joins in some scenarios. Suppose we have relations A, B, C where $A = \{0, \cdots, 2n-1\}$, $B = \{n, \cdots, 3n-1\}$, and $C = \{0, \cdots, n-1, 2n, \ldots, 3n-1\}$. Any pairwise join will produce n results, but the intersection $A \cap B \cap C$ is empty; the leapfrog join determines this in $O(1)$ steps.

3.3 Trie iterators

We extend the linear iterator interface to handle relations of arity > 1. Relations such as $A(x, y, z)$ are presented as *tries* with each tuple $(x, y, z) \in A$ corresponding to a unique path through the trie from the root to a leaf (Figure 2). (Note however that relations need not be stored as tries; in practice we use B-tree-like data structures, and present their contents via a trie iterator interface.)

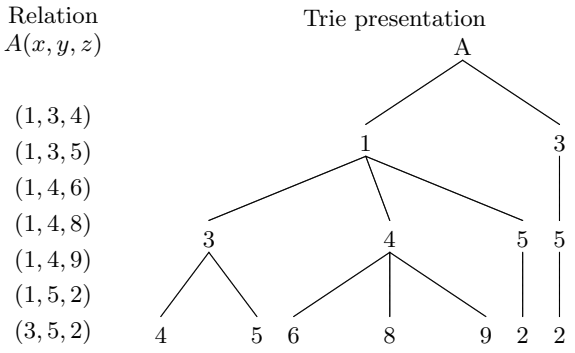


Figure 2: Example: Trie presentation of a relation $A(x, y, z)$. After open() is invoked at some node n, the linear iterator methods next(), seek() and atEnd() present the children of n. In the above example, invoking open() thrice on an iterator positioned at A would move to the leaf node $[1, 3, 4]$; next() would then move to leaf node $[1, 3, 5]$; another next() would result in the iterator being atEnd(). The sequence up(), next(), open() would then advance the iterator to the leaf node $[1, 4, 6]$.

Upon initialization, trie iterators are positioned at the root. The linear iterator API is augmented with two methods for trie-navigation:

void open();	Proceed to the first key at the next depth
void up();	Return to the parent key at the previous depth

A trie iterator for a materialized relation is required to have $O(\log N)$ time for the open() and up() methods.

With a bit of bookkeeping, it is straightforward to present Btree-like data structures as TrieIterators, with each operation taking $O(\log N)$ time.[3]

3.4 Leapfrog Triejoin

We now describe the *Leapfrog Triejoin* algorithm for full conjunctive joins.

The triejoin algorithm requires the optimizer to choose a *variable ordering*, i.e., some permutation of the variables appearing in the join. For example, in the join $R(a, b), S(b, c), T(a, c)$ we might choose the variable ordering $[a, b, c]$. Choosing a good variable ordering is crucial for performance, in practice, but immaterial for the worst-case complexity analysis presented here. Techniques for choosing an advantageous variable ordering are the subject of a forthcoming paper; for the complexity analysis we fix an arbitrary ordering.

Leapfrog triejoin requires a restricted form of conjunctive joins, attained via some simple rewrites:

1. Each variable can appear at most once in each argument list. For example, $R(x, x)$ would be rewritten to $R(x, y), x = y$ to satisfy this requirement. The $x = y$ term may be presented as a nonmaterialized view of a predicate $Id(x, y) \Leftrightarrow (x = y)$, implemented by a variant of the TrieIterator interface.

2. Each argument list must be a subsequence of the variable ordering. For example, if the chosen variable ordering were $[a, b, c]$ and the join contained a term $U(c, a)$, we would rewrite this to $U'(a, c)$ and define a materialized view $U'(a, c) \equiv U(c, a)$. (In practice we install indices automatically when required by such rewrites, and maintain them for use in future queries.)

3. To simplify the complexity analysis, each relation symbol may appear at most once in the query. For a query such as $E(x, y)$, $E(y, z)$ we introduce a copy $E' \equiv E$ and rewrite to $E(x, y)$, $E'(y, z)$. This avoids awkwardness in the complexity analysis, but is not required for implementation purposes.

4. Constants may not appear in argument lists. A subformula such as $A(x, 2)$ is rewritten to $A(x, y)$, $\mathsf{Const}_2(y)$, where $\mathsf{Const}_2 = \{2\}$. In practice Const_α is presented as a nonmaterialized view, using a variant of the TrieIterator interface.

Leapfrog triejoin employs one leapfrog join for each variable. Consider the example $R(a, b)$, $S(b, c)$, $T(a, c)$ with the variable ordering $[a, b, c]$. The leapfrog joins employed for the variables a, b, c in the example are:[4]

Variable	Leapfrog join	Remarks
a	$R(a, \_), T(a, \_)$	Finds a present in R, T projections
b	$R_a(b), S(b, \_)$	For specific a, finds b values
c	$S_b(c), T_a(c)$	For specific a, b, finds c values

The topmost leapfrog join iterates values for a which are in both the projections $R(a, \_)$ and $T(a, \_)$. When this leapfrog join emits a binding for a, we can proceed to the next level join and seek bindings for b from $R_a(b), S(b, \_)$. For each such b, we can proceed to the next level and seek a binding for c in $S_b(c), T_a(c)$. When a leapfrog join exhausts its bindings, we can retreat to the previous level and seek another binding for the previous variable. Conceptually, we can regard triejoin as a backtracking search through a 'binding trie.'

3.5 Triejoin implementation

At initialization, the triejoin is provided with a trie iterator for each relation (or more generally, subformula) of the join.

The triejoin initialization constructs an array of leapfrog join instances, one for each variable. The leapfrog join for a variable x is given an array of pointers to trie-iterators, one for each atom in which x appears. For example, in the join $R(a, b)$, $S(b, c)$, $T(a, c)$, the leapfrog join for b is given pointers to the trie-iterators for R and S. There is only one instance of the trie-iterator for R, which is shared by the leapfrog joins for a and b.

The leapfrog joins use the linear-iterator portion of the trie iterator interfaces; the open/up trie navigation methods are used only by the triejoin algorithm. The triejoin uses a variable *depth* to track the current variable for which a binding is being sought; initially $depth = -1$ to indicate the triejoin is positioned at the root of the binding trie (i.e.,

[3]For example, to perform a next() operation when positioned at the node $x = 1$ of Figure 2, one would seek the least upper bound of $(1, +\infty, +\infty)$ in the B-tree representation; this would reach the record $(3, 5, 2)$.

[4]Recall that $R(a, \_)$ is the projection $\{a : \exists b \,.\, (a, b) \in R\}$, and $R_a(b)$ is the 'curried' form $\{b : (a, b) \in R\}$.

before the first variable.) Depths $0, 1, \ldots$ refer to the first, second, etc. variables of the variable ordering.

Leapfrog triejoin presents a nonmaterialized view of the query result, presented via a trie-iterator interface. The linear iterator portions of the trie-iterator interface (namely key(), atEnd(), next(), and seek()) are delegated to the leapfrog join for the current variable. (At depth -1, i.e., the root, only the operation open() is permitted, which moves to the first variable.) It remains to define the open() and up() methods, which are trivial (Algorithms 5 and 6).

Algorithm 5: triejoin-open()

```
// Advance to next var
depth := depth + 1 ;
for each iter in leapfrog join at current depth do
  | iter.open() ;
end
call leapfrog-init() for leapfrog join at current depth
```

Algorithm 6: triejoin-up()

```
for each iter in leapfrog join at current depth do
  | iter.up() ;
end
// Backtrack to previous var
depth := depth - 1 ;
```

This completes the trie iterator interface. To obtain the satisfying assignments of the query formula, we simply walk the trie presented by leapfrog triejoin, a simple exercise we omit here.

4. COMPLEXITY ANALYSIS

We consider now the complexity of leapfrog triejoin for full conjunctive joins of materialized relations.

4.1 The proof strategy

We introduce the proof strategy informally, before proceeding to the formal proof of Theorem 4.2. Consider the example join:

$$Q(a, b, c) \equiv R(a, b), S(b, c), T(a, c)$$

with variable ordering $[a, b, c]$. Suppose that $|R| \leq n$, $|S| \leq n$, and $|T| \leq n$. The fractional cover bound yields $|Q| \leq n^{3/2}$.

We wish to show that the triejoin runs in $O(n^{3/2} \log n)$ time for this example. Recall that a leapfrog join of two unary relations U, V requires at most $2 \cdot \min\{|U|, |V|\}$ iterator operations. It is readily seen that the cost at the first two trie levels $[a, b]$ cannot exceed $O(n)$ linear iterator operations: at the first trie level the leapfrog join is limited by $\min(|R(a, \_)|, |T(a, \_)|) \leq |R(a, \_)| \leq |R| \leq n$, and at the second trie level the number of iterator operations is controlled by:

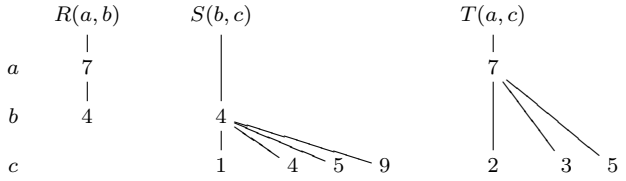
$$\begin{aligned} &\sum_{a \in R(a,\_), T(a,\_)} \min\{|R_a(b)|, |S(b, \_)|\} \\ &\leq \sum_{a \in R(a,\_), T(a,\_)} |R_a(b)| \\ &\leq |R| \end{aligned}$$

Therefore the total number of linear iterator operations at the first two trie levels is $O(n)$. At the third trie level, the number of linear iterator operations is controlled by:

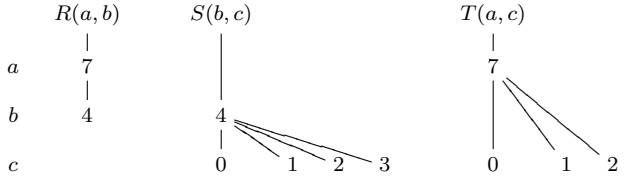
$$\sum_{(a,b) \in R(a,b), S(b,\_), T(a,\_)} \min\{|S_b(c)|, |T_a(c)|\} \tag{5}$$

We now wish to show that the quantity (5) is $\leq n^{3/2}$. We do this by renumbering the c values of the relations such that the join produces a number of results equal to (5), without increasing the amount of work. Since the join can produce at most $n^{3/2}$ results (from the fractional cover bound), this will establish that (5) is $\leq n^{3/2}$.

For a concrete example, suppose we had these trie presentations of R, S, T:



This would produce only the result tuple $(7, 4, 5)$. To obtain a result size equal to (5) we renumber the c values, resulting in a new problem instance which produces one result for every leaf of T (the smaller relation):



This results in exactly three results $(7, 4, 0)$, $(7, 4, 1)$, and $(7, 4, 2)$, equalling (5).

In general, the renumbering produces modified relations S', T' which each have cardinality $\leq n$. Since $n^{3/2}$ is an upper bound on the result size, it follows that (5) is at most $n^{3/2}$.

The renumbering is accomplished as follows:

(i) Construct $S'(b, c)$ by renumbering the c values of each S_b-subtree to be $0, 1, \ldots$, i.e.:

$$\begin{aligned} S'(b, \_) &= S(b, \_) \quad \text{(Keep } b \text{ values the same)} \\ S'_b &= \{0, 1, \ldots, |S_b| - 1\} \quad \text{(Renumber } c \text{ values)} \end{aligned}$$

(ii) Similarly, renumber the c values of each T_a subtree:

$$\begin{aligned} T'(a, \_) &= T(a, \_) \quad \text{(Keep } a \text{ values the same)} \\ T'_a &= \{0, 1, \ldots, |T_a| - 1\} \quad \text{(Renumber } c \text{ values)} \end{aligned}$$

When we compute the leapfrog join of $S'_b = \{0, 1, \ldots, |S_b| - 1\}$ with $T'_a = \{0, 1, \ldots, |T_a| - 1\}$, we get exactly $\min\{|S_b|, |T_a|\}$ results. This holds for every join at the third trie level; therefore the query result size is exactly the quantity (5). Since the fractional cover bound gives an upper bound of $n^{3/2}$ on the query result size, we have:

$$\sum_{(a,b) \in R(a,b), S(b,\_), T(a,\_)} \min\{|S_b(c)|, |T_a(c)|\} \leq n^{3/2}$$

Hence the running time of leapfrog triejoin for the example is $O(n^{3/2} \log n)$.

The above example illustrates the proof technique we employ for the leapfrog triejoin complexity analysis. The following sections generalize the renumbering transform (Section 4.2), develop the sum-min cost bound (Section 4.3), and formalize classes of databases to which the complexity bound applies (Section 4.4). These lead up to the proof, in Section 4.5, of the complexity bound for leapfrog triejoin (Theorem 4.2).

4.2 The renumbering transform

We generalize the renumbering transformation introduced in the previous section. For an atom $R(x, y, z)$, *a renumbering at variable* $v \in \{x, y, z\}$ is obtained by traversing the trie representation of R, and:

- If the variable v appears in the argument list at depth d, then for each node at depth $d-1$ renumber its children to be $0, 1, \ldots$; otherwise, do nothing.
- Replace all values for variables appearing after v in the key-ordering with 0.
- Eliminate any duplicate tuples.

The resulting relation R' is called a renumbering of R. Figure 3 illustrates renumberings of a relation $R(x, y, z)$ at various depths.[5]

4.3 Triejoin costs

Let $R^1, \ldots, R^m$ be the relations in the join, and $V = [v_0, \ldots, v_{k-1}]$ be the chosen variable ordering. Each atom (relation) in the join takes as arguments some subset of the variables V, in order. For a relation $R(v_0, v_1, v_2, v_3)$, we use this notation for currying:

$$R_{v_0,v_1}(v_2, v_3) = \{(v_2, v_3) \ : \ (v_0, v_1, v_2, v_3) \in R\}$$

We write $R_{<i}(v_i, \ldots)$ for the curried version of all variables strictly before v_i in the ordering; e.g. $R_{<3}(v_3) = R_{v_0,v_1,v_2}(v_3)$.

Write $Q_i(v_0, v_1, \ldots, v_i)$ for the join 'up to and including' variable v_i; this is obtained by replacing variables $v_{i+1}, \ldots, v_{k-1}$ with the projection symbol _ in the query, and omitting any atoms which contain only projection symbols.[6] For example, with $Q = R(a, b), S(b, c), T(a, c)$, and key order $[a, b, c]$, we would have:

$$\begin{aligned} Q_0 &= R(a, \_), T(a, \_) \\ Q_1 &= R(a, b), S(b, \_), T(a, \_) \\ Q_2 &= R(a, b), S(b, c), T(a, c) \end{aligned}$$

Let $R^\alpha_{<i}(v_i, \ldots), R^\beta_{<i}(v_i, \ldots), \cdots$ be the relations in the leapfrog join at depth i. Let C_i be the sum-min of the leapfrog triejoin at tree depth i:

$$C_i = \sum_{(v_0,\ldots,v_{i-1}) \in Q_{i-1}} \min \ \{|R^\alpha_{<i}(v_i, \_, \ldots, \_)|, \\ |R^\beta_{<i}(v_i, \_, \ldots, \_)|, \cdots\}$$

To compute the join result, one uses the trie iterator presented by leapfrog triejoin to completely traverse the trie.

[5]It is worth noting that alternate renumbering schemes might be useful for certain classes of problems. But for the purposes of this paper, we stick to $0, 1, 2, \ldots$.

[6]Note that Q_i is generally a strict superset of the projection of the query result $Q(v_0, v_1, \ldots, v_i, \_, \_, \ldots, \_)$.

PROPOSITION 4.1. *The running time of leapfrog triejoin is* $O((\sum_{i=0}^{k-1} C_i) \log N_{max})$.

PROOF. Let N_{max} be the cardinality of the largest input relation. At levels $0, \ldots, k-2$, each result of a leapfrog join incurs the cost of an open() and up() operation, totalling $O((\sum_{i=0}^{k-2} C_i) \log N_{max})$ time by the $O(\log N)$ performance requirement for open() and up(). At levels $0, \ldots, k-1$ the time cost of the leapfrog joins is $O((\sum_{i=0}^{k-1} C_i) \log N_{max})$ from Prop. 3.1. □

4.4 Families of problem instances

We now formalize some concepts in preparation for asymptotic arguments. Chief among these is a *family of problem instances*; this concept encompasses familiar examples such as *graphs with at most n edges*, and *binary relations R,S,T with each relation of size* $\leq n$.

We write $\mathrm{Str}[\sigma]$ for finite structures with signature (vocabulary) σ. A *family of problem instances* is a countable set $(\mathbf{K}_n)_{n \in \mathbb{N}}$ indexed by a parameter $n \in \mathbb{N}$, where each $\mathbf{K}_n \subseteq \mathrm{Str}[\sigma]$ is a class of finite relational structures, and $(i \leq j) \implies (\mathbf{K}_i \subseteq \mathbf{K}_j)$. (Example: *graphs with at most n edges* is a family of problem instances.)

More generally, we can choose a tuple of parameters $\overline{n} = [n_1, \ldots, n_k] \in \mathbb{N}^k$, with the usual partial ordering on tuples, such that if $\overline{n}' = [n'_1, \ldots, n'_k]$ and $n_1 \leq n'_1, \ldots, n_k \leq n'_k$, then $\mathbf{K}_{[n_1,\ldots,n_k]} \subseteq \mathbf{K}_{[n'_1,\ldots,n'_k]}$. (Example: let σ contain the binary relation symbols R, S, T, and define $\mathbf{K}_{r,s,t}$ to be structures with $|R| \leq r$, $|S| \leq s$, and $|T| \leq t$.)

A query Q is defined by some first-order formula $\varphi(\overline{x})$. For a structure $\mathcal{A} \in \mathbf{K}_n$ we write $Q^{\mathcal{A}}$ to mean the satisfying assignments of $\varphi(\overline{x})$ in $\mathcal{A}$. For simplicity, we take $\overline{x}$ to be the variable ordering for the triejoin.

4.5 Proof of the complexity bound

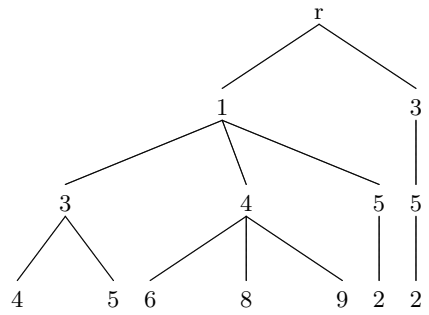
Fix a variable ordering V. Given structures $\mathcal{A}, \mathcal{A}'$, we say $\mathcal{A}'$ is a renumbering of $\mathcal{A}$ if it is obtained by selecting some relation of $\mathcal{A}$ and renumbering it at some depth, as per Section 4.2. A family of problem instances is *closed under renumbering* when for every $\mathcal{A} \in \mathbf{K}_n$, if $\mathcal{A}'$ is a renumbering of $\mathcal{A}$, then $\mathcal{A}' \in \mathbf{K}_n$ also.

THEOREM 4.2. *Let* $Q(v_0, \ldots, v_{k-1})$ *be a full conjunctive query satisfying the syntactic restrictions of Section 3.4, and*

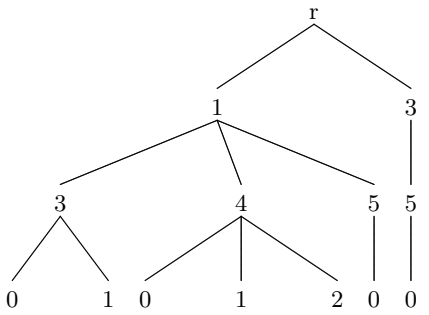
1. $(\mathbf{K}_n)_{n \in \mathbb{N}}$ *be a family of problem instances closed under renumbering,*
2. $q(n) = \max_{\mathcal{A} \in \mathbf{K}_n} |Q^{\mathcal{A}}|$ *be the largest query result size for any structure in* $\mathbf{K}_n$*, and*
3. $M(n)$ *be the cardinality of the largest relation in any structure of* $\mathbf{K}_n$.

Then, Leapfrog Triejoin computes Q *in* $O(q(n) \log M(n))$ *time over* $(\mathbf{K}_n)_{n \in \mathbb{N}}$ *using variable ordering* $[v_0, \ldots, v_{k-1}]$.

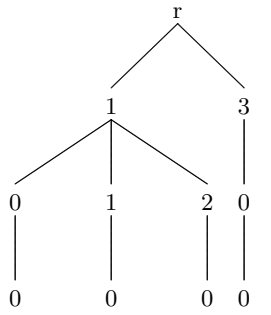
PROOF. (By contradiction). Suppose the running time is not $O(q(n) \log M(n))$. From Prop. 4.1, the running time of leapfrog triejoin is $O((C_0 + \cdots + C_{k-1}) \log M(n))$, where C_i is the sum-min for the leapfrog join of variable v_i. For this to not be $O(q(n) \log M(n))$, some variable v_i must have $C_i \in \omega(q(n))$ for infinitely many instances $\mathcal{A}$. For each such $\mathcal{A}$, renumber all relations for variable v_i, and revise $Q(v_0, \ldots, v_{k-1})$ appropriately. This results in structures $\mathcal{A}'$



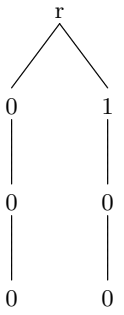
(a) A relation $R(x, y, z)$



(b) Renumbered at depth 2, for variable z



(c) Renumbered at depth 1, for variable y



(d) Renumbered at depth 0, for variable x

Figure 3: Example of the renumbering transform applied to a relation $R(x, y, z)$.

with $|Q^{\mathcal{A}'}| = C_i$. Since the family is closed under renumbering, $\mathcal{A}' \in \mathbf{K}_n$; but $|Q^{\mathcal{A}'}| \in \omega(q(n))$, contradicting the definition of $q(n)$. □

Note that Theorem 4.2 does not depend on the fractional edge cover bound (Section 2.2). The fractional edge cover bound provides a means to bound $q(n)$ for families of problem instances defined by constraints on the size of input relations. Since renumbering does not increase the sizes of relations, such families are closed under renumbering. The worst-case optimality in the sense of NPRR [8] is immediate:

COROLLARY 4.3 (THEOREM 4.2). *The run time of Leapfrog Triejoin is bounded by the fractional edge cover bound, up to a log factor.*

Example: for the R, S, T example we could define the family of instances by $|R| \leq n$, $|S| \leq n$, $|T| \leq n$; the fractional edge cover bound provides $q(n) = n^{3/2}$, and therefore the running time of leapfrog triejoin is $O(n^{3/2} \log n)$.

5. IMPROVING ON THE NPRR BOUND

In this section we show that leapfrog triejoin achieves optimal worst-case running time (up to a log factor) over finer-grained families of problem instances than those defined by the AGM (fractional edge cover) bound, and that NPRR is *not* worst-case optimal for such families.

5.1 Instances defined by projection bounds

Corollary 4.3 established that the leapfrog triejoin complexity bound of $O(q(n) \log M(n))$ from Theorem 4.2 applies to families of problem instances defined by constraints on the sizes of input relations. We demonstrate that Theorem 4.2 applies to finer-grained families defined by constraints on the size of *projections* of input relations. This establishes that leapfrog triejoin is worst-case optimal for such families. The NPRR algorithm is not; we exhibit a family of problem instances for which leapfrog triejoin is optimal, and NPRR is asymptotically slower. This may partially explain the faster performance of LFTJ observed in practice [9].

By way of example, we return to $Q(a, b, c) = R(a, b)$, $S(b, c)$, $T(a, c)$. Consider a family of problem instances $(\mathbf{K}_n)_{n \in \omega}$ defined by the following constraints on projection sizes of R, S, T (recall that $R(a, \_) = \pi_1(R)$):

$$\begin{array}{llll} |R(a,\_)| \leq n^{3/8} & & |R(\_,b)| \leq n^{5/8} \\ |S(b,\_)| \leq n^{5/8} & & |S(\_,c)| \leq n^{3/8} \\ |T(a,\_)| \leq n & & |T(\_,c)| \leq 1 \end{array}$$

From the definition of the renumbering transform (Section 4.2), the following is evident:

PROPOSITION 5.1. *Applying a renumbering transform to a relation R does not increase the cardinality of any projections of R.*

Therefore families defined by constraints on projection cardinalities are closed under renumbering, and the following is immediate from Theorem 4.2:

THEOREM 5.2. *Leapfrog triejoin is worst-case optimal for families of problem instances defined by cardinality constraints on projections of input relations.*

Continuing our example, from the above constraints on projections of R, S, T it is easily inferred that $|Q(a, \_, \_)| \leq n^{3/8}$, $|Q(\_, b, \_)| \leq n^{5/8}$, and $|Q(\_, \_, c)| \leq 1$. Hence $|Q| \leq n$. By Theorem 5.2, leapfrog triejoin runs in time

$O(n \log n)$ over this family. In the next section we establish that NPRR has running time $\Theta(n^{1.375})$ for this family. This counterexample establishes:

PROPOSITION 5.3. *NPRR is* not *worst-case optimal for families of problem instances defined by cardinality constraints on projections of input relations.*

5.1.1 Counterexample for Prop. 5.3

Consider the behaviour of the NPRR algorithm for an instance with:

$$\begin{array}{lcccccc} R & = & [n^{3/8}] & \times & [n^{5/8}] & & \\ S & = & & & [n^{5/8}] & \times & [n^{3/8}] \\ T & = & [n] & & & \times & [1] \\ Q & = & [n^{3/8}] & \times & [n^{5/8}] & \times & [1] \end{array}$$

We follow the exposition of Example 2 of [8]. Let $\tau \geq 0$ be a parameter, which is used to define a threshold for *heavy join keys*. A join key $b \in R(\_, b)$ is heavy if it appears in more than τ tuples of R; let D be the set of heavy join keys. The algorithm handles tuples $(a, b) \in R$ for heavy join keys $b \in D$ separately from those with $b \notin D$. Let $G \subseteq R$ be those tuples containing no $b \in D$. The algorithm (1) constructs $D \times T$ and filters using hash tables on S and R; and (2) constructs $G \bowtie S$ and filters using a hash table on T. The union of these two results yields Q.

We now consider the running time. There are two cases, which depend on the choice of τ (which is taken to be $n^{1/2}$ in Example 2 of [8], but we consider arbitrary choice of τ here.)

Case 1: $\tau \geq n^{3/8}$. Then D will be empty, and $G = R$; the result will be constructed using only step (2): constructing $G \bowtie S = R \bowtie S$ and filtering using T. Since $|R \bowtie S| = n^{1+3/8}$, the running time will be $\Theta(n^{1.375})$.

Case 2: $\tau < n^{3/8}$. Then $D = [n^{5/8}]$, and the result will be constructed using only step (1): since $|D \times T| = n^{1+5/8}$, the running time will be $\Theta(n^{1.625})$.

With the best choice of τ the running time is $\Theta(n^{1.375})$. Since leapfrog triejoin has running time $O(n \log n)$ for the family of problem instances containing this example, we have demonstrated that leapfrog triejoin can be asymptotically faster than the NPRR algorithm.

6. DISCUSSION AND FUTURE WORK

6.1 Removing the log factor

Ken Ross suggested the following variant of leapfrog triejoin which eliminates the $\log M(n)$ factor of the complexity bound [10]. For a relation $R(a, b)$, maintain a hash table for $R(a, \_)$ i.e. for the projection $\pi_1(R)$. For each $a \in R(a, \_)$ maintain a hash table for $R_a(b)$. Each entry in the hash table for $R(a, \_)$ contains a pointer to the hash table for $R_a(b)$. (Similarly for k-ary relations with $k > 2$). Replace each leapfrog join with a scan of the smallest relation, with lookups into hash tables for the other relations. This eliminates the log factor, giving a running time of $O(q(n))$.

It will be interesting to investigate when the asymptotic improvement offered by hash tables translates into practical advantage, and whether query optimizers can be trained to efficiently select trie versus hash table representations. There are countervailing factors to be weighed against the asymptotic improvement:

- The leapfrog join of unary relations $A_1, \ldots, A_k$ can require substantially fewer than $\min\{|A_1|, \ldots, |A_k|\}$ iterator operations in practice, due to differences in data distribution amongst the relations. Using leapfrog join ensures that you do not pay for the relation sizes per se, but rather for the interleavings where one relation interposes itself into another. One example of this is given in Section 3.2, where a join of three relations of size n is performed with $O(1)$ iterator operations. This advantage is not obviously achievable by the hash table variant.

- The $\log M(n)$ factor in the leapfrog triejoin complexity bound is a tax not always applied; the log factor reflects the potential cost of sparse access patterns into relations, when leaping between distant keys. When access patterns are dense, the log factor vanishes. For example, taking $R = S = T = [n^{1/2}] \times [n^{1/2}]$, and representing R, S, T as tries, the running time is $O(n^{3/2})$.

- Hash tables imply random memory access patterns, which are notoriously costly in steep memory hierarchies; leapfrog triejoin frequently exhibits sequential access patterns, which are better exploited by current architectures.

6.2 Extension to $\exists_1$ queries

The implementation of leapfrog triejoin in our commercial database system LogicBlox extends the basic algorithm described here in several useful ways. We sketch these extensions here, as they provide basic functionality essential for implementors.

The LogicBlox runtime evaluates rules defined using the following fragment of first-order logic:

$$\begin{aligned} \mathsf{conj} &::= [\ \exists \overline{x}\ .\ ]\ \mathsf{dform}\ (\ \wedge \mathsf{dform}\ )^* \\ \mathsf{dform} &::= \mathsf{atom} \mid \mathsf{disj} \mid \mathsf{negation} \\ \mathsf{atom} &::= R(\overline{y}) \mid F[\overline{y}] = \overline{z} \\ \mathsf{disj} &::= \mathsf{conj}\ (\ \vee \mathsf{conj})^+ \\ \mathsf{negation} &::= \neg \mathsf{conj} \\ \mathsf{rule} &::= \forall \overline{x}\ .\ \mathsf{conj} \rightarrow \mathsf{head} \\ \mathsf{head} &::= \mathsf{atom}\ (\ \wedge \mathsf{atom})^* \end{aligned}$$

Each conjunction bears an optional existential quantifier block. Atoms can be either relations or functions, which may represent either concrete data structures (representing edb functions/relations, or materialized views), or primitives such as addition and multiplication. The use of negation comes with some further restrictions not captured by the above grammar. We extend leapfrog triejoin to tackle such rules as follows.

1. *Disjunctions.* A simple variant of the leapfrog algorithm computes a disjunction of unary relations $A_1(x) \vee \cdots \vee A_k(x)$, using the standard algorithm for merging sorted sequences presented by iterators. We handle a disjunction of k-ary formulas $\varphi_1(\overline{x}) \vee \cdots \vee \varphi_k(\overline{x})$ in the following manner. Each subformula $\varphi_i(\overline{x})$ is required to have the same free variables. The extension from disjunction of unary subformulas to k-ary subformulas mostly follows the triejoin algorithm of Section 3.5, with the exception that the triejoin-open() method selects only those iterators positioned at the current key

for opening at the next level. The implementation of disjunction presents $\varphi_1(\overline{x}) \vee \cdots \vee \varphi_k(\overline{x})$ as a nonmaterialized view using the trie iterator interface; since leapfrog triejoin likewise presents conjunctions as nonmaterialized views, we can permit arbitrary nesting of conjunctions and disjunctions without materializing intermediate results or DNF-conversion, in most cases.

2. *Functions.* We distinguish between relations $R(x, y)$ and functions $F[x] = y$. For the function $F[x] = y$, where F is represented by a concrete data structure, the variable x is said to occur in *key position*, and the variable y in *value position*. A free variable of a conjunction is a key if it is a key of any subformula; every free variable of a disjunction is deemed to be a key. Only variables occurring in key position are considered for the variable ordering. To handle a query such as $F[x] = y, G[y] = z$ with a variable ordering $[x, y]$, we treat it as $F[x] = \alpha, I_\alpha(y), G[y] = z$, where $I_\alpha(y)$ presents a nonmaterialized view of the relation $\{\alpha\}$.

3. *Primitives.* Primitives are scalar operations such as addition and multiplication. In a subformula such as $z = y+1$, we deem all variable occurrences to be value-position. In a query such as $A(x, y), z = y+1$, we handle primitives such as $z = y + 1$ by attaching *actions* to the triejoin which are triggered whenever a specified variable is bound. With the key ordering $[x, y]$, the primitive $z = y + 1$ would be triggered whenever y is bound. We order actions attached to the same variable so as to respect order-of-operation dependencies. For a query such as $A(x, y), z = y + 1, B(z)$ with variable ordering $[x, y, z]$, we use the same technique as above, treating it as $A(x, y), \alpha = y + 1, I_\alpha(z), B(z)$. Actions can either succeed or fail; if they fail, the leapfrog triejoin algorithm searches for the next binding of the trigger variable.

4. *Negation.* We distinguish two cases of negation: complementation, and scalar negation. Complementation occurs when we have a formula of the form $\varphi_1(\overline{x}, \overline{y}), \neg\varphi_2(\overline{x})$, where each variable in $\overline{x}$ occurs in key-position of φ_1. In this case we handle $\neg\varphi_2(\overline{x})$ by an action attached to the last variable of $\overline{x}$, which performs a lookup into $\varphi_2(\overline{x})$, succeeding just when $\varphi_2(\overline{x})$ fails. Scalar negation occurs when we have a subformula $\neg\varphi_2(\overline{x})$, where each variable in $\overline{x}$ occurs in value-position in φ_2; this implies φ_2 contains only primitive operations. In such cases we permit existential quantifiers to occur in φ_2, to handle subexpressions such as $\neg\exists t \,.\, x+y = t, t > 0$, which depart from $\exists_1$ in a trivial way. We handle these by an action attached to the last variable of $\overline{x}$ which computes $\varphi_2(\overline{x})$ and succeeds just when φ_2 fails.

5. *Projections.* Projections are currently handled by using data structures which support reference counts. we anticipate introducing an optimization to handle a projection $\exists z \,.\, \varphi(\overline{x}, z)$ by a special nonmaterialized view which produces only the first z for given $\overline{x}$. We anticipate this will be more efficient when z occurs after $\overline{x}$ in the variable ordering.

6. *Ranges.* We handle inequalities such as $x \geq c$ by including a nonmaterialized view of a predicate representing an interval $[c, +\infty)$; similarly for $\leq, <, >$. It is a simple exercise to implement a trie-iterator for an interval such as $[c, +\infty)$.

The complexity analysis presented for leapfrog triejoin (Theorem 4.2) does not immediately encompass the above extensions, but can be applied in some cases by considering nested subformulas to be materialized, even though in actual evaluation they are not. For example, in the formula $A(x, y), (B(y, z) \vee C(y, z))$, we can consider a hypothetical materialization of $T(y, z) \equiv B(y, z) \vee C(y, z)$, and analyze $A(x, y), T(y, z)$ using whatever properties for T we can establish. For instance, if we know $|A| \leq n_1$, $|B| \leq n_2$ and $|C| \leq n_3$, it follows that $|T| \leq (n_2 + n_3)$, and we can invoke Corollary 4.3 using the fractional cover bound. This technique yields a valid bound for the nonmaterialized presentation of T if trie iterator operations on the presentation of $B(y, z) \vee C(y, z)$ take $O(\log n)$ time, which is the case for disjunctions. However, this is not the case for projections. Laurent Oget made the promising suggestion of lazily materializing subformulas as they are evaluated, which would limit the cost to that of materializing all subexpressions.

Conclusions

Leapfrog triejoin is a variable-oriented join algorithm which achieves worst-case optimality (up to a log factor) over large and useful families of problem instances. It provides the core evaluation algorithms of the LogicBlox Datalog system. It improves on the NPRR algorithm in its simplicity, and its optimality for finer-grained families of problem instances. The algorithm is easily understood and straightforward to implement.

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