On the Expressiveness and Complexity of MongoDB

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ABSTRACT
A significant number of novel database architectures and data models have been proposed during the last decade. While some of these new systems have gained in popularity, they lack a proper formalization, and a precise understanding of the expressiveness and the computational properties of the associated query languages. In this paper, we aim at filling this gap, and we do so by considering MongoDB, a widely adopted document database managing complex (tree structured) values represented in a JSON-based data model, equipped with a powerful query mechanism. We provide a formalization of the MongoDB data model, and of a core fragment, called MQuery, of the MongoDB query language. We study the expressiveness of MQuery, showing its equivalence with nested relational algebra. We further investigate the computational complexity of significant fragments of it, obtaining several (tight) bounds in combined complexity, which range from LOGSPACE to alternating exponential-time with a polynomial number of alternations.

1. INTRODUCTION
As was envisioned by Stonebraker and Cetintemel [21], during the last ten years a diversity of new database (DB) architectures and data models has emerged, driven by the goal of better addressing the widely varying demands of modern data-intensive applications. Notably, many of these new systems do not rely on the relational model but instead adopt a less rigid data format, and alternative query mechanisms, which combine an increased flexibility in dealing with semi-structured data, with a higher efficiency (at least for some types of common operations). Hence the emergence of the term NoSQL (for “not only SQL”) [8, 17].

A large portion of the so-called non-relational systems (e.g., MongoDB, CouchDB, and Hadoop) organize data in collections of semi-structured, tree-shaped documents in the JavaScript Object Notation (JSON) format, which is commonly viewed as a lightweight alternative to XML. Such documents can be seen as complex values [14, 1, 26, 12], in particular due to the presence of nested arrays. As an example, consider the document in Figure 1, containing standard personal information about Kristen Nygaard (such as name and birth-date) together with information about the awards he received, the latter being stored inside an array.

Among the non-relational languages that have been proposed for querying JSON collections (see, e.g., [3, 19, 24] and the MongoDB aggregation framework [4]), languages with rich capabilities have unsurprisingly many similarities with well-known query languages for complex values, such as monad algebra (MA) [5, 16], nested relational algebra (NRA) [23, 25] and Core XQuery [16]. For instance, Jaql [3], one of the most prominent query language targeting map-reduce frameworks [13], supports higher-order functions, which have their roots in MA, and the group and unwind operators of the MongoDB aggregation framework are similar to the nest and unnest operators of NRA. While some of these query languages have been widely used in large-scale applications, there have been only few attempts at capturing their formal semantics, e.g., through a calculus for Jaql [4], and even less at understanding their computational properties.

In this paper, we consider the case of MongoDB, a widely adopted distributed JSON-based document database, and conduct the first major investigation into the formal foundations and properties of its data model and query language. MongoDB provides rich querying capabilities by means of the aggregation framework, which is modeled on the notion of data processing pipelines. In this framework, a query is a multi-stage pipeline, where each stage defines a transformation, using a MongoDB-specific operator, applied to the set of documents produced by the previous stage.

Our first contribution is a formalization of the Mon-
goDB data model and of the fragment of the aggregation framework query language that includes the \textit{match}, \textit{unwind}, \textit{project}, \textit{group}, and \textit{lookup} operators, and which we call \textit{MQuery}. Each of these operators roughly corresponds to an operator of NRA: match corresponds to select, project to project, lookup to left join, and as mentioned above, group to nest, and unwind to unnest. As a useful side-effect of our formalization effort, we point out different “features” exhibited by MongoDB’s query language that are somewhat counter-intuitive, and that might need to be reconsidered by the MongoDB developers for future versions of the system. In our investigation, we consider various fragments of MQuery, which we denote by $M^\alpha$, where $\alpha$ consists of the initials of the stages that can be used in the fragment.

Our second contribution is a characterization of the expressive power of MQuery obtained by comparing it with NRA. We define the relational view of JSON documents, and devise translations in both directions between MQuery and NRA, showing that the two languages are equivalent in expressive power. We also consider the $M^{\text{MUGL}}$ fragment, where we rule out the recently (in Version 3.2) added lookup operator, which allows for joining a given document collection with external ones. Actually, we establish that already $M^{\text{MUGL}}$ is equivalent to NRA over a single relation, and hence is capable of expressing arbitrary joins (within one collection), contrary to what believed in the community of MongoDB practitioners and users. Interestingly, all our translations are compact (i.e., polynomial), hence they allow us also to carry over complexity results between MQuery and NRA.

Finally, we carry out an investigation of the computational complexity of $M^{\text{MUGL}}$ and its fragments. In particular, we establish that what we consider the minimal fragment, which allows only for match, is LOGSPACE-complete (in combined complexity). Projecting and grouping allow one to create exponentially large objects, but by representing intermediate results compactly as DAGs, one can still evaluate $M^{\text{MUGL}}$ queries in PTIME. The use of unwind alone causes loss of tractability in combined complexity, specifically it leads to NP-completeness, but remains LOGSPACE-complete in query complexity. Adding also project or lookup leads again to intractability even in query complexity, although $M^{\text{MUGL}}$ stays NP-complete in combined complexity. In the presence of unwind, grouping provides another source of complexity, since it allows one to create doubly-exponentially large objects; indeed we show PSPACE-hardness of $M^{\text{MUG}}$. Finally, we establish that the full language and also the $M^{\text{MUGL}}$ fragment are complete for exponential time with a polynomial number of alternations (in combined complexity). As mentioned, our polynomial translations between MQuery and NRA, allow us to carry over the complexity results also to NRA (and its fragments). In particular, we establish a tight $\text{TA}[2^{\text{O}(n)} , n^{\text{O}(1)}]$ result for the combined complexity of Boolean query evaluation in NRA, whose exact complexity was open.

The rest of the paper is structured as follows. In Section 2 we introduce NRA. In Section 3 we provide our formalization of MongoDB documents, and in Section 4 of the MongoDB query language. In Section 5 we study the expressiveness of such language by providing translations to and from NRA, and in Section 6 we study its computational complexity. We conclude the paper in Section 7. Selected proofs are given in the Appendix.

2. PRELIMINARIES

We recap the basics of nested relational algebra (NRA) \cite{10, 25}, mainly to fix the notation of the operators. For their semantics we refer to \cite{10}.

Let $A$ be a countably infinite set of attribute names and relation schema names. A relation schema of a relation can have the form $R(S)$, where $R \in A$ is a relation schema name and $S$ is a finite set of attributes, each of which is an atomic attribute (i.e., an attribute name in $A$) or a relation schema of a sub-relation. A relation schema can also be obtained through a NRA operation (see below). We use the function $\text{att}$ to retrieve the attributes from a relation schema name, i.e., $\text{att}(R) = S$. A relation schema $R(S)$ is called \textit{flat} if $S$ consists of atomic attribute only. In the following, when convenient, we refer to relation schemas by their name only.

Let $\Delta$ be the domain of all the atomic attributes in $A$. An \textit{instance} of a relation schema $R(S)$ is a finite set of tuples over $R(S)$. A \textit{tuple} $t$ over $R(S)$ is a finite set \{$a_1, v_1; a_2, v_2; \ldots; a_n, v_n$\} such that if $a_i$ is an atomic attribute, then $v_i \in \Delta$, and if $a_i$ is a relation schema, then $v_i$ is an instance of $a_i$.

A filter $\psi$ over a set $A \subseteq A$ is a Boolean formula constructed from the form of $v \in a_i$, $(v = a_i)$, or $(a = a')$, where \{$a, a'$\} $\subseteq A$, and $v$ is an atomic value or a relation. Let $R$ and $R'$ be relation schemas. We make use of the following relational algebra operators: (1) set union $R \cup R'$ and set difference $S \setminus S'$, for $\text{att}(R) = \text{att}(R')$; (2) cross-product $R \times R'$, resulting in a relation schema with attributes \{$\text{rel1}.a \mid a \in \text{att}(R)$\} $\cup$ \{$\text{rel2}.a \mid a \in \text{att}(R')$\}; (3) selection $\sigma_\psi(R)$, where $\psi$ is a filter over $\text{att}(R)$; (4) projection $\pi_A(R)$, for $A \subseteq \text{att}(R)$; (5) extended projection $\pi_P(S)$, where $P$ may also contain elements of the form $b/f(a_1, \ldots, a_n)$, for a computable function $f$ and \{$a_1, \ldots, a_n$\} $\subseteq \text{att}(R)$.

We also use the two operators of NRA: (6) nest $\nu_{\pi_1(a_1, \ldots, a_n) \rightarrow b}(R)$, resulting in a schema with attributes \{$\text{att}(R) \setminus \{a_1, \ldots, a_n\}$ $\cup$ \{$b(a_1, \ldots, a_n)$\}$\}$ and (7) unnest $\chi_a(R)$, resulting in a schema with attributes \{$\text{att}(R) \setminus \{a\}$ $\cup$ \{$\text{att}(a)$\}$\}$. We note that $\chi_a(R)$ will not preserve tuples $t$ if $\pi_a(t) = \emptyset$. We also assume that in NRA the project operator $\pi$ can access sub-relations at all levels as in \cite{10}.

3. MONGODB DOCUMENTS

In this section we propose a formalization of the syntax and the semantics of MongoDB documents. In our formalization, we make two simplifying assumptions with respect to the way such documents are treated by the MongoDB system: (i) we view documents as expressed in JSON, as opposed to BSON, since we abstract away document order, and (ii) we consider set-semantics as opposed to bag-semantics. In particular, we avoid deep comparison of objects, which does not follow the standard semantics but is based on their binary representation and is deprecated.\cite{https://docs.mongodb.org/manual/reference/bson-types/}

\footnote{Personal communication by the MongoDB development team.}
A MongoDB database stores collections of documents, where each document is an object consisting of key-value pairs, and a value can itself be a nested object. A collection corresponds to a table in a (nested) relational database, and a document corresponds to a row in a table.

We start by defining the syntax of MongoDB documents in the JSON format. Literals are atomic values, such as strings, numbers, and booleans. A JSON object is a finite set of key-value pairs, where a key is a string and a value can be a literal, an object, or an array of values, constructed according to the grammar in Figure 3 (where terminals are written in blue). We require that the set of key-value pairs constituting a JSON object does not contain the same key twice. A (MongoDB) document is a JSON object (not nested within any other object) with a special key ‘_id’, which is used to identify the document. Figure 1 shows a MongoDB document in which, apart from _id, the keys are birth, name, awards, etc. Notice that the value of name is an object consisting of two key-value pairs, and the value of awards is an array of objects, each describing an award.

Given a collection name C, a (MongoDB) collection for C is a finite set F_C of documents, such that each document is identified by its value of _id, i.e., each value of _id is unique in F_C. Given a set C of collection names, a MongoDB database instance D (over C) is a set of collections, one for each name C ∈ C. We write D.C to denote the collection for name C.

We formalize MongoDB documents as finite unordered, unranked, node-labeled, and edge-labeled trees. We assume three disjoint sets of labels: the sets K of keys and I of indexes (non-negative integers), used as edge-labels, and the set V of literals, containing the special elements null, true, and false, and used as node labels. A tree is a tuple (N, E, L_n, L_e), where N is a set of nodes, E is a successor relation, L_n : N → V ∪ {‘{}’, ‘[]’} is a node labeling function, and L_e : E → K ∪ I is an edge labeling function, such that (i) (N, E) forms a tree, (ii) a node labeled by a literal must be a leaf, (iii) all outgoing edges of a node labeled by ‘[]’ must be labeled by keys, and (iv) all outgoing edges of a node labeled by ‘{}’ must be labeled by distinct indexes. Given a tree t and a node x, the type of x in t, denoted type(x, t), is literal if L_n(x) ∈ V, object if L_n(x) = ‘{}’, and array if L_n(x) = ‘[]’. The root of t is denoted by root(t). A forest is a set of trees. If root(t) has an outgoing edge labeled with _id, we call the tree t a document.

Given a tree t, we define inductively for each node x in t, the value represented by x in t, denoted value(x, t), as follows: (i) if x is a leaf in t, then value(x, t) = L_n(x); (ii) let x_1, . . . , x_m be all the children of x with the corresponding edges labeled by k_1, . . . , k_m. If type(x, t) = object, then value(x, t) = {k_1; value(x_1, t), . . . , k_m; value(x_m, t)}, and if type(x, t) = array, then value(x, t) = [value(x_1, t), . . . , value(x_m, t)].

The tree corresponding to a value v, denoted tree(v), is defined as (N, E, L_n, L_e), where N is the set of x_v such that v is an object, array, or literal value appearing in v, and for x_v ∈ N: (i) if v is a literal, then L_n(x_v) = v and x_v is a leaf; (ii) if v = {k_1; v_1, . . . , k_m; v_m}, for m ≥ 0, then L_n(x_v) = ‘{}’, x_v has m children x_v_1, . . . , x_v_m with L_n(x_v_1, x_v) = k_1; (iii) if v = [v_1, . . . , v_m], for m ≥ 0, then L_n(x_v) = ‘[]’, x_v has m children x_v_1, . . . , x_v_m with L_e(x_v_1, x_v) = k_1.

4. MongoDB QUERIES

The basic query mechanism of MongoDB are so-called find queries, which are subsumed by the more powerful query mechanism provided by the aggregation framework. In this paper, we present and formalize only the query language derived from the aggregation framework, and we refer to this query language (or rather, family of languages) as MQuery.

4.1 Syntax of MQuery

An MQuery is a sequence of stages, also called a pipeline,
applied to a collection name, where each of the stages transforms a forest into another forest.

The grammar of the MQuery language is presented in Figure 4. MQuery allows for five types of stages: (i) match \( \mu \), which selects trees of interest, (ii) unwind \( \omega \), which flattens an array from the input trees to output a tree for each element of the array, (iii) project \( \rho \), which modifies trees by projecting away paths, renaming paths, or introducing new paths. (iv) group \( \gamma \), which groups trees according to the values of a set of paths, and (v) lookup \( \lambda \), which joins trees in the pipeline with trees in an external collection \( C \), using a local path and a path in \( C \) to express the join condition, and an additional path to store the matching trees. We consider also various fragments of MQuery, and we denote each fragment by \( M^\alpha \), where \( \alpha \) consists of the initials of the stages that can be used in queries in the fragment. Hence, \( M_{\text{MUPGL}} \) denotes MQuery itself, and, e.g., \( M_{\text{MUP}} \) denotes the fragment of \( M_{\text{MUPGL}} \) that does not use lookup, and \( M_{\text{MIP}} \) the fragment that additionally does not use group. We observe that MongoDB find queries correspond to a simple case of \( M_{\text{MP}} \), where a match stage is followed by a project stage in which each projection element is of the form PATH: \text{true} and \_id: false.

We provide some comments and additional requirements on the grammar in Figure 4. A PATH (which in MongoDB terminology is actually called a “field”), is a non-empty concatenation of keyPath, where elements for KEYS are from the set \( K \). Elements for VALUE are defined according to the grammar in Figure 3. COLLECTION is a collection name, that is, a non-empty string. The empty path, which can be used in a path reference, is denoted in MongoDB by the string \$ROOT. In the following, a path is either the empty path or an element constructed according to PATH. For two paths \( p \) and \( p' \), we say that \( p' \) is a strict prefix of \( p \), if \( p = p'.p'' \), for some non-empty path \( p'' \). Also, \( p' \) is a prefix of \( p \) if \( p' \) is either a strict prefix of \( p \) or equal to \( p \). We assume that a projection \( p_1:d_1, \ldots, p_n:d_n \) is such that there are no \( i \neq j \) where \( p_i \) is a prefix of \( p_j \). By default the \_id key is kept in a projection, and to project it away the projection must contain an element \_id: false. The comparison operators used in a value definition \text{VALUEDEF} accept only arrays of length 2. We observe that, with respect to the official MongoDB syntax, we have removed/introduced some syntactic sugar. In particular, for \text{CRITERION} we disallow expressions of the form "name.first": "john". Instead they can be expressed as "name.first": \{\text{seq: "john"}\}. Moreover, we allow for the use of \$nor in \text{VALUEDEF}, as it can be expressed using \$not and \$and.

### 4.2 Semantics of MQuery

To abstract away syntactic aspects of MQuery, and allow us to formalize its semantics, we first propose for it an algebra, shown in Figure 5. In this algebra, \( p \) stands for a path, \( v \) for a value, \( \varphi \) for a criterion, \( d \) for a value definition, \( \beta \) for a Boolean value definition, \( \kappa \) for a conditional value definition, \( s \) for a stage, and \( C \) for a collection name. For simplicity of presentation, the only comparison operator that we kept in MQuery is equality. Adding also order comparison would not affect any of the results on expressiveness and complexity presented later. Moreover, we denote the query stages as follows:

- \( \mu_\varphi \) for a match stage;
- \( \omega^p \) for an unwind stage that does not preserve null and empty arrays, and \( \omega^p_+ \) for an unwind stage that preserves
**Figure 6:** The semantics of MQuery stages

- **Match**
  \[ t \models (p = v), \text{ if there is } x \in [p]^t \text{ or } [p,i]^t \text{ for } i \in I, \text{ with } t \models \text{value(x, t)} = v. \]
  \[ t \models (\exists p), \text{ if } [p]^t \neq \emptyset. \]
  \[ t \models \neg \varphi, \text{ if } t \models \varphi_1 \text{ and } t \models \varphi_2. \]
  \[ t \models \psi, \text{ if } t \models \varphi_1 \lor \varphi_2. \]
  \[ F \models \mu = \{ t \mid t \in F \text{ and } t \models \varphi \}. \]

- **Project**
  \[ t \models (p_1 = p_2), \text{ if there is a value } v \text{ such that } t \models (p_1 = v) \text{ and } t \models (p_2 = v), \text{ or } t \models \neg (\exists p_1), j = 1, 2. \]
  \[ t \models (v_1 = v_2), \text{ if } (v_1 = v_2) \text{ and } v \text{ is a value, for } v \notin \{ \text{null, false, 0} \}. \]
  \[ t \models [d_1, \ldots, d_n], \text{ if } t \models (\exists p), \text{ and } t \models \neg (p = v) \text{ for } v \in \{ \text{null, false, 0} \}. \]
  \[ t \models (c^d_1, d_2) \text{ if } t \models c \text{ and } t \models d_1, \text{ or if } t \models \neg c \text{ and } t \models d_2. \]
  \[ \rho_p(t) = \text{subtree}(t, N_p), \text{ where } N_p \text{ are the nodes in } t \text{ on a path from root}(t) \text{ to a leaf through some } x \in [p]^t \]
  \[ \rho_{q/d}(t) = \begin{cases} \text{attach}(q, \text{tree}(v)), & \text{if } t \models \exists p, \\ \emptyset, & \text{otherwise} \end{cases} \]
  \[ \rho_{q/d}(t) = \text{attach}(q, \text{tree}(v)) \]
  \[ F \models \rho_p^m = \{ \rho_p^m(t) \mid t \in F \}. \]

- **Unwind**
  \[ \omega_p(t) = \begin{cases} \{ t \} \cup \text{subtree}(t, p) & \text{if } \rho_p(t) \neq \emptyset, \\ \emptyset, & \text{otherwise}. \end{cases} \]
  \[ \omega_{p}^+ = \bigcup_{p \in P} \omega_{p}(t). \]

- **Group**
  \[ F \models \gamma_{\text{null}}{a_1/b_1, \ldots, a_m/b_m} = \text{attach}(\_i.d, \text{null}) \oplus \text{attach}(a_j, \text{array}(F, b_j)) \]
  \[ F \models \gamma_{g_1, g_2, \ldots, g_n/a_1/b_1, \ldots, a_m/b_m} = \begin{cases} \text{attach}(\_i.d, \emptyset) \oplus \text{attach}(a_j, \text{array}(F \triangleright \mu_p, b_j)) \mid \varphi = \bigwedge_{i=1}^m (\neg \exists g_i), (F \triangleright \mu_p) \neq \emptyset \} \cup \\ \bigoplus_{t \in I} \text{attach}(\_i.d, g_i(t)) \oplus \text{attach}(a_j, \text{array}(F \triangleright \mu_p, b_j)) \mid I \subseteq \{1, \ldots, n\} \setminus \emptyset, \end{cases} \]
  \[ t_i \in \text{forest}(F, y_i) \text{ for } i \in I, \varphi = \bigwedge_{i \in I} (y_i = t_i) \land \exists y_i \land \bigwedge_{i \in I} (\neg \exists y_i), (F \triangleright \mu_p) \neq \emptyset \}

- **Lookup**
  \[ \lambda_{\text{p}_1 \in C, \text{p}_2}[F^m](t) = t \oplus \text{attach}(p, \text{array}(F \triangleright \mu_{\text{p}_2 = v_1, e})), \text{ where } v_1 = \text{value(subtree}(t, p_1)) \]
  \[ F \models \lambda_{\text{p}_1 \in C, \text{p}_2}[F^m] = \{ \lambda_{\text{p}_1 \in C, \text{p}_2}[F^m](t) \mid t \in F \}. \]

For a project stage, where \( P \) is a sequence of elements of the form \( p \) or \( q/d \), where \( p \) is a path to be kept, and \( q \) is a new path with value definition \( d \). We observe that we included \( \exists p \) as an atomic Boolean value definition \( \beta \) since it can be expressed using a conditional value definition (see Appendix B.1). When the \( \_i.d \) must be omitted, we write \( \rho_{p}^\rightarrow \);

for a group stage, where the group condition \( G \) and the aggregation paths \( A \) are (possibly empty) sequences of elements of the form \( p/p' \), for paths \( p \) and \( p' \), and \( p \) must be a key in \( A \). In these sequences, if \( p \) coincides with \( p' \), then we simply write \( p \) instead of \( p/p' \). When \( G \) is the empty sequence, it corresponds to the grouping condition being \( \text{null} \) and

for a lookup stage, where \( p_1 \) is the local path, \( p_2 \) is the path from the external collection \( C \), and \( p \) is the path to store the matching trees.

Finally, we use \( e \) to denote the empty path.

Our semantics of the MQuery algebra is based on sets. Before introducing it formally, we show how to interpret paths over trees.

**Definition 4.1.** Given a tree \( t = (N, E, L_n, L_e) \), we interpret a (possibly empty) path \( p \), and its concatenation \( p_{1} \ldots p_{m} \) with indexes \( i_1, \ldots, i_m \), as sets of nodes as follows, where \( k \) is a key:

\[ \begin{align*}
[q]^t &= \{ \text{root}(t) \} \\
[y]^n &= \{ y \in N \} \text{ there exist } i_1, \ldots, i_m, m \geq 0, \text{ and } x \in [p_{i1} \ldots i_m] \text{ s.t.} \\
&(x, y) \in E \text{ and } L_e(x, y) = k \} \\
[y]^n &= \{ y \in N \} \text{ there is } x \in [p_{i1} \ldots i_{m-1}] \text{ s.t.} \\
&(x, y) \in E \text{ and } L_e(x, y) = i_m \}
\end{align*} \]

When \( [p]^t = \emptyset \), we say that the path \( p \) is missing in \( t \).

Observe that, in the above definition, the semantics of paths allows for skipping over intermediate arrays at every step in the path.

Given a tree \( t \) and a path \( p \), when type\((x, t) = ty \), for each \( x \in [p]^t \), where \( ty \in \{ \text{array, literal, object} \} \), we define the type of \( p \) in \( t \), denoted type\((p, t) \), to be \( ty \). Also, when type\((p, t) = \text{array} \) and type\((x, t) = ty \) for each \( x \in [p,i]^t \).
for \( i \in I \), we write type\((p[i], t) = ty \). We say that \( p \) is a first level array in \( t \) if type\((p, t) = \) array and type\((p', t) \neq \) array, for each strict prefix \( p' \) of \( p \).

In Figure 4 we define the semantics of the MQuery stages: specifically, given a forest \( F \) and a stage \( s \), we define the forest \( F \triangleright s \), depending on the form of \( s \) (for a lookup stage, we also require an additional forest \( F' \) as parameter).

For the match and project stages, we define when a tree \( t \) satisfies a criterion \( \varphi \), denoted \( t \models \varphi \), or a value definition \( d \), denoted \( t \models d \). In this definition we assume that for each pair of values \( v_1 \) and \( v_2 \), the comparison \((v_1 = v_2)\) evaluates to a Boolean value. We write \((v_1 = v_2)\) when \((v_1 = v_2)\) evaluates to true in our formalization. In our semantic framework, we employ the classical semantics for “deep” comparison of non-atomic values, which differs from the actual semantics provided by MongoDB. We conclude this section by discussing some of the features in which our semantics differs from the current version of the MongoDB system. The reason for this divergence is that with respect to these features, the behavior of MongoDB might be considered counterintuitive, or even an inconsistency in the semantics of operators.

### Notes on Our Semantics

We conclude this section by discussing some of the features in which our semantics differs from the current version of the MongoDB system. The reason for this divergence is that with respect to these features, the behavior of MongoDB might be considered counterintuitive, or even an inconsistency in the semantics of operators.

### Group.

In MongoDB, the group operator behaves differently when grouping by one path and when grouping by multiple paths. In the former case missing is treated as null, while in the latter case it is treated differently. More specifically, when grouping by one path (e.g., \( g/y \)), MongoDB puts the trees with \( y = \text{null} \) and those where \( y \) is missing into the same group with \( _\text{id} = \emptyset \). On the contrary, when grouping with multiple paths (e.g., \( g_{y_1}/g_{y_2}/g_{y_3}/... \)), the trees with all \( y_i \) missing are put into a separate group with \( _\text{id} = \emptyset \).

### Comparing value and path.

The criteria in match and Boolean value definitions in project behave differently. For instance, when comparing a path \( p \) of type array with a value \( v \) using equality, match checks \((1)\) whether \( v \) is exactly the array value of \( p \), or \((2)\) whether \( v \) is an element inside the array value of \( p \). Instead, project only checks condition \((I)\). More generally, for match, \( t \models (p = v) \) if there is a node \( x \) in \([p]\) for some \( i \in I \) such that \( v(x, t) = v \), but for project, \( t \models (p = v) \) if \((v = v)\) coincides with subtree\((t, p)\).

### Null and missing values.

Moreover, for match, \( (p = \text{null}) \) holds \((a)\) when \( p \) exists and its value is \text{null}, or \((b)\) when \( p \) is missing. Instead, for project, \( (p = \text{null}) \) holds only for \((a)\).

### 5. Expressiveness of MQuery

In this section we characterize the expressiveness of MQuery in terms of nested relational algebra (NRA). More precisely, we show that MQuery is actually equivalent to NRA, by developing translations in both directions.
5.1 Nested Relational View of MongoDB

To know what is the relational database corresponding to a MongoDB database, we define a nested relational view of MongoDB. Intuitively, paths correspond to attributes, which might be atomic or relation schemas.

In order to define the relation schema of the relational view independently of the actual database instance, we first introduce the notion of type of a tree, which is analogous to complex object types [16], and similar to JSON schema [20].

**Definition 5.1.** Consider JSON values constructed according to the following grammar:

\[
\text{Type} ::= \text{literal} \mid \{ \text{ListKey:Type} \} \mid \{ \text{Type} \}
\]

Given such a JSON value \(d\), we call the tree \(\text{tree}(d)\) corresponding to \(d\) a type.

We say that a tree \(t\) is of type \(\tau\) if for every path \(p\) we have that \(t \models \exists p\ implies \tau \models \exists p\), \(\text{type}(p,t) = \text{type}(p,\tau)\), and \(\text{type}(p)\), \(t) = \text{type}(p[\tau], \tau)\). A forest \(F\) is of type \(\tau\) if all trees in \(F\) are of type \(\tau\).

We now associate to each type \(\tau\) a relation \(R_{\tau}\) in which, intuitively, each nested relation corresponds to an array in \(\tau\). In the following definition, given paths \(p\) and \(q\), we say that \(p,q\) is a simple extension of \(p\) if there is no strict prefix \(q'\) of \(q\) such that \(\text{type}(p,q', \tau) = \text{array}\).

**Definition 5.2.** Given a type \(\tau\), the schema of the relation \(R_{\tau}\), denoted \(\text{rschema}(\tau)\), is defined as \(R_{\tau}(\text{atts}(\tau))\), where, for a path \(p\) in \(\tau\), \(\text{atts}(p)\) is the set of simple extensions \(p'\) of \(p\) such that

- \(p'\) is an atomic attribute if \(\text{type}(p', \tau) = \text{literal}\), and
- \(p'\) is a sub-relation if \(\text{type}(p', \tau) = \text{array}\).

In the latter case, if \(\text{type}(p'[\tau], \tau) = \text{literal}\), then \(p'\) has one atomic attribute \(p'.\text{lit}\); otherwise \(p'\) has attributes \(\text{atts}(p')\).

Observe that the names of sub-relations and of atomic attributes in \(\text{rschema}(\tau)\) are given by paths in \(\tau\) (from the root), and therefore are unique.

Next, we define the relational view of a forest with respect to a type. In this view, to capture the semantics of the missing paths, we introduce the new constant **missing**.

**Definition 5.3.** Let \(\tau\) be a type and \(F\) a forest of type \(\tau\). The relational view of \(F\) with respect to \(\tau\), denoted \(\text{rel}_{\tau}(F)\), is defined as \(\{ \text{rtuple}_{\tau}(R_{\tau}, e, t) \mid t \in F \}\), where, for a relation name \(R\) in \(\text{rschema}(\tau)\) and a path \(p\), \(\text{rtuple}_{\tau}(R, p, t)\) is the \(R\)-tuple \((p,q : \text{rval}(p,q,t))_{p,q \in \text{atts}(p)}\).

When \([q]^t = \emptyset\), \(\text{rval}(p,q,t)\) is defined as **missing**, otherwise \(\text{rval}(p,q,t)\) is defined as

- \(L_\tau(x), for \{x\} = [q]^t, if p.q is atomic;
- \{([p.q.lit : v] | i \in I, x \in [q.i]^t, L_\tau(x) = v), if \text{atts}(p.q) = \{p.q.lit\}; and
- \{rtuple\((p.q.p.q, \text{subtree}(t,q.i)) \mid i \in I, [q.i]^t \neq \emptyset\), otherwise.

**Example 5.4.** Consider the type \(\tau_{\text{bios}}\) for \(\text{bios}\):

\[
\{ "id": "literal", "awards": ["award": "literal", "year": "literal"], "birth": "literal", "contribs": ["literal"], "name": ["first": "literal", "last": "literal"] \}
\]

Then, \(\text{rschema}(\tau_{\text{bios}})\) is defined as

\[
\text{bios}_{\text{id}}, \text{awards(awards.award, awards.year), birth, contribs(contribs.lit), name.first, name.last).}
\]

Moreover, for the tree \(t_{\text{bios}}\) in Figure 1, the relational view \(\text{rel}_{\tau_{\text{bios}}}(\{t_{\text{bios}}\})\) is illustrated in Figure 7.

To define the relational view of MongoDB database instances, we introduce the notion of (MongoDB) type **constraints**, which are given by a set \(S\) of pairs \((C, \tau)\), for a collection name \(C\) and a type \(\tau\), one for each collection name.

We say that a database instance \(D\) satisfies the constraints \(S\) if \(D, C\) is type \(\tau\) for each \((C, \tau) \in S\). For a given \(S\), for each \((C, \tau) \in S\), we refer to \(\tau\) by \(\tau_{\text{C}}\). Moreover, we assume that in \(\text{rschema}(\tau_{\text{C}})\), the relation name \(R_{\tau_{\text{C}}}\) is actually \(C\).

**Definition 5.5.** Let \(S\) be a set of type constraints, and \(D\) a MongoDB database instance satisfying \(S\). The relational view \(\text{rdbs}(D)\) of \(D\) with respect to \(S\) is the instance \(\{\text{rel}_{\tau}(D,C) \mid (C, \tau) \in S\}\).

Finally, given a MongoDB query and an NRA query, we define when the two can be considered as equivalent. To this purpose, we define equivalence between two kinds of answers: forests and nested relations.

**Definition 5.6.** Let \(F\) be a forest and \(R\) a nested relation. Then \(F\) is equivalent to \(r\), denoted \(F \simeq r\), if \(F\) is of some type \(\tau\) and \(\text{rel}_{\tau}(F) = r\).

**Definition 5.7.** Let \(S\) be a set of type constraints. An MQuery \(q\) is equivalent to an NRA query \(Q\) (with respect to \(S\)), denoted \(q \equiv_{S} Q\), if \(\text{ans}_{\text{m}}(q, D) \simeq \text{ans}_{\text{na}}(Q, \text{rdbs}(D))\), for each database instance \(D\) satisfying \(S\).
5.2 From NRA to MQuery

We now show that NRA can be fully captured by \( \mathcal{M}^{\text{MUPG}} \), while \( \mathcal{M}^{\text{MUPG}} \) captures NRA over a single collection.

In our translation from NRA to MQuery, we have to deal with the fact that an NRA query in general has a tree structure where the leaves are relation names, while an MQuery consists of a sequence of stages. So, we first show how to “linearize” tree-shaped NRA expressions into a MongoDB pipeline. More precisely, we show that it is possible to combine two \( \mathcal{M}^{\text{MUPG}} \) queries \( q_1 \) and \( q_2 \) into a single \( \mathcal{M}^{\text{MUPG}} \) query pipeline\( (q_1, q_2) \) so that the results of \( q_1 \) and \( q_2 \) can be accessed from the result of pipeline\( (q_1, q_2) \) for further processing (here we actually assume that \( q_1 \) and \( q_2 \) are sequences of stages). The idea of pipeline\( (q_1, q_2) \) is to duplicate each tree \( t \) in the input forest as \( t_1 \) and \( t_2 \) so that \( t_i = (\text{rel} = i) \), for \( i \in \{1, 2\} \), and the copy of \( t \) is stored in \( t_i \) under the key \( \text{rel} \), and then to execute \( q_i \)'s one after another:

\[
\text{pipeline}(q_1, q_2) = \rho_{\text{origDoc/rel, actRel/\{1,2\}}} \triangleright \omega_{\text{actRel}} \\
\rho_{\text{actRel, \{rel/((\text{actRel}=i)\&\text{origDoc/dummy}\})}_{i=1,2} \triangleright \text{subq}_1(q_1) \triangleright \text{subq}_2(q_2)
\]

where dummy is a path that does not exist in any collection, and each subq\( _j(q_j) \) implements the subquery \( q_j \) so as not to affect the result of the other subquery \( q_{3-j} \). Specifically, subq\( _j(q_j) = \text{subq}_j(s_1) \cdots \text{subq}_j(s_n) \), for \( q_j = s_1 \cdots s_n \), \( j \in \{1, 2\} \), and subq\( _j \) for single stages is defined as follows:

\[
\begin{align*}
\mu_{\text{rel}} &\triangleright \rho_{\text{actRel}} \triangleright \omega_{\text{rel}j,p} \\
\omega_{\text{rel}j,p} &\triangleright \rho_{\text{actRel}} \triangleright \omega_{\text{rel}j,p} \\
\rho_{p, q/d} &\triangleright \rho_{\text{rel}(3-j), \text{actRel}, \text{rel}j, \text{id}, \text{id}, \text{rel}p, \\
\gamma_{g/y:a/b} &\triangleright \gamma_{\text{rel}j, g, \text{rel}j, \text{y}, \text{a}, \text{rel}j, \text{rel}j, \text{b}, \text{rel}(3-j), d} \\
\rho &\triangleright \rho_{\text{rel}(3-j), \text{actRel}, \text{rel}j, \text{id}, \text{id}, \text{rel}j, \\
\gamma_{g/y:a/b} &\triangleright \gamma_{\text{rel}j, g, \text{rel}j, \text{y}, \text{a}, \text{rel}j, \text{rel}j, \text{b}, \text{rel}(3-j), d} \\
\rho &\triangleright \rho_{\text{rel}(3-j), \text{actRel}, \text{rel}j, \text{y}, \text{a}, \\
\gamma_{g/y:a/b} &\triangleright \gamma_{\text{rel}j, g, \text{rel}j, \text{y}, \text{a}, \text{rel}j, \text{rel}j, \text{b}, \text{rel}(3-j), d} \\
\rho &\triangleright \rho_{\text{rel}(3-j), \text{actRel}, \text{rel}j, \text{y}, \text{a}, \\
\gamma_{g/y:a/b} &\triangleright \gamma_{\text{rel}j, g, \text{rel}j, \text{y}, \text{a}, \text{rel}j, \text{rel}j, \text{b}, \text{rel}(3-j), d} \\
\rho &\triangleright \rho_{\text{rel}(3-j), \text{actRel}, \text{rel}j, \text{y}, \text{a}, \\
\gamma_{g/y:a/b} &\triangleright \gamma_{\text{rel}j, g, \text{rel}j, \text{y}, \text{a}, \text{rel}j, \text{rel}j, \text{b}, \text{rel}(3-j), d}
\end{align*}
\]

where \( e[p \\rightarrow q] \) denotes the expression \( e \) in which every occurrence of the path \( p \) is replaced by the path \( q \).

**Example 5.8.** Consider the sequences of stages \( q_1 = \mu_{\text{name.first}="John" \triangleright \rho_{\text{name}} \text{ and } q_2 = \mu_{\text{awards}} \triangleright \rho_{\text{awards}} \). Then

\[
\text{pipeline}(q_1, q_2) \text{ is the following sequence of stages:}
\]

\[
\rho_{\text{origDoc/rel, actRel/\{1,2\}}} \triangleright \omega_{\text{actRel}} \\
\rho_{\text{actRel, \{rel/((\text{actRel}=i)\&\text{origDoc/dummy}\})}_{i=1,2} \triangleright \text{subq}_1(q_1) \triangleright \text{subq}_2(q_2)
\]

Let \( t \) be the tree in Figure 8. The result of \( \{t\} \triangleright \text{pipeline}(q_1, q_2) \) consists of two trees:

\[
\{ \{\text{actRel}: 1, \\
\text{"reli": 4,} \\
\text{"name": { "first": "Kristen",} \\
\text{"last": "Nygaard" } \\
\} \\
\}
\]

and

\[
\{ \{\text{actRel}: 2, \\
\text{"reli": 4,} \\
\text{"name": { "first": "Kristen",} \\
\text{"last": "Nygaard" } \\
\} \\
\}
\]

So, the result of \( \{t\} \triangleright q_1 \) is found in the first tree under the key \( \text{reli} \), and the result of \( \{t\} \triangleright q_2 \) is found in the second tree under the key \( \text{reli} \).

We start with a singleton set \( S = \{(C, \tau)\} \) of type constraints for a collection name \( C \), and consider an NRA query \( Q \) over the relation \( C \) (with schema \( rschema(\tau_C) \)). The translation of \( Q \) is the \( \mathcal{M}^{\text{MUPG}} \) query \( C \triangleright nra2mq(Q) \), where \( nra2mq(Q) \) is defined recursively in Figure 8. In Figure 8 we reload the function \( att \) and assume that for an NRA query \( Q' \), \( att(Q') \) is the attribute set of the schema implied by \( Q' \). Also, for \( Q_1 \cup Q_2 \) and \( Q_1 \setminus Q_2 \) we assume that \( att(Q_i) = \{p_1, \ldots, p_n\} \).

**Theorem 5.9.** Let \( Q \) be an NRA query over \( C \). Then \( C \triangleright nra2mq(Q) \equiv_s Q \).

**Example 5.10.** Consider the following NRA queries over \( rschema(\tau_{\text{bios}}) \), where \( \text{fn} \) stands for name.first, \( \text{ln} \) for
name.last, an for awards.award, and ay for awards.year:

\[ Q = \pi_{\text{fn}, \text{ln}, \text{an}, \text{ay}}(\chi\text{awards(bios)}) \]

\[ Q' = \sigma_{(\text{rel1}.\text{ay} \leftrightarrow \text{rel2}.\text{ay}) \land ((\text{rel1}.\text{fn} \neq \text{rel2}.\text{fn}) \lor (\text{rel1}.\text{ln} \neq \text{rel2}.\text{ln}))}(Q \times Q) \]

Thus, \( Q' \) asks for a pair of computer scientists that received an award in the same year. We illustrate some steps of \( \text{nra2mq} \):

- \( \text{nra2mq}(Q) = \rho_{\text{id}, \text{awards}, \text{birth}, \text{contribs}, \text{fn}, \text{ln}, \phi} \)
- \( \text{subq}_1(\text{nra2mq}(Q)) \) is the sequence
  \[ \rho_{\text{rel2}, \text{actRel}.\text{rel}, \text{rel1}.\text{id}, \text{rel1}.\text{awards}, \text{rel1}.\text{birth}, \phi} \]
- And \( \text{nra2mq}(Q) \) is the sequence pipeline(\( \text{nra2mq}(Q), \text{nra2mq}(Q) \))

Next, we consider NRA queries across several collections, and show their translation to the \( \mathcal{M}_{\text{MUPGL}} \) fragment of MQuery. Let \( S \) be a set of type constraints, and \( Q \) an NRA query over the schemas for collections named \( C_1, \ldots, C_n \), with \( n \geq 2 \). Let us take \( C_1 \) to be the collection over which we evaluate the generated MQuery. Then, we first need to “bring in” the trees from the collections \( C_2, \ldots, C_n \), which we do in a preparatory phase bring(\( C_2, \ldots, C_n \)):

\[ \gamma_{\text{coll1} / e} \triangleright \chi_{\text{coll2}} \triangleright \cdots \triangleright \chi_{\text{coll} n} \]

\[ \rho_{\text{coll1}, \ldots, \text{colln}, \text{actColl} / (1 .. n)} \triangleright \omega_{\text{actColl}} \]

\[ \rho_{\text{actColl}, \text{coll} / ((\text{actColl} = 1) ? \chi_{\text{coll1}} : \cdots) \triangleright \omega_{\text{colln}} \]

Second, we define a function \( \text{nra2mq}^*(Q) \) that differs from \( \text{nra2mq}(Q) \) in the translation of the collection names:

\[ \text{nra2mq}^*(C_i) = \mu_{\text{actColl} = i} \triangleright \rho_{\text{p}/\text{coll}i, p \in \text{att}(C_i)} \]

Finally, the translation of \( Q \) is the \( \mathcal{M}_{\text{MUPGL}} \) query \( C_1 \triangleright \text{bring}(C_2, \ldots, C_n) \triangleright \text{nra2mq}^*(Q) \).

**Theorem 5.11.** Let \( Q \) be an NRA query over \( C_1, \ldots, C_n \). Then \( C_1 \triangleright \text{bring}(C_2, \ldots, C_n) \triangleright \text{nra2mq}^*(Q) \) is an NRA query.

**Theorem 5.12.** \( \mathcal{M}_{\text{MUPGL}} \) captures full NRA, and \( \mathcal{M}_{\text{MUPGL}} \) captures NRA over a single collection.

We observe that the above translation serves the purpose of understanding the expressive power of MQuery, but is likely to produce queries that MongoDB will not be able to efficiently execute in practice, even on relatively small database instances. We also note that the translation from NRA to MQuery works even if we allow for database instances \( D \) such that \( D \cdot C \) is not strictly of type \( \tau_C \), but may also contain other paths that are not in \( \tau_C \).

5.3 From MQuery to NRA

We show now how to translate MQuery to (recursive) NRA. First, given a set \( S \) of constraints, and an MQuery stage \( s \), we define an NRA query \( \text{mq2nra}(s) \). Then, for an arbitrary MQuery \( C > s_1 > \cdots > s_n \), the corresponding NRA query is defined as \( \text{mq2nra}(s_1) \circ \cdots \circ \text{mq2nra}(s_n) \). Below we assume that the input to \( \text{mq2nra}(s) \) is a query \( Q \) with the associated attributes \( \text{att}(Q) \), and \( \tau \) is the type corresponding to the schema of \( Q \). We say that a path \( p \) is nested in \( \tau \) if type \( p' \), \( \tau \) = array for some strict prefix \( p' \) of \( p \).

In the following, we present the translation of each stage.

**MATCH.** We assume match criteria \( \phi \) to be in negation normal form, that is, negation appears directly in front of the atoms of the form \( (p = v) \) or \( \exists p \).

We first introduce the translation for conjunction- and disjunction-free criteria \( \phi \) according to the type \( \tau \), that is, when \( \phi \) is of the form \( (p = v) \) or \( \exists p \), or \( \neg \exists p \). To this purpose, we define an auxiliary function \( \text{fun}(\phi) \), whose goal is to translate the criteria properly also when \( p \) is not an attribute name in \( \text{rschema}(\tau) \).

For \( \phi = (p = v) \), we need to check whether \( p \) and \( v \) are “compatible” with respect to \( \tau \), that is, whether \( v \) is of type subtree(p, \( \tau \)) or of type subtree(p, \( \tau \)). When they are incompatible, we set \( f(p = v) = \text{false} \); otherwise if \( v \) is of type subtree(p, \( \tau \)), we define \( f(p = v) \) as

- \( (p = v) \), if type(p, \( \tau \)) = literal;
- \( (p = \text{rel}(F)) \) where \( F = \{ \text{attach}(\text{p}, \text{tree}(v_i)) \}_{i=1}^{n} \), if type(p, \( \tau \)) = array and \( v = [v_1, \ldots, v_n] \);
- \( \bigwedge_{p' \in \text{tuple}_{\tau}^{-}(R_{\tau}, \text{attach}(p, v), v') \neq \text{missing}(p' = v') \), if type(p, \( \tau \)) = object;

and if \( v \) is of type subtree(p, \( \tau \)) (hence, type(p, \( \tau \)) = array), we define \( f(p = v) \) as

- \( (v \in p) \), if type(p, \( \tau \)) = literal;
- \( (\text{tuple}_{\tau}^{-}(R_{\tau}, \text{attach}(p, v), v) \neq \text{missing} \), if type(p, \( \tau \)) = object.

For \( \phi = \neg(p = v) \), we set \( f(p = v) = \neg(f(p = v)) \).

For \( \phi = \exists p, f(\phi) \) is defined as follows (we write \( q \neq v \) as a shortcut for \( (q = v) \)):

- \( (p \neq \text{missing}) \), if type(p, \( \tau \) \) \( \in \{ \text{literal}, \text{array} \} \);
- \( \bigvee_{p,q \in \text{att}_{\tau}^{+}(\phi)} \neg q \neq \text{missing} \), if type(p, \( \tau \)) = object.

For \( \phi = \neg \exists p \), we set \( f(\phi) = \neg(f(\exists p)) \).

If the path \( p \) in \( \phi \) is not nested in \( \tau \), we translate \( \mu_{\phi} \) as \( \sigma_{\phi}(\cdot, \text{mq2nra}(\phi)) \).

Consider now the case when the path \( p \) in \( \phi \) is nested, and for simplicity, assume there is only one level of nesting. Further, assume that \( p = q.p' \), \( q \) is a sub-relation of \( R_{\tau} \) (we call it the parent relation of \( p \)), and \( p \) is a prefix of some path in \( \text{att}_{\tau}^{+}(q) \). Then to check the condition on \( q \) according to the semantics of match, we need to be able to access the contents of the sub-relation \( q \) by unnesting it, but to return the original (i.e., nested) relation \( q \). So before actually doing a selection, we apply several preparatory phases.

- \( \text{AddID} = \text{att}(Q), \text{id} \text{att}(Q) \circ ([V_{\text{idatt}(Q)} \rightarrow \text{ID}] \end{array} \) creates an identifier for each tuple (required for negative \( \phi \), for which we need to unnest and then to nest back):
• AddDup_ψ = π_{att}(Q), ID, q′/q creates a copy q′ of the sub-relation q.
• Prep_ψ does proper preprocessing of the new attribute q′.
  \[ \text{Prep}_\psi = \chi_{q′} \circ \pi_{att}(Q), ID, \{a′/a \in att(q′)\} \]
  for positive \( \psi \).
  \[ \text{Prep}_\neg \psi = \chi_{q′} \circ \pi_{att}(Q), ID, \text{res}/f(\neg \psi) \circ \nu_{\{\text{res}\}} \rightarrow \text{cond} \]
  for \( \neg \psi \).

Then, we apply selection with the condition \( f(\psi) \) defined as \( f(\psi_{\neg a\rightarrow a'}) \) for positive \( \psi \) and as \( \text{cond} = \{\{\text{res, false}\}\} \) for negative \( \psi \), and finally, project away the auxiliary columns q and ID. More precisely,

\[ \text{mq2nra}(\mu_\psi) = \text{AddID} \circ \text{AddDup}_\psi \circ \text{Prep}_\psi \circ \sigma_f(\psi) \circ \pi_{att}(Q). \]

This translation can be extended to the case of multiple levels of nesting, and we omit the details, which are tedious but straightforward.

Now we deal with arbitrary criteria \( \psi \). Let \( \alpha_1, \ldots, \alpha_n \) be all positive literals with nested paths in \( \psi \), \( \beta_1, \ldots, \beta_m \) all negative literals with nested paths in \( \psi \), and \( \delta_1, \ldots, \delta_k \) all literals with not nested paths in \( \psi \). For each literal about a nested path \( p \), we need to create a separate duplicate of the parent relation \( q \) of \( p \). So below we assume that \( \text{AddDup}_{\alpha_1, \ldots, \alpha_n, \beta_1, \ldots, \beta_m} \) creates a new column named uniquely for each literal \( \alpha_k \) and \( \beta_j \), and that \( \text{Prep}_{\beta_j} \) projects all these new columns and gives a unique names to the sub-relations \text{cond} (and projects them as well). We set \( f(\delta) = f(\delta_i) \) and let \( f(\phi) \) be the result of replacing in \( \phi \) each literal \( \ell \) by \( f(\ell) \) (respecting the unique names of the attributes and sub-relations for each literal about a nested path).

Then \( \text{mq2nra}(\mu_\psi) \) is the query

\[ \text{AddID} \circ \text{AddDup}_{\alpha_1, \ldots, \alpha_n, \beta_1, \ldots, \beta_m} \circ \text{Prep}_{\alpha_1} \circ \cdots \circ \text{Prep}_{\alpha_n} \circ \text{Prep}_{\beta_m} \circ \text{Prep}_{\alpha_1} \circ \cdots \circ \text{Prep}_{\alpha_n} \circ \sigma_f(\psi) \circ \pi_{att}(Q). \]

UNWIND. The unwind operator \( \omega_p \) can be translated to unnest in NRA: \( \text{mq2nra}(\omega_p) = \chi_p \).

With \( \omega_p \), we first replace empty sub-relations \( p \) with \( \{(a : \text{missing})\}_{a \in att_r(p)} \), and then apply the normal unnest. Hence, \( \text{mq2nra}(\omega_p) \) is defined as

\[ \pi_{att}(Q) \setminus \{p, \nu((p=\{\})?\{(a : \text{missing})\}_{a \in att_r(p)} : p) \circ \chi_p \}. \]

PROJECT. A project stage \( p_p \) can be translated to the NRA project operator.

Let \( p \) be a path in \( \tau \). We define a function \( \text{proj}(p) \).
If \( \text{type}(p, \tau) \in \{\text{literal, array}\} \), then \( \text{proj}(p) = \{p\} \).
If \( \text{type}(p, \tau) \) is object, then \( \text{proj}(p) = \{p, p'/p' \in att_r(\psi)\} \), where \( q \) is the shortest prefix of \( p \) such that \( \text{type}(q, \tau) = \text{array} \), when \( p \) is nested, and \( q = \epsilon \), if \( p \) is not nested.

We define the function \( \text{proj} \) also for expressions \( q/d \). If \( d \) is a path \( p \), we set \( \text{proj}(q/p) = \{q/p\} \), if \( \text{type}(p, \tau) \in \{\text{literal, array}\} \), and \( \text{proj}(q/p) = \{q.r/p.r \mid p.r \in \text{proj}(p)\} \), if \( \text{type}(p, \tau) = \text{object} \). If \( d \) is a (JSON) value, then simply \( \text{proj}(q/d) = \{q/d\} \).

For complex value definitions \( d \), \( \text{proj}(q/d) \) can be defined by analogy using \( \text{proj}(p) \) when needed.

Then \( \text{mq2nra}(p_p) = \pi_{\text{proj}(p)} \), where \( \text{proj}(P) = \bigcup_{p \in P} \text{proj}(p) \cup \bigcup_{q \in D} \text{proj}(q/d) \).

GROUP. To translate a group operator \( \gamma_{\text{G}_{\alpha_1, \beta_1}, \ldots, \beta_m} \), intuitively we rename attributes according to \( \gamma \) and \( \alpha_i/b_i \), nest the attributes \( \alpha_i \) into \( \text{acc} \), and project each \( \alpha_i \) from \( \text{acc} \) independently. For simplicity, we only show the translation when all types of paths in \( G \) and \( b_i \)'s are either literal or array. In this case, \( \text{mq2nra}(\gamma_{\text{G}_{\alpha_1, \beta_1}, \ldots, \beta_m}) = \)

\[ \pi_{\text{id}(G), \alpha_1/b_1, \ldots, \alpha_n/b_m} \circ \nu_{\{\alpha_1, \ldots, \alpha_n\}} \rightarrow \text{acc} \circ \]

\[ \pi_{\text{idAtt}(G), \alpha_1/\text{acc}, \alpha_1, \ldots, \alpha_n/\text{acc}} \]

where \( \text{id}(G) = \land \text{id}.g_1/y_1, \ldots, \text{id}.g_m/y_m \) and \( \text{idAtt}(G) = \land \text{id}.g_1, \ldots, \text{id}.g_m \) if \( G = g_1/y_1, \ldots, g_m/y_m \), and \( \text{id}(G) = \land \text{id}.\emptyset \) and \( \text{idAtt}(G) = \land \text{id} \), if \( G \) is empty. This translation can be extended to the case in which some types are object by using the proj function defined above. We omit the details.

LOOKUP. For a lookup operator \( \lambda_{\rho_1 = C'.p_2} \), we assume that \( C' \) is of type \( \tau' \). For simplicity, we present a translation using the left join operator \( R \bowtie_{\rho_2} R' \) that keeps the tuples in \( R \) for which it does not find matching tuples in \( R' \), by filling in the rest of the attributes by \( \text{null} \). It is possible to avoid using left join, but would make the translation less readable. To translate lookup, we first compute the left join of \( Q \) and \( C' \) according to the join condition \( p_1 = C'.p_2 \), then nest all attributes from \( C' \) into a sub-relation \( p \), and finally make sure that the value of \( p \) is \( \{\} \) for unmatched tuples. More precisely, we define \( \text{mq2nra}(\lambda_{\rho_1 = C'.p_2})(Q, C') \) as

\[ \pi_{\text{att}(Q)/\text{rel1 att}(Q), \text{proj}(p)/((p=\{\})?\{(a : \text{missing})\}_{a \in \text{att}_r(p)} : p) \circ \chi_p \circ \left( (\nu_{\text{rel2 att}(C')} \rightarrow \text{proj}(Q \bowtie_{\rho_2} \text{proj}(p_1) = C'.\text{proj}(p_2)) \right) \]

where \( Q.\text{proj}(p_1) = C'.\text{proj}(p_2) \) is an abbreviation of a conjunction of multiple equality conditions, if subtree(\( \tau, p_1 \)) coincides with subtree(\( \tau', p_2 \)), and false otherwise.

We illustrate the translation of MQuery to NRA in the following examples.

EXAMPLE 5.13. Consider a collection of type \( \tau_{\text{bios}} \) in Example 5.4. First, we provide the translation of some atomic criteria:

• \( f(\text{name.first} = "Kristen") = (\text{name.first} = "Kristen") \)

• \( f(\text{name.first} = \{\text{first}: "Kristen"\}) = \text{false} \) since according to \( \tau_{\text{bios}} \), the object under the key name should contain also the key last.

• \( f(\text{name.first} = "Kristen", \text{last} = "Nygaard") = (\text{name.first} = "Kristen") \land (\text{name.last} = "Nygaard") \)

• \( f(\text{contribs} = \{\text{"OOP", "Simula"}\}) \), \( f(\psi) \) computes a comparison between a sub-relation name and a relation value: \( \text{and} (\text{\{contribs.lit: \"OOP\}"}, (\text{\{contribs.lit: \"Simula\}"})) \)

• \( f(\text{contribs} = \{\text{"OOP"}\} = \{\text{\"OOP\}" \in \text{\{contribs.lit\}} \}

Second, we provide the translation of match stages for a
criterion about a nested path and for a complex criterion:

\[
\text{mq2nra}(\mu(\text{awards.year}=2001)) = \\
\pi_{\text{id.year}}/\text{awards.year}, \text{persons.first}/\text{name.first}, \text{persons.last}/\text{name.last} \\
\chi_{\text{awards1}} \circ \pi_{\text{att(bios)}}, \text{awards.award1}/\text{awards.award}, \\
\sigma_{\text{awards.year1}/\text{awards.year}} \\
\Sigma(\text{awards.year}=2001) \circ \pi_{\text{att(bios)}}
\]

\[
\text{mq2nra}(\gamma_{\text{year}/\text{awards.year}:\text{persons/name}}) = \\
\pi_{\text{id.year}/\text{awards.year}, \text{persons.first}/\text{name.first}, \text{persons.last}/\text{name.last}} \\
\chi_{\text{persons.first}/\text{persons.last}} \circ \text{acc} \\
\pi_{\text{id.year}, (\text{persons.first}, \text{persons.last})/\text{acc} (\text{persons.first}, \text{persons.last})}
\]

where for the first stage we omitted the creation of the identifier column. Finally, we provide the translation of a group stage:

\[
\text{mq2nra}(\gamma_{\text{year}/\text{awards.year}:\text{persons/name}}) = \\
\pi_{\text{id.year}/\text{awards.year}, \text{persons.first}/\text{name.first}, \text{persons.last}/\text{name.last}} \\
\chi_{\text{persons.first}/\text{persons.last}} \circ \text{acc} \\
\pi_{\text{id.year}, (\text{persons.first}, \text{persons.last})/\text{acc} (\text{persons.first}, \text{persons.last})}
\]

It is easy to see that the translation of MQuery to NRA is of polynomial size. Although it is perhaps not surprising that MQuery can be translated to NRA, we note that it required some care to work out the details that allowed us on the one hand to correctly capture the semantics of MQuery, and on the other hand to keep the translation compact.

**Theorem 5.14.** Let \( F \) be a forest of type \( \tau \) and \( s \) a stage of MQuery, then \( F \triangleright s \simeq \text{mq2nra}(s)(\text{rel}_r(F)) \) if \( s \) is not a lookup stage; otherwise \( F \triangleright s[F'] \simeq \text{mq2nra}(s)(\text{rel}_r(F), \text{rel}_r(F')) \) for a forest \( F' \) of type \( \tau' \).

**Proof.** Straightforward considering the semantics of the MQuery stages and of NRA.

**Theorem 5.15.** Let \( S \) be a set of type constraints, and \( q \) an MQuery \( C \triangleright s_1 \triangleright \ldots \triangleright s_m \). Then \( q \equiv_s (\text{mq2nra}(s_1) \circ \ldots \circ \text{mq2nra}(s_m))(C) \).

### 6. COMPLEXITY OF MQuery

In this section we report results on the complexity of different fragments of MQuery. Specifically, we are concerned with the combined and query complexity of the *Boolean query evaluation* problem, which is the problem of checking whether the answer to a given query over a given database instance is non-empty.

Our first result establishes that the full \( \mathcal{M}_{\text{MPGL}} \) and also \( \mathcal{M}_{\text{MPUG}} \) are complete for exponential time with a polynomial number of alternations under \( \text{LOGSPACE} \) reductions. That is, have the same complexity as monad algebra with atomic equality and negation \( \mathcal{M}_{\text{MUG}} \), which however is strictly less expressive than NRA.

**Theorem 6.1.** \( \mathcal{M}_{\text{MPUG}} \) and \( \mathcal{M}_{\text{MPGL}} \) are \( \text{TA}[2^{O(n^3)}, n^{O(1)}] \)-complete in combined complexity, and in \( \text{AC}^0 \) in data complexity.

**Proof Sketch.** The proof of the lower bound follows the line of the \( \text{TA}[2^{O(n^3)}, n^{O(1)}] \)-hardness proof in \( \mathcal{M}_{\text{MUG}} \).

As for the upper bound, we provide an algorithm that follows a strategy based on starting the alternating computation from the last stage, inspired by a similar one in \( \mathcal{M}_{\text{MUG}} \). Let \( q \) be an \( \mathcal{M}_{\text{MPGL}} \) query and \( D \) a database instance. We check whether there is a tree in \( \text{ans}_{\text{mq2nra}}(q, D) \) using an alternating Turing machine running in exponential time with polynomially many alternations.

Intuitively, for a forest \( F' \) resulting from applying a stage \( s \) in \( q \) to a previous result \( F \), i.e., \( F' = F \triangleright s \), in general we need to check whether there is a tree and/or all trees in \( F' \) that satisfy some conditions (such as, the value of a path \( p \) in such a tree should/should not be \( v \), or a path \( p \) should/should not exist), without explicitly constructing \( F' \). To do so, we derive from the conditions on \( F' \) suitable conditions to be checked on \( F \). Such conditions are obtained/guess from the criteria in match stages, and Boolean value definitions and conditional value definitions in project stages. Both branching and alternations happen because of the group stage. For instance, if \( s = ?a_1/a_1, a_2/a_2 \) and the conditions on \( F' \) contain \( a_1 \not= [\cdot] \), then we need to check that there is no tree in \( F \) satisfying \( \exists b_1 \). If \( s = ?g/y/a_1/a_2/a_2 \) and the conditions on \( F' \) contain \( \_id.g = v \), \( a_1 \not= [\cdot] \) and \( a_2 \not= [\cdot] \), then we need to check whether in \( F \) there is a tree satisfying \( y = v \) and \( \exists b_1 \), and there is a tree satisfying \( y = v \) and \( \exists b_2 \).

The overall computation starts from \( F' = \text{ans}_{\text{mq2nra}}(q, D) \), and propagates the constraints on the intermediate forests to the previous stages. The “depth” of the checks is given by the number of stages, the branching and the number of alternations are bounded by the size of \( q \), which gives us \( \text{TA}[2^{O(n^3)}, n^{O(1)}] \) upper bound.

The data complexity follows from the data complexity of NRA that is known to be in \( \text{AC}^0 \). \( \square \)

Next, we study some of the less expressive fragments of MQuery. We consider match to be an essential operator, and we start with the minimal fragment \( \mathcal{M}^m \), for which we show that query answering is tractable and very efficient.

**Theorem 6.2.** \( \mathcal{M}^m \) is \( \text{LogSpace-complete in combined complexity}. \)

**Proof Sketch.** The lower-bound can be shown by a reduction from the directed forest accessibility problem, known to be complete for \( \text{LOGSPACE} \) under \( \text{NC}^1 \) reducibility to the problem whether \( t \models \exists p \), for a tree \( t \) and a path \( p \).

The upper-bound follows from the following facts: (i) we can check in \( \text{LOGSPACE} \) whether \( t \models (p = v) \) and whether \( t \models \exists p \), for a tree \( t \), a path \( p \), and a value \( v \); (ii) tree-isomorphism, needed to check equality between the sub-tree reached through a path \( p \) and a complex value \( v \) is in \( \text{LOGSPACE} \); (iii) the Boolean formula value problem is \( \text{ALOGTIME-complete} \), and hence in \( \text{LOGSPACE} \). \( \square \)
Theorem 6.3. \( \mathcal{M}_{\text{MP}} \) is \textit{PTIME}\textit{-hard} in query complexity and \( \mathcal{M}_{\text{MPGL}} \) is in \textit{PTIME} in combined complexity.

\textbf{Proof Sketch.} The lower-bound follows from the fact that we can compute the value of a monotone Boolean circuit consisting of assignments to \( n \) variables in \( n \) project stages, and in the final match stage we can check whether the output variable evaluates to 1.

For the upper-bound, we notice that it is not necessary to materialize the exponentially large trees, instead we can work on their compact representations in the form of directed acyclic graphs (DAGs). Thus, we can devise an algorithm for which the result of each stage grows at most linearly in the size of the stage and its input set of DAGs. Hence, we can evaluate each stage on a structure that is at most polynomial.

We can identify the unwind operator as one of the sources of complexity, as it allows one to multiply the number of trees each time it is used in the pipeline. Indeed, adding the unwind operator alone causes already loss of tractability, provided the input tree contains multiple arrays (hence in combined complexity).

Theorem 6.4. \( \mathcal{M}_{\text{MU}} \) is \textit{LOGSPACE-complete} in query complexity and \( \text{NP-complete} \) in combined complexity.

\textbf{Proof Sketch.} For the LOGSPACE upper-bound, we observe that the number of times the unwind operation can actually multiply the number of trees is bounded by the number of arrays that are present in the input tree, and hence by a constant. Hence, we can both compute the result of the unwind stages, and evaluate the match conditions in LOGSPACE in the size of the query.

The NP lower-bound results from a straightforward encoding of the Boolean satisfiability problem: we start from an input forest containing \( n \) arrays \([0,1]\), then we generate with \( n \) unwind stages all \( 2^n \) assignments, and finally we check with a match stage whether there is a satisfying one. The NP upper-bound follows from the next theorem.

Adding project and lookup does not increase the combined complexity, but does increase the query complexity, since they allow for creating multiple arrays from a fixed input tree.

Theorem 6.5. \( \mathcal{M}_{\text{MUP}} \) and \( \mathcal{M}_{\text{MUL}} \) are \textit{NP-hard} in query complexity, and \( \mathcal{M}_{\text{MPGL}} \) is in \textit{NP} in combined complexity.

\textbf{Proof Sketch.} The proof of the lower-bound is analogous to the one for the NP lower-bound in Theorem 6.3 except that now we can use either project or lookup to generate the forest with \( n \) arrays \([0,1]\).

For the upper-bound, we extend the idea of using DAGs as compact representations of trees. We only specify how to evaluate an unwind stage: instead of creating a separate DAG for each element of the array, we guess an element of the array and produce at most one DAG for each input DAG. This is sufficient, since without group, we can evaluate each original tree independently of the other ones.

In the presence of unwind, the group operator provides another source of complexity, since in \( \mathcal{M}_{\text{MUG}} \) we can generate doubly exponential large trees, analogous to monad algebra \cite{MUP}. Let \( t_0 = \text{tree}(\{i : 0\}) \) and \( t_1 = \text{tree}(\{i : 1\}) \). Then the result of applying the following \( \mathcal{M}_{\text{MUG}} \) query to \( \{t_0, t_1\} \) is a forest containing \( 2^{2^n} \) trees, each encoding one \( 2^n \)-bit value.

\[ \gamma_1 d_1, x_1 ., x_n \rightarrow \omega_{i.d_1,x_1} d_1 \rightarrow \omega_{i.d_2,x_2} d_2 \rightarrow \ldots \rightarrow \omega_{i.d_n,x_n} d_n \rightarrow \mu_1 \rightarrow \mu_2 \rightarrow \psi \]

Below we show that already \( \mathcal{M}_{\text{MUG}} \) queries are \textit{PSPACE-hard}.

Theorem 6.6. \( \mathcal{M}_{\text{MUG}} \) is \textit{PSPACE-hard} in query complexity.

\textbf{Proof.} Proof by reduction from the validity problem of QBF. Let \( \varphi \) be a quantified Boolean formula over the variables \( x_1, \ldots, x_n \) of the form \( Q_1 x_1 Q_2 x_2 \ldots Q_n x_n \psi \), for \( Q_i \in \{\exists, \forall\} \). We construct a forest \( F \) and an \( \mathcal{M}_{\text{MUG}} \) query \( q \) such that \( F > q \) is non-empty iff \( \varphi \) is valid.

\( F \) contains a single document \( d \) of the form \( \{x:0[1]\} \), and \( q \) is as follows:

\[ \gamma_1 x_1 / \ldots / x_n x_1 / \omega_{i.d_1,x_1} d_1 / \ldots / \omega_{i.d_n,x_n} d_n / \mu_1 \rightarrow \mu_2 / \psi \rightarrow \]

The query \( q \) consists of two logical parts. In the first one we create \( n \) arrays \([0,1]\), unwind each of them, thus creating all possible \( 2^n \) variable assignments and then filter only the satisfying ones. In the second part, for each quantifier \( Q_i x_i \), we filter the assignments to the variables \( x_1, \ldots, x_i-1 \) satisfying the formula \( Q_i x_i \ldots Q_n x_n \psi \) by using group.

7. CONCLUSIONS

Here we carried out a first formal investigation of MongoDB, a widely used NoSQL database system, with the aim of understanding its query expressiveness and complexity. We provided a formalization of the MongoDB data model, and of a core fragment, called MQuery, of the MongoDB query language. We studied the expressiveness of MQuery, showing its equivalence with NRA by developing compact translations between these two query languages. We further investigated the computational complexity of significant fragments of MQuery, obtaining several (tight) bounds in combined complexity, which range from LOGSPACE to alternating exponential-time with a polynomial number of alternations. As a byproduct, we have also established a tight complexity bound for NRA.

We briefly comment on our choice of the MongoDB query language for carrying out our investigation, as opposed to adopting a (possibly abstract and novel) language that would capture also additional features of other existing query languages for processing semi-structured or complex valued data (such as Jaql \cite{Jaql} or Pig Latin \cite{pigLatin}). First of all, we see value in studying a real-world system that, although widely
adopted, still lacks a proper formalization and an understanding of its computational properties. Also, since MongoDB is still under active development, some of the insight provided by our work might help the developers to tune the system, and possibly backtrack on some choices that appear difficult to justify from a formal point of view. Turning to Jaql and Pig Latin, these are script languages, compiled into sets of map-reduce jobs for the Hadoop platform, for batch processing (note, however, that also in MongoDB the output can be stored in another collection, so it is compatible with batch processing). Moreover, Jaql is highly composable since it supports higher-order functions (all language operators can be applied to any level of nested data). This contrasts with a regular query language as the one provided by the MongoDB aggregation framework, in which the operators cannot take stage operators as parameters, and which is mostly intended to be used in an online setting. Hence, a thorough comparison with these languages would require a full investigation of their formal and computational properties, not much different in scope than what provided here, and left for future work.

We are currently working on applying the results presented here, and specifically the translation from NRA to MUPGL, to provide high-level access to MongoDB data sources relying on the ontology-based data access paradigm [7], thus avoiding hard-coded post-processing transformations [4].

Acknowledgements. We thank Christoph Koch and Dan Suciu for helpful clarifications on nested relational algebra, and Henrik Ingo for information about MongoDB. We also thank Martin Rezk for his participation to initial work on the topic of the paper.

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APPENDIX

A. EXAMPLES OF MongoDB QUERIES

MongoDB provides two main query mechanisms. The basic form of query is a `find` query, which allows one to filter out documents according to some (Boolean) criteria and to return, for each document passing the filter, a tree containing a subset of the key-value pairs in the document. Specifically, a find query has two components, where the first one is a criterion for selecting documents, and the second one is a projection condition.

**Example A.1.** The following MongoDB find query selects from the `bios` collection the documents talking about scientists whose first name is Kristen, and for each document only returns the full name and the date of birth.

```
db.bios.find(
    {
        "name.first": {
            "$eq": "Kristen"
        },
        "name": 1, "birth": 1
    }
)
```

When applied to the document in Figure 1 it returns the following tree:

```
{  
    "_id": 4,
    "birth": "1926-08-27",
    "name": {
        "first": "Kristen", "last": "Nygaard"
    }
}
```

Observe that by default the document identifier is included in the answer of the query.

Note that with a find query we can either obtain the original documents as they are, or we can modify them by specifying in the projection condition only a subset of the keys, thus retaining in the answer only the corresponding key-value pairs. However, we cannot change the shape of the individual pairs.

A more powerful querying mechanism is provided by the aggregation framework, in which a query consists of a pipeline of stages, each transforming a forest into a new forest. We call this transformation pipeline an MQuery. One of the main differences with find queries is that MQuery can manipulate the shape of the trees.

**Example A.2.** The following MQuery essentially does the same as the previous find query, but now it flattens the complex object `name` into two key-value pairs.

```
db.bios.aggregate([  
    {  
        "$match": {"name.first": {"$eq": "Kristen"}}},  
        {"$project": {  
            "birth": true, "firstName": "$name.first", "lastName": "$name.last" } }  
    ])
```

So the document from our running example will be transformed into the following tree:

```
{  
    "id": 4,
    "birth": "1926-08-27",
    "firstName": "Kristen",
    "lastName": "Nygaard"
}
```

**Example A.3.** Consider the MQuery

```
db.bios.aggregate([  
    {"$project": {"name": true,  
        "award1": "$awards", "award2": "$awards" } }},  
    {"$unwind": "$award1"},  
    {"$unwind": "$award2"},  
    {"$project": {  
        "name": true, "award1": true, "award2": true,  
        "twoInOneYear": {  
            "$and": [  
                {"$eq": ["$award1.year", "$award2.year"]},  
                {"$ne": ["$award1.award", "$award2.award"]}  
            ]}  
    }},  
    {"$match": {"twoInOneYear": true}},  
    {"$project": {  
        "firstName": "$name.first",  
        "lastName": "$name.last",  
        "awardName1": "$award1.award",  
        "awardName2": "$award2.award",  
        "year": "$award1.year" } }],
```

It consists of 6 stages and retrieves all persons who received two awards in one year. The first stage keeps the complex object name, creates two copies of the array awards, and projects away all other fields. The second and third stages flatten (unwind) the two copies (award1 and award2) of the array of awards (which intuitively creates a cross-product). The fourth step compares awards pairwise and creates a new key (twoInOneYear) whose value is true if the scientist has two awards in one year. The fifth one selects the documents of interests (those where twoInOneYear is true), and the final stage renames and projects keys.

By applying the query to the document in Figure 1 we obtain:

```json
{
  "id": 4,
  "firstName": "Kristen",
  "lastName": "Nygaard",
  "awardName1": "IEEE John von Neumann Medal",
  "awardName2": "Turing Award",
  "year": 2001
}
```

We note that the unwind operator creates a new document for every element in the array. Thus, unwinding awards (once) in the document in our running example will output 3 documents, only one of which satisfies the subsequent selection stages. In the example below we illustrate the group stage, which combines different documents into one.

**EXAMPLE A.4.** The following query returns for each year all scientists that received an award in that year.

```javascript
db.bios.aggregate([
  {
    "$unwind": "$awards",
    "$group": {
      _id: { "year": "$awards.year" },
      "names": {$addToSet: "$name" } },
  }
])
```

Running this query over the database consisting of the document in Figure 1 produces the following output:

```json
{
  "_id": { "year": 2001 },
  "names": [
    { "first": "Kristen", "last": "Nygaard" } ]
},
{
  "_id": { "year": 1999 },
  "names": [
    { "first": "Kristen", "last": "Nygaard" } ]
}
```

### B. TREE OPERATIONS

In the following, let $t = (N, E, L_n, L_e)$ be a tree. Below, when we mention reachability, we mean reachability along the edge relation.

**subtree** the subtree of $t$ rooted at $x$ and induced by $M$, for $n \in M$ and $M \subseteq N$, denoted subtree($t, x, M$), is defined as $(N', E|_{N' \times N'}, L_n|_{N'}, L_e|_{E'})$ where $N'$ is the subset of nodes in $M$ reachable from $x$ through nodes in $M$. We write subtree($t, M$) as abbreviation for subtree($t, \text{root}(t), M$).

For a path $p$ with $|[p]| = 1$, the subtree subtree($t, p$) of $t$ hanging from $p$ is defined as subtree($t, r_p, N'$) where $\{r_p\} = [p]$ and $N'$ are the nodes reachable from $r_p$ via $E$. For a path $p$ with $|[p]| = 0$, subtree($t, p$) is defined as tree(null).

**attach** the tree attach($k_1 \ldots k_n, t$) constructed by inserting the path $k_1 \ldots k_n$ on top of the tree $t$, for $n \geq 1$, is defined as $(N', E', L'_n, L'_e)$, where

- $N' = N \cup \{x_0, x_1, \ldots, x_{n-1}\}$, for fresh $x_0, \ldots, x_{n-1}$,
- $E' = E \cup \{(x_0, x_1),(x_1, x_2),\ldots,(x_{n-1}, \text{root}(t))\}$,
- $L'_n = L_n \cup \{(x_0, \emptyset), \ldots, (x_{n-1}, \emptyset)\}$,
- $L'_e = L_e \cup \{(x_0, x_1), k_1, \ldots, (x_{n-2}, x_{n-1}), (x_{n-1}, \text{root}(t)), k_n\}$.

**intersection** Let $t_1$ and $t_2$ be trees. The function $t_1 \cap t_2$ returns the set of pairs of nodes $(x_n, y_n) \in N_1 \times N_2$ reachable along identical paths in $t_1$ and $t_2$, that is, such that there exist $(x_0, x_1), \ldots, (x_{n-1}, x_n)$ in $E_1$, for $x_0 = \text{root}(t_1)$, and $(y_0, y_1), \ldots, (y_{n-1}, y_n)$ in $E_2$, for $y_0 = \text{root}(t_2)$, with $L_{E_1}(x_i) = L_{E_2}(y_i)$ and $L_{E_1}(x_{i-1}, x_i) = L_{E_2}(y_{i-1}, y_i)$, for $1 \leq i \leq n$.

**merge** Let $t_1, t_2$ be trees $(N^j, E^j, L_{n}^j, L_{e}^j)$, $j = 1, 2$, such that $N_1 \cap N_2 = \emptyset$, and for each path $p$ leading to a leaf in $t_2$, i.e., $t_2 \models (p = v)$ for some literal value $v$, we have that $t_1 \nvdash \exists p$ and the other way around. Then the tree $t_1 \oplus t_2$ resulting from merging $t_1$ and $t_2$ is defined as $(N, E, L_n, L_e)$, where
• $N = N^1 \cup N^2$, for $N^{2'} = N^2 \setminus \{(x_1, x_2) \in t_1 \cap t_2\}$
• $E = E^1 \cup (E^2 \cap (N^{2'} \times N^{2'})) \cup ((t_1 \cap t_2) \circ E^2)$
• $L_n = L^1_n \cup L^2_n |_{N^2'}$
• $L_e = L^1_e \cup L^2_e |_{N^{2'} \times N^{2'}} \cup \{(x_1, y_2), \ell \} |_{L^2_e(y_1, y_2) = \ell, (x_1, y_1) \in t_1 \cap t_2\}$

minus $t_1 \setminus t_2$ is subtree $(t_1, N')$ where $N' = N_1 \setminus N_2$.

array Let $\{t_1, \ldots, t_n\}, n \geq 0$, be a forest and $p$ a path. The operator $\text{array}(\{t_1, \ldots, t_n\}, p)$ creates the tree encoding the array of the values of the path $p$ in the trees $t_1, \ldots, t_n$. Let $t^p_j = \text{subtree}(t_j, p)$ with $(N^j, E^j, L^1_e, L^2_e)$ where all $N^j$ are mutually disjoint, and $r_j = \text{root}(t^p_j)$. Then, $\text{array}(\{t_1, \ldots, t_n\}, p)$ is the tree $(N, E, L_n, L_e)$ where

• $N = \left( \bigcup_{j=1}^n N^j \right) \cup \{v_0\}$
• $E = \left( \bigcup_{j=1}^n E^j \right) \cup \{(v_0, r_1), \ldots, (v_0, r_n)\}$
• $L_n = \left( \bigcup_{j=1}^n L^1_e \right) \cup \{(v_0, "1")\}$
• $L_e = \left( \bigcup_{j=1}^n L^2_e \right) \cup \{(v_0, r_1, 0), \ldots, (v_0, r_n, n-1)\}$

We also define subtree $(t, p)$ for paths $p$ such that $\lceil |p^t| \rceil > 1$. In this case it returns the tree encoding the array of all subtrees hanging from $p$. Formally, $\text{subtree}(t, p) = \text{array}(\{t_1, \ldots, t_n\}, \varepsilon)$, where $\{r_1, \ldots, r_n\} = \lceil |p^t| \rceil$. $N_j$ the set of nodes reachable from $r_j$ via $E$, and $t_j = \text{subtree}(t, r_j, N_j)$. We observe that the definition of the array operator is recursive as it uses the generalized subtree operator.

B.1 Expressing $\exists p$ in value definition

We can express $\exists p$ as $(p?true:((-p=null) \land (p=false) \land (p=0))?true:false)$.

C. NESTED RELATIONAL ALGEBRA TO MQuery

**Lemma C.1.** The result of pipeline$(q_1, q_2)$ contains the result of $q_k$ in the trees with $\text{actRel} = i$ under the key $\text{rel}_i$.

**Proof.** Let $F$ be a forest, and $F_0$ the result of evaluating of the first 3 stages in pipeline$(q_1, q_2)$ over $F$. Then $F_0$ satisfies the property:

(∗) for each tree $t$ in $F_0$, if $t \models \text{actRel = 1}$, then $t \models \exists \text{rel}_1 \land \neg \exists \text{rel}_2$, and if $t \models \text{actRel = 2}$, then $t \models \exists \text{rel}_2 \land \neg \exists \text{rel}_1$.

Moreover, for each tree $t$ in $F$, there are exactly two trees $t_1$ and $t_2$ in $F_0$ such that $t_1 \models \text{actRel = 1}$, subtree$(t_1, \text{rel}_1)$ coincides with $t$, and $t_2 \models \text{actRel = 2}$, subtree$(t_2, \text{rel}_2)$ coincides with $t$. These follow from the semantics of conditional value definition and of $\rho_{p/q}$ when $q$ is missing from the input trees.

Let $F_1 = F_0 \circ \text{subq}_1(q_1)$. We prove that

- **(clean) $F_1$ satisfies (∗),**
- **(own) $F_1 \circ \text{actRel}=1_{\text{actRel}=1}$, coincides with $F \circ q_1$, and**
- **(other) $F_1 \circ \text{actRel}=2$ coincides with $F_0 \circ \text{actRel}=2$, which coincides with $F$ (i.e., the “other” trees are not affected).**

It is sufficient to prove the above for the case of $q_1$, being a single stage pipeline $s$. It follows the following cases:

• $s$ is a match stage $\mu_{\varphi}$. Then $\text{subq}_1(q_1) = \mu_{\text{actRel}=1} \lor \varphi[p/\text{rel}_1,p]$. Since match does not alter the structure of the trees, $F_1$ satisfies (∗).

• $s$ is an unwind stage $\omega^+_p$. Then $\text{subq}_1(q_1) = \omega^+_\text{rel}_1,p$. First, $\text{subq}_1(q_1)$ does not affect the trees with $\text{actRel}=2$ because there does not exist the path $\text{doc}1.p$, and $\text{subq}_1(q_1)$ will preserve all such trees as they are. Second, the trees that contain the path $\text{doc}1.p$ (hence, with $\text{actRel}=1$), will be affected in exactly the same way as the trees in $F$ would be affected by $q_1$. Finally, since unwind does not affect other paths than $p$, we have that $F_1$ satisfies the clean specialization property.

• $s$ is an unwind stage $\omega^-_p$. Then $\text{subq}_1(q_1) = \mu_{\text{actRel}=1} \lor (\exists \text{rel}_1,p) \land (\text{rel}_1,p \neq 0) \lor \omega^+_\text{rel}_1,p$. Again, $\text{subq}_1(q_1)$ does not affect the trees with $\text{actRel}=2$ because they will all pass the match stage and the subsequent unwind will preserve them as they are. Second, we note that evaluating $q_1$ over $F$ will remove trees where path $p$ does not exist, or $p$ exists and its value is null, or empty array. This is done by $\text{subq}_1(q_1)$ in the match stage. The subsequent unwind acts as the unwind above. Again, we have that $F_1$ satisfies the clean specialization property.
• s is a project stage \( \rho_{p,q/d} \). Then, \( \text{subq}_1(q_1) = \rho_{\text{subq}_2, \text{actRel}, \text{rel}_1._id, \text{rel}_1.p, \text{rel}_1.q}\). It is easy to see that (clean) and (other) are satisfied. As for (own), the trees with \( \text{actRel} = 1 \) will keep the paths \( \text{rel}_1._id, \text{rel}_1.q \) and the value of the path \( \text{rel}_1.p \) will be defined by \( d \). Hence, (own) also holds.

• s is a group stage \( \gamma_{y/\alpha/b} \). Then \( \text{subq}_1(q_1) = \gamma_{\text{rel}_1.g/\text{rel}_1.y, \text{actRel}_{\text{rel}_1.a/\text{rel}_1.b, \text{rel}_2} \)

\[
\rho_{\text{rel}_2, \text{actRel}._id, \text{actRel} \_id, \text{rel}_1.a, \text{rel}_1._id, g/\_id, \text{rel}_1.g} \\
\rho_{\text{actRel} \_id, \{\text{rel}_i/\text{rel}_i/\text{dummy}\}} \_id, 1, 2 \supset \omega_{\text{rel}_2}
\]

The result of the first stage is \( n + 1 \) trees where
- one tree originates from all trees with \( \text{actRel} = 2 \), the value of \( \text{rel}_2 \) is the array of all such \( \text{rel}_2 \) and \( \text{rel}_1.a \) is an empty array.
- \( n \) is the number of different values \( v_1, \ldots, v_n \) of \( \text{rel}_1.g \) in all trees with \( \text{actRel} = 1 \), and each of the \( n \) trees originates from a subset of the trees with \( \text{actRel} = 1 \) and \( \text{rel}_1.g' = v_i \), the value of \( \text{rel}_2 \) is the empty array, the value of \( \text{rel}_1.a \) is all \( \text{rel}_1.a' \) in this subset of trees, and the value of \( \text{rel}_1.g \) is \( v_i \).

The result of the second stage is \( n + 1 \) trees where some paths in \_id are renamed. The result of the third stage is a forest satisfying the clean specialization property. In the forth stage, the array \( \text{rel}_2 \) is unwound, hence the trees with \( \text{actRel} = 2 \) are brought in the original shape. It is easy to see that all properties are satisfied.

Since the translation is symmetric, we have also that \( F_2 = F_1 \supset \text{subq}_2(q_2) \) satisfies the corresponding properties (clean), (own) and (other). \( \square \)

**Theorem 5.9** Let \( Q \) be a NRA query over \( C \). Then \( C \supset \text{nra2mq}(Q) \equiv_{S} Q \).

**Proof.** Follows from the definition of \( \text{rschema}_{\_}(C) \), Lemma 3.1 and the semantics of MQuery stages. \( \square \)

### D. COMPLEXITY OF MQUERY

**Theorem 6.1** \( \mathcal{M}_{\text{UPG}} \) and \( \mathcal{M}_{\text{MPG}} \) are \( \text{TA}[2^n, n^0] \)-hard in complexity and in \( \text{EXPSPACE} \) in combined complexity and in \( \text{AC}^0 \) in data complexity.

**Lemma D.1.** \( \mathcal{M}_{\text{MPG}} \) is \( \text{TA}[2^n, n^0] \)-hard in combined complexity.

**Proof.** We adapt the proof of \( \text{TA}[2^n, n^0] \)-hardness from [16].

Let \( M = (\Sigma, Q, \delta, q_0, F) \) be an alternating Turing machine that runs in time \( 2^{p_1(n)} \) with \( p_2(n) \) alternations on inputs of size \( n \), where \( \Sigma \) the tape alphabet, \( Q \) is the set of states partitioned into existential \( Q_2 \) and universal \( Q_\gamma \) states, \( \delta : Q \times \Sigma \times \{1, 2\} \rightarrow Q \times \Sigma \times \{-1, 0, +1\} \) the transition function, which for a state \( q \) and symbol \( s \) gives two instructions \( \delta(q, s, 1) \) and \( \delta(q, s, 2) \), \( q_0 \) the initial state and \( F = \cup Q \) the set of accepting states.

Following Koch, we simulate the computation of \( M \) in \( \mathcal{M}_{\text{MPG}} \). Each run of \( M \) is a tree of configurations of depth bounded by \( p_2(n) \cdot 2^{p_1(n)} \), and each configuration consists of a tape of length bounded by \( 2^{p_1(n)} \), a current state and a position marker on the tape. We construct an \( \mathcal{M}_{\text{MPG}} \) \( q \) and a forest \( F \) such that \( F \supset q \) is non-empty iff \( M \) accepts its input. \( F \) consists of a single document containing the key-value pair \_id \_id: 1.

- The tape of a configuration is modeled as a nested object of nested depth \( p_1(n) \) and with \( 2^{p_1(n)} \) leaves. The position of the head on the tape is represented by an extended tape alphabet \( \Sigma' = \Sigma \cup \{ \# \mid s \in \Sigma \} \). That is, the symbol \( s \) in a tape cell indicates that the cell stores symbol \( s \) and it is the current position of the head. The following is a valid tape:

\[
\text{"tape"}: \{ \#1^1, \#0^0, \#s^\sigma, \#x^\tau \}, \#1^1: \{ \#1, \#\#, \#x, \#\# \}.
\]

We can compute the set of all \( m^{p_1(n)} \) tapes (including non-valid ones) by the query:

\[
\text{Tapes} = \rho_{\text{tape} / |\Sigma'|} \supset \rho_{\text{tape}, r/tape} \supset \omega_1 \supset \omega_r \supset \rho_{\text{tape}, l/tape, r/r} \supset \gamma_{\text{tape}} \supset \ldots \supset \rho_{\text{tape}, tape, r/r} \supset \omega_1 \supset \omega_r \supset \rho_{\text{tape}, l/tape, r/r} \supset \gamma_{\text{tape}} \supset \rho_{\text{tape}, state / |\Sigma|} \supset \omega_{\text{tape}} \supset \omega_{\text{state}} \supset \rho_{\text{c.tape/tape}, c.state/state}
\]

Where for a set \( S \), the value definition \( [S] \) means a constant array consisting of all elements in \( S \) (we view everything as strings). The result of this query (on \( F \)) is a single document containing an array of all possible tapes under the key \_tape.

- In turn, a configuration is a pair, consisting of a tape and a state. We can compute all possible (including non-valid ones) configurations by the following \( \mathcal{M}_{\text{MPG}} \):

\[
\text{Configs} = \text{Tapes} \supset \rho_{\text{tape}, state / |\Sigma|} \supset \omega_{\text{tape}} \supset \omega_{\text{state}} \supset \rho_{\text{c.tape/tape}, c.state/state}
\]

The result of \( \text{Configs} \) is a set of trees, each containing one possible configuration under the key \_c.
Next, we are going to construct a query that computes the pairs of configurations $c_1$ and $c_2$ such that $c_2$ is a possible immediate successor of $c_1$ according to $\delta$ (also including pairs of non-valid configurations). First, we create all pairs of configurations $c_1$ and $c_2$, and make working copies $w_1$ and $w_2$ of the tapes.

\[
\text{Prepare-succ} = \text{Configs} \triangleright \gamma_{c_1/c, c_2/c} \triangleright \omega_{c_1} \triangleright \omega_{c_2} \triangleright \rho_{\text{succ}/\{c_1/c, c_2/c\}}, w_1/c, \text{tape}, w_2/c, \text{tape}
\]

Second, to check that $c_1$ is a possible successor of $c_2$, we verify that $w_1$ and $w_2$ differ at at most two consecutive tape positions. The tapes are of exponential length, but we can find these two positions by doing a number of checks that is equal to the depth of the value encoding a tape minus 1. Namely, we iteratively compare the halves of the working copies, and in the next step the working copies become the halves which are not equal (see [16] for more details):

- If $w_1.l = w_2.l$ (the left halves of the tapes are equal), we replace $w_1$ by $w_1.r$ and $w_2$ by $w_2.r$.
- If $w_1.r = w_2.r$ (the right halves of the tapes are equal), we replace $w_1$ by $w_1.l$ and $w_2$ by $w_2.l$.
- If $w_1.l \neq w_2.l$ and $w_1.r \neq w_2.r$ (the left and the right quarters of the tapes are equal), the difference should be in the “inner” part of the tree), we replace $w_1.l$ by $w_1.l.r$, $w_1.r$ by $w_1.r.l$ and $w_2.l$ by $w_2.l.r$, $w_2.r$ by $w_2.r.l$.

We implement zoom-in by the query:

\[
\text{Zoom-in} = \rho_{\text{succ}, w_1/((w_1.l=w_2.l)\land w_1.r=(w_1.r=w_2.r))\land ((w_1.1.l\neq w_2.1.l)\lor (w_1.1.r\neq w_2.1.r))}\triangleright \rho_{\text{succ}/\{c_1/c, c_2/c\}}, w_1/c, \text{tape}
\]

After finding the two positions where the tapes differ, we check that the head is over one of these positions.

\[
\text{Head} = \mu_{\forall \in \Sigma}(w_1.l=\hat{z}) \lor (w_1.r=\hat{z})
\]

Then, we check that the difference is according to the transition function $\delta$. Let criterion $\varphi_{\delta}$ be the disjunction of the following formulas $\varphi_{q,s,q',z,l}$, for each instruction $\delta(q,s,i) = (q',s,z,l)$:

- $\varphi_{q,s,q',z,l} = (\text{succ.c.1.state} = q) \land (\text{succ.c.2.state} = q') \land ((w_1.l = \hat{s}) \land (w_2.l = \hat{z}) \lor \bigvee_{b \in \Sigma}(w_1.r = b) \land (w_2.r = b)) \lor (w_1.r = \hat{s}) \land (w_2.r = \hat{z}) \lor \bigvee_{b \in \Sigma}(w_1.l = b) \land (w_2.l = b))$
- $\varphi_{q,s,q',z,l+1} = (\text{succ.c.1.state} = q) \land (\text{succ.c.2.state} = q') \land ((w_1.l = \hat{s}) \land (w_2.l = \hat{z}) \lor \bigvee_{b \in \Sigma}(w_1.r = b) \land (w_2.r = b)) \lor (w_1.r = \hat{s}) \land (w_2.r = \hat{z}) \lor \bigvee_{b \in \Sigma}(w_1.l = b) \land (w_2.l = b))$
- $\varphi_{q,s,q',z,l-1} = (\text{succ.c.1.state} = q) \land (\text{succ.c.2.state} = q') \land ((w_1.l = \hat{s}) \land (w_2.l = \hat{z}) \lor \bigvee_{b \in \Sigma}(w_1.r = b) \land (w_2.r = b)) \lor (w_1.r = \hat{s}) \land (w_2.r = \hat{z}) \lor \bigvee_{b \in \Sigma}(w_1.l = b) \land (w_2.l = b))$

Finally, the query Succ that computes pairs of successor configurations is:

\[
\text{Succ} = \text{Prepare-succ} \triangleright \text{Zoom-in} \triangleright \cdots \triangleright \text{Zoom-in} \triangleright \text{Head} \triangleright \mu_{\varphi_{\delta}} \triangleright \rho_{\text{succ}}
\]

To encode alternations, we first need to compute computation paths of length up to $2^{p_1(n)}$ that we represent by pairs $(c_1, c_2)$: $c_2$ is reachable from $c_1$ in at most $2^{p_1(n)}$ steps, moreover if the state of $c_1$ is existential, then each of the intermediate configurations before reaching $c_2$ must be existential, and likewise if the state of $c_1$ is universal. We implement “at most” by means of the “stay transitions” $(c, c)$ added to Succ. We compute these computation paths iteratively:

- $\text{CP}_0 = \text{Succ}$
- $\text{CP}_{i+1} = \text{CP}_i \triangleright \gamma_{s_1/\text{succ}, s_2/\text{succ}} \triangleright \omega_{s_1} \triangleright \omega_{s_2} \triangleright \mu_{s.1.c.2.e/c.2.s.1} \triangleright \mu_{s.1.c.1.e/c.2.s.2} \triangleright \rho_{\text{succ}/\{c_1/c, c_2/c, s_2/c\}}$

where $(p \in A)$, for a set $A$, is a shortcut for $\forall a \in A(p = a)$, and $\varphi_1 \iff \varphi_2$ is a shortcut for $(\neg \varphi_1 \lor \varphi_2) \land (\neg \varphi_2 \lor \varphi_1)$.

We can now compute the states $A_i$ of configurations that lead to an accepting state in $i$ alternations:

\[
A_1 = \text{CP}_{p_1(n)} \triangleright \gamma_{\text{cp}/\text{succ}} \triangleright \rho_{\text{cp.s/cp}} \triangleright \omega_{s} \triangleright \mu_{s.1.c.2.e/c.2.s.1} \triangleright \rho_{\text{cp.s.1.c.1.e/c.2.s.2}} \triangleright \gamma_{\text{cp.s.1.c.1.e/c.2.s.2}} \triangleright \rho_{\text{cp.s.1.c.1.e/c.2.s.2}} \triangleright \gamma_{\text{cp.s.1.c.1.e/c.2.s.2}} \triangleright \rho_{\text{cp.s.1.c.1.e/c.2.s.2}} \triangleright \gamma_{\text{cp.s.1.c.1.e/c.2.s.2}} \triangleright \rho_{\text{cp.s.1.c.1.e/c.2.s.2}}
\]

Finally, we check that the initial computation is in $A_{p_2(n)}$. The initial configuration has a tape, where the input string $w$ of length $n$ is padded with $2^{p_1(n)} - n$ #-symbols. Let $w_u$ be the nested value of depth $\lceil \log_2 n \rceil$ representing $w$ padded with $2^{\lceil \log_2 n \rceil} - n$ #-symbols (it can be computed in LOGSPACE). Then the initial configuration can be computed, and checked whether in $A_{p_2(n)}$ as follows:

\[
C_0 \text{in } A_{p_2(n)} = \rho_{a, \text{tape.l}, \text{tape.r}/w_u, \text{tape.r}/w_u} \triangleright \rho_{a, \text{tape.l}, \text{tape.r}/\{1/\text{tape.r}/r/\text{tape.r}\}} \triangleright \cdots \triangleright \rho_{a, \text{tape.l}, \text{tape.r}/\{1/\text{tape.r}/r/\text{tape.r}\}} \triangleright \rho_{a, c.0.\text{tape.c.0.state}/w_u} \triangleright \rho_{a, c.0.\text{tape.c.0.state}/w_u} \triangleright \rho_{a, c.0.\text{tape.c.0.state}/w_u}
\]

\[
\omega_u \triangleright \rho_{u=c_0}
\]
Thus we obtain that \( \{ \text{tree}([\{ _id: 1 \}] ) \} \rightarrow C_0 \in A_{p_1(n)} \) is non-empty iff \( M \) accepts \( w \). 

\textbf{LEMMA D.2}. \( \mathcal{M}^{\text{MUPGL}} \) is in \( \text{TA}[2^{nO(1)}, nO(1)] \) in combined complexity.

\textbf{Proof}. Let \( q = C \triangleright s_1 \cdots \triangleright s_n \) be an \( \mathcal{M}^{\text{MUPGL}} \) query, and \( D \) a MongoDB instance. We provide an algorithm to check that \( \text{ans}_\text{mo}(q, D) \) is non-empty.

We assume that \( q \) is of the following form:

\begin{itemize}
  \item we consider atoms of the form \( p = v, p \neq v, p = p, p \neq p, \exists p, \lnot \exists p \), and assume that the criteria in match stages, Boolean value definitions and conditions in conditional value definitions are monotone Boolean expressions over such atoms (i.e., use only conjunction and disjunction). To make sure that the atomic expressions in such value definitions are of this form, we replace atomic expressions \( p \), for a path \( p \), with \( \exists p \land (p \neq \text{null}) \land (p \neq \text{false}) \land (p \neq 0) \), and get rid of the “constant” expressions of the form \( v \) for a value \( v \), and \([d_1, \ldots, d_k]\) as follows. First, replace the former with \text{true} when \( v \neq \text{null} \), \( v \neq \text{false} \) and \( v \neq 0 \), and with \text{false} otherwise, and replace the latter by \text{true}. Second, simplify the Boolean combinations with \text{true} and \text{false} in the standard way (e.g., \text{true} \lor \text{false} becomes \text{true}, and \text{true} \land \text{false} becomes \text{false}), and simplify conditional value definitions that have \text{true} or \text{false} as the condition in the obvious way.
  
  \item each project stage is of the form \( p^\omega_{m_1} \cdots p^\omega_{m_p}, q/d \), that is, contains at most one projection element defining the value of a path \( q \). We can achieve it for an arbitrary project stage \( p^\omega_{m_1} \cdots p^\omega_{m_p}, q/d_1 \ldots q/d_m \) by splitting it into \( m \) project stages:

\[
\rho^\omega_{m_1} \cdots p^\omega_{m_p}, q/d_1 \triangleright p^\omega_{m_1} \cdots p^\omega_{m_p}, q/d_1 \triangleright \cdots \triangleright p^\omega_{m_1} \cdots p^\omega_{m_p}, q/d_1 \cdots q/d_m.
\]

Let \( \text{ans}_\text{mo}(q, D) = F_n \). The algorithm is to check whether there is a tree in \( F_n \). We do it recursively as follows. Assume that \( F_d = F' \) and we want check whether a tree satisfying a set \( \psi \) of atoms (of the considered form) is in \( F' \). Then, the check amounts to the following:

\begin{itemize}
  \item if \( s = \mu_p \), then we guess atoms \( e_1, \ldots, e_m \) appearing in \( \varphi \) so that assigning them the true value makes \( \varphi \) true, add to \( \psi \) the conditions \( e_1, \ldots, e_m \). If the new conditions \( \psi' \) are consistent, we check whether there is a tree satisfying \( \psi' \) in \( F \). Otherwise, we report a failure.
  
  \item if \( s = \omega_\varphi \), then we replace \( \rho_q \) by \( p, i \) in all conditions in \( \psi \) about \( p \) and check whether there is a tree with the new conditions \( \psi' \) in \( F' \).
  
  \item if \( s = \omega^+ \), then we guess whether with or without index, and in the former case we replace \( p \) by \( p, i \) in all conditions in \( \psi \) about \( p \), in the latter \( \psi \) is not changed. Then we check whether there is a tree with the new conditions \( \psi' \) in \( F' \).
  
  \item if \( s = \rho^\omega_{m_1} \cdots p^\omega_{m_p}, q/d \), we do not do anything for \( p_i \). As for \( q/d \), we remove \( \exists q \) if it is in \( \psi \), and proceed as follows:

\begin{enumerate}
  \item if \( d \) is a path \( q' \), we replace each occurrence of \( q \) in \( \psi \) by \( q' \).
  
  \item if \( d \) is a constant non-array value,

\begin{enumerate}
    \item if there is a condition of the form \( q = v \) in \( \psi \), we remove it from \( \psi \), check whether \( v = d \), and if not, we report failure.
  
    \item if there is a condition of the form \( q \neq v \) in \( \psi \), we remove it from \( \psi \), check whether \( v \neq d \), and if not, we report failure.
  
    \item if there is a condition of the form \( q' = v' \) in \( \psi \), for a prefix \( p' \) of \( q \), we extract the value \( v \) for \( p \) (it will be the value of the subtree in \( v \) reachable by path \( q' \) such that \( p'.q' = q \)) if it is possible and proceed as in (a), otherwise we report a failure.
  
    \item if there is a condition of the form \( q.p' = v' \) or \( q.p' \neq v' \) in \( \psi \), we extract the value definition \( d' \) from \( d \) reachable by path \( p' \) if it is possible and proceed as in the case \( q.p'/d' \), otherwise we report a failure.
  
    \item if there is a condition of the form \( q.i = v' \) in \( \psi \), we report a failure.
\end{enumerate}

3. if \( d \) is a Boolean value definition

\begin{enumerate}
  \item if there is a condition of the form \( q = v \) (resp., \( q \neq v \)) in \( \psi \), we remove it from \( \psi \). Then we check whether \( v \) is \text{true} or \text{false}, if not, we report failure. Otherwise, we guess atoms \( e_1, \ldots, e_n \) appearing in \( d \) so that \( d \) evaluates to \( v \) (resp., to the negation of \( v \)) under assigning the atoms \( e_i \) the true value, and add to \( \psi \) the conditions \( e_1, \ldots, e_n \).
  
    \item analogous to 2.(c)
  
    \item analogous to 2.(d)
  
    \item analogous to 2.(e)
\end{enumerate}

4. if \( d = [d_1, \ldots, d_k] \),
\end{itemize}

\]
Once we reach the first stage, then we directly check whether there is a tree in $D.C.$ bounded by the size of $L$. We add conditions $\gamma_1/y_1,\ldots,y_m/a_1/b_1,\ldots,a_n/b_n$. We replace all conditions of the form $\gamma_i.a_i = v$ in $\psi$ by $y_i = v$. For each $a_j/b_j$ by analogy with group by $null$, where also need to take into account conditions on $\gamma_i.a_i$.

If there is a condition of the form $q = v$ in $\psi$, we remove it from $\psi$, check whether $v$ is of the form $[v_1,\ldots,v_k]$, if not, we report failure. Otherwise we guess the pairs $(d_i,v_j)$, and for each pair $(d_i,v_j)$ we break it down and proceed similarly the case as if we had $q'/d_i$ and a condition $q' = v_j$ in $\psi$.

If there is a condition of the form $q' = v'$ in $\psi$, we remove it from $\psi$, check whether $v' = d$, and if not, we report failure.

If there is a condition of the form $p' = v'$ in $\psi$, for a prefix $p'$ of $q$, we extract the value $v$ for $p$ (it will be the value of the subtree in $v$ reachable by path $q'$ such that $p'.q' = q$) if it is possible and proceed as in (a), otherwise we report a failure.

If there is a condition of the form $q.p = v'$ or $q.p' = v'$ in $\psi$, we guess $d_i$, extract the value definition $d'$ from $d_i$ reachable by path $p'$ if it is possible and proceed as in the case $q.p'/d'$, otherwise we report a failure.

If there is a condition of the form $q,i = v'$ in $\psi$, we guess $d_i$ and proceed similarly to the case as if we had $q'/d_i$ and a condition $q' = v'$ in $\psi$.

If $D$ is a conditional value definition $(?d_1;d_2)$, we guess atoms $e_1,\ldots,e_n$ appearing in $c$ so that $\psi \cup \{e_1,\ldots,e_n\}$ is consistent, and if $c$ evaluates to true under assigning the atoms $e_i$ the true value, then we consider the inductive case when $d = d_1$, otherwise when $d = d_2$. In any case, we add to $\psi$ the conditions $e_i$.

Then we check whether the new conditions $\psi'$ are consistent. If not, we report failure. Otherwise we check whether there is a tree satisfying $\psi'$ in $F$.

- $s = \gamma_{a_1/b_1} \ldots a_n/b_n$. If there is a condition $\cdot i.a \neq \text{null}$ in $\psi$, we report failure. Otherwise, we remove all conditions on $\cdot i.a$ from $\psi$, and for each $a_j/b_j$ we proceed as follows:
  - if $\psi$ contains a condition of the form $a_j = \emptyset$, then we check that there is no tree satisfying $\exists b_j$ in $F$.
  - if $\psi$ contains a condition of the form $a_j = \{v_1,\ldots,v_k\}$, $k > 0$, then for each $i = 1,\ldots,k$, we check whether each tree in $F$ satisfies $b_j \in \{v_1,\ldots,v_k\}$.
  - if $\psi$ contains a condition of the form $a_j = \{v_1,\ldots,v_k\}$, $k > 0$, then we guess either “subset” or “superset”, in the former case we guess a subset $\{v_1,\ldots,v_m\}$ of $\{v_1,\ldots,v_k\}$ and check whether each tree in $F$ satisfies $b_j \in \{v_1,\ldots,v_m\}$ if $m > 0$, or whether each tree in $F$ satisfies $\exists b_j$ if $m = 0$; in the latter case we check whether there is a tree satisfying $\{b_j \neq v_1,\ldots,b_j \neq v_k\}$ in $F$.
  - if $\psi$ contains a condition of the form $a_j = v$ for a non-array value, then we report failure.
  - if $\psi$ contains a condition of the form $a_j,i = v$, then we replace it by $b_j = v$ and check whether there is a tree with the new conditions $\psi'$ in $F$.
  - if $\psi$ contains a condition $\exists a_j$, then it is satisfied and can be removed. We check whether there is a tree in $F$.

- $s = \lambda_{p_1=C_2,p_2}$. We replace all conditions of the form $\cdot i.a.g_i = v$ in $\psi$ by $y_i = v$. For each $a_j/b_j$ by analogy with group by $null$, where also need to take into account conditions on $\cdot i.a.g_i$.

Once we reach the first stage, then we directly check whether there is a tree in $D.C.$ satisfying the conditions, or whether all trees in $D.C.$ satisfy the conditions.

By analysing how we deal with various stages, we can see that both branching and alternations occur only because of the group stages. The overall algorithm works in alternating exponential time with a polynomial (actually, linear) number of alternations: the “depth” of the checks is given by the number of stages, the branching and the number of alternations are bounded by the size of $q$.

**Lemma 6.2.** Boolean query evaluation for $\mathcal{M}^q$ queries is LOGSPACE-complete in combined complexity.
Proof. First, we prove the upper bound. Let $D$ be a MongoDB database, and $q$ an $\mathcal{M}^q$ query of the form $C \triangleright \mu_\varphi$, where $\varphi$ is a criterion. We can view $\varphi$ as a Boolean formula constructed using the connectors $\land$, $\lor$ and $\neg$ starting from the atoms of the form $(p \text{ op } v)$ and $\exists p$, where $p$ is a path, $v$ a literal value, and $\text{ op }$ is a comparison operator. Given a tree $t$ and an atom $\alpha$ of the above form, we can check in LogSpace whether $t \models \alpha$: for each node $x$ in $t$, we can check in LogSpace if $\text{ path } (x, t) = p$ and we can check in LogSpace if $L_n(x) = v$.

Now, we define a LogSpace reduction from the problem of whether $\text{ ans}_{\mathcal{M}^q}(q, D) \neq \emptyset$ to the problem of determining the truth value of a variable-free Boolean formula, known to be ALogTIME-complete [6]. We construct a Boolean formula $\psi$ as the disjunction of $\varphi_t$ for each $t \in D, C$, where $\varphi_t$ is a copy of $\varphi$, where each atom $\alpha$ is substituted with $1$ if $t \models \alpha$ and with $0$, otherwise. Then $\text{ ans}_{\mathcal{M}^q}(q, D) \neq \emptyset$ if and only if the value of $\psi$ is true.

We show the lower bound by NC$^1$ reduction from the directed forest accessibility (DFA) problem known to be complete for LogSpace under NC$^1$ reducibility [11]. The DFA problem is, given an acyclic directed graph $G$ of outdegree zero or one, nodes $u$ and $v$, to decide whether there is a directed path from $u$ to $v$.

Let $G = (V, T)$, $u, v \in V$ such that $G$ has precisely two weakly connected components, $u$ has indegree $0$ and $v$ has outdegree $0$: the lower bound still holds in this case. Let $v'$ be the other vertex in $G$ with outdegree $0$. We construct a tree $t = (N, E, L_n, L_e)$ and a path $p$ such that $t \models (\exists p)$ if there is a directed path from $u$ to $v$ in $G$. We add a fresh node $r$ that will be the root of the tree with two children $v$ and $v'$, and a fresh node $l$ that will be the only child of $u$, also we invert all edges in $G$: $N = V \cup \{r, l\}$, $E = T^- \cup \{(r, v), (v, v'), (u, l)\}$. Then we set $L_n(r, v) = a$, $L_n(r, v') = c$, $L_e(u, l) = b$, and the rest of the edges is labeled by index $0$. The node labels are set as $L_n(r) = \{\text{ }\}$, $L_n(u) = \{\text{ }\}$ and the rest of the nodes are labeled with $\{\text{ }\}$.

Now, the obtained tree $t$ is not a valid tree according to our definition of a tree, as the children of array nodes are not labeled by distinct indexes. However, by inspecting the semantics of $[p]$, we see that $t \models (\exists p)$ if $t' \models (\exists p)$, where $t'$ is the version of $t$ with all distinct indexes. Thus, we obtain that $t \models (\exists \alpha b)$ iff there is a directed path from $u$ to $v$ in $G$. $\square$

The project operator allows one to create new values by duplicating the existing ones; hence, it can make trees grow exponentially in the size of the query, and similarly with the group operator. Nevertheless, we can still check whether the answer to a query is non-empty in polynomial time by reusing the "old" tree nodes when it is necessary to duplicate values.

Lemmas 6.3. Query evaluation for $\mathcal{M}^{\text{MPGL}}$ queries is PTIME-complete.

Lemmas D.3. The query emptiness problem for $\mathcal{M}^p$ queries is PTIME-hard in combined complexity.

Proof. The proof by a straightforward reduction from the Circuit Value problem, known to be PTIME-complete. For completeness, we provide the reduction. Given a monotone Boolean circuit $C$ consisting of a finite set of assignments to Boolean variables $X_1, \ldots, X_n$, of the form $X_i = 0$, $X_i = 1$, $X_i = X_j \land X_k$, $j, k < i$, or $X_i = X_j \lor X_k$, $j, k < i$, where each $X_i$ appears on the left-hand side of exactly one assignment, check whether the value $X_n$ is $1$ in $C$.

We construct a query $q$ such that on each non-empty forest $F$, $F \triangleright q$ is non-empty iff the value $X_n$ is $1$ in $C$. We set $q = s_1 \triangleright \cdots \triangleright s_n \triangleright \mu_{X_n=1}$, where for $i \in \{1, \ldots, n\}$, $s_i = \rho_{x_1, \ldots, x_i-1, x_i/\text{ass}_i}$, where $\text{ass}_i = v$, if $X_i = v$ for $v \in \{0, 1\}$, $\text{ass}_i = x_j \land x_k$, if $X_i = X_j \land X_k$, and $\text{ass}_i = x_j \lor x_k$, if $X_i = X_j \lor X_k$. $\square$

Lemmas D.4. The query emptiness problem for $\mathcal{M}^{\text{MPGL}}$ queries is in PTIME in combined complexity.

Proof. We provide a PTIME algorithm for checking whether, given an $\mathcal{M}^{\text{MPGL}}$ query (over collection $C$), a forest $F_0$ for $C$, and forests $G_C$, for each external collection $C'$ used by $q$, $F_0 \triangleright q$ is non-empty.

The algorithm computes the result of each stage by representing the intermediate trees as DAGs in order to avoid exponential growth of trees that is possible due to multiple duplication of existing values. Suppose that $q = s_1 \triangleright \cdots \triangleright s_m$. Then we compute $F_1, \ldots, F_m$, where each $F_i$ is a set of DAGs, and we can obtain from $F_i$ the forest $F_0 \triangleright s_1 \triangleright \cdots \triangleright s_i$ by "unravelling" each DAG into a proper tree.

We are going to consider connected DAGs with labeled nodes and edges and that have only one source node, that is, one node that has no incoming edges. Similarly to trees, a DAG is a tuple $(N, E, L_n, L_e)$, where $N$ is a set of nodes, $E$ is a successor relation, $L_n : N \rightarrow V \cup \{\text{ }\}$ is a node labeling function, and $L_e : E \rightarrow K \cup I$ is an edge labeling function such that (i) $(N, E)$ forms a DAG with a single node that has no incoming edges, (ii) a node labeled by a literal must be a node without outgoing edges, (iii) all outgoing edges of a node labeled by $\{\text{ }\}$ must be labeled by keys, and (iv) all outgoing edges of a node must be labeled by distinct indexes. Clearly, a tree is a connected DAG with a single source node. We denote the source node of a DAG $t$ by $\text{ root}(t)$. For a DAG $t$, the path type $\text{ type}(p, t)$, the interpretation of path $[p]$, satisfaction of criteria $t \models \varphi$ and value definitions $d \models d$ is defined in the same way as for trees.

First, we show, given a set $F$ of DAGs and a stage $s$, how to compute the set $F'$ of DAGs resulting from evaluating $s$ over $F$.

- Suppose $s$ is a match stage $\mu_\varphi$. Then $F' = \{ t \mid t \in F \text{ and } t \models \varphi \}$. Clearly, $F' \subseteq F$, hence is linear in $F$ and $s$.
- Suppose $s$ is a project stage $\rho_{p_1, \ldots, p_m, q_1/d_1, \ldots, q_n/d_n}$. Let $t \in F$ be a DAG. We show how to transform it into a DAG $t'$ according to $s$. Initially, $t'$ contains one fresh node $r$ with $L_n(r) = \{\text{ }\}$. Then, for each $i \in \{1, \ldots, n\}$, we do the following changes to $t'$. Suppose $q_i = k_1 \cdots k_l$, we first insert into $t'$ fresh nodes $x_1, \ldots, x_{l-1}$ and edges $(x_j, x_{j+1})$ with $L_e(x_j, x_{j+1}) = k_j$, $L_n(x_j) = \{\text{ }\}$ for $x \in \{x_1, \ldots, x_{l-1}\}$. Note that here, if $l = 1$, $x_{l-1}$ refers to $r$. Then, by induction on the structure of $d$, we proceed as follows:
(a) $d_i$ is a literal value $v$: we insert a fresh node $x_i$ and an edge $(x_{i-1}, x_i)$ with $L_e(x_{i-1}, x_i) = k_i$ and $L_n(x_i) = v$.

(b) $d_i$ is a path reference $p$. If $[p] = \emptyset$, we remove from $t'$ all nodes $x_1, \ldots, x_{i-1}$ (and edges) inserted previously. If $[p] = \{\} = 1$, let $x_p \in [p]$: we add to $t'$ the node $x_p$ and its label, an edge $(x_{i-1}, x_p)$ with $L_e(x_{i-1}, x_p) = k_i$, and copy all other nodes (hence the edges and labels) reachable from $x_p$ in $t$. Otherwise let $[p] = \{y_1, \ldots, y_m\}$: we insert into $t'$ a fresh node $x_i$ with $L_n(x_i) = \{\}$, edges $(x_{i-1}, x_i), (x_i, y_1), \ldots, (x_i, y_m)$, with $L_e(x_{i-1}, x_i) = k_i$ and $L_n(x_i, y) = j - 1$ and copy all other nodes (and edges and labels) reachable from $y_j$ in $t$.

(c) If $d_i$ is a Boolean value definition, let $v_i$ be the Boolean value of $t \models d_i$. We proceed as in the case $d_i$ is a literal value $v_i$.

(d) If $d_i$ is a conditional value definition $(d_i ? e_1 : e_2)$, then whenever $t \models d_i$, we proceed as in the case $d_i$ is $e_1$, otherwise as in the case $d_i$ is $e_2$.

(e) If $d_i$ is an array definition $[e_1, \ldots, e_m]$, then we insert into $t'$ a fresh node $x_i$ with $L_n(x_i) = \{\}$ and an edge $(x_{i-1}, x_i)$ with $L_e(x_{i-1}, x_i) = k_i$. Further, for each $e_j$, let $y_i$ be the node defined according to the structure of $e_j$ and the cases above (e.g., if $e_j$ is a literal value, then $y_i$ is a fresh node, and of $e_j$ is a path reference, it is an already existing in $t$ node). We add an edge $(x_i, y_i)$ with $L_e(x_i, y_i) = j - 1$. Note that if $e_j$ is a path reference and this path does not exist in $t$, then it is equivalent to $e_j$ being null.

Thus, we have constructed the DAG $t'$ with a single source node. The size of $t'$ has grown at most linearly in the size of $t$ and $s$. In the resulting set $F'$, each DAG is obtained from exactly one DAG in $F$.

- Suppose $s$ is a group stage $\gamma_{g_1} \cdot \ldots \cdot \gamma_{g_n} / y_n \cdot y_{n+1} / b_1 \cdot \ldots \cdot b_m$. If $n > 1$, let $F_1$ be a subset of $F$ such that

(1) there exist indexes $i_1, \ldots, i_k$, $k \leq n$, and values $\gamma_{g_1}, \ldots, \gamma_{g_k}$ such that for each DAG $t \in F_1$ the following holds: $t \models (\exists y_i)$ and $t \models (y_i \equiv v_i)$ for $i \in \{i_1, \ldots, i_k\}$ and $t \models \neg (\exists y_i)$ for $i \in \{1, \ldots, n\} \setminus \{i_1, \ldots, i_k\}$.

We show how to transform $F_1$ into a DAG $t'_{F_1}$. Initially, $t'_{F_1}$ contains two fresh nodes $r$ and $x_0$ with $L_n(r) = L_n(x_0) = \{\}$, and an edge $(r, x_0)$ with $L_e(r, x_0) = \_id$. We now show how $t'_{F_1}$ is built.

First, for each $i \in \{i_1, \ldots, i_k\}$, we proceed as follows. Fix a tree $t \in F_1$. Suppose $g_i = k_1 \cdot \ldots \cdot k_i$, we insert into $t_{F_1}$ fresh nodes $x_1, \ldots, x_{l_i-1}$ with $L_n(x) = \{\}$ for $x \in \{x_1, \ldots, x_{l_i-1}\}$, and edges $(x_j, x_{j+1})$ with $L_e(x_j, x_{j+1}) = k_i$. We proceed as above (hence the edges and labels reachable from $x_{l_i}$ in $t$). Otherwise let $[y_i] = \{z_1, \ldots, z_l\}$: we insert into $t_{F_1}$ a fresh node $x_i$ with $L_n(x_i) = \{1\}$ and edges $(x_{i-1}, x_i), (x_i, z_1), \ldots, (x_i, z_l)$, with $L_e(x_{i-1}, x_i) = k_i$, and $L_n(x_i, z_j) = \_j - 1$, and copy all other nodes (hence the edges and labels) reachable from $z_j$ in $t$.

Second, for each $i \in \{1, \ldots, m\}$, we proceed as follows. We insert into $t_{F_1}$ a fresh node $x$ with $L_n(x) = \{1\}$ and an edge $(r, x)$ with $L_e(r, x) = \_a$. Now, for each DAG $t \in F_1$, we insert an element to the array rooted at $x$ as follows: if $[y_i] = \emptyset$, then we do not insert anything into $t_{F_1}$; if $[y_i] = \{1\}$, we add to $t_{F_1}$ an edge $(x, z)$ with $L_e(x, z)$ being the index of the new element, and copy all other nodes (hence the edges and labels) reachable from $z$ in $t$; otherwise we insert into $t_{F_1}$ a fresh node $z$ with $L_n(z) = \{1\}$ and edges $(x, z), (z, z_1), \ldots, (z, z_l)$ with $L_e(x, z)$ being the index of the new element, $L_e(z, z_j) = \_j - 1$, and copy all other nodes (hence the edges and labels) reachable from $z_j$ in $t$.

The resulting DAG $t'_{F_1}$ has the single source node $r$, and its size is linear in the size of $F_1$ and $s$. Let $F_1, \ldots, F_s$ be the partition of $F$ into subsets satisfying (1). Such a partition can be computed in time polynomial in $F$ and $s$: for each $t \in F$, we can determine its “partition” and then group the DAGs accordingly. Then $F'$ is obtained as $\{t_{F_1}, \ldots, t_{F_s}\}$, and its size is linear in the size of $F$ and $s$.

- Suppose $s$ is a lookup stage $\lambda_{\beta_1 \cdots \cdot \beta_s}$, and $G$ is the forest for $C$. Let $t \in F'$ with the source node $x_0$, we show how to transform it into a DAG $t'$ according to $s$. Initially $t'$ coincides with $t$. Suppose $p = k_1 \cdot \ldots \cdot k_i$, we insert into $t'$ fresh nodes $x_1, \ldots, x_l$ with $L_n(x_j) = \{1\}$ for $x \in \{x_1, \ldots, x_{l_i-1}\}$, $L_n(x) = \{1\}$, and edges $(x_j, x_{j+1})$ with $L_e(x_j, x_{j+1}) = k_j$. Let $v$ be the value of $p_1$ in $t$, that is $v = value(subtree(t, p_1))$, and let $G_1$ be the subset of $G$ such that value(subtree$(g, p_2)$) = $v$ for each $g \in G_1$. Now, for each $g \in G_1$, let $x_g$ be the root of $g$: we add to $t'$ an edge $(x_l, x_g)$ with $L_e(x_l, x_g)$ being the consecutive index, and copy the whole tree $g$ to $t'$.

The resulting DAG $t'$ is linear in the size of $F, G$ and $s$.

Now, we obtain that for a query $q = s_1 \cdot \ldots \cdot s_m$ and an input forest $F_0$, each set of DAGs $F_i$, $i \in \{1, \ldots, m\}$ computed from $F_{i-1}$ and $s_i$ is linear in the size of $F_{i-1}$ and $s_i$, therefore $F_m$ is polynomial in the size of $F_0$ and $q$. It should be clear that $F_0 \models q$ is non-empty iff $F_m$ is non-empty.

Next, we show that adding unwind causes the loss tractability, while project and lookup do not add complexity.

**Lemma 6.5.** Boolean query evaluation for $\mathcal{M}^{mu}$ and $\mathcal{M}^{mu,pl}$ queries is NP-complete in combined complexity.

**Proof.** We prove the lower bound by reduction from the Boolean satisfiability problem. Let $\varphi$ be a Boolean formula over $n$ variables $x_1, \ldots, x_n$. We fix a collection name $C$, and construct a collection $F$ for $C$ and an $\mathcal{M}^{mu}$ query $q$ such that $ans_{mu}(q, F)$ is non-empty iff $\varphi$ is satisfiable.
\( F \) contains a single document \( d \) of the form \( \{ "x1": [true, false], \ldots, "xn": [true, false] \} \), and \( q \) is the query:
\[
C \triangleright \omega_{x1} \triangleright \ldots \triangleright \omega_{xn} \triangleright \mu_{\varphi}, \text{ denoted } q_{\text{NP}}, \text{ where } \varphi \text{ can be viewed as a criterion.} \]

**Corollary D.6.** The query emptiness problem for \( \mathcal{M}^{\text{MUP}} \) queries is NP-hard in query complexity.

**Proof.** Since it is possible to use project to create copies of arrays, we can modify the above reduction so that \( F \) contains a single document of the form \( \{ "\text{values}": [true, false] \} \), and \( q = C \triangleright \rho_{x1}/\text{values}, \ldots, xn/\text{values} \triangleright q_{\text{NP}}. \]

**Corollary D.7.** The query emptiness problem for \( \mathcal{M}^{\text{MUL}} \) queries is NP-hard in query complexity.

**Proof.** Now, we can use lookup to create copies of arrays. In this case again, \( F \) contains two documents of the form \( \{ "\text{values}": \text{true} \} \) and \( \{ "\text{values}": \text{false} \} \). The query is as follows: \( q = C \triangleright \lambda_{x1}^{\text{dummy}=C, \text{dummy}} \triangleright \ldots \triangleright \lambda_{xn}^{\text{dummy}=C, \text{dummy}} \triangleright \omega_{x1} \triangleright \ldots \triangleright \omega_{xn} \triangleright \mu_{\varphi'}, \) where \( \varphi' \) is the variant of \( \varphi \) where each variable \( x \) is replaced by \( x.\text{values} \).

**Lemma D.8.** Boolean query evaluation for \( \mathcal{M}^{\text{MUL}} \) is in NP in combined complexity.

**Proof.** We modify the PTIME algorithm for \( \mathcal{M}^{\text{MUL}} \) as follows. Given an \( \mathcal{M}^{\text{MUL}} \) \( q \) (over collection \( C \)), a forest \( F_0 \) for \( C \), and forests \( G_{C'} \) for each external collection \( C' \) used by \( q \), we compute in non-deterministic polynomial time \( F_0 \triangleright q \) and check whether the result is empty or not.

We only show how to compute the set \( F' \) of DAGs resulting from evaluating an unwind stage \( s \) over a set \( F \) of DAGs.

- Suppose \( s = \omega_p \). Let \( t \in F \), we show how to transform it into \( F_1 \), which is either the empty set or a singleton set \( \{ t' \} \), for a DAG \( t' \). If \( p \) is first level array in \( t \), let \( \{ x_o \} = [p]^t \) and \( \{ x_1, \ldots, x_n \} \) all nodes such that \( (x_a, x_i) \) are edges in \( t \). If \( n = 0 \), then \( F_1 = \emptyset \). Otherwise, we guess \( k \in \{ 1, \ldots, n \} \) and \( F_1 = \{ t' \} \). Initially, the new DAG \( t' \) coincides with \( t \) but on the nodes reachable from \( x_o \). If \( L_a(x_b) = \ell \) in \( t \), then \( L_n(x_a) = \ell \) in \( t' \) and we add to \( t' \) the edges \( (x_a, y) \) such that \( (x_k, y) \) is in \( t \) and copy to \( t' \) all other nodes (hence the edges and labels) reachable from \( y \) in \( t \).

- Suppose \( s = \omega_p^+ \). The difference with the previous stage is that if \( n = 0 \), then \( F_1 = \{ t \} \).

\( F' \) is obtained as \( \bigcup_{t \in F} F_1 \). Clearly, \( F' \) is linear in the size of \( F \) and \( s \).

As a query contains a linear number of unwind stages, our algorithm requires to do a linear number of guesses (of polynomial size), and the whole computation runs in polynomial time.

To conclude, we also show that evaluation of \( \mathcal{M}^{\text{MUP}} \) queries with additional array operators \( \text{filter, map} \) and \( \text{setUnion} \) is NP-hard in query complexity. The map operator \( m_d(p) \) allows to transform each element inside an array \( p \) according to the new definition \( d \), and the filter operator \( f_d(p) \) filters the elements of an array \( p \) that satisfy \( d \):

\[
\{ \text{filter: \{ input: PATHREF, as: PATH, cond: VALUEDEF \}} \}
\]

\[
\{ \text{map: \{ input: PATHREF, as: PATH, in: VALUEDEF \}} \}
\]

\[
\{ \text{setUnion: \[ VALUEDEF \]} \}
\]

**Lemma D.9.** The query emptiness problem for \( \mathcal{M}^{\text{MUP}} \) queries with filter, map and set union operators is NP-hard in query complexity.

**Proof.** Proof by reduction from the Boolean satisfiability problem. Let \( \varphi \) be a Boolean formula over \( n \) variables \( x_1, \ldots, x_n \). We construct a query \( q \) such that for each non-empty forest \( F \), \( F \triangleright q \) is non-empty iff \( \varphi \) is satisfiable.

\[
q = \rho_{a_0}/(x_1=0), a_1/(x_1=1) \triangleright \rho_{a_0}/[a_0, a_1] \triangleright \rho_{a_0}/m_{x_1, x_2}(a), a_1/m_{x_1, x_2}(a) \triangleright \rho_{a_0}/(a_0, a_1) \triangleright \cdots
\]

\[
\rho_{a_0}/m_{x_1, x_2, \ldots, x_{n-1}, x_n}(a), a_1/m_{x_1, x_2, \ldots, x_{n-1}, x_n}(a) \triangleright \rho_{a_0}/(a_0, a_1) \triangleright \cdots
\]

\[
\rho_{\text{assignments}}/f_a(a) \triangleright \mu_{\text{assignments}}(\neq \emptyset)
\]

The stages \( (a_1) \) to \( (a_n) \) construct an array \( a \) of \( 2^n \) elements, where each element is an object encoding an assignment to the variables \( x_1, \ldots, x_n \). In the stage \( (a_i) \), the map operator is used to extend each current element with the an assignment to the variable \( x_i \). The (filter) stage then uses the filter operator to check for each element of the big array, whether it is a satisfying assignment, and if not, it is removed from the array. Finally, match will check that the resulting array is non-empty. If it is the case, then we have a satisfying assignment. All satisfying assignments will be stored in \( a \).