Evo-Path: Querying Data Evolution through Complex Changes

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Abstract: Evo-graph is a model for data evolution that captures data versions and treats changes as first-class citizens. A change in evo-graph can be compound, comprising disparate changes, and is associated with the data items it affects. In previous work, we specified how an evo-graph can be reduced to a snapshot holding under a specific time instance, we presented an XML representation of evo-graph called evoXML, we defined how evo-graph is constructed as the current snapshot evolves, as well as presented and evaluated the C2D framework that implements these concepts using XML technologies. In this paper, we formally define evo-path, an XPath extension for querying the data history and change structure in a uniform way over evograph. We specify the evo-path syntax, semanties and implementation, and present several query categories.

1 INTRODUCTION

The dynamic nature of web data poses new challenges for data management. In particular, revisiting past data snapshots may not be enough for users of scientific data. Additionally, they would like to review how and why data have evolved, in order to reassess and compare previous and current results. Such an activity may require a search that moves backwards and forwards in time, spread across disparate parts of a database, and perform complex queries on the semantics of the changes that modified the data. The need for tracing past changes and data lineage is evident in a wide range of web information management domains.

Consider an example taken from Biology, the revision in the classification of diabetes, which was caused by a better understanding of insulin (National research council, 2005). Initially, diabetes was classified according to the age of the patient, as *juvenile* or *adult onset*. As the role of insulin became clearer two more subcategories were added: *insulin dependent* and *non-insulin dependent*. All *juvenile* cases of diabetes are *insulin dependent*, while *adult onset* may be either *insulin dependent* or *non-insulin dependent*. In Figure 1, the leftmost/rightmost image depicts a tree representation of the initial/revised diabetes classification. Supposing that a scientist examines the revised classification, she may realize that diabetes categories are not as expected. She

would like to know: Which may be the previous structure of categories? Which changes are responsible for the reorganization of diabetes categories? What are the previous versions of the data nodes that changed due to the reorganization of diabetes categories? However, these representations are not informative on which parts of the data evolved and how, which changes led from one version to another, or what changes were applied on which parts of data. Recording change operations in a log or computing deltas between successive versions do not solve the problem. In most cases, it difficult to interpret a posteriori isolated is operations because they usually form more complex, semantically rich changes, each comprising many small changes on disparate parts of data. As a result, answering such questions may require complex queries in different parts of a database, a task which may be even more intensive for large datasets.

We argue that in systems where evolution issues are paramount, changes should not be treated solely as transformation operations on the data, but rather as first class citizens retaining structural, semantic, and temporal characteristics. In previous work, we proposed a graph model, evo-graph (Stavrakas and Papastefanatos, 2010), and its XML representation, evoXML (Stavrakas and Papastefanatos, 2011), capturing relationships between evolving data and changes applied on them. Evo-graph models changes explicitly as first class citizens and thus, enables

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Figure 1: Snap-models of diabetes classification before (left) and after (right) revision and the relevant evo-graph (middle).

querying data and changes in a uniform way. In (Papastefanatos et al., 2013) we showed how evograph is constructed, recording data history and structured changes step by step as current snapshot evolves, and evaluated the C2D framework, which implements these concepts via XML technologies.

In this paper, we formally define evo-path, an XPath (Robie, Dyck and Spiegel, 2017) extension for performing time- and change-aware queries on evo-graph. Evo-path allows querying both data history and change structure in a uniform way, taking advantage of changes in order to retrieve and relate data that are otherwise irrelevant to each other. Temporal, evolution and causality queries are supported. In O(Stavrakas and Papastefanatos, 2010) and (Stavrakas and Papastefanatos, 2011) evo-path was introduced, but only a syntax outline and a byexample translation into equivalent XQuery expressions over evoXML were presented. In this paper, we contribute the following: a) we enrich the evo-path syntax, b) we define evo-path formal semantics, c) we present an implementation based on a formal translation of evo-path into equivalent XPath expressions over evoXML.

Section 2 covers previous work on evo-graph, evoXML, basic and complex changes. Section 3 formally defines evo-path: syntax, semantics, implementation and examples. Section 4 revises related work. Section 5 concludes the paper.

2 PRELIMINARIES

Snap-model. In terms of this work, we assume that data is represented by a rooted, node-labelled, leaf-valued tree called snap-model. A snap-model S(V, E) consists of a set of nodes V, divided into complex

and atomic, with atomic being the tree leaves, and a set of directed edges E. At any time instance, snap-model undergoes arbitrary changes.

Evo-graph. An evo-graph G is a graph-based model that captures all the instances of an evolving snap-model across time, together with the changes responsible for the transitions. It consists of: Data nodes (complex and atomic) and data edges, departing from every complex data node. Change nodes (complex and atomic), representing change events, depicted as triangles to distinguish from circular data nodes. Change edges connect every complex change node to change nodes it contains. Evolution edges connect each change node with two data nodes, the version before and after the change. r_D is the *data root*, such that there is a path formed by data edges from r_D to every other data node. r_C is the *change root*, such that there is a path formed by change edges from r_C to every other change node. Intuitively, evo-graph consists of a data graph, holding the data versions, and a tree of changes, which interconnect via evolution edges. Change nodes are annotated with timestamps denoting the time instance each change occurred. Although valid time may be considered, we rely on transaction time, assuming a linear time domain constituted by consecutive discrete values and two special time instances: 0 for the beginning of time and now for the current time. Timestamps are used for determining the validity timespan of data nodes and data edges in evo-graph. Evo-graph can then be reduced to a snap-model holding under a specified time instance through the reduction process (Stavrakas and Papastefanatos 2010).

An evo-graph example is the middle image in Figure 1, representing the revision in the diabetes classification from the graph of Figure 1 left to right. The revision process is denoted by the complex change *reorg_diab_cat* (node &21) composed by 5 basic changes (in order they occurred): *clone* (node &8), *add* (node &11), *remove* (node &13), *create* (node &15), and *create* (node &18). The reduction of the evo-graph for T=*start* (i.e. 0)/*now* results in the snap-model of the leftmost/rightmost image of Figure 1.

EvoXML. In (Stavrakas and Papastefanatos, 2011) we presented an XML representation of evograph, the *evoXML*. Table 1 presents the evoXML for time instance 1 of the evo-graph in Figure 1, including only the *clone* operation (node &8, lines 12-16, 19-20). Notice that the edge from node &7 to node &6 (denoting that &6 remains a child of the next version of &4) is represented via the evoXML reference *evo:ref* in line 14, which points to the element in line 10. Also, notice the change node &8 in lines 19-20. Comparing to (Stavrakas and Papastefanatos 2011), we explicitly encode the timespan of each data node on it, via attributes *evo:ts* and *evo:te*, to facilitate evo-path evaluation.

Basic and Complex Changes. The following basic change operations may be applied on a snapmodel: create, add, remove, update, clone. A complex change applied on a node of a snap-model is a sequence of basic and other complex change operations that are applied on the node itself or/and its descendants, formulating semantically coherent sequences (Papastefanatos et al., 2013). A complex change example is reorg_diab_cat applied on categories node of Figure's 1 leftmost image:

reorg-diab-cat(&2) { clone(&4, &6, &9) add(&3, &6) remove(&4, &6) create(&3, &16, 'type', 'insulin dependent') create(&4, &19, 'type', 'non insulin dependent') }

Table 1: EvoXML for time instance 1.

1	<evo:evoxml xmlns="" xmlns:evo="http://web.</th></tr><tr><td>2</td><td>imis athena-innovation gr/projects/c2d"></evo:evoxml>	
3	<evo:dataroot evo:id="dataroot"></evo:dataroot>	
4	<diabetes evo:id="1" evo:te="now" evo:ts="0"></diabetes>	
5	<categories 2"="" evolte="now" evolts="0"></categories>	
6	<cat evold="3" evolte="now" evolts="0"></cat>	
7	<age evolid="5" evolte="now" evolts="0"></age>	
8	iuveniles/age>	
9	<pre>scat evo:id="4"evo:ts="0" evo:te="1"></pre>	
10	< are evold="6" evolts="0" evolte="now">	
11	adult onset / age / cat>	
11		
12	<cat <="" evo:id="/" evo:te="now" evo:ts="1" td=""></cat>	
13	evo:previous="4">	
14	<age evo:ref="6"></age>	
15	<age evo:id="9" evo:te="now" evo:ts="1"></age>	
16	adult onset	
17		
18	<evo:changeroot evo:id="changeroot"></evo:changeroot>	
19	<clone <="" evo:before="4" evo:id="8" evo:tt="1" td=""></clone>	
20	evo:after="7"/>	

21 </evo:evoXML >

3 EVO-PATH

3.1 Syntax

Similar to XPath, evo-path uses path expressions to move through and select data nodes. In addition, evo-path allows the navigation through change nodes on evo-graph. Consequently, there are two types of path expressions in evo-path: *data path* and *change path expressions*. Also, several predicates are supported to express conditions on evo-graph temporal properties and evolution edges.

Data path expressions start from the data root of evo-graph and return data nodes. Similar to XPath, they are written as a sequence of *location steps* separated by "/" characters and shortcuts can be used as in the two equivalent evo-paths below:

```
/child::A/
descendant-or-self::node()/
child::B/child::*[position()=1]
/A//B/*[1]
```

Change path expressions start from the change root of evo-graph and return change nodes. They have the same syntax as data path expressions, but are enclosed in square brackets:

</location step1/.../location stepN>

Temporal predicates are introduced in evo-path in order to express temporal conditions on the evograph nodes. The following types are employed:

1) On data node timespan:

[ts() operator (t_1, t_2)], where ts() evaluates to the validity timespan of the context data node, operator may be [not] (in | contains | meets | equals) covering the standard operations between sets, allowing the use of not in front of any of the operators, and t_1, t 2 are specified timestamps defining a timespan.

[ts() operator t], where ts() evaluates to the validity timespan of the context data node, operator may be [not] covers, and t is a specified timestamp, for the case where a specified timestamp exists or not in the validity timespan.

2) On data node timespan start time:

[tstart() operator t], where tstart() evaluates to the start of the validity timespan of the context data node, operator may be (> | >= | = | < | <=), and t is a specified timestamp.

3) On data node timespan end time:

[tend() operator t], where tend()
evaluates to the end of the validity timespan of the

context data node (operator and t as in case 2).

4) On change node timestamp:

[tt() operator t], where tt() evaluates to the timestamp of the context change node (operator and t as in case 2).

Evolution predicates are used to assert the existence of evolution edges at specific points in the graph. They combine a data path expression with a change path expression and vice versa, implying that the specified data are affected by the specified change. Their general form is:

```
5) data_path_expr
[evo-filter(<change_path_expr>)]
6) <change_path_expr
[evo-filter(data_path_expr)]>
```

where evo-filter may be one of: evobefore(), evo-after() and evo-both().

Each evo-filter evaluates into true or false, in case there is or not an evolution edge involving the data or change node in context. evo-before() and evo-after() refer on a specific side of the evolution edge, while evo-both () on both sides. In case 5 evo-before() and evo-after() validate whether the data node in context holds before and after respectively the application of the change being represented by the change node in context. evoboth() validates whether the data node holds either before or after the change. In case 6 evobefore() and evo-after() validate whether the change node in context represents the change before and after which the data node in context holds respectively. evo-both() validates whether the change node represents the change either before or after which the data node holds.

3.2 Example Queries

The evo-path examples refer to and are evaluated on the evo-graph of Figure 1 regarding diabetes.

1) Temporal queries - Querying the history of data elements: Suppose that a scientist examines the current diabetes snapshot and realizes that the categories structure is not as expected. She wants to retrieve the previous versions of data node &20.

//Diabetes/categories [ts() not covers
'now'] (Q1)

This is a data path expression with a temporal predicate that evaluates false for the current version of categories and true for every other version. It returns node &2 with timespan [0, 5].

2) Evolution queries - Querying changes applied on data elements: The scientist observes the creation of several new nodes under the categories node. She wants to know the complex changes that contain a relevant create operation, to check if create was part of a larger modification.

<//* [evo-both(//Diabetes//*)] [.//create [evo-both(//Diabetes/ categories/cat)]]> (Q2)

This is a change path expression. The first predicate is an evolution predicate for returning all the change nodes that are applied to Diabetes node or any of its descendants. The second predicate dictates that only changes with a create descendant applied on a cat object can be returned. It returns node &21 with timestamp 6, i.e. the complex change reorg_diab_cat, affecting data node &2 and resulting into data node &20.

The scientist can now retrieve all the changes associated with *reorg_diab_cat*, in order to understand its full effect.

<//reorg diab cat/*> (Q3)

This change path expression returns nodes &8, &11, &13, &15 and &18.

3) Causality queries - Querying relationships between change and data elements: Realizing that the modifications on diabetes categories are related to the complex change &21 reorg_diab_cat, the scientist decides to check all the previous versions of the data nodes affected by reorg_diab_cat and its descendant changes.

The data path expression returns all data nodes being connected through evolution edges with a $reorg_diab_cat$ change node (&21) or one of its descendant change nodes, specifically those before each change due to evo-before(). The nodes &3 with timespan [0, 1], &4 [0, 1), &7 [1, 2], &10 [2, 3] and &12 [3, 4] are returned. The scientist now realizes the sequence of data evolution.

3.3 Semantics

In XPath, the meaning of a path expression is the sequence of nodes, at the end of each path, that matches the expression. In evo-path, the meaning of a data path expression is a sequence of (data-node, interval) pairs such that the data-node has been at the end of a matching data path continuously during that interval. The interval is the validity timespan of the data-node. In evo-path, the meaning of a change

path expression is a sequence of (change-node, instance, data-node-before, data-node-after) tuples such that the change-node is at the end of a matching change path at the specific instance and it references the data-node-before and the data-node-after the change. The instance is the timestamp (transaction time) when the change was applied on the datanode-before, leading to the data-node-after.

For specifying the evo-path semantics the formal XPath semantics introduced by (Wadler, 1999) have been adapted. The meaning of an XPath expression is specified with respect to a context node. For a data path expression, this is extended to a context pair of a data-node and a time interval. For a change path expression, its meaning is specified with respect to a context tuple of a change-node, a time instance, a data-node before and data-node after the change. For the data part, four semantic functions are defined: S,Q,Q_T and Q_E . S[[p]]x denotes the sequence of pairs (data-node, interval) selected by pattern p when x is the context pair. It may also denote a sequence of values. The boolean expression Q[[q]]x denotes whether or not the qualifier q is satisfied when the context pair (data-node, interval) is x. The boolean expression $Q_T[[q_T]]x$ denotes whether or not a temporal condition q_T is satisfied, while the boolean

Table 2: Formal Semantics of Evo-Path.



expression $Q_E[[q_E]]x$ denotes whether or not an evolution condition q_E is satisfied. For the change part, four similar semantic functions are defined: S_c, Q_c, Q_{cT} and Q_{cE} . $S_c[[p]]x$ denotes the sequence of tuples (change-node, instance, data-node-before, datanode-after) selected by pattern p when x is the context tuple. It may also denote a sequence of values. The boolean expression $Q_c[[q]]x$ denotes whether or not the qualifier q is satisfied when the context tuple (change-node, instance, data-node-before, data-nodeafter) is x. The boolean expression $Q_{cT}[[q_T]]x$ denotes whether or not a temporal condition q_T is satisfied, while the boolean expression $Q_{cE}[\![q_E]\!]x$ denotes whether or not an evolution condition q_E is satisfied. In Table 2 the formal semantics of the most common evo-path constructs are presented.

For the *data root* and *change root* it holds: The validity timespan of the *data root* is by definition [0, now], as it is always valid in time. The timestamp of the *change root* is by definition 0, the data-node-before and data-node-after are undefined (\emptyset) , as it does not represent an actual change.

3.4 Implementation

In order to implement evo-path, each valid evo-path expression is translated into an equivalent XPath expression over evoXML. Table 3 summarizes the translation rules. Each data/change path expression (case A) is evaluated starting from the data/change root. Each temporal predicate (case B) is mapped to an XPath predicate over evoXML attributes evo:ts, evo:te and evo:tt. Each evolution predicate (case C) is mapped to an XPath predicate over the evoXML attributes evo:before or/and evo:after. These attributes appear on change elements and should be equal to evo:id attribute of data elements. Moreover, recall that evoXML encodes evo-graph in a top-down non-replicated approach (Stavrakas and Papastefanatos, 2011): if a child node is pointed to by multiple parent versions, the element corresponding to the child node is contained in the oldest parent element, while subsequent parent versions contain "clone" elements of the child. These are empty elements pointing to the "original" child element via evo:ref attribute. This feature is handled while translating a data path expression to an equivalent XPath expression (case D). The returned nodes of a data path expression should be the "original" ones, i.e. those with an evo:id attribute (rule 1). Similar holds for predicates that are used to find a specific node, e.g. based on position (rule 2). For predicates that are used to find a node that contains a specific value, the returned nodes should be the "original"

ones and the contained value should be checked in an "original" child node. However, the node in context may have either an "original" or a "clone" child node. In the latter case, the "clone" child node is used to access the pointed "original" one. Thus, in rule 3 two cases are identified: p1 is an "original" node and contains the "original" node p2 with value, or p1 is an "original" node and contains the "clone" node p2 pointing to an "original" node with value. This is extended in rule 4 with an additional location step. For p3 a third case is identified: p1 is an "original" node which contains the "original" node p2 with value and the "clone" node p3, which is used to access the "original" pointed node p3. The case of having p1 as "original" node and p2 and p3 as "clone" nodes is not identified, since it eventually ends up to one of the rest cases. Finally, note that XPath predicates on other node types, like attributes, are not considered, since in evoXML evolving data are represented on element nodes.

Below, we show the XPath expressions for the Section 3.2 evo-path queries, generated following the translation rules. For simplicity evo namespace is omitted. evoXML.xml contains the evoXML representation of evo-graph in Figure 1.

```
(Q1) let $d:=doc("evoXML.xml")/evo:evoXML/
            evo:DataRoot
    return $d//Diabetes/categories
               [@evo:te!='now']
(Q2) let $d:=doc("evoXML.xml")/evo:evoXML/
            evo:DataRoot,
  $c:=doc("evoXML.xml")/evo:evoXML/
            evo:ChangeRoot
    return $c//*[@evo:before=
           $d//Diabetes//*/@evo:id or
                 @evo:after=
           $d//Diabetes//*/@evo:id]
         .//evo:create[@evo:before=
    $d//Diabetes/categories/cat/@evo:id or
                      @evo:after=
    $d//Diabetes/categories/cat/@evo:id] ]
(Q3) let $c:=doc("evoXML.xml")/evo:evoXML/
            evo:ChangeRoot
    return $c//reorg_diab_cat/*
(Q4) let $d:=doc("evoXML.xml")/evo:evoXML/
            evo:DataRoot,
        $c:=doc("evoXML.xml")/evo:evoXML/
            evo:ChangeRoot
    return $d//*[@evo:before=
           $c//reorg diab cat//*/@evo:id]
```

4 RELATED WORK

An early work (Chawathe, Abiteboul and Widom 1999) proposes DOEM, an extension of OEM, representing changes as annotations on the nodes

Table 3: Evo-Path to XPath translation.

	Evo-Path	XPath	
	А.	Data and Change Path Expressions	
data_path_expr		<pre>doc("evoXML.xml")/evo:evoXML/evo:DataRoot/mapped_data_path_e xpr</pre>	
<ch< td=""><td>ange_path_expr></td><td><pre>doc("evoXML.xml")/evo:evoXML/evo:ChangeRoot/mapped_change_pa th expr</pre></td></ch<>	ange_path_expr>	<pre>doc("evoXML.xml")/evo:evoXML/evo:ChangeRoot/mapped_change_pa th expr</pre>	
B. Temporal Predicates			
[ts() in (t_1, t_2)],where $t_2 \in \mathbb{N}$	[@evo:ts>= t_1 and (if @evo:te='now' then false() else @evo:te<= t 2)]	
[ts(whe) contains (t_1, t_2)], re <i>t</i> 2 ∈ N	[@evo:ts<= t_1 and (if @evo:te='now' then true() else @evo:te>= t 2)]	
[ts() meets (t_1, t_2)], where $t_2 \in \mathbb{N}$		<pre>[if @evo:te='now' then (@evo:ts>= t_1 and @evo:ts<= t_2) else((@evo:ts>= t_1 and @evo:ts<= t_2) or (@evo:te>= t_1 and @evo:te<= t_2))]</pre>	
[ts(t_2 e) equals (t_1, t_2)], where \mathbb{N}	<pre>[@evo:ts = t_1 and (if @evo:te='now' then false() else @evo:te = t_2)]</pre>	
[ts() in (t_1, 'now')]	[@evo:ts>= t_1]	
[ts() contains (t_1, 'now')]	[@evo:ts<=t_1 and @evo:te='now']	
[ts() meets (t_1, 'now')]	<pre>[[11 @evo:te='now' then true()eise (@evo:ts>=t_i or @evo:te>=t 1)]</pre>	
[ts() equals (t_1, 'now')]	[@evo:ts = t_1 and @evo:te='now']	
[ts	() covers t], where $t\in\mathbb{N}$	<pre>[@evo:ts<= t and (if @evo:te='now' then true() else @evo:te>= t)]</pre>	
[ts	() covers 'now']	[@evo:te='now']	
[ts	tart() operator t], where $t \in \mathbb{N}$	[@evo:ts operator t]	
[te:	nd() > t], where $t \in \mathbb{N}$	[if @evo:te='now' then true() else @evo:te> t]	
[te:	nd() >= t], where $t \in \mathbb{N}$	[if @evo:te='now' then true() else @evo:te>= t]	
[te:	$nd() = t]$, where $t \in \mathbb{N}$	[if @evo:te='now' then false() else @evo:te = t]	
[te:	nd() < t], where $t \in \mathbb{N}$	[if @evo:te='now' then false() else @evo:te< t]	
[te:	nd() <= t], where $t \in \mathbb{N}$	[if @evo:te='now' then false() else @evo:te<= t]	
[te:	nd() = 'now']	[@evo:te='now']	
[tend()< 'now']		[true()]	
[tend()<= 'now']		[liue()]	
[tt() operator t], where ten [leevolt operator t]			
C. Evolution Predicates			
data_path_expr		<pre>doc("evoxML.xml")/evo:evoxML/evo:DataRoot/data_path_expr[dev o.id=</pre>	
before(<change_path_expr>)]</change_path_expr>		<pre>doc("evoXML.xml")/evo:evoXML/evo:ChangeRoot/change_path_expr/ @evo:before]</pre>	
data_path_expr [evo-		<pre>doc("evoXML.xml")/evo:evoXML/evo:DataRoot/data_path_expr[@ev o:id=</pre>	
after(<change_path_expr>)]</change_path_expr>		doc("evoXML.xml")/evo:evoXML/evo:ChangeRoot/change_path_expr/ @evo:after]	
dat	a_path_expr	<pre>doc("evoXML.xml")/evo:evoXML/evo:DataRoot/data_path_expr[@ev </pre>	
[evo-both(<change_path_expr>)]</change_path_expr>		0:10= doc("evoXMI.xml")/evo:evoXMI/evo:ChangeRoot/change_path_expr/	
		<pre>@evo:before or @evo:id=</pre>	
		<pre>doc("evoXML.xml")/evo:evoXML/evo:ChangeRoot/change_path_expr/ @evo:after1</pre>	
<pre><change_path_expr [evo-filter(data_path_expr)]=""> where evo-filter is evo-before or evo-after or evo-both are defined symmetrically</change_path_expr></pre>			
D. Plain Data Path Expressions			
1	/p	/p[@evo:id]	
2	/p[position predicate]	<pre>/p[(@evo:id and position predicate) or /@evo:id=(n[position predicate]/@evo:usf)]</pre>	
3	/nl[n2 on value]	<pre>(devo:ru=/p[posttion predicate]/devo:rei)] /n1[@evo:id and n2 on value] </pre>	
5	NATING ON MATRE!	<pre>/p1[@evo:id and p2/@evo:ref=/p1[p2 op value]/p2/@evo:id]</pre>	
4	/p1[p2 op value]/p3	<pre>(/p1[@evo:id and p2 op value] /p1[@evo:id and p2/@evo:ref=/p1[p2 op value]/p2/@evo:id] /p1[m2/@evo:id=(m1/m2 on value]/p2/@evo:id] </pre>	
L		/pi[p3/@evo:ld=/pi[p2 op value]/p3/@evo:rei])/p3[@evo:ld]	

and edges of the OEM graph. In (Marian et al., 2001), a diff algorithm is employed for detecting changes between two versions of an XML document and storing them as edit scripts or deltas. A similar approach is in (Chien, Tsotras and Zaniolo, 2001), where a referenced-based identification of objects is used across versions. In (Gergatsoulis and Stavrakas, 2003) MXML, an XML extension that uses context information to express time and model multifaceted documents, is proposed. Other works deal with change modelling (Rizzolo et al., 2009) and detection (Papavassiliou et al., 2009), (Galani, Papastefanatos and Stavrakas, 2016) on semantic data and RDF.

In (Rizzolo and Vaisman, 2008), an XML document is modelled as a directed graph and transaction time is attached at the edges. In (Gao and Snodgrass, 2003), a temporal query language for adding valid time support in XQuery is presented. In (Wang and Zaniolo, 2003) a temporally grouped data model is employed for uniformly representing and querying versions. In (Moon et al., 2008), this technique is extended for publishing the history of a relational database in XML and a set of schema modification operators (SMOs) is used for representing mappings between successive schema versions. (Amagasa, Yoshikawa and Uemura, 2000) deal with archiving curated databases for scientific data, using timestamps and merging all versions into one hierarchy. (Buneman, Chapman and Cheney, 2006) deal with provenance in curated databases. User actions are recorded in sequence and stored as provenance links.

Our model introduces a change-based view for evolving data. Changes are not derived by data versions, but are modelled as first class citizens along with data. Changes are not described via diffs or transformations with edit scripts between versions, but are complex objects operating on data, exhibiting structural, semantic, and temporal properties. Thus, querying evolution involves searching on both data and change structure, using temporal- and change-based conditions. Changecentric modelling can provide additional information on *what*, *why*, and *how* data evolved.

5 CONCLUSIONS

In this paper, we formally defined evo-path: a language for querying evolving data and changes in a uniform way. Evo-path operates on evo-graph, a model that captures data versions and structured changes. We also defined evo-path translation into

plain XPath expressions, which are evaluated on evoXML, an XML representation of evo-graph. Our next steps involve experimenting evo-path.

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REFERENCES

- Amagasa, T., Yoshikawa, M., Uemura, S. (2000). A Data Model for Temporal XML Documents. In DEXA.
- Buneman, P., Khanna, S., Tajima, K., Tan, W.C. (2004). Archiving Scientific Data. In ACM Transactions on Database Systems, Vol. 20, pp 1-39.
- Buneman, P., Chapman, A. P., Cheney, J. (2006). Provenance Management in Curated Databases. In SIGMOD'06.
- Chawathe, S., Abiteboul, S., Widom, J. (1999). Managing Historical Semistructured Data. In Journal of Theory and Practice of Object Systems, Vol. 24(4), pp.1-20.
- Chien, S-Y., Tsotras, V. J., Zaniolo, C. (2001). Efficient Management of Multiversion Documents by Object Referencing. In *VLDB*.
- Gao, D., Snodgrass, R. T. (2003). Temporal Slicing in the Evaluation of XML Queries. In *VLDB*.
- Gergatsoulis, M., Stavrakas, Y. (2003). Representing Changes in XML Documents using Dimensions. In *1st International XML Database Symposium*.
- Marian, A., Abiteboul, S., Cobena, G., Mignet, L. (2001). Change-Centric Management of Versions in an XML Warehouse. In *VLDB*.
- Moon, H.J., Curino, C., Deutsch, A., Hou, C.Y., Zaniolo, C. (2008). Managing and querying transaction-time databases under schema evolution. In *VLDB*.
- National research council Committee on Frontiers at the Interface of Computing and Biology (2005). Catalyzing Inquiry at the Interface of Computing and Biology. Edited by J. C. Wooley, H. S. Lin., National Academies Press.
- Papavassiliou, V., Flouris, G., Fundulaki, I., Kotzinos, D., Christophides, V. (2009). On Detecting High-Level Changes in RDF/S KBs. In *ISWC*.
- Rizzolo, F., Vaisman, A. A. (2008). Temporal XML: modeling, indexing, and query processing. In *VLDB J.*, 17(5): 1179-1212.

- Rizzolo, F., Velegrakis, Y., Mylopoulos, J., Bykau, S. (2009). Modeling Concept Evolution: a Historical Perspective. In *ER*.
- Stavrakas, Y., Papastefanatos, G. (2010). Supporting Complex Changes in Evolving Interrelated Web Databanks. In *CoopIS*.
- Stavrakas, Y., Papastefanatos, G. (2011). Using Structured Changes for Elucidating Data Evolution. In DaLi (with ICDE 2011).
- Papastefanatos, G., Stavrakas, Y., Galani, T. (2013). Capturing the History and Change Structure of Evolving Data. In *DBKDA*.
- Galani, T., Papastefanatos, G., Stavrakas, Y. (2016). A language for defining and detecting interrelated complex changes on RDF(S) knowledge bases. In *ICEIS*.
- Wadler, P. (1999). A Formal Semantics of Patterns in XSLT. In *Markup Technologies*.
- Wang, F., Zaniolo, C. (2003). Temporal Queries in XML Document Archives and Web Warehouses. In *TIME*.
- Robie, J., Dyck, M., Spiegel, J. (2017, March 21). XML Path Language (XPath) 3.1 W3C Recommendation. https://www.w3.org/TR/2017/REC-xpath-31-20170321/.