Discovering Multi-Table Functional Dependencies Without Full Join Computation

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Abstract

In this paper, we study the problem of discovering join FDs, i.e., functional dependencies (FDs) that hold on multiple joined tables. We leverage local inferencing, selective mining, and sampling and show that we can discover most of the exact join FDs from the single tables participating to the join and avoid the full computation of the join result. We propose algorithms to speed-up the join FD discovery process and mine FDs on the fly only from necessary data partitions. We introduce JEDI (Join Dependency Discovery), our solution to discover join FDs without computation of the full join beforehand. Our experiments on a range of real-world and synthetic data demonstrate the benefits of our method over existing FD discovery methods that need to precompute the join results before discovering the FDs. We show that the performance depends on the cardinalities and coverage of the join attribute values: for join operations with low coverage, JEDI with selective mining outperforms the competing methods using the straightforward approach of full join computation by one order of magnitude in terms of runtime and can discover three-quarters of the exact join FDs using mainly local inference in half of its total execution time on average. For higher join coverage, JEDI with sampling reaches precision of 1 with only 63% of the table input size on average.

1 Introduction

The problem of computing all functional dependencies (FDs) that hold on a given relational table has received much attention from the academia and the industry due to numerous application demands. FDs capture deterministic relations between attributes of a database. Typically, an FD \( X \rightarrow Y \) with column sets \( X \) and \( Y \) in a given table expresses that the combination of values in \( X \) columns uniquely determines the value of every column in \( Y \). This can be of critical use for the database design process, table decomposition, database normalization, and for many data management applications, such as data cleaning [25], data profiling [4], and query optimization [10, 23]. Although FDs are essential for many aspects of database management, the problem of discovering FDs in an entire database with multiple joined tables has been considered so far only by computing FDs from single tables in isolation without much investigation on the effect of the join operation on FD discovery. Trivially, one can compute the join results between multiple tables beforehand and then run an existing method to discover FDs. However, such computation could be significantly reduced by inferring FDs from each separate table and computing the join result only when and with what is needed. In this paper, we address the problem of frugal computation of join FDs and rename it as the Join FD discovery problem that aims at finding FDs that hold on the join result of multiple relational tables without computing the full join operations.

The Join FD discovery problem is interesting for many reasons: (1) Join FDs can be used to assess whether the FDs discovered from a single table are meaningful for the entire database when they still hold in the join results of multiple tables. Inversely, join FDs can be used to prune the set of FDs discovered from a single table when they are not persistent across the joined tables. In certain cases, they may hold incidentally on a single table due to some data errors or table incompleteness; (2) New FDs can be discovered through join operations and they can be useful for database administration, query optimization [23], and other applications. Therefore, it is beneficial to discover them efficiently; and (3) Most join FDs can be inferred from the single tables participating to the join. This can save computation time since there is no need to compute the join result entirely before FD discovery. To address the Join FD discovery problem, we combine three strategies in one approach: logical inference, selective mining (with vertical data partitions), and selective sampling (with horizontal partitions) for FD discovery and we propose JEDI, an efficient solution for automatically discovering multi-table join FDs with frugal computation, rather than the trivial and costly approach of computing the result of a join operation tables before FD discovery.

Challenges. The first challenge is the exponential complexity of join FD discovery. The straightforward approach is very costly for two reasons: (1) the numbers of attributes of the tables participating in the join are added. Many of the existing methods exhibit poor scalability as the number of attributes increases (despite the efficiency of their pruning methods to search over the lattice of attribute combinations). This problem is already well-known for FD discovery from a single table [14] but is amplified in the join FD discovery problem; and (2) the execution times of the join and the FD discovery are also cumulated.

As a second challenge, real-world data sets are plagued with missing or erroneous values that may lead to spurious FDs or low recall in terms of genuine FDs [1]. More particularly, the problem of fully missing records has not been much investigated although it may have a significant impact on the validity of the FD discovery results. We can also observe disparate value cardinalities in the join attributes of the participating tables. The assumption of Preservation of Join Value Sets [7] is often violated due to many "dangling tuples", that is, for \( R \approx S \), tuples of \( R \) that join with no tuple of \( S \) (and inversely). Moreover, some join attribute values (e.g., keys) may be repeated and joined multiple times. Because of these disparities and partial coverage, the union of the FD sets obtained from single tables is not equivalent to the FD set obtained from the join result.
Finally, pruning the join FD search space efficiently is challenging. Existing methods identify minimal FDs from a single table. However, minimality does not guarantee that the set of discovered FDs will be parsimonious [14, 28] and minimal FDs from single tables are not necessarily minimal multi-table FDs. In this paper, we propose the first approach that discovers efficiently join FDs from multiple tables of a database.

The main contributions of our paper are the following:

- We demonstrate several useful properties for inferring exact FDs that can be obtained from various join operators between two tables (i.e., inner join, left and right semi-joins, left and right outer joins) without computing the full join result beforehand;
- We propose four algorithms that leverage these properties, and efficiently compute the exact FDs from two or more tables without computing full joins;
- We propose JEDI, a system implementing our algorithms. JEDI is available at https://github.com/xxxx with code, scripts, and data sets for the reproducibility of our experiments;
- We provide the results of an extensive experimental evaluation: we compare JEDI against three state-of-the-art FD discovery methods over a diverse array of real-world and synthetic data sets with varying numbers of tuples, attributes, domain sizes, types, and coverage of the join operations. We find that JEDI outperforms the competing methods by one order of magnitude in terms of execution time for discovering exact FDs while preserving the smallest memory consumption on average.

Outline. Section 2 presents an illustrative example. Section presents the necessary background and notations. In Section 3, we formalize the Join FD discovery problem and provide an overview of JEDI. In Section 4, we present our main contributions as the algorithms at the core of JEDI. We describe our performance experiments evaluating the efficiency and precision of JEDI in Section 5. Finally, we discuss related work in Section 6 and conclude in Section 7.

2 AN ILLUSTRATIVE EXAMPLE

To motivate our approach, we consider the following example illustrated in Figure 1. Samples of two tables are extracted from the clinical database MIMIC-III\(^1\) [11]: PATIENT table contains information of 5 patients: their identifier (subject_id), gender, date of birth (dob), date of death (dod), and expire_flag. ADMISSION table contains some administrative and clinical information about each patient such as the hospital admission time (admittime), the admission location (admission_location), the insurance, the diagnosis, and h_expire_flag indicating whether the patient died at the hospital. The table contains 10 admission records. We can opt for the NULL semantics where missing values are all equal and extract exact FDs from each table. We obtain 9 exact FDs for PATIENT and 14 exact FDs for ADMISSION. The figure also shows relevant approximate FDs (with degree \(\alpha = 1\)) from both tables. In addition, the figure presents the join result of the two tables over the join attribute subject_id. In our example, 42 exact minimal and canonical FDs can be discovered from the join result. Interestingly, we can observe that the 9 exact FDs from the PATIENT table in the left side of the join are preserved (in green), as well as 9 (out of the 14) exact FDs from the ADMISSION table (in pink). Additionally, 10 FDs discovered from the join result can be obtained by inference between the sets of exact FDs discovered respectively from each single table (in blue). For example, admittime \(\rightarrow\) dob is obtained from admittime \(\rightarrow\) subject_id in ADMISSION and subject_id \(\rightarrow\) dob in PATIENT. In the PATIENT table, the subject_id values are unique, whereas in the ADMISSION table, we can observe two repeated records for patients #252 and #249. Moreover, the patient #257 is absent in the ADMISSION table, whereas s/he is present in the table PATIENT, similarly patient #247 is absent in the PATIENT table but present in the ADMISSION table. Due to these cardinality disparities in the domain of the join attribute subject_id, some approximate FDs discovered from the single tables can become exact FDs in the join result (we will use the term “upstaged” AFDs in the rest of the paper) as it is the case for 4 join FDs in the join result (in grey). The approximation degree \(\alpha\) means that \(\alpha\) tuples violate the exact FD. In the case of the AFD expire_flag \(\rightarrow\) dod in PATIENT table, removing one tuple, either patient #257 or patient #250 will make the AFD

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\(^1\)https://physionet.org/content/mimiciii/1.4/
become exact. When the two tables are joined, patient #257 is removed due to the absence of the corresponding subject_id value in the ADMISSION table. The same phenomenon occurs for the 3 AFDs with approximation degree 1 discovered from the ADMISSION table, namely: diagnosis → subject_id, diagnosis → insurance, and diagnosis → admission_location. We note that the 5 remaining exact FDs from the ADMISSION table are reduced to minimal exact FDs in the set of FDs discovered from the join result. Finally, 10 exact FDs (in orange) that hold over the entire join result have to be discovered from the join result. However, if we join the two tables partially, only with the following combinations of tuples: [(#249, #252) or (#249, #251)] and [(#250, #251) or (#250, #252)], we can obtain the remaining 10 join FDs without the full join computation. Note that finding semantically correct FDs is orthogonal to our work and still an open problem for FD discovery from single tables: e.g., dob → dod discovered from PATIENT and admittime → diagnosis from ADMISSION, both also present in the join result, are not semantically correct. All FDs (from single or multiple tables) must be validated by domain experts before they can be used by downstream applications. Similarly, AFDs can be either semantically incorrect (e.g., diagnosis → insurance) or correct (e.g., expire_flag → dod) and can only surface as exact FDs in a join result due to errors in the single tables. Moreover, we would like to point out that these observations can be made regardless of the NULL semantics. A better understanding of the mechanisms underlying the appearance of FDs in multi-table settings is hence needed. Based on these observations, the questions that motivated our work were the following: Instead of fully computing the join result before FD discovery, can we infer most of the FDs and accelerate the overall computation? Do we need to compute the full join anyway? How can we select the necessary tuples and attributes in a principled way?

The rest of the paper will attempt to answer these questions and propose efficient solutions as parts of our JEDI framework for discovering join FDs from multiple relational tables.

3 PRELIMINARIES

Next, we recall the necessary definitions of FDs and join operators with their application to our problem.

Definition 1 (Functional dependency satisfaction). Let I be an instance over a relation R, and X, Y be two sets of attributes from R. I satisfies a functional dependency d : X → Y, denoted by I ⊨ d if and only if:
\[ \forall t_1, t_2 \in I. t_1[X] = t_2[X] \Rightarrow t_1[Y] = t_2[Y]. \] (1)

Definition 2 (Logical implication between FDs). Let R be a relation, and X, Y, Z be three sets of attributes from R. Then a functional dependency d : X → Z logically implies a functional dependency d' : Y → Z if, and only if, for every instance I over R:
\[ I \models d \text{ implies that } I \models d'. \] (2)

Definition 3 (Approximate functional dependency). The approximate functional dependency (AFD), also called partial FD, denoted a : X → Y of a functional dependency between X and Y that holds if and only if the minimum fraction of tuples at most equal to e is removed from the relation such that X → Y can hold.

The minimal fraction of tuples is computed as
\[ e(X \rightarrow Y) = 1 - \sum_{c \in \mathcal{X}} \frac{\max \{c'[|c' \in \pi_X \mathit{Y} \text{ and } c' \subseteq c]\}}{|R|} \] (3)

with \( \mathcal{X} \) the set of equivalence classes defining a partition of R under X, \( \pi_X = \{|t| t \in R\} \). The equivalence class of a tuple t ∈ R with respect to a given set X ⊆ R is \( t|X = \{u \in R | t[A] = u[A] \forall A \in X\} \).

Next, we provide the definition of the natural join. Let us consider S and T, two relations with at least one common attribute; L and R, two instances over the relations S and T, respectively; atts( ), a function taking an relational instance as input and returning its set of attributes. The set of common attributes between S and T is denoted \( X = \text{atts}(L) \cap \text{atts}(R) \).

Definition 4 (Natural join). The natural join between L and R, denoted by \( L \Join R \), is the instance such that:
• \( \forall t \in L \Join R, t \in (L \times R) \)
• \( \forall t \in L \ Join R \) there exists two tuples \( t_L \in L \) and \( t_R \in R \) such that \( t_L[ atts(L) ] = t_R[ atts(R) ] \) \( \wedge (\pi_X(t_L) = \pi_X(t_R)) \).

We recall the definitions of left and right semi-joins.

Definition 5 (Semi-join). The left and right semi-joins between L and R, denoted by \( L \bowtie_R L \) and \( L \bowtie_L R \) respectively, are the instances such that \( L \bowtie_R L = \text{atts}(L)(L \bowtie_R L) \) and \( L \bowtie_L R = \text{atts}(R)(L \bowtie_L R) \).

In the case of relational instances without common attributes, the equi-join operator can be used. The equi-join operator is defined as follows.

Definition 6 (Equi-join). Let a ∈ atts(L) and b ∈ atts(R) be two attributes. The equi-join between L and R on a = b, denoted by \( L \bowtie_{a=b} R \), is the instance such that \( \forall t \in L \bowtie_{a=b} R, \) there exists two tuples \( t_L \in L \) and \( t_R \in R \) such that \( t_L[a] = t_R[b] \) = \( t_R[a] = t_R[b] \).

Finally, we recall the definitions of left and right outer joins as follows.

Definition 7 (Left outer join). Let v represent the null value. The left outer join between L and R, denoted by \( L \bowtie L \), is the instance such that \( L \bowtie L = \{t | t \in (L \bowtie R) \cup (L \bowtie \{\pi_{atts(L)}(L) \bowtie \{t \mid v, \ldots, v\})\} \) = \( L \bowtie L = \{t | t \in (L \bowtie R) \cup (L \bowtie \{\pi_{atts(L)}(L) \bowtie \{t \mid v, \ldots, v\})\} \)

Definition 8 (Right outer join). The right outer join between L and R, denoted by \( L \bowtie L \), is the instance such that:
\( L \bowtie L = \{t | t \in (L \bowtie R) \cup (L \bowtie \{\pi_{atts(L)}(L) \bowtie \{t \mid v, \ldots, v\})\} \) = \( L \bowtie L = \{t | t \in (L \bowtie R) \cup (L \bowtie \{\pi_{atts(L)}(L) \bowtie \{t \mid v, \ldots, v\})\} \)

From the previous definitions, we can define the notion of full outer join as follows.

Definition 9 (Full outer join). The right outer join between L and R, denoted by \( L \bowtie L \), is the instance such that:
\( L \bowtie L = (L \bowtie L) \cup (L \bowtie R) \).

4 EFFICIENT DISCOVERY OF JOIN FDs

In this section, we describe the problem we address and explain how we can infer and compute FDs that remain valid through a join operation with frugal computation. First, we focus on the FDs discovered from single relations separately, then we consider the FDs between attributes coming from the two (or more) joined relations.
We propose the workflow illustrated in Figure 2. It consists in three steps corresponding to: (1) Discovery of approximate single-table FDs that are upstaged and become exact FDs via the join operation (JEDI step 1); (2) Logical inference and minimality reduction of join FDs (JEDI step 2); and (3) Computation of the remaining join FDs from partial join over selective mining or sampling (JEDI step 3). The steps are detailed in the next sections.

4.1 From AFDs to Exact FDs Through Join

New FDs may appear mechanically due to the join operation when tuples from one table cannot be joined with their counterpart in the other table, i.e., when some join attribute values are missing in one of the tables. In certain cases, FDs that were approximate in a single table become exact in the join result. This mechanism is expressed more formally in the following theorem:

**Theorem 2 (Join FDs from Upstaged AFDs).** Let $L$ and $R$ be two instances over relations $S$ and $T$, respectively, and $D_L$ and $D_R$ be the two sets of all FDs such that $L \models D_L$ and $R \models D_R$, respectively. Then the sets of upstaged FDs denoted $D_L^{\text{new}}$ and $D_R^{\text{new}}$ are the sets:

$$D_L^{\text{new}} = \{d \mid d \notin D_L \land (L \otimes_X Y \models \pi_Y(R)) \models d \}$$

and

$$D_R^{\text{new}} = \{d \mid d \notin D_R \land (\pi_X(L) \otimes_X Y R) \models d \}$$

**Example 1.** To illustrate the case of upstaged AFDs using the example of Figure 1, let us consider the NULL semantics where all null values are identical. The approximate FD $\text{expire}_{\text{flag}} \rightarrow 1$ does not violate the FD. However, in the join result of $\text{PATIENT \#subject}_{\text{id}}$ $\text{ADMISSION}$, the violating tuple $\#257$ has no counterpart in the ADMISSION table and it disappears from the join result. Consequently, the FD $\text{expire}_{\text{flag}} \rightarrow d$ becomes exact in the join result.

To compute join FDs from upstaged AFDs, we propose Algorithm 1. Lines 2–10 handle the inputs of the user if $s$ he can provide FDs and/or AFDs for each table participating in the join operation. If not, exact FDs are computed from each single table. For each side of the join, if exact FDs have been provided, the subroutine upstagedFDs is executed (lines 8 and 12) and computes partially the join only with the join attributes from the left side table (line 12) to check the assumption of the join value set preservation [7]. If the assumption is violated (i.e., if some tuples have been deleted through the join operation (line 13)), some upstaged join FDs are produced. The subroutine discovers the FDs in the input instance by taking into account the previously discovered FDs and improves the pruning (line 17 of upstagedFDs). On the other hand, if AFDs are provided as inputs of Algorithm 1 (lines 5–6 and 25), the subroutine upstagedAFDs will check for each AFD if the join of its set of violating tuples with the instance from the other side of the join leads to an empty instance (line 26). In this case, the AFD becomes exact in the joined instance and thus is added to the output set of exact FDs. In this algorithm, the computation is performed over one table at a time, and not over the complete join result. Thus, the FD discovery focuses on FDs whose attributes belong to one joined table only. Next, we discover the FDs containing attributes from both instances by relying on the characteristics of the join and on the FDs discovered previously.

4.2 Exact FDs from Joined Tables

Other join FDs are FDs containing attributes from the result of a join operation between multiple tables. Compared to the previous join FDs from upstaged AFDs, they will include a mix of attributes coming from each table participating in the join. Their definition is formalized as follows.
Algorithm 1: Find Join FDs from Upstaged AFDs

**Input:** L and R, two relational instances; X and Y, the sets of join attributes for L and R respectively; \( \oplus \in [\leq, \prec, \times, \geq, \succ, =] \) the join operator.

**Optional Input:** \( D_L \) and \( D_R \), the sets of AFDs or exact FDs over L and R respectively.

**Result:** the FD sets \( D_{LUP} \) and \( D_{RUP} \)

1. \( D_{LUP} \), \( D_{RUP} \) \( \leftarrow \) \( \emptyset \);
2. for each pair of instances \((i, j) \in \{(L, R); (R, L)\}\) do
   3. if \( D_i \) is not provided then
      4. \( D_i \) \( \leftarrow \) computeFDs(i);
   5. if \( D_i \) contains AFDs then
       6. \( D_{iUP} \) \( \leftarrow \) upstagedAFDs(i, j, X, Y, \( D_i \));
     else
        7. \( D_{iUP} \) \( \leftarrow \) upstagedAFDs(i, j, X, Y, \( D_i \));
   8. end
9. \( D_{cand} \) \( \leftarrow \) generate candidate FDs for first level of \( I_{join} \);
   10. repeat
       11. prune FDs in \( D_{cand} \) logically implied by FDs in \( D_{out} \);
       12. prune FDs in \( D_{cand} \) logically implied by FDs in \( D \);
       13. add to \( D_{out} \) the FDs from \( D_{cand} \) holding in \( I \);
       14. \( D_{cand} \) \( \leftarrow \) generate candidate FDs for next level;
    until \( D_{cand} \) \( = \) \( \emptyset \);
15. return \( D_{out} \)

16. Subroutine upstagedAFDs(I, J, X, Y, D)
17. \( D_{out} \) \( \leftarrow \) \( \emptyset \);
18. for \( d \in D \) do
19. \( V \) \( \leftarrow \) get violating tuples for \( d \) in \( I \);
20. if \( V \cap \pi_X \pi_Y (J) = \emptyset \) then
       21. add \( d \) to \( D_{out} \);
22. prune FDs in \( D_{out} \) implied by each others return \( D_{out} \)

Definition 10. Let L and R be two instances over relations S and T, respectively. An FD d is said to be multi-table and specific to the joined instance \( L \otimes X \rightarrow Y \) if \( d \) holds in \( L \otimes X \rightarrow Y \); and \( d \) contains at least one attribute occurring in \( \text{atts}(L) \setminus \text{atts}(R) \) and one attribute occurring in \( \text{atts}(R) \setminus Y \).

Example 2. In our example of Figure 1, FDs specific to the joined result are highlighted in orange. For example, gender, h_expire_flag \( \rightarrow \) insurance is specific to the join of Patient and Admission. It holds in PATIENT \( \models \) ADMISSION. Attributes gender and expire_flag come from PATIENT and attribute insurance comes from ADMISSION.

Next, we consider the case of FDs that have all attributes in their left-hand side coming from only one relational instance and we prove several interesting properties about these logically inferable FDs. Then, we examine the properties of multi-table join FDs with left-hand side attributes obtained from both initial instances.

4.2.1 Logically inferable join FDs. We will now show that the join FDs with left-hand side (1hs) attributes coming from only one initial instance can be deduced from the sets of FDs over the initial instances. To prove the theorem, we first state the following lemma showing that an FD with 1hs attributes coming from only one single instance cannot exist if their right-hand side (rhs) is not functionally defined by the set of join attributes.

Theorem 3. Let L and R be two instances over relations S and T, respectively. Let \( L \otimes X \rightarrow Y \) be a join result with \( X \subseteq \text{atts}(L), Y \subseteq \text{atts}(R) \). For all \( A \subseteq \text{atts}(L) \setminus X \) and \( B \subseteq \text{atts}(R) \setminus Y \):

- if \( L \otimes X \rightarrow Y \not\models X \rightarrow B \) then \( L \otimes X \rightarrow Y \not\models A \rightarrow B \)

Sketch. Let \( x_1, \ldots, x_n \) being values over the attributes in X, and \( b_1, \ldots, b_m, b'_1, \ldots, b'_m \) being values over the attributes in B. If \( L \otimes X \rightarrow Y \not\models X \rightarrow B \) then there exist two tuples:

- \( t_R(x_1, \ldots, x_n, b_1, \ldots, b_m, \ldots) \)
- \( t'_R(x_1, \ldots, x_n, b'_1, \ldots, b'_m, \ldots) \)

in R such that: \( \exists i \in \{1, \ldots, n\}, b_i \neq b'_i \) and there exists a tuple \( t_I(x_1, \ldots, x_m, a_1, \ldots, a_k, \ldots) \) in L with \( a_1, \ldots, a_k \), the values of the attributes in A (otherwise, tuples \( t_R \) and \( t'_R \) would have been filtered during the join operation). Thus, the join \( L \otimes X \rightarrow Y \) leads to the two tuples:

- \( t(x_1, \ldots, x_n, a_1, \ldots, a_k, b_1, \ldots, b_m, \ldots) \)
- \( t'(x_1, \ldots, x_n, a_1, \ldots, a_k, b'_1, \ldots, b'_m, \ldots) \)

which violate the FD \( A \rightarrow B \) and \( L \otimes X \rightarrow Y \not\models A \rightarrow B \) \( \Box \)

Example 3. To illustrate the property proved in Theorem 3, we observe that the diagnosis is not determined by the patient identifier in Figure 1, for example patient #249 has been admitted three times for a different pathology each time, i.e.: PATIENT \( \models \) subject_id \( \models \) diagnosis. From Theorem 3, we know that diagnosis in the join result PATIENT \( \models \) subject_id can not be determined by any set of attributes coming from PATIENT table. Such similar inferences may be trivial for the user, but they usually require the knowledge of the attribute semantics. If not encoded, they are difficult to capture by a system. However, the property proved in Lemma 3 can be used to drastically reduce the set of possible FDs that can appear after a join operation.

From our proof of Theorem 3, we can characterize a subset of the set of FDs with 1hs attributes coming from only one initial instance and that hold in the joined instance.

Theorem 4. Let L and R be two instances over relations S and T, respectively. Let \( L \otimes X \rightarrow Y \) be a join result with \( X \subseteq \text{atts}(L), Y \subseteq \text{atts}(R) \). For all \( A \subseteq \text{atts}(L) \setminus X \) and \( B \subseteq \text{atts}(R) \setminus Y \):

- if \( L \otimes X \rightarrow Y \models X \rightarrow B \) then \( L \otimes X \rightarrow Y \models A \rightarrow B \)

Proof. This is trivially proved by transitivity, with the use of Armstrong’s transitivity axiom. \( \Box \)

Example 4. In PATIENT \( \models \) subject_id ADMISSION result illustrated in Figure 1, we observe that the diagnosis determines the date of birth,
4.2.2 FDs with 1hs attributes from multiple tables. Now, we characterize the set of FDs which hold on a join result and such that their 1hs attributes come from both initial instances. We characterize two kinds of FDs with multi-table attributes in 1hs: (1) FDs that can be deduced directly using a simple logical reasoning, and (2) FDs that need to be discovered and validated from the data. For example, gender, expire_flag→insurance of our example has attributes from PATIENT in 1hs and attributes from ADMISSION in rhs and it cannot be inferred logically. Other FDs with the same properties are illustrated in orange in Figure 1. In the following theorem, we show that if 1hs attributes of an FD come from the instances participating in the join, then we cannot predict their validity without checking them directly with some representative (if not all) tuples of the join result:

**Theorem 5.** Let L and R be two instances over relations S and T, respectively. Let \( L \odot X = Y R \) be a join result with \( X \subseteq \text{atts}(L) \), \( Y \subseteq \text{atts}(R) \). We cannot guarantee that all FDs over \( L \odot X = Y R \) can be inferred from Armstrong’s axioms over the FDs over L and R taken separately.

**Proof.** In the two following instances L and R, we can see that only the FDs \( YA’ \rightarrow b \) and \( Yb \rightarrow A’ \) hold.

\[
\begin{array}{c|c|c|c|c|c}
L & R & L \odot X = Y R \\
\hline
X & A & Y & A’ & b & X = Y & A’ & b \\
\hline
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 \\
1 & 1 & 1 & 1 & 1 & 0 & 1 & 1 \\
2 & 2 & 2 & 1 & 0 & 1 & 0 & 0 \\
2 & 2 & 1 & 0 & 2 & 1 & 0 & 0 \\
\end{array}
\]

In the join result, the FD \( AA’ \rightarrow b \) holds but it cannot be inferred using Armstrong’s axioms over the FDs discovered from each instance L and R.

This theorem motivates the need for designing a new method for computing FDs from partial join results, as we cannot always infer all the FDs only using logical reasoning. However, we can rely on the following theorem to greatly reduce the number of remaining FDs to check from the data:

**Theorem 6.** Let L and R be two instances over relations S and T, respectively. Let \( L \odot X = Y R \) be a join result with \( X \subseteq \text{atts}(L) \), \( Y \subseteq \text{atts}(R) \). For all \( A \subseteq \text{atts}(L) \), \( A’ \subseteq \text{atts}(R) \) and \( b \in \text{atts}(R) \): If \( L \odot X = Y R \models AA’ \rightarrow b \), Then \( L \odot X = Y R \models YA’ \rightarrow b \).

In-line with Theorem 6, we propose Algorithm 3 for selective mining and use the FDs previously discovered with Algorithms 1 and 2 to compute the remaining join FDs. Intuitively, Theorem 6 shows that a given attribute \( b \) can be a rhs of a remaining join FDs only if we have previously found an FD of the form \( YA \rightarrow b \) with \( Y \) being the join attributes of the instance containing \( b \). Thus, it allows us to focus only on the plausible rhs (lines 6 and 10 in subroutine discover) and explore their candidate 1hs (lines 7-12). In practice, there is no need to generate every candidate FDs initially. Instead, candidate FDs can be explored by generating a first level containing only the smallest candidates and by generating upper levels only when currently evaluated candidates are not valid. Moreover, we can avoid the computation of the full join by deleting a given 1hs attribute \( a \) if \( a \) is not a possible rhs and, for every FD...
Algorithm 3: Discover Join FDs with selective mining

**Input:** L and R, two relational instances; X and Y, the sets of join attributes for L and R respectively; \( D_L \) and \( D_R \), exact FDs sets from L and R; \( D_{L \cap R} \), set of FDs inferred from \( L \bowtie X \sim Y \cdot R \); \( \Delta \in \{\subseteq, \cap, \subset \subseteq, \bowtie \} \) a join operator;

**Result:** \( D_{final} \), the final set of FDs from \( L \bowtie X \sim Y \cdot R \);

\[ D_{out} \leftarrow \text{discover}(L, R, X, Y, D_L, D_R, D_{L \cap R}); \]
\[ D_{final} \leftarrow D_{out} \cup \text{discover}(R, L, Y, D_L, D_{L \cap R}); \]
\[ \text{return} \ D_{final} \]

Subroutine \( \text{discover}(I, J, X, Y, D_I, D_{L \cap R}) \)

\[ \forall J \rightarrow b \in D_J \]
\[ \forall A \subseteq \text{atts}(I) \setminus X \]
\[ \text{if } \exists A' \subseteq A, A' \rightarrow b \in D_{L \cap R} \text{ and } A \rightarrow b \text{ holds in } L \bowtie J \]
\[ \text{add } A \rightarrow b \text{ to } D_{out}; \]
\[ \text{forall } Y' \rightarrow b \in D_J \text{ such that } A' \nrightarrow b \]
\[ \text{if } A \cup A' \rightarrow b \text{ holds in } L \bowtie J \]
\[ \text{add } A \cup A' \rightarrow b \text{ to } D_{out}; \]
\[ \text{return} \ D_{out}; \]

4.2.3 Sampling-based Discovery of Join FDs. As the computation of the join FDs by Algorithm 3 can be expensive both in time and space, we propose Algorithm 4 which relies on selective sampling. To this extent, Algorithm 4 starts with the \( \text{micro_join} \) subroutine that compute FDs from micro-joins only between the tuples from L and R that are selected by the \( \text{selective_sampling} \) subroutine (lines #6 and #19–25). The set of tuple ids to join is generated in the \( \text{generate_ids_set} \) subroutine (lines #23-24, #26-38). It builds a tree where the depth levels correspond to the order of the attributes with the fewest number of distinct values as the first level and \( n_b \), the last level to consider (line #29); the nodes correspond to distinct values per attribute (i.e., level) (line #33). Then, if an attribute value corresponds to a unique tuple for a level less than \( n_b \), the tuple id is selected as the representative tuple of a branch to be considered for the micro-join; if multiple tuples share the same value, \( n_b \) tuples will be selected. Then, for each sample, the instances are joined (line# 9) and the FDs over the resulting instance are computed and added to \( E_{out} \), the set of all computed FDs (lines# 10 and 11). Finally, subroutine \( \text{computeLVLFDs} \) (line# 3) extracts from the set \( E_{out} \) the FDs that are valid in every sample. An FD \( d \) can be considered as valid in a set of FD \( D \) if either (1) there exists a logically equivalent FD in \( D \) or (2) there exists an FD logically implying \( d \) in \( D \). However, we cannot guarantee that an FD discovered from samples is exact in the joined instance without the full exploration. Indeed, for a given FD \( d \), in the worst case, the projection of \( L \bowtie R \) over the attributes in \( d \) needs to be explored to check the non-existence of a pair of tuples violating \( d \). We refer to [5] for a formal proof of the NP-completeness of finding minimal FDs.

Algorithm 4: Sampling-based discovery of Join FDs

**Input:** L and R, two instances; X and Y, the sets of join attributes for L and R respectively; \( D_L \) and \( D_R \), exact FDs sets of L and R; \( \Delta \in \{\subseteq, \cap, \subset \subseteq, \bowtie \} \) a join operator;

**Result:** \( D_{out} \), the FDs over \( L \bowtie X \sim Y \cdot R \);

\[ E_D, P \leftarrow \emptyset; \]
\[ E_D \leftarrow \text{micro_join}(L, R, X, Y, n_b, n_o); \]
\[ D_{out} \leftarrow \text{compute_FDs}(E_D); \]
\[ \text{return} \ D_{out}; \]

Subroutine \( \text{micro_join}(L, R, X, Y, n_b, n_o) \)

\[ \text{ids} \leftarrow \text{selective_sampling}(L, R, n_b, n_o); \]
\[ P \leftarrow (\sigma_{X \in \text{ids}}(L), \sigma_{Y \in \text{ids}}(R)); \]
\[ \text{forall } (L_i, R_i) \in P \]
\[ J_i \leftarrow L_i \cup R_i; \]
\[ D_i \leftarrow \text{compute exact FDs over } J_i; \]
\[ \text{add } D_i \text{ to } E_D; \]
\[ \text{return} E_D; \]

Subroutine \( \text{compute_FDs}(\{D_1; \ldots; D_n\}) \)

\[ D_{out} \leftarrow \emptyset; \]
\[ \text{forall } d \in \bigcup_{i \in [1, n]} D_i \]
\[ \text{if } \forall D_i \in \{D_1; \ldots; D_n\}, \exists d' \in D_i, d' \Rightarrow d \]
\[ \text{add } d \text{ to } D_{out}; \]
\[ \text{return} D_{out}; \]

Subroutine \( \text{selective_sampling}(L, R, X, Y, n_b, n_o) \)

\[ E_{ids} \leftarrow \pi_X(L) \cap \pi_Y(R); \]
\[ L_{ids} \leftarrow \sigma_X \in E_{ids}(L); \]
\[ R_{ids} \leftarrow \sigma_Y \in E_{ids}(R); \]
\[ E_{ids}', E_{ids}'' \leftarrow \text{generate_ids_set}(L_{ids}, X, n_b, n_o); \]
\[ E_{ids}'' \leftarrow \text{generate_ids_set}(R_{ids}, Y, n_b, n_o); \]
\[ \pi_X(E_{ids}') \cap \pi_Y(E_{ids}''); \]

Subroutine \( \text{generate_ids_set}(I, A, n_b, n_o) \)

\[ ids_{out} \leftarrow \emptyset; \]
\[ I' \leftarrow I; \]
\[ noList \leftarrow \text{list the attributes in atts}(I') \setminus A \text{ in ascending order of distinct values with size limit } n_o; \]
\[ \text{forall } a \in \text{noList} \]
\[ I'' \leftarrow \pi_a(I'); \]
\[ \text{forall } b \in I'' \]
\[ I''' \leftarrow \pi_a(\sigma_{a = b}(I'')); \]
\[ \text{if } |I'''| = 1 \]
\[ \text{add } I''' \text{ to } ids_{out}; \]
\[ \text{else} \]
\[ \text{add } n_b \text{ tuples from } I''' \text{ to } ids_{out}; \]
\[ \text{return} ids_{out}; \]
4.3 The 4 C’s

4.3.1 Coverage. We observed that the cardinalities and overlap of the join attribute values are rarely preserved through a join operation and this has a great impact on FD discovery depending on the join operator used. Various sets of join FDs can be computed and we summarized the different cases in Figure 3 that recaps when JEDI algorithms are executed. Our example corresponds to the last line and \( \text{cov}_{\text{core}} \) column of the table with \((0..N;0..N)\) cardinalities where the join attribute \( \text{subject}_\text{id} \) with value \#257 in PATIENT has no counterpart in ADMISSION table; \#247, 248, and \#253 in ADMISSION have no counterpart in PATIENT table, and \#252 and \#249 in PATIENT are present multiple times in ADMISSION table. To quantify this phenomenon, we define the notion of join coverage and compute it as follows:

\[
\text{Coverage}(R \bowtie L) = \frac{1}{2} \left( \text{Cov}(R \bowtie L, L, X) + \text{Cov}(R \bowtie L, R, Y) \right)
\]

with \( \text{Cov}(\text{Join}, I, a) = \frac{1}{|\sigma_I(a)|} \sum_{\sigma(a) = \varepsilon(\text{Join})} \sigma(a = \text{Join}) \). X and Y denote the join attributes of L and R, respectively. I is a considered instance and a the considered join attribute. If \( \text{Coverage}(R \bowtie L) = 0 \), no tuple from L can be joined with tuples in R. For \( \text{Coverage}(R \bowtie L) > 1 \), some tuples in L (or R) may be missing from the join result. For \( \text{Coverage}(R \bowtie L) = 1 \), there are as many tuples in both tables L and R as in the join result.

For \( \text{Coverage}(R \bowtie L) < 1 \), there are more tuples in the join result than in tables L or R as some tuples may be repeated through the join: for example, one patient may have multiple admissions. In Figure 1, \( \text{Coverage}(	ext{PATIENT} \bowtie 	ext{ADMISSION}) = \frac{1}{2} \cdot (\frac{2}{3} + \frac{2}{3}) = 0.99 \).

4.3.2 Completeness and correctness of JEDI with Selective Mining. Algorithm 1 either checks if the tuples violating the AFDs are excluded by the join operation or, if AFDs are not provided, it mines the exact FDs after the tuples are filtered by the join operation. Algorithm 2 retrieves the minimal FDs from the logically inferred FDs, thus no 1hs subset of FDs remains unchecked. Theorem 6 indicates which part of the candidate FD lattice can be pruned. Then, Algorithm 3 explores the candidate FDs using a classic bottom-up approach, thus no minimal FDs remains unchecked. Overall, our algorithms explore the lattice of candidate FDs until they find minimal FDs; they avoid only the parts of the lattice that do not contain valid candidate FDs, thus JEDI with selective mining retrieves the complete set of minimal candidate FDs.

In Algorithm 1, valid exact FDs are either discovered from the data or deduced (because the join operation filters the tuples violating some FDs that became consequently exact after the join). Both cases of FDs are guaranteed to hold on the joined instance and only minimal 1hs are kept. Theorem 4 shows the correctness of the set of FDs inferred through logical inference. Then, the subroutine refine checks the correctness of its candidates FDs holding on the data. Therefore, the set of FDs \( D_2 \) discovered by Algorithm 2 is such that \( D_2 \models D_0 \). In Algorithm 3, Theorem 6 enforces the retrieval of FDs based only on the attributes that can become rhs in the joined instance, then only plausible candidate FDs are explored. Therefore, every discovered FD holds in the joined instance. By construction, Algorithm 2 and 3 lead to the retrieval of FDs with minimal 1hs only.

4.3.3 Completeness and Correctness of JEDI with sampling. JEDI with sampling uses Algorithm 1 and 2 with the same completeness and correctness guarantees exposed previously for JEDI with selective mining. Algorithm 4 uses Algorithm 3 over samples, the retrieved FDs are minimal exact FDs holding on the samples. If there exists a minimal FDs \( A \rightarrow b \) in a sample, an FD \( A' \rightarrow b \) such that \( A' \subset A \) cannot become a minimal FD in the full instance. Therefore, the FDs retrieved in from the samples imply the set of FDs over the full joined instance. The correctness of Algorithm 4 cannot be guaranteed as there is a probability of not sampling a pair of counter-example tuples for a given AFD, and thus to confound the AFD with exact FDs in the join results. Due to the NP-completeness of the minimal FD mining problem[5], every pair of tuples must be checked in order to find a possible counter-example, thus to guarantee that the discovered FDs from samples are exact FDs. We would like to note that developing a framework to guarantee the accuracy of the sampling-based FD discovery approach is a challenging problem and a focus of our future research.

4.3.4 Complexity. Algorithm 1 subroutine updstagedFDs is based on a level-wise algorithm through the attributes lattice. Its complexity is exponential in the number of attributes of the considered table. It prunes candidates at each level when it is possible. In terms of memory, only two levels are required. The memory size is bounded by \( O(k^2) \) where \( k \) is the number of attributes. The complexity of the second subroutine updstagedAFDs of Algorithm 1 is \( O(n \cdot f) \) where \( n \) is the maximal number of tuples and \( f \) the maximal number of FDs either from the left or the right table. The join computation is linear because we use a merge join algorithm over indexed data. It should be noted that subroutine updstagedAFDs does not

| Use Cases | JEDI Use Cases | Type of JOIN | Result of join FD Discovery from L \( \bowtie \) R |
|-----------|----------------|--------------|---------------------------------------------|
| JEDI 1    | \( D_0 \) = \{L.R\} \[\{0;0\}\] | L \( \bowtie \) R | \( L.R \) = \( R.\) \[\{0;0\}\] |
| JEDI 2    | \( D_0 \cup D_1 \) = \{L.R\} \[\{0;0\}\] | L \( \bowtie \) R | \( L.R \) = \( R.\) \[\{0;0\}\] |
| JEDI 3    | \( D_0 \cup D_1 \cup D_2 \) = \{L.R\} \[\{0;0\}\] | L \( \bowtie \) R | \( L.R \) = \( R.\) \[\{0;0\}\] |
| JEDI 4    | \( D_0 \cup D_1 \cup D_2 \cup D_3 \) = \{L.R\} \[\{0;0\}\] | L \( \bowtie \) R | \( L.R \) = \( R.\) \[\{0;0\}\] |

Figure 3: Computation of join FD sets depending on the join type and cardinalities of join attributes in \( L \bowtie R \) \((0;1..N)\) means that some tuples are absent in L, whereas they are present once or multiple times in R; \((0;N;1..N)\) means that some tuples are absent or repeated multiple times in L, whereas they are always present in R at least once and multiple times.
compute the full join but instead a subset of the full join (Algorithm 2 line 10). Algorithm 2 infers and refines FDs coming from the previous step with complexity \( O(n \cdot f) \), where \( f \) is the number of validated FDs and \( n \) the maximal number of tuples in the left or right instance. The complexity of Algorithm 3 is \( O(f \cdot f_{2}) \) where \( f_{2} \) is the maximal number of validated FDs in the left or right instance and \( f \) the number of validated FDs in the join instance. Algorithm 4 operates on micro-joins computed by micro_join subroutine with complexity \([P] + O(|L_{i}| \cdot |R_{i}|) + O(|\mathcal{E}_{D}|)\) with \([P]\) the number of tuples in the micro-join \( i \), \(|L_{i}|\) and \(|R_{i}|\) the number of tuples in \( L \) and \( R \) participating to the micro-join, and \( |\mathcal{E}_{D}| \), the set of consistent FDs discovered from multiple micro-joins FD sets. The complexity of selective sampling is \( O(|L| + |R|) + O(n_{z} \cdot k_{\max}), \) with \( k_{\max} \), the maximum number of attributes in \( L \) or \( R \).

5 EXPERIMENTS

Evaluation Goal. We compare the two variants of our method which computes only necessary micro-joins on-the-fly against the straightforward approach that consists of computing first the full join of two or more tables and then mine all the FDs from the joined result. The two main points we seek to validate are: (1) Does our approach enable us to discover join FDs accurately (i.e., high precision) in an efficient manner and faster than the straightforward approach? (2) What is the impact of different data and joins characteristics on JEDI performance?

Setup. We perform all experiments on a laptop Dell XPS machine with an Intel Core i7-7500U quad-core, 2.8 GHz, 16 GB RAM, powered by Windows 10 64-bit. Our algorithm implementation in Java use only one thread. Our code, scripts, and data sets are available at https://github.com/xxxx.

Methods. We compare JEDI algorithms for selective mining (JEDI_SM) and sampling-based join FD discovery (JEDI_SB) against with four state-of-the-art FD discovery methods: (1) TANE [8, 9], (2) Fast_FDs [26], and (3) FUN [17], and (4) HyFD [21], using Java implementation of Metanove [19]. Data sets are stored in a Postgres DBMS. Join attributes are indexed with B-Tree and hash indexes.

Evaluation Metrics. To measure the performances of join FD discovery, we use precision defined as the fraction of correctly discovered FDs on-the-fly by JEDI from partial joins that are common with the true FDs discovered from the full join result by the straightforward method over the total number of discovered true FDs. For each experiment, we consider ten runs per setting and report the average performance of each method. We examine precision, runtime, and memory consumption for different join operators with varying: (1) the size of the input tables and joins, (2) the cardinalities of the join attribute values and join coverage, and (3) the sample size.

Data. We use three real-world datasets and one synthetic data set in our experiments: (1) the clinical database MIMIC-3\(^2\) [11]; (2) PTE\(^3\), a database for predictive toxicology evaluation, used to predict whether the compound is carcinogenic, and (3) PTC\(^4\), the data set from the Predictive Toxicology Challenge that consists of more than three hundreds of organic molecules marked according to their carcinogenicity on male and female mice and rats; and (4) the TPC-H Benchmark\(^5\) with scale-factor 1. Data sets characteristics are given in Table 1 and the characteristics of the join operations in Figure 4.

5.1 Efficiency and Effectiveness Evaluation

In a first set of experiments, we evaluate the runtime and memory consumption of JEDI algorithms compared to the state-of-the-art FD discovery methods that follow the straightforward approach over a total of 55 join operations on the real-world and synthetic data sets with various coverage values illustrated in Figure 4. Variants of the same join operation with different orderings of the participating tables have the same coverage. We want to evaluate the gain of the key components of JEDI for join FD discovery and therefore focus on JEDI Algorithm 1 (join FD discovery from upstaged AFDs), Algorithm 2 (logical inference), and Algorithm 3 (selective mining of the remaining FDs from the join result) for JEDI_SM and algorithms 1,2, and 4 (selective sampling) for JEDI_SB.

5.1.1 Runtime. Figure 5 shows the average runtime (in seconds) for the two variants of JEDI. We log the average total runtime of

![Figure 4](https://example.com/figure4.png)

**Figure 4:** Coverage of the join operations considered in our experiments. The number of variants of each join operation (with different orderings) is indicated in parentheses.

![Table 1](https://example.com/table1.png)

**Table 1:** Data characteristics for our experiments.

![Database Joins](https://example.com/databasejoins.png)

**Database Joins (Nb of variants) (log(Coverage))**

---

\(^2\)https://physionet.org/content/mimiciii/1.4/
\(^3\)https://relational.fit.cvut.cz/dataset/PTE
\(^4\)https://relational.fit.cvut.cz/dataset/PTC
\(^5\)http://www.tpc.org/tpch/
join FD discovery (including data loading) for all methods over 10 runs. For the competing methods, we added the average execution time of each join operation over the indexed data. For PTE and PTC data sets with low coverage, JEDI_SM is much faster than the other methods operating on the pre-computed full join results with one order of magnitude on average. However, for MIMIC3 and joins with higher coverage, JEDI_SM is not as competitive as HyFD applied to the full join result. This result actually motivated the design of a sampling-based method that can be more efficient when join coverage is high (\( \log(Coverage) > 1 \)) in large table sizes (i.e., when many tuples from one table are repeated in the join operation). JEDI_SB shows similar or better performances for low coverage joins PTE and PTC with a sampling size around 28% in average to reach precision 1 as shown for MIMIC3 to compete with HyFD that operates over the precomputed full join. Also, the figure shows that both variants of JEDI are sensitive to the table ordering in the join operation, even more when the join size increases.

5.2 Evaluation of JEDI with Selective Mining

In Figure 7, we report the average runtime breakdown of each algorithm 1, 2, and 3 in JEDI_SM (in the horizontal histograms) and their respective percentages of discovered FDs (in the adjacent pie charts with the same color coding). Error bars represent the standard deviation of the average total runtime of the algorithms over ten runs. The data distributions, cardinalities of the join attribute values, and the join coverage have very different characteristics across the data sets to illustrate the behavior of our algorithms on different join orderings and different coverage values for PTC and MIMIC3. We observe the same behavior in PTE which is not shown due to space limitation. Algorithm 1 manipulates different sets of upstaged AFDs per input table, as we can see with the 3-size joins in MIMIC3. The logical inference made by Algorithm 2 from Algorithm 1 output will lead to different resulting sets of inferred FDs. For MIMIC3, JEDI 1 alone retrieves 52% of the true FDs on average. Algorithm 2 helps only for patients \( \Rightarrow [\text{diagnoseicd} \Rightarrow \text{dicddiagnoses}] \), the only case when the logical inference can be triggered from the FDs discovered by Algorithm 1.

The figure shows that different orderings in the tables participating in the join operations change not only the runtime but also the contribution of each algorithm in retrieving the true FDs. The reason is that various orderings of the input tables lead to different sets of potential upstaged AFDs and trigger different logical inferences. Consequently, the remaining set of join FDs to discover (by Algorithm 3 or 4) will be different. Future work will be to find the optimal ordering of the input tables and predict the cases where logical inference could prevail over selective mining to discover FDs more efficiently.
5.3 Coverage Analysis

In this experiment reported in Figure 8, we use subsets of MIMIC3 database with 100, 500, and 1000 tuples of PATIENT joined with 100 to 1000 tuples of ADMISSION with (a) inner, (b) outer left, and (c) outer right join operators for PATIENT ¥ ADMISSION. We evaluate the precision of the three algorithms of JEDI_SM (Y-axis) as the coverage rate (X-axis) increases across 30 joins for each join operator (90 joins). Coverage increases with the size of the rhs table participating in the join operation which indicates cardinalities $(0..N;0..N)$ as more and more tuples are repeated through the join operation. Precision of Algorithm 1 decreases as the coverage and sizes of both lhs and rhs tables of the join increase for the three types of join showing the difficulty of leveraging AFDs when the number of repetitions increases. JEDI 1 precision is relatively low for inner and outer right joins with best values (around .45) when coverage is below .5. Precision of Algorithm 2 is close to 0 because logical inference cannot be leveraged from Algorithm 1’s outputs, when the coverage and sizes of the joined table increase. We observed that Algorithms 1 and 2 tend to be more effective when the coverage is relatively low as shown in Figure 8 for the three types of join operations.

5.4 Evaluation of JEDI with Sampling

In this last set of experiments, we evaluate JEDI 1,2,4 and show that it outperforms JEDI_SM and other competing methods in terms of runtime for precision equals to 1, in particular for the worst case scenarios when coverage is high. First, we investigate the effect of the sample size on the precision of JEDI Algorithms 1, 2, and 4. Figure 9 shows precision of selective sampling with JEDI 1,2,4 compared to JEDI 1,2 followed by random sampling (averaged over 10 runs) for the inner join between 1,000 tuples of PATIENT and 1,000 tuples of ADMISSION with high coverage (>1) (cf. Figure 8(a)). For this experiment, we used $n_s = 1$ as input parameter for selective sampling to pick only one tuple as the representative tuple of a branch and we vary $n_s$ from 0 to $|atts(PATIENT ¥ ADMISSION)|$ to exclude the attributes with the highest number of distinct values. JEDI 1,2,4 reaches precision (and recall) of 1 when the size of the selected sample is 62.3% of the table input size. Interestingly, even for a sample of size of 10% with tuples selected by Algorithm 4, we can see an improvement of +0.153 over JEDI 1 and 2 precision.
This shows the main advantage of our approach, reducing drasti-
cally the execution time of the join FD discovery. Table 2 com-
pletes the comparative study of the two variants of JEDI against the
competing methods for the worst case scenarios when join coverage is
high for large table size. Recall that JEDI_SM has shown the best
performances over the state-of-the-art methods for PTE and PTC
joints with relatively low join coverage and small table sizes (from
2 to 5 attributes and 300 to 24k tuples). So, we focus on MIMIC3 and
TPC-H joins and report for each join: its coverage, the Join size ratio
(expressed as the sample size over the full join size, and as a percent-
age in parentheses, and the average runtime of JEDI_SM, JEDI_SB at
precision 1, FUN, TANE, HyFD, and FastFDs.

For MIMIC3, we observe that JEDI_SB outperforms all the meth-
ods with at least one of the variants of the join ordering, otherwise
HyFD applied to the full join result is slightly faster. This shows
that the ordering of large tables is critical for size 3 and more joins
but most importantly, high coverage impacts the sampling strategy.
The reason is that many tuples from each input table are repeated
through the join operation and the choice of more than one represen-
tative tuples jeopardizes the sampling result, in particular when
it does not preserve the balance and distributions of the repeated
tuples from the full join to the multiple micro-joins.

For TPC-H, we observe the same phenomenon for the 3-size join
where the straightforward approach with HyFD is slightly more
efficient (or equal with TANE). We observe that the join size ratio
to reach precision 1 is influenced by the coverage and also the num-
er of distinct values for each attributes of the joined tables. For
example, for the join part=partsupp, the average number of distinct
values per attribute is 52,984 for part and 223,971 for partsupp which
facilitates the sampling strategy in selecting violating tuples and
reducing the space of candidates FDs. This can explain the relatively
low ratio (22%) despite high join coverage.

These observations show that there is room for improvement in the
two following directions: (1) to find the optimal ordering of the
tables to maximize the performance of FD discovery (in particular
in Algorithm 1) and and (2) to improve the sampling strategy and
better tune the sample size \( n_p \) to maximize the number of violations
and reduce the space of candidate join FDs.

6 RELATED WORK

In the last three decades, numerous approaches from the database
and the data mining communities have been proposed to extract
automatically valid exact and approximate FDs from single relation
al tables [3, 13]. Liu et al. [15] have shown that the complexity of FD
discovery is in \( O(n^3(\frac{k}{2})^{1.2k^2}) \) where \( k \) is the number of attributes
and \( n \) the number of records considered. To find FDs efficiently,
existing approaches can be classified into three categories: (1) Tuple-
oriented methods (e.g., FastFDs [26], DepMiner [16]) that exploit
the notion of tuples agreeing on the same values to determine the
combinations of attributes of an FD; (2) Attribute-oriented meth-
oxds (e.g., Tane [8, 9], Fun [17, 18], FDMine [27]) that use pruning
techniques and reduce the search space to the necessary set of
attributes of the relation to discover exact and approximate FDs.
HyFD [22] exploits simultaneously the tuple- and attribute-oriented
approaches to outperform the previous approaches; and more re-
cently (3) Structure learning methods relying on sparse regression
[28], or on entropy-based measures [12] to score candidate con-
straints (not limited to FDs alone). More particularly, FDX [28]
performs structure learning over a sample constructed by taking
the value differences over sampled pairs of tuples from the raw data.
In addition, incremental approaches [2, 24] have been developed to
tackle data volume and velocity with updating all valid FDs when
new tuples are inserted outperforming classical approaches that
recalculate all FDs after each data update. Extensive evaluations
of FD discovery algorithms can be found in [6, 20]. To the best of
our knowledge, previous work on FD discovery did not attempt to
address the problem join FD discovery in an efficient manner. Our
approach combining logical inference, partitioning, and selective
sampling is the first solution in this direction.

7 CONCLUSIONS

We introduced JEDI, a framework to solve the problem of FD
discovery from multiple joined tables without the full computa-
tion of the join result beforehand. The salient features of our work are
the following: (1) We leverage single-table approximate FDs that
become exact join FDs due to the join operation when the join
value sets are not preserved; (2) We leverage logical inference to
discover join FDs from the sets of single-table FDs without com-
puting the full join result; and (3) We find new multi-table join
FDs from partial join and micro-joins using respectively selective
mining on the necessary attributes and selective sampling on the
necessary tuples. We empirically show that JEDI outperforms, both
in terms of runtime and memory consumption, the state-of-the-art
FD discovery methods applied to the join results that have to be
computed beforehand. We hope that this will open a new line of
research where the community will examine FDs across multiple
and an entire database. Since join FDs are resilient to the
join operators, they can be leveraged for pruning and assessing the
validity and prevalence of a large set of discovered single-table FDs.

Table 2: Average runtime comparison on MIMIC3 and TPC-H data.
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