Query Refinement for Diversity Constraint Satisfaction

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ABSTRACT

Diversity, group representation, and similar needs often apply to query results, which in turn require constraints on the sizes of various subgroups in the result set. Traditional relational queries only specify conditions as part of the query predicate(s), and do not support such restrictions on the output. In this paper, we study the problem of modifying queries to have the result satisfy constraints on the sizes of multiple subgroups in it. This problem, in the worst case, cannot be solved in polynomial time. Yet, with the help of provenance annotation, we are able to develop a query refinement method that works quite efficiently, as we demonstrate through extensive experiments.

1 INTRODUCTION

With increasing awareness of the need to improve representation of historically underrepresented population groups, many companies, government agencies, educational institutions, professional societies, and other organizations have adopted diversity initiatives as part of their selection processes for recruitment, award nomination, etc., aiming to challenge long-standing biases, creating a diverse environment in the long run. For example, fellowship programs often require a diverse pool of nominees, ensuring representation from underrepresented demographic groups in a particular field [1, 2]. The NFL's Rooney Rule [3] mandates that teams interview at least one candidate from racially or ethnically diverse backgrounds for senior leadership positions, aiming to disrupt entrenched biases, although it does not dictate the final hiring decision. In these contexts, relational databases are frequently employed to select candidates.

Traditional relational queries output tuples that meet specified conditions in the query predicates. If a query is used as part of some

Table 1: `Applicants` table with primary key ID. Job applicants selected by queries `Q1`, `Q2`, and `Q3` are marked with ✓.

ID	Gender	Race	Major	GPA	Q1	Q2	Q3
1	F	White	ME	3.65			
2	F	White	CS	3.95	✓	✓	✓
3	F	Black	CS	3.40			
4	F	White	ME	3.60			
5	F	White	EE	3.85		✓	
6	F	Black	EE	3.90		✓	✓
7	F	Asian	EE	3.85		✓	
8	M	White	CS	3.65			
9	M	White	CS	3.90	✓	✓	✓
10	M	Black	CS	3.85	✓	✓	
11	M	White	CS	3.40			
12	M	White	EE	3.85		✓	
13	M	Asian	EE	3.95		✓	✓
14	M	Black	ME	3.60			

Table 2: `Internships` table, with primary key (ID, Type).

ID	Type	Hours
2	r.l.	80
2	t.c.	90
3	t.c.	90
6	g.a.	120
7	t.c.	40
7	g.a.	60
9	r.l.	60
13	g.a.	100
14	t.c.	100

high-stakes selection process, it would be natural to state diversity requirements as cardinality constraints for including specific demographic groups in the query result, like inviting a certain number of individuals from different demographic groups for job interviews. Unfortunately, such constraints are currently not supported by relational systems: We can specify criteria on how to select candidates for a job interview, but cannot impose constraints on demographic group membership of the selected candidates. In this paper, we propose a method to augment relational queries with group cardinality constraints to fulfill diversity requirements. Our approach is based on existing *query refinement* literature, which modifies queries to meet overall cardinality bounds [4–12]. However, existing methods do not handle constraints over specific groups in the query result. We further explain the need for such constraints and provide an overview of our approach using an example.

Example 1.1. Table 1 shows a dataset D of 14 job candidates applying to a tech company, with five attributes: ID, gender, race, (college) major, and GPA. Among these, gender and race are the *sensitive attributes* that denote demographic group membership. The employer may wish to state cardinality constraints w.r.t. such attributes, to counteract the effects of historical discrimination. Major and GPA are *qualification attributes*, and can be used in selection conditions. The company would like to interview applicants who graduated from college with a technical major and a high GPA. To start, the data analyst uses the following query to select candidates:

```
Q1: SELECT *
    FROM Applicants AS a
        WHERE a.Major = 'CS' AND a.GPA >= 3.85
```

Query Q1 selects candidates #2, #9, and #10, as marked in Table 1. Notably, only one female applicant is chosen despite half of the

applicants being female, and no Asian is selected, although Whites, Blacks and Asians are all present in the applicant pool. To increase diversity, the company aims to interview at least two females, and at least one applicant of each race. These requirements can be expressed as *group cardinality constraints*, achieved by slightly adjusting the selection criteria, such as expanding the set of majors to also include Electrical Engineering (EE), thus *relaxing* the query:

```
Q2: SELECT *
    FROM Applicants AS a
        WHERE (a.Major = 'CS' or a.Major = 'EE')
        AND a.GPA >= 3.85
```

In addition to Q1, query Q2 adds applicants #5, #6, #7, #12 and #13 to be interviewed, as marked in Table 1. The selected set includes four women and at least one individual of each race, satisfying the diversity requirement on both gender and race.

Next, the data analyst observes that a total of eight candidates will be interviewed based on Q2. This will require a substantial time commitment from the company's human resources department, who then impose an additional requirement — to limit the number of selected candidates to no more than five, thus introducing an upper-bound constraint on the size of the overall result set. To satisfy this additional constraint, the query can, once again, be refined, this time *restricting* the GPA range:

```
Q3: SELECT *
    FROM Applicants AS a
        WHERE (a.Major = 'CS' or a.Major = 'EE')
        AND a.GPA >= 3.90
```

The result of Q3 consists of 4 applicants, #2, #6, #9, and #13, with 2 of each gender and at least 1 of each race, satisfying all constraints.

Example 1.2. Next, suppose the employer introduces an additional requirement of selecting applicants with internship experience, with information in Table 2. To select applicants with at least 80 internship hours, the data analyst uses this query:

```
Q4: SELECT *
    FROM Applicants, Internships AS a, i
        WHERE a.ID = i.ID
        WHERE (a.Major = 'CS' or a.Major = 'EE')
        AND a.GPA >= 3.85 AND i.Hours >= 80
```

To have a team with diverse professional backgrounds, the company may wish to interview at least one applicant for each internship type: research lab (r.l.), tech company (t.c.), and government agency (g.a.). This can, once again, be expressed as a cardinality constraint, using attributes from `Internships` (Table 2). Thus, together with predicates and constraints from Example 1.1, we now have multiple selection predicates and cardinality constraints involving attributes from both tables. Then we can continue to refine the predicates in this query, as already discussed.

Outline of our approach. In this paper, we study the problem of finding minimal refinements of a query so that its result satisfies the given group cardinality constraints. Our goal is to modify selection predicates *just enough* to meet all the constraints, while preserving the intention of the original query as much as possible. Note that unlike the running example, our solution does not divide the process into steps. Instead, it considers all constraints and returns all minimal refinements that comply with them.

Finding minimal refinements presents two challenges: 1) the time-consuming execution of candidate query refinements to test constraint satisfaction, especially for large datasets or remote databases,

and 2) the computationally expensive exhaustive analysis due to the combinatorially large number of possible predicate changes. To address these challenges, we adopt a provenance model that annotates tuples with relevant predicate information and translates cardinality constraints into algebraic expressions for constraint testing, following Green *et al.* [13]. Additionally, we introduce Possible Value Lists (PVL), a data structure encompassing all possible predicate values, and employ an efficient searching algorithm with pruning techniques to identify minimal refinements.

Diversity is a compelling need when distributing resources and opportunities in a society, as we saw in our running example. Furthermore, it is also desirable in many other settings. For example, we usually want search and recommendation systems to produce diverse results [14]. While we use a running example about fairness (in the sense of representation), we underscore that the techniques we propose in this paper can be applied in many other contexts.

Alternative approaches. One way to satisfy group cardinality constraints is to modify the result set directly in a post-processing step, adding or removing tuples: Adding candidate #7, who is both female and Asian, to the result of Q1 would meet the diversity requirements. However, this method may be illegal in some jurisdictions and application contexts (e.g., it would be illegal in the US in the context of employment, housing, and lending), because it uses demographic group membership explicitly as part of decision making, effectively subjecting applicants from different demographic groups to different processes. Even where legal, this method may have undesirable side effects, such as tarring all members of a group, including its best-qualified members, as "weaker", on account of there being a different standard applied to the group.

Unlike post-processing, modifying the query predicates is usually legal, as it applies the same evaluation process to all individuals. One famous case involves the University of Texas, which was not permitted to give African Americans explicit (post-processing) preference in admissions; however, it was allowed to use rank in school as the basis for admission, thereby admitting top students from poor-performing segregated schools in preference to second-tier white students from top schools who may have better test scores.

Another alternative approach proposed by Shetiya *et al.* [15] shares similar motivation with our work but differs in four important ways. The first three are technical. First, they only handle constraints over a single binary sensitive attribute (e.g., male vs. female gender *or* majority vs. minority ethnicity), while we handle multiple sensitive attributes and do not limit them to be binary. Second, we support both query relaxation (i.e., generating more result tuples, asquery Q2) and query contraction (i.e., generating fewer result tuples, as Q3), while [15] only supports query relaxation. Third, [15] only focuses on queries over a single relation, while we support SPJ queries with predicates and constraints of attributes over multiple tables joined together, as shown in Example 1.2.

The fourth difference between our work and [15] is conceptual. Their diversity objective aims to minimize the distance between the *result sets* of the original query and the rewritten query, while our objective is to minimize the distance between the *queries themselves*. Although this difference might seem subtle, it leads to fundamentally different objectives in the rewriting process: preserving the salient properties of the selection process while potentially changing the result substantially vs. preserving the result as much as

possible while potentially making substantial changes to the selection process. For example, in the running Example 1.1, Q2 and Q3 are two refinements of Q1. Shetiya et al. would consider Q3 to have higher similarity (0.4) to Q1 than Q2 (0.375), while we consider Q2 to have higher similarity to Q1 based on the query predicates.

Contributions and roadmap. In Section 2, we formally define the QUERY REFINEMENT PROBLEM, the problem of finding minimal refinements of a query sequence given a dataset and a set of constraints on the query results, analyze its theoretical complexity, and prove its hardness. In Section 3, we describe our provenance model based on [13]. Then, Section 4 introduces the Possible Value Lists (PVL), a data structure that represents possible refinements based on provenance expressions. The PVL aims to enhance the efficiency of searching for minimal refinements. Our algorithm for generating minimal refinements using the PVL is detailed in Section 5, along with proposed optimizations for special cases. In Section 6, we experimentally evaluate our solution with multiple datasets, queries, and constraints. We give an overview of related work in Section 7 and conclude in Section 8.

2 PROBLEM DEFINITION

In this section, we introduce the notion of query refinement, cardinality constraints, and formally define the QUERY REFINEMENT PROBLEM. Additionally, we prove that the defined problem is not solvable in polynomial time, in the worst case. Table 3 summarizes the notations used in this paper.

2.1 Query Refinement

We support the class of queries considered in [4], conjunctive Select-Project-Join (SPJ) queries with selection predicates over *numerical* or *categorical* attributes. Selection predicates over numerical attributes include range ($<, \leq, \geq, >$) and equality ($=$). Categorical predicates are of the form `attribute = constant_1 OR...OR attribute = constant_n`. For ease of presentation, in the rest of the paper, we assume numerical predicates are of the form `attribute <op> constant`.[1], where `<op>` can be one of $\{<, \leq, \geq, >\}$. Equality predicates `attribute = constant` are translated into two predicates `attribute >= constant` and `attribute <= constant`.

For a query Q, we use Q_n and Q_c to denote the set of numerical and categorical selection predicates, respectively. The parts of a predicate are represented as $p.A$, $p.op$, and $p.C$. Specifically, for numerical predicates in the form `attribute >= constant`, $p.A$ represents the attribute, $p.op$ represents the operator $\geq$, and $p.C$ represents the constant. Similarly, for categorical predicates of the form `attribute = constant_1 OR...OR attribute = constant_n`, $p.A$ represents the attribute, and $p.C$ represents the set of constants $\{constant_1, \ldots, constant_n\}$ in predicate p.

We use the notion of query refinement defined in [4] to formally state our problem. For a numerical predicate, refinements are changes to the value of the constant; while for categorical predicates, a refinement is done by adding and/or removing predicates from the original constant list. We say that a query Q' is a *refinement* of query Q if Q' is obtained from Q by refining some predicates of Q. For example, query Q3 (selecting applicants with CS or EE major

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[1]Extending our solution to support other forms of numerical predicates, such as `attribute1 <op> constant·attribute2` is straightforward, and we do not discuss them in this paper.

Table 3: Notation Table

Notation	Description
D	dataset
Q	query or refinement query
$Q(D)$	result of executing Q over D
Q_n, Q_c	numerical predicates, categorical predicates of Q
$p.A, p.C, p.op$	attribute, constant, and operator of predicate p
$\mathcal{G}$	conjunction of conditions
$Q(D)_\mathcal{G}$	group of tuples in $Q(D)$ satisfying $\mathcal{G}$
Cr	cardinality constraints defining a group
$\mathcal{V}_{Q(D)}$	set of variables in provenance expressions
$prov(t)$	annotation of tuple $t \in D$
$\mathcal{I}_{Q(D)}^{Cr}$	provenance expression set
$val_{Q'}(A_v)$	valuation of $A_v \in \mathcal{V}_{Q(D)}$ with refinement Q'
$Tval_{Q'}(\mathcal{I}_{Q(D)}^{Cr})$	truth value of expression set $\mathcal{I}_{Q(D)}^{Cr}$
$L_{D,Q}$	PVL given D, Q
$Q.R$	list of indices representing Q in PVL $L_{D,Q}$
$Q\vert_P$	partial query of Q containing predicates in set P

and GPA at least 3.90) is a refinement of Q1 (selecting applicants with CS major and GPA at least 3.85) from Example 1.1.

2.2 Group Cardinality Constraints

Let $Q(D)$ be the result of executing query Q over dataset D, and $\mathcal{G}$ be a group defined by a conjunction of conditions with specified the value of some attributes. For instance, the group of Black females is $\{Gender = F, Race = Black\}$. We use $Q(D)_\mathcal{G}$ to denote the group of tuples in $Q(D)$ that satisfy the condition $\mathcal{G}$. A cardinality constraint Cr over $Q(D)_\mathcal{G}$ is a conjunction of expressions of the form $|Q(D)_\mathcal{G}| \; op \; x$, where $op \in \{=, \leq, <, >, \geq\}$ and x is a constant, or a function of the size of some other data group defined using $\mathcal{G}'$. We say that $Q(D)$ satisfies Cr if all the expressions hold. Namely, multiple cardinality constraints should be satisfied conjunctively.

Given a dataset D, a query Q, and a set of cardinality constraints Cr such that $Q(D)$ does not satisfy Cr, there can be multiple ways to refine Q so as to satisfy the constraints, as we demonstrate next.

Example 2.1. Recall in that our running example (Example 1.1), the original query (Q1) selects applicants with CS major and GPA of at least 3.85, resulting in only one female being selected. However, the company aims to select at least two females, which can be formally expressed as $Q(D)_{Gender=F} \geq 2$. Both Q2 (adding EE major) and Q3 (adding EE major and restriting GPA to be at least 3.90) are refinements of Q1 that select at least two females. Another plausible refinement that qualifies at least two females is to adjust the GPA predicate to be `a.GPA >= 3.40`.

The above example suggests that the company can achieve its diversity goal through various query modifications. Minimal modifications to the original query are preferred, prioritizing `a.GPA >= 3.60` over `a.GPA >= 3.55`. However, refinements modifying different attributes might be incomparable without additional preference information provided by the end user (as long as they all satisfy the constraints). Thus, we define the set of minimal refinements.

For query Q and its refinements Q' and Q'', Q' *dominates* Q'' if Q' is "closer" to Q than Q'' for every refined predicate. For example, in the job applicant context, `a.GPA >= 3.85` has refinement `a.GPA >= 3.90` dominating `a.GPA >= 3.60`. Similarly, for the predicate `a.Major = 'CS'`, refinement `a.Major = 'EE'` dominates refinement `a.Major = 'EE' or a.Major = 'ME'`. A *minimal refinement* of Q w.r.t. Cr satisfies three conditions: (i) Q' is a

refinement of Q, (ii) $Q'(D)$ satisfies Cr, and (iii) there is no other refinement Q'' that satisfies conditions (i) and (ii) while dominating Q'. Our goal is to find all minimal refinements of a query with respect to a set of cardinality constraints as we next define.

Problem 2.2 (Query Refinement Problem). *Given a dataset D, a SPJ query Q, and a set of cardinality constraints Cr, find all minimal refinements of Q with respect to Cr.*

Note that multiple minimal refinements may exist, and our objective is to report all of them. It is also possible that no refinement meets the constraints, resulting in an empty result set. A straightforward approach to address the Query Refinement Problem would be to traverse all possible refinements. For each refinement, we would check whether it satisfies the constraints and if so, add it to a result set R. Queries in R that are dominated by others will finally be removed. However, this naive approach exhibits exponential time complexity, and as demonstrated shortly, no polynomial time algorithm can solve the Query Refinement Problem.

2.3 Hardness Analysis

Theorem 2.3. *Given a dataset, an SPJ query, and a set of cardinality constraints, no polynomial time algorithm in the number of selection predicates can guarantee the enumeration of the set of all minimal refinements.*

	A_1	A_2	A_3	...	A_N	Gender
t_1	0	1	1	...	1	F
t_2	1	0	1	...	1	F
t_3	1	1	0	...	1	F
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	F
t_N	1	1	1	...	0	F
t_{N+1}	0	0	0	0	0	F
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	F
t_n	0	0	0	0	0	F

Table 4: Dataset for proof

Proof. We prove the theorem by constructing an example with an exponential number of minimal refinements. Consider a dataset with n tuples and query Q with N predicates over attributes $A_1 \cdots A_N$. Assume all N predicates are numeric predicates where the value of attribute $A_i (1 \leq I \leq N)$ can be either 0 or 1. Without loss of generality, we assume $n > N$ and $N \% 2 = 0$. Figure 4 shows the dataset, where the values of an attribute A_i for a tuple t is represented as either 1 or 0, meaning the value of $t.A_i$. For t_i where $1 \leq i \leq N$, $t_i.A_i = 0$, and $t_i.A_j = 1, j \neq i$. That is, for $t_1 - t_N$, only values on the diagonal are 0. For t_i where $i \geq N+1$, $t_i.A_j = 0, 1 \leq j \leq N$.

As in Figure 4, all n tuples have attribute gender as female, and we assume the cardinality constraint is to have at least $N/2$ females. With the original query Q, no female is selected, so we need to refine Q so that at least $N/2$ tuples satisfy the query. Since all values are binary, a refinement is to refine some predicates from $p.c = 1$ to $p.c = 0$. Any refinement that refines $N/2$ of the predicates to be $p.c = 0$ is a minimal refinement, for the following two reasons. First, such a refinement R makes $N/2$ of the tuples among $t_1 - t_N$ selected by the query, thus satisfying the cardinality constraint. Second, for any refinement R' dominated by R, R' has at most $N/2 - 1$ predicates

refined with $p.c = 0$, making at most $N/2 - 1$ tuples among $t_1 - t_N$ selected by the query, and zero tuples among $t_{n+1} - t_n$ selected, thus not satisfying the cardinality constraint.

Therefore, any refinement refining half of the predicates is a minimal refinement, so the number of minimal refinements is $\binom{N}{N/2} = O(\sqrt{2}^N)$. □

In what follows, we will present a solution that largely increase the efficiency by using provenance model to avoid redundant database access, and a searching algorithm with pruning methods.

3 PROVENANCE MODEL

Given a query, the number of possible refinement queries can be extremely large, especially when dealing with queries involving multiple tables and numerous attributes. Evaluating their satisfaction of cardinality constraints can be expensive, particularly with large or remote databases, and/or a large number of constraints. However, this costly query evaluation process can be eliminated using data annotations based on provenance theory. In fact, we can generate provenance annotations within a linear pass over the dataset, and then propagate them throughout the query evaluation to generate provenance expression as we next explain.

Our provenance model is inspired by the idea of hypothetical reasoning using provenance presented in [6]. Intuitively, we generate provenance expressions, using the data, the given SPJ query, and the cardinality constraints. We leverage the idea of conditional tables (c-tables) [16], where tuples are associated with conditions. To capture the possible refinements, we annotate tuples in the data with the query selection conditions.

3.1 Provenance expressions

We first define a set of variables used in the provenance expressions. Given a query Q over the data D, the set of variables $\mathcal{V}_Q$ is defined as $\mathcal{V}_{Q(D)} = \{A_{[t.A]} \mid \exists p \in Q_n \cup Q_c, p.A = A, t \in D\}$, where $[t.A]$ denotes the value of the attribute A in t.

Example 3.1. In Examples 1.1 and 1.2, when the company aims to select job applicants based on their majors (M), GPA values (G) (Table 1), and internship hours (H) (Table 2), we have the following variables involved in this query: $\mathcal{V}_{Q(D)} = \{M_{CS}, M_{EE}, M_{ME}, G_{3.95}, G_{3.90}, G_{3.85}, G_{3.65}, G_{3.60}, G_{3.40}, H_{40}, H_{60}, H_{80}, H_{90}, H_{100}, H_{120}\}$.

We use the set of variables $\mathcal{V}_{Q(D)}$ to generate provenance annotations, and use $\widetilde{Q}$ to denote the query obtained from Q when omitting the selection predicates. We generate provenance annotations for each tuple $t \in \widetilde{Q}(D)$: $prov(t) = \prod_{i=1}^{i=k} A_{i[t.A_i]}$ where each A_i is an attribute that is involved in Q (i.e., $\exists p \in Q_n \cup Q_c, p.A = A_i$), and k is the number of such attributes. Intuitively, the annotated output $\widetilde{Q}(D)$ includes all the tuples after executing only join operations, and it represents the output of all possible refinements of Q, where the provenance annotation of each tuple can be used to determine whether it satisfies any given refinement.

Finally, given a dataset D and a query Q, and a cardinality constraint $Q(D)_{\mathcal{G}}$ op x, where $op \in \{>, \geq, <, \leq\}$, we define expressions that express the cardinality constraints using the resulting provenance annotations: $\left(\sum_{t \in Q(D)_{\mathcal{G}}} prov(t) \right)$ op x. For a given set of cardinality constrains Cr over $Q(D)$ we use $\mathcal{I}_{Q(D)}^{Cr}$ to denote the corresponding set of provenance expressions.

Example 3.2. Equation 1 represents the constraint of selecting at least two females based on their majors, GPA values and internship hours in our job applicant example (Example 1.1 and 1.2). We get this expression by joining Table 1 and Table 2 by attribute ID, and choosing annocations of females applicants #2, #3, #6, #7.

$$M_{CS} \cdot G_{3.95} \cdot H_{170} + M_{CS} \cdot G_{3.40} \cdot H_{90} + \\ M_{EE} \cdot G_{3.90} \cdot H_{120} + M_{EE} \cdot G_{3.85} \cdot H_{100} \geq 2 \tag{1}$$

3.2 Refinements through valuation

For a query Q on data D, each possible refinement query Q' corresponds to an assignment to the variables set $\mathcal{V}_{Q(D)}$ in the corresponding provenance expression, known as a *valuation* in the provenance literature. Variables that satisfy the query are assigned the value 1 ($val_{Q'}(A_v) = 1$), while others get 0 ($val_{Q'}(A_v) = 0$). Such value assignments can then be used for the valuation of the provenance expressions associated with each tuple in the data and in turn, the truth values of the provenance expressions. Given provenance expressions $\mathcal{I}_{Q(D)}^{Cr}$ and the value assignment $val_{Q'}$, we use $Tval_{Q'}(I)$ to denote the truth value of the expression $I \in \mathcal{I}_{Q(D)}^{Cr}$, obtained by applying $val_{Q'}(A_{iv})$ on each variable A_{iv} in I. Overloading notation we use $Tval_{Q'}(\mathcal{I}_{Q(D)}^{Cr})$ to denote the truth value of the expression set $\mathcal{I}_{Q(D)}^{Cr}$, namely $Tval_{Q'}(\mathcal{I}_{Q(D)}^{Cr}) = \wedge_{I \in \mathcal{I}_{Q(D)}^{Cr}} Tval_{Q'}(I)$

Example 3.3. Recall in our running example (Example 1.1 and 1.2), the company would like to have at least two females selected, which gives us the provenance expression Equation (1) from Example 3.2. With query Q4 (selecting applicants with CS or EE major, GPA at least 3.85 and at least 80 hours of internship experience), only variable $G_{3.40}$ is 0, and others are 1, so the truth value is true.

PROPOSITION 3.4. *Let D be a dataset and Q a query. Q satisfies a set of cardinality constraints Cr if and only if $Tval_Q(\mathcal{I}_{Q(D)}^{Cr}) = True$.*

Namely, given the provenance expressions of the cardinality constraints, we can efficiently examine the effect of refinements on constraint satisfaction without the need to access the data and execute the potential refinements. Furthermore, the provenance expressions may guide the refinement search as we next explain.

4 POSSIBLE VALUE LISTS (PVL)

With a provenance model available for testing potential refinements without accessing the data itself or repetitively evaluating refinement queries, the next question is how to find all the minimal refinements efficiently. A straightforward method is to traverse all possible refinements one by one, but this can be computationally prohibitive given the combinatorial number of refinements. Our solution uses a set of lists depicting the possible refinements based on the variables in the provenance expression, called the Possible Value Lists (PVL), as we next describe.

The PVL is used to enumerate the possible refinement queries. Each such query can be defined by the modifications, to the original query, in the predicates' values. For numerical predicates, minimal refinements can only include numerical values from the tuples in the data that are involved in cardinality constraints. For example, for the constraint over the number of female applicants in our running example, a refinement changing the GPA predicate to a.GPA >= 3.45 cannot be minimal. This is because it yields the same output as refining the GPA predicate to a.GPA >= 3.60 since

no female applicant has a GPA within the range of $3.45 \leq$ GPA $<$ 3.60. However, the latter refinement dominates the former.

Given a dataset D, query Q, and cardinality constraints Cr, the PVL $L_{D,Q,Cr}$ represents possible modifications using lists of values. The values in the lists are sorted based on their distance from the values in the original query Q. Each numerical predicate p_n (A op c) are stored in a single list ($l_{p_n.A}$) of possible values for $p_n.A$, sorted by their absolute distance from c ($|x - c|, x \in l_{p_n.A}$). Categorical predicates p_c ($A \in C$) are represented using multiple lists, including l_{A_v} for each possible value v of A, with values of 1 (existence) or 0 (absence) to indicate the presence of v in C. The order of 1 and 0 is determined based on whether v is already part of p_c. In other words, 1 (existence) is placed higher than 0 (absence) if v is already part of the original predicate p_c; and vice versa.

Example 4.1. Figure 1a depicts the PVL $L_{D,Q1,Cr}$ of Example 1.1 with dataset D, query Q1 (a.Major = 'CS' AND a.GPA >= 3.85), and Cr over the number of females, people of each race, and the overall size of the result. The Major predicate has CS but not EE or ME, so 1 is placed above 0 in the list $l_{M_{CS}}$, and 0 is placed above 1 in the lists $l_{M_{EE}}, l_{M_{ME}}$. Note that values 4.00, 3.95, and 3.90 in l_G correspond to values 3.95, 3.90 and 3.85 in D, respectively. The meaning of colors highlighting some values will be explained later.

Note that depending on $p_n.op$ (operators in predicates) and values in D, the values in list $l_{p_n.A}$ may be $v \pm precision(p_n.A)$, where v is a value of numerical attribute $p_n.A$ in D and $precision(p_n.A)$ is its precision, e.g., in our running example $precision(GPA) = 0.05$. Specifically, when $p_n.op$ is $\geq$ ($<$), for values $v \geq p_n.C$, $l_{p_n.A}$ should contain $v + precision(p_n.A)$ instead of v; when $p_n.op$ is $\leq$ ($>$), for values $v \leq p_n.C$, $l_{p_n.A}$ should contain $v - precision(p_n.A)$ instead of v. In the running example, to contract GPA predicate (a.GPA >= 3.85) so that it disqualifies a 3.85 (3.90, 3.95) GPA value, it needs to be refined to a.GPA >= 3.90 (3.95, 4.00).

Intuitively, each value in a list of PVL $L_{D,Q,Cr}$ demonstrates a possible refinement of a specific predicate. A combination of one value from each list corresponds to a refinement of the query Q. In this manner, PVL encompasses all minimal refinements. The relationship between PVL and refinements of query Q is summarized in the following proposition.

PROPOSITION 4.2. *Given a query Q_0 over the dataset D and cardinality constraint Cr, let $\mathbf{Q}^*$ be the set of all possible refinement queries that can be generated using values from D.*

(1) Every minimal refinement query must be in $\mathbf{Q}^*$.
(2) $\forall Q' \in \mathbf{Q}^*$, Q' can be represented using a set of indexes $Q'.R$ in the PVL $L_{D,Q_0,Cr}$ such that $Q'.R[l]$ is the index in the list $l \in L_{D,Q_0,Cr}$. $\forall p_n \in Q'_n, \exists l_{p_n.A} \in L_{D,Q_0,Cr}, p_n.C = l_{p_n.A}[Q'.R[l_{p_n.A}]]$. $\forall p_c \in Q'_c, \exists l_{p_c.A_v} \in L_{D,Q_0,Cr}$ such that $l_{p_c.A_v}$ consists of 0 and 1. If $v \in p_c.C$ then $Q'.R[l_{p_c.A_v}]$ is the index of 1, and 0 otherwise.
(3) Every possible index set $Q'.R$ corresponds to a query $Q' \in \mathbf{Q}^*$.

Example 4.3. Revisiting Example 1.1 with PVL in Figure 1a, refinement query Q2, compared to the original query Q1, adds EE as a recognized major, so can be represented as $Q2.R = [2, 1, 1, 1]$. This corresponds to values $l_{M_{EE}}[2] = 1, l_{M_{ME}}[1] = 0, l_{M_{CS}}[1] = 1, l_G[1] = 3.85$. The refinement query Q3, which adds EE and adjust GPA range to be a.GPA >= 3.90, can be represented as $Q3.R = [2, 1, 1, 2]$, as highlighted in blue.
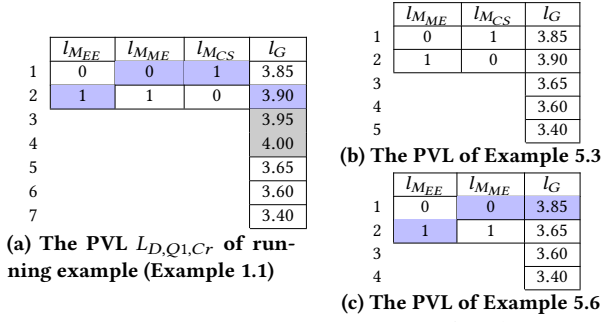
	$l_{M_{EE}}$	$l_{M_{ME}}$	$l_{M_{CS}}$	l_G
1	0	0	1	3.85
2	1	1	0	3.90
3				3.95
4				4.00
5				3.65
6				3.60
7				3.40

(a) The PVL $L_{D,Q1,Cr}$ of running example (Example 1.1)

	$l_{M_{ME}}$	$l_{M_{CS}}$	l_G
1	0	1	3.90
2	1	0	3.90
3			3.65
4			3.60
5			3.40

(b) The PVL of Example 5.3

	$l_{M_{EE}}$	$l_{M_{ME}}$	l_G
1	0	0	3.85
2	1	1	3.65
3			3.60
4			3.40

(c) The PVL of Example 5.6

Figure 1: Possible value lists (PVL).

Our algorithm for generating minimal refinements utilizes the PVL to traverse the possible refinements. As stated in Proposition 4.2, all minimal refinements can be represented from the PVL. This representation holds the following properties that serve as the foundation for the correctness of our algorithm.

PROPOSITION 4.4. *Let D be a dataset, Q be a query, and Cr be constraints, and $L_{D,Q,Cr}$ be the corresponding PVL consisting of n_l lists. Additionally, let $Q_1, Q_2 \in \mathbf{Q}$ be two different refinement queries.*
(1) Q_1 dominates $Q_2 \iff \forall j, 1 \le j \le n_l, Q_1.R[j] \le Q_2.R[j]$.
(2) If Q_1 and Q_2 are minimal refinements then $\exists j, 1 \le j \le n_l$, such that $Q_1.R[j] \le Q_2.R[j]$ and $\exists j', 1 \le j' \le n_l$, such that $Q_1.R[j'] > Q_2.R[j']$

5 GENERATING MINIMAL REFINEMENTS

We present the algorithm for searching minimal query refinements using PVL. We will describe the algorithm and then discuss optimizations that can be applied in specific scenarios.

5.1 The algorithm

The algorithm uses the notion of partial queries as we next define.

Definition 5.1 (Partial queries). Given a query Q with the set of predicates $Q_n \cup Q_c$ and a subset $P \subseteq Q_n \cup Q_c$, the query $Q|_P$ is similar to Q but consists only of the predicates in the set P. We say that $Q|_P$ is a *partial query* of Q.

Example 5.2. Consider the original query Q1 in Example 1.1 with predicates `a.Major = 'CS' AND a.GPA >= 3.85`. For $P = \{a.GPA >= 3.85\}$, $Q1|_P$ is a partial query of Q1.

The high-level idea of the algorithm is to generate refinement queries that satisfy the constraints by completing the predicate set of partial queries to obtain refinements of the given query Q. This process is done for different partial queries using a recursive function. We next provide details on the different parts of the algorithm.

Finding a minimal refinement (from a partial query). Given a partial query $Q'|_P$ (where Q' is a refinement of Q), the algorithm generates one minimal refinement query by completing the predicates of P to obtain a refinement of the input query Q, which is procedure findRefinement (line 1). Procedure findRefinement traverses the PVL in a top-down manner, setting each predicate of P according to values in the lists of PVL. It attempts all possible refinements by exhaustive search but with pruning methods (as shown in paragraph "Reducing the search space") until a suitable refinement is found. Each refinement is represented by an index set, one in each list. The general principle is to check the index set with smaller indexes earlier. For instance, when searching in PVL in Figure 1a, we start from an index set with three 1's and one 2: [2, 1, 1, 1], [1, 2, 1, 1], [1, 1, 2, 1], [1, 1, 1, 2], but nothing works.

Algorithm 1: Search for all minimal refinements

input : PVL L, query Q, and cardinality constraints $\mathcal{I}$.
output: All minimal relaxations
Function Search($L, Res, Q|_P, \mathcal{I}$):
1    $Q_b \leftarrow$ findRefinement $(L, \mathcal{I}, Q|_P)$
2   **if** $Q_b.R \ne \emptyset$ **then**
3   update (Res, Q_b)
4   **if** *there are more than one list in L* **then**
5   **foreach** $l \in L$ **do**
6          $k \leftarrow Q_b.R[l]$
7   **for** *i from $k - 1$ to 1* **do**
8            $Q'|_{P'} \leftarrow$ addPredicate $(Q|_P, l[i])$
9            $\mathcal{I}_r \leftarrow$ inequalities of $\mathcal{I}$ requiring relaxations
10   **if** $Tval_{Q'|_{P'}}(\mathcal{I}_r) = True$ *and there are other lists l' s.t. $Q_b.R[l]$ is not the last index in l'* **then**
11              $L' \leftarrow$ remove l from L
12              $Res \leftarrow$ Search$(L', Res, Q'|_{P'}, \mathcal{I})$
13   remove values above index $Q_b.R[l]$ in list l

14   **return** Res

Then we continue with an index set with two 1's and two 2's: $[2, 2, 1, 1], [2, 1, 2, 1], \cdots$. We stop when we find the first refinement satisfying the cardinality constraints. Since the traversal starts from values at the top of PVL, which are the closest to the original predicates, the first first satisfying refinement found must be a minimal one. There can be more than one minimal satisfying refinement, and findRefinement returns the one it encounters first.

Recursive search. The core of the algorithm is a recursive search function depicted in Algorithm 1. Given a partial query $Q|_P$ with a fixed predicate set P (as part of a minimal refinement), a temporary result set Res, a PVL L, and a set of provenance inequalities, Search function performs the following steps. First, using the findRefinement procedure, the function identifies a minimal refinement Q_b (line 1). If no such refinement exists, the current result set Res is returned. Otherwise, Res is updated with Q_b (line 3). Next, the algorithm generates new refinements by adding a predicate with a value from a list $l \in L$ to P (addPredicate), removing l from L, and recursively searching for new refinements (lines 4–13). In this process, for each list $l \in L$, the algorithm considers all possible predicates that can be generated using values above $Q_b.R[l]$ in l. This adds a new predicate to P and removes one list from L in each iteration. The recursive search continues until no refinements are found in the PVL or when the PVL contains only one list.

Reducing the search space. When we traverse the possible refinements, the search space can be reduced using the notion of *partial dissatisfaction* as we next explain. For a given set of provenance inequalities $\mathcal{I}$, we use $\mathcal{I}_r \subseteq \mathcal{I}$ to denote the subset of inequalities that are of the form $Q(D)_G \ op \ x$, where $op \in \{>, \ge\}$ and x is a constant. These constraints are referred to as *relaxation constraints*. For any given (refinement) query Q', if there exists a predicate set $P \subset Q'_n \cup Q'_c$ such that $Tval_{Q'|_P}(\mathcal{I}_r) = False$, then $Tval_{Q'}(\mathcal{I}^{Cr}_{Q(D)}) = False$. In other words, if a partial query $Q|_P$ fails to satisfy certain relaxation constraints, it implies that the entire constraint set is not satisfied by Q'. For example, if a partial query $Q|_P$ disqualifies 6 out of 7 females, then any query Q would not satisfy the constraint of selecting at least 2 females.

Putting it all together. Given a query Q over D and a set of provenance inequalities $\mathcal{I}^{Cr}_{Q(D)}$ generated form the cardinality constraints

Cr, we find the set of all minimal refinements by calling the Search function. We initiate the search by invoking Search with the initial parameters: LD, Q, Cr, an empty result set *Res*, a partial query $Q|P$ where $P = \emptyset$, and $\mathcal{I}^{Cr}Q(D)$. Search calls findRefinement procedure, as described earlier, to generate new refinements. The search is optimized by avoiding refinements that can not satisfy the constraints based on partial dissatisfaction (lines 9 – 10). Moreover, to prevent redundant checks, at the end of the recursive call with values in list *l*, the algorithm removes all these values (values above index $Q_b.R[l]$) from consideration (line 13). This is because refinements with these values have already been examined.

Example 5.3. Consider Example 1.1, where job applicants are selected based on their majors and GPA values shown in Figure 1. The original query Q1 (CS major and GPA at least 3.85) has constraints over the number of females, individuals of each race, and the overall result size. Provenance expressions of the constraints are generated using the provenance model, and PVL is built as shown in Figure 1a. To reduce the search space, 3.95 and 4.00 in l_G (highlighted in grey) are removed since partial queries with a.GPA >= 3.95 (or a.GPA >= 4.00) do not satisfy the requirement of selecting at least two females. We search in PVL for base minimal refinement by a top-down traversal, and obtain Q_b s.t. $Q_b.R = [2, 1, 1, 2]$, as highlighted in blue, refining Major predicates to a.Major = 'EE' or a.Major = 'CS' and GPA predicate to a.GPA >= 3.90. Next, we explore further refinements by checking values above the blue ones in PVL. We examine the value in $l_{M_{EE}}[1]$ and $l_G[1]$. For $l_{M_{EE}}[1]$, we add EE to the Major predicate, generate a new PVL (Figure 1b), and recursively search, but no base minimal refinements are found. Similarly, when fixing GPA predicate with value $l_G[1] = 3.85$, we generate another new PVL (Figure 1a), and the recursive search does not find any more minimal refinements either. The final result contains only one minimal refinement.

We prove that our algorithm can find all minimal refinements without reporting any non-minimal refinements, as stated in the following theorem.

THEOREM 5.4. *Given a dataset D, a SPJ query Q, and a set of provenance inequalities $\mathcal{I}_{Q(D)}^{Cr}$, our algorithm can find all minimal refinements, and all of those reported are minimal refinements.*

PROOF. The second part of the theorem is trivial as the algorithm always verifies each refinement before adding it, ensuring that anything reported by the algorithm is a minimal refinement. To prove the first half of the theorem, we use induction. Based on Algorithm 1, the lists in the Possible Value Lists (PVL) represent predicates to be refined, and Q'_P is a partial query with fixed predicates *P*. We aim to show that each iteration of Search(L, Res, Q'_p) can find all minimal refinements.

Base case: When there is only one list in PVL, there is a single remaining predicate *p* with at most one minimal refinement. Algorithm 1, in line 1, can identify any refinement of *p* that satisfies the condition $Tval_{Q'|P}(\mathcal{I}_{Q(D)}^{Cr}) = True$, if such a refinement exists.

Induction step: Assuming that with an *x*-list PVL, Algorithm 1 can find all minimal refinements, we need to prove it can still do so with an $(x + 1)$-list PVL. Suppose there are *y* minimal refinements with an $(x + 1)$-list PVL, where $y \geq 1$. During the traversal process, one of these refinements, Q_b, will be identified as the base minimal refinement. Among the remaining $(y - 1)$ refinements Q,

---

Algorithm 2: Find a minimal relaxation

input : A *PVL L* and cardinality constraints $\mathcal{I}$.
output: A minimal relaxation $\mathcal{R}$

1 **Procedure** findRelaxation($L, \mathcal{I}, Q|_P$)
2     $Q_b \leftarrow$ binarySearch($L, \mathcal{I}, Q|_P$)
3   **if** $Q_b.R \neq \emptyset$ **then**
4   **foreach** $l \in L$ **do**
5           $foundMin \leftarrow False$
6   **while** $Q_b.R[l] \geq 1$ *or foundMin* **do**
7              $Q_b.R[l] \leftarrow Q_b.R[l] - 1$
8   **if** $Tval_{Q_b}(\mathcal{I}) = False$ **then**
9                 $Q_b.R[l] \leftarrow Q_b.R[l] + 1$
10                 $foundMin \leftarrow True$
11   **return** Q_b

---

each refinement *Q* is more refined in some lists and less refined in others compared to Q_b, based on Proposition 4.4. Thus, there must be at least one list *l* in the PVL where $Q.R[l] < Q_b.R[l]$. Let *l* be the left-most list satisfying this condition. If *l* is a numerical list corresponding to predicate *p*, Algorithm 1 updates the partial query $Q'|_{P'}$ by adding a predicate p' with $p'.A = p.A$, $p'.op = p.op$, and $p'.c = l[Q.R[l]]$. Similarly, if *l* is a categorical list corresponding to A_v of predicate *p*, the algorithm updates the partial query $Q|_P$ by either adding or not adding *v* to $p.C$, depending on whether the value to fix is 1 or 0. Then, the algorithm performs iteration Search($L'_{D,Q,Cr}, Res, Q'|_{P'}$), where $L'_{D,Q,Cr}$ is the PVL without list *l*. Based on our induction hypothesis, Search($L'_{D,Q,Cr}, Res, Q'|_{P'}$) can find all minimal refinements since $L'_{D,Q,Cr}$ consists of *x* lists. Hence, *Q* can be found by Search($L'_{D,Q,Cr}, Res, Q'|_{P'}$). The removal of values above the base minimal refinement Q_b (line 13 in Algorithm 1) does not affect the generation of query *Q* since they are removed after being checked already. □

Complexity analysis. Generating the provenance inequalities is polynomial in the data size, as it requires a single linear pass over the dataset to annotate the data in addition to the query evaluation. For the searching algorithm, the worst case is to traverse all possible refinements, so the time complexity is the number of all possible refinements is the product of the length of all lists in PVL is

$$O\left(\left(\prod_{i=1}^{N_n}(|Dom(A_i)| + 1)\right) \cdot 2^{\sum_{j=1}^{N_c} |Dom(A_j)|}\right)$$

where N_n, N_c denote the number of numeric predicates and categorical predicates, respectively; A_i, A_j denote numeric attributes and categorical attributes, respectively, and $Dom(A)$ denotes the domain of attribute *A*. In the worst case, $|Dom(A_i)| = |D| = n$, thus we have $O\left(\left(n^{N_n}\right) \cdot 2^{\sum_{j=1}^{N_c} |Dom(A_j)|}\right)$

While the time complexity is exponential to the number of numerical predicates and the size of domains of categorical predicates in the worst case, we show in our experiments that in practice, the running time of our algorithm is typically much better, due to our search space pruning.

5.2 Optimizations

We next describe some optimizations that can be applied when 1) numerical predicates do not have an equality (=) operator; and 2) all the constraints are relaxation constraints or all are contraction

constraints, i.e., $C(D)_G$ op x, where x is a constant and $op \in \{>, \geq\}$ (or $op \in \{<, \leq\}$) for *all* the constraints. For simplicity of presentation, in what follows, we present the case of relaxation. The case of contraction is symmetric.

First of all, note that tuples in D that already satisfy the cardinality constraints do not impact the refinement process and can therefore be excluded from both the provenance inequalities and the PVL. Furthermore, when all constraints are relaxation constraints, the process of finding a minimal refinement from a partial query and the subsequent recursive searches can be optimized, owing to the monotonicity property of relaxation queries in the following proposition.

PROPOSITION 5.5. *Let D be a dataset, Q be a query, and $L_{D,Q,Cr}$ be the corresponding PVL which consists of n_c lists. Let $\mathcal{I}^{Cr}_{Q(D)}$ be a set of provenance inequalities such that Cr are all relaxation constraints. Let Q_1, Q_2 be two different relaxations such that $Tval_{Q_1}(\mathcal{I}^{Cr}_{Q(D)}) = True$ and Q_1 dominates Q_2. Then $Tval_{Q_2}(\mathcal{I}^{Cr}_{Q(D)}) = True$.*

PROOF. Without loss of generosity, assume for all numerical predicates p, $p.op$ is $\geq$, i.e., they are all of the form $p.A \geq p.c$. To prove the proposition, we only need to show that $\forall A_v \in \mathcal{V}_{Q(D)}$ s.t. $val_{Q_1}(A_v) = 1$, we have $val_{Q_2}(A_v) = 1$. Let p_1, p_2 be the predicate corresponding to A_v in Q_1, Q_2, respectively. First, when A is a numerical attribute, based on Proposition 4.4, with list l_A, we have $Q_1.R[l_A] \leq Q_2.R[l_A]$, thus $p_1.c \geq p_2.c$. Based on the definition of valuation, $val_{Q_1}(A_v) = 1$ means $v \geq p_1.c$, so $v \geq p_2.c$, thus $val_{Q_2}(A_v) = 1$. Second, when A is a categorical attribute, with list l_A, based on Proposition 4.4, we assume $Q_2.R[l_A] = 2, Q_1.R[l_A] = 1$ (because other cases are trivial), so $p_2.C \subset p_1.C$. Based on the definition of valuation, $val_{Q_2}(A_v) = 1$ means $v \in p_1.C$, so $v \in p_2.C$, thus $val_{Q_2}(A_v) = 1$. □

Based on the above proposition, minimal refinements can be efficiently identified. Rather than employing a top-down search that traverses all potential refinements, we optimize this procedure by implementing a binary search to locate a refinement that satisfies the cardinality constraints. Following that, we "tighten" the refinement to make it minimal. This process is depicted in Algorithm 2. We first use a binary search (line 2) to obtain an initial query Q_b such that $\forall l \in L, Q_b.R[l] = k$ and $val_{Q_b}(\mathcal{I}^{Cr}_{Q(D)}) = True$. For lists l with length smaller than k, we set $Q.R[l]$ to be the length of l. Next, we tighten Q_b – make it minimal by moving up the index values in each list as much as possible (lines 4 – 10). The refinement we get at the end of the process is a minimal relaxation.

Proposition 4.4 also provides us with another optimization so that some recursions can be avoided. When we recursively search for other relaxations by fixing a predicate with values above $Q_b.R$, (lines 7 – 12 in Algorithm 2), if there is a value $l[i]$ that fixing it ends up adding no new minimal relaxation to the result set, we do not need to check values above index i in list l. In other words, from line 7 to line 12 in Algorithm 2, if one of the iterations in the for loop does not update the result set Res with any new minimal relaxations, we execute a "break" after line 12 to end the for loop in advance, because the following iterations would check values that relax the query less, and based on monotonicity, will definitely not satisfy the cardinality constraints.

Example 5.6. To show a simple example with relaxation constraints, in our running example (Example 1.1) where job applicants are selected based on their majors and GPA values in Table 1, we only consider the constraint that at least two females are selected. As mentioned before, when all constraints are relaxation constraints, provenance inequalities can be simplified by removing tuples satisfying query already, so the provenance expression is

$$M_{ME} \cdot G_{3.65} + M_{CS} \cdot G_{3.40} + M_{ME} \cdot G_{3.60}$$
$$+ M_{EE} \cdot G_{3.85} + M_{EE} \cdot G_{3.90} + M_{EE} \cdot G_{3.85} \geq 1 \quad (2)$$

Compared to Figure 1a, the PVL in Figure 1c does not contain list $l_{M_{CS}}$ and values greater than 3.85 in list l_G since they already satisfy Q1. To get an initial relaxation Q_b, we do a binary search and find that 2 is the smallest index k such that $\forall l \in L, Q_b.R[l] = k$ and $val_{Q_b}(\mathcal{I}^{Cr}_{Q1(D)}) = True$. Then we tighten Q_b by moving up values in each list as much as possible, and get $Q'_b.R = [2, 1, 1]$, highlighted in blue color, which is a minimal relaxation that adds EE to be a recognized major. Then, we fix the value in $l_{M_{EE}}[1]$ and search for other relaxations recursively, and find another two minimal relaxations: (1) modifying GPA predicate to be a.GPA >= 3.40; and (2) adding ME to the major list, and modifying GPA predicate to be a.GPA >= 3.65.

6 EXPERIMENTS

We empirically evaluate our proposed solutions to demonstrate their usefulness and effectiveness. We describe the experimental setup and provide a real-world case study, and then present a quantitative study assessing the efficiency of our algorithm, considering various datasets, queries, and cardinality constraints, and comparing it to the baseline solution. We analyze the impact of data size, query selectivity, and constraint properties on running time and the number of checked refinements. Moreover, we validate the effectiveness of the optimization presented in Section 5.2, provide comparison between our approach and [15]. The results show that our PVL-based search algorithm performs well across diverse scenarios, achieving up to 100 times faster execution than baseline traversal. The optimizations improve performance by up to 99.87%. For more comprehensive experiments.

6.1 Experiment Setup

To the best of our knowledge, there is no available benchmark for query refinement testing that provides datasets, queries, and constraints. For our evaluation, we choose the Healthcare and ACSIncome datasets, which are commonly used public demographic datasets in the context of fairness and diversity. We select attributes such as gender, race, age, marital status, and relationships to form the constraints, as these attributes are commonly employed as sensitive attributes that reflect membership in various demographic groups. Other other attributes are used to form the queries. We also use TPC-H benchmark which comes with queries, and we use attributes such as order priority and order status to form constraints.

Datasets: We use three different datasets to do experiments:
- **The Healthcare dataset**[2] is a dataset used in [17] to train a classifier identifying patients at risk for serious complications. It contains demographic and clinical history information of 887

Q_1^H	Q_2^H
SELECT * FROM Healthcare WHERE	
income >= 200K and **num-children >= 3** and **county in ("county2", "county3")**	**income <= 100K** and **complications >= 5** and **num-children >= 4** and
Q_3^H	Q_4^H
SELECT * FROM Healthcare WHERE	
income >= 150K and **num-children <= 4** and **complications <= 8** and **county in ("county2", "county4")**	**income >= 300K** and **complications >= 5** and **county in ("county1", "county4")**
Q_1^A	Q_2^A
SELECT * FROM ACSIncome WHERE	
working_hours >= 40 and **Educational_attainment >= 19** and **Class_of_worker in ("local_gov", "state_gov", "federal_gov")**	**working_hours <= 40** and **Educational_attainment <= 19** and **income in ("<20K", "20K-40K")**
Q_3^A	Q_4^A
SELECT * FROM ACSIncome WHERE	
working_hours >= 60 and **Educational_attainment <= 16** and **income in ("<20K")**	**working_hours >= 60** and **Educational_attainment >= 22** and **income in (">60K")** and **Class_of_worker in ("self_empl_inc", "self_empl_not_inc")**
Q_3^T	
SELECT * FROM customer, order, lineitem WHERE c_custkey = o_custkey and l_orderkey = o_orderkey and **c_mktsegment = 'BUILDING'** and **o_orderdate < date 1995-03-28** and **l_shipdate > date 1995-03-28**	
Q_{12}^T	
SELECT * FROM order, lineitem WHERE l_orderkey = o_orderkey and l_commitdate < l_receiptdate and l_shipdate < l_commitdate **l_shipmode in ('RAIL', 'AIR')** and **l_receiptdate >= date 1995-01-01** and **l_shipdate < date 1996-01-01**	

Figure 2: Queries used in experiments

C_1^H	C_2^H	C_3^H
{race = race2} {age = group1}	{race = race1} {age = group2} {age = group3}	{age = group1} {race = race1}
C_4^H	C_5^H	C_6^H
{race = race3} {race = race1, age = group1}	{race = race2} {age = group2}	{race = race2} {age = group2}
C_7^H	C_8^H	C_9^H
{smoker = no} {race = race2}	{smoker = yes} {race = race3}	{smoker = no} {race = race3}
C_1^A	C_2^A	C_3^A
{sex = F, marital = Married} {race = Black}	{sex = M, relationship = husband/wife} {age = 30 − 60, marital = divorced}	{sex = M, race = Asian} {sex = F, marital = Married}
C_4^A	C_5^A	C_6^A
{sex = F} {race = Black}	{race = White} {age = 30 − 60}	{race = Black} {age = 30 − 60}
C_7^A	C_8^A	C_9^A
{sex = F} {race = Black} {marital = Divorced}	{race = White} {sex = M}	{sex = F} {race = White}
$C_1^{T,3}$	$C_2^{T,3}$	$C_3^{T,3}$
{c_nationkey = 23} {l_shipmode = MAIL}	{c_nationkey = 2} {o_orderstatus = P, l_returnflag = N} {l_shipmode = MAIL} {l_shipinstruct = COLLECT COD} {l_linenumber = 5}	{l_linenumber = 6, l_shipmode = SHIP, o_orderstatus = F, o_orderpriority = 1-URGENT}, {l_shipinstruct = DELIVER IN PERSON, o_orderstatus = P, o_orderpriority = 2 − HIGH}
$C_1^{T,12}$	$C_2^{T,12}$	$C_3^{T,12}$
{o_orderpriority = 5-LOW, l_linenumber = 3}, {l_shipinstruct = COLLECT COD}, {l_returnflag = A}	{o_orderpriority = 1-URGENT}, {l_linenumber = 1} {l_returnflag = A, o_orderstatus = F};	{l_linenumber = 7, l_shipinstruct = NONE, o_orderpriority = 5-LOW, o_orderstatus = F}, {o_orderpriority = 4-NOT SPECIFIED, l_shipinstruct = TAKE BACK RETURN, l_linenumber = 7, l_returnflag = A}

Figure 3: Constraints used in experiments

patients, with attributes like number of children, income, number of complications, county, race, age, etc..

- **ACSIncome dataset** is one of five datasets created by [18] as an improved alternative to the popular UCI Adult dataset. The data was compiled from the American Community Survey (ACS) Public Use Microdata Sample (PUMS). It covers all 50 states and Puerto Rico, with 1,664,500 rows and 11 features.

- **TPC-H benchmark**[3] is a standard benchmark for measuring the performance of relational database management systems (RDBMS) and data warehousing systems. The benchmark consists of a suite of 22 SQL queries and a database schema with 8 relational tables, and is designed to simulate the decision support systems of a typical data warehousing environment. We use TPC-H 3.0.1 to generate datasets and queries 100M data size.

Queries: We generated four queries each for Healthcare and ACSIncome dataset (denoted as $Q_1^H, Q_2^H, Q_3^H, Q_4^H, Q_1^A, Q_2^A, Q_3^A, Q_4^A$) without JOIN operations as each dataset has a single relation. From TPC-H benchmark queries, we randomly chose #3 and #12 (Q_3^T, Q_{12}^T), which both include JOIN operations. The TPC-H query was simplified by removing GROUP BY, ORDER BY, and LIMIT clauses which are not considered in our setting and only affect tuple display. This modification doesn't affect the experiment's validity. Additionally, we replaced attribute sets in the query projections with SELECT * for simplicity and to ensure all attributes in the cardinality constraints were included. One predicate over l_receiptdate in query #12 is replaced with attribute l_shipdate, which enables us to explore different scenarios and apply optimizations. An overview of all queries used in the experiments is presented in Figure 2.

Cardinality constraints: Figure 3 summarizes the constraints used in experiments. We form three sets of cardinality constraints for each of the Healthcare, ACSIncome, and TPC-H datasets, by using representative sensitive attributes such as race and gender for the first two demographic datasets, and attributes from multiple tables that are not used in queries for non-demographic TPC-H dataset. Each set contains 2 to 5 constraints that must be fulfilled simultaneously. The first set of constraints for each dataset contains relaxation constraints, the second contains contraction constraints, and the third contains a combination of both: first group being relaxed to 105% and second being contracted to 95%. Similar results were observed for other queries and constraints.

Platform: All experiments were performed on a macOS Ventura 13.2 machine with a Apple M2 Max chip, 64 GB memory. The algorithms were implemented using Python3.

Compared algorithms: In the experimental section, we compare three approaches: a baseline method, our fully optimized proposed solution (as detailed in Sec. 5.2), and our proposed solution without optimizations. Each method operates on in-memory data and utilizes provenance expressions to evaluate potential refinements. The baseline approach also uses provenance expressions, as managing data on an external database would be less efficient due
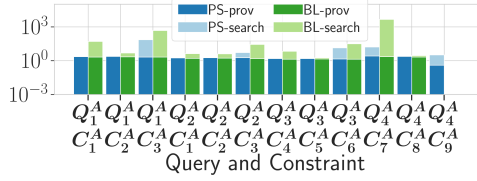
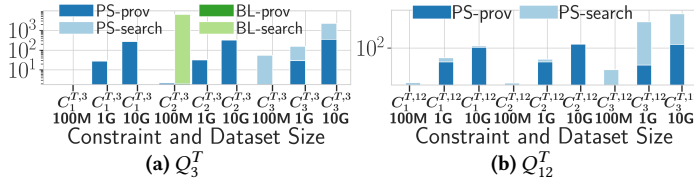**Figure 4: ACSIncome**

Figure 5: Healthcare

(a) Q_3^T

(b) Q_{12}^T

Figure 6: TPC-H benchmark, running time

Figure 7: ACSIncome, number of refinements checked

Figure 8: Healthcare, number of refinements checked

(a) Q_3^T

(b) Q_{12}^T

Figure 9: TPC-H benchmark, number of refinements checked

to multiple I/O accesses. In contrast, our solution only requires a single access to generate provenance inequalities. We begin by comparing our fully optimized proposed solution with the baseline approach. Then, we investigate the impact of various parameters on the performance of our optimized solution. Next, we compare our optimized solution with the non-optimized version. Finally, we contrast our approach with existing work in the field. Here are the three approaches used in the experiments. Note that they all report all minimal refinements, so the quality of results are the same. They differ in efficiency due to different searching strategies.

- **Baseline Algorithm (Baseline).** This naive algorithm, introduced in Section 4, utilizes a provenance model to avoid multiple database accesses. However, it identifies minimal refinements by navigating through all potential refinements.
- **PVL-based Search (PS).** This is Algorithm 1 with all optimizations in Section 5.2 to identify minimal refinements with PVL.
- **PVL-based Search without optimization (PS_no_opt).** This version of our proposed approach is also Algorithm 1, but without the optimizations described in Section 5.

Metrics: We compare the running time and number of possible refinements checked by each algorithm.

6.2 Real-world applications

As mentioned in Section 1, adding cardinality constraints to query results has important real-world applications, particularly where diversity matters. For example, consider a hospital that wants to offer financial assistance to patients in need, specifically those with low incomes, a high number of children, and a high complication rate, using the Healthcare dataset. They execute query Q_2^H (please see Figure 2) to select patients with an income less than 100K, more than 4 children, and more than 5 complications, resulting in 42 out of 887 patients being selected. However, the hospital notices under-representation of certain demographic groups in the query result. Only 17% of the selected patients belong to race2 among the three races, and there are fewer individuals from age group1 compared to other age groups. The hospital worries about
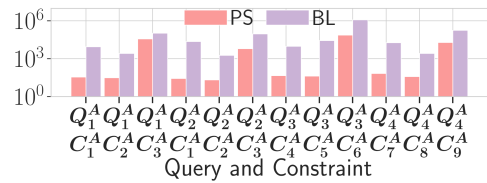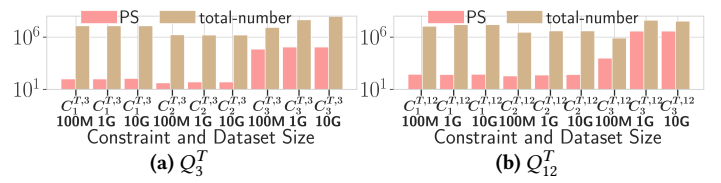
criticism for a financial assistance program that is skewed in this manner. To achieve a more balanced demographic distribution among the recipients of financial assistance, the hospital introduces cardinality constraint C_1^H to relax query Q_2^H, aiming to increase the representation of individuals from these two groups to 105%. Our algorithm provides three methods to minimally refine query Q_2^H: 1) adjusting the lower bound of the number of children to 3, 2) modifying the lower bound of the number of complications to 4, and 3) changing the upper bound of income to 134K. The hospital can choose any of these refinement queries based on their preference. Additionally, the hospital may utilize constraint C_2^H to limit the selection of patients from dominant groups, or combine both approaches, as demonstrated by C_3^H.

6.3 Experiment Results

We first conduct experiments to compare the running time of our algorithm with that of the baseline. Subsequently, we investigate the impact of various parameters on our algorithm's running time by systematically altering them, enabling us to identify the scalability of our algorithm.

Running time. The first set of experiments assesses the running time for different scenarios by executing our algorithm and comparing its running with the baseline naive algorithm. In all tested scenarios, our algorithm outperforms a baseline naive algorithm by more than 100 times, as shown in Figures 4, 5, and 6. The blue bar depicts the running time of our solution (provenance search), and the green bar shows the running time for the baseline algorithm. The dark section represents the provenance generation time, and the light blue section shows the searching time for minimal refinements. The x-axis displays the query and constraint used, while the y-axis shows the running time in seconds. In some experiments the green bar is omitted because the program of baseline approach cannot terminate within a 3-hour time-out. Our solution performs well with various flavors of constraint sets, including relaxation, contraction, and a mix of both, because our solution searches through
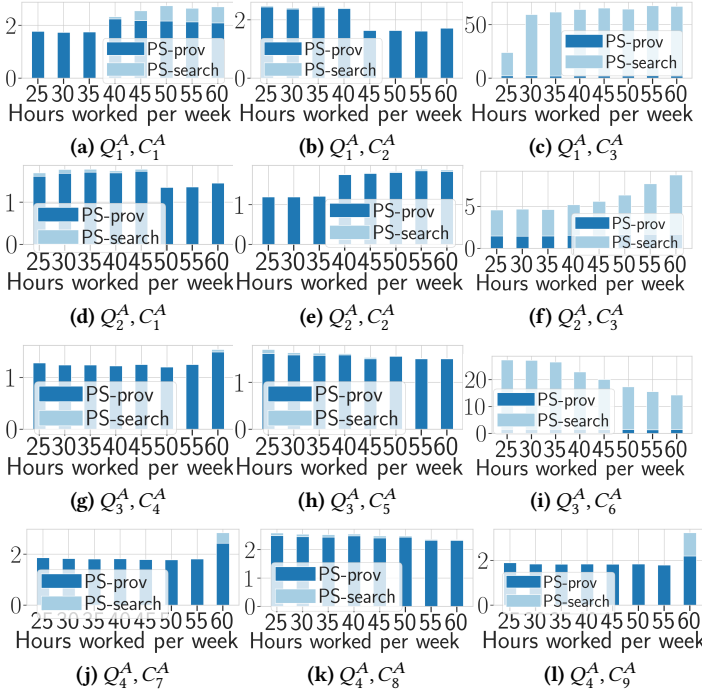
Figure 10: Effect of query selectivity on the running time, ACSIncome data, x-axis shows different constants in a predicate, y-axis is running time (s)
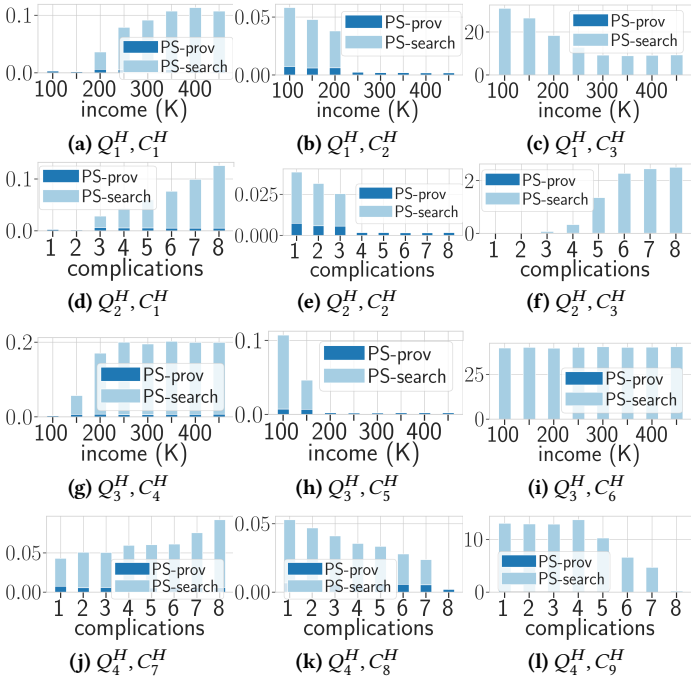

Figure 11: Effect of query selectivity on the running time, Healthcare data, x-axis shows different constants in a predicate, y-axis is running time (s)
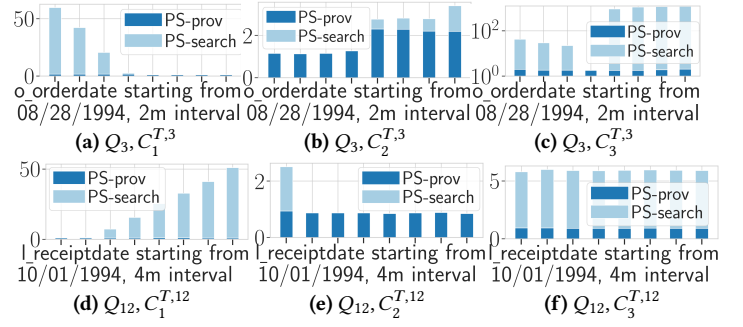

Figure 12: Effect of query selectivity on the running time, TPC-H benchmark, 100M data sizes, x-axis shows different constants in a predicate, y-axis is running time (s)

and the distance between the original query and queries satisfying cardinality constraints, as we demonstrate next.

Running time. The first set of experiments compares the running time of our algorithm with a baseline naive algorithm. In all tested scenarios, our algorithm consistently outperforms the baseline by more than 100 times, as shown in Figures 4, 5, and 6. The blue bar represents the running time of our solution with PVL, while the green bar shows the running time for the baseline algorithm. The dark section represents provenance generation time, and the light section shows the searching time for minimal refinements. In some cases, the green bar is omitted because the baseline approach cannot terminate within a 3-hour time-out. Our solution performs well with various constraint sets, including relaxation, contraction, and a mix of both, due to the efficient search checking fewer refinements using the PVL. The running time for different query-constraint combinations varies significantly due to factors such as the search space and the distance between the original query and queries satisfying cardinality constraints, as demonstrated next.

Data size. We examined the effect of data size on running time using the TPC-H dataset, and present our findings in Figure 6, which shows the running time for data sizes of 100M, 1G, and 10G. Data size affects running time in two primary ways: the time to generate provenance expressions and the search space size. The time needed to generate provenance expressions and assign values to them scales linearly with the data size, while the size of the Provenance Value List (PVL) generally with the number of attribute values in larger datasets. Due to these factors, for each query and constraints pair, we observed a clear trend of increasing running time as the data size increased.

Query Selectivity. To examine the effect of query selectivity, we varied the value of a single constant in the predicate of each query. The results are shown in Figures 10, 11, 12, where the x-axis is the value of the constant in the predicate being varied, and the y-axis is the running time in seconds. Intuitively, the selectivity of the query (with respect to the constraints) determines the search space the algorithm traverses to find refinement queries. When increasing the selectivity, we expect the search space to increase for relaxation, as it starts from refinements close to the original query. Thus we expect to see an increase in the running time, as in Figures 10a, 10e, 10g, 10j, 11a, 11d, 11g, 11j, 12b, 12d. For contraction constraints, we expect to see an opposite trend, as in Figures 10b, 10d, 10h, 10k, 11b, 11e, 11h, 11k, 12a, 12d. In the general
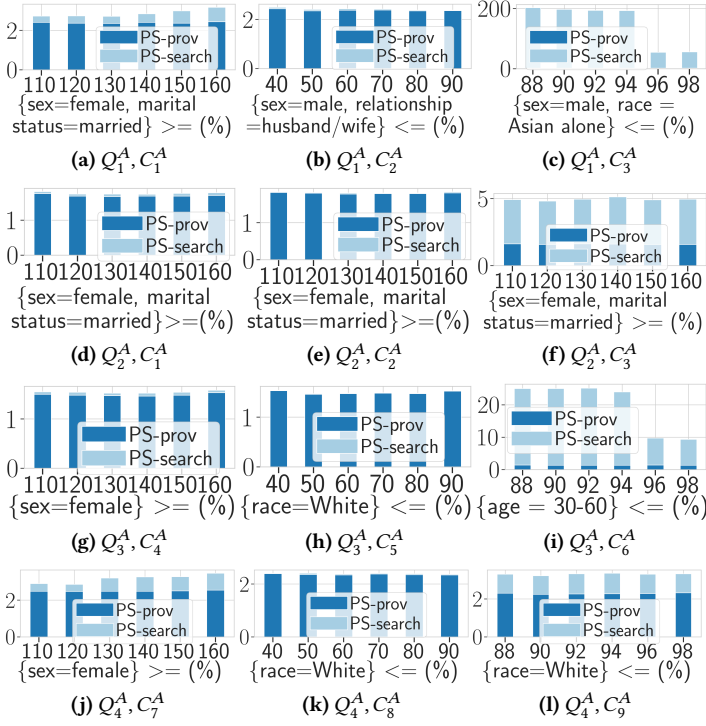
fewer refinements using the PVL. The running time for different query-constraint combinations varies significantly, because the running time is affected by many factors such as the search space

Figure 13: Effect of constraints on the running time, ACSIncome dataset, y-axis is running time (s)

case (constraint set $C_3^A, C_3^H, C_3^{T,3}, C_3^{T,12}$), increasing the constant in a predicate does not affect the size of the provenance expression which contains the entire data, but it does impact the relaxation and contraction constraints in opposite ways, resulting in a trade-off between the constraints. The running time is primarily influenced by the contraction constraint for lower selectivity, while for higher selectivity, it is mainly devoted to meeting the relaxation constraint, so there can be a turning point. A similar trend is observed in Figure 11l, 12c. However, some figures, such as Figure 10c, 10f, 10i, 10l, 11c, 11f, 11i, 12f, display a monotonic increase or decrease without a turning point, which is due to the satisfaction of either the contraction or relaxation constraints dominating the overall running time of the algorithm.

Constraints satisfaction properties. To analyze the effect of the cardinality constraint on the running time, we varied the ratio to which one group is relaxed or contracted in the constraint while keeping the ratio of the other groups unchanged and observed its impact. Specifically, for relaxation constraints, we relax one of the groups to 110%, 120%, 130%, 140%, 150%, 160%; for contraction constraints, we contract one of the groups to 40%, 50%, 60%, 70%, 80%, 90%; and for refinement constraints, we either relax one group to 102%, 104%, 106%, 108%, 110%, 112%, or contract one group to 88%, 90%, 92%, 94%, 96%, 98%. Altering the constant in the cardinality constraint does not affect the size of the Provenance Value List (PVL), as it depends on the dataset, query, and groups definition in constraints rather than constants in constraints. We intuitively expect that as constraints are tightened or relaxed, the running time of algorithms will increase or decrease respectively, as queries satisfying the constraints move further or closer to the original query. Figures 13, 14, and 15 display the results

of these experiments for three datasets. We observed an increase in the running time when constraints were more difficult to satisfy, as in Figure 13a, 13j, 14a, 14c, 14d, 14f, 14g, 14i, 14j, 15a, 15d. Opposite trends are observed in other figures when the queries becomes more and more easy to satisfy. But some figures, like Figure 13b, 13d, 13e, 13f, 13g, 13h, 13k, 13l, 15b, 15e, 15f, exhibit negligible changes in running time when a constraint changes, indicating that the impact of these changes is minor. This can be attributed to the uneven distribution of data groups in the constraints, where adjusting a predicate to a particular value can qualify or disqualify multiple tuples simultaneously, satisfying various relaxation/contraction ratios. This effect is particularly noticeable when there are many tuples with the same value in an attribute, resulting in minimal refinements that are almost the same for different relaxation/contraction ratios.

Effect of optimizations. To assess the impact of the optimizations for the searching algorithm described in Section 5.2, we conducted experiments using algorithms both with and without optimizations and compared their search times. These optimizations incorporate the use of binary search instead of a top-down traversal when searching for a refinement, exploiting the monotonicity property of queries when all constraints are relaxation constraints or all are contraction constraints. We used queries (Q_1^H, Q_2^H, Q_3^H, Q_4^H, Q_1^A, Q_2^A, Q_3^A, Q_4^A, Q_3^T, Q_{12}^T) and the constraints C_1^H, C_2^H, $C_4^H, C_5^H, C_7^H, C_8^H, C_1^A, C_2^A, C_4^A, C_5^A, C_7^A, C_8^A, C_1^{T,3}, C_2^{T,3}, C_1^{T,12}, C_2^{T,12}$ for the three datasets, and the results are shown in Figure 16. The light blue bar represents the searching time with optimization, and the light orange bar represents the time without optimization. Our results indicate that the optimizations significantly reduced execution times across all tested scenarios and enhance the efficiency of the algorithm with gains of up to 99.87%.

6.4 Comparison with Related Work

We compared our algorithm with the one by Shetiya *et al.* [15], which also addresses group cardinality constraints but with different objectives and settings. Since [15] only supports numerical predicates with a single binary sensitive attribute, all the comparison experiments are conducted in this setting. We use the C++ implementation provided by Shetiya *et al.* [15].

Result comparison. To be consistent with [15] and allow for easy comparison, we use TexasTribune dataset (used by [15]), containing salary information for Texas state employees, to compare the returned results. Our query imposes both upper and lower bounds for the salary attribute (`a.salary >= 10000` and `a.salary <= 20000`), resulting in a gender disparity of 69 with 100 males and 169 females in the result set. For [15], the query selects tuples with salaries in range [10000, 20000]. As for cardinality constraints, we require the gender disparity to be no larger than 62 (90% of the original disparity), resulting in constraint: $|Q(D)_{gender=M} - Q(D)_{gender=F}| \leq 62$. The refinement returned by [15] is a salary range $r_1 = [10135.7, 19701.5]$ (Jaccard similarity 0.95), which is also returned by our algorithm. Additionally, our algorithm returns seven other refinements: $r_2 = [10000, 19629.6]$, $r_3 = [11305.8, 20000]$, $r_4 = [11274.1, 19999.9]$, $r_5 = [11205.2, 19999.2]$, $r_6 = [11138.4, 19759.9]$,
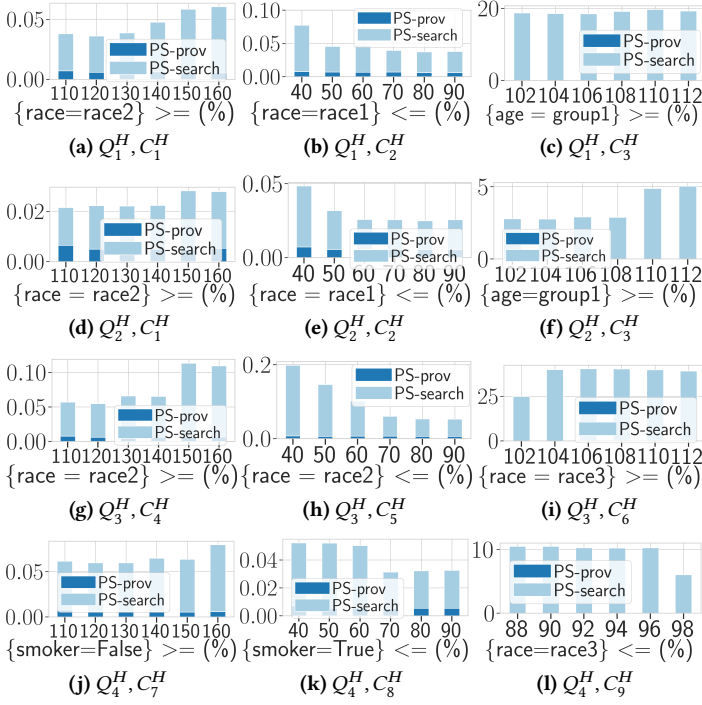
(a) Q_1^H, C_1^H (b) Q_1^H, C_2^H (c) Q_1^H, C_3^H

(d) Q_2^H, C_1^H (e) Q_2^H, C_2^H (f) Q_2^H, C_3^H

(g) Q_3^H, C_4^H (h) Q_3^H, C_5^H (i) Q_3^H, C_6^H

(j) Q_4^H, C_7^H (k) Q_4^H, C_8^H (l) Q_4^H, C_9^H

Figure 14: Effect of constraints on the running time, Healthcare dataset, y-axis is running time (s)

(a) $Q_3^T, C_1^{T,3}$ (b) $Q_3^T, C_2^{T,3}$ (c) $Q_3^T, C_3^{T,3}$

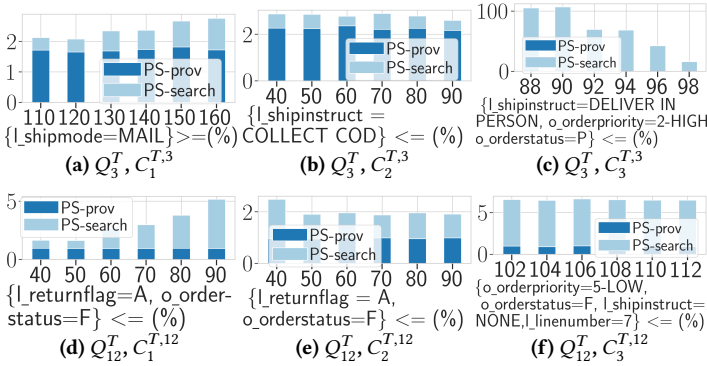(d) $Q_{12}^T, C_1^{T,12}$ (e) $Q_{12}^T, C_2^{T,12}$ (f) $Q_{12}^T, C_3^{T,12}$

Figure 15: Effect of constraints on the running time, TPC-H benchmark, x-axis shows how much groups are relaxed/contracted, y-axis is running time (s)

$r_7 = [11036.2, 19723.8]$, and $r_8 = [10764.0, 19705.7]$ (Jaccard similarity 0.95, 0.90, 0.90, 0.90, 0.88, 0.89, 0.91, respectively). All the returned refinements are minimal. The differences in the results are due to the different minimality definitions: distance between queries v.s. distance in the result sets. Our definition of minimality allows the user to select the most suitable refinement based on their preferences. For instance, if the user prefers to minimize changes to the lower bound of the salary, r_2 would be the best refinement with the same best Jaccard similarity as r_1, but it would be ignored by [15].

Running time comparison. To compare the running time of the two algorithms, considering [15] uses different algorithms for single-attribute and multiple-attribute queries, we employ both

the one-dimensional TexasTribune dataset used earlier and a two-dimensional uniform dataset from [15]. The uniform dataset consists of 10,000 points uniformly sampled within a square of length 1,000 units, with two numerical attributes (x and y) and a sensitive attribute (color). For each dataset, we use two queries with different disparities. For TexasTribune dataset, we use queries 1) selecting salary $\in [5000, 15000]$, with a disparity of 62, and 2) selecting salary $\in [10000, 20000]$, with a disparity of 69. For uniform dataset, we use queries 1) selecting records with $x \in [400, 600]$ and $y \in [400, 600]$, with a disparity of 30, and 2) selecting records with $x \in [550, 700]$ and $y \in [550, 700]$, with a disparity of 35. We evaluate the running time for different original queries, setting target disparities at 80%, 70%, 60%, 50%, 40%, 30%, 20% of the original disparity as cardinality constraints. Figures 17 presents the comparison results with 1-attribute and 2-attribute queries, with the x-axis representing the target disparity and the y-axis showing the execution time. To account for the possibility of our algorithm outputting more than one refinement, the figures have the bar labeled PVL-first, representing the time to find the first minimal refinement using our algorithm, in comparison with [15]. In general, the running time increases as the target disparities become smaller, as satisfying harder constraints takes more time. For single-attribute queries, the running time of [15] remains stable as disparity has small impact on their algorithm, which mainly depends on data size. In most cases, PVL-first and [15] exhibit comparable running times, with the same order of magnitude, indicating similar efficiency in finding the first minimal refinement. However, there is an exception in multiple-attribute queries, where [15] is much faster when the target disparity is high (90% or 80% of the original), but even in this situation, both algorithms finish within 3 seconds. It is worth noting that besides comparable execution times in the covered settings of [15], our algorithm handles multiple relations, constraints, and non-binary sensitive attributes, providing more versatility than the compared approach of [15]. Additionally, our algorithm includes further optimizations to improve efficiency in some situations, as discussed in Section 5.2.

7 RELATED WORK

We next overview multiple lines of related work.

Query refinement. The problem of query refinement has been addressed in previous studies such as [4, 5, 15, 19–22]. They focus on modifying queries to satisfy cardinality constraints, mostly emphasizing the overall output size rather than specific data groups within the output. For example, [5, 19] aim to relax queries with an empty result set to produce some answers. Other works like [4, 20] address the issues of too many or too few answers by refining queries to meet specific cardinality constraints on the result's size. An exception is the recent work by Shetiya et al.[15], which aims to refine queries to satisfy constraints on the size of specific data groups in the result. We discuss and demonstrate the differences in Section6.4. Other related work by [23, 24] aims to satisfy cardinality constraints through minimal query refinement but does not consider categorical attributes and provides only cardinality estimations without exact results. Furthermore, the work of [21, 22] studies the problem of explaining missing tuples in the query result through query refinement. A key difference is that [21, 22] aim
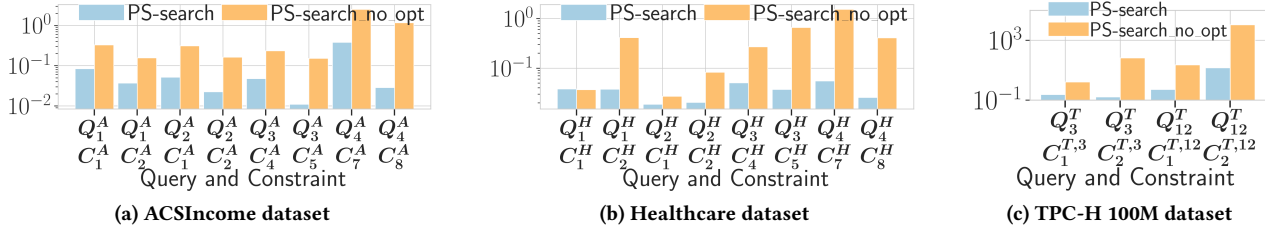
(a) ACSIncome dataset   (b) Healthcare dataset   (c) TPC-H 100M dataset

Figure 16: Effect of optimizations on the searching time, y-axis is searching time (s)
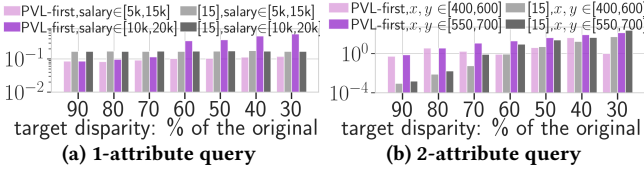

(a) 1-attribute query   (b) 2-attribute query

Figure 17: Comparison between [15] and our PVL-based searching algorithm, y-axis is running time (s)

to include user-specified missing tuples in the result set through refinement, rather than imposing constraints over groups, where including or removing tuples not specified by the user may apply.

Query result diversification. Query result diversification is another related topic aiming to increase result diversity while maintaining relevance of results to the original query [25–28]. In some settings, relevance and diversity are tradeoffs [29], and in others, user information is used to select the result set. However, there are two main differences between this line of research and our approach. First, query result diversification involves ranking items based on their relevance to the query, aiming to select items that are ranked as high as possible and, at the same time, as diverse as possible. In contrast, our approach does not involve ranking: an item is either selected or not based on the query. Second, while query result diversification explores item selection based on the given query but without modifying the query, our approach achieves result diversity through query refinement itself.

Provenance. Data provenance has been studied extensively in recent years. An early approach to user provenance for RDBMS [30, 31] finds a set of tuples that contribute to a certain output tuple. The model proposed in [32] collects contributing input tuples separately for each step in the derivation of the output tuple so that it shows how the output is obtained. Then a general framework proposed in [13] introduced tuple annotations using a semiring K to evaluate queries over annotated relations. The Caravan system [6] enables efficient what-if analysis by creating provisioned representations for hypothetical reasoning, eliminating the need to access original data or execute complex queries. MONDRIAN [33] proposes an annotation-oriented data model, facilitating manipulation and querying of both data and annotations. It allows annotations to be specified on sets of values, thus enabling efficient querying of information based on their association. Glavic et al. [34] outlined a propagation-based method for provenance generation through operator instrumentation. Their approach modifies operators to generate and transfer detailed provenance information across the query network. Our provenance model is inspired by [6], with tuple annotations propagated through query valuation as in [13].

Fairness constraints in other settings. While our work does not only apply to fairness context, fairness is an important topic in data selection and there are many prior works focusing on satisfying fairness constraints in some settings. Some works aim to satisfy fairness constraints under a certain diversity model [35–37], and others focus on fairness constraints in the optimization of an additive utility [38]. There is also some work on fairness in set selection and ranking [39], fairness in classification [40], and diversity in top-k results [41–43]. Other works consider constraint query languages [44], presenting a declarative language with extensions to SQL to support fairness constraints in queries [45].

8 CONCLUSION AND FUTURE WORK

In this paper, we address the problem of finding all minimal refinements of a given query that satisfy specific cardinality constraints for data groups within the result set. Unlike many previous studies that primarily examine query refinement based on the overall result set size, our focus lies in satisfying size constraints for specific data groups within the result set. Furthermore, our approach extends beyond existing research by supporting a wider range of queries and constraints. Specifically, we enable SPJ queries that involve multiple constraints on multiple relations, encompassing sensitive attributes that are more than binary, and supporting both query relaxations and query contractions. To achieve this, we have proposed a solution that uses a provenance model to annotate tuples in the source data with the necessary predicate information. The cardinality constraints are translated into algebraic expressions, allowing for efficient verification of constraint satisfaction without accessing the original data. Furthermore, we also propose a search algorithm that efficiently explores the search space and finds potential refinements, which are then verified using our proposed provenance-based approach. Experimental results demonstrate the effectiveness and efficiency of our solution on a variety of datasets and constraints. For future work, it would be beneficial to investigate the general applicability of the proposed approach to other SQL clauses. For instance, queries involving NOT operators would require searching the complementary space. Moreover, queries combining ranges with both AND and OR operators would translate provenance expressions that incorporate both logical AND and OR operations. We left these for future research.

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