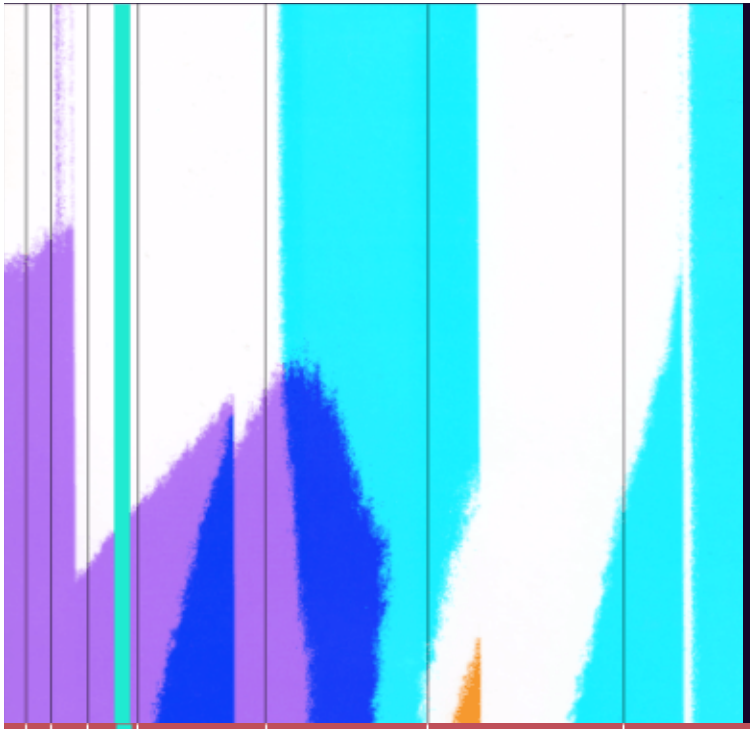

Path sequence-based XML query processing

BDA 2004, Montpellier

INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET EN AUTOMATIQUE

INRIA

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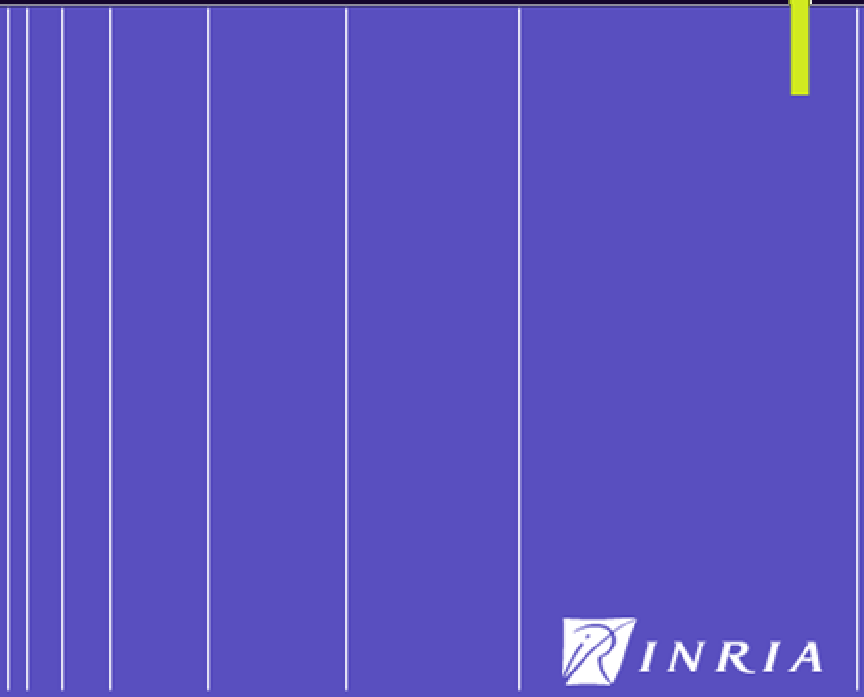
Plan

- Path sequence based XML storage
  - Logical path sequence model
  - Physical storage
- Path sequence based query processing
  - Path sequence-based XQuery optimization
    - FOR-WHERE
    - RETURN
  - Physical operators
  - Putting it all together
- Conclusion and future work

The path sequence model for storing XML documents



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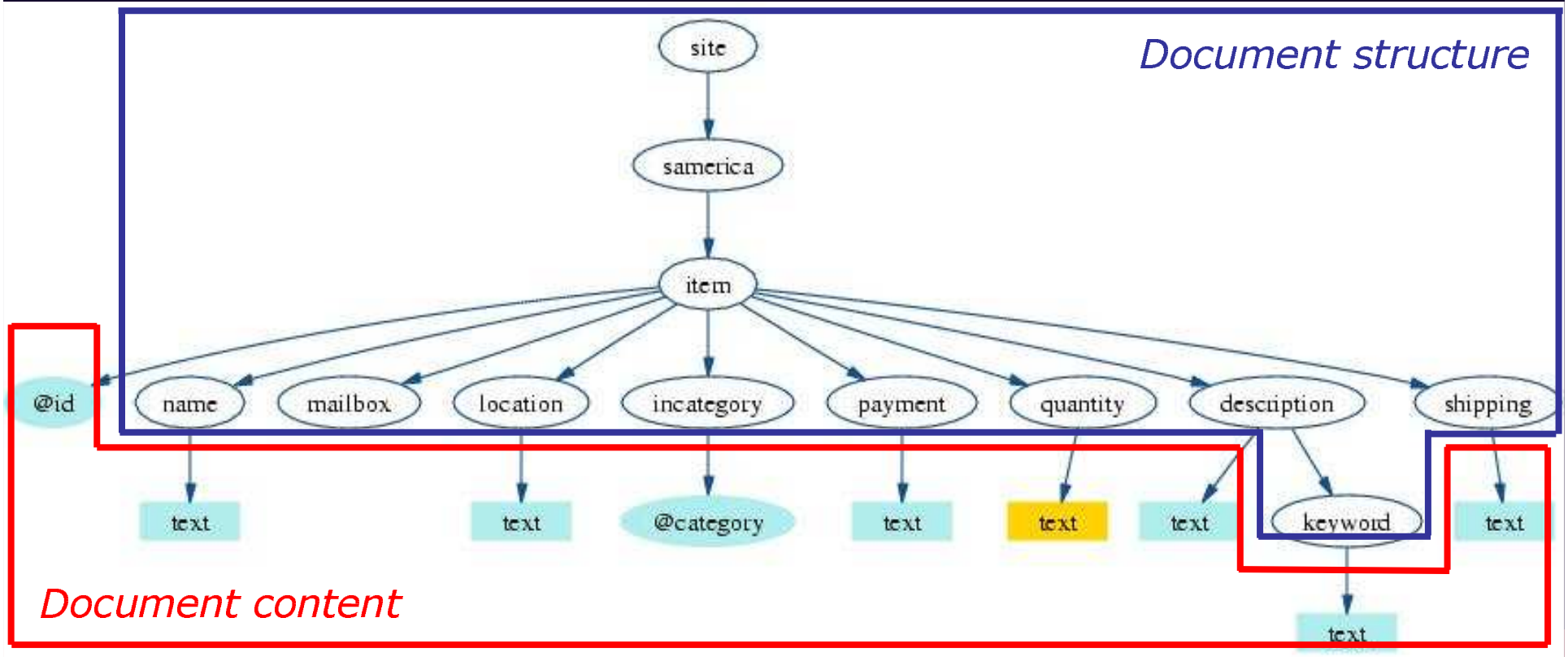
The logical path sequences storage model

- Separate XML structure from content
  - Structure is useful
  - Content is large
- Split structure and content by the incoming path
  - Sequences of element IDs
  - Sequences of values
  - Selective data access, efficient twig pattern query evaluation
- Store structure and content in path sequences
  - Built-in document order

Separating structure from content



Storing document structure in path sequences

Assign a structural identifier to elements [pre, post, depth]

As in Timber, Natix ...

Direct establishment of structural relationships

ID1 ancestor of ID2 iff ID1.pre < ID2.pre and ID1.post > ID2.post

For parent, test also ID1.depth = ID2.depth - 1

Storing the document structure:

1 path in the doc = 1 sequence of structural element identifiers

Stored in pre (document) order

Structural identifiers

[1, 8, 1] <item @id=''item0''>
[2, 1, 2] <description> Beany Crocodile </description>
[3, 3, 2] <seller>
[4, 2, 3] <personRef>Joe</personRef>
</seller>
[5, 4, 2] <payment>Visa</payment>
[6, 5, 2] <payment> MasterCard </payment>
[7, 6, 2] <mailbox> </mailbox>
[8, 7, 2] <shipping> UPS in US only </shipping>
</item>

[1, 8, 1] ancestor of [5, 4, 2], [6, 5, 2]
[3, 3, 2] parent of [4, 2, 3]

Structural identifier sequences

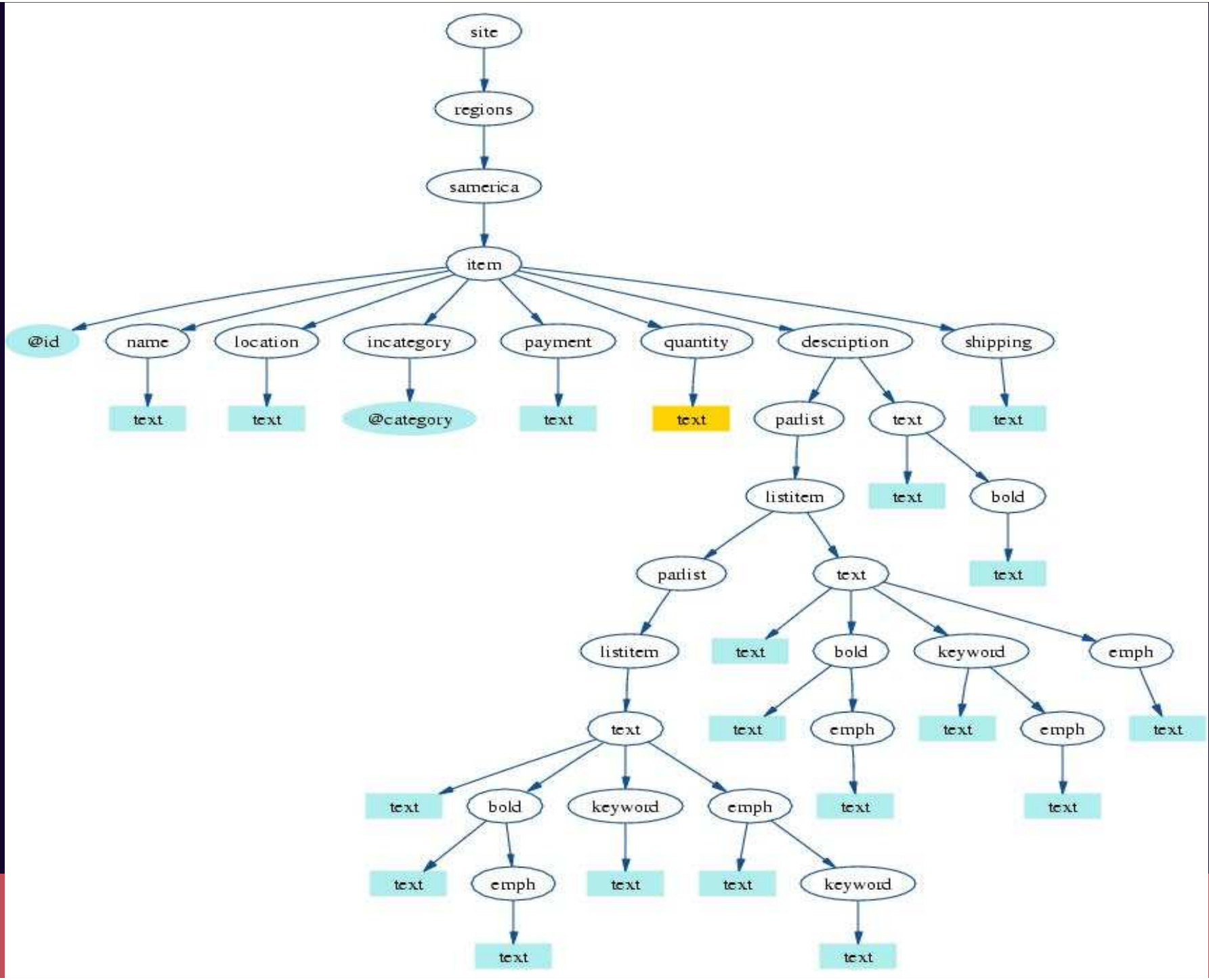
[1, 8, 1] <item @id=''item0''>
[2, 1, 2] <description> Beany Crocodile </description>
[3, 3, 2] <seller>
[4, 2, 3] <personRef>Joe</personRef>
</seller>
[5, 4, 2] <payment>Visa</payment>
[6, 5, 2] <payment> MasterCard </payment>
[7, 6, 2] <mailbox> </mailbox>
[8, 7, 2] <shipping> UPS in US only </shipping>
</item>

Path sequence for /site/auctions/samerica/item: { [1, 8, 1] }
Path sequence for ../item/payment: { [5, 4, 2], [6, 5, 2] }

Structural identifier sequences

[1, 8, 1] <item @id=''item0''>
[2, 1, 2] <description> Beany Crocodile </description>
[3, 3, 2] <seller>
[4, 2, 3] <personRef>Joe</personRef>
</seller>
[5, 4, 2] <payment>Visa</payment>
[6, 5, 2] <payment> MasterCard </payment>
[7, 6, 2] <mailbox> </mailbox>
[8, 7, 2] <shipping> UPS in US only </shipping>
</item>

Path sequence for /site/auctions/samerica/item: { [1, 8] }
Path sequence for ../item/payment: { [5, 4], [6, 5] }


site
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samerica
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@id
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payment
quantity
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listitem
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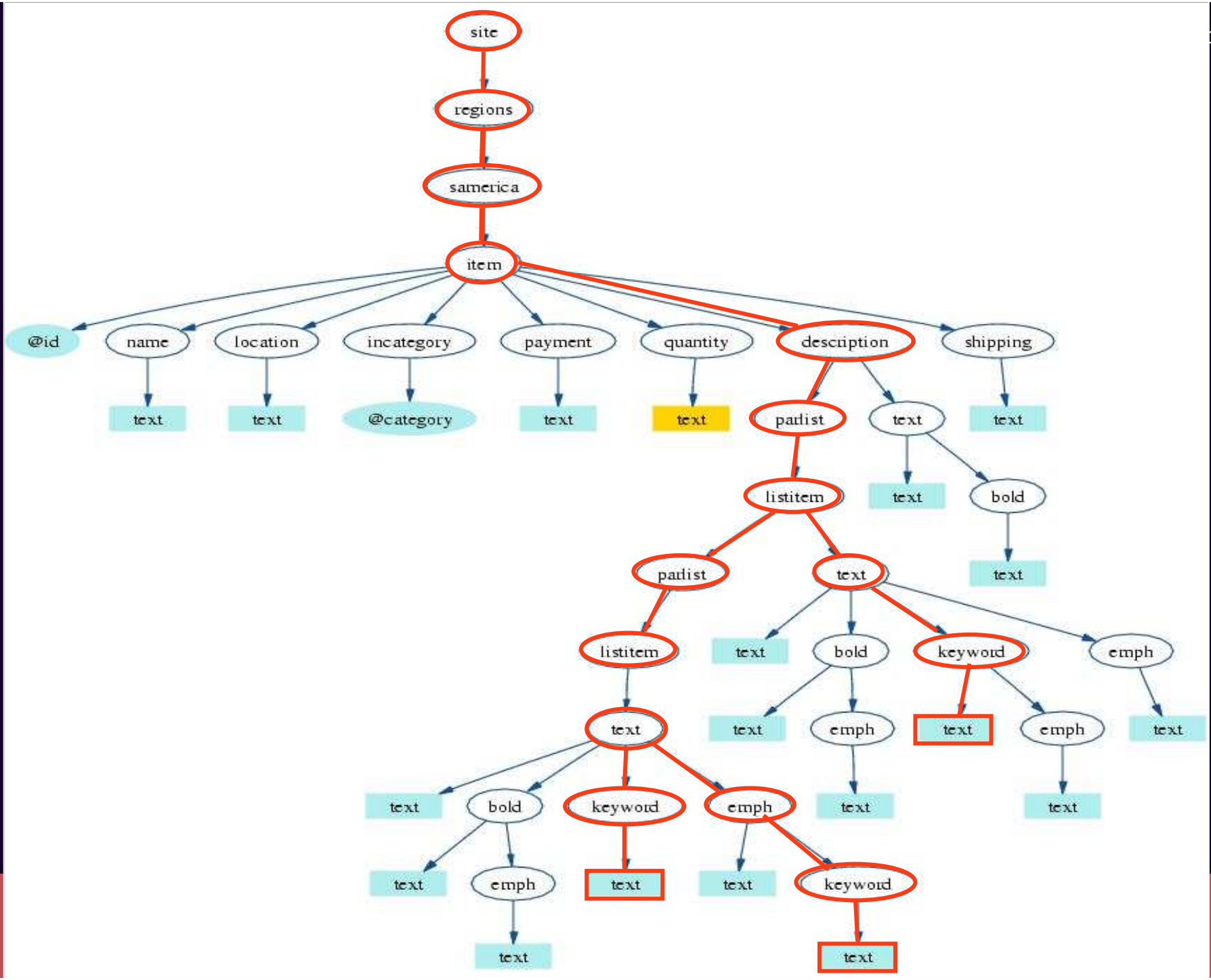
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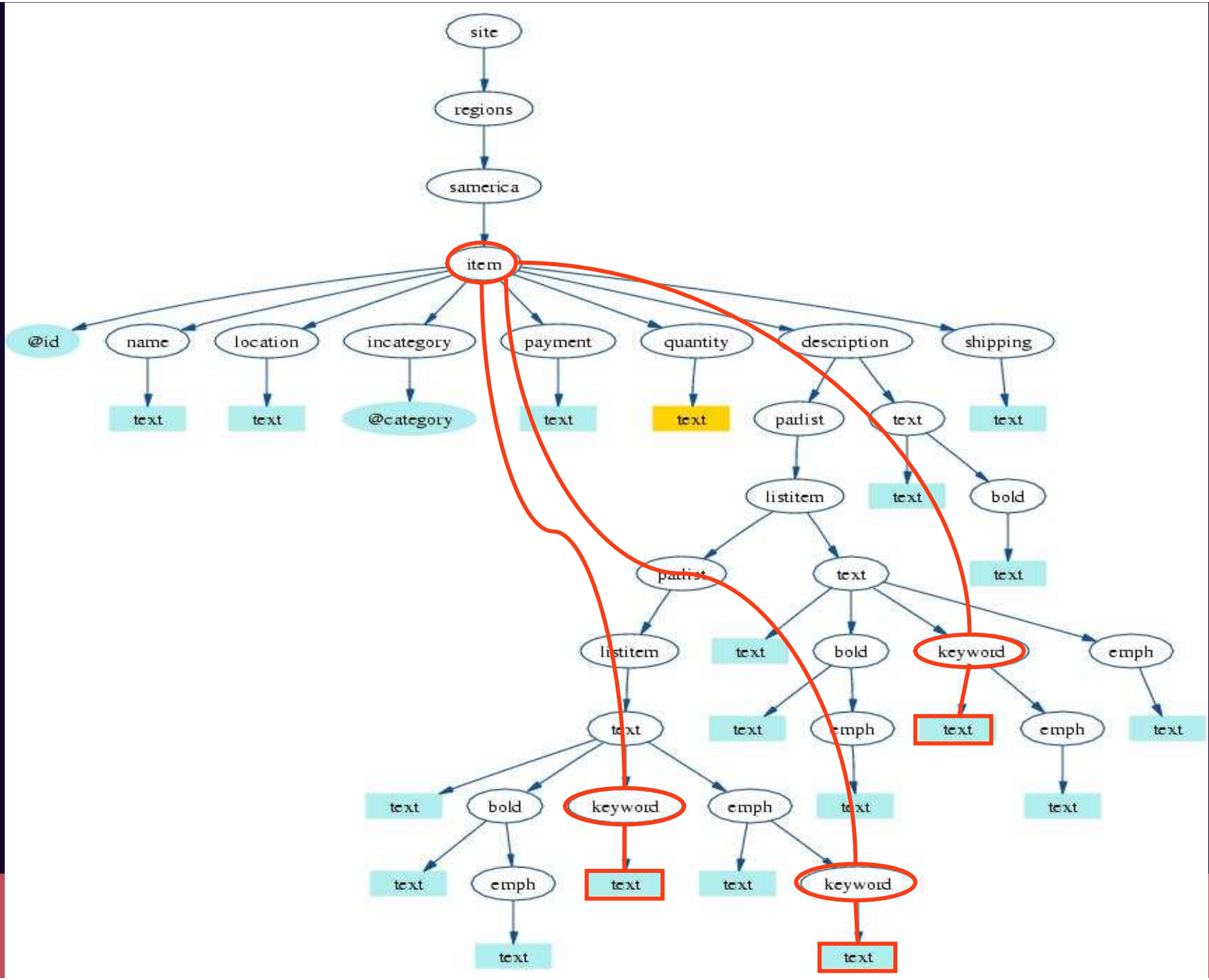
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listitem
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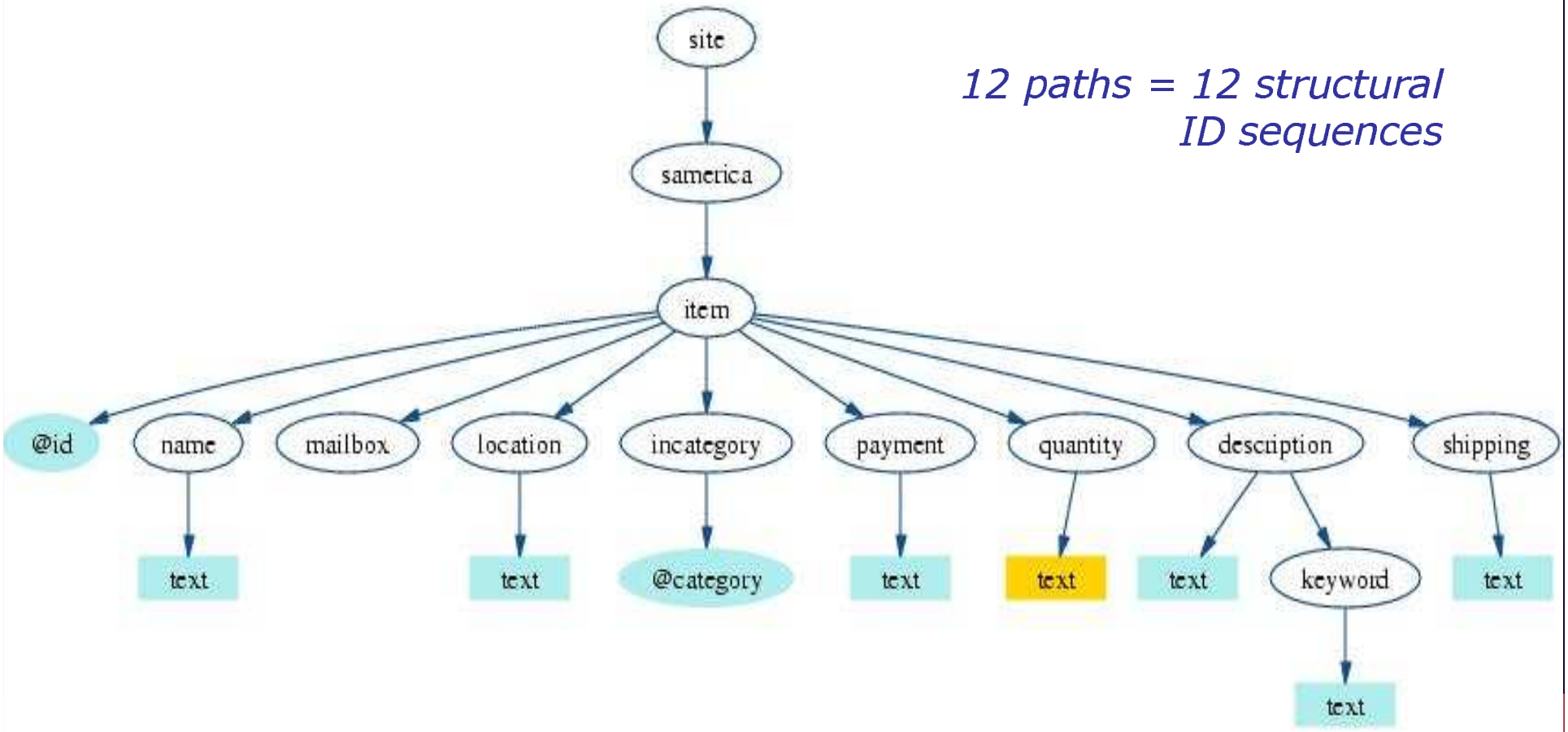
Structural identifier sequences



12 paths = 12 structural ID sequences

Storing document content in path sequences

For each root-to-leaf path in the XML document, store a *container: a sequence of (ID, value) pairs*

Text nodes: IDs of the parent elements

Attributes: IDs of the enclosing elements

Container for /site/samerica/item/payment:

{ ([5, 4, 2], "Visa")
  [6, 5, 2], "MasterCard") }

Other persistent storage structures

Required:

- Path sumary
  - Dataguide on tree (XML) structure
  - Easy to build, compact

Optional:

- Statistics associated to the path summary
- Value / full text indexes on containers...
- Structural indexes...

Physical storage for path sequences

ID sequences: fixed-length items

Containers: varying-length items

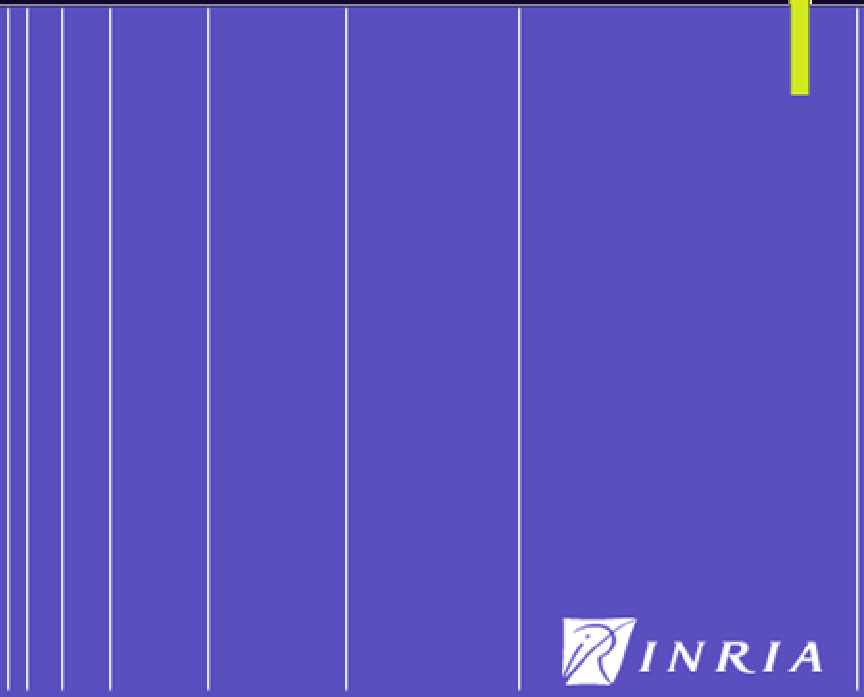
Ordered sequences (document order):

- B+ - trees
- Compact (continuous) sequences

Trade-off: compactness vs. suitability to updates

Implementation supports both, we mostly used sequences

XML query processing based on path sequences



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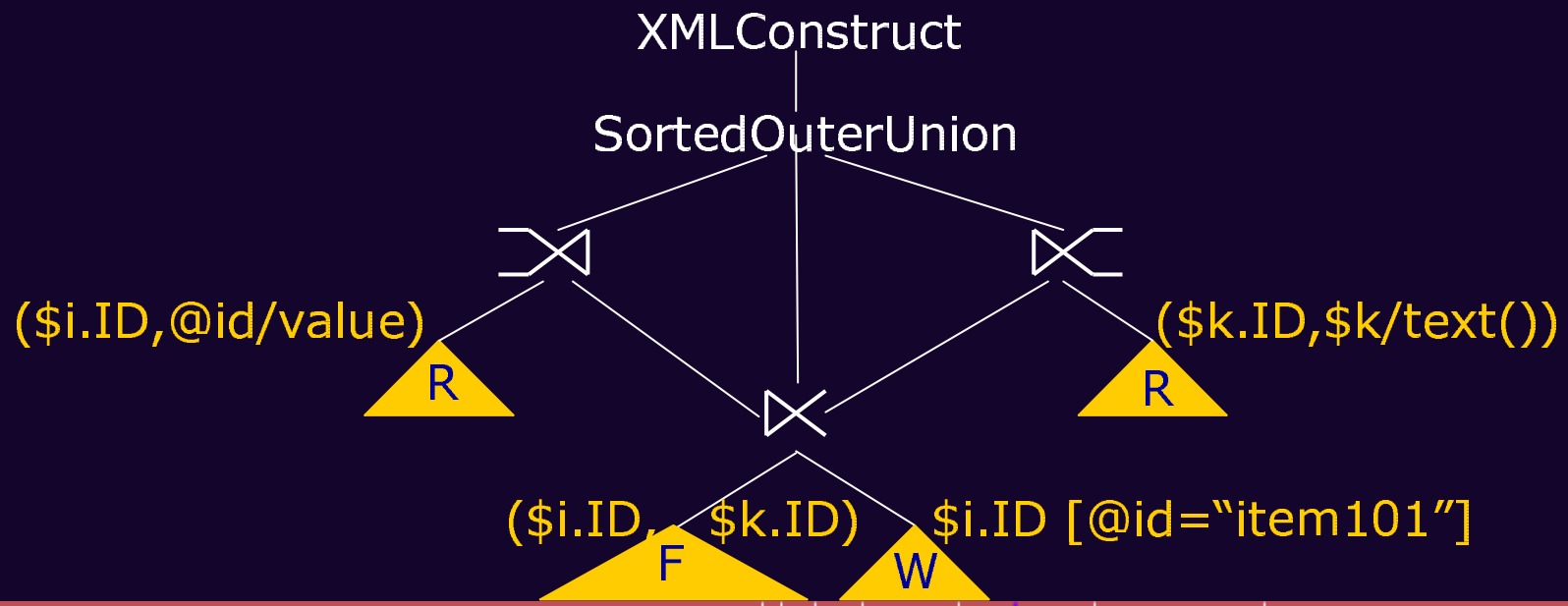
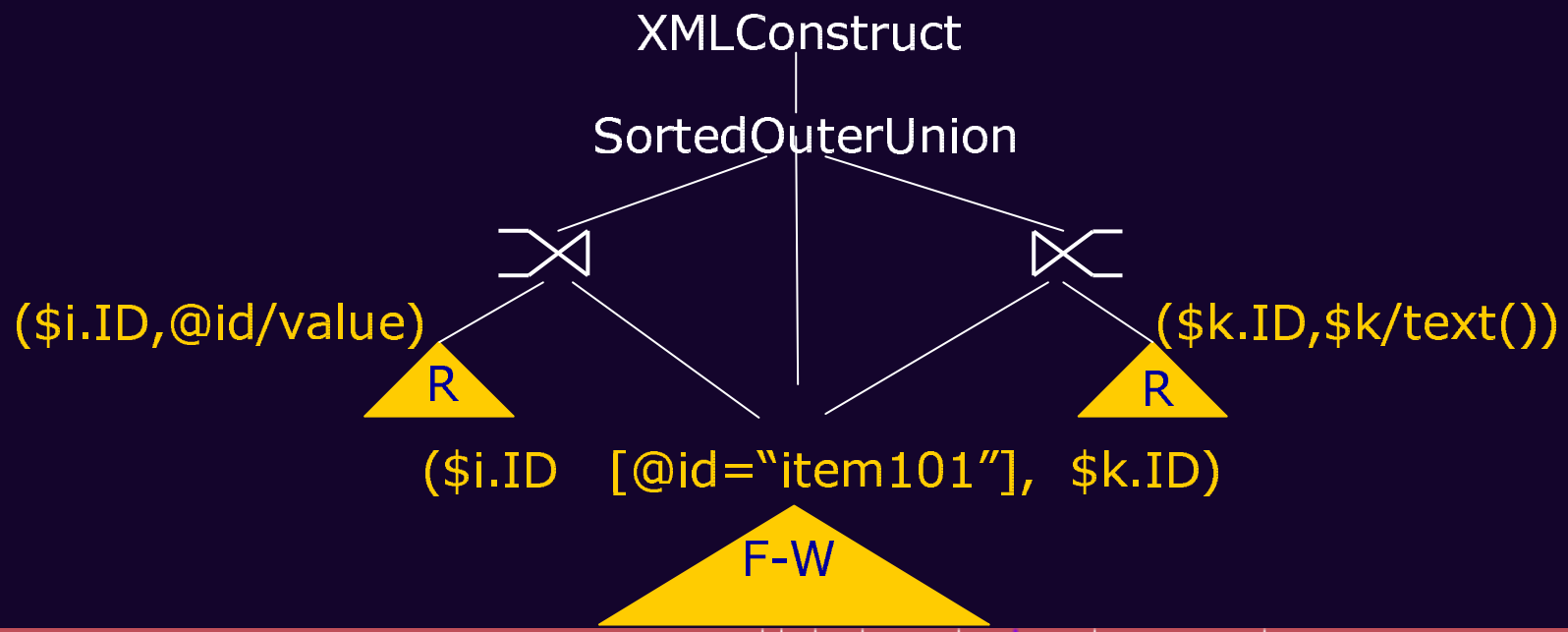
XQuery optimization approach (1)

```
for $i in //samerica/item
    $k in $i//keyword
where $i/@id="item101"
return <article>
            <numero> $i/@id/value() </numero>
            <mot-cle> $k/text() </mot-cle>
       </article>
```



XQuery optimization approach (2)

```
for $i in //samerica/item
    $k in $i//keyword where $i/@id="item101"
return <article>
            <numero> $i/@id/value() </numero>
            <mot-cle> $k/text() </mot-cle>
       </article>
```



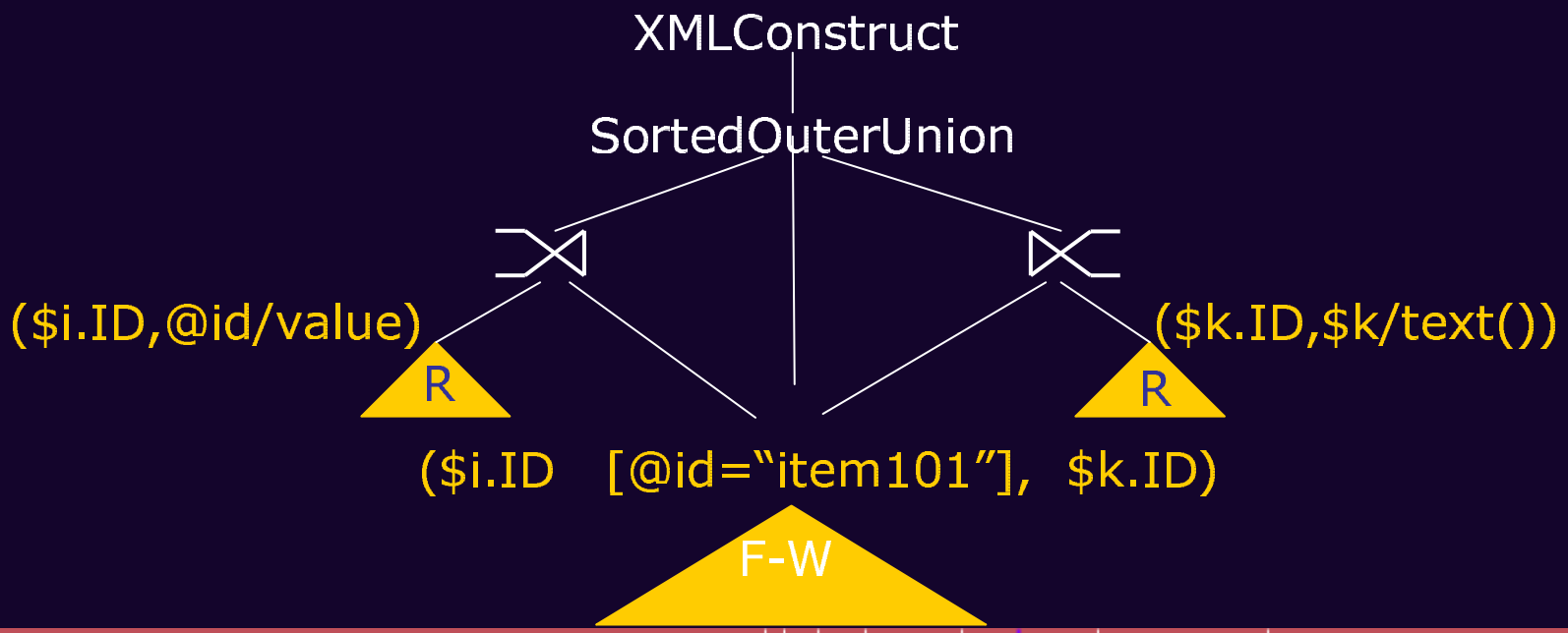
Steps in XQuery optimization

Optimize the FW plan (aka “twig pattern”):

- Variables on one or many paths; value predicates
- Output: tuples of IDs, sorted in doc order

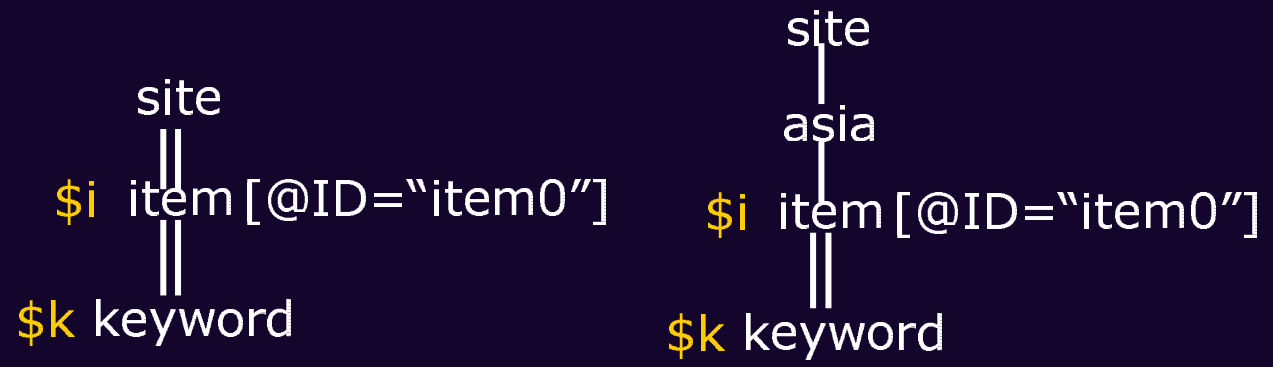
Optimize the R plan(s)

- Similar
- Based on the FW plan result



Optimizing the for-where clauses

Input: twig pattern; path summary



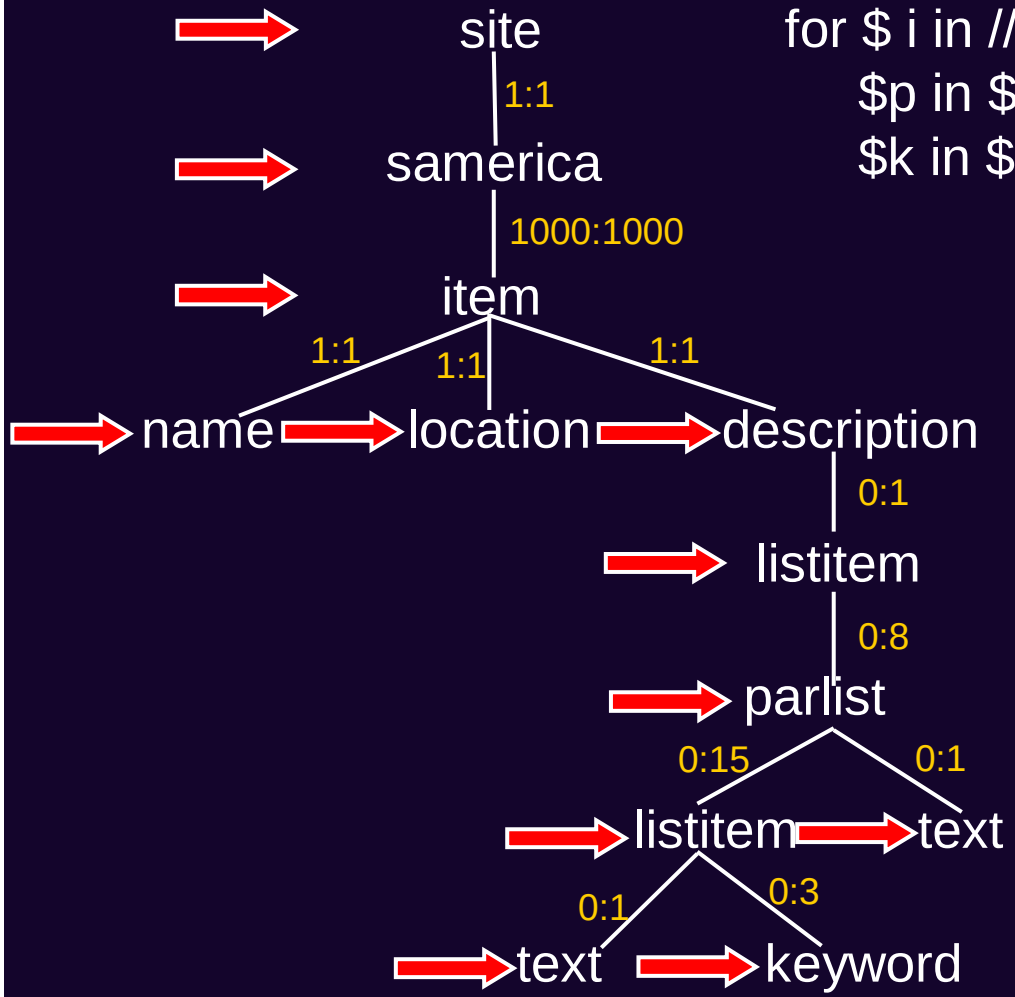
Output: *path list pList of each variable*

$i.pList = { /site/regions/africa/item, /site/regions/asia/item,
/site/regions/europe/item, /site/regions/namerica/item,
/site/regions/samerica/item }

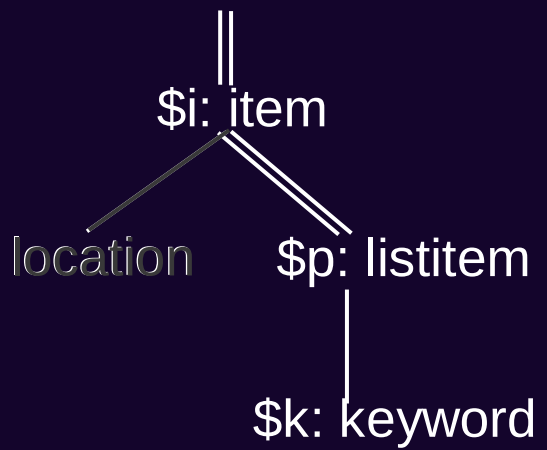
$k.pList is too large ☺

Variable path inference

Variable path inference



for $ i in //item[location],
$p in $i//listitem,
$k in $p/keyword

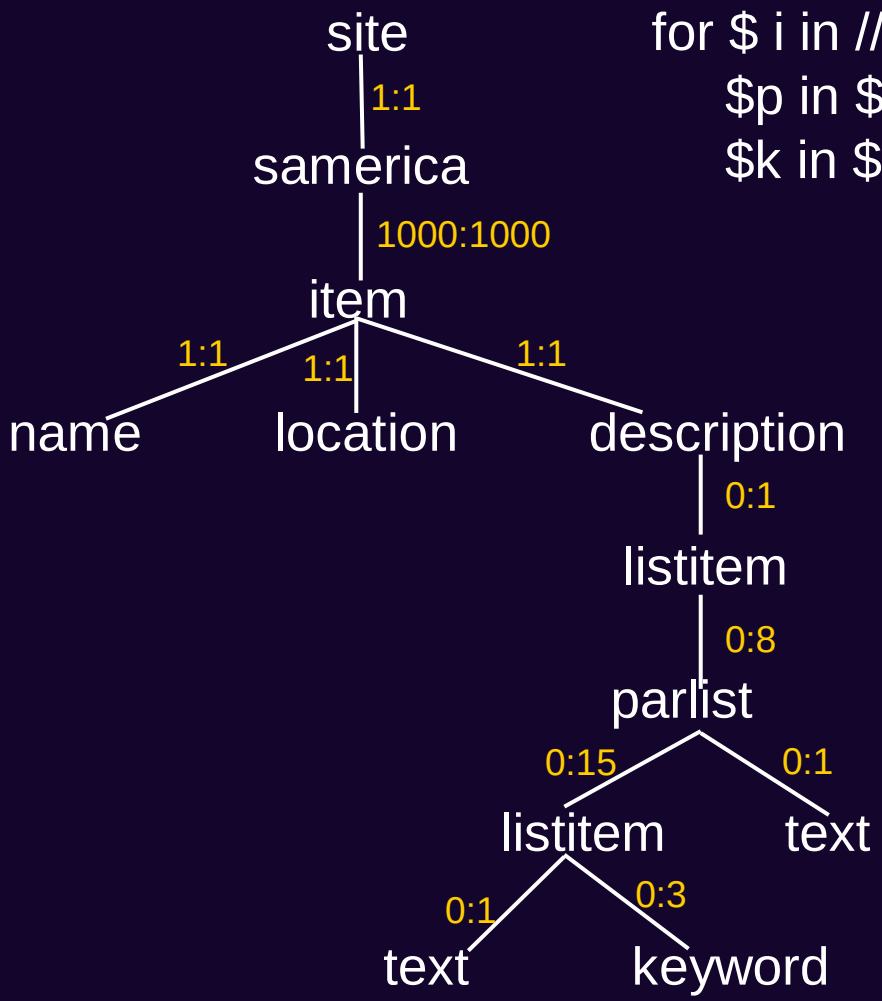


$i.pList /site/samerica/item

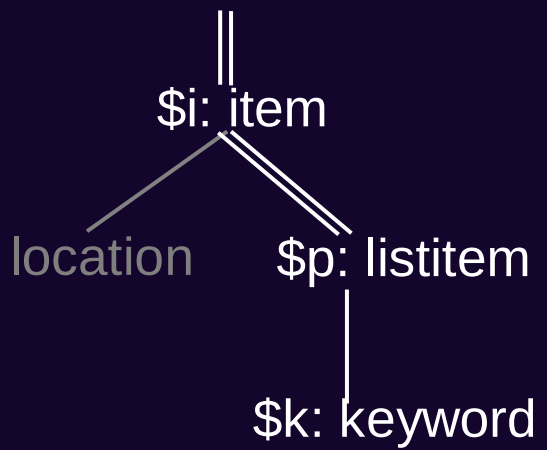
$p.pList /site/sam/item/descr/listitem
/site/sam/item/descr/litem/parlist/listitem

$k.pList
/site/sam/item/descr/litem/plist/litem/kwd

Variable path inference



for $ i in //item[location],
$p in $i//listitem,
$k in $p/keyword



$i.pList /site/samerica/item

$p.pList
/site/sam/item/descr/litem/parlist/listitem
$k.pList
/site/sam/item/descr/litem/plist/litem/kwd

Variable path inference

Traverse in parallel the path summary and the query

- Find the minimal set of paths for each variable
- Eliminate redundant branches
- Infer new structural relationships between variables

Implementation

- In memory: recursive traversals
- On disk-resident path summary: streaming query evaluation on the path summary

Physical operators

Iterator interface

Flat tuple algebra

PathScan: returns all IDs on a given path

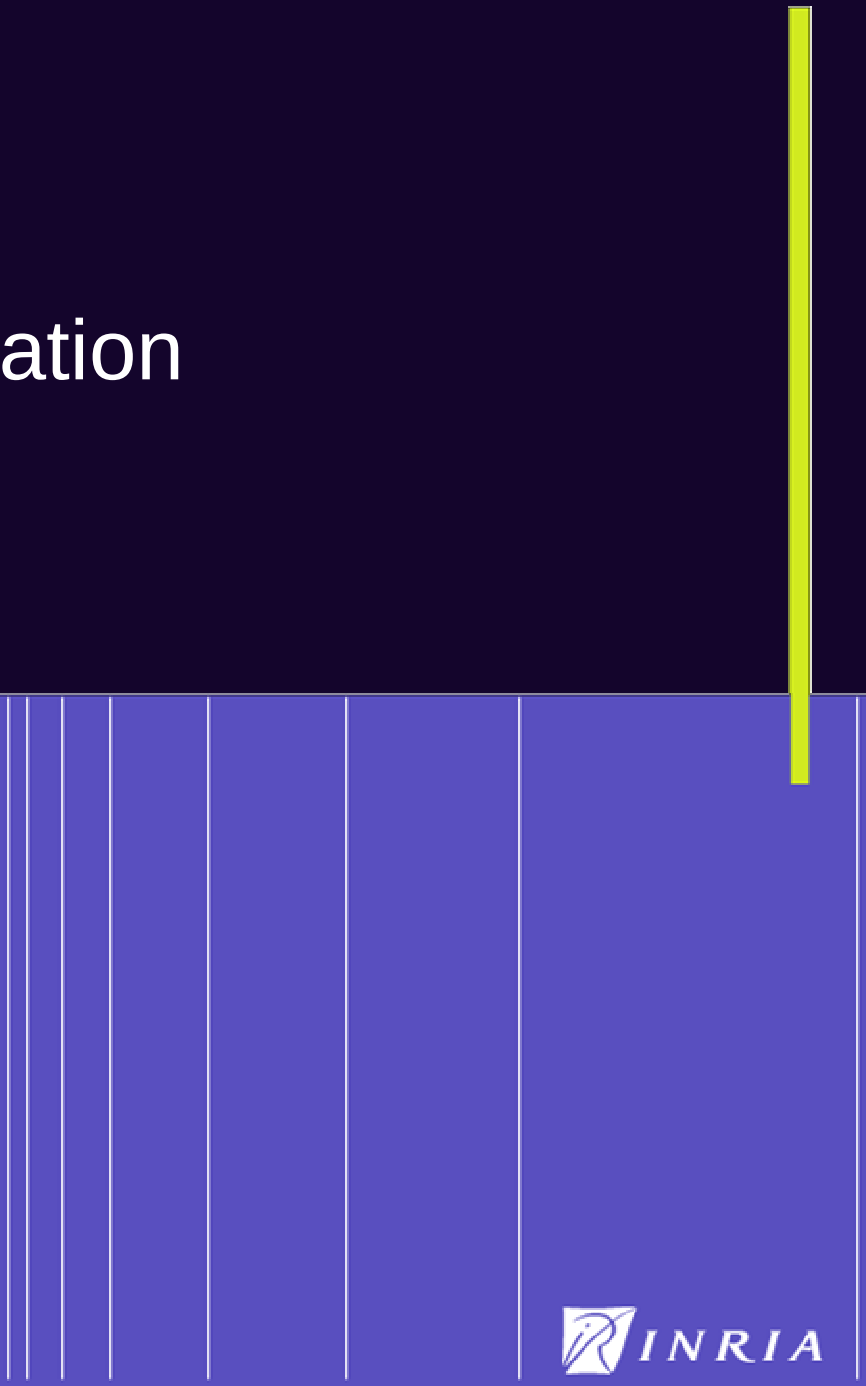
ContainerScan: returns all (ID, value) pairs on a given path

Merge: sequence fusion in document order

StackTreeDesc (structural join), outer- and semi-join variants

SortedOuterUnion for reconstruction

Performance evaluation



Physical storage

Implemented based on BerkeleyDB: free library of persistent storage structures

B+-trees, hash tables, fixed- and varying-length sequences

	B+-trees	Sequences
Path partitioning	√	√
Tag partitioning	√	√

Sequence-based storage 4 times more compact than B+-tree based

No overhead pages

Path partitioning more compact than tag-partitioning

Tags are stored only once per path

B+-trees better support updates

Query processing performance based on path sequences

Query performance depends on:

Selective data access

Path sequence access much more selective than tag-based access (e.g. Natix, Timber)

Efficient intermediary (e.g. join) algorithms

StackTreeDesc efficient (linear time); skipping joins
Path sequences enable more skipping

Query plan quality

Precise plan construction + minimization based on path summary

Path partitioning vs. tag partitioning: does it make a difference ?

Many paths lead to common tags (different meanings)

Name, title, address, comment, keyword, paragraph...

A given tag may appear in many contexts with the same meaning

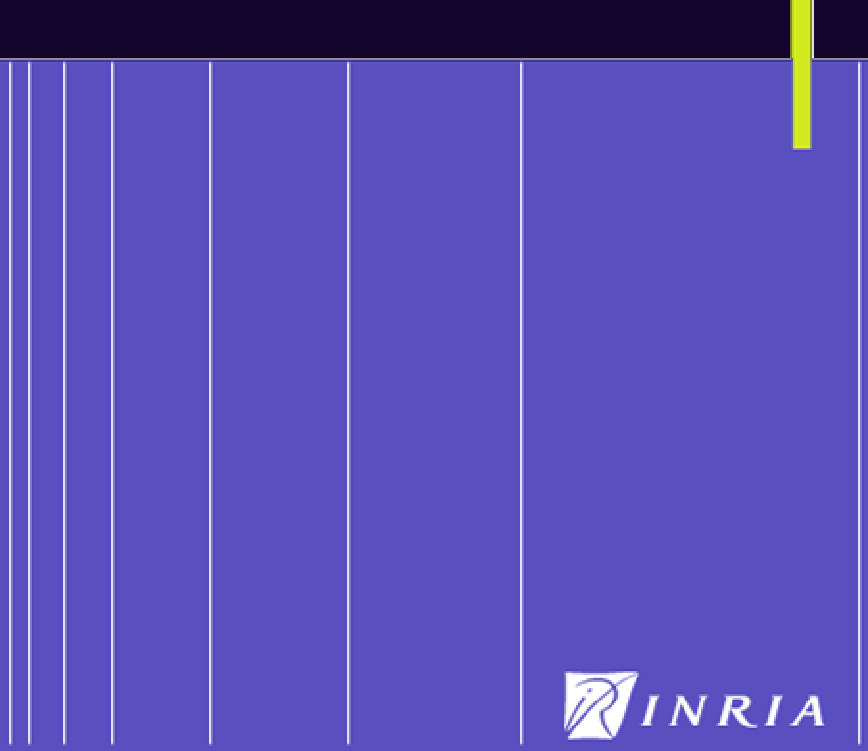
"Horizontal partitioning" e.g. auction items

Measured on a set of frequent XML documents *median fan-in*:

weighted average of #paths leading to a given tag
Values between 2.75 and 15.5

Only counter-example (median fan-in = 1): toy dataset designed by a UW CS grad student

Summary



Summary and perspectives

Path-sequence based storage model

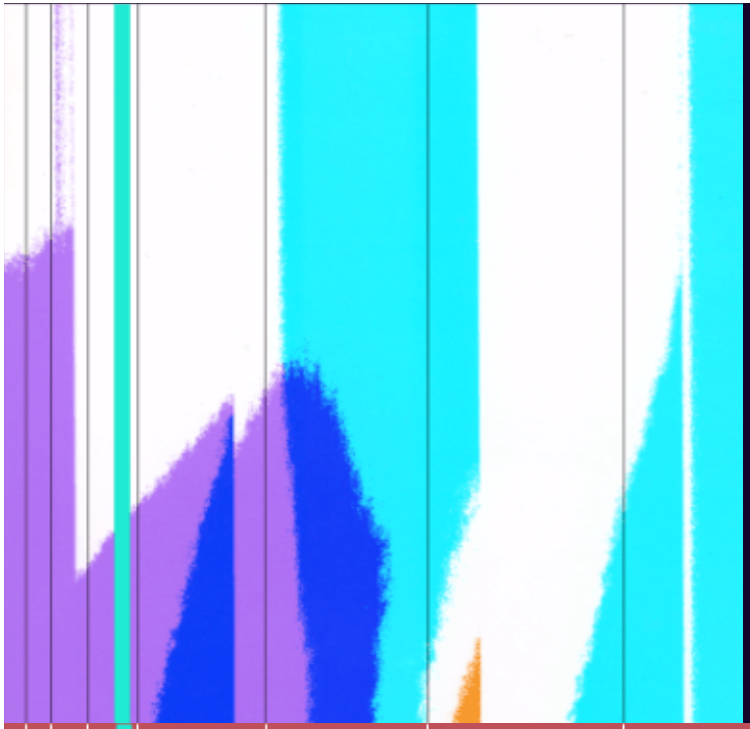
- Logical storage: Extreme "vertical" fragmentation
- Physical access: trade-offs B+-trees / sequences
- Data access: selective

Query processing on a path sequence storage

- Query optimization: minimization and pruning based on path summary
- Data reconstruction: very complex plans, good scaleup

Perspectives

- Finish up the code...
- Intermediary *physical* fragmentation degrees (path-tag)



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