Rewriting XPath Queries using View Intersections: Tractability versus Completeness

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The standard approach for optimization of XPath queries by rewriting using views techniques consists in navigating inside a view’s output, thus allowing the usage of only one view in the rewritten query. Algorithms for richer classes of XPath rewritings, using intersection or joins on node identifiers, have been proposed, but they either lack completeness guarantees, or require additional information about the data. We identify the tightest restrictions under which an XPath can be rewritten in polynomial time using an intersection of views and propose an algorithm that works for any documents or type of identifiers. As a side-effect, we analyze the complexity of the related problem of deciding if an XPath with intersection can be equivalently rewritten as one without intersection or union. We extend our formal study of the view-based rewriting problem for XPath by describing also (i) algorithms for more complex rewrite plans, with no limitations on the number of intersection and navigation steps inside view outputs they employ, and (ii) adaptations of our techniques to deal with XML documents without persistent node IDs, in the presence of XML keys. Complementing our computational complexity study, we describe a proof-of-concept implementation of our techniques and possible choices that may speed up execution in practice, regarding how rewrite plans are built, tested and executed. We also give a thorough experimental evaluation of these techniques, focusing on scalability and the running time improvements achieved by the execution of view-based plans.

1. INTRODUCTION

The problem of equivalently rewriting queries using views is fundamental to several classical data management tasks. While the rewriting problem has been well studied for the relational data model, its XML counterpart is not yet equally well understood, even for basic XML query languages such as XPath, due to the novel challenges raised by the features of the XML data model.

XPath [Clark and DeRose 1999] is the standard for navigational queries over XML data and it is widely used, either directly, or as part of more complex languages (such as XQuery [Boag et al. 2007]). Early research [Xu and Özsoyoglu 2005; Mandhani and Suciu 2005; Tang and Zhou 2005; Yang et al. 2003] studied the problem of equivalently rewriting an XPath by navigating inside a single materialized XPath view. This is the only kind of rewritings supported when the query cache can only store or can only obtain copies of the XML elements in the query answer, and so the original node identities are lost.

We have recently witnessed an industrial trend towards enhancing XPath queries with the ability to expose node identifiers and exploit them using intersection of node sets (via identity-based equality). This trend is supported by such systems as [Balmin et al. 2004] and has culminated in the adoption of intersection as a first-class primitive of the XPath standard, starting from XPath 2.0 [Berglund et al. 2007] and through the new XPath 3.0 standard [Robie et al. 2010]. In a more general setting, intersection between collections of nodes can be based not only on physical node identifiers, but also on logical ids or keys. Research on keys for XML, such as the ones proposed in [Buneman et al. 2005], led to the introduction of a special key construct in the XML Schema [Falisrade and Walmsley 2004] standard, which allows to uniquely identify a node based on the result of an XPath expression.

This development enables for the first time multiple-view rewritings obtained by intersecting several materialized view results. The single-view rewritings considered in early XPath research have only limited benefit, as many queries with no single-view rewriting can be rewritten using multiple views. Our work is the first to characterize the complexity of the intersection-aware rewriting prob-
lem. We are interested in sound and complete algorithms, which are guaranteed to find a rewriting whenever one exists.

Our main objective is to identify a fragment of XPath that is as large as possible, while admitting polynomial-time rewriting that remains complete. We exhibit a fragment of XPath with these properties showing that it is maximal in the sense that extending it renders the rewriting problem intractable (coNP hard). The fragment is practically interesting as it permits expressive queries and views with child and descendant navigation and path filter predicates, but no wildcard labels.

As a side-effect of our study on rewriting, we analyze the complexity of the problem of deciding if an XPath with intersection can be equivalently rewritten as one without intersection or union, case in which we say it is union-free. We also study the effect of intersection on the complexity of containment. Our hardness results thus immediately apply to XPath 2.0 and XPath 3.0 queries.

Prior work on XPath containment derived coNP lower bounds in the presence of wildcard navigation, yet showed PTIME for tree patterns without wildcard [Miklau and Suciu 2004]. In contrast, we show that extending wildcard-free tree patterns with intersection already leads to intractability.

**Running example.** Throughout the paper we will consider an example based on XPath queries over a digital library, which consists in a large number of publications, including scientific papers. A paper is organized into a hierarchy of sections, which may include, among other things, figures and images, usually related to the theorems and other results stated in the papers.

Let us assume that there has already been a query \( v_1 \), that retrieved all images appearing in sections with theorem statements:

\[
v_1 : \text{doc}(\text{L}')//\text{paper}//\text{section}[\text{theorem}]//\text{image}
\]

The result of \( v_1 \) is stored in the cache as a materialized view, rooted at an element named \( v_1 \). Later, the query processor had to answer another XPath \( v_2 \) looking for images inside (floating) figures that can be referenced:

\[
v_2 : \text{doc}(\text{L}')//\text{lib/paper//section}[\text{figure}[\text{caption//label}]]//\text{image}
\]

The result of \( v_2 \) is not contained in that of \( v_1 \), so it was also executed and its answer cached.

Let us first look at an incoming query \( q_1 \), asking for all postscript images that appear in sections with theorems:

\[
q_1 : \text{doc}(\text{L}')//\text{paper}//\text{section}[\text{theorem}]//\text{image}[\text{ps}]
\]

\( q_1 \) can be easily answered by navigating inside the view \( v_1 \), using the following XPath query:

\[
r_1 : \text{doc}(v_1)/v_1//\text{image}[\text{ps}]
\]

Now, consider a query \( q_2 \) looking for the files corresponding to images inside labeled figures from sections stating theorems:

\[
q_2 : \text{doc}(\text{L}')//\text{lib/paper//section}[\text{theorem}]//\text{figure}[\text{caption//label}]/\text{image}//\text{file}
\]

It is easy to see that \( q_2 \) cannot be answered in isolation using only \( v_1 \) or only \( v_2 \), because, for instance, there is no way to enforce that an image is both in a section having theorems and inside a labeled figure. However, by intersecting the results of the two views (assuming they both preserve the identities of the original image elements), one can build a rewriting equivalent to \( q_2 \):

\[
r_2 : (\text{doc}(v_1)/v_1//\text{image} \cap \text{doc}(v_2)/v_2//\text{image})//\text{file}
\]

**Outline.** This paper is organized as follows. We discuss related work in Section 2. Section 3 introduces general notions for tree and DAG patterns, and the rewriting problem. In Section 4 we give a high-level view on our rewriting algorithm REWRITE. We then zoom in on the rewrite rules on which it is based in Section 5. We discuss in Section 6 how these techniques can apply even in the absence of persistent node IDs, under XML key constraints. We present the formal guarantees of algorithm REWRITE in Section 7 in terms of soundness, completeness and complexity bounds; we
also analyze the related problem of union-freedom for DAG patterns. As the general rewriting problem is coNP-complete, we then study the most permissive restrictions on the language of queries or rewrite plans that enable a sound and complete approach (Sections 8 and 9). We consider a richer language for rewrite plans in Section 10 which can have arbitrary many steps of intersection and compensation of views. We discuss implementation issues and optimization opportunities in Section 11 and we present our experiments is Section 12. We conclude in Section 13. We detail two of the more involved proofs in an appendix, in Sections A and B.

2. RELATED WORK

The area of rewriting XPath queries using views lacks in general theoretical foundations, as most related works propose incomplete algorithms or impose strong limitations.

XPath rewriting using only one view (no intersection) was the target of several studies [Xu and Ozsoyoglu 2005; Mandhani and Suciu 2005; Tang and Zhou 2005; Yang et al. 2003; Wu et al. 2009], possibly in the presence of DTD constraints [Aravoglidi and Vassalos 2011]. Previously proposed join-based rewriting methods either give no completeness guarantees [Balmin et al. 2004; Tang et al. 2008] or can do so only if the query engine has extra knowledge about the structure and nesting depth of the XML document [Arion et al. 2007]. Others [Tang et al. 2008] can only be used if the node ids are in a special encoding, containing structural information. Our algorithm works for any documents and type of identifiers, including application level ids, such as the id attributes defined in the XML standard [Bray et al. 2006] or XML Schema keys [Fallside and Walmsley 2004]. In [Lakshmanan et al. 2006; Gao et al. 2007; Wang et al. 2011], the authors look at a different problem, that of finding maximally contained rewritings of XPath queries using views. Rewriting more expressive XML queries using views was studied in [Chen and Rundensteiner 2002; Deutsch and Tannen 2003; Onose et al. 2006], but without considering intersection. Fan et al. [Fan et al. 2007] define views using DTDs instead of queries and study the problem of rewriting an XPath using one view DTD. In [Afrati et al. 2011], for a different XPath fragment (including wildcard labels), the authors describe a sound but incomplete algorithm for finding equivalent rewritings as unions of single-view rewritings. Several works considered the problem of choosing the optimal set of views to materialize in order to support a given query workload (see [Katsifodimos et al. 2012] and the main references therein).

Most related prior work. This article extends the results we present in the extended abstract [Cautis et al. 2008], with respect to which it brings several new important contributions. We provide a more complete study on the computational complexity of the view-based rewriting problem, describing decision procedures for settings in which the techniques of [Cautis et al. 2008] would not be applicable. More precisely, (i) we consider more complex rewrite plans, with no limitations on the number of intersection steps they employ, and (ii) we describe how our techniques can be modified to deal with XML documents without persistent node Ids, in the presence of XML keys. Moreover, we report on a systems contribution, pertaining to the implementation of an XPath rewriting engine. Optimization issues – on how rewrite plans are chosen, built and evaluated – were not considered in [Cautis et al. 2008], whose focus was on computational complexity only. We discuss such issues in this paper, as well as certain implementation choices that may speed up execution in practice. In particular, we introduce the theoretical foundations and we report on the implementation of a PTIME technique for partially minimizing redundancy in rewritings without paying the price of full minimization (which is NP-complete). We also give a thorough experimental evaluation of the presented techniques. We provide the complete proofs for all theoretical results (no proofs were given in [Cautis et al. 2008]). We believe these are of interest on their own, as they are based on various novel techniques for analyzing and reasoning about XPath. We also present additional examples, whose role is to illustrate more complex rewrite plans or to complement our proofs.

Sound and complete algorithms for rewriting XML queries using multiple views were also proposed later (after the publication of [Cautis et al. 2008]), in [Manolescu et al. 2011]. There, the focus is not on tractable rewriting. Indeed, the authors target a more expressive language, tree pattern queries with value joins and multiple arity, for which equivalence is intractable and no complete
rewriting algorithm implementation can go below the exponential bound; this is for two reasons: (i) the coNP-hardness result (ref. theorem), even in the absence of value joins and unary tree pattern queries, and (ii) the NP-hardness of relational conjunctive query rewriting, which can be encoded by tree patterns with joins (Chandra and Merlin 1977; Onose et al. 2006). Moreover, [Manolescu et al. 2011] focuses on the minimality of rewrite plans, which brings another exponential in the total running time. In essence, both the algorithm in [Manolescu et al. 2011] and the one in [Cautis et al. 2008] (for the intractable case) amount to reformulating an intersection of tree patterns into a union of intersection-free tree patterns (a.k.a. interleavings; see Section 3). There can be exponentially many interleavings, which is unavoidable given the coNP lower bound.

In contrast to [Manolescu et al. 2011], this submission studies the most expressive language for input queries (XPath with a few restrictions) for which finding a rewriting is tractable (we present a sound and complete procedure for which we can guarantee polynomial time under these restrictions). In addition, we study the more general problem of rewriting XPath queries using multiple views joined by Ids, show intractability beyond our restrictions and for that case we present an exponential rewriting algorithm that is sound and complete.

Ways to explore the space of possible rewrite plans using views, for minimization purposes, have been considered in previous literature (see for instance [Popa et al. 2000]). Intuitively, they start from a rewriting and randomly prune certain components of the plan while maintaining equivalence; this reveals a threshold on the size of minimal plans (in terms of number of views) to be considered. Even though minimization lies beyond the scope of our paper, we note that the techniques presented here do create the search space in which all minimal rewritings are to be found, creating the opportunity to plug in techniques for exploring the search space, such as in [Popa et al. 2000].

Containment and satisfiability for several extensions of XPath with intersection have been previously investigated, but all considered problems were at least NP-hard or coNP-hard. For our language, containment is also intractable, but the equivalence test used in the rewriting algorithm is in PTIME for practically relevant restrictions. Satisfiability of XPath in the presence of the intersect operator and of wildcards was analyzed in [Hidders 2003], which proved its NP-completeness. As noticed in [Benedikt et al. 2005], there is a tight relationship between satisfiability and containment for languages that can express unsatisfiable queries. If containment is in the class K, satisfiability is in coK and if satisfiability is K-hard, containment is coK-hard. We give even stronger coNP completeness results for the containment of an XPath \( p_1 \) into an XPath \( p_2 \), by allowing intersection only in \( p_1 \) and disallowing wildcards. Satisfiability is analyzed in [Benedikt et al. 2005] for various fragments of XPath, including negation and disjunction, which could together simulate intersection, but lead to coPSPACE-hardness for checking containment. Richer sublanguages of XPath 2.0, including path intersection and equality, are considered in [ten Cate and Lutz 2007], where complexity of checking containment goes up to EXPTIME or higher. None of these studies tries to identify an efficient test for using intersection in query rewriting. A different approach, taken by [Groppe et al. 2006] is to replace intersection by using a rich set of language features, and then try to simplify the expression using heuristics.

Finally, closure under intersection was analyzed in [Benedikt et al. 2005] for various XPath fragments, all of which use wildcard. We study the case without wildcard and prove that union-freedom (equivalence between an intersection of XPaths and an XPath without intersection or union) is coNP-hard. However, under restrictions similar to those for the rewriting problem, union-freedom can be solved in polynomial time. Thus, we also answer a question was previously raised in [Cautis et al. 2007] regarding whether an intersection of XPath queries without wildcard can be reduced in PTIME to only one XPath.

[Cautis et al. 2011] describes an algorithm for rewriting using multiple views, designed especially for views specified by means of a program (a Query Set Specification). Completeness is achieved there for input queries having at least one descendant edge in the root to output-node path (so called multi-token queries), and for a restricted language for rewrite plans (intersections of views). For

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This is based on the observation that a query is satisfiable iff it is not contained in a query that always returns the empty set.
Rewriting XPath Queries using View Intersections: Tractability versus Completeness

3. PRELIMINARIES

We consider an XML document as an unranked, unordered rooted tree $t$ modeled by a set of edges $\text{EDGES}(t)$, a set of nodes $\text{NODES}(t)$, a distinguished root node $\text{ROOT}(t)$ and a labeling function $\lambda_t$, assigning to each node a label from an infinite alphabet $\Sigma$. Every node $n$ of a tree has a text value $\text{text}(n)$, possibly empty.

We consider XPath queries with child `/' and descendant `//' navigation, without wildcards. We call the resulting language $\text{XP}$ and define its grammar as:

\[
\begin{align*}
apath &::= \text{doc}(\text{"name"})/\text{rpath} \mid \text{doc}(\text{"name"})//\text{rpath} \\
rpath &::= \text{step} \mid \text{rpath}/\text{rpath} \mid \text{rpath}//\text{rpath} \\
\text{step} &::= \text{label} \text{pred} \\
\text{pred} &::= \epsilon \mid \text{[rpath]} \mid \text{[rpath = C]} \mid \text{[//rpath]} \mid \text{[///rpath = C]} \mid \text{pred pred}
\end{align*}
\]

Expressions in $\text{XP}$ are produced from the symbol $\text{apath}$, and they correspond to absolute paths, that is, queries expressed starting from the document root. The $\text{rpath}$ symbol generates relative path expressions, i.e. encoding navigation relative to a given document context. The sub-expressions inside brackets are called predicates. $C$ terminals stand for text constants.

The semantics of $\text{XP}$ can be defined as follows:

\textbf{Definition 3.1 (XP Semantics).} The result of evaluating an XP expression $q$ over an XML tree $t$ is defined as a binary relation over $\text{NODES}(t)$:

1. $[[\text{label}]]_t = \{(n, n') | (n, n') \in \text{EDGES}(t), \lambda_t(n') = \text{label}\}$
2. $[[\text{pred}]]_t = \{n | n \in \text{NODES}(t), \text{pred}(n) = \text{true}\}$
   
   (a) Let $\text{pred}$ be defined as $[\text{rp}]$ or $[//\text{rp}]$ and let $t_n$ denote the subtree rooted at $n$ in $t$. We say that $\text{pred}(n) = \text{true}$ iff $[[\lambda_t(n)//\text{rp}]]_{t_n} \neq \emptyset$ (or $[[\lambda_t(n)//\text{rp}]]_{t_n} \neq \emptyset$, resp.).

   (b) If $\text{pred}$ is of the form $[\text{rp} = C]$ (or $[//\text{rp} = C]$) then $\text{pred}(n) = \text{true}$ iff $\text{text}([[\lambda_t(n)//\text{rp}]]_{t_n}) = C$ (or $\text{text}([[\lambda_t(n)//\text{rp}]]_{t_n}) = C$, resp.).

3. $[[\text{pred}_1 \text{pred}_2]]_t = [[\text{pred}_1]]_t \cap [[\text{pred}_2]]_t$
4. $[[\epsilon]]_t = \text{NODES}(t)$
5. $[[\text{label pred}]]_t = \{(n, n') | (n, n') \in [[\text{label}]]_t, n' \in [[\text{pred}]]_t\}$
6. $[[\text{rpath} \text{rpath}]]_t = \{(n, n') | (n, n') \in [[\text{rpath}]]_t \circ [[\text{rpath}]]_t\}$
7. $[[\text{rpath} //\text{rpath}]]_t = \{(n, n') | (n, n') \in [[\text{rpath}]]_t \circ \text{EDGES}^*(t) \circ [[\text{rpath}]]_t\}$
8. $[[\text{doc("name")rpath}]]_t = \{ (\text{ROOT}(t), n) | (\text{ROOT}(t), n) \in [[\text{rpath}]]_t\}$
9. $[[\text{doc("name")//rpath}]]_t = \{ (\text{ROOT}(t), n') | (\text{ROOT}(t), n') \in \text{EDGES}^*(t) \circ [[\text{rpath}]]_t\}$

$\text{doc("name")}$ returns the root of the document storing $t$. We denote by $\circ$ the standard binary relation composition, that is $R \circ S = \{(r, s) | (r, x) \in R, (x, s) \in S\}$.

In the following, we will prefer for XML queries an alternative representation widely used in literature, the unary tree patterns $\text{Miklau and Suciu 2004}^4$.

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4Miklau and Suciu (and most follow-up works) provide a node set semantics for tree patterns. Our semantics is equivalent to node set semantics, despite the binary representation. We just repeat the context node with each of the selected nodes, instead of writing it once for the entire set as in [Miklau and Suciu 2004]. This will prove more convenient for our formal development. There exists a line of work on distinguishing the expressive power between binary (path set semantics) and node set semantics [Wu et al. 2009], but it does not apply here. In [Wu et al. 2009], the distinction boils down to allowing one versus two distinguished nodes in the pattern. In our work we only have one distinguished node.
Definition 3.2. A tree pattern \( p \) is a non-empty rooted tree, with a set of nodes \( \text{NODES}(p) \) labeled with symbols from \( \Sigma \), a distinguished node called the output node \( \text{OUT}(p) \), and two types of edges: child edges, labeled by / and descendant edges, labeled by //. The root of \( p \) is denoted \( \text{ROOT}(p) \). Every node \( n \) in \( p \) has a test of equality \( \text{test}(n) \) that is either the empty word \( \epsilon \), or a constant \( C \). If \( n \) is on a path between \( \text{ROOT}(p) \) and \( \text{OUT}(p) \), then \( \text{test}(n) \) is \( \epsilon \).

Any \( XP \) expression can be translated into a tree pattern query and vice versa (see, for instance [Miklau and Suciu 2004]). For a given \( XP \) expression \( q \), by \( \text{pattern}(q) \) we denote the associated tree pattern \( p \) and by \( \text{spath}(p) \equiv q \) the reverse transformation.

The semantics of a tree pattern can be given using embeddings:

Definition 3.3. An embedding of a tree pattern \( p \) into a tree \( t \) over \( \Sigma \) is a function \( e \) from \( \text{NODES}(p) \) to \( \text{NODES}(t) \) that has the following properties:

1. \( e(\text{ROOT}(p)) = \text{ROOT}(t) \);
2. for any \( n \in \text{NODES}(p) \), \( \text{LABEL}(e(n)) = \text{LABEL}(n) \);
3. for any \( n \in \text{NODES}(p) \), if \( \text{test}(n) = C \) then \( \text{test}(e(n)) = C \);
4. for any /-edge \( (n_1, n_2) \) in \( p \), \( (e(n_1), e(n_2)) \) is an edge in \( t \);
5. for any //-edge \( (n_1, n_2) \) in \( p \), there is a path from \( e(n_1) \) to \( e(n_2) \) in \( t \).

The result of applying a tree pattern \( p \) to an XML tree \( t \) is the set:

\[ \{ (\text{ROOT}(t), e(\text{OUT}(p))) \mid e \text{ is an embedding of } p \text{ into } t \} \]

We will consider in this paper the extension \( XP^\cap \) of \( XP \) with respect to intersection. Expressions in \( XP^\cap \) are generated from the symbol \( \text{ipath} \), by adding the following rules to the grammar of \( XP \):

\[
\begin{align*}
\text{ipath} & ::= \text{cpath} | (\text{ipath}) | (\text{cpath})/\text{rpath} | (\text{cpath})//\text{rpath} \\
\text{cpath} & ::= \text{apath} | \text{cpath} \cap \text{apath}
\end{align*}
\]

The symbol \( \text{cpath} \) defines a single level of intersection of \( XP \) expressions, e.g.

\[
\text{doc}("v_1")/v_1/\text{image} \cap \text{doc}("v_2")/v_2/\text{image}.
\]

\( \text{ipath} \) adds to this intersection an \( \text{rpath} \) expression, thus allowing additional (relative) navigation from the nodes in the intersection result, e.g.

\[
(\text{doc}("v_1")/v_1/\text{image} \cap \text{doc}("v_2")/v_2/\text{image}/\text{file})
\]

Note that by definition \( XP^\cap \) does not include arbitrary nested intersections of \( XP \) queries. We defer the analysis of the language expressing such nested intersections (a superset of \( XP^\cap \)) to Section 10.

Formally, \( XP^\cap \) has the following semantics:

1. \( \text{cpath} \cap \text{apath} = [\text{cpath}]_t \cap [\text{apath}]_t \]
2. \( [\text{cpath}//\text{rpath}]_t = \{(n, n') \mid (n, n') \in [\text{cpath}]_t \circ [\text{rpath}]_t\} \)
3. \( [\text{cpath}/\text{rpath}]_t = \{(n, n') \mid (n, n') \in [\text{cpath}]_t \circ \text{EDGES}^*(t) \circ [\text{rpath}]_t\} \)

By \( XP^\cap \) expressions over a set of documents \( D \) we denote those that use only \( \text{apath} \) expressions that navigate inside the documents \( D \). For a fragment \( \mathcal{L} \subseteq XP \), by \( \mathcal{L}^\cap \subseteq XP^\cap \) we denote the \( XP^\cap \) expressions that use only \( \text{apath} \) expressions from \( \mathcal{L} \).

Similar to the \( XP - \) tree pattern duality, we can represent \( XP^\cap \) expressions using the more general \( \text{DAG} \) patterns:

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Footnote: We overloaded the intersection operator: while on the left side it refers to the \( XP^\cap \) syntax, on the right side it denotes the classic set set intersection operation.
Definition 3.4. A DAG pattern $d$ is a directed acyclic graph, with a set of nodes $\text{NODES}(d)$ labeled with symbols from \( \Sigma \), a distinguished node called the output node \( \text{OUT}(d) \), and two types of edges: child edges, labeled by / and descendant edges, labeled by //, $d$ has to satisfy the property that any $n \in \text{NODES}(d)$ is accessible via a path starting from a special node \( \text{ROOT}(d) \). In addition, all the nodes that are not on a path from \( \text{ROOT}(d) \) to \( \text{OUT}(d) \) (denoted predicate nodes) have only one incoming edge. Every node $n$ in $d$ has a test of equality $\text{test}(n)$ that is either the empty word \( \epsilon \), or a constant $C$. If $n$ is on a path between \( \text{ROOT}(d) \) and \( \text{OUT}(d) \), then $\text{test}(n)$ is always $\epsilon$.

Figure (a) gives an example of a DAG pattern. \( \text{ROOT}(d) \) is the \text{doc}(L) node and \( \text{OUT}(d) \) is the image node indicated by a square.

In our algorithm (Section 4) we obtain the $\text{XP}^\cap$ expressions that are rewriting candidates directly. We only use the DAG pattern representation for the equivalence check involved in validating these candidates. We therefore only need to translate from $\text{XP}^\cap$ into DAG patterns, but not conversely. We specify the one-way translation below.

Representing $\text{XP}^\cap$ by DAG patterns. For a query $q$ in $\text{XP}^\cap$, we construct the associated pattern, denoted $\text{dag}(q)$, as follows:

1. for every apath ($\text{XP}$ path with no \( \cap \)), $\text{dag}(\text{apath})$ is the tree pattern corresponding to the \text{apath}.
2. $\text{dag}(p_1 \cap p_2)$ is obtained from $\text{dag}(p_1)$ and $\text{dag}(p_2)$ as follows: (i) provided there are no labeling conflicts and both $p_1$ and $p_2$ are not empty, by coalescing $\text{ROOT}(\text{dag}(p_2))$ with $\text{OUT}(\text{dag}(p_1))$ with $\text{OUT}(\text{dag}(p_1))$ respectively, (ii) otherwise, as the empty pattern.
3. $\text{dag}(x/rpath)$ and $\text{dag}(x/lrpath)$ are obtained as follows: (i) for non-empty $x$, by appending the pattern corresponding to $rpath$ to $\text{OUT}(\text{dag}(x))$ with a /- and a ll-edge respectively, (ii) as $x$, if $x$ is the empty pattern.

By a pattern from the language $\mathcal{L}$ we denote any pattern built as $\text{dag}(q)$, for any $q \in \mathcal{L}$. Note that a tree pattern is a DAG pattern as well. The notion of embedding and the semantics of a pattern can be extended in straightforward manner from trees to DAGs. In the following, unless stated otherwise, all patterns are DAG patterns. We can prove the following:

Theorem 3.5. For any $q \in \text{XP}^\cap$ and any tree $t$, $q(t) = \text{dag}(q)(t)$.

By the main branch nodes of a pattern $d$, MBN($d$), we denote the set of nodes found on paths starting with \( \text{ROOT}(d) \) and ending with \( \text{OUT}(d) \). We refer to main branch paths between \( \text{ROOT}(d) \) and \( \text{OUT}(d) \) as main branches of $d$. The (unique) main branch of a tree pattern $p$ is denoted MB($p$).

Definition 3.6. A pattern $d_1$ is contained in another pattern $d_2$ iff for any input tree $t$, $d_1(t) \subseteq d_2(t)$. We write this shortly as $d_1 \sqsubseteq d_2$. We say that $d_1$ is equivalent to $d_2$, and write $d_1 \equiv d_2$, iff $d_1(t) = d_2(t)$ for any input tree $t$. 

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We say that a pattern $p$ is minimal \cite{Amer-Yahia2002} if it is equivalent to none of its strict sub-patterns.

**Definition** 3.7. A mapping between two patterns $d_1$ and $d_2$ is a function $h : \text{NODES}(d_1) \to \text{NODES}(d_2)$ that satisfies the properties\cite{Mandhani2005} of an embedding (allowing the target to be a pattern) plus three others:

1. for any $n \in \text{MBN}(d_1)$, $h(n) \in \text{MBN}(d_2)$;
2. for any $l$-edge $(n_1, n_2)$ in $d_1$, $(h(n_1), h(n_2))$ is a $l$-edge in $d_2$.
3. for any $n \in \text{NODES}(d_1)$, if $\text{test}(n) = C$ then $\text{test}(h(n)) = C$.

A root-mapping is a mapping that satisfies (1). A containment mapping is a root-mapping $h$ such that $h(\text{OUT}(d_1)) = \text{OUT}(d_2)$.

**Lemma** 3.8. If there is a containment mapping from $d_1$ into $d_2$ then $d_2 \subseteq d_1$.

**Lemma** 3.9. Two tree patterns are equivalent iff they are isomorphic after minimization.

**Proof.** It is a direct consequence of Theorem 1 from \cite{Mandhani2005}, because equivalence in $XP$ (we remind that our language $XP$ has no wildcard) is always witnessed by containment mappings in both directions. \hfill $\Box$

**Lemma** 3.10. A tree pattern $p$ is contained into a DAG pattern $d$ iff there is a containment mapping from $d$ into $p$.

**Proof Sketch.** Consider the model $\text{mod}_p$ of $p$ in which $l$-edges are replaced by a sequence /$z$/ (two child edges), where $z$ is a fresh new label. If $p \subseteq d$, then in particular $d(\text{mod}_p) \neq \emptyset$. Since $z$ is a new label, $d$ can only embed a $l$-edge in a path fragment containing $z$. \hfill $\Box$

Note that in $XP$ unsatisfiable DAG patterns are possible (when there exists no model with non-empty results). For the purposes of this paper, we assume in the following only satisfiable patterns. We say that two $XP$ queries $q_1$ and $q_2$ are incomparable if there is no containment mapping between them.

We now prove that we can always reformulate a DAG pattern as a (possibly empty) union of tree patterns.

As in \cite{Benedikt2005}, a code is a string of $\Sigma$ symbols alternating with either / or $\ell$.

**Definition** 3.11 (Interleaving). By the interleavings of a pattern $d$ we denote any tree pattern $p_i$ produced as follows:

1. choose a code $i$ and a total onto function $f_i$ that maps $\text{MBN}(d)$ into $\Sigma$-positions of $i$ such that:
   a. for any $n \in \text{MBN}(d)$, $\text{LABEL}(f_i(n)) = \text{LABEL}(n)$
   b. for any $l$-edge $(n_1, n_2)$ in $d$, the code $i$ is of the form $\ldots f_i(n_1)/f_i(n_2) \ldots$
   c. for any $l$-edge $(n_1, n_2)$ in $d$, the code $i$ is of the form $\ldots f_i(n_1) \ldots f_i(n_2) \ldots$

2. build the smallest pattern $p_i$ such that:
   a. $i$ is a code for the main branch $\text{MB}(p_i)$,
   b. for any $n \in \text{MBN}(d)$ and its image $n'$ in $p_i$ (via $f_i$), if a predicate subtree $st$ appears below $n$ then a copy of $st$ appears below $n'$, connected by same kind of edge.

Two nodes $n_1, n_2$ from $\text{MBN}(d)$ are said to be collapsed (or coalesced) if $f_i(n_1) = f_i(n_2)$, with $f_i$ as above. The tree patterns $p_i$ thus obtained are called interleavings of $d$ and we denote their set by $\text{interleave}(d)$.
For instance, one of the seven interleavings of $d$ in Figure 1(a) is the pattern in Figure 1(c) and another one corresponds to the XPath $\text{doc}(L)/\lib/paper/paper//section[theorem]/figure[caption//label]/image$

We say that a pattern $d$ is satisfiable if it is non-empty and the set $\text{interleave}(d)$ is non-empty. By definition, there is always a containment mapping from a satisfiable pattern into each of its interleavings. Then, by Lemma 3.8, a pattern will always contain its interleavings. Similar to a

By definition, there is always a containment mapping from a satisfiable pattern into each of its

We can now construct the interleaving $p_i$ and its embedding $e_i$, such that $(\text{ROOT}(t), n) \in e_i(t)$. Let $\text{id}$ be defined by $\text{MBN}(d)$ to $c$, such that all the child/descendant relationships between main branch nodes are accordingly translated in the ordering of $c$. Let $c'$ denote the code obtained from $c$ by: Step 1) replacing by the empty string all the positions that are not the image of some node $n' \in \text{MBN}(d)$ under $e \circ \text{id}$, Step 2) replacing any sequence of consecutive /-characters of length more than 2 (i.e., “///...”) by the slash-slash sequence (i.e., “/”).

We can now construct the interleaving $p_i$ and its embedding $e_i$, such that $(\text{ROOT}(t), n) \in e_i(t)$.

Let us book keep by a partial function $f_i$, the correspondence between used $e$ positions and $c$ positions. Let $p_i$ be defined by the code $i = c'$, and let $f_i$ be defined by $f_i \circ \text{id} \circ e$ on all the nodes in $\text{MBN}(d)$. It is easy to see that $i$ and $f_i$ give indeed an interleaving $p_i$, as it obeys all the conditions and $p_i$ is minimal. Let $i''$ denote the one-to-one mapping from $\text{MB}(p_i)$ into $c'$. Now, we can define its embedding $e_i$ into $t$ as follows: for all main branch nodes $n' \in \text{MB}(p_i)$ we have $e_i(n') = \text{id}^{-1} \circ f_i^{-1} \circ \text{id}''$. It is easy to see that for any node $n'' \in \text{MBN}(d)$ such that $n_i'' = \text{id}''(f_i(n''))$, we have $e(n'') = e_i(n')$ so all the predicate subtrees in $p_i$ can be mapped at $e_i(n')$ for all $n'$. Since $t$ and $n$ were chosen at random, this concludes the proof of containment for $d \subseteq \bigcup_i p_i$. □

The following also hold:

**Lemma 3.12.** Any DAG pattern is equivalent to the union of its interleavings.

**Proof.** We only need to consider the other inclusion, from $d$ into $\bigcup_i p_i$. We show that for any XML tree $t$ and any node $n \in t$ such that $(\text{ROOT}(t), n) \in e(t)$, for some embedding $e$ of $d$ into $t$ (so $e(\text{OUT}(d)) = n$), we can always find an interleaving $p_i$ and embedding $e_i$ of $p_i$ in $t$ such that $(\text{ROOT}(t), n) \in e_i(t)$. This would be enough to conclude the proof of inclusion (and equivalence).

Let $p$ denote the linear path from $\text{ROOT}(t)$ to $n$ (endpoints included) and let $c$ denote the code of $p$. Let $\text{id}$ denote the one-to-one mapping from $p$ to $c$. Note that $e$ gives us a mapping $\text{id} \circ e$ from $\text{MBN}(d)$ to $c$, such that all the child/descendant relationships between main branch nodes are accordingly translated in the ordering of $c$. Let $c'$ denote the code obtained from $c$ by: Step 1) replacing by the empty string all the positions that are not the image of some node $n' \in \text{MBN}(d)$ under $e \circ \text{id}$, Step 2) replacing any sequence of consecutive /-characters of length more than 2 (i.e., “///...”) by the slash-slash sequence (i.e., “/”).

We can now construct the interleaving $p_i$ and its embedding $e_i$, such that $(\text{ROOT}(t), n) \in e_i(t)$.

Let us book keep by a partial function $f_i$, the correspondence between used $e$ positions and $c$ positions. Let $p_i$ be defined by the code $i = c'$, and let $f_i$ be defined by $f_i \circ \text{id} \circ e$ on all the nodes in $\text{MBN}(d)$. It is easy to see that $i$ and $f_i$ give indeed an interleaving $p_i$, as it obeys all the conditions and $p_i$ is minimal. Let $\text{id}''$ denote the one-to-one mapping from $\text{MB}(p_i)$ into $c'$. Now, we can define its embedding $e_i$ into $t$ as follows: for all main branch nodes $n' \in \text{MB}(p_i)$ we have $e_i(n') = \text{id}^{-1} \circ f_i^{-1} \circ \text{id}''$. It is easy to see that for any node $n'' \in \text{MBN}(d)$ such that $n_i'' = \text{id}''(f_i(n''))$, we have $e(n'') = e_i(n')$ so all the predicate subtrees in $p_i$ can be mapped at $e_i(n')$ for all $n'$.

Since $t$ and $n$ were chosen at random, this concludes the proof of containment for $d \subseteq \bigcup_i p_i$. □

**Lemma 3.13.** If a tree pattern is equivalent to a union of tree patterns, then it is equivalent to a member of the union.

**Lemma 3.14.** Let $p = \bigcup_i p_i$ and $q = \bigcup_j q_j$ be two finite unions of tree patterns. Then $p \equiv q$ iff $\forall i, \exists j$ s.t. $p_i \equiv q_j$.

Given an DAG pattern $d$, by the normal form of $d$ (in short, $\text{nf}(d)$) we denote the equivalent formulation of $d$ as the union of incomparable interleavings with respect to containment.

Note that the set of interleavings $\mathcal{I}$ of a DAG pattern $p$ can be exponentially larger than $p$. Indeed, it was shown that the $XP^2$ fragment is not included in $XP$ (i.e., the union of its interleavings cannot always be reduced to one $XP$ query by eliminating interleavings contained in others) and that a DAG pattern may only be translatable into a union of exponentially many tree patterns ([Benedikt et al. 2005]). Nevertheless, testing if a DAG is satisfiable can be done in polynomial time.

**Definition 3.15.** A DAG pattern is union-free iff it is equivalent to a single tree pattern.

---

This is reminiscent of similar results from relational database theory, on comparing conjunctive queries with unions of conjunctive queries.
By Lemmas 3.12 and 3.13, a satisfiable pattern is union-free iff it has an interleaving that contains all other possible interleavings. A naive, exponential-time procedure to test union-freedom would thus be to generate all possible interleavings and to check whether one of them contains all others.

### 3.1. Additional notation

A /-pattern is a tree pattern that has only /-edges in the main branch. We call predicate subtree of a pattern $p$ any subtree of $p$ rooted at a non-main branch node. By a /-sub predicate $st$ we denote a predicate subtree whose root is connected by a /-path to the main branch node to which $st$ is associated. A //predicate is a predicate subtree connected by a //edge to the main branch. A tree skeleton is a tree pattern without //edges in predicate subtrees.

A prefix $p$ of a tree pattern $q$ is any tree pattern with $\text{ROOT}(p) = \text{ROOT}(q)$, $m = MB(p)$ a subpath of $MB(q)$ and having all the predicates attached to the nodes of $m$ in $q$. For instance, the pattern shown in Figure 1(c) is a prefix of the pattern of $q_2$, since it has all the nodes of $q_2$, except for the output one.

A lossless prefix $p$ of a tree pattern $q$ is any tree pattern obtained from $q$ by setting the output node to some other main branch node (i.e., an ancestor of $\text{OUT}(q)$). Note that this means that the rest of the main branch becomes a side branch, hence a predicate.

For a pattern $d$ and node $n \in \text{MBN}(d)$, by $\text{SP}_d(n)$ we denote the subpattern rooted at $n$ in $d$.

The compensate function generalizes the concatenation operation from [Xu and Özsoyoglu 2005], by copying extra navigation from the query into the rewrite plan. For $r \in XP^\cap$ and a tree pattern $p$, $\text{compensate}(r, p, n)$ returns the query obtained by deleting the first symbol from $x = \text{xpath}(\text{SP}_p(n))$ and concatenating the rest to $r$. For instance, the result of compensating $r = a/b$ with $x = b[c][d]/e$ at the $b$-node is the concatenation of $a/b$ and $[c][d]/e$, i.e., $a/b[c][d]/e$.

We also refer to the tokens of tree pattern $p$: more specifically, the main branch of a tree pattern $p$ can be partitioned by its sub-sequences separated by //edges, and each /-pattern from this partitioning is called a token. We can thus see a pattern $p$ as a sequence of tokens (/patterns) $p = t_1//t_2//\ldots//t_k$. We call $t_1$, the token starting with $\text{ROOT}(p)$, the root token of $p$. The token $t_k$, which ends by $\text{OUT}(p)$, is called the result token of $p$. The other tokens are denoted intermediary tokens, and by the intermediary part of a tree pattern we denote the sequence of intermediary tokens. Note that a tree pattern may have only one token, if it does not have //edges in the main branch. By a token-suffix of $p$ we denote any tree pattern defined by a suffix of the sequence of tokens $(t_1, \ldots, t_k)$. Symmetrically, we introduce the notion of token-prefix of $p$.

### 3.2. The rewriting problem

Given a set of views $V$, defined by $XP$ queries over a document $D$, by $D_V$ we denote the set of view documents $\{\text{doc}(v)|v \in V\}$, in which the topmost element is labelled with the view name. Given a query $r \in XP^\cap$ over the view documents $D_V$, we define $\text{unfold}(r)$ as the $XP^\cap$ query obtained by replacing in $r$ each $\text{doc}(v)/v$ with the definition of $v$.

We are now ready to describe the view-based rewriting problem. Given a query $q$ and a finite set of views $V$ over $D$ in a language $L \subseteq XP$, we look for an alternative plan $r$, called a rewriting, that can be used to answer $q$. We define rewritings as follows:

**Definition 3.16.** For a given document $D$, an $XP$ query $q$ and $XP$ views over $D$, a rewrite plan of $q$ using $V$ is a query $r \in XP^\cap$ over $D_V$. If $\text{unfold}(r) = q$, then we also say $r$ is a rewriting.

According to the definition above and the definition of $XP^\cap$, a rewriting $r$ is of the form $I = (\bigcap_{i,j} u_{ij}), I/\text{xpath}$ or $I//\text{xpath}$, with $u_{ij}$ of the form $\text{doc}(v_{ij})/v_{ij}/p_i$ or $\text{doc}(v_{ij})/v_{ij}//p_i$.

**Lemma 3.17.** A rewrite plan from $XP^\cap$ can be evaluated over a set of view documents $D_V$ in polynomial time in the size of $D_V$.

**Proof Sketch.** Consider a plan $r$ over a set of view documents $D_V$. $r$ gives a tractable evaluation strategy that: start from the document nodes and navigate from each of them down to the intersection node. All navigations can be done in PTIME, as they can be seen equivalently as tree navigation.
patterns. We can prove by induction on the structure of $r$ that the input of each intersection node is polynomial, hence its input is also polynomial, because the result is always a set (arity is 1), and it has at most as many elements as the largest of its inputs. Hence the size of each intermediate result is bounded by the size of the largest view. As the number of steps, navigation and intersections is constant w.r.t. $t$ (it is proportional to the size of $r$), the overall computation is in PTIME in $|D_V|$. 

**Completeness.** Hereafter, an algorithm is said to be complete for rewriting $L \subseteq XP$ if it solves the rewriting problem for queries and views in $L$, i.e., it finds a rewriting whenever one exists.

## 4. THE REWRITING ALGORITHM

Our approach for testing the existence of a rewriting (algorithm $\text{REWRITE}$) is the following: for each rewrite plan $r$ using views that satisfies certain conditions w.r.t the query $q$, we test whether its unfolding is equivalent to $q$. A remarkable feature of the algorithm is that it considers only a linear number of candidate plans. Indeed, we show in Section 7 that if a rewriting exists then one of these candidate plans is a rewriting, which implies the completeness of our algorithm. This result is a pleasant surprise, given that intuitively one would expect the number of distinct plans to be inspected to reflect the number of distinct subsets of views.

Testing equivalence between the tree pattern $q$ and a DAG pattern $d$ corresponding to the unfolding of $r$ will be the central task in our algorithm. As by construction the plans / DAGs to be considered will always contain $q$, testing equivalence will amount to testing the opposite containment, of $d$ into $q$.

However, Lemmas 3.12 and 3.13 imply that equivalence holds iff $d = \text{unfold}(r)$ has an interleaving $p_i$ such that $d \equiv p_i \equiv q$. From this observation, a naïve approach for the rewrite test would be to simply compute the interleavings of $d$ (a union of interleavings), check that this union reduces by containments to one interleaving $p_i$ (union-freedom), and that $p_i$ is equivalent to $q$. The reason we call this approach naïve is that the number of interleavings in the union can be exponential (recall Section 3), even when the unfolding of $r$ is equivalent to a single tree pattern. In this case, one "dominant" interleaving in the union will contain all others.

To avoid the cost of the naïve approach in these cases, we set out to directly detect the dominant interleaving prior to checking equivalence. We devise an algorithm, $\text{APPLY-RULES}$, that operates a series of transformations on the candidate rewrite plans, expressed in the form of nine rewrite rules. Starting from $d$, each rule application will produce an equivalent DAG pattern that is one step closer to the dominant interleaving that contains all others, if one such interleaving exists, i.e., if $d$ is union-free.

Our rule-based rewriting algorithm applies to any DAG patterns and is a decision procedure for union-freedom under practically relevant restrictions. More precisely, we show in Section 7 that under the restrictions, $\text{APPLY-RULES}(d)$ is a tree whenever $d$ is union-free. In general, this is not guaranteed and additional containment tests between the remaining possible interleavings may be necessary to find one $p_i$ such that $p_i \equiv d$. Nevertheless, using $\text{APPLY-RULES}$ can be beneficial even in the general case, by reducing the number of interleavings we have to check.

We give below the global form of our rule-based algorithm. Section 5 will be dedicated to the detailed description of each of the nine rules, showing that they preserve equivalence. We will discuss several possible optimizations and strategies for triggering rewrite rules in Section 11. Section 7 shows PTIME complexity for $\text{APPLY-RULES}$.

**APPLY-RULES**($d$)

1. repeat
2. repeat apply R1 to $d$
3. until no change
4. repeat apply R2-R9 to $d$, in arbitrary order
5. until no change
6. until no change

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We use APPLY-RULES in the REWRITE algorithm, that rewrites \( q \) using views \( \mathcal{V} \):

\[
\text{REWRITE}(\mathcal{V}, \mathcal{V})
\]

1. \( \text{Prefs} \leftarrow \{(p, \{v_i, b_i\}) \mid v_i \in \mathcal{V}, p \text{ a lossless prefix of } q, b_i \in \text{MB}(p), \exists \text{ a root-mapping } h \text{ from } u_i = \text{pattern}(v_i) \text{ into } p, h(\text{OUT}(u_i)) = b_i\} \)

2. \( \text{for } (p, W) \in \text{Prefs} \)

3. \( \text{do let } \mathcal{V}' \leftarrow \{\text{compensate}(\text{doc}(\text{"v"})/v, p, b) \mid (v, b) \in W\} \)

4. \( \text{let } r \text{ be the } \mathcal{X} \mathcal{P} \mathcal{R} \text{ query } \left(\bigcap_{v_j \in \mathcal{V}'} v_j\right) \)

5. \( \text{let } d \text{ be the DAG corresponding to } \text{unfold}(r) \)

6. \( \text{APPLY-RULES}(d) \)

7. \( \text{if } d \subseteq p \)

8. \( \text{then return } \text{compensate}(r, q, \text{OUT}(p)) \)

9. \( \text{return fail} \)

REWRITE starts the construction of rewrite-plan candidates by collecting the sets of relevant compensated views w.r.t. the input query or lossless prefixes thereof. For each prefix \( p \) in separation, all possible compensated views are combined in the intersection step. The resulting DAG pattern is then tested for equivalence w.r.t. \( p \), and if this holds (i.e., we have a rewriting for \( p \)) this prefix is compensated once more to obtain a rewriting for \( q \). At line 8, if \( p \) is \( q \) itself, compensate returns just \( r \), as all needed navigation had already been added at line 3. Note that \( d \) is, in all cases, satisfiable, because we intersect views that contain a satisfiable query. Note also that, while the output of APPLY-RULES may be an arbitrary DAG, the algorithm always returns the initial DAG (plus some compensation), thus ensuring straight-forward conversion towards an \( \mathcal{X} \mathcal{P} \mathcal{R} \) expression.

As an extension to REWRITE, ALL-REWRITES searches for all the rewritings of \( q \) using views \( \mathcal{V} \):

\[
\text{ALL-REWRITES} \quad \text{– same code as REWRITE with the modifications:}
\]

— replace line 2 with: \( \{\text{for } (p, U) \in \text{Prefs for } W \subseteq U\} \)

— remove line 8

— continue to run even when the return at line 8 is reached.

While we will show in Theorem 7.2 that REWRITE is sound and complete for all queries and views in \( \mathcal{X} \mathcal{P} \), its complexity depends on that of the containment test on line 7. While in general this containment test is hard, it becomes efficient if \( d \) is a tree. We identify fairly permissible restrictions under which the resulting \( d \) is always a tree (thus allowing the containment test in \( \text{PTIME} \)), and consider a specialized version of REWRITE, as below:

EFFICIENT-RW – same code as REWRITE, with the following modification

— line 7 becomes: \( \text{if } d \text{ is a tree then if } d \subseteq p. \)

As mentioned above, the number of plans to be considered is linear, and both APPLY-RULES and the containment test when \( d \) is a tree have \( \text{PTIME} \) complexity, thus announcing overall polynomial complexity for EFFICIENT-RW. We indeed show in Section 7 that EFFICIENT-RW always runs in \( \text{PTIME} \). Moreover, we show that under fairly permissible and practically relevant restrictions, the resulting \( d \) is always a tree, thus EFFICIENT-RW becomes sound and complete.

5. THE REWRITE RULES (OF SUBROUTINE APPLY-RULES)

We present in this section a set of rewrite rules, such that each application of one of the rules brings the DAG pattern one step closer to a tree pattern. We will prove that the result of APPLY-RULES is always equivalent to the original DAG. This implies that REWRITE gives a sound algorithm for the rewriting problem, and we will show it is also a decision procedure.

We present the rules R1-R9 as pairs formed by a test condition, which checks if the rule is applicable, and a graphical description, which shows how the rule transforms the DAG. The left-hand
side of the rule description will match main branch nodes and paths in the DAG. If the matching
nodes and paths verify the test conditions, then the consequent transformation is applied on them.
Each transformation either

— collapses two main branch nodes \( n_1, n_2 \) into a new node \( n_{1,2} \) (which inherits the predicate sub-
trees, incoming and outgoing main branch edges),
— removes some redundant main branch nodes and edges, or
— appends a new predicate subtree below an existing main branch node.

**Graphical notation.** We use the following notation in the illustration of our rewrite rules: linear
paths corresponding to part of a main branch are designated in italic by the letter \( p \), nodes are
designated by the letter \( n \), the result of collapsing two nodes \( n_i, n_j \) will be denoted \( n_{ij} \), simple lines
represent \(-\)edges, double lines represent \(/\)-edges, simple dotted lines represent \( -\)-paths, and double
dotted lines represent arbitrary paths (may have both \(-\) and \(/\)). We only represent main branch nodes
or paths in the depiction of rules (predicates are omitted). Exception are rules R5 and R9, where
we need to refer to a subtree predicate, respectively a \(/\)-subpredicate, by its XP expression \([Q]\). We
refer to the tree pattern containing just a main branch path \( p \) simply by \( p \), and to the tree pattern
having \( p \) as main branch by \( \text{TP}_d(p) \): for a main branch path \( p \) in \( d \), given by a sequence of nodes
\((n_1, \ldots, n_k)\), we define \( \text{TP}_d(p) \) as the tree pattern having \( p \) as main branch, \( n_1 \) as root and \( n_k \) as
output, plus all the predicate subtrees (from \( d \)) of the nodes of \( p \). We represent by a rhombus main
branch paths that are not followed by any \( / \) (main branch) edge. Paths include their end points.

**Test Conditions.** In the test conditions, we say that a pattern \( d \) is immediately unsatisfiable if
by applying to saturation rule R1 on it we reach a pattern in which either there are two \(-\)-paths of
different lengths but with the same start and end node, or there is a node with two incoming
\(-\)-edges \( \lambda_1/\lambda \) and \( \lambda_2/\lambda \), such that \( \lambda_1 \neq \lambda_2 \). Note that the test of immediate unsatisfiability is just a
sufficient condition for the unsatisfiability of the entire DAG. For instance, a DAG pattern that has
in parallel the branches \( \text{doc}(["L"])/\text{paper}/\text{section} \) and \( \text{doc}(["L"])/\text{book}/\text{section} \) is not satisfiable yet R1
does not apply on it.

**Definition 5.1.** We say that two \(-\)-patterns \( p_1, p_2 \) are similar if (a) their main branches have the
same code, and (b) both have root mappings into any pattern \( p_{1,2} \) built from \( p_1, p_2 \) as follows:

1. choose a code \( i_{1,2} \) and a total onto function \( f_{1,2} \) that maps the nodes of \( m_{1,2} = \text{MBN}(p_1) \cup
\text{MBN}(p_2) \) into \( i_{1,2} \) such that:
   a) for any node \( n \) in \( m_{1,2} \), \( \text{LABEL}(f_{1,2}(n)) = \text{LABEL}(n) \)
   b) for any \(-\)-edge \( (n_1, n_2) \) in the main branch of \( p_1 \) or \( p_2 \), the code \( i_{1,2} \) contains
      \( f_{1,2}(n_1)/f_{1,2}(n_2) \)
2. build the minimal pattern \( p_{1,2} \) such that:
   a) \( i_{1,2} \) is a code for the main branch \( \text{MB}(p_{1,2}) \),
   b) for each node \( n \) in \( \text{MBN}(p_1) \cup \text{MBN}(p_2) \) and its image \( n' \) in \( \text{MB}(p_{1,2}) \) (via \( f_{1,2} \)), if a
predicate subtree \( st \) appears below \( n \) then a copy of \( st \) appears below \( n' \), connected by the
same kind of edge.

**Example 5.2.** For instance, the patterns \( p_1 = \text{a}/\text{b}/\text{c}/\text{d}/\text{e} \) and \( p_2 = \text{a}/\text{b}/\text{e}/\text{b}/\text{d}/\text{c} \) are similar,
given that the patterns \( p_{1,2} \) that can be built from them, according to Definition 5.1 are of the
form (before minimization) \( p_{1,2} = \text{a}/\text{b}/\text{e}/\text{b}/\text{d}/\text{c}/\text{e} \), \( p_{1,2} = \text{a}/\text{b}/\text{e}/\text{b}/\text{d}/\text{c}/\text{e} \) or
\( p_{1,2} = \text{a}/\text{b}/\text{e}/\text{b}/\text{d}/\text{c}/\text{e} \).

For two nodes \( n_1, n_2 \in \text{MBN}(d) \), such that \( \lambda_d(n_1) = \lambda_d(n_2) = \lambda \), by \( \text{collapse}_d(n_1, n_2) \) we
denote the DAG obtained from \( d \) by replacing \( n_1 \) and \( n_2 \) with a \( \lambda \)-labeled node \( n_{1,2} \) that inherits the
incoming and outgoing edges of both \( n_1 \) and \( n_2 \). We say that two nodes \( n_1, n_2 \) are collapsible if
they have the same label and the DAG pattern \( \text{collapse}_d(n_1, n_2) \) is not immediately unsatisfiable.

We have now all the ingredients to present the rewrite rules. With each rule presentation we will
also prove soundness, i.e., that equivalence is preserved. We thus have the following result:
**Proposition 5.3.** The application of any of the rules from the set R1-R9 on a DAG \( d \) produces another DAG \( d' \) such that \( d' \equiv d \).

We use the following schema for the soundness proofs. Each rule \( r \) in our set has an associated function \( f_r \), that takes a DAG \( d \) as input and outputs another DAG \( f_r(d) \) that is the result of applying \( r \) to \( d \). By the way rules transform \( d \), the containment \( f_r(d) \subseteq d \) is immediate. We will thus discuss why \( d \subseteq f_r(d) \) holds after any rule \( r \) triggers, proving in fact the following lemma.

**Lemma 5.4.** For a rule \( r \), a DAG \( d \) and a document \( t \), if \( d \) has an embedding \( e \) in \( t \) and \( r \) is applicable to \( d \), then \( f_r(d) \) has also an embedding \( e' \) into \( t \) such that \( e(\text{OUT}(d)) = e'(\text{OUT}(f_r(d))) \).

**Remark 1.** Lemma 5.4 implies that \( d \subseteq f_r(d) \) and since the opposite containment mapping trivially holds, Proposition 5.3 follows immediately (i.e., \( d \equiv f_r(d) \)).

5.1. Rule R1

This rule triggers when \( \lambda_d(n_1) = \lambda_d(n_2) \)

\[
(R1.i) \quad n_1 \rightarrow \quad n_2 \qquad \rightarrow \quad n_{1,2} \\
(R1.ii) \quad n_2 \rightarrow \quad n_1 \qquad \rightarrow \quad n_{1,2}
\]

**Example 5.5.** The DAG pattern that would be obtained by intersecting some two views `doc("L")/paper/...` and `doc("L")/paper/...` would be subject to R1’s application, with \( n_1 \) and \( n_2 \) being its two nodes labeled `paper`.

**Proof for Lemma 5.4 - Soundness of R1.** \( n_1 \) and \( n_2 \) belong to two different main branches, but they have a common parent \( n \). (Remember that all paths depicted in the rules are part of main branches.) Remember also that, by the definition of a main branch, the branches of \( n/n_1 \) and \( n/n_2 \) have at least one common node below \( n \) \( \text{OUT}(d) \). Then, in any embedding \( e \) of \( d \) into a tree \( t \), \( n/n_1 \) and \( n/n_2 \) need to map in the same path of \( t \) and it must be true that \( e(n_1) = e(n_2) = x \), where \( x \in \text{NODES}(t) \). Thus there is also an embedding \( e' \) from \( f_{R1}(d) \) into \( t \) that maps \( n_{1,2} \) into \( x \) and is equal to \( e \) on all the other nodes. \( \Box \)

5.2. Rule R2

This rule triggers if \( n_1 \) and \( n_2 \) are not collapsible and \( n_2 \) is not reachable from \( n_1 \) (resp. \( n_1 \) is not reachable from \( n_2 \), in the case of R2.ii).

\[
(R2.i) \quad n_1 \rightarrow \quad n_2 \qquad \rightarrow \quad n_{2,1} \\
(R2.ii) \quad n_2 \rightarrow \quad n_1 \qquad \rightarrow \quad n_{1,2}
\]

**Example 5.6.** Notice the application of rule R2.i in our running example (Figure 1), with \( n_1 \) being the node labeled `lib` and \( n_2 \) being the node labeled `paper` in the left branch of the DAG pattern. Symmetrically, rule R2.ii applies with \( n_1 \) being the node labeled `figure` and \( n_2 \) being the node labeled `section` in the left branch of the DAG pattern.

**Proof for Lemma 5.4 - Soundness of R2.** We first discuss R2.i. Let \( n_0 \) be the parent of \( n_1 \) and \( n_2 \). From the condition that \( n_1 \) and \( n_2 \) are not collapsible, we infer that either they have different labels, or the pattern obtained by trying to collapse \( n_1 \) and \( n_2 \) is immediately unsatisfiable.
Both cases imply that, for an embedding \( e \) into \( t \), we cannot have \( e(n_1) = e(n_2) \). The former case is obvious. For the latter, supposing that \( e(n_1) = e(n_2) = x \), we observe that the beginning of main branches under \( n_1 \) and \( n_2 \), formed only by /-edges, call them \( p_{n_1} \) and \( p_{n_2} \) respectively, need to map into the same nodes under \( x \) (as all main branches have at least one common ending point, \( \text{OUT}(d) \), and we are mapping them into a tree). Then the pattern obtained by collapsing \( n_1 \) and \( n_2 \) would also have an embedding into \( t \), that can be computed from \( e \) by equating nodes \( n_1 \) and \( n_2 \). But this contradicts the assumption that the pattern obtained by trying to collapse \( n_1 \) and \( n_2 \) is immediately unsatisfiable. Hence, for an embedding \( e \) into \( t \), \( e(n_1) \neq e(n_2) \), and, since \( e(n_1) \) has to be a child of \( e(n_0) \), \( e(n_2) \) has to be a strict descendant of \( e(n_1) \). This guarantees that \( n_0/n_1/n_2 \) will also map into \( t \) if \( d \) does.

The proof for R2.ii is very similar to the one for R2.i. \( \square \)

5.3. Rule R3.i

This rule triggers if the following conditions hold:

— \( p_1 \equiv p_2 \),
— each of \( p_2 \)'s nodes has only one incoming main branch edge,
— \( \text{TP}_d(p_2) \) contains \( \text{TP}_d(p_1) \).

Example 5.7. Notice the application of this rule in our running example (Figure 1), with \( n_1 \) and \( n_2 \) being the two nodes labeled paper and the paths \( p_1 \) and \( p_2 \) consisting of only these nodes.

Proof for Lemma 5.4 - Soundness of R3.1. Let \( n_0 \) be the parent of \( n_1 \) and \( n_2 \). For convenience, let us first rename \( n_1 \) by \( n'_1 \) and \( n_2 \) by \( n'_2 \), let \( p_1 \) be defined by the sequence of nodes \( (n'_1, \ldots, n'_k) \) and let \( p_2 \) be defined by the sequence of nodes \( (n''_1, \ldots, n''_k) \). We know that \( \lambda_d(n'_i) = \lambda_d(n''_i) \), for each \( i = 1, k \).

Note that by applying R1 to saturation (after R3.i) all the pairs \( (n'_i, n''_i) \) will be collapsed. By \( f_{\text{R3i}}(d) \) we denote directly the result of R3i followed by these R1 steps. Let \( n_{1i} \in \text{MBN}(f_{\text{R3i}}(d)) \) denote the node that results from the collapsing of the \( (n'_i, n''_i) \) pair.

First, if the two main branches \( n_0/p_1 \) and \( n_0/p_2 \) contain the output node, for any embedding \( e \), \( e(n'_i) \) needs to be equal to \( e(n''_i) \) and likewise, for each \( i \) the image of \( n'_i \) needs to be equal to the one of \( n''_i \). The reason is that the two branches have the same endpoints \( (n_0 \) and \( \text{OUT}(d)) \), the same length and, since \( p_1 \) has no /-edge, \( n_0/p_1 \) needs to be isomorphic to the path from \( e(n_0) \) to \( e(\text{OUT}(d)) \). Thus, it is obvious that by merging each \( n'_i \) and \( n''_i \) we obtain a pattern that also has an embedding, if \( d \) does, and it maps \( \text{OUT}(d) \) into the same node.

Let us now assume that \( p_2 \) ends above \( \text{OUT}(d) \). Let \( m \) be the function from \( d \) into \( d \) that maps \( \text{TP}_d(p_2) \) into \( \text{TP}_d(p_1) \) and is the identity everywhere else (in particular, \( m(p_2) = p_1 \)). We can show that \( e \circ m \) is another embedding of \( d \) into \( t \), one that takes each pair \( n'_i, n''_i \) into the same image and preserves the image of the output. The main reason is that \( p_1 \) and \( p_2 \) contain only /-edges, hence they can map only into a sequence of /-edges in \( t \). And since the branches containing \( p_1 \) and \( p_2 \) respectively both start at \( n_0 \) and meet at \( \text{OUT}(d) \) or at some other node above it, they have to map into the same path \( p \) of \( t \), from \( e(n_0) \) to \( e(\text{OUT}(d)) \). So \( e(n'_i) \) is either above or equal to \( e(n''_i) \), because \( n'_i \) is connected by a /-edge to its parent \( n_0 \). But then all the nodes on \( p_1 \) map above or in the same place in \( p \) as the nodes of \( p_2 \); in particular \( e(n'_k) \) is above the image of any main branch node \( n \) that is /-child of \( n''_k \). Therefore \( e \circ m \) satisfies the condition imposed by the /-edge between \( n'_k \) and \( n \). All the other conditions for showing \( e \circ m \) is an embedding follow directly from the fact \( e \) is an embedding. The image of \( \text{OUT}(d) \) is the same in \( e \circ m \) and \( e \), since \( \text{OUT}(d) \) is not part of \( p_2 \).
We argue now that \( e \circ m \) is also an embedding for the DAG \( d' \) obtained from \( d \) as follows: (a) for each \( i \), append the predicate subtrees of \( n''_k \) below \( n'_i \), (b) remove the edge \( n_0/n''_1 \) and the tree pattern \( TP_d(p_2) \), and (c) connect the dangling incoming \( \ell\)-edges of children of \( n''_k \) to \( n \). (By the test conditions these must be the only dangling edges.)

But \( f_{R3}(d) \) has a straightforward mapping \( h \) into \( d' \), as \( h = \{ n_{ii} \mapsto n'_i; x \mapsto x \text{ elsewhere} \} \), hence we obtain the desired embedding \( e' \) as \( h \circ e \circ m \), with \( e'(\text{OUT}(f_{R3}(d))) = e(\text{OUT}(d)) \). □

5.4. Rule R3.ii

This rule triggers if the following conditions hold:

— \( p_1 = p_2 \),
— each of \( p_2 \)'s nodes has only one outgoing main branch edge,
— \( TP_d(p_2) \) contains \( TP_d(p_1) \).

**Proof for Lemma 5.4 - Soundness of R3.ii.** We can use same argument as for R3.i. □

5.5. Rule R4.i

The rule triggers if the following conditions hold for all nodes \( n_4 \):

— \( n_3 \) has one incoming main branch edge, all other nodes of \( p_2 \) have one incoming and one outgoing main branch edge,
— there exists a mapping from \( TP_d(p_2) \) into \( SP_d(n_1) \), mapping all the nodes of \( p_2 \) into nodes of \( p_1 \).
— the path \( p_2//n_4 \) does not map into \( p_1 \).

**Example 5.8.** The DAG pattern that would be obtained by intersecting some two views \( \text{doc("L")//lib//paper//section//...//figure//caption} \) and \( \text{doc("L")//lib[//caption]//section//theorem//...} \) would be subject to R4.1's application, with \( p_1 \) being the path corresponding to \( \text{lib//paper//section} \), \( p_2 \) being the path corresponding to \( \text{lib//section} \), and \( n_4 \) being the node labeled theorem.

**Proof for Lemma 5.4 - Soundness of R4.1.** Let \( n_0 \) be the parent of \( n_1 \) and \( n_2 \). Suppose that \( d \) has an embedding \( e \) into a tree \( t \). \( p_1 \) and \( p_2 \) are parts of main branches starting from \( n_0 \) and ending in a common node, at or above \( \text{OUT}(d) \). Hence, if \( d \) has an embedding \( e \) into a tree \( t \), the nodes of \( p_1 \), of \( p_2 \) and each \( n_4 \) must all map into the same path \( p \) of \( t \). Moreover, since \( n_0/p_1 \) has only \( \ell \)-edges, it is necessarily isomorphic to the fragment of \( p \) starting at \( n_0 \) and of length \( |p_1| + 1 \).

Let \( n_5 \) be the end node of \( p_1 \) and \( n_3 \) the end node of \( p_2 \). With necessity, either there is a node \( n' \in p_1 \) such that \( e(n_3) = e(n') \) or \( e(n_3) \) is below \( e(n_5) \). In the former case, we can show that for any \( n_4 \) there is no node \( n'' \) of \( p_1 \) such that \( e(n'') = e(n_4) \). For a given \( n_4 \), let us assume that such a node \( n'' \) exists. Since \( p_1 \) is isomorphic to \( e(p_1) \), and the mapping of \( p_2//n_4 \) through \( e \) would imply also a mapping of \( p_2//n_4 \) into a suffix of \( p_1 \), this leads to a contradiction. Since \( n_0/p_1 \) is isomorphic to the beginning of \( p \), it means that \( e(n_4) \) is below \( e(n_5) \). But then we can also map all nodes of

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$f_{R4i}(d)$ exactly following $e$ because $e$ verifies the condition imposed by the $//\text{-edge}$ between $p_1$ and $n_4$ and the part that was removed ($p_2$) was not connected to other main branches. Moreover, the image of the output is the same, because $\text{OUT}(d)$ is below $p_1$ and $f_{R4i}(d)$ keeps all nodes under $p_1$ unchanged.

If $e(n_3)$ is below $e(n_5)$ in $t$, then, following the same reasoning, we can argue that $e$ can be reused to map the nodes of $f_{R4i}(d)$ into $t$.  

5.6. Rule R4.ii

This rule triggers if the following conditions hold for all nodes $n_4$:

— $n_3$ has only one outgoing main branch edge, all the other nodes of $p_2$ have one incoming and one outgoing main branch edge,

— there exists a mapping from $\text{TP}_d(p_2)$ into $\text{TP}_d(p_1)$, mapping all the nodes of $p_2$ into nodes of $p_1$,

— the path $n_4//p_2$ does not map into $p_1$.

PROOF FOR LEMMA 5.4 - SOUNDNESS OF R4.ii. Proof similar to R4.i: here the rule’s test condition guarantees that, in any embedding, the beginning of $p_1$ is mapped below $n_4$.  

5.7. Rule R5

This rule triggers if the following conditions hold:

— $n_2$ and $n_3$ are collapsible and $p_1 \equiv p_3$,

— pattern $\lambda_d(n_2)[Q]$ does not have a root-mapping into $\text{SP}_d(n_2)$,

— for any node $n_4$ in $p_2$ such that $d' = \text{collapse}_d(n_4, n_3)$ is not immediately unsatisfiable, pattern $\lambda_d(n_2)[Q]$ has a root mapping into $\text{SP}_d(n_2)$,

— if there is no path from $n_3$ to a node of $p_2$, there has to be a root-mapping from pattern $\lambda_d(n_2)[Q]$ into the pattern obtained from $\text{TP}_d(p_2)$ by appending $[Q]$’s pattern, via a $//\text{-edge}$, below the node $\text{OUT}(\text{TP}_d(p_2))$.

(Special case: $p_1$ and $p_3$ empty.)

Example 5.9. The DAG pattern that would be obtained by intersecting some two views doc("L")/lib/paper/section//... and doc("L")//paper[.//caption]/... would be subject to R5’s application, copying the predicate [./caption] on the node labeled paper coming from the former view.

PROOF FOR LEMMA 5.4 - SOUNDNESS OF R5. Let $st$ denote the subtree predicate introduced by $f_{R5}(d)$ on $n_2$, and let $st'$ denote its copy under $n_3$. Given the embedding $e$ of $d$ in $t$, there are three possible cases:

(1) the image of $n_3$ is the same with the image of $n_2$,

(2) the image of $n_3$ is the same with the image of some other node $n_4$ from $p_2$.  

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(3) the image of \( n_3 \) is below the image of any node from \( p_2 \).

In the first case, \( e \) gives immediately an embedding \( e' \) of \( f_{R5}(d) \) in \( t \), since \( st' \) has already an image in the subtree rooted at \( e(n_3) \).

In the second case, we can first conclude that the DAG pattern \( d' = collapse_e(n_4, n_3) \) must not be immediately unsatisfiable. This is because \( e \) gives also an embedding \( e'' \) from \( d' \) in \( t \), one that maps the node \( n_{3,4} \) into \( e(n_3) = e(n_4) \). Let us now consider the tree pattern \( p = pattern(\lambda_d(n_2)[Q]) \), which modulo renaming is the pattern formed by the main branch node \( n_2 \) and the predicate subtree \( st \). Since we know that \( p \) maps into \( SP_e(p_2) \), by some mapping \( f \), we can also build a containment mapping \( \bar{f} \) from \( f_{R5}(d) \) into \( d' \), defined as follows: (a) \( n_3 \) and \( n_4 \) have the same image, \( n_{3,4} \), (b) \( \bar{f} = f(n) \) for all the nodes \( n \) of \( st \) and (c) \( \bar{f} \) is the identity mapping for all the other nodes. Finally, we obtain the embedding \( e' \) as the composition \( e'' \circ \bar{f} \).

In the third case, let us consider the DAG pattern \( d' \) obtained from \( d \) by appending the pattern of \( Q \) below \( OUT(TP_d(p_2)) \), via an \( \ll \)-edge (as described in the rule condition). Note that since the image of \( n_3 \) under \( e \) is below the image of any node from \( p_2 \), we can easily obtain from \( e \) an embedding \( e'' \) from \( d' \) into \( t \).

Moreover, by the test condition, we have a root-mapping \( f \) from \( pattern(\lambda_d(n_2)[Q]) \) into the modified pattern, \( TP_d(p_2) \). From \( f \) we will construct a mapping \( \bar{f} \) from \( f_{R5}(d) \) in \( d' \).

Let \( st \) be new subtree predicate in \( f_{R5}(d) \), corresponding to \( [Q] \) at node \( n_2 \). We define \( \bar{f} \) from \( f_{R5}(d) \) in \( d' \) as follows: (a) \( \bar{f} \) is the identity function for nodes outside \( st \) and (b) \( \bar{f}(n) = f(n) \) for all the nodes \( n \) in \( st \).

Finally, by the composition \( e'' \circ \bar{f} \) we obtain an embedding of \( f_{R5}(d) \) into \( t \). □

5.8. Rule R6

This rule triggers if the following conditions hold:

— \( n_3, n_4 \) have only one incoming main branch edge, all other nodes of \( p_1 \) and \( p_2 \) have one incoming and one outgoing main branch edge,

— \( TP_d(p_1) \) and \( TP_d(p_2) \) are similar.

![Diagram](image.png)

Example 5.10. The DAG pattern that would be obtained by intersecting some two views `doc("L")//lib/paper[.//caption//section//...` and `doc("L")//lib[//figure//paper//section//...` would be subject to R6’s application, with the paths \( p_1 \) and \( p_2 \) corresponding to the `lib/paper/section` parts of the views.

**Proof for Lemma 5.4 - Soundness of R6.** Let \( n_0 \) be the parent of \( n_4 \) and \( n_2 \). For convenience, let us first rename \( n_1 \) by \( n'_1 \) and \( n_2 \) by \( n'_2 \), let \( p_1 \) be defined by the sequence of nodes \( (n'_1, \ldots, n'_k) \) and let \( p_2 \) be defined by the sequence of nodes \( (n''_0, \ldots, n''_k) \). We know that \( \lambda_d(n'_i) = \lambda_d(n''_i) \), for each \( i = 1, k \).

As mentioned, our rule-rewriting algorithm would behave in the same way if R6 collapsed the entire \( p_1 \) and \( p_2 \) paths. To simplify the presentation of the rules, we delegated to R1 this task. However, to simplify the presentation of the proof, we will consider the pattern \( d'' \), representing the result of applying R6 followed by these R1 steps. Let \( n_{ii} \in MBN(d'') \) denote the node that results from the collapsing of the \( (n'_i, n''_i) \) pairs. It is easy to see that there is always a mapping \( h \) from \( f_{R6}(d) \) into \( d'' \), given by the composition of the applications of \( f_{R1} \) that merge all these \( (n'_i, n''_i) \) pairs. Hence, it is sufficient to show that for any embedding \( e \) of \( d \) into a tree \( t \), there is an embedding \( e' \) of \( d'' \) into \( t \), which guarantees that \( e' \circ h \) is an embedding of \( f_{R6}(d) \) into \( t \).
Let us consider any embedding \( e \) of \( d \) in a tree \( t \). We have three possible cases:

1. the image of \( n_1' \) is the same with the image of \( n_1'' \),
2. the image of \( n_1' \) is above the image of \( n_1'' \),
3. the image of \( n_1' \) is above the image of \( n_1'' \).

In the first case, \( e \) gives immediately an embedding \( e' \) of \( d'' \) into \( t \), since the nodes of \( p_1 \) and \( p_2 \) have the same images.

In the second case, let \( e(p_1) \) denote the image of \( p_1 \) in \( t \). We show that the function \( e' \) from \( d'' \) into \( t \) which: (a) for each \( i \) maps \( n_{ii} \) into \( e(n_{ii}') \), and (b) maps \( n \) into \( e(n) \) for all the nodes \( n \) outside \( TP_d(n_{11}/\ldots/n_{kk}) \), can be extended to a full embedding of \( d'' \) into \( t \). For that, we must show that all the predicate subtrees rooted at \( n_{ii} \) nodes can be mapped in the subtree rooted at \( e(n_{ii}') \). Since predicate subtrees from \( n_i' \) obviously have an image at \( e(n_i') \), \( e' \) is defined by \( e \) on these nodes. What remains is to describe \( e' \) over the predicates subtrees that originate at \( n_i'' \) nodes.

Since \( TP_d(p_1) \) and \( TP_d(p_2) \) are similar, we always have a root-mapping from both \( l \)-patterns into any \( p_{12} \), as given in Definition 5.1. Note that the embedding \( e \) (as any other embedding of \( d \) in general) imposes an order on the nodes of \( p_1 \) and \( p_2 \), consistent with their \( l \)-edges. We can thus always find an associated pattern \( p_{12} \) that has an embedding in the subtree rooted at \( e(n_{ii}') \) in \( t \). Let the pattern fixed in this way be \( p \) and let his embedding into the subtree rooted at \( e(n_{ii}') \) be \( e'' \). Let \( f_2 \) be the root-mapping of \( TP_d(p_2) \) into \( p \) (by definition, we can always find such an \( f_2 \)).

We can now define \( e' \) over the predicates subtrees of \( n_{ii} \)'s that originate at \( n_i'' \)'s using \( e'' \circ f_2 \).

By symmetry, the third case can be handled in the same manner. \( \square \)

5.9. Rule R7

This rule triggers if the following conditions hold:

— the nodes of \( p_2 \) have only one incoming and one outgoing main branch edge,
— there exists a mapping from \( TP_d(p_2) \) into \( SP_d(n_1) \), such that the nodes of \( p_2 \) are mapped into nodes of \( p_1 \).

![Diagram](image)

Example 5.11. Notice the application of this rule in our running example (Figure 1), with \( p_1 \) and \( p_2 \) corresponding to the two paths paper//section//figure in parallel.

Proof for Lemma 5.4. Soundness of R7. With \( n_3 \) and \( n_4 \) denoting the end points of \( p_2 \), \( n_1 \) denoting the common parent of \( p_1 \) and \( p_2 \), let \( n_2 \) denote the image of \( n_3 \) under the mapping from \( TP_d(p_2) \) into \( SP_d(n_1) \).

Since \( n_3, n_4 \) and \( p_2 \) are not connected to any other parts of the DAG, for any embedding \( e \) into a tree \( t \), the restrictions \( e' \) of \( e \) to \( NODES(d) \setminus \{n|n \in p_2\} \) is a partial embedding into \( t \) (because \( n_3, n_4, p_2 \) do not affect the conditions needed to embed the other nodes of \( d \). But \( e' \) is a total embedding for \( f_{\pi}(d) \) and \( e'(OUT(f_{\pi}(d))) = e'(OUT(d)) = e(OUT(d)) \). \( \square \)

5.10. Rule R8

This rule triggers if the following conditions hold:

— the nodes of \( p_2 \) have only one incoming and one outgoing main branch edge,
— in any possible mapping of \( p_2 \) into \( p_1 \) the image of \( n_2 \) is \( n_1 \).
Example 5.12. The DAG pattern that would be obtained by intersecting some two views `doc("L")/lib/paper/section/figure/image` and `doc("L")//paper[.//caption]//image` would be subject to R8’s application, with $n_1$ and $n_2$ corresponding to the two nodes labeled `paper`.

Proof for Lemma 5.4 - Soundness of R8. Let $n_0$ denote the common parent of the two branches in parallel, and let $n_3$ denote their common child node. As the branches of $p_1$ and $p_2$ are fragments of main branches between the nodes $n_0$ and $n_3$, and $n_0/p_1/n_3$ has only /-edges, we can argue, as for R7, that for any embedding $e$ into a tree $t$, $p_1$ and $e(p_1)$ are isomorphic. Also, $e(p_2) \subseteq e(p_1)$, as the nodes of $e(p_2)$ must lie on the same path fragment, between $e(n_0)$ and $e(n_3)$. Since $p_1 \rightarrow e(p_1)$ is an isomorphism, there is an inverse mapping $i$ from $e(p_1)$ into $p_1$ which is surjective. But $e(p_2) \subseteq e(p_1)$, hence $g = i \circ e$ is a mapping from $p_2$ into a suffix of $p_1$. As we assumed the conditions of R8 to be satisfied, it follows that $g(n_2) = n_1 \Leftrightarrow e(n_2) = e(n_1)$, for any embedding $e$. But then, if we take

$$e'(x) = \begin{cases} e(n_1)(= e(n_2)), & \text{if } x = n_{1,2} \\ e(x), & \text{otherwise} \end{cases}$$

$e'$ will be an embedding for $f_{R8}(d)$ with $e'(\text{OUT}(f_{R8}(d))) = e(\text{OUT}(d))$. □

5.11. Rule R9

For any /-subpredicate $Q$ in $d$, any node $n$ in $p_1$ s.t. the presence of $Q$ as predicate at $n$ on $p_1$ would verify the condition of extended skeletons (see Section 7), the rule triggers if

— the nodes of $p_2$ have only one incoming and one outgoing main branch edge, and
— for all mappings $\psi_i$ of $p_2$ into $p_1$,
— for $d'$ being the pattern obtained from $d$ by collapsing each $n_i \in p_2$ with $\psi(n_i)$,
— we have that $\text{pattern}(\lambda_d(n)[Q])$ has a root-mapping into $\text{SP}_{d'}(n)$.

(Special cases: $Q$ is attached to a node of $p_2$ itself, or $Q$ is a full predicate in $d$, or both.)

Remark. This rule was not included in the extended abstract published in [Cautis et al. 2008], but it is required to achieve completeness.

Example 5.13. The DAG pattern that would be obtained by intersecting some two views `doc("L")/lib/section/section/section[figure]/image` and `doc("L")//section[figure]/section[figure]/image` would be subject to R9’s application, with predicate $Q$ being [figure] and the node $n$ corresponding to the second node labeled section in the former view. Note that only after adding $Q$ on node $n$ R7 can apply, removing the branch from the latter view and yielding a tree pattern `doc("L")/lib/section/section[figure]/section[figure]/image`.

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PROOF FOR **LEMMA 5.4 - SOUNDNESS OF R9.** The conditions ensure that in any possible interleaving of $d$, in particular in any interleaving of the parts $p_1$ and $p_2$, the predicate $[Q]$ will be present at the position of $n$. Equivalence follows.

**Remark.** Some of the rules, such as R3 or R6, could safely collapse several nodes, without changing any of the results in Section 7. We opted for the current version for ease of presentation.

**Example 5.14.** We illustrate in Figure 1 how the unfolding of the intersection of views $v_1$ and $v_2$ from the running example is rewritten it into a prefix of $q_2$ (see Figure 1(c)). Then, line 8 in REWRITE adds the navigation /file and the intuitive rewriting $r_2$ that we described there is obtained.

### 6. USING XML KEYS

We discuss in this section a more general setting in which view-based rewriting can be solved by the techniques of our paper, even when nodes do not necessarily have persistent Ids. More precisely, in the presence of **key constraints**, the kind of rewrite plans we considered here can still be supported. For example, key attributes are often present in XML documents, e.g., an SSN attribute could be associated with patient elements in a medical record, and could play the role of node identifiers in a plan which intersects view results at the level of patient elements.

Several formalisms for specifying integrity constraints on XML data have been consider in standards and research literature [Buneman et al. 2003; Hartmann and Link 2009]. In general, they specify in terms of path expressions three components: (i) a context, either the root or a set of nodes, (ii) the target of the key constraint, namely the nodes that should be uniquely identified within the given context, and (iii) the key nodes, descendants of the target ones, whose values will form the keys. The key constraints for which the context is the root of the document are called absolute, while the others are called relative. One of the most important problems over key constraints is the one of **constraint implication**, which consists in inferring new constraints from the existing ones. For our purposes, only absolute constraints (explicit or inferred) are relevant, given that query results are always computed in the root context.

In the presence of key constraints, additional steps of reasoning about node identity are necessary in order to understand which rewrite plans (involving the intersection operator) are valid. A naive approach would be to perform a complete pass over the data, annotating each node that is the scope of at least one key constraint with a (fresh) node Id. Then, only plans that intersect result sets in which at least one of the sets is composed only of annotated notes will be valid and executable. This would allow us to transparently apply algorithm **REWRITE** on XML data under key constraints, modulo this final validation step that needs to inspect the actual view results.

An alternative approach could be to perform the additional reasoning step directly at the query level. More precisely, the algorithm **REWRITE** could be modified to handle also XML data with key constraints by replacing line 1 with the following one (modification in italic):

$$
\text{1} \quad \text{Prefs} \leftarrow \{(p, \{(v_i, b_i)\}) \mid v_i \in \mathcal{V}, p \text{ a lossless prefix of } q \text{ and } p \text{ contained in a target path,}
\quad b_i \in \text{MB}(p), \exists \text{ a mapping } h \text{ from } u_i = \text{pattern}(v_i) \text{ into } p, h(\text{OUT}(u_i)) = b_i\}
$$

Testing whether a certain path selects only nodes that are uniquely identified by a key would only require some containment tests (depending on the formalism in which target paths are formulated).

Following these two possible approaches - either by Id-annotating the XML data based on keys or matching the input query and prefixes thereof against the specified key target paths - all the results formulated under the assumption of persistent Ids remain valid in this new setting and **REWRITE** remains a decision procedure for view-based rewriting.

### 7. FORMAL GUARANTEES OF ALGORITHM **REWRITE**

Using Proposition 5.3, we first show that algorithm **REWRITE** (and **EFFICIENT-RW** and **ALL-REWITES**) is sound, i.e. it gives no false positives.
Theorem 7.1. If algorithm Rewrite (or Efficient-Rw or All-Rewrites) returns a DAG pattern $r$, then $\text{unfold}(r)$ \equiv $q$.

Proof. By construction $d = \text{dag}(\text{unfold}(r))$ maps into $\text{pattern}(q)$, hence, by Lemma 3.8, $q' \subseteq d$, where $q'$ is $q$ modified to have its output at the last main branch node of the prefix $p$.

By Proposition 5.3, every rule application preserves equivalence. Hence the final $d$ is equivalent to the $d$ initially built. Let $r'$ be the rewriting returned at line 8. Since $r'$ is just $r$ with, possibly, some more navigation, and navigation is monotonic, then $d \sqsubseteq p$ guarantees that $\text{unfold}(r') \subseteq q$. We already knew that $d$ had a containment mapping into $q'$. Then, the last compensation just “moves” the output node lower, and guarantees that $q \sqsubseteq \text{unfold}(r')$. Hence $\text{unfold}(r') \equiv \text{pattern}(q)$. \qed

Moreover, it is also complete, in the sense described in Section 3.

Theorem 7.2. (1) Algorithm Rewrite is complete for rewriting $XP$.

(2) If the input query $q$ is minimal, All-Rewrites finds all minimal rewritings.

We say a rewriting $r$ is minimal if the DAG pattern corresponding to $r$ has no equivalent strict sub-pattern.

Proof of Point (1). If there is a DAG $d$ equivalent to the query $q$, then $q \sqsubseteq d$, and then, by Lemma 3.10, there must be a containment mapping from $d$ into $q$.

The completeness of algorithm Rewrite is not affected by the usage of APPLY-RULES, in the following sense: the result of applying the containment test directly on the DAG pattern corresponding to the unfolding of $r$ is the same as when applying it to the result of APPLY-RULES. This follows from the equivalence preservation property of the rules. For this reason, we do not need to consider APPLY-RULES in the completeness proof.

Thus, if there is a rewriting of the form $I$ or $I/\text{comp}$ or $I/\text{comp}$, where $I$ is an intersection, in particular there must be a root-mapping from $\text{unfold}(I)$ into $q$. Then, looking for all rewrite plans amounts to testing for all prefixes of $\text{MB}(q)$ if there is an intersection of views, with possibly some compensation on each branch, that map their main branches into that prefix, then add the compensation below the prefix, which will guarantee a containment mapping from the unfolding into the entire $q$.

Step 1 in Rewrite tries all prefixes of $\text{MB}(q)$ and for each such prefix it finds all views that map their main branch inside that prefix. Hence, for each $I$ as before, there will be a $I'$, built at step 4. of the form $I \cap J$, where $J$, possibly empty, is an intersection of other views (with maybe compensation) that map their main branches inside the same prefix. But then $q \sqsubseteq I' \sqsubseteq I$, so $I$ is a rewriting iff $I'$ is one.

We argue next that in order to test whether $r' = \text{compensate}(r, q, \text{OUT}(p))$ is an equivalent rewrite plan (which amounts here to testing that $\text{unfold}(r') \subseteq q$) it is sufficient (and obviously necessary) to test that $d \sqsubseteq p$ (in Rewrite at line 7). In other words, if the test $d \sqsubseteq p$ fails, then $r$ (potentially compensated) cannot yield an equivalent rewriting.

The test for $d \sqsubseteq p$ amounts to (a) testing that $d$ is union-free, with some interleaving of such that $i \equiv d$, and (b) testing that $i \sqsubseteq p$. If $d$ is union-free, then the statement $\text{unfold}(r') \subseteq q$ if $d \sqsubseteq p$ can be proven in straightforward manner.

To conclude the proof of completeness, we use Claim 7.1, which shows that $d' = \text{unfold}(r')$ cannot be union-free if $d$ is not union-free (proof given separately hereafter).

Claim 7.1. $d'$ is union-free only if $d$ is union-free.

Finally, since Rewrite is sound (Th. 7.1), any rewrite plan that is output is indeed a rewriting. \qed

\footnote{The focus on minimal rewritings is standard in the literature on rewriting using views. One reason is that, for a large class of cost models, minimal size rewritings are provably also cost minimal. This class corresponds to monotonic cost models, in which the cost of evaluating the entire query is never less than the cost of evaluating any of its subqueries. While there are exceptions to monotonicity in real-life scenarios, the class is still quite prevalent in practice. An additional reason for the traditional focus on minimal rewritings is that the set of non-minimal rewritings is infinite even in the most basic scenarios (relational conjunctive queries and views), rendering a search for all non-minimal rewritings meaningless.}

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PROOF OF POINT (2). If \( q \) is minimal, all the subtrees added by the function \( \text{compensate} \) are also minimal, hence the rewritings that are produced are minimal. It is left to prove that \textit{ALL-REWRITES} finds them all. We already saw that if there is a rewriting, \textit{REWRITE} tries one which is equivalent to it. \textit{ALL-REWRITES} does even more: it really tries all the rewrite plans, because it considers all subsets of views that map down to a certain position in \( \text{MB}(q) \), at line [2]. Any other compensation that may be needed is copied from \( q \) in the call to \( \text{compensate} \) from the return clause (line [3]). It is easy to prove that a tree pattern is minimal iff one cannot drop subtrees from it (which is the definition of minimality in \cite{Mandhani and Suciu 2005}). Therefore, if \( q \) is minimal, all its subtrees are also minimal. \( \Box \)

PROOF OF CLAIM [7,1]. Let \( d = i_1 \cup \ldots \cup i_k \), for \( i_1, \ldots, i_k \) being the non-reducible interleavings of \( d \) (for each \( i_j \) we cannot build another, i.e. non-equivalent, interleaving that contains \( i_j \)). For each \( i_j \), let \( i'_j \) denote the compensated interleaving \( i'_j = \text{compensate}(i_j, q, \text{OUT}(p)) \).

First, it is immediate that \( d' = \bigcup_j i'_j \) by showing containment mappings in both directions.

We show next that if \( d \) is not union-free, then \( \bigcup_j i'_j \) is not union-free either (there is no query in this union that contains all other queries). We will rely on the following two observations:

(1) The compensation applied on \( d' \)'s interleavings will only extend the main branch, but will not bring (or qualify) new predicates for the existing main branch nodes, hence yielding no new mapping opportunities in this sense. This is because the node \( \text{OUT}(p) \) in prefix \( p \) is assumed to have already “inherited” the rest of \( q \) as a predicate (\( p \) is a lossless prefix).

In other words, if there exists a containment mapping between \( i'_j \) and \( i'_l \) then there must exist a root-mapping between the corresponding \( i_j \) and \( i_l \).

(2) We can partition the interleavings of \( d \) into two classes:

(a) those that have a “minimal” (or certain) result token (essentially obtained after applying \( R1 \) rewrite steps on the result tokens of \( d' \)'s parallel branches),

(b) the remaining ones, which by definition must have a result token that cannot map in the result token of interleavings of the first kind (the result token has a longer main branch or some predicates that are not necessarily present in all interleavings [4]).

The first class cannot be empty, the second one may be empty.

By the first observation, for any two interleavings of \( d, i_j \) and \( i_l \), knowing that \( i_j \not\subseteq i_l \), we can have \( i'_j \subseteq i'_l \) only if there exists already a root-mapping \( \phi \) from \( i_j \) into \( i_l \) which fails to be a full containment mapping only because the image of \( \text{OUT}(i_l) \) is not \( \text{OUT}(i_j) \). If such an root-mapping does not exist then surely we have that \( i'_j \not\subseteq i'_l \).

By the second observation, for interleavings of the first kind, their result token will always map in the result token of any other interleaving (of both kinds) such that the image of the output node is the output node in the other interleaving.

Putting everything together, since the first class cannot be empty, in order to prove the claim it is now sufficient to show that a query \( i'_j \) corresponding to an interleaving \( i_j \) of the second kind cannot reduce (contain) a query \( i'_j \) corresponding to an interleaving \( i_j \) of the first kind. Let \( i_j \) and \( i_l \) be the two interleavings, with \( t'_j \) and \( t'_l \) denoting their result tokens, such that there exists a root-mapping \( \phi \) which takes \( \text{OUT}(i_j) \) into some main branch node that is not part of \( t'_j \) (by the definition of the two kinds of interleavings \( t'_j \) cannot map into \( t'_l \)).

We show that this leads to a contradiction, namely that \( i_j \) is not minimal, in the sense that a main branch node of \( i_j \) can be removed, obtaining another (simpler) valid interleaving of \( d \).

Each of the branches in parallel in \( d \) (denoted hereafter \( x \)) must have a containment mapping \( \psi_x \) into \( i_l \) (and a containment mapping \( \tau_x \) into \( i_j \) as well), so we obtain by \( \phi \circ \psi_x \) a root-mapping from any branch \( x \) into \( i_j \). Importantly, the image of \( \text{OUT}(x) \), \( n = \phi(\psi_x(\text{OUT}(x))) \), is some main branch node of \( i_j \) above \( t'_j \). This means that we can also map (by a root-mapping) each \( x \) branch into \( i_j \) somewhere higher than the result token \( t'_j \). But this hints that we can in fact simplify \( i_j \) into

---

8Since this is the result token and everything else can be put “above” it, it is easy to obtain this minimal, certain result token.
an interleaving having a shorter main branch, yet containing \(i_j\). More precisely, this interleaving of the parallel branches \(x\), described by a code-mapping pair \((i, f_i)\), can be obtained as follows:

1. take as the code \(i\) the main branch of \(i_j\) without \(n_i\).
2. define \(f_i\) as (a) for the main branch nodes of each \(x\) except those of the result token, by the \(\phi \circ \psi_x\) mapping, (b) for the main branch nodes of the result token of \(x\) by \(\tau_x\).

It is easy to check that the interleaving obtained in this way has a containment mapping into \(i_j\) based on the “identity” mapping for the main branch nodes.

We now consider the computational complexity of \(\text{REW}rite\). We can observe that it runs in worst-case exponential time, as it uses a containment check (line 7) that is inherently hard:

**Theorem 7.3.** Containment of an XP\(^\ominus\) query \(d\) into an XP query \(p\) is coNP-complete in \(|d|\) and \(|p|\).

**Proof.** To show that our problem is in coNP, we can use an argument similar to the one used in [Neven and Schwentick 2006] for the case of XPath with disjunction. We know that \(\eta(d) = U\), where \(U\) is a union of queries from XP. A non-deterministic algorithm that decides \(d \not\subseteq p\) guesses \(u \in U\) (without computing \(U\)), making a certain choice at each step of interleaving. Then, it checks that \(u \not\subseteq p\), which can be done in PTIME as \(u, p \in XP\).

coNP-hardness is proven by reduction from the 3DNF-tautology problem [Garey and Johnson 1979], which is known to be coNP-complete. We start from a 3DNF formula \(\phi(x) = C_1(x) \lor C_2(x) \lor \ldots \lor C_n(x)\) over boolean variables \(x = (x_1, \ldots, x_n)\), \(C_i(x)\) being conjunctions of literals.

Out of \(\phi\) we build \(d \in XP\) \(\cap U\) and \(p \in XP\) over \(\Sigma = \{x_1, \ldots, x_n, b, v, true, false, yes\}\) such that \(\phi\) is a tautology iff \(d \subseteq p\). Intuitively, \(d\) will encode all possible truth assignments for \(\phi\).

We build \(d\) by intersecting two branches, based on the following gadgets (illustrated in Figure 2):

1. the pattern \(x_1[yes]/x_2[yes]/\ldots/x_n[yes]\) (denoted \(T\))
2. the pattern \(x_1[true]/x_1[false]/x_2[true]/x_2[false]/\ldots/x_n[true]/x_n[false]\) (denoted \(S\))
3. for each clause \(C_i\), the pattern obtained from \(x_1/a/x_1/a/x_2/a/\ldots/x_n/a/x_n/a\) by putting the \([yes]\) predicate below each of the 3 nodes corresponding to the literals of \(C_i\) (this pattern is denoted \(P_{C_i}\)). For instance, for \(C_i = (x_1 \land x_2 \land x_3)\), we have the pattern \(P_{C_i} = x_1/a/yes/x_1/a/x_2/a/yes/x_3/a/yes/x_3/a/\ldots/x_n/a/x_n/a\).
4. for each clause \(C_i\), \(Q_{C_i}\) denotes the predicate \(c/c/c/\ldots/c/v[//P_{C_i}]\), with \(m - i + 1\) \(c\)-nodes.
5. for each \(C_i\), the predicate \(Q_{C} = [Q_{C_1}, Q_{C_2}, Q_{C_3}, \ldots, Q_{C_n}]\), that is the list of all \(Q_{C_j}\) predicates for \(j \neq i\).
6. the pattern \(c[Q_1]/c[Q_2]/\ldots/c[Q_m]/c\) (denoted \(U\))

Now, we define \(d\) as \(d = (doc(A)///T//out) \cap (doc(A)///U//v//S//out)\).

An important observation is that \(Q_{C_i}\) predicates are not inherited at \(c\)-nodes. This is ensured by the \(v\) node we introduced in \(Q_{C_i}\)'s and in \(U\) (for inheritance, the last \(c\)-node of \(Q_{C_i}\)'s branch would have to match with a \(v\)-node).

Next, when interleaving the two branches in \(d\), \(x_k\) in the left branch can either be coalesced with the first \(x_k\) (having predicate \(true\)) in the second branch, corresponding to the case \(x_k = true\), or with the second \(x_k\) (having predicate \(false\)), corresponding to \(x_k = false\). Hence interleavings correspond to truth assignments for the variables of \(\phi\).

Note also that when some clause \(C_i\) is made \(true\) by a truth assignment (i.e., all its literals are \(true\)), then the predicate \(P_{C_i}\) will hold at the last \(c\) node in the \(U\) part, or, put otherwise, the \(Q_{C_i}\) predicate will now hold at the \(i\)th \(c\) node in \(U\).

Finally, let \(p\) be the pattern \(doc(a)///c[Q_{C_1}, Q_{C_2}, Q_{C_3}, \ldots, Q_{C_m}]///out\).

We can now argue that \(d \subseteq p\) iff \(\phi\) is a tautology. The if direction is immediate since in this case each truth assignment makes at least one \(C_i\) true. This means that the \(Q_{C_i}\) predicate will now hold at the \(i\)th \(c\)-node in \(d\) and, since all other \(Q_{C_j}\) predicates, for \(j \neq i\), were already explicitly present
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Fig. 2: The patterns used in the reduction of TAUTOLOGY to DAG containment

Fig. 3: Interaction between R2.i and R2.ii

at this node, it is now easy to see that there exist now a containment mapping from \( p \) into \( d \) that takes \( p \)'s \( c \)-node into \( d \)'s \( i \)th \( c \)-node.

The only if direction is similar. If for some truth assignment, none of the clauses is TRUE (in the case \( \phi \) is not a tautology), then it is easy to check that \( p \) will not have a containment mapping into the interleaving corresponding to that truth assignment.

One might hope there is an alternative polynomial time solution for the rewriting problem, which would not require such a potentially expensive containment test. We prove this is not the case, showing that that the rewriting problem itself is hard.

**Theorem 7.4.** The rewriting problem for queries and views from XP is coNP-complete.

**Proof.** For the coNP-hardness proof, we refer the reader to the proof of Theorem 8.5 which shows an even stronger result, as it deals with a restricted fragment of XP.

We discuss now the complexity upper-bound. Let \( q \) be the input query, let \( V \) be the set of views. First, note that rewriting could be solved using an oracle for union-freedom, but this does not provide any easy map reduction. This is why we prove the following result independently.

For each node of \( \text{MB}(q) \) in which some of the views \( V_j \subseteq V \) map, it is enough to guess one interleaving of \( \bigcap_{j \in I_j} v_j \) in which \( q \) does not map. If we put together a polynomial number of polynomially large witnesses, they make up a polynomial witness for the entire problem. In other words, one can verify in polynomial time that there is no rewriting.

However, we show next that our rule rewriting procedure is polynomial, hence rewritings can be found efficiently whenever the containment test of REWRITE’s line 6 can be done efficiently:
LEMMA 7.5. The rewriting of a DAG d using APPLY-RULES always terminates, and it does so in \(O(|\text{NODES}(d)|^2)\) steps.

PROOF. First, let us notice that none of the rules increases the number of main branch nodes, and in fact R1, R3, R4, R6, R7, R8 always decrease it, hence the number of times they are applied is less than \(|\text{MBN}(d)| = O(|\text{NODES}(d)|)\). R5 can also fire only a finite number of times, as the number of predicates to be introduced is bound by the initial number of predicates in the pattern \(d\), which is in \(O(|\text{NODES}(d)|)\).

R2 leaves the number of nodes unchanged and may decrease the number of edges by one or leave it the same. R2.i always progresses down main branches, and R2.ii always up, respectively. The only possibility of going into a loop would come from the interaction of R2.i and R2.ii.

Consider the generic case depicted in Figure 3(a), in which R2.ii would apply for nodes \(n_1, n_2, n_3\). (The case in which we apply an R2.i step is symmetrical). Suppose that \(n_3\) also has a // edge towards a node \(n_4\). There would be a danger of looping if R2.i had been previously applied to nodes \(n_3, n_2, n_4\), and now it would apply again because \(n_2//n_3\) would be re-introduced. But then, R2.i applied to those nodes would have introduced an edge \(n_4//n_2\) and any later applications of R2 (or of any other rule) would have maintained \(n_2\) reachable from \(n_3\), as in Figure 3(b). In this case, R2.ii would not introduce any // edge between \(n_3\) and \(n_2\), as it is explicitly specified in the rule.

Thus, R2 can fire at most \(|\text{MBN}(d)|^2\) times, because at each step it infers the order, in all interleavings, of a pair of nodes from \(\text{MBN}(d)\) whose ordering was unknown before. So, rewriting with R1-R9 always terminates in at most \(O(|\text{NODES}(d)|^2)\) steps.

Each of the rules R1-R8 can be tested in polynomial time in straightforward manner. They are mostly based on existence or non-existence of mappings. For some of them (in particular, for R7, R8 and R9), we will discuss certain implementation choices that may speed-up execution in Section 11. Similarity can also be tested in polynomial time, since the number of patterns \(\text{MBN}(d)\) whose ordering was unknown before. So, rewriting with R1-R9 always terminates in at most \(O(|\text{NODES}(d)|^2)\) steps.

We discuss next how R9 can be tested.

For the given \(n, p_1, p_2, Q\) (the number of such predicates is of the order of \(|d|\)), we can check in polynomial time whether the rule triggers as follows. \(Q\) can be seen as having the following form (Figure 4): a // path \(l_1/.../l_k\) followed by either (a) one or more // edges, (b) one or more // edges and one or more // edges, or (c) one or more // edges. In other words, \(l_k\) denotes the highest node having either several outgoing edges (of either kind) or one outgoing edge, of the // kind.

**Case a.** If \(Q\) is of the first kind, since at node \(n\) in \(p_1\) the predicate \(Q\) would verify \(XP_{eq}(\text{see the following section})\), it means that \(n\) is followed by a main branch that is incompatible with \(l_1/l_2/.../l_k\). Let \(l_1/.../l_{k'}\), for \(1 \leq k' < k\), be the maximal prefix that is compatible with the main branch (if one exists). This means that the main branch below \(n\) starts by a sequence of labels \(l_1/.../l_{k'/l}\), where \(l \neq l_{k'+1}\).

For \(Q\) to hold at \(n\) in each interleaving of \(p_2\) with \(p_1\), it means that in it we have either:

1. \(Q\) or a predicate into which \(Q\) can map attached to \(n\) itself (i.e. we do not need the main branch descendants of \(n\) and their predicates), or
(2) the predicate $l_2/\ldots/l_k[Q_1]\ldots[Q_s]$ or a predicate into which it can map attached to $n$’s main branch child $n'$ (i.e. we do not need the main branch descendants of $n'$ and their predicates), or
(3) the predicate $l_2/\ldots/l_k[Q_1]\ldots[Q_s]$ or a predicate into which it can map attached to $n$’s main branch descendant at distance 2, $n''$ (i.e. we do not need the main branch descendants of $n''$ and their predicates), or so on, . . .
(k') the predicate $l_{k+1}/\ldots/l_k[Q_1]\ldots[Q_s]$ or a predicate into which it can map attached to $n$’s main branch descendant at distance $k'$, $n^{(k')}$, (i.e. we do not need the main branch descendants of $n^{(k')}$ and their predicates).

Accordingly, in order to test that $Q$ holds at $n$ in each interleaving of $p_2$ with $p_1$, we need to test the non-existence of a mapping from $p_2$ into $p_1$ that would not bring a predicate as the ones described above on any of the nodes $n, n', n'', \ldots, n^{(k')}$. This test can be done in polynomial time, top-down and one token at a time, by choosing as long as possible for each token of $p_2$ the highest-possible image that does not contribute any predicates like the ones described above.

Case a. This case is similar to the previous since we have the same setting, i.e., $n$ is followed by a main branch that is incompatible with $l_1/l_2/\ldots/l_k$ and we have at most a prefix of it $l_1/\ldots/l_{k'}$, for $1 \leq k' < k$, that is compatible (if such a prefix exists).

Case c. If $n$ is followed by a main branch that is incompatible with $l_1/l_2/\ldots/l_k$, then the same reasoning of the two previous cases applies here as well. Otherwise, for $Q$ to hold at $n$ in each interleaving of $p_2$ with $p_1$, it means that in each interleaving we have either:

(1) $Q$ or a predicate into which $Q$ can map attached to $n$ itself (i.e. we do not need the main branch descendants of $n$ and their predicates), or
(2) predicate $l_2/\ldots/l_k[Q_1]\ldots[Q_s]$ or one into which it can map attached to $n$’s main branch child $n'$ (i.e., we do not need the main branch descendants of $n'$ and their predicates), or so on, . . .
(k) the predicate $l_k[Q_1]\ldots[Q_s]$ or a predicate into which it can map being present (as a predicate) on $n$’s main branch descendant at distance $k$, $n^{(k)}$, (i.e. we do not need the main branch descendants of $n^{(k)}$ and their predicates), or
(k+1) all the predicates $[Q_1], \ldots, [Q_s]$ verified at $n$’s main branch descendant at distance $k+1$, $n^{(k+1)}$.

So a similar test for the non-existence of a mapping has to be done, but with some minor adjustments. Top-down, we will chose a mapping image for each token of $p_2$ into $p_1$, as long as we do not arrive at the position of $n^{(k+1)}$ or below it (i.e. we will chose an image for a token if it does not overpass this position and does not contribute predicates like the ones described by the items (1) to (k) above). Then, for the remaining suffix of $p_2$, we check the existence of a mapping for it that would (i) not contribute predicates like the ones given in conditions (1) to (k), and (ii) would not contribute all the predicates of the last condition, i.e., that there is a mapping for the remaining part of $p_2$ in the remaining part of $p_1$ s.t. among $Q_1, \ldots, Q_s$ there is at least one predicate $Q_i$ which will not be verified at $n^{(k+1)}$ after coalescing $p_2$’s nodes with their mapping images. This can be seen as a recursive call, that can be run for each $Q_i$, individually, and will take us back to the three cases depending on the shape of $Q_i$. (Note that all the predicates $Q_1, \ldots, Q_s$ at node $n^{(k+1)}$ on $p_1$ will verify the condition for extended skeletons.)

A dynamic programming approach can be used to perform all these tests in polynomial time, based on the to-be-mapped suffix of $p_2$, the target suffix of $p_1$ and the predicate to be tested (it is not necessary to perform the test several times for a given such triple). □

An immediate corollary of Lemma 7.5 is the following.

**Corollary 7.6.** Efficient-RW always runs in PTIME.

To summarize the results so far, we showed that **Rewrite** is complete for XP, and we gave matching (coNP) complexity bounds for this problem. Moreover, we described a variant of this algorithm (Efficient-RW) which runs in polynomial time, but is only sound.
We consider next restrictions by which Efficient-Rw becomes also complete, thus turning into a complete and efficient rewriting algorithm. Note that one may impose restrictions on either the XP fragment used by the query and views, or on the rewrite plans that Rewrite deals with. We consider both cases, by this charting a tight tractability frontier for this problem.

The next section shows that Efficient-Rw is complete under fairly permissive restrictions on the input query, and this without restricting the language of views (which remains XP).

8. TRACTABILITY FRONTIER - XP FRAGMENT FOR PTIME

We introduce in this section a fragment of XP that, intuitively, limits the use of // -edges in predicates, in the following manner: any token t of a pattern p will not have predicates with // -edges that may become redundant in some interleaving p might be involved in, due to descendants of t and their respective predicates.

Let us first fix some necessary terminology. By a // -subpredicate st we denote a predicate subtree whose root is connected by a // -edge to a // -path p that comes from the main branch node n to which st is associated (as in n[...[//st]]), p is called the incoming // -path of st and can be empty.

By extended skeletons (XPes) we denote tree patterns having the following property: for any main branch node n \(\not\in\) OUT(p) and // -subpredicate st of n, there is no mapping (in either direction) between the code of the incoming // -path of st and the one of the // -path following n in the main branch (where the empty code is assumed to map in any other code). For instance, the patterns a[b//c//d]/e//d or a[b//c//d]/b//d, a[b//c]/d, a[//b]/c/d or a[//b]/c/e are not.

Observe that the above definition imposes no restrictions on predicates of the output node. This relaxation was not present in [Cautis et al. 2008]’s definition of extended skeletons but it is easy to show that it does not affect any of the results that were obtained with the more restrictive definition. This is because there is only one choice for ordering the output nodes in interleavings of an intersection; they are collapsed into one output node. Note that this XP sub-fragment does not restrict in any way the use of descendant edges in the main branch or the use of predicates with child edges only. Note also that all the paths given in the running example are from this fragment.

We denote by XPes the fragment of XP in which only XPes expressions are used. For any tree pattern v, by its extended skeleton, we denote the XPes query s(v) obtained by pruning out all the // -subpredicates violating the XPes condition. This notion can be easily generalized to extended skeletons s(d) for any DAG patterns d.

The following two lemmas have the auxiliary role of allowing us to rewrite input queries from XPes in polynomial time, without imposing any restrictions on the views.

**Lemma 8.1.** A DAG pattern d is union-free only if its extended skeleton DAG pattern s(d) is so.

**Proof.** The proof is based on the following property: modulo // -predicates, the sets of tree patterns interleave(d) and interleave(s(d)) are the same. More precisely, for each \(p_i \in\) interleave(d) there exists \(p'_i \in\) interleave(s(d)) such that \(s(p_i) = p'_i\) and the other way round. Supposing that s(d) is not union-free, let us assume towards a contradiction that d is union-free. Let \(p_i\) denote the interleaving such that \(p_i \equiv d\) and let \(p'_i\) denote the associated interleaving from s(d), \(p'_i = s(p_i)\).

Since s(d) is not union-free, there exists some \(p'_{i'} \in\) interleave(s(d)) such that \(p'_{i'} \not\subseteq p'_i\). Then there is \(p_j \in\) interleave(d) such that \(s(p_j) \not\subseteq s(p_i)\). Finally, since \(p_j \subseteq p_j\), we also have \(p_j \subseteq s(p_i)\).

Suppose for the sake of contradiction that \(p_j \subseteq s(p_i)\) and \(s(p_j) \not\subseteq s(p_i)\) both hold. Then any containment mapping \(\psi\) from s(p_i) into p_j should use some of the predicates of p_j starting with a // -edge (otherwise we would have a containment mapping from s(p_i) into s(p_j) as well). But this is not possible since for any // -subpredicate st, its incoming // -path is incompatible (does not map) with the path l' following the main branch node (see Figure 5).

The following result also follows similarly to Lemma 8.1.
Rewriting XPath Queries using View Intersections: Tractability versus Completeness

Lemma 8.2. There exists an $XP^\cap$ rewriting of an input query $q \in XP_{es}$ using a set of $XP$ views iff there exists one using the extended skeletons of the views.

Proof. The if direction is immediate. For the only if direction, it suffices to see that since $q$ is an extended skeleton, any containment mapping from $q$ into the unfolding of the rewrite plan will actually use only parts that are not violating the $XP_{es}$ condition. This means that a containment mapping from $q$ into this plan also gives a containment mapping from $q$ into the corresponding plan using instead of the original views their extended skeletons.

By Lemma 8.2, assuming $XP_{es}$ input queries, without loss of generality all views can be assumed in the rest of this section to be from $XP_{es}$ as well (when this is not the case, the views can be substituted by their extended skeletons before the DAG rewriting, for instance at Step 3 in REWRITE).

A key result of our paper is the following (for readability purposes, proof given in Section A):

Theorem 8.3. For any pattern $d$ in $XP^\cup_{es}$, $d$ is union-free iff the algorithm APPLY-RULES rewrites $d$ into a tree.

From this, it follows immediately that:

Corollary 8.4 ($XP_{es}$). Algorithm EFFICIENT-RW is complete for rewriting $XP_{es}$ queries using $XP$ views.

We show next that relaxing the extended skeleton restrictions leads to hardness for union-freedom and rewriting using views. We consider here as middle-ground between extended skeletons and $XP$ the fragment $XP//_{es}$ obtained from extended skeletons by allowing predicates that are connected by a $//-$edge to the main branch (such as in $v'_2$) and freely allowing $//-$edges in these predicates. Obviously, $XP_{es} \subseteq XP//_{es}$. We denote by $XP//_{es}$ the fragment of $XP^\cap$ in which only $XP//_{es}$ expressions are used.

We first prove the following complexity lower bound for union-freedom:

Theorem 8.5. For a pattern $d$ in $XP//_{es}$, the problem of deciding if $d$ is union-free is coNP-hard.

Proof. We use a reduction from tautology of 3DNF formulas, which is known to be coNP-complete. We start from a 3DNF formula $\phi(\bar{x}) = C_1(\bar{x}) \lor C_2(\bar{x}) \lor \ldots C_m(\bar{x})$ over the boolean variables $\bar{x} = (x_1, \ldots, x_n)$, where $C_i(\bar{x})$ are conjunctions of literals.

Out of $\phi$, we build patterns $p_0, p_1, \ldots, p_n \in XP//_{es}$ over $\Sigma = \{x_1, \ldots, x_n, a, c, yes, out\}$ such that the DAG pattern $d = p_0 \cap p_1 \cap \cdots \cap p_n$ is union-free iff $\phi$ is a tautology.

We build the patterns $p_0, p_1, \ldots, p_n$, based on the gadgets $P, P_{yes}, P_{C_1}, \ldots, P_{C_m}, M, Q_{C_1}, \ldots, Q_{C_m}, C, Q,$ and $P_X$ where $X$ can be any set of one, two or three variables (see Figure 6). More precisely, these gadgets are defined as follows:

1. the linear pattern with $m + 1$ c-nodes, $c/c/\ldots/c$ (denoted $M$)
(2) the pattern \( x_1/x_2/\ldots/x_n \) (denoted \( P \))
(3) the pattern \( x_1/\text{yes}/x_2/\text{yes}/\ldots/x_n/\text{yes} \) (denoted \( P_{\text{yes}} \))
(4) patterns \( P_X \), where \( X \) is a set of variables of size at most 3, obtained from \( P \) by putting a \([\text{yes}]\)
predicate below the nodes labeled by the variables in \( X \).
(5) for each clause \( C_i \), the pattern \( P_{X_i}[\text{true}]/a/M/P_{X_i}[\text{false}]/a/M/P/out \), where \( X_i \) is the
set of positive variables in \( C_i \) and \( X_f \) is the set of negated variables in \( C_i \) (this pattern
is denoted \( P_{C_i} \)). For instance, for \( C_i = (x_1 \land \bar{x}_2 \land x_3) \), we have the pattern \( P_{C_i} = P_{[1.5]}/[\text{true}]/a/M/P_{[2]}/[\text{false}]/a/M/P/out \).
(6) for each clause \( C_i \), \( Q_{C_i} \) denotes the predicate \([c/c/c/\ldots/c[P_{C_i}]]\), with \( m - i + 1 \) \( c \)-nodes,
(7) for each \( C_i \), the predicate \( Q_i = [Q_{C_1}, \ldots, Q_{C_{i-1}}, Q_{C_{i+1}}, \ldots, Q_{C_m}] \), that is the list of all \( Q_{C_j} \)
predicates for \( j \neq i \).
(8) the pattern \([c[Q_1]/c[Q_2]/c[Q_3]/\ldots/c[Q_m]]/c \) (denoted \( C \)), the predicate \( Q = [Q_{C_1}, \ldots, Q_{C_m}] \).

The \( n + 1 \) patterns are then given in the last section of Figure 6.

First, note that no inheritance of predicates occurs in these patterns. \( Q_{C_i} \) predicates are not inher-
ited in the \( C \) part of \( p_0 \) because that would require some \( x_1 \)-label to be equated with the \( c \)-label.
Similarly, the \( P_{yes} \) part of the main branch does not put implicit \( Q_{C_i} \) predicates at \( c \)-nodes either.

We argue that the candidate interleaving \( p_c \) such that \( p_c \equiv d \) is unique: \( p_c \) is obtained by the
code \( i \) corresponding to the main branch of \( p_0 \), and the function \( f_i \) that maps the first \( a \)-node (the
one with a predicate \([/a/\text{false}] \)) of each pattern \( p_1, \ldots, p_n \) in the same image as the third \( a \)-node of \( p_0 \)
(the parent of the \( C \) part). This is the interleaving that will yield the “minimal” extended skeleton
(namely the one of \( p_0 \)), since nodes with a \([\text{yes}]\) predicate are coalesced with \( p_0 \) nodes having
already that predicate. All others would at least have additional \([\text{yes}]\) predicate branches and even
longer main branches and thus cannot not map into \( p_c \). Hence no other interleaving can contain \( p_c \).
We show in the following that \( p_c \) will contain (and reduce) all other interleavings of \( p_0 \cap \cdots \cap p_n \) iff \( \phi \) is a tautology. Moreover, it is easy see that \( p_c \) contains some interleaving \( p \) if and only if its \( \left[ //Q \right] \) predicate can be mapped at the third \( a \)-node from the root in \( p \).

Note now that \( p_c \) will contain all interleavings \( p \) that for at least some pattern \( p_j \) “put” its first \( a \)-node either below or in the third \( a \)-node of \( p_0 \). This is because \( \left[ //Q \right] \) would be either explicitly present at the third \( a \)-node in \( p \) or it would be inherited by this node from some \( a \)-labeled descendant.

So, the interleavings that remain be considered are those described by a function \( f' \) which takes all the first \( a \)-nodes from \( p_1, \ldots, p_n \) higher in \( p_0 \), i.e. in either the first or the second \( a \)-node of \( p_0 \). Each of these interleaving will basically make a choice between these two \( a \)-nodes.

For some \( p_j \), by choosing to coalesce its first \( a \)-node with the first \( a \)-node of \( p_0\) we get an \([yes]\) predicate at the \( x_i \) node of the \( \true P \) part of \( p_0 \). Similarly, by coalescing with the second \( a \)-node we get an \([yes]\) predicate at the \( x_i \) node of the \( false P \) part of \( p_0 \). So, these \( n \) individual choices of

where to coalesce \( a \)-nodes amount to a truth assignment for the \( n \) variables, and in each interleaving the \( yes \) predicate will indicate that assignment.

Recall that in order for \( p_c \) to contain such an interleaving \( p \), it must be possible to map the predicate \( \left[ //Q \right] \) of the third \( a \)-node of \( p_c \) at the third \( a \)-node of \( p \).

We can now argue that \( p_0 \cap p_1 \cap \cdots \cap p_n \subseteq p_c \) iff \( \phi \) is a tautology. The if direction (when each truth assignment \( t \) makes at least one clause \( C_i \) true) is immediate. For a truth assignment with clause \( C_i \) being true, in the corresponding interleaving \( p \), the \( P_{C_{C_j}} \) predicate will hold at the last \( c \)-node in the \( C \) part, hence the \( Q_{C_j} \) predicate will hold at the \( i \)th \( c \)-node in \( C \). Since all other \( Q_{C_j} \) predicates, for \( j \neq i \), were already explicitly present at this \( i \)th \( c \)-node, it is now easy to see that the \( \left[ //Q \right] \) predicate would be verified at the \( a \)-labeled ancestor. Hence there exists a containment mapping from \( p_c \) into \( p \).

The only if direction is similar. If for some truth assignment, none of the clauses is \( \true \) (in the case \( \phi \) is not a tautology), then it is easy to check that \( p_c \) will not have a containment mapping into the interleaving \( p \) corresponding to that truth assignment. This is because the \( \left[ //Q \right] \) predicate would not map at the third \( a \)-node in \( p \).  

We next prove that the \( \coNP \) lower bound is tight, showing that union-freedom for patterns from \( XP_{\setminus} \) is in \( \coNP \) (recall that the problem was shown to be tractable for extended skeletons).

**Theorem 8.6.** For a pattern \( d \) in \( XP_{\setminus} \), the problem of deciding if \( d \) is union-free is in \( \coNP \).

**Proof.** To show that union-freedom is in \( \coNP \) we use the following approach: we show that one can always build an interleaving \( p_c \) that is the unique candidate for \( p_c \equiv d \). Then, we can use an argument similar to the one used in the proof of Theorem 7.3 to check in \( \coNP \) if \( d \subseteq p_c \).

If there are no views that have only \( l \)-edges in their main branch, we start can with \( d \) being a DAG pattern as the one illustrated in Figure 11a. This is the result of applying R1 steps until saturation, on what will be the root and result tokens of interleavings of \( d \). Let \( t_r \) denote the root token (ending with node \( n_r \)) and let \( t_o \) denote the result token (starting with node \( n_o \)). We have some branches in parallel \( i_1, \ldots, i_k, i_{k+1}, \ldots, i_{k+t} \), starting and ending at various nodes of \( t_r \) and \( t_o \), with the first \( k \) ones being connected to \( n_r \) and \( n_o \). We proceed towards building \( p_c \).

Let us first assume that \( l = 0 \), i.e., all the branches in parallel are connected to \( n_r \) and \( n_o \).

We know by Lemma 8.1 that \( d \) is union-free only if its extended skeleton \( s(d) \) is union-free. This in turn means that there exists some branch in \( d \), say \( i_1 \), such that all other \( s(i_j) \) map into \( s(i_1) \) (Lemma A.4). So, all the branches in parallel map their extended skeletons into the branch \( i_1 \), while predicates starting by a \( l \)-edge may not map (these are allowed in \( XP_{\setminus} \), contrary to \( XP_{es} \)).

It is now easy to see that \( p_c \) can only have an extended skeleton of the form \( s(t_r) //s(i_1) //s(t_o) \) (this is the minimal skeleton). Note that several choices for mapping each \( s(i_j) \) into \( i_1 \) may be available, and each such mapping can be seen as a way of coalescing \( i_j \) nodes with the \( i_1 \) ones. In fact, interleavings that do not use one of these choices cannot lead to \( p_c \) (they will no longer yield the minimal candidate extended skeleton).
Among these coalescing choices that do not modify the candidate extended skeleton, it now easy to pick the one that gives the unique candidate \( p_c \). For each \( i_j \) let \( \psi_{i_j} \) denote the mapping of \( s(i_j) \) in \( i_1 \) that uses the highest possible image for each token of \( s(i_j) \). We build \( p_c \) from \( d \) by transformation steps that coalesce each \( n \in MB(i_j) \) with the node \( \psi_{i_j}(n) \in MB(i_j) \).

We argue that the pattern \( p_c \) we obtained is the only interleaving candidate for \( p_c \equiv d \). This is because all other interleavings that do not modify the candidate extended skeleton will be subsumed (as contained interleavings) by this one. This is because all the predicates that were missing from \( i_1 \) and were added by coalesce steps must start by a \(/-edge. If they would be added below this first possible image, they would anyway be inherited by the main branch nodes above.

Now, since we have a clear candidate \( p_c \), obtained in polynomial time, we can guess a witness interleaving \( p_w \) of \( d \) such that \( p_w \not\subseteq p_c \) in polynomial time.

We now consider the case when, after the initial phase of R1 steps, \( l \neq 0 \), i.e., some of the branches in parallel are not from \( n_r \) to \( n_o \). In this case, we can advance towards the unique candidate interleaving and a new DAG as the one discussed above by the following coalescing choices. For \( j \) from \( k+1 \) to \( k+l \), for each \( i_j \), let \( n_j^r \) denote the node in \( t_r \) that is sibling of the first node in \( i_j \), and let \( n_j^p \) denote the node of \( t_p \) that is “parent-sibling” of \( i_j \) (they have the same child node). Let \( pr_j \) denote its maximal token-prefix such that its extended skeleton \( s(pr_j) \) maps in \( TP_d(n_j^r/\ldots/n_r) \). (Note that some of the predicates - among those starting by a \(/-edge - may not fully map.)

Then, for each \( i_j \), by \( sf_j \) we denote the maximal token-suffix such that \( sf_j \) fully maps in \( TP_d(n_0/\ldots/f_{j}^r) \). We can thus write each \( i_j \) as \( i_j = pr_j/sf_j \), for \( j = k+1,l+1 \). If, for some \( i_j \), \( pr_j \) and \( sf_j \) overlap then in this case the \( m_j \) part is considered empty.

Now, we consider the DAG pattern \( d' \) obtained from \( d \) by replacing each \( i_j \) branch by the branch \( m_j \), but connected this time by \(/-edges to \( n_r \) and \( n_o \). We argue that \( d \) is union-free only if \( d' \) is union-free. and that if \( d' \equiv p_c \), then \( p_c \) is also the only interleaving candidate for \( p_c \equiv d \). This is because all other interleavings are either subsumed by those of \( d' \), or change the extended skeleton of \( t_r \), or add some predicates on \( t_o \) that will not be present in all interleavings (the candidate must end exactly by \(/\backslash t_o \). From this point on, we can continue with the initial line of reasoning, over \( d' \).

Finally, the case when at least one of the views has no \(/-edges in the main branch can be handled by a similar construction of the unique candidate interleaving. \( \square \)

It is now easy to show that the same complexity lower bound holds for the rewriting problem.

**Theorem 8.7.** For queries and views from \( XP_{/\backslash} \), the rewriting problem is coNP-hard.

**Proof.** We can use the same construction as in the proof of Theorem \([8.5]\) for a reduction from tautology of a formula \( \phi \). We define \( n+1 \) views, \( v_0 = p_0 \), \( v_1 = p_1, \ldots, v_n = p_n \). We define \( q = p_c \), for \( p_c \) being the unique candidate interleaving for the DAG \( d = dag(unfold(v_0 \cap v_1 \cap \ldots \cap v_n)) \). Moreover, it is easy to see that the only rewrite plan that has chances to be a rewriting is \( r = v_0 \cap v_1 \cap \ldots \cap v_n \) (the output node of each view can only be mapped in the output node of \( q \)). From this, it follows that \( r \) is an equivalent rewriting if \( d \equiv q \) or \( d \) is union-free if the formula \( \phi \) is valid. This shows that deciding the existence of an equivalent rewriting \( r \) for queries and view from \( XP_{/\backslash} \) is coNP-hard. \( \square \)

**9. Tractability Frontier: Rewrite-Plans for PTIME**

We also identify a large class of rewrite plans that lead to PTIME completeness.

We say that two (or several) tree patterns are akin if their root tokens have the same main branch codes. For instance, while the views \( v_1 \) and \( v_2 \) from our example are not akin, \( v_1 \) is akin to:

\[
v_1' = \text{doc(L)}/figure[//caption//label]/subfigure/image[ps]
\]

Under the assumption of akin views, we can relax the syntactic restrictions of the \( XP_{cs} \) fragment for tractability and accept the class of patterns \( XP_{/\backslash} \). Our main result for restricted rewrite plans is following (for readability purposes, the proof is given in Section \([8]\):

ACM Journal Name, Vol. V, No. N, Article A, Publication date: January YYYY.
**Theorem 9.1.** For DAG patterns of the form \( d = \bigcap_j p_j \), where all \( p_j \) are in \( XP// \) and akin, \( d \) is union-free iff the algorithm APPLY-RULES rewrites \( d \) into a tree.

From this, it follows that:

**Corollary 9.2 (\( XP// \)).** EFFICIENT-RW always finds a rewriting for \( XP// \), provided there is at least a rewriting \( r \) such that the patterns intersected in \( \text{unfold}(r) \) are akin.

Once again, we can show that dropping the restriction of akin patterns leads to hardness for both union-freedom and rewriting using views.

**Theorem 9.3.** For a pattern \( d = \bigcap_j p_j \), where all \( p_j \) are in \( XP \) and akin, deciding if \( d \) is union-free is \( \text{coNP-hard} \).

**Proof.** Similar to the proof of Theorem 8.5.

It follows easily that the same lower-bound holds for the rewriting problem as well.

**Theorem 9.4.** For queries and views from \( XP \), deciding the existence of a rewriting \( r \) such that the patterns intersected in \( \text{unfold}(r) \) are akin is \( \text{coNP-hard} \).

**Proof.** Similar to the proof of Theorem 8.7.

10. NESTED INTERSECTION

We have considered so far the \( XP^\cap \) formalism, for rewritings that may first compensate the views, may then perform an intersection, and finally may compensate the result of this intersection. Such rewritings may not be sufficient for certain input queries, as illustrated in the following example.

**Example 10.1.** Let us assume that we have a view \( v_1 \), that retrieved all sections from papers:

\[
v_1 : \text{doc}("L")/\text{paper//section}
\]

The result of \( v_1 \) is stored in the cache as a materialized view, rooted at an element named \( v_1 \). Later, the query processor had to answer another XPath \( v_2 \) looking for sections having at least one theorem:

\[
v_2 : \text{doc}("L")/\text{section[theorem]}
\]

The result of \( v_2 \) is not contained in that of \( v_1 \), so it is also executed and its answer cached.

A third view has to be processed then, looking for library images in figures:

\[
v_3 : \text{doc}("L")/\text{lib//figure/image}
\]

and \( v_3 \) has to be computed as well, since it cannot be answered using the results of \( v_1 \) and \( v_2 \).

Let us now look at an incoming query \( q \), asking for all images in figures that appear in sections of papers with theorems:

\[
q : \text{doc}("L")/\text{lib//paper//section[theorem]//figure/image}
\]

However, by intersecting the results of the first two views we get the right section elements. Then, we can further navigate inside them, and intersect their image descendants with the images selected by \( v_3 \). So one can build a rewriting equivalent to \( q \):

\[
r_2 : (\text{doc}(v_1)/v_1 \cap \text{doc}(v_2)/v_2)/\text{figure/image} \cap \text{doc}(v_3)/v_3
\]

In the following, we will consider an extension \( XPint \) of \( XP \) with respect to intersection, which includes \( XP^\cap \), and allows us to handle rewritings with arbitrary many levels of intersection and compensation over views (i.e., nested intersections). The grammar of \( XPint \) is obtained from that of \( XP^\cap \) by adding the rule

\[
\text{jpath} ::= \text{ipath} \mid (\text{jpath}) \mid \text{jpath} \cap \text{cpath} \mid (\text{jpath})/\text{rpath} \mid (\text{jpath})//\text{rpath},
\]

having the straightforward semantics.
Let us notice that \( \text{XPint} \) queries can also be represented by DAG patterns having the particular property that if there are two distinct main branches from a node \( n_1 \) to another node \( n_2 \), then \( n_1 \) must be the root of the DAG.

As before, given a query \( r \in \text{XPint} \) over the view documents \( D_V \), we define \( \text{unfold}(r) \) as the \( \text{XPint} \) query obtained by replacing in \( r \) each \( \text{doc}(“V”) \)/\( V \) with the definition of \( V \). The notion of rewriting also extends naturally.

Definition 10.2. For a given XML document \( D \), an \( \text{XPint} \) query \( q \) and \( \text{XPint} \) views \( V \) over \( D \), an \( \text{XPint} \) -rewrite plan of \( q \) using \( V \) is a query \( r \in \text{XPint} \) over \( D_V \).

If \( \text{unfold}(r) \equiv q \), then we also say \( r \) is an \( \text{XPint} \) -rewriting.

We can show that this more general flavor of rewritings is no more expensive to evaluate (over view documents) than the \( \text{XP} \) ones.

Lemma 10.3. An \( \text{XPint} \) -rewrite plan can be evaluated over a set of view documents \( D_V \) in polynomial time in the size of \( D_V \).

Proof Idea. This a direct consequence of Courcelle’s theorem \cite{Courcelle1990} and generalizations thereof \cite{Flum2002}, on evaluating in linear time (data complexity) monadic second-order (MSO) formulas on trees or bounded tree-width structures. MSO is known to capture the navigational XPath outputting sets of nodes \cite{Gottlob2002}, a fragment that strictly subsumes \( \text{XPint} \).

Equally important, the rewriting problem stays in the same complexity class, even if the expressivity of the rewriting language increases.

Theorem 10.4. Deciding the existence of an \( \text{XPint} \) -rewriting for a query and views from \( \text{XP} \) is coNP-complete.

Proof. Similar to the proof of Theorem 7.4.

For the purposes of this section, we introduce the notion of rewriting graphs, which are similar to DAG patterns, with the following differences:

— in addition to \( \Sigma \) nodes, they have view nodes with labels of the form \( \text{doc}(“v”) \) where \( v \) is a symbol from a set of views \( V \); a view node cannot have any incoming edge.

— they do not have a distinguished node \( \text{ROOT} \).

We also generalize the function \( \text{unfold}(r) \) to return the \( \text{XPint} \) query that corresponds to the following transformation: replace every \( \text{doc}(“v”) \)/\( v \) with the query that defines \( v \), coalescing the newly introduced node corresponding to \( \text{OUT}(v) \) with its unique main branch child. This leads to a DAG pattern, since the views are assumed to be evaluated over the same, unique document.

Starting from the pattern of the input query \( q \) and the views \( V \), we will build step by step a rewriting graph \( \text{cand}_{RW}(q,V) \) that we call the rewriting candidate. We will then prove that the obtained candidate is minimally containing w.r.t. \( q \), i.e. \( \text{cand}_{RW}(q,V) \) is contained in any query over the view documents that contains \( q \). This guarantees completeness in the sense that if an \( \text{XPint} \) rewriting exists, \( \text{xpath}(\text{cand}_{RW}(q,V)) \) is also a rewriting.

Algorithm BuildRewriteCandidate

input: query \( q \in \text{XP} \), set of views \( V \) defined by \( \text{XP} \) queries
output: candidate rewriting \( \text{cand}_{RW}(q,V) \)

(1) set \( r \) to \( \text{pattern}(q) \)
(2) let \( S \leftarrow \{(v_i, o) \mid \text{if there is a mapping } h \text{ from } v_i \text{ into } q, o = h(\text{OUT}(v))\}\)
(3) foreach \( (v, o) \) in \( S \)
   add to \( r \) a new view-node labeled \( \text{doc}(“v”) \), with a child labeled \( v \) connected by a \( / \)-edge to \( o \)
(4) keep in \( r \) only paths accessible starting from view-nodes
(5) if OUT(q) is not in r, then fail
(6) set OUT(r) to OUT(q)
(7) return candRW(q, V) := r

Algorithm NestedRewrite
(1) candRW(q, V) ← BuildRewriteCandidate(q, V)
(2) if unfold(candRW(q, V)) ≡ q then output candRW(q, V)
else fail

As the step (7) of Rewrite, the equivalence test at step (2) uses Lemma 3.12. We show next that our algorithm always produces the minimally containing rewriting, in the following sense.

LEMMA 10.5. For q ∈ XP, V a set of XP views and r′ a rewriting graph, if q ⊆ unfold(r′), then unfold(candRW(q, V)) ⊆ unfold(r′).

PROOF. Let d be dag(unfold(candRW(q, V))), d′ be dag(unfold(r′)) and p be dag(q). As q ⊆ unfold(r′), we can write d = \cup_i d_i, d′ = \cup_j d′_j and p = \cup_k p_k as the union of their interleavings. By Lemma 3.14 there are containment mappings h_i from each d_i into some p_k and h′_j from every d′_j into some p_k.

We show by structural induction that there is a containment mapping from every d′_j into some d_i.

(1) Suppose r′ is of the form doc(V)/V, where V ∈ V. Since every d′_j maps into some p_k and candRW(q, V) is built using all possible mappings of the views, there is at least one occurrence of V in d connected to a node o. Moreover, since q ⊆ unfold(r′), there must be such an occurrence in which o actually corresponds to OUT(p). Hence there is trivially a containment mapping from every d′_j into some d_i.

(2) Consider now the case in which r′ corresponds to a query of the form \(\alpha/x\), where every interleaving \(\alpha_j\) of the pattern unfold(\(\alpha\)) has a mapping \(m^1_j\) into some \(d_i\) and \(x\) is a relative path. Let \(n_{\alpha}\) be the last node on the main branches of unfold(\(\alpha\)). Let \(d'_j\) be \(\alpha/x/\). By construction, the subgraph of \(d_i\) accessible starting from \(m^1_j(n_{\alpha})\), call it \(t_{ij}\) is a tree that is isomorphic to a subtree of \(h'_j(d'_j)\), where \(h'_j\) is the mapping from \(d'_j\) into some interleaving \(p_k\). Hence the identity function id is a mapping from \(st\) into \(t_{ij}\), therefore \(m^1_j\) can be extended to a mapping \(m^2_j\) from \(d'_j\) into \(d_i\). If OUT(d′) is in the pattern of \(\alpha\), then from the containment of \(q\) into \(\alpha/x\) we can also infer the containment of \(q\) into \(\alpha\) and the induction hypothesis guarantees that \(m^1_j\) can be chosen such that it is a containment mapping. Otherwise, OUT(d′) is part of the pattern of \(x\) and \(h'_j(\text{OUT}(d')) = \text{OUT}(p)\). But then \(m^2_j(\text{OUT}(d')) = h'_j(id(\text{OUT}(d'))) = \text{OUT}(d)\) and \(m^2_j\) is a containment mapping.

(3) Suppose that r′ is of the form \((\alpha \cap \text{doc}(V)/V)\), where every interleaving \(\alpha_j\) of the pattern unfold(\(\alpha\)) has a mapping \(m^1_j\) into some \(d_i\). Let \(n_{\alpha}\) be the last node in the main branches of \(\text{dag}(\text{unfold}(\alpha))\) and \(n'_\alpha = m^1_j(n_{\alpha})\), unique for all j. Then again we can find \(\text{doc}(V)/V\) in d that was added to candRW(q, V) by a set of mappings \{m^1_j\} into p that agree with \(h'_j\) on unfold(doc(V)/V) and such that \(m^1_j(n'_\alpha) = \text{OUT}(p), \forall l\). Hence \(n'_\alpha\) is the output node of \(d\) and \(m^1_j\) can be extended to a mapping \(m^2_j\) from \(d'_j\) into \(d_i\) such that \(m^2_j(\text{OUT}(d')) = n'_\alpha = \text{OUT}(d)\).

Then by Lemma 3.8 we have that \(d \subseteq d'\).

THEOREM 10.6. For any query q ∈ XP and any XP rewriting r′ such that unfold(r′) ⊆ q, unfold(candRW(q, V)) ⊆ unfold(r′).

Remark. Note that algorithm BuildRewriteCandidate runs in PTIME, but NestedRewrite is worst-case exponential, which is the best we can hope for, given the hardness result of Theorem 10.4.

It is remains open whether for XPint the complexity of union-freedom and view-based rewriting drops to PTIME under the input query restrictions (extended skeletons) or the rewrite plan ones.
discussed in the previous section. This represents one of our main directions for future research on XML view-based query rewriting, and challenging one.

11. OPTIMIZATION OPPORTUNITIES
The implementation of the REWRITE algorithm revealed several possible refinements, and we discuss in this section the most relevant high-level optimizations that enabled performance improvements in practice. We stress that, by this implementation, our main goal was to provide a proof-of-concept prototype, illustrating advantages and scalability. Many other directions for optimization, including low-level aspects and supporting data structures, remain to be explored.

11.1. Optimizing plans
We start by introducing the theoretical foundations of a PTIME technique for partially minimizing redundancy in rewrite plans, without paying the price of full minimization. We show that, at line 3 of REWRITE, for a given view participating in a plan, we can always choose one unique compensation instead of all the valid compensations. To this end, for a view $v$ that maps into $p$, $\text{bestcomp}(v, p)$ returns $v'$ formed by $v$ plus some compensation, such that $v'$ is contained in all other compensated versions of $v$.

**Lemma 11.1.** For a given prefix $p$ of the input query and a given view $v$, $\text{bestcomp}(v, p)$ is well-defined. It is sufficient to use in algorithm REWRITE, for the corresponding rewrite plan, only $v$’s $\text{bestcomp}(v, p)$ compensation.

**Proof Idea.** It is immediate that compensations that are subsumed (contain) by others will be redundant in the rewrite plan and can be safely discarded (this could be performed by applying R7 to saturation on the original plan). However, the best compensation is uniquely defined for each prefix and view, and can be constructed and used directly in the plan, in this way avoiding expensive rule testing and application. More precisely, the compensated view $\text{bestcomp}(v, p)$ corresponds to the longest possible compensation — in terms of main branch nodes of $p$ — that can be applied on $v$ in REWRITE, which in turn corresponds to the highest possible mapping image of $v$ in $p$. It can be easily verified that the $\text{bestcomp}(v, p)$ compensation obtained in this way will be contained in all the other compensations of $v$.

We also identified as potentially beneficial a test for the existence of a sub-plan equivalent to the input query formed by akin views, even for input queries outside the fragment $\text{XP}$. Intuitively, rule application on the akin plan is likely to advance faster towards a conclusion. Note however that whenever the resulting DAG is not a tree we cannot conclude whether the initial plan is union-free, and this plan has to be processed as well.

Regarding the simplification of plans, due to the compensation steps, many redundant predicates may be present on nodes of the initial plan. These can be pruned out, before the APPLY-RULES subroutine, in this way making the various mapping tests for rule applications lighter.

Finally, we can use some efficient tests to detect plans that cannot be equivalent to the input query and can be discarded before the APPLY-RULES subroutine. For example, in the case of input queries with only /-edges in the main branch, a view having that same main branch must be available. Similar tests on the main branches of the root and output tokens of the query and the plan’s views can be used to discard plans.

11.2. Optimizing rule applications
First, the implementation of the rewrite rules uses as a key building block the “bottom-up” computation of mappings. While for mappings into tree structures we can rely directly on a dynamic programming approach as in [Miklau and Suciu 2004], extending this approach for mapping of trees into DAGs requires to maintain the DAG nodes in topological order.
Rewriting XPath Queries using View Intersections: Tractability versus Completeness

Second, complementing the steps discussed in the proof of Lemma 7.5 – for testing in polynomial time the premises of the rules – other optimizations are possible in the DAG rewrite phase. Regarding rule R1, note that the only DAG changes that may trigger it, besides R1 itself, can come from the rules R2, R6 and R8. Therefore, we can (i) start by applying R1 to saturation, and (ii) go through the rest of the rules and reapply rule R1 to saturation only after one of these three rules triggered. Rule application can be tested efficiently when the various paths involved can be easily identified, due to either being “single incoming edge, single outgoing edge” or being |-paths; for identifying |-paths, one must however apply to saturation rule R1, before any tests involving such paths. The test for R7 is slightly more involved, since part of its input, namely the p1 candidates, is not easily identifiable. However, it is sufficient to test the existence of such candidates and to handle them implicitly, contrary to p2 candidates which can be found easily by the properties required by the rule. Given a p2 candidate, any mapping of p2 nodes in the DAG rooted at node n1 will also determine at least one such path p1, and we only need to keep track of the allowed images for nodes of p2 (between n1 and the common descendant of n1 and p2’s nodes).

Third, regarding the tests for collapsible nodes, the formal definition does not necessarily lead to the most efficient implementation. We can in fact bypass the computation of tentative DAGs and simply compare the incoming and outgoing |-paths for the tested nodes.

Fourth, in order to efficiently check the applicability of rule R8, instead of the naïve test for each possible pair of nodes (n1, n2), we can rely on two parallel mapping computations: one that is bottom-up, ending at the common ancestor node, and one that is top-down, ending that the common descendant node. Then, the intersection of the valid mappings for nodes of p2 can reveal those that are relevant for R8, having only one possible image in p1.

11.3. Other optimization opportunities
Some general adjustments that proved to be useful for the overall performance include dedicated data structures, such as adjacency lists for incoming and outgoing main branch edges, predicates, child and descendant edges – as many of the rules involve iterating on specific children types – as well as lists of topologically-sorted nodes, built with the candidate plan and updated only when needed, after certain rules were applied.

12. EXPERIMENTS
We performed our experiments on an Intel(R) Core(TM) i7-2760QM@2.40GHz machine, with 8G of RAM and the Ubuntu 11.10 operating system.

We evaluated the performance and scalability of the Rewrite algorithm, focusing on two main aspects:

— the rewrite time, i.e., the time necessary to find an equivalent rewriting, when one exists, and
— the improvements on evaluation time, i.e., the comparison between the evaluation time of the input query over the data, on one hand, and the rewrite time cumulated with the evaluation time of the rewriting, over the view documents, on the other hand.

In the space of analysis, we looked at how these two performance indicators vary with the size and the type of input queries – w.r.t. the various XPaths fragment that were discussed in the paper, the size of the view set that may give a rewriting, and the size of the input data.

12.1. Documents, queries and views
Our experimental setup was guided by: (a) our focus on measuring rewrite time as well as improvements on evaluation time, (b) the intention to stress-test our implementation for performance evaluation purposes. We thus needed:

— queries and views spanning the XP fragments analyzed in our theoretical study,
— a set of documents the queries and views would apply to,
— the ability to scale query, view and document sizes, for performance assessment.
Given our needs in terms of variation of query and view structure, number and size, we could not benefit from existing benchmarks or real-life settings publishing queries and views. Therefore we designed our own synthetic query and views generator, suiting our testing purposes. Starting from a given XML input document, this generator produces queries and views over that document (i.e. yielding a non-empty result), controlling their structure, number and size, as well as pair-wise containment.

While our synthetic queries and views generator can be plugged on any XML document, our need to scale with the document size limited the usefulness of existing XML documents. We have therefore adopted in our experiments the extensively cited XMark document generator [Schmidt et al. 2002]. This generator allows varying the size of its output, while ensuring similar structure and properties across the XML documents it produces.

Three input documents were generated with the XMark generator, of sizes 41KB, 91MB and 18GB. On each of the documents, we used our custom generator to produce input queries and view sets.

We generated, for each of the documents, input queries of main branch size 5, 7 and 9 (the XMark documents have a maximal depth of 11). We considered input queries from three categories: $X_{P_{ee}}$, beyond $X_{P_{ee}}$ but in $X_{P_{ff}}$, and in $X_{P}$ but beyond $X_{P_{ff}}$, i.e., without restrictions.

For input queries, each possible pairing of main-branch size and category for input queries was used to generate 10 random input queries, for a total of 90 input queries. Importantly, these queries were generated from the data, in a way that ensures that they all have a non-empty result on the three input documents. This was to avoid meaningless evaluation time measurements and to preclude the case when an alternative detection of unsatisfiability would shortcut the rewrite time.

For the generation of views, to each of the input queries we associated five randomly generated view sets of variate size, namely consisting of 40, 80, 160, 320, or 640 views, for a total of 450 view sets. We had the following guidelines in the generation of view sets:

1. While we wanted many views, we wanted to control the percentage of views that would be useful in a rewriting; more precisely, all the view sets consisted of 10% useful views (for the rewriting), while the remaining 90% were useless (i.e., they did not map in the input query).\footnote{We adopted this 10% − 90% ratio as a reasonable one for most practical scenarios.}

2. We wanted views that were not equivalent to the input query nor a prefix thereof, and did not allow single-view rewritings. This was to exercise precisely the non-trivial, multiple-view rewritings that our algorithm achieves.

3. We wanted only view sets that gave an equivalent rewriting for the input query they were associated to. This was in order to be able to evaluate rewritings and to check their benefit over the evaluation of the input queries.

4. For the fragment $X_{P_{ee}}$, no restrictions were imposed on the views, consistent with our theoretical results (completeness does not depend on view restrictions).

Note that, although all views have a non-empty result by construction, the size of their result and their selectivity could vary significantly and were not controlled in the generator. Other aspects that were not controlled by our query generator were (i) the overall size of input queries (only the size of the main branch was chosen), (ii) the overall size of the views, and (iii) the overall size of the plans built and tested in REWRITE.

12.2. REWRITE vs. EFFICIENT-RW

As a first experiment, through the random generation of sets of views, we took a first step towards understanding how often one may lose completeness in practice, if interleavings are not computed. In other words, we wanted to quantify how often, at line (7) in REWRITE, a positive containment test has to deal with a DAG pattern in the left-hand side. (Recall that the only difference introduced by the EFFICIENT-RW variant of the algorithm is that the containment test is done only if the DAG transformations yield a tree pattern.) This is important for input queries from $X_{P_{ff}}$ and $X_{P}$, as the
computation of interleavings – potentially exponentially many – is expected to represent the main overhead in the search for a rewriting.

To this end, the random generation flow was the following: (a) a set of views would be generated, for a given input query and a given set size, and (b) the rewrite plans would be constructed and each would be tested for equivalence in REWRITE, within a limit of 30 minutes of execution time.

This experiment gave us valuable insight: within the time limit of this random process, yielding 450 sets of views, we obtained no view set that did provide an equivalent rewriting, but only by performing interleavings, after APPLY-RULES (line (7) in REWRITE). In the process, for all the generation tentatives, a large majority of the allotted time was spent in computing interleavings, when a tree pattern was not outputted by APPLY-RULES. Moreover, in many of these cases, the time limit was met without reaching a conclusion. This outcome, on one hand, confirms the fact that the computation of interleavings is very costly. More importantly, while this represents just a preliminary set of results, it does suggest that one could “turn off” the computation of interleavings: while we know that interleavings are needed for completeness, it seems that we may not have a sufficiently important gain in finding rewritings by computing them; if supported by further evidence, we can suggest avoiding the computation of interleavings, using EFFICIENT-RW instead of REWRITE.

Consequently, with the 450 sets of views we obtained, we continued our empirical evaluation using the EFFICIENT-RW variant of our algorithm.

12.3. Rewrite time

For this set of measurements, for each input query size and category, for the corresponding 10 input queries, we recorded the average time to find a rewriting for each possible size of the view set (among the 5 sizes given previously). This allowed us to understand how the rewrite time using EFFICIENT-RW varies with the input query size and category, on one hand, and with the size of the view set, on the other hand.

We present our measurements for the running time of EFFICIENT-RW in Figure 7. There, we give one set of results (a sub-figure) for each query length. In each sub-figure, we give five groups of three columns. A group corresponds to one possible size of the view set, and in each group the first column corresponds to XPes input queries, the second column corresponds to XP// input queries, and the third column corresponds to input queries without restrictions.

We can draw several important conclusions from the results of in Figure 7. First, our proof-of-concept prototype of EFFICIENT-RW can process efficiently, in a fraction of a second, queries of significant size – up to 9 nodes in the main branch, with 3 – 4 predicates in average on each main branch node and with predicates of average depth of 3 – and view sets of significant size as well (order of hundreds). Note that the measurements follow closely a linear progression with respect to the size of the view set. With respect to varying the query size, the observed progression is even less pronounced – for example, for queries without restrictions, from 110ms to 210ms to 250ms.
12.4. Evaluation time

Regarding evaluation time, we compared the time necessary to evaluate the initial (input) queries over the input documents with the time necessary to build, test and then evaluate the rewriting over the view documents. We present these measurements in Figure 8. For the sake of conciseness, we present only the results for the input queries of maximal size (9 nodes in the main branch). We give one set of results (a sub-figure) for each document size. As before, in each sub-figure, we give five groups of three columns, with one group for each possible size of the view set. As for rewrite time, we measured the average time in each setting. Since the time necessary to run the input query over the input documents does not depend on the views, it is represented by a horizontal line in the plot.

Query evaluation was done using the SAXON query engine, which we extended with the Id-based JOIN functionality across multiple documents (the view documents), as SAXON’s ability to perform this task was incomplete.

Query evaluation was done using the SAXON query engine, which we extended with the Id-based JOIN functionality across multiple documents (the view documents), as SAXON’s ability to perform this task was incomplete.

A first important aspect to be noted in Figure 8 is that, over all input documents, the time necessary to evaluate the rewriting is smaller than the one for the input query, for all sizes of view sets. Moreover, the evaluation time based on view documents exhibits a linear progression and, overall, remains quite low, roughly 0.5 seconds for the smallest document, around 1 second for the intermediary document, and around 2.5 seconds for the largest document.

One can note the intuitive trend indicating that the larger the set of views in the rewriting, the less important the performance benefit over the original query plan. (Note that we measured the plans consisting of all the useful views.) In our results, this trend stems from the way we set up the experiments, doubling at each step the number of views that were applicable in a rewriting (while this seems to be an unlikely scenario in practice, it represents a suited stress test for our algorithm). In
our experimental configuration, many views meant, inevitably, more data and many opened documents, hence the overhead related to managing them, which for Saxon starts being noticeable.

Within one group of columns, the differences in evaluation time based on views between the three categories of queries are mainly due to the variations in terms of selectivity and view documents’ size. For instance, on the smallest document, the views generated for extended skeletons were significantly less selective, yielding view documents almost two times larger than the ones corresponding to the other two categories. Similar differences could be observed for the second document, between views for the $XP_{es}$ and $XP_1$ queries on one hand, with larger view documents, and the views for arbitrary queries on the other hand.

Finally, we also considered the execution time of EFFICIENT-RW over the view sets without the 10% useful views, measuring the ratio between the direct evaluation of the query and the overhead of unsuccessful EFFICIENT-RW runs. Without listing the precise measurements, we mention here that we observed negligible overhead in all cases – up to 2% – even over the smallest document.

12.5. Discussion

Our main conclusions from this experimental evaluation are the following:

— EFFICIENT-RW scales to large sets of views, with rewrite time under one second, in all cases. Recall ours is an initial prototype and there is certainly room for further optimization, therefore these are very encouraging results. Moreover, the rewrite time represented a small percentage of the evaluation time. At the same time, there are many scenarios (e.g., with security views) where rewriting is not done for performance purposes, and in which the comparison between rewrite time and evaluation time is immaterial.

— The evaluation of the rewriting, including the rewrite time, is significantly more efficient than the evaluation of the input query, under assumptions that are widely-applicable in practice. Despite the fact that views were generated randomly, without means to control their selectivity or how they may “cover” the input query, the rewriting was evaluated two to three times faster than the input query, even for hundreds of views. Note that in the random generation process we do control the percentage of useful views and, for stress testing the algorithm, this was increased exponentially; this is certainly not what one would expect in practice. Finally, the evaluation time depends undoubtedly on the particular query engine that is used, and it is not clear whether the one that we relied on had an optimal behavior when handling many opened, large documents.

— The benefit of our tractable techniques for equivalently rewriting XPath queries using multiple views is significant. Indeed, interleavings are key to achieving completeness (as our theoretical results show) yet, at the same time, our experiments show that the benefit of computing interleavings is limited; therefore, EFFICIENT-RW is a good candidate for practical, performance-oriented scenarios, even when completeness cannot be guaranteed (e.g., beyond $XP_{es}$).

13. CONCLUSION

We considered the problem of rewriting XPath queries using multiple views, characterizing the complexity of the intersection-aware rewriting problem. More precisely, our work identified the tightest restrictions under which an XPath query can be rewritten in PTIME using an intersection of views and we propose an algorithm that works for any type of identifiers. A side effect of this research was to establish a similar tractability frontier for the problem of deciding if an intersection of XPaths can be equivalently rewritten as an XPath without intersection or union. We extended our formal study of the view-based rewriting problem for XPath to more complex rewrite plans, with no limitations on the number of intersection and navigation steps inside view outputs they may employ. We also presented a proof-of-concept implementation of our techniques and a thorough experimental evaluation, focusing on scalability and the comparison between the evaluation time of the initial query plan and the evaluation time of the rewriting, using the view documents.

An important open question remains to provide a more accurate characterization for the complexity of XPath rewriting with multiple levels of intersection and compensation ($XPint$ rewritings).
In particular, an important question is whether view-based rewriting for $XP_{es}$ input queries allows tractable, sound and complete procedures when rewrite plans are from $XPint$.

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Rewriting XPath Queries using View Intersections: Tractability versus Completeness

A. PROOF OF THEOREM

APPENDIX

The proof is organized as follows. We first show that APPLY-RULES is complete over DAG patterns in which the root and the output node are connected by a path having only /-edges (Lemma A.1).

We then consider the complementary case when all the branches in parallel (the compensated views) have at least one //-edge in the main branch. For clarity, we prove completeness progressively, starting with the case of intersecting two views under certain restrictions: their root tokens have the same main branch, their result tokens have the same main branch as well (Lemma A.2). We then extend to the case of arbitrary many views, with these restrictions (Lemma A.3). Then we consider the general case, which will rely on results proven for the limited cases.

We start with DAG patterns – unfoldings of the rewrite plan – in which the root and the output node are connected by a path having only /-edges, i.e. there one of the views involved in the intersection has only one token.

**Lemma A.1.** For $n$ XP$_{es}$ patterns $v_1, v_2, \ldots, v_n$, where $v_1$ has only one token, $\text{dag}(v_1 \cap v_2 \cap \cdots \cap v_n)$ is union-free iff APPLY-RULES rewrites it into a tree.

**Proof.** Without loss of generality, we can consider that $v_2, v_3, \ldots, v_n$ have more than one token. Suppose that the output of the rewriting algorithm, call it $d'$, is not a tree pattern. It is easy to see that there is a subpattern $sd'$ in $d'$ that is not a tree and it has a //Edge, otherwise R1 (plus maybe R7) would have reduced that subgraph to a tree. Then there must be a node $n_1$ in $d'$ such that there are at least 2 main branch paths ($p_1$ and $p_2$) going out of $n_1$: one starting with a //edge $n_1//n_2$ and another one starting with a //edge $n_1//n_3$, such that the 2 paths meet again starting from a node $n_4$. We can also infer that on the $n_1//n_3$ branch, the last edge before $n_4$ is a //edge $n_5//n_4$, as in Figure 10b otherwise R1.ii would have applied or the pattern would have been unsatisfiable.

Since R2 did not apply, it means that $n_2$ and $n_3$ are collapsible and, moreover, that the root token of $p_2$ is a prefix of $p_1$ yet there is at least one predicate attached to a node of it that does not map in the corresponding position in $p_1$.

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Besides these two branches, other branches may be present in parallel with the /-only main branch in \(d'\) of which \(p_1\) is part of.

In general, since R7 does not apply, it means that \(p_2\) does not fully map into \(p_1\). This means that an interleaving \(i\) of \(d'\) s.t. \(d' \equiv i\) (witness for union-freedom), built by some choice \(\psi\) of mapping \(p_2\)'s main branch nodes into \(p_1\)'s main branch nodes, must for at least some node \(n_7\) in \(p_2\) and predicate \(Q\) attached to it collapse \(n_7\) with \(n_8 = \psi(n_7)\) of \(p_1\), even though \(\text{pattern}(\lambda_d(n_7)[Q])\) did not map into \(\text{SP}_{d'}(n_8)\).

We will show that there exists at least one other interleaving \(i'\) of \(d'\) in which the predicate \(Q\) does not hold at \(n_8\). Since R7 did not apply, it means that \(Q\) did not hold at \(n_8\) before any possible application of R9 and it still does not hold after R9 steps. But this basically tells us there there exists an interleaving in which \(Q\) does not hold at \(n_8\). This implies that \(d\) is not union-free.

We now consider the case when all the branches in parallel (the compensated views) have at least one // edge in the main branch.

We start by proving the following lemma.

**Lemma A.2.** For two XP_e patterns \(v_1, v_2\) s.t. their root and result tokens have the same main branch, the DAG pattern \(d = \text{dag}(v_1 \cap v_2)\) is union-free iff APPLY-RULES rewrites \(d\) into a tree.

**Proof.** Let us first consider what rule steps may apply in order to refine \(d\). First, since we are dealing with patterns with root and result tokens having the same main branch, R1 steps will first apply, coalescing the root and result tokens of the two branches. At this point, the only rules that remain applicable are R6 and R7. This is because we do not have nodes with incoming (or outgoing) /-edges and // -edges simultaneously and R5 will only apply to predicates starting by a // -edge.

We argue now that \(d\) is union-free iff rule R7 applies on it.

Note that since we only have 2 parallel branches an application of rule R7 would immediately yield a tree. So the if direction is straightforward. For the only if direction, if R7 does not apply this translates into (†) there is no mapping (not necessarily root-mapping) between the intermediary part of \(v_1\) and the intermediary part of \(v_2\).

Assuming that (†) holds, rule R6 remains the only option. So, possibly after some applications of R6, followed by applications of R1 collapsing entire tokens, we obtain a refined DAG \(d\) as illustrated in Figure 9a (only the main branches of \(d\) are illustrated). \(p_r\) has the common main branch following the root (may have several tokens if R6 applied) and \(t_o\) denotes the result token. \(t_1\) and \(t_2\) denote the two sibling /-patterns for which R6 no longer applies. As \(t_1, t_2\) are dissimilar we have that \(t_1 \neq t_2\).

We show that \(d\) is not union-free by the following approach: we build two interleavings, \(p'\) and \(p''\), that do not contain one another, and then show that by assuming the existence of a third interleaving \(p\) that contains both we obtain the contradiction \(t_1 \equiv t_2\).
We continue with the following observation which follows easily from the $XP_{ex}$ restriction on usage of //edges in predicates: given two $l$-patterns $t_1$ and $t_2$ from $XP_{ex}$, if $t_1$ does not map in $t_2$ then, for any tree pattern $q$ of the form $...//t_2//...$ with $t_2'$ being an isomorphic copy of $t_2$, we have that $t_1$ does not map into $t_2'$.

The following steps will implicitly use this observation.

Let $p_1 = t_1//p_3$ denote the left branch and let $p_2 = t_2//p_4$ denote the right branch in $d$. Because of (1), there is no mapping (not necessarily root-mapping) between $p_1$ and $p_2$.

Let $sf_1$ be the maximal token-suffix of $p_1$ that can map into $p_2$, and let $pr_1$ be the remaining part (i.e., a token-prefix). Note that $pr_1$ cannot be empty, so we can write it as $p_1 = pr_1//sf_1$.

Similarly, let $sf_2$ denote the maximal token-suffix of $p_2$ that can map into $p_1$, and let $pr_2$ denote the remaining part, non-empty as well. So we can write $p_2 = p_2//sf_2$.

We build $p'$ and $p''$ as follows:
\[
p' = p'_r // p'_{r1} // p'_{o1} // t'_o = p'_r // p'_{r2} // p'_{o2} // s'_{f1} // t'_o
\]
\[
p'' = p''_r // p''_{r1} // p''_{o1} // t''_o = p''_r // p''_{r2} // p''_{o2} // s''_{f2} // t''_o
\]

where the $#'$, $''$ parts are isomorphic copies of the # parts of $d$.

Note that $pr'_{r1}$ (resp. $pr''_{r2}$) starts by token $t'_1$ (resp. $t''_2$).

These two queries are obviously in $XP_{es}$, hence no containment mapping between $p'$ and $p''$ since, by the way $sf_1$ and $sf_2$ were defined, $pr'_{r1}$ (resp. $pr''_{r2}$) could only map in $pr''_{r1}$ (resp. $pr'_{r2}$).

So neither $p'$ nor $p''$ can be the interleaving that reduces all the others. We show in the following that no other interleaving $p$ of $d$ can reduce both $p'$ and $p''$ unless $t_1 \equiv t_2$.

Let us assume that such a $p$ exists. Without loss of generality, let $p$ be of the form
\[
p = p_r//m//t_o.
\]

(interleavings that are not of this kind will not remain in the normal form of $d$).

We assume a containment mapping $\phi'$ from $p$ to $p'$ and another one $\phi''$ from $p$ to $p''$. Obviously, $v_1$, $v_2$ must have containment mappings into $p$, since $p \equiv v_1 \cap v_2$. In particular, their sub-sequences $p_1$ and $p_2$ have images in the $m$ part of $p$. Let $\psi'$ and $\psi''$ be these containment mappings.

With a slight abuse of notation, let $\psi'(pr_1)$ denote the minimal token-prefix of $m$ within which the image under $\psi'$ of the $pr_1$ part of $v_1$ occurs. $\psi'(pr_1)$ is well defined because $v_1$ and $v_2$, and hence $p_1$ and $p_2$, are in $XP_{es}$, hence the image of a token of $p_1$ and of its predicates is included into a token of $m$. In other words, $\psi'(pr_1)$ starts with the root token of $m$ and ends with the token into which the output token of $pr_1$ maps. Similarly, let $\psi''(pr_2)$ denote the minimal token-prefix of $m$ within which the image under $\psi''$ of the $pr_2$ part of $v_2$ occurs.

We can thus write $p$ in two forms, as
\[
p = p_r//\psi'(pr_1) ... \psi'(sf_1)//t_o
\]
\[
p = p_r//\psi''(pr_2) ... \psi''(sf_2)//t_o
\]

Next, we argue that in the containment mapping $\phi''$ of $p$ in $p''$, we must have $\phi''(\psi'(pr_1)) = pr''_{r1}$.

Similarly, we must have that $\phi''(\psi''(pr_2)) = pr''_{r2}$. This follows easily from the way $sf_1$ and $sf_2$ were defined. (For instance, no node of $\psi'(pr_1)$ can map below $pr''_{r2}$ in $p''$, otherwise $sf_1$ would not be maximal. And $MB(p_r) = MB(p''_r)$ and $\psi'(pr_1) \geq pr''_{r1}$, hence no node of $\psi'(pr_1)$ can map higher than $pr''_{r1}$ either, otherwise $p_r$ would not map into $p''$.) And it then implies that $\psi'(pr_1) \equiv pr_1$ and $\psi''(pr_2) \equiv pr_2$.

But since $m$ starts by both the token-prefix $\psi'(pr_1)$ and by $\psi''(pr_2)$, hence by token-prefixes $pr_1$ and $pr_2$, $pr_1$ and $pr_2$ should at least start by the same token. Hence $t_1 \equiv t_2$, which is a contradiction.

In other words, we showed that $d$ is union-free iff, after a sequence of $R1$ steps, $R7$ applies, transforming the pattern into a tree. As we know from Lemma [7.5] that APPLY-RULES also terminates, it follows that $d$ is union-free iff APPLY-RULES rewrites $d$ into a tree. 

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Fig. 10: DAG patterns for the proof of Theorem 8.3.

For $d = v_1 \cap v_2$, where $v_1$ and $v_2$ are two skeleton patterns such that their root and result tokens have the same main branch, with the previous notations, we can also easily prove the following.

**Lemma A.3.** All the interleavings of $nf(d)$ are of the form $p_r//...//t_o$.

We know so far that the intersection $d$ of two skeleton queries such that their root and result tokens have the same main branch is union-free iff APPLY-RULES rewrites $d$ into a tree. Moreover, this happens iff there is a mapping between the intermediary part of one into the intermediary part of the other. If $d$ is not union-free, the result is a union of queries having the same root and result tokens, as described in Lemma A.3.

We now consider intersections of more than two patterns.

**Lemma A.4.** Given $XP_{es}$ patterns $v_1, \ldots, v_n$ s.t. their root and result tokens have the same main branch, the DAG pattern $d = \text{dag}(v_1 \cap \cdots \cap v_n)$ is union-free iff APPLY-RULES rewrites $d$ into a tree. If the skeletons are of the form $v_i = p_r//p_i//t_o$, $1 \leq i \leq n$, then $d$ is union-free iff there is a query among them, $v_j$, having an intermediary part $p_j$ such that all other $p_i$ map into $p_j$.

**Proof.** We prove this by induction on the number of patterns (Lemma A.2 covers $n = 2$). As in the case of Lemma A.2, we first rewrite $d$ by rule R1, coalescing the root and result tokens of the parallel branches. At this point, the only rules that remain applicable are R6 and R7.

Let us now assume that some run of APPLY-RULES terminates on $d$ without outputting a tree. Then, it is easy to check that APPLY-RULES will also stop in the particular run, in which we start by applying only R7 until it does not apply anymore.

We show in the following that $d$ resulting from this run is not union-free.

We continue with $d$ obtained, as said previously, possibly after some applications of R7 that removed some of the branches in parallel, yielding a DAG pattern as the one illustrated in Figure 9b. $2 \leq k \leq n$ denotes the number of remaining branches in parallel and $i_1, \ldots, i_k$ denote these branches. Without loss of generality, let these be the intermediary parts of $v_1, \ldots, v_k$ respectively.

Note that we are now in a setting in which $d \equiv v_1 \cap \cdots \cap v_k$ and the following holds: (†) there is no mapping between the intermediary parts of any of $v_1, \ldots, v_k$.

Next, starting from the DAG pattern $d$ in Figure 9b by (†), only rule R6 is applicable.

For convenience, we assume that R6 steps are applied by a slightly different strategy: we take an R6 step only if it applies to all the parallel branches simultaneously. At some point, this process will stop as well and we obtain a refined $d$ as illustrated in Figure 10a (only the main branches are given). Let $p_i = t_i//r_i$ denote the branches in parallel. Note that the $t_i$ tokens cannot all be equivalent (recall that in $XP_{es}$ similar patterns must be equivalent).
Let us assume towards a contradiction that \( d \) is union-free and let \( q \) be the interleaving such that \( q \equiv d \). Without loss of generality, let \( q \) be of the form \( q = p_r//t//m//t_o \), where \( t \) is the token immediately following \( p_r \). (the \( m \) part might be empty).

Without loss of generality, let us also assume that \( t_1 \neq t \) (we know that there must be at least one such token among \( t_1, \ldots, t_k \)). We show that by assuming \( q \equiv d \) we obtain the contradiction \( t \equiv t_1 \).

For \( p_1 \) chosen in this way, let \( d' \) denote the DAG pattern obtained from \( d \) by removing its \( p_1 \) branch. Introducing for each \( i \) the pattern \( v'_i = p_r//p_i//t_o \), by (1) all incomparable, note that \( d' \) can be seen as \( d' = d\text{ag}(v'_2 \cap \cdots \cap v'_k) \) and note also that \( d' \equiv \bigcap_{i=1}^k (p_r//t_1//r_1//t_o) \).

By the inductive hypothesis, \( d' \) is not union-free, i.e., there is some \( x \geq 2 \) and some patterns \( q_1, \ldots, q_x \), which are some incomparable interleavings of \( d' \) (such their root and result tokens have the same main branch), all of the form \( p_r//\cdots//t_o \) (by induction, from Lemma \( \text{A.3} \), such that \( d' \equiv q_1 \cup \cdots \cup q_x \).

So can conclude that \( d \equiv v'_1 \cap (q_1 \cup q_2 \cup \cdots \cup q_m) = (v'_1 \cap q_1) \cup (v'_1 \cap q_2) \cup \cdots \cup (v'_1 \cap q_m) \).

Note now that we cannot have \( v'_1 \subseteq q_i \), for any \( q_i \), since this would mean that \( v'_1 \subseteq v'_2, \ldots, v'_k \), in contradiction with (1).

We proceed by an exhaustive case analysis:

**Case 1:** for all \( q_i \), we have \( q_i \not\subseteq v'_1 \).

In this case, each intersection of two given above will not be union-free. This follows easily from Lemmas \( \text{A.2} \) and \( \text{A.3} \) since \( v'_1 \) and \( q_i \) have the same root tokens and result tokens (there is no containment mapping between them, so there can be no mapping between their intermediary parts).

Hence any interleaving resulting from some DAG pattern \( d_i = \text{dag}(q_1 \cap v'_1) \) cannot even reduce all the other interleavings of \( d_i \), so \( d \) cannot be union-free in this case, since \( d = \cup d_i \). This case can be thus discarded.

**Case 2:** at least two interleavings of \( d' \), say \( q_1 \) and \( q_2 \), are such that \( q_1 \subseteq v'_1 \) and \( q_2 \subseteq v'_1 \).

We can thus reformulate \( d \) as \( d = q_1 \cup q_2 = (v'_1 \cap q_1) \cup (v'_1 \cap q_2) \cup \cdots \cup (v'_1 \cap q_m) \). Now, each DAG pattern \( v'_1 \cap q_1 \) is not union-free and, moreover, their interleavings cannot contain \( q_1 \) or \( q_2 \) (since \( q_1, q_2 \not\subseteq q_i \) in the first place). Also, obviously, \( q_2 \not\subseteq q_1 \) and \( q_1 \not\subseteq q_2 \). So again can not be union-free and this case can be discarded as well.

**Case 3:** exactly one of the interleavings of \( d' \), call it \( q_i \), is contained in \( v'_1 \) (\( q_i \subseteq v'_1 \)).

In this case, \( d \) can be reformulated as \( d = q_i \cup (v'_1 \cap q_2) \cup \cdots \cup (v'_1 \cap q_m) \) and cannot be union-free unless it is in fact equivalent to \( q_i \). This means that for all other \( q_i \)'s we must have \( v'_1 \cap q_i \subseteq q_i \). Of course, \( q_i \) should be equivalent (isomorphic modulo minimization, by Lemma \( \text{A.3} \)) to \( q_i \), the interleaving of \( d \) for which we supposed \( d \equiv q_i \), i.e. \( q_1 \equiv p_r//t//m//t_o \).

We continue by assuming for instance that \( v'_1 \cap q_2 \subseteq q_1 \).

Recall that \( v'_1 \) is of the form \( v'_1 = p_r//p_1//p_2//t_o \) and let \( q_2 \) be of the form \( q_2 = p_r//m//t_o \).

Since \( q_2 \not\subseteq v'_1 \) and they have the same root and result tokens, there is no mapping from \( p_1 \) into \( m \). Consequently, let \( s_f \) denote the maximal token-suffix of \( p_1 \) that can map into \( m \), and let \( pr_1 \) denote the remaining part (i.e., a token-prefix). Since \( pr_1 \) cannot be empty, we can write \( v'_1 \) as \( v'_1 = p_r//pr_1//s_f//t_o \), where \( pr_1 \) is an isomorphic copy of \( pr_1 \).

Let us now consider the interleaving \( u \) of \( v'_1 \cap q_2 \), of the form \( u = p_r//pr_1//m//t_o \), where \( pr_1 \) is an isomorphic copy of \( pr_1 \) as well.

As we assumed that \( u \subseteq v'_1 \cap q_2 \subseteq q_1 \), there must exist a containment mapping \( \phi \) from \( q_1 \) to \( u \).

Since \( q_1 \subseteq v'_1 \), let \( \phi \) be a containment mapping from \( v'_1 \) into \( q_1 \). So we have \( v'_1 \overset{\phi}{\rightarrow} q_1 \).

In particular, \( \phi \) must map the \( pr'_1//s_f \) part of \( v'_1 \) in the \( m//t \) part of \( q_1 \). With a slight abuse of notation, let \( \phi(pr'_1) \) denote the minimal token-prefix of \( t//m \) within which the image under \( \phi \) of \( pr'_1 \) occurs. In other words \( \phi(pr'_1) \) starts with the root token of \( t \) and ends with the token into which the output token of \( pr'_1 \) is mapped. (Again, \( \phi(pr'_1) \) is well defined because all patterns are skeletons and tokens can only map strictly inside tokens.)

We can thus write \( q_1 = p_r//\phi(pr'_1) \cdots \phi(s_f) //t_o \).

Next, we argue that in the containment mapping \( \psi \) of \( q_1 \) into \( u \), we must have \( \psi(\phi(pr'_1)) = pr''_1 \).

(This follows easily from the definition of \( s_f \).) And this implies that \( \phi(pr'_1) = pr''_1 = pr_1 \). Hence
$q_1$ and $v'_1$ start by some common non-empty token-prefix. Since one of them starts by $t$ and the other by $t_1$ this means in the end that $t \equiv t_1$, which is a contradiction.

**Remark.** We can also generalize Lemma [A,3] as follows: the interleavings of $nf(d)$ are of the form $p_r/\ldots/t_o$ (see Figure 10a). 

So we now know for now that APPLY-RULES is complete for the case of DAG patterns that are defined as the intersection of skeleton queries when their root and result tokens have the same main branch. Such an intersection is union-free iff there is a query $v_i$ among them having an intermediary part into which all the other intermediary parts map. If this is not the case, the DAG is equivalent to a union of interleavings having the same root tokens and result tokens.

We are now ready to give sum up the results so far and conclude the completeness proof for $XP_{eq}$.

**Proof Summing-up.** We will show that, given $n$ (extended) skeletons $v_1, \ldots, v_n$, all having several tokens, APPLY-RULES is complete for deciding union-freedom for the DAG pattern

$$d = dag(v_1 \cap \ldots \cap v_n).$$

We first rewrite $d$ by R1 steps. We obtain after this phase a DAG pattern $d$ in which the root token of $d$ may have several main branch nodes with outgoing $//$-edges. Similarly, the result token may have several nodes with incoming $//$-edges. If this is not the case, neither for the root token nor for the result token, then we know that the algorithm APPLY-RULES is in this case complete by Lemma [A,4].

Let us assume that some run of APPLY-RULES ends without a tree. We can easily prove that in this case the following run APPLY-RULES would also stop without yielding a tree:

— first refine by rules R2, R3 and R4 the root token and the result token w.r.t. their outgoing/incoming $//$-edges,
— then rewrite some of the branches in parallel by applying R7.

We continue assuming that we do not obtain a tree by the above run. At this point, $d$ is a DAG pattern as the one illustrated in Figure 11a, where $t_r$ denotes the root token (ending with node $n_r$) and $t_o$ denotes the result token (starting with $n_o$). Rules R2, R3 and R4 no longer apply, hence each $//$-edge outgoing from a node of $t_r$ that is ancestor of $n_r$ cannot be refined into connecting it to a lower node in $t_r$. Similar for $//$-edges incoming for nodes of $t_o$ that are descendants of $n_o$.

The intermediary branches $i_1, \ldots, i_k$ denote those that start from $n_r$ and end at $n_o$ (we use this notation, even if there may be no such $i_1, \ldots, i_k$ and $k = 0$). The other branches in parallel, $i_{k+1}, \ldots, i_{k+l}$, denote those that do not obey both conditions. If $l = 0$, i.e. there are no such branches, we fall again in the case handled by Lemma [A,4] for which the algorithm is complete. We continue with the assumptions that $k \geq 0$ and $l \geq 1$ as well.

We next prove that $d$ is not union-free.

We introduce some additional notation. For each $i_j$, $k + 1 \leq j \leq k + l$, such that $i_j$ starts above $n_r$, let $n'_r$ denote the node in $t_r$ that is sibling of the first node in $i_j$ (i.e., $n'_r$ and the first node in $i_j$ have the same parent node, a node in $t_r$). Note that $n'_r$ is ancestor-or-self of $n_r$. Let $n'_o$ denote the node of $t_o$ that is “parent-sibling” of $i_j$ (they have the same child node). $n'_o$ is defined if $i_j$ ends below $n_o$ and is descendant-or-self of $n_o$.

For each $i_j$, by $pr_j$ we denote its maximal token-prefix that can map in $TP_d(n'_r/\ldots/n_r)$. Similarly, for each $i_j$ by $sf_j$ we denote its maximal token-suffix that can map in $TP_d(n_o/\ldots/n'_o)$. Note that $pr_j$ and $sf_j$ cannot overlap since in this case $i_j$ would have been rewritten away by R7. We can thus write each $i_j$ as $i_j = pr_j/sf_j$, for $1 \leq j \leq l + 1$.

Now, we consider a second DAG pattern $d'$ obtained from $d$ by replacing each $i_j$ branch by $m_{ij}$, connected now by $//$-edges to $n_r$ and $n_o$ (Figure 11b), instead of the parent of $n'_r$ and the child of $n'_o$.

We argue now that the set of interleavings of $d'$ is included in the set of interleavings of $d$ (set inclusion). Moreover, $d$ is union-free only if $d'$ is union-free, such that if $d' \equiv p$, for an interleaving...
p, then p is the only candidate for \( d = p \). First, it is straightforward that all the interleavings of \( d' \) are interleavings of \( d \) as well. The particularity of \( d' \) is that its interleavings do not modify the tokens \( t_r \) and \( t_o \). More precisely each interleaving will be of the form \( t_r // ... // t_o \). Moreover, by the way \( d' \) was defined and given that no R2, R3 or R4 steps applied on \( d \), we argue that all other interleavings of \( d \) will either (a) be redundant, i.e. contained in those of \( d' \), (b) add some predicate on \( t_r \) or \( t_o \) or (c) have a longer root token (resp. result token) than \( t_r \) (resp. \( t_o \)). But this means that an interleaving \( p \in n\ell(d) - n\ell(d') \) cannot have a containment mapping into an interleaving of the form \( t_r // ... // t_o \). Hence it cannot be equivalent to \( d \). So the only interleaving \( p \) candidates for \( p = d \) are those of \( n\ell(d') \). From this it follows that \( d \) can be union-free only if \( d' \) is union-free.

Note now that by Lemma 8.4, \( d' \) is union-free if there exists some \( m_j \) into which all \( i_1, \ldots, i_k \) and all the \( m_i \)’s map. This is because of the assumption that among \( i_1, \ldots, i_k \) there is no branch \( i_j \) into which all other \( i_i \)’s map.

We continue towards showing that \( d \) is not union-free with this assumption and let \( m \) denote the branch into which all others map. Note that among \( m_{k+1}, \ldots, m_{k+l} \) there can be more than one “copy” of \( m \) (i.e., equivalent to \( m \)). By \( m_c \) we denote all these copies. Among \( i_1, \ldots, i_k \) there is no copy of \( m \) (otherwise R7 would have triggered).

Let \( d' \equiv p = t_r // m // t_o \), for \( m = t // m' \). We build next an interleaving \( w \) of \( d \) s.t. \( w \not\subset p \).

W.l.g. let us assume that all the \( m_c \) copies of \( m \) are connected in \( d \) to a node that is strict ancestor of \( n_o \).

Since R2 or R4 did not apply on these copies of \( m \), it means that a strict prefix of the main branch of \( m \)’s root token \( t \) maps in a suffix of the main branch of \( t_r \), when the possibly non-empty preceding token-prefix \( p_r \) is collapsed somewhere “higher”.

Let \( \psi \) denote the partial mapping from \( t \) into \( t_r \) that uses the maximal possible prefix of \( t \) across all the copies \( m_c \). Let \( t = t' / t'' \), where \( t' \) is this maximal prefix (not empty).

We are now ready to build \( w \).

We build first the root token \( t'_r \) of the \( w \) interleaving as follows: let \( t'_r \) denote an interleaving of \( t_r \) and \( t \) defined by the code \( i = MB(t_r) / MB(t'') \), and \( f_x \) defined as “identity” on \( t_r \) and \( t'' \), and \( f_x(n) = \psi(n) \) for the main branch nodes of \( t' \).

We build the intermediary part \( p \) of the \( w \) interleaving as follows: starting from \( i_x \in \{i_1, \ldots, i_k, m'\} \) (or simply from \( i_x \in \{i_1, \ldots, i_k\} \) in the case \( m' \) is empty), let us interpret them as the intermediary parts of the following skeleton patterns \( s_x = start / i_x \ / end \).

\[ 1 \] The remaining cases when

- all the \( m_c \) copies of \( m \) are connected in \( d \) to a node that is strict descendant of \( n_o \), or
- all the \( m_c \) copies of \( m \) but one (we cannot have more than one, otherwise R7 would have triggered leaving only one) are connected in \( d \) to a node that is strict ancestor of \( n_r \) and all the \( m_c \) copies of \( m \) but one are connected in \( d \) to a node that is strict descendant of \( n_o \),

can be handled similarly.
Let also $s$ denote the pattern $s = \text{start}/**/\text{end}$.

Let us now consider now the DAG pattern $d' = \text{dag}(\cap x s_x)$. Since none of the $s_x$ patterns is equivalent to $s$, from Lemma [A.4] we have that $d' \neq s$. Moreover, since $s \subseteq d'$ (because $s_x \subseteq s$), we must have that $d' \nsubseteq s$. In other words, there must exist an interleaving $w'$ of $d'$, of the form $\text{start}/**/\text{end}$ such that $w' \nsubseteq s$. Finally, this means $p$ is such that while all the $i_1, \ldots, i_k, m'$ map into it, we have that $m$ does not map into it.

Finally, we define $w$ as $w = t_r/**/p/**/t_o$. It is easy to check that $w$ is an interleaving of $d$ (a containment mapping into $w$) but $w \nsubseteq p = t_r/**/t/**/m'/**/t_o$. Hence $d$ is not union-free. \qed

Remark. We can draw the following conclusions from the proof of Theorem [8.3]. When APPLY-RULES is applied to DAG patterns built from multi-token views from $XP_{cs}$, after R1 steps, followed eventually by R2, R3 and R4 steps, we obtain the branches in parallel $i_1, \ldots, i_k$ starting from the last node of the root token ($t_r$) and ending with the first node of the result token ($t_o$). Other branches in parallel may exist in $d$, but connected to other nodes of $t_r$ and $t_o$. Then, by eventually some R7 steps, the DAG pattern must become a tree, otherwise it is not union-free. Under the extended skeletons restrictions, R5 and R6 are not necessary for completeness. The resulting tree is $t_r/**/i_1/**/t_o$, where $i_1$ is one of the branches in parallel, into which all other, $i_2, \ldots, i_k$ map.

B. PROOF OF THEOREM ?? (REWITE-PLANS FOR PTIME)

We give in this section the completeness proof for rewrite plans formed by akin patterns.

We show that, given $n$ akin tree patterns $v_1, \ldots, v_n$, APPLY-RULES decides union-freedom for $d = \text{dag}(v_1 \cap \cdots \cap v_n)$. Let each $v_j$ be defined as $v_j = t_j**/i_j/**/t_{o,j}$.

Special case. We start by considering the special case when the patterns have the same main branch for their result tokens as well.

By Lemmas [8.1] and [A.4], we know that $d$ is union-free only if the intermediary parts $i_j$ are such that their skeletons map in the skeleton of one of them. Without loss of generality, let us assume that all $s(i_j)$ map in $s(i_1)$. We continue with this assumption.

First, the initial R1 steps coalesce the root and result tokens of the $n$ branches, yielding a DAG pattern similar to the one illustrated in Figure [9a]. Then, the only rules that may be applicable are R6 and R7. Let us assume that APPLY-RULES stops outputting a pattern that is not a tree. We show that $d$ is not union-free.

If the algorithm APPLY-RULES stops without outputting a tree in some run, then it will also stop without outputting a tree in the following particular rewriting strategy

— we first apply R6 on the “biggest”branches in parallel $i_j, i_k$ such that $s(i_j) \equiv s(i_k) \equiv s(i_1)$, if any. It is straightforward that R6 must apply for these branches, coalescing entirely the two branches into one branch. After this phase, there will be no other parallel branch with skeleton $s(i_1)$, besides $i_1$ itself.

— Then, R6 is applied only if applicable on all the branches in parallel at once. This phase will terminate with a refined $d$ similar to the one illustrated in Figure [10a] where $2 \leq k \leq n$, $p_r$ denotes the common pattern following the root (may have several tokens if R6 was applied) and $t_1, \ldots, t_k$ denote the sibling tokens on which R6 no longer applies (i.e., they are not all similar hence they do not all have the same skeleton).

Also, rule R7 is applied freely, and it can rewrite out some of the branches in parallel.

After this phase, while there exists a mapping from each $s(p_i)$ into $s(p_1)$, there is no mapping from $p_i$ into $p_1$. Note also that, by the first phase of the rewriting strategy, we cannot have the opposite mapping from $s(p_1)$ into $s(p_i)$.

— Finally, rule R6 is applied only between $p_1$ on the one hand, and other branches $p_i$ on the other hand, while R7 is still applied freely.

We obtain a DAG pattern similar to the one in Figure [12]. Let us assume that besides $p_1$ there are $l$ remaining branches in parallel, connected by a //edge either to $p_r$ or to various tokens of $p_1$. 

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Show next that for any such the branches function $f$ corresponds branch in parallel that token included, denoted $t_i$. (We know that such a node $n$ must start with a $//$-edge and must come from a node of some (maybe several) branches $p_i$. For each $i=1, l$, we can thus reformulate $p_1$ as $p_1 = pr_i // sf_i$, where the root token of $sf_i$ is $t_i$. Note that for each $i$ we have that $s(p_i')$ maps into $s(sf_i)$, while the opposite is not true.

It is immediate that $d$ can be union-free, for some $c$ such that $d \equiv c$, only if $c$ is of the form $c = pr_i // m // t_o$ where $s(m) = s(p_1)$, since this is the minimal skeleton for an interleaving.

All the candidate interleavings $c$ will be defined by the code $i = MB(p_r // m // t_o)$ and some function $f_i : MBN(d) \rightarrow i$. What distinguishes the various $c$'s is the definition of $f_i$ on the nodes of the branches $p_i', \ldots, p_i'$ (since the other main branch nodes in $d$ have only one possible image). We show next that for any such $f_i$ and associated interleaving $c$ we can build the $w$ witness with $w \not\subseteq c$.

Let $f_i$ be fixed and let $c$ denote the corresponding interleaving for code $i$ and function $f_i$. Note that we can interpret $f_i$ as a series of rewrite steps over $d$ that collapse the pairs of nodes $(n, f_i(n))$, for all the nodes $n$ in the $p_i', \ldots, p_i'$ branches, outputting as end result the tree pattern $c$. These steps do not modify the skeleton of $p_1$, hence can only bring some new predicates starting by $//$-edge.

Next, we describe how the interleaving $w \not\subseteq c$ is built, from the current pattern $d$ of Figure\[12\].

Let $n_e \in MB(c)$ denote the lowest main branch node in $c$'s $m$ part which has a subtree predicate $st$ that is not present (in other words, cannot be mapped) at the associated node $n_1$ in the $p_1$ part of $d$. $st$ must start with a $//$-edge and must come from a node of some (maybe several) branches $p_i'$. (We know that such a node $n_e$ must exist, otherwise the $p_i'$ branches would fully map in the corresponding branch in parallel $sf_i$ and rule R7 would have applied).

Without loss of generality, let $n_i', \ldots, n_i'$, for $\{i_1, \ldots, i_s\} \subseteq \{1, \ldots, l\}$, denote the nodes from the branches $p_i', \ldots, p_i'$, that are the “source” of $st$\[12\] So we have $f_i(n_i1) = f_i(n_i') = \cdots = f_i(n_i') = n_e$ and we can say that $n_e$ is the result of coalescing $n_1$ with $n_i', \ldots, n_i'$.

Now, we can see the left branch $p_1$ as being divided into two parts, the one down to the token of $n_1$ (that token included), denoted $p_{11}$, and the rest, denoted $p_{12}$. So we can write $p_1$ as $p_1 = p_{11} // p_{12}$.

\[12\]They have a predicate $st'$ into which $st$ maps.
Similarly, for each \( x \in \{i_1, \ldots, i_s\} \) we can see each main branch \( pr_{x}^1//p_x^l \) as being divided into two parts, the one down to the token of \( n_x^l \) (that token included), denoted \( p_x^l \), and the rest, denoted \( p_x^{l+1} \). So we can write each main branch \( pr_{x}^1//p_x^l \) of \( d \) as \( pr_{x}^1//p_x^l = p_x^l//p_x^{l+1} \).

Note that by the way \( n_x \) was chosen (as the lowest node) we can conclude that by \( f_1 \) (on the main branch nodes) we can fully map \( TP_d(p_x^{l+1}) \) into \( SP_d(n_1) \), for all \( x \) (i.e., there are no other added predicates below \( n_1 \)'s level). It is also easy to see that while \( s(p_x^{l+1}) \) maps in \( s(p_1) \) (by \( f_1 \)), the opposite is not true, otherwise R6 steps would have applied up to this point.

We are now ready to construct \( w \). First, we obtain a part \( p \) of the \( w \) interleaving as follows: starting from the set of skeleton queries \( s(p_x^l) \), for all \( x \in \{i_1, \ldots, i_s\} \), let us interpret them as the intermediary parts of the following skeleton patterns \( s_x = start//s(p_x^1)////end. 

Let also \( s \) denote the skeleton pattern \( s = start//s(p_1)////end. 

Let us now consider the DAG pattern \( d' = dag(\cap_x s_x) \). Since none of the skeleton patterns \( s_x \) is equivalent to \( s \), from Lemma [A.4] we have that \( d' \neq s \). Moreover, since \( s \subseteq d' \) (because \( s \subseteq s_x \), by the way \( c \) was defined), we must have that \( d' \nsubseteq s \). In other words, there must exist an interleaving \( w' \) of \( d' \), of the form \( start//p////end \) such that \( w' \nsubseteq s \). Finally, this means \( p \) is such that while all the \( s(p_x^l) \) map into it, we have that \( s(p_1) \) does not map into it. We will use this property. For each \( p_x^l \), let \( f_x \) denote a mapping from \( s(p_x^l) \) into \( p \).

Next, we obtain a second part of \( w \) as follows. Let \( pr_{11} \) denote the maximal token-suffix of \( p_1 \) such that \( s(p_11) \) can map in \( p \), and let \( sf_{11} \) denote the remaining part. \( sf_{11} \) cannot be empty, so it is formed by at least the output token of \( p_{11} \), the one with node \( n_1 \). So we can see \( p_{11} \) as \( p_{11} = p_{11}^l//sf_{11}. 

Let \( f_{x} \) denote a partial mapping from \( s(p_{11}) \) into \( p \) that exhibits \( sf_{11}. 

We will define \( w \) by a code \( i' \) and function \( f_{i'} \) as follows:

\[ i' = \lambda (pr_l//p//sf_{11}//p_{12}//t_o), \]

\[ f_{i'} \text{ maps nodes of MBN}(d) \text{ into } i' \text{ positions as follows:} \]

\[ f_{i'} \text{ is "identity" for the main branch nodes of } pr_r, t_o, \text{ for the } sf_{11} \text{ part of the } p_{11} \text{ prefix of } p_1 \]

\[ \text{and for the } p_{12} \text{ suffix of } p_1, \]

\[ \text{for the remaining main branch nodes } p_{11} \text{ (i.e., those of } pr_{11}, f_{i'}(n) = f_p(n), \]

\[ \text{for the main branch nodes } n \text{ of the } p_{x1} \text{ prefix of the } p_{x1}^1//p_{x1}^l \text{ branch in } d, \text{ for } x \in \{i_1, \ldots, i_s\}, \]

\[ f_{i'}(n) = f_{x1}(n) \]

\[ \text{for the remaining nodes } n \text{ in the } p_{x1}^1//p_{x1}^l \text{ branches (i.e. those in } p_x^{l+1}, f_{i'}(n) = f_{x1}(f_i(n)), \]

\[ \text{finally, for all the main branch nodes of the remaining branches } p_y^l, \text{ for } y \notin \{i_1, \ldots, i_s\}, \]

\[ f_{i'}(n) = f_{i'}(f_i(n)). \]

We now argue that \( w \) is an interleaving of \( d \) and \( w \nsubseteq c \). First, it is easy to check that \( w \) is an interleaving for \( d \). Recall that \( c \) is s.t. \( s(c) = s(p_r//p_{11}//t_o) = s(p_r//pr_{11}//sf_{11}//p_{12}//t_o) \). Second, it is also easy to check that \( c \) can have a containment mapping in \( w \) iff its \( sf_{11} \) part maps in the \( sf_{11} \) of \( w \). But this is not possible because the \( st \) subtree predicate is not present on the \( f_{i'}(n_1) \) node of \( w \) (which is found somewhere in the output token of the \( sf_{11} \) part).

**General case.** We now consider the general case, when the result tokens do not necessarily have the same main branch. After the possible rewrite steps of \( R1(i) \) steps on the root tokens, and after the possible rewrite steps of \( R1(ii) \), \( R2(ii) \), \( R3(ii) \) and \( R4(ii) \) on the result tokens, we may now obtain a DAG pattern in which the branches in parallel may not be "connected" to \( t_o \) at its highest node \( (n_o) \), but at some other node that is strict descendant of \( n_o \). If this is not the case, then we are back to the special case discussed previously.

Otherwise, let us now consider the DAG pattern \( d' \) obtained from \( d \) by connecting the endpoints of the branches in parallel at \( n_o \). We can easily see that the interleavings of \( d' \) are all among those of \( d \) and moreover, \( d \) is union-free only if \( d' \) is union-free, with \( d' \equiv d \equiv p \), for some \( p \in \text{interleave}(d') \). This is because the interleavings of \( d \) that are not interleavings of \( d' \) as well are those that add some predicates on \( t_o \) that are not present in all the interleavings.
By Lemmas 8.1 and 8.4, we know that $d$ is union-free only if the intermediary parts $i_j$ are such that their skeletons map in the skeleton of one of them, which in addition, in the current $d$ pattern, must start at $n_r$ and end at $n_l$. Without loss of generality, let us assume that this is $i_1$ (note that the $i_1$ branch will not be affected by the transformation from $d$ to $d'$).

From the special case, we know under what conditions $d'$ is union-free, and it is immediate that, when they hold, the interleaving $p$ is obtained from $i_1$ possibly by adding some predicates of the form $[//\ldots]$ to some of its main branch nodes. Importantly, each such predicate is added on the highest possible main branch node of $i_1$.

Finally, it is now easy to check that an interleaving $p$ of $d'$ obtained in this way will always have a containment mapping in any interleaving $p'$ of $d$: everything except the added predicates will map (by identity), while the added predicates (of the form $[//\ldots]$) will map in their respective occurrence in $p'$ (by necessity, found at a lower main branch node then in the one in $p$).

This ends the completeness proof of APPLY-RULES over unfoldings of rewrite plans that intersect only akin views from $XP_{//}$. 