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MEASURING THE STRUCTURAL SIMILARITY AMONG XML DOCUMENTS AND DTDS

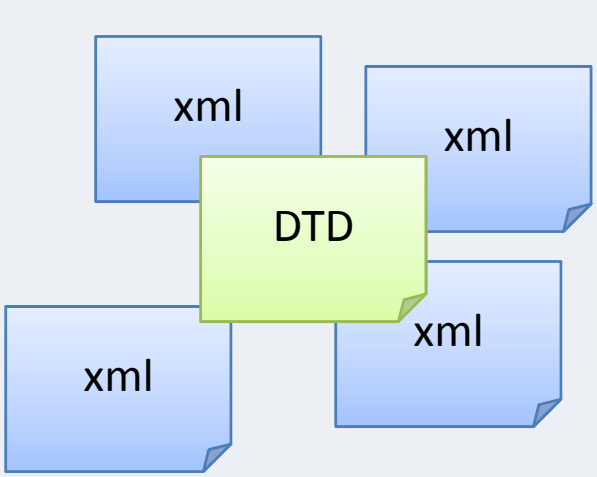
<Paper 1>

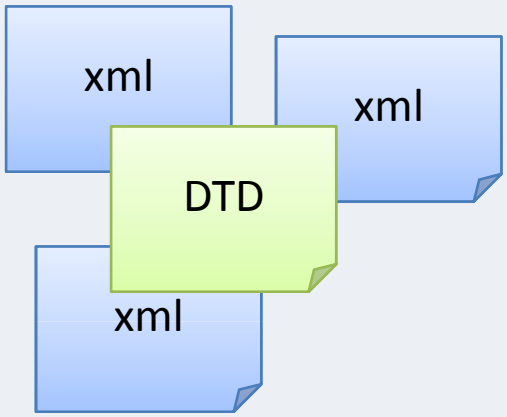
Volker Grabsch und Christine Janischek

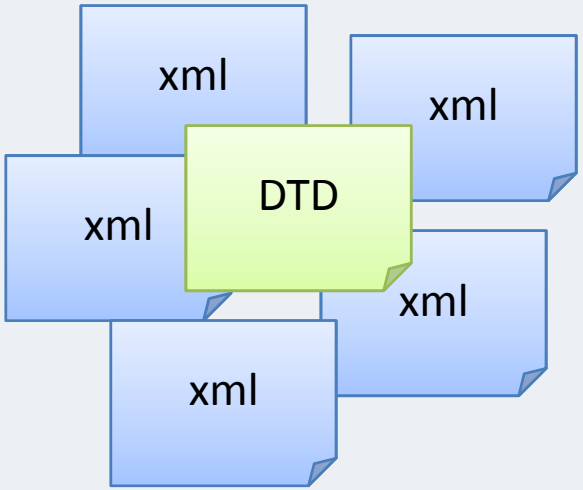
Übersicht

1. Einführung
2. Grundbegriffe
3. Algorithmen
4. Schwachstelle

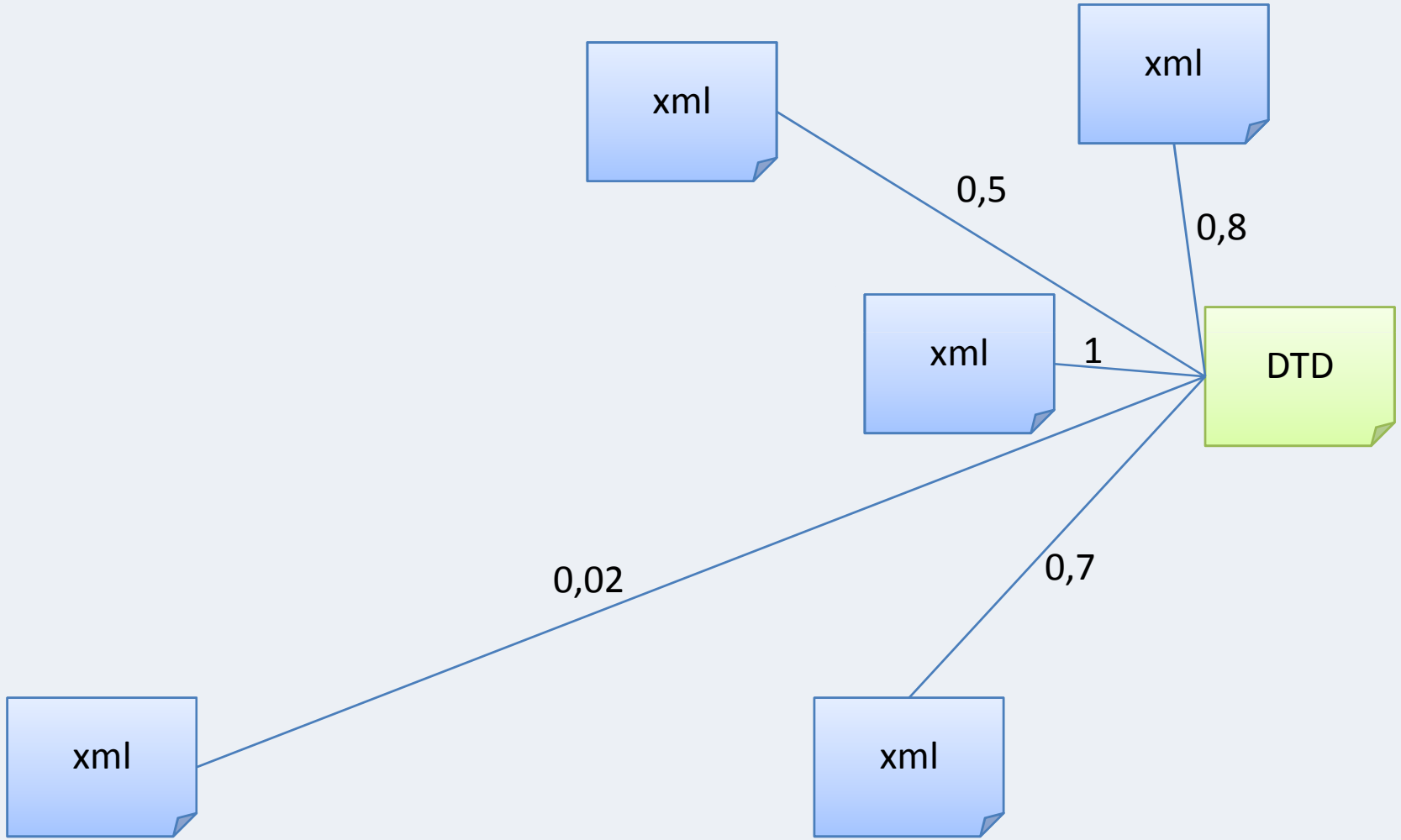
Welches Dokument gehört zu welcher DTD?







Ähnlichkeitsmaß zwischen Dokument und DTD



Vereinfachungen

- Ignorieren der Tag-Reihenfolge (DTD)
- Ignorieren der Textknoten (datenzentriert)

Unkritische Vereinfachungen:

- Verzicht auf den „+“-Operator in der DTD
- Ignorieren der Attributknoten
- Gleiche Semantik bedeutet gleicher Tagname

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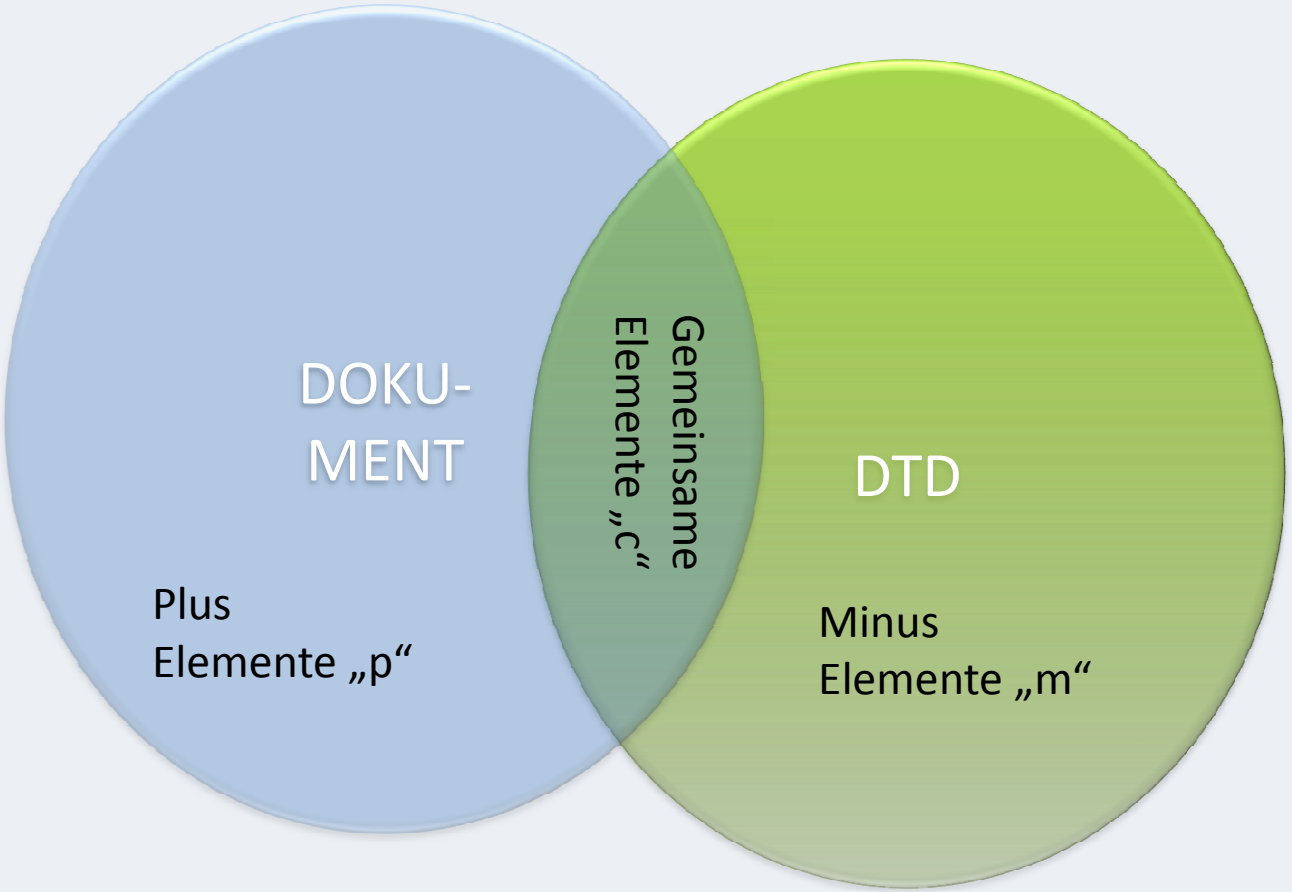
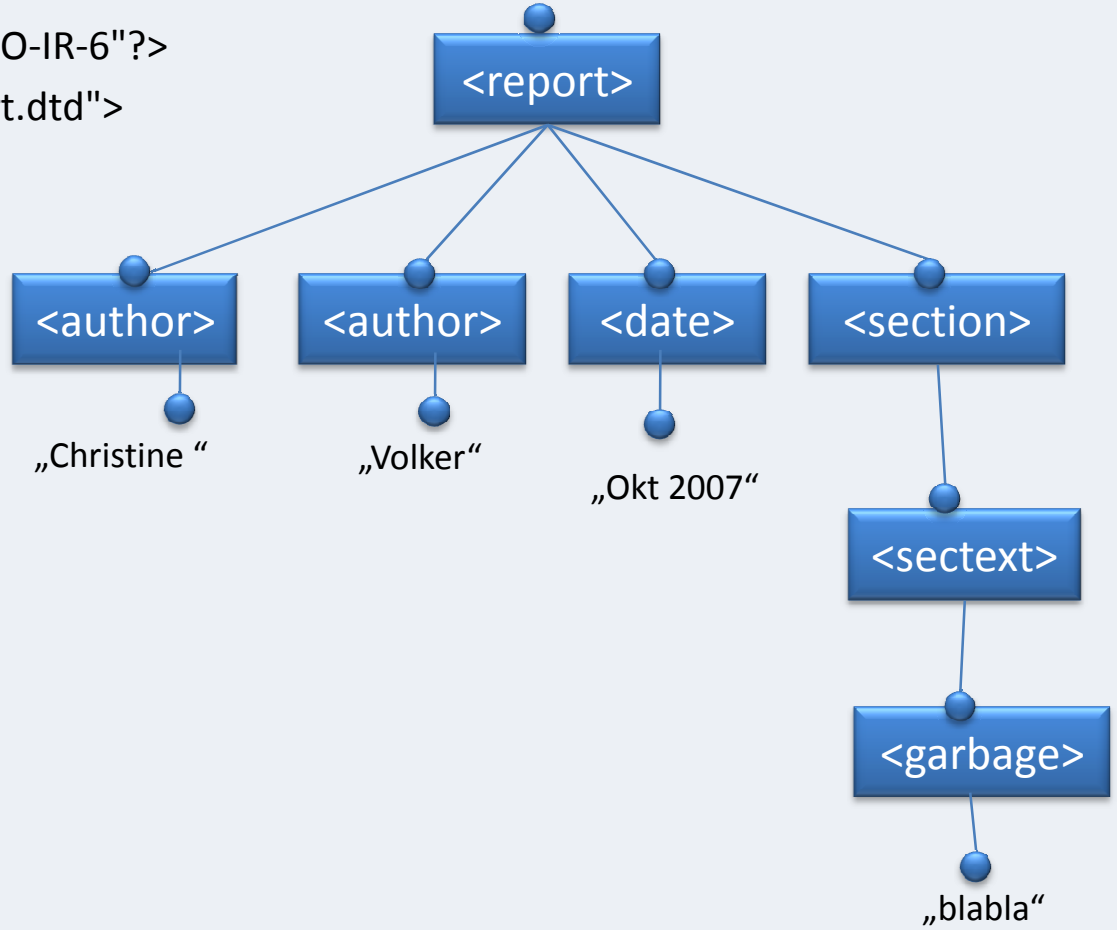
Gemeinsame, Plus-, und Minus-Elemente



Report.xml

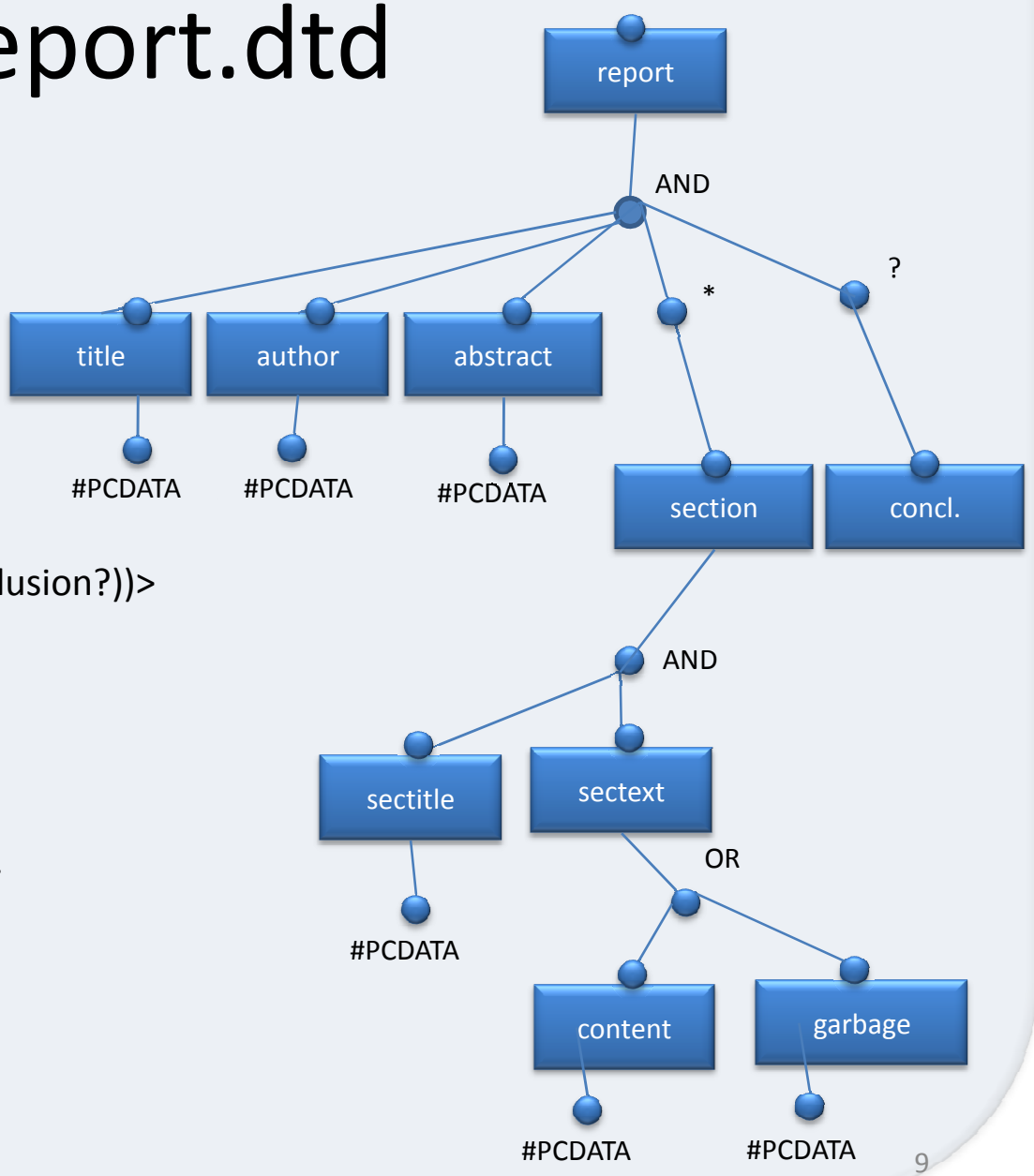
```
<?xml version="1.0" encoding="ISO-IR-6"?>
<!DOCTYPE report SYSTEM "report.dtd">
<report>
 <title>Titel</title>
 <author>Christine</author>
 <author>Volker</author>
  <date>Okt 2007</date>
  <section>
   <sectext>
     <garbage>blabla</garbage>
   </sectext>
  </section>
</report>
```



Report.dtd

```
<!-- XML DTD "report.dtd" -->

<!ELEMENT report
     (title,author,abstract,(section*),(conclusion?))>
 <!ELEMENT title (#PCDATA)>
 <!ELEMENT author (#PCDATA)>
 <!ELEMENT abstract (#PCDATA)>
 <!ELEMENT section (sectitle,sectext)>
  <!ELEMENT sectitle (#PCDATA)>
  <!ELEMENT sectext (content|garbage)>
     <!ELEMENT content (#PCDATA)>
     <!ELEMENT garbage (#PCDATA)>
 <!ELEMENT conclusion (#PCDATA)>
```



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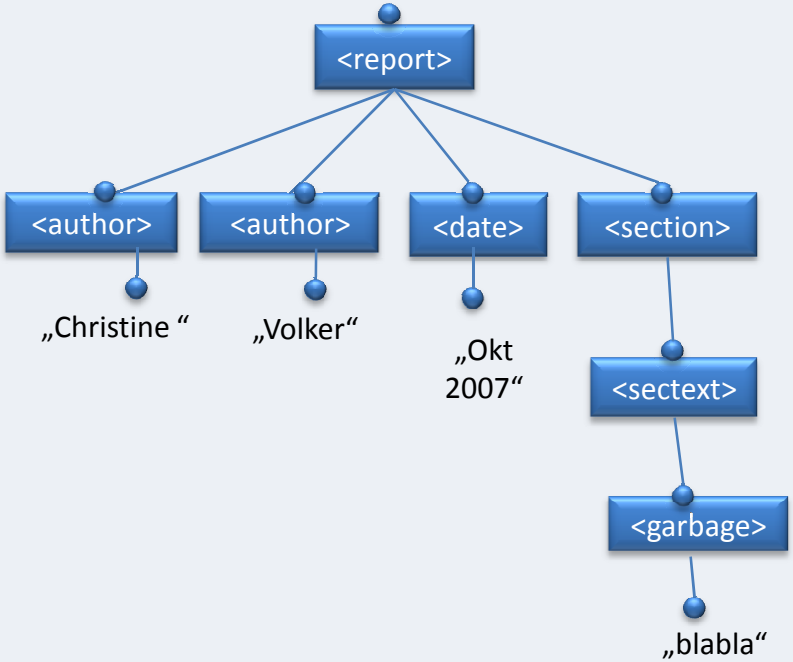
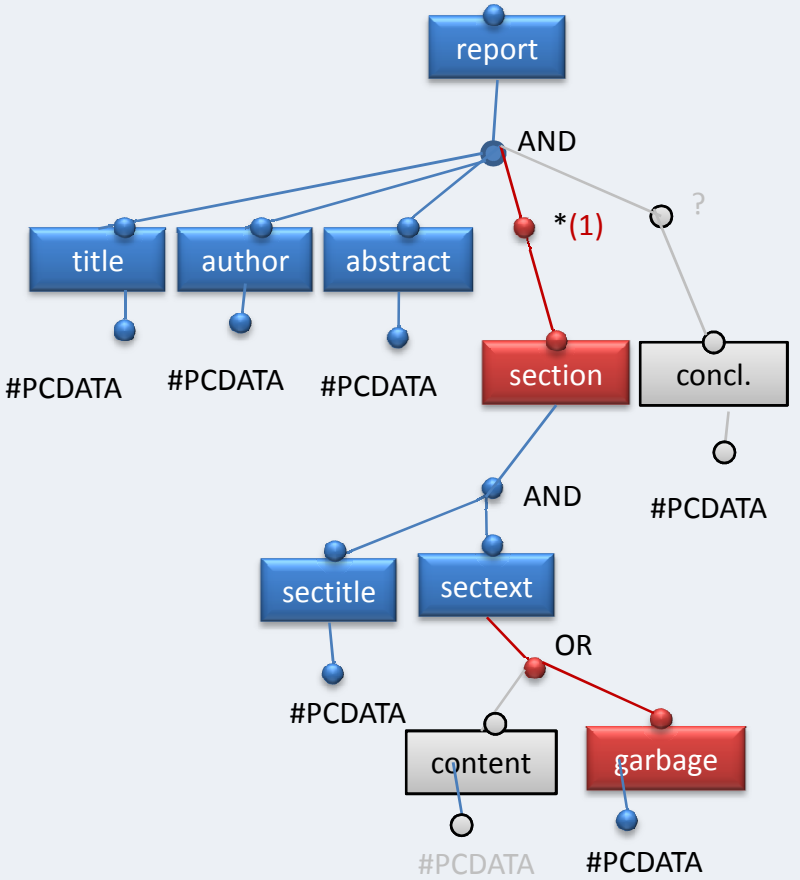
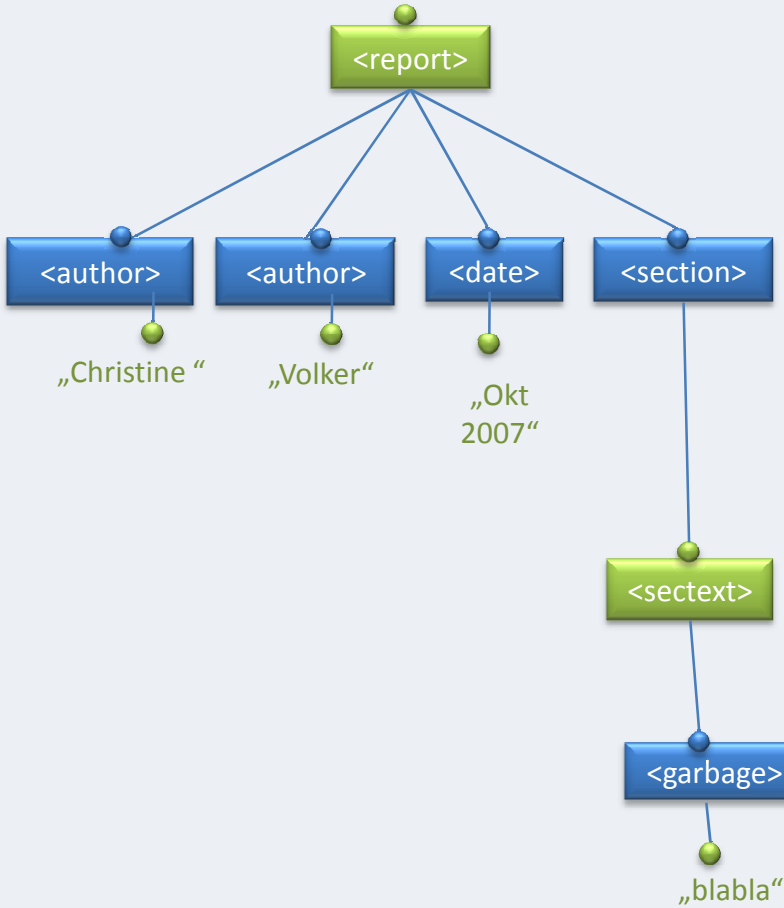
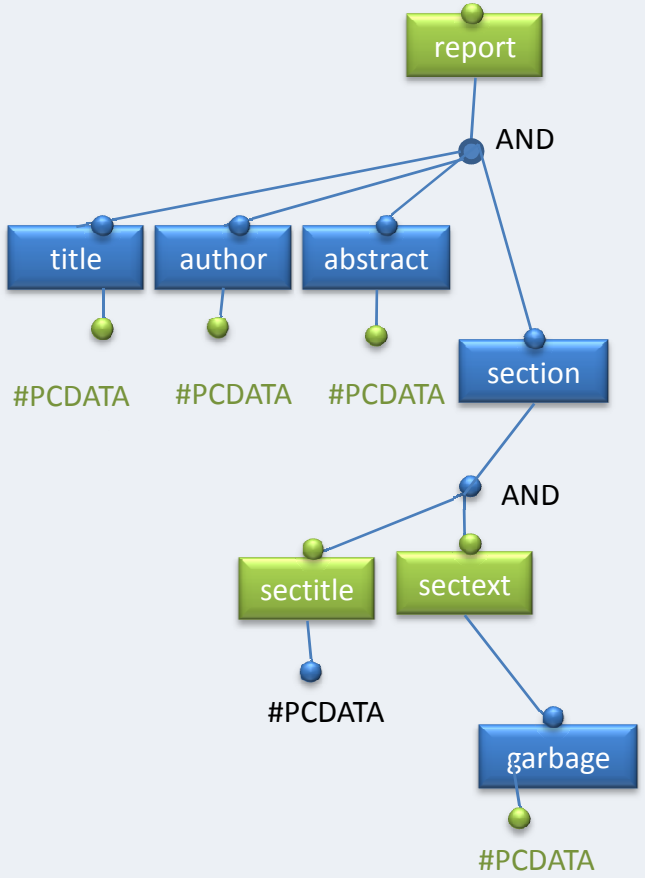
Auswahl der Instanz-DTD





Ähnlichkeit zur Instanz-DTD





(p, m, c)
(0,0,1)
(2,2,2)
(2,3,2)
(0,1,1)
(0,0,1)

Ähnlichkeitsmaß

(p, m, c)	Level Weight (γ=2)	W · (p,m,c)
(0,0,1)	16	(0,0,16)
(2,2,2)	8	(16,16,16)
(2,3,2)	4	(8,12,8)
(0,1,1)	2	(0,2,2)
(0,0,1)	1	(0,0,1)
		(24,30,43)

α,β (≥ 0) sind die Gewichtung der Plus- und Minus-Elemente.

$$\varepsilon((p, m, c)) = \frac{c}{\alpha * p + c + \beta * m}$$

Konvention: $\alpha = \beta = 1$

$\varepsilon((24,30,43)) = 0,44$

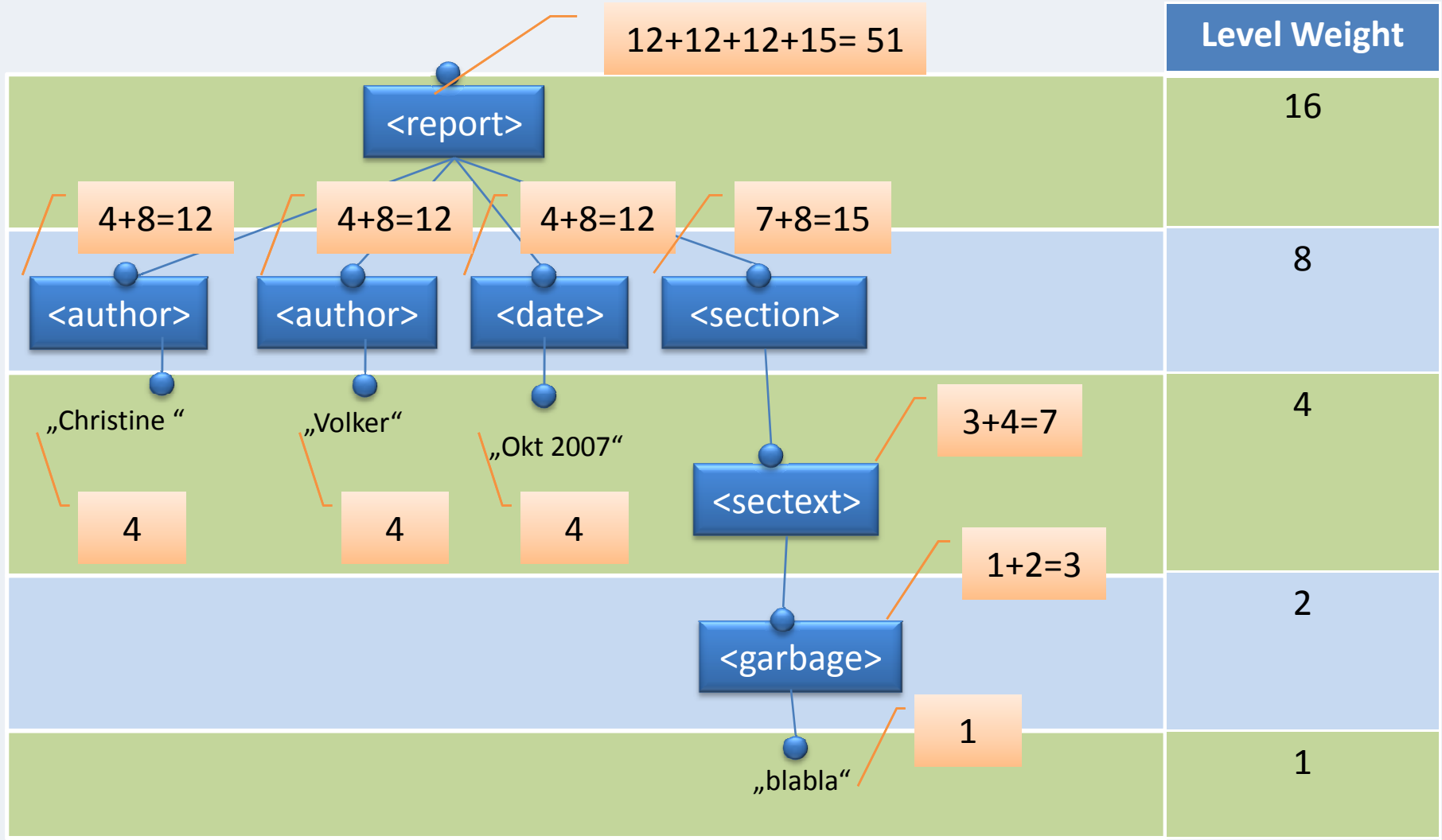
ε liegt immer zwischen 0 und 1.

ε = 1 gilt bei Dokumenten, die mit der DTD bis auf die Tag-Reihenfolge übereinstimmen.

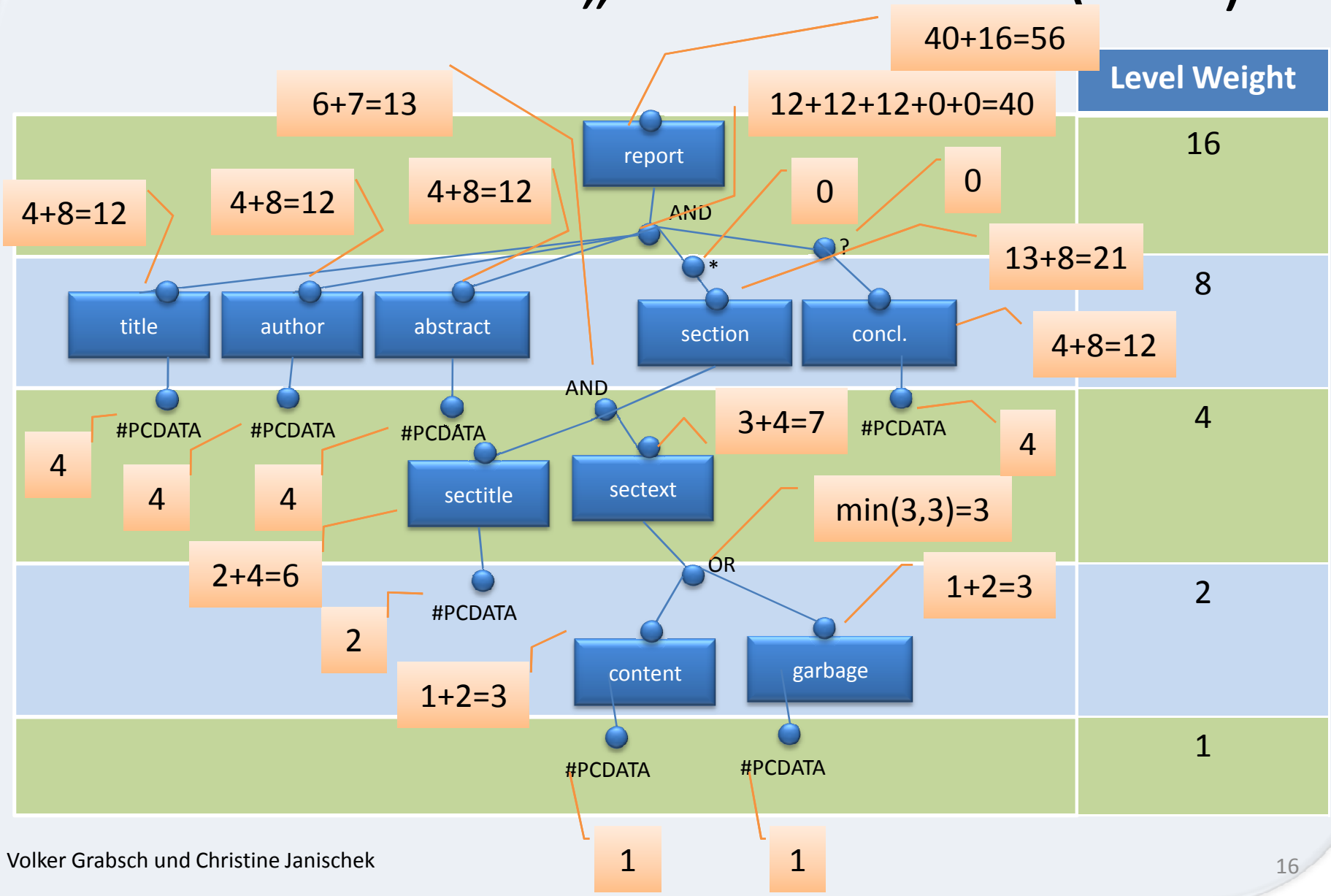
Gewicht eines Teilbaums (W)

- In der „Weight function“ wird die Anzahl der Elemente mit dem jeweiligen Level multipliziert und dann kummuliert.
- Wurzelnahe Elemente sind mehr Wert als entfernte Elemente.
- DTD: Optionale oder wiederholende Elemente werden dabei nicht berücksichtigt
- DTD: Bei „OR“ wird der Teilbaum mit dem kleinsten Gewicht ausgewählt.

Gewicht eines „p“-Teilbaums (XML)



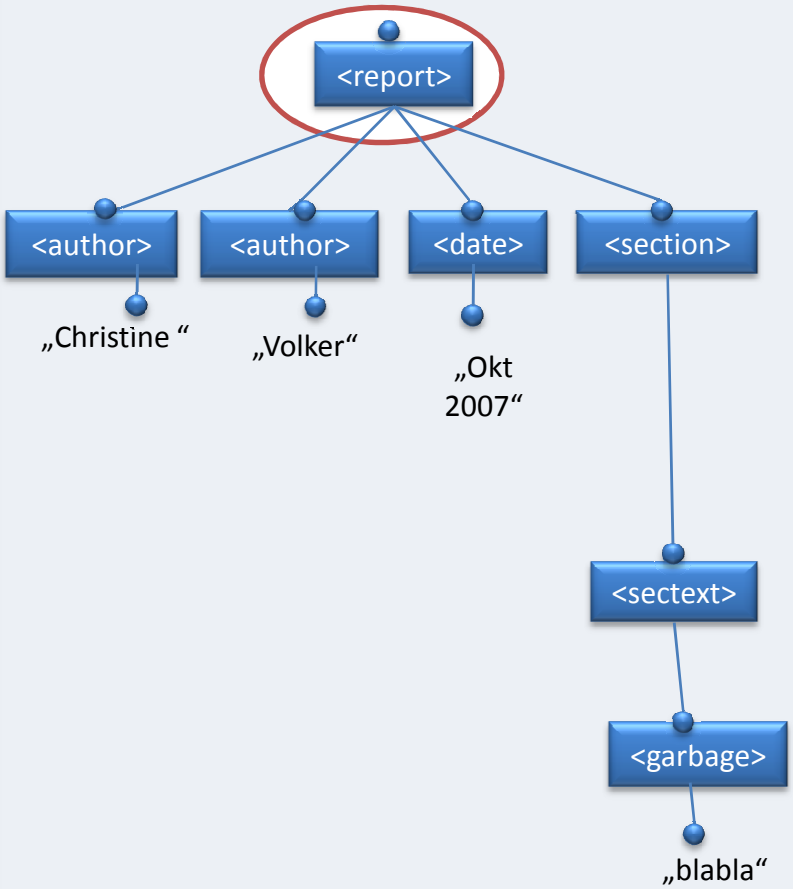
Gewicht eines „m“-Teilbaums (DTD)

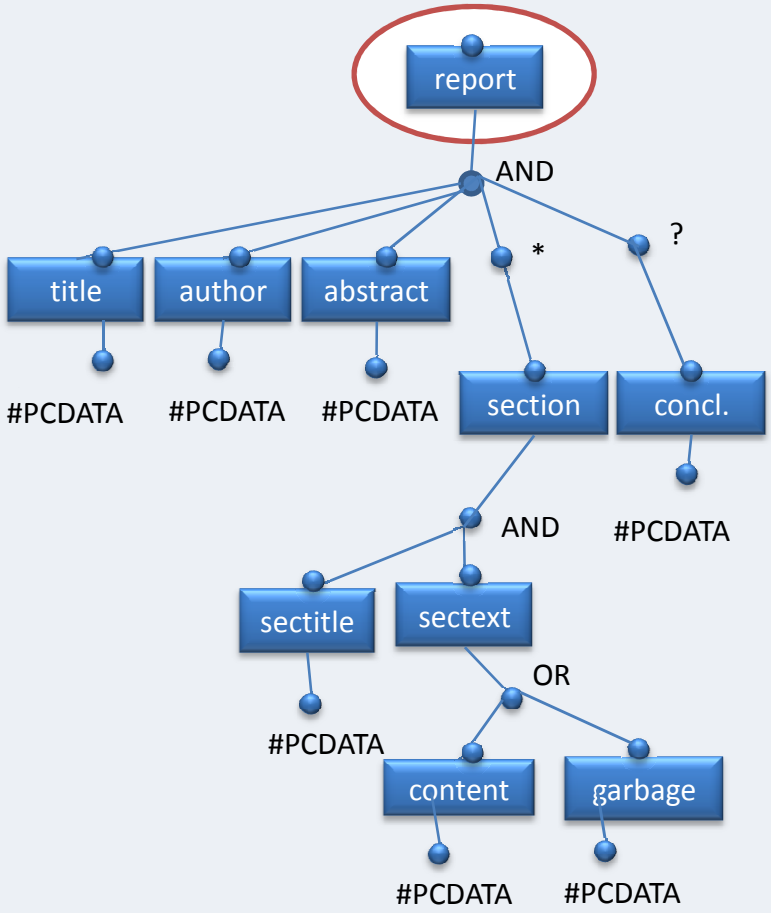


Matching Algorithm (M)

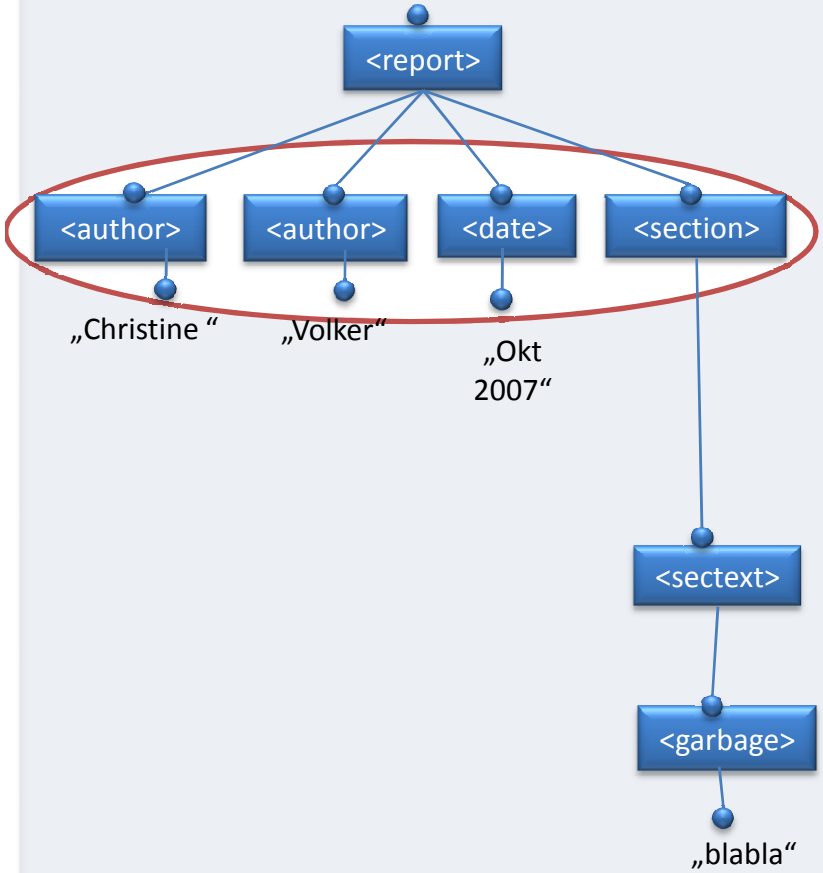
- Naive Lösung: „generate and test“ für alle Instanz-DTDs – nicht praktikabel.
- Besserer Weg:
  - Phase 1: Vom Wurzelelement (root) abwärts , werden die Teile des Baumes rekursiv abgearbeitet.
  - Phase 2: Bei der Rückkehr des rekursiven Aufrufs (backtracking) werden die Alternativen ausgewertet und die Beste ausgewählt.

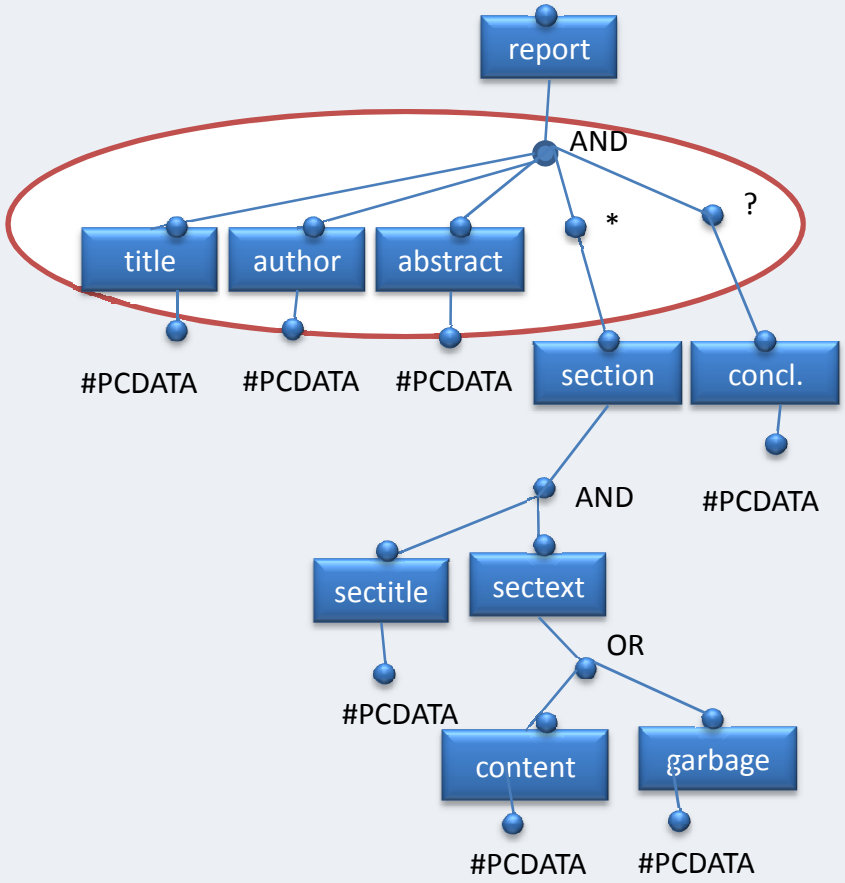
Matching Algorithm (M)



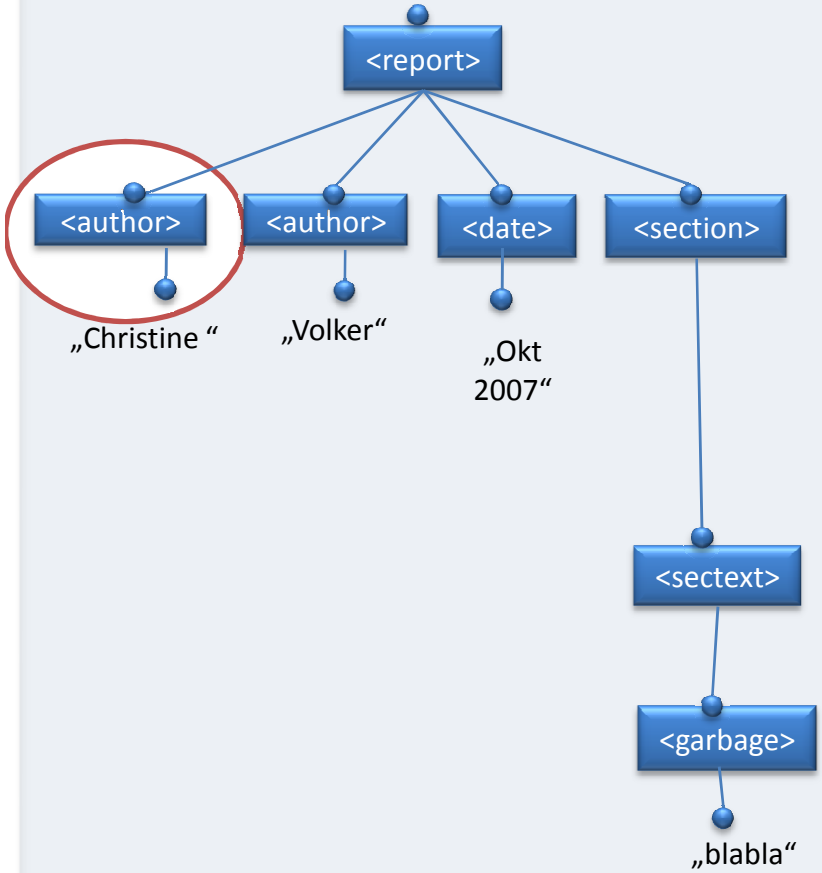


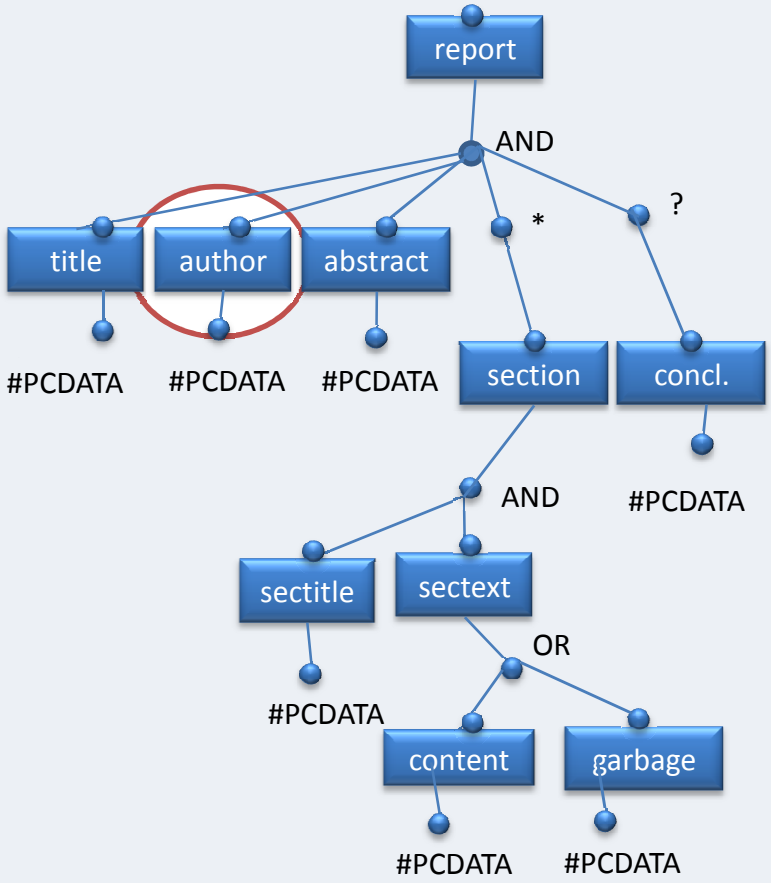
Matching Algorithm (M)





Matching Algorithm (M)





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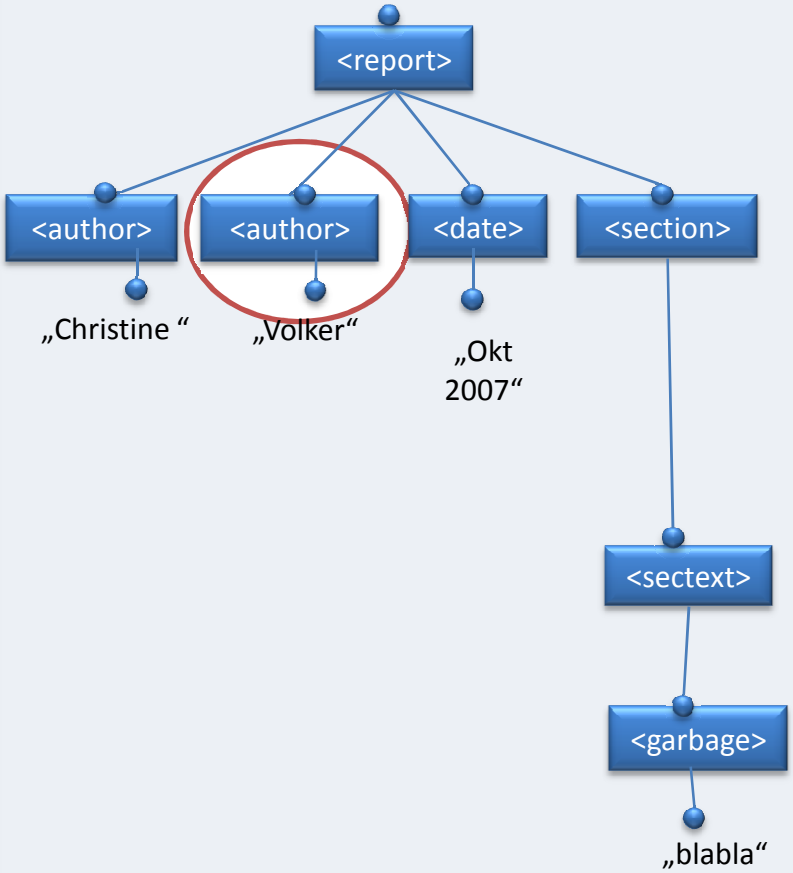
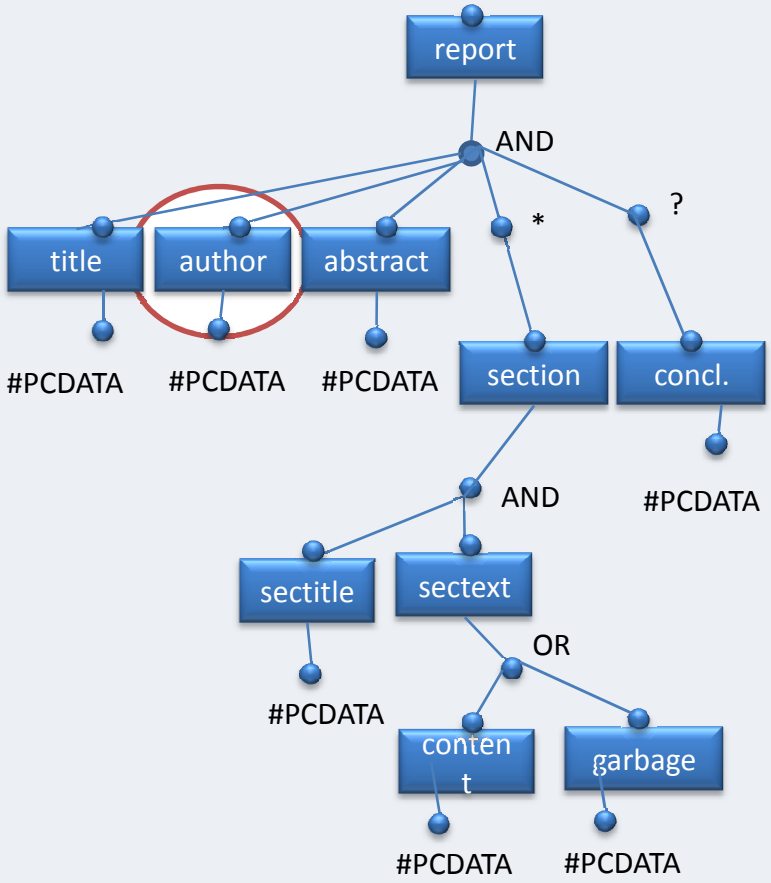
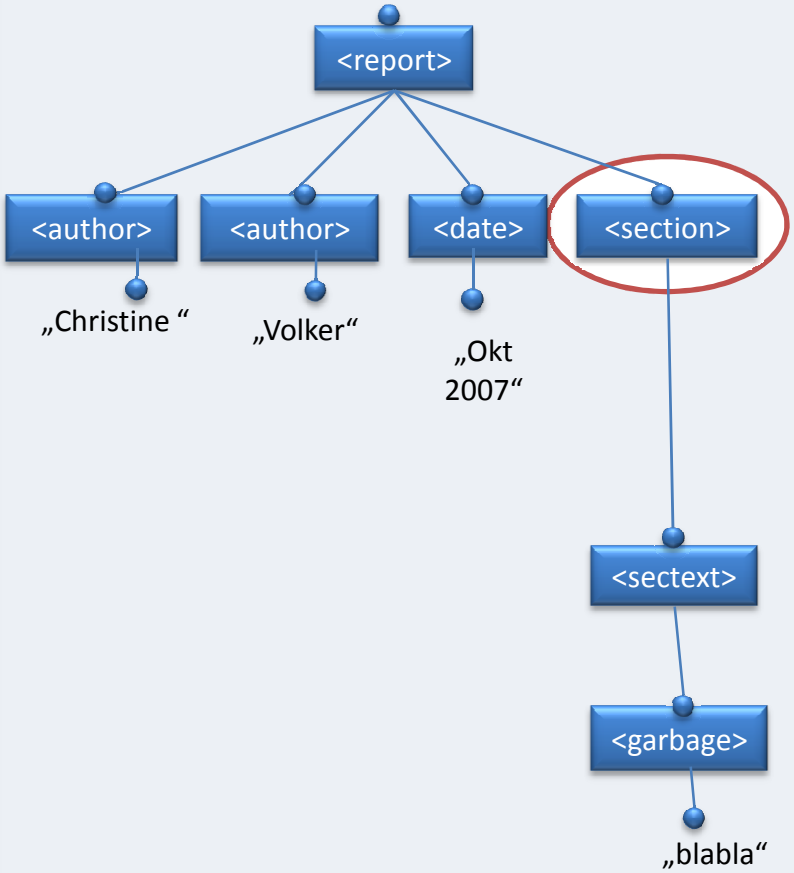
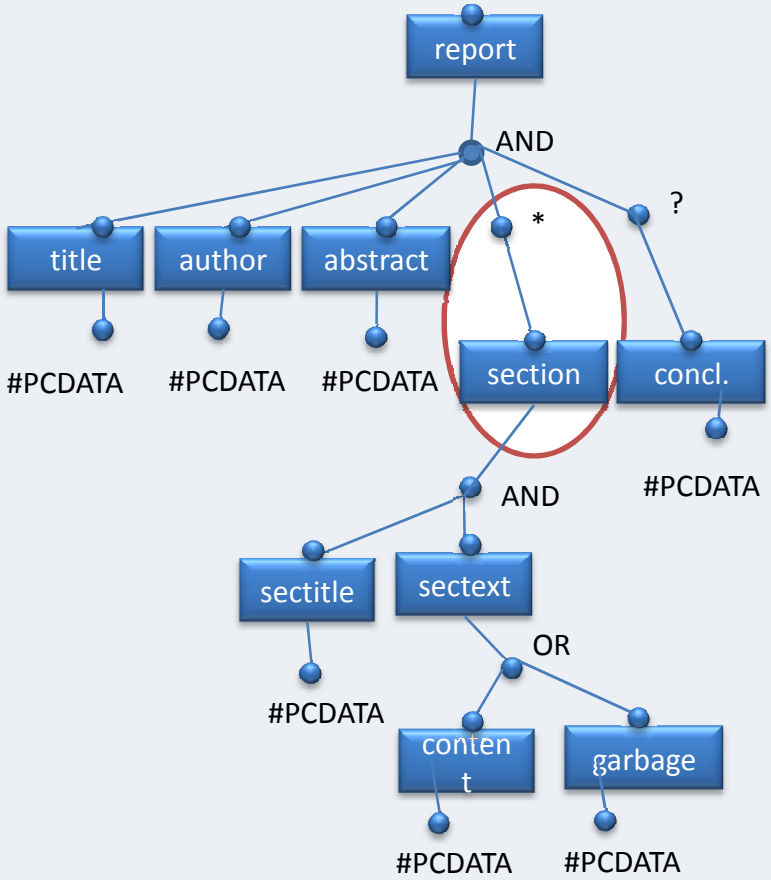




Matching Algorithm (M)





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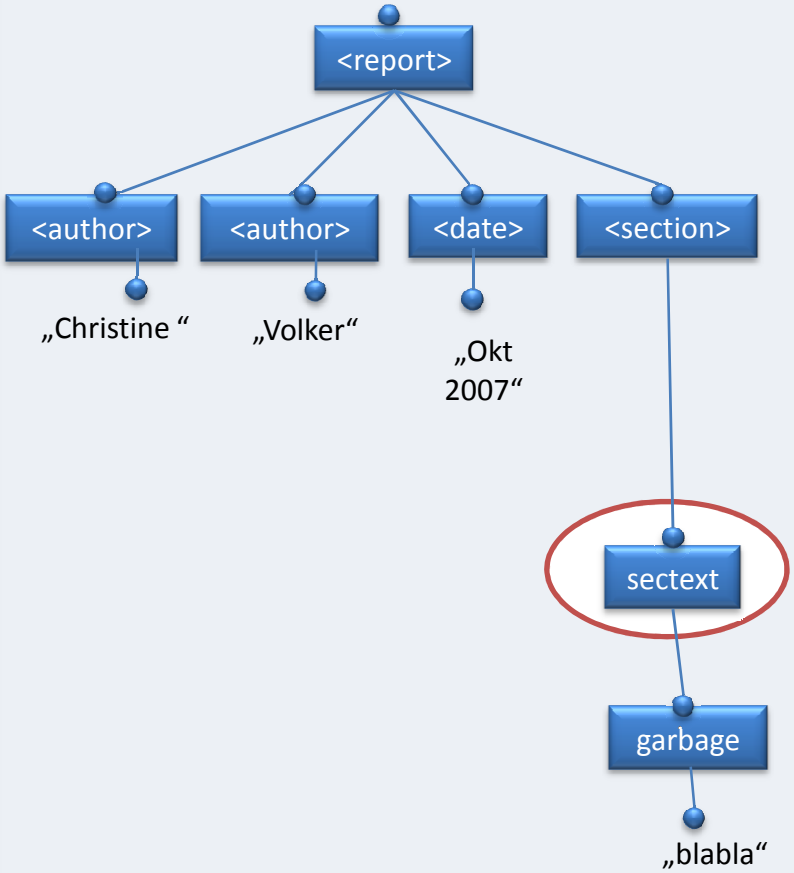

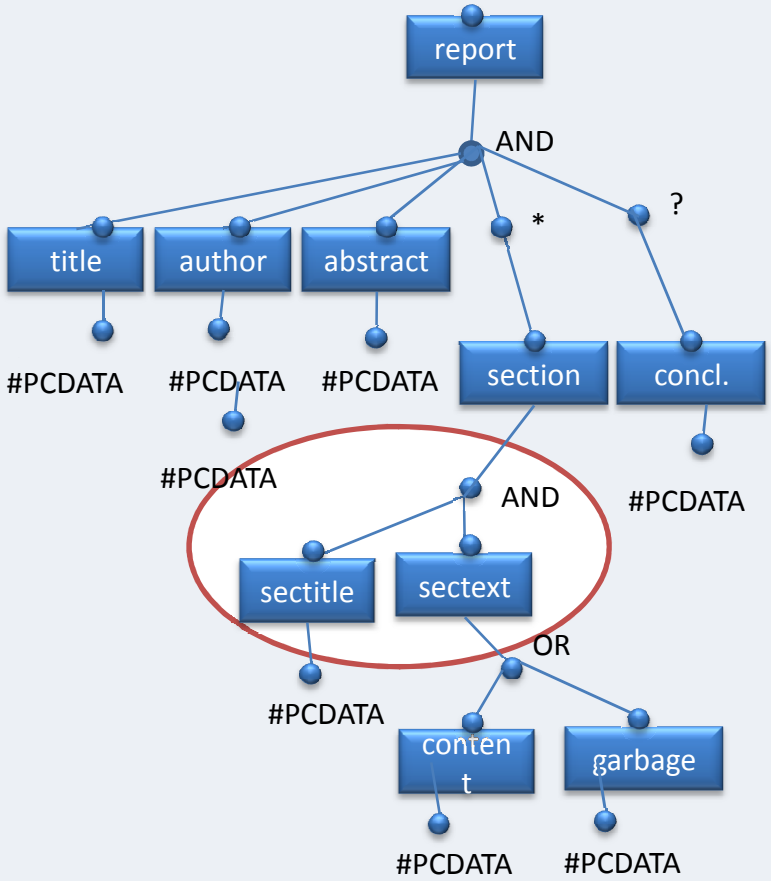

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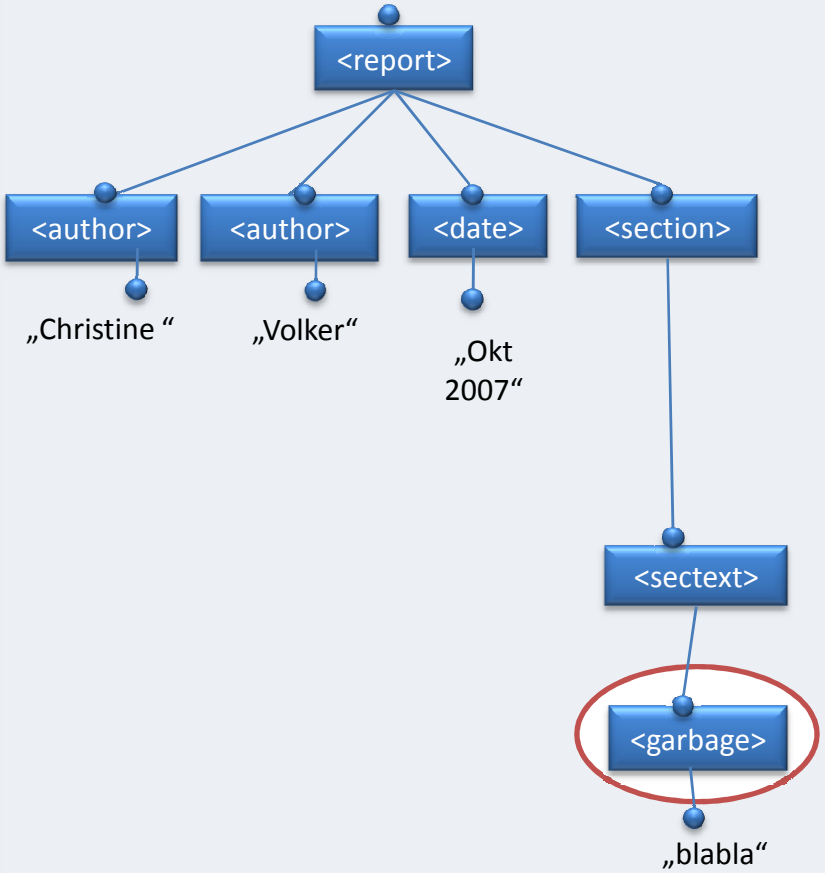

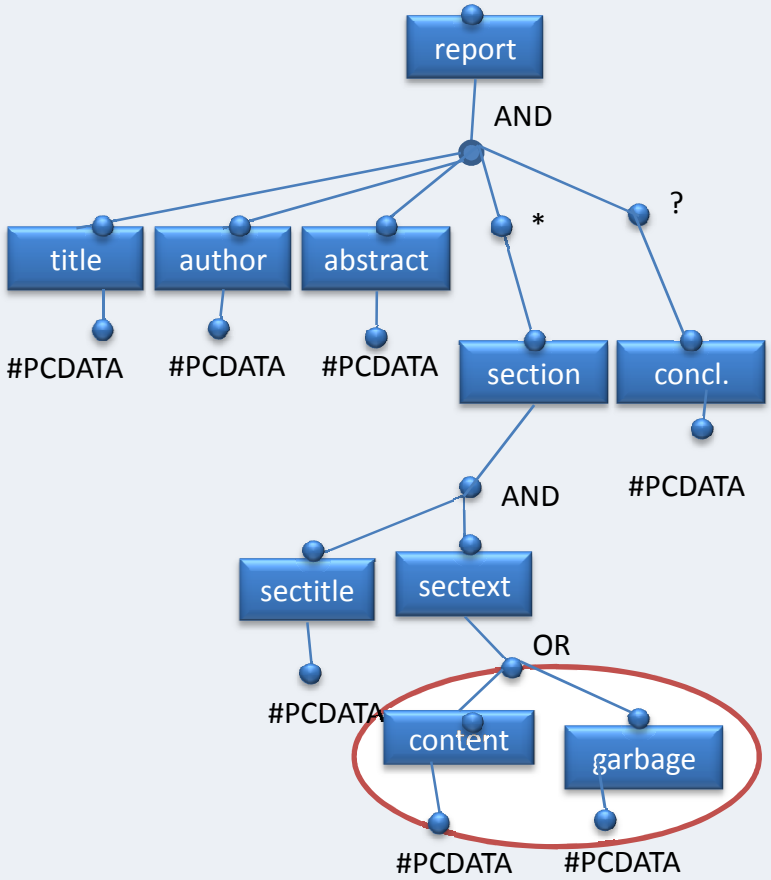

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