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How to build a Search-Engine with Common Unix-Tools

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Resources available

http://www.smiffy.de/dbkda-2018/ [1]

- Slideset
- Exercises
- Command refcard

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Outlook

- General Architecture of an IR-System
  - Naive Search
  - Boolean Search
  - Vector Space Model
  - Inverted Index
  - Query Processing
- Overview of useful Unix Tools
- Implementation Aspects
- Summary

+ 2 hands on exercices

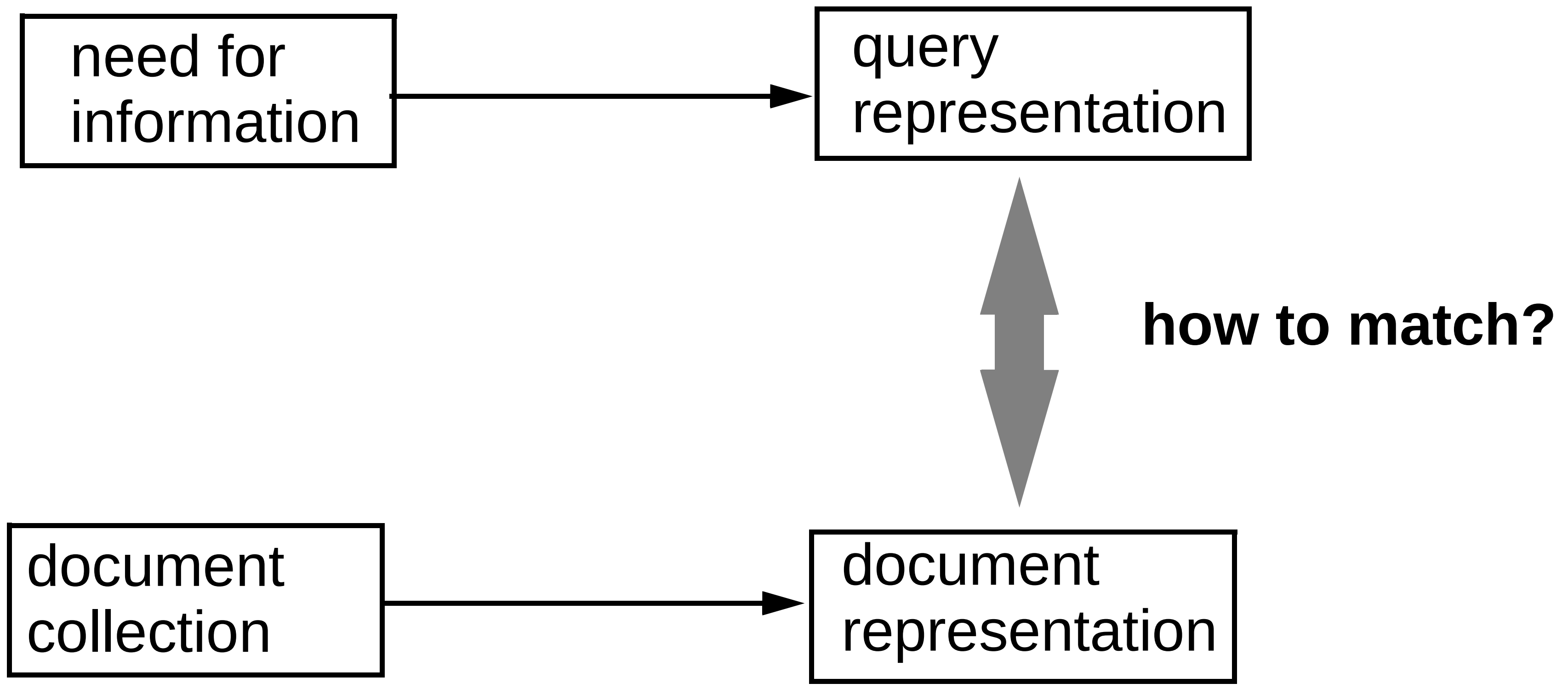
- Text analytics
- Building an Inverted Index & Query processing

What is Information Retrieval ?

Information Retrieval (IR) is finding material (usually documents) of an unstructured nature (usually text) that satisfies an information need (usually a query) from within large collections (usually stored on computers).

[Manning et al., 2008]

What is Information Retrieval ?



Keyword Search

- Given:
  - Number of Keywords
  - Document collection
- Result:
  - All documents in the collection, cotaining the keywords
  - (ranked by relevance)

Naive Approach

- Iterate over all documents d in document collection
  - For each document d, iterate all words w and check, if all the given keywords appear in this document
  - if yes, add document to result set
- Output result set

- Extensions/Variants
  - Ranking
  - multiword terms (***New York***)
  - ’near’ semantic (i.e. ***trump*** near ***russia***)

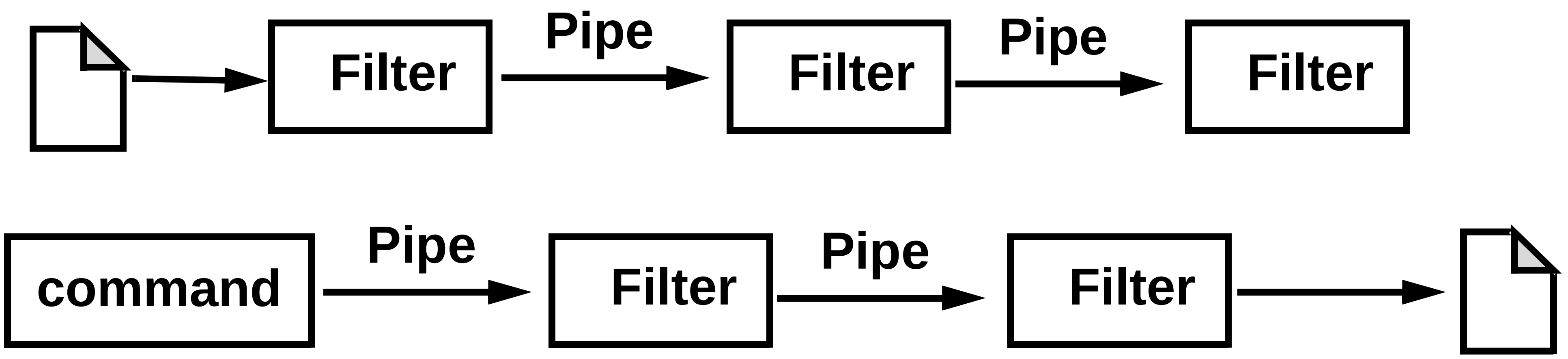
see examples later ....

Naive Approach

- Advantages:
  - Good for small and medium size datasets
  - No index need to be build before
  - Speed: up to 2 GB per second
- Disadvantages:
  - Not feasable for larger datasets (100 GB: 1 min. per search request)
  - Potentiell additional preprocessing for each query needed
- Implementation with the shell using the commands
  - grep (main work)
  - tr, sort, sed, uniq, sort, cut, join (pre-/postprocessing)

Data Processing with the Shell

- Architectural Pattern: Pipes and Filters (Douglas McIlroy, 1973)
- Data exchange between processes
- Loose coupling
- POSIX Standard
- Filter represent data-sources and data-sinks



Shell commandos in the Linux/Unix/Cygwin Environment

- Input-/Output channels
  - Standardinput (STDIN)
  - Standardouput (STDOUT)
  - Standarderror (STDERR)
- In-/Output Redirection
  - > : Redirect Standardoutput (into file)
  - < : Redirect Standardinput (from file)
  - 2> : Redirect Standarderror (into file)
  - >> : Redirect Standardoutput (append into file)
  - | : Pipe operator: Connect Standardoutput of a command with Standardinput of the next command
- Example:

```
cut -d, -f1 city.csv | sort | uniq -c | sort -nr | \
    awk  '$1>1 {print $2}' > result.txt
```

Overview of Commands used in this Tutorial

- **grep**: print lines matching a pattern
- **tr**: translate or delete characters
- **comm**: compare two sorted files line by line
- **uniq**: report or omit repeated lines
- **join**: join lines of two files on a common field
- **cat**: concatenate files and print on the standard output
- **sort**: sort lines of text files
- **sed**: stream editor for filtering and transforming text
- **awk**: pattern scanning and processing language
- **wc:** Counts words, bytes, lines
- **cut:** Extracts columns from a file
- ...

General comment

- Most of the commands accept the input from file or from STDIN. If no (or not enough) input files are given, it is expected that the input comes from STDIN

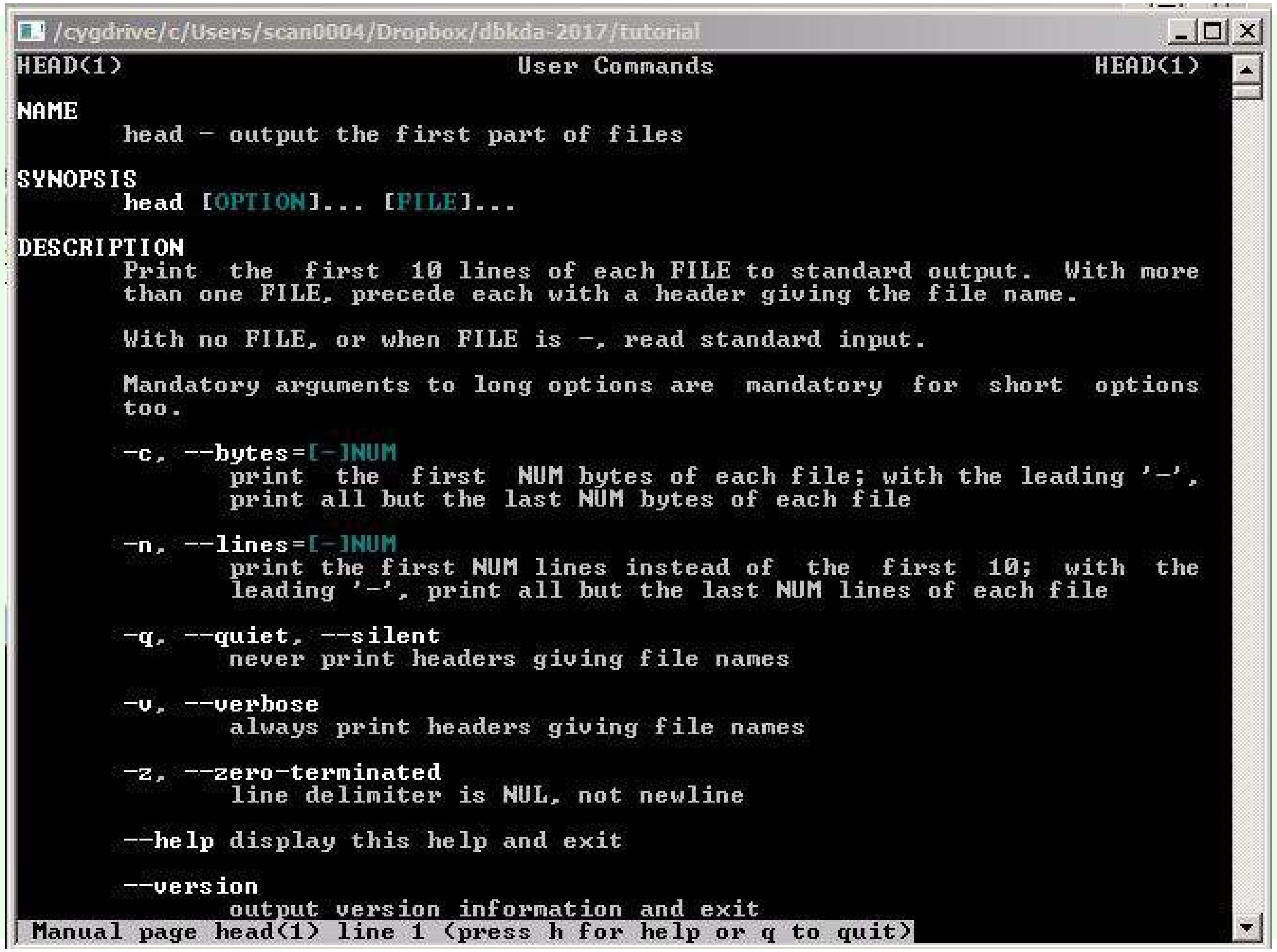
```
head -n4 my-file.txt
cat -n my-file.txt | head -n4
```

- Most of the commands have a lot of options which couldn’t be explained in detail. To get an overview of the possibilities of a command, simple type

```
man command
```

- Example:

```
man head
```



```
HEAD(1)                          User Commands                          HEAD(1)

NAME
       head - output the first part of files

SYNOPSIS
       head [OPTION]... [FILE]...

DESCRIPTION
       Print  the  first  10 lines of each FILE to standard output.  With more
       than one FILE, precede each with a header giving the file name.

       With no FILE, or when FILE is -, read standard input.

       Mandatory arguments to long options are  mandatory  for  short  options
       too.

       -c, --bytes=[-]NUM
              print  the  first  NUM bytes of each file; with the leading '-',
              print all but the last NUM bytes of each file

       -n, --lines=[-]NUM
              print the first NUM lines instead of  the  first  10;  with  the
              leading '-', print all but the last NUM lines of each file

       -q, --quiet, --silent
              never print headers giving file names

       -v, --verbose
              always print headers giving file names

       -z, --zero-terminated
              line delimiter is NUL, not newline

       --help display this help and exit

       --version
              output version information and exit
 Manual page head(1) line 1 (press h for help or q to quit)
```

Online Search using grep

- Multi line phrase match:

```
$ cat multiline-match.txt
This is an example of a multi line
match. In this case the phrase 'multi line match'
should be found, even if the words appear in
separate lines.
$ cat multiline-match.txt | tr '\n' ' '| grep -o 'multi line
match'
multi line match
multi line match
```

Search for ’teaching’ near ’students’

```
$ less papers/1273.txt
The teaching is created with
students despite the number
which is about one hundred and
fifty. The lecturer asks ques-
tions related to the study ...
```

```
$ tr -cs < papers/1273.txt \
    'A-Za-z'  '\n' | less
The
teaching
is
created
with
students                n-words distance
despite
the
number
which
is
about
one
hundred
```

Search for ’teaching’ near ’students’

```
$ tr < ../proceedings/papers/1273.txt  -cs 'A-Za-z0-9'  '\n'| \
   grep -5 teaching|less
--
ask
questions
fig
1
The
teaching
is
created
with
students
despite
--
the
```

grep with additional context
(n-lines before/after the match)

Search for ’teaching’ near ’students’

```
export MAX_DIST=5
export TXT_DOCS=papers/*.txt
rm -f result.txt
for f in $TXT_DOCS; do
     tr -sc '[A-Za-z]+' '\n' < $f | tr 'A-Z' 'a-z' > $f.2;
     grep -H -$MAX_DIST -i teaching $f.2 | grep -i students | \
      sed -r 's#\.2[-:][a-z]+$##' >> result.txt
done
rm -f $TXT_DOCS.2
uniq -c result.txt | sort -nr|less
```

- Output (sorted by decreasing relevance)

```
11 ../proceedings/papers/1273.txt
 8 ../proceedings/papers/1442.txt
 3 ../proceedings/papers/1351.txt
 3 ../proceedings/papers/1250.txt
 3 ../proceedings/papers/1210.txt
 3 ../proceedings/papers/1140.txt
 3 ../proceedings/papers/1121.txt
 3 ../proceedings/papers/1114.txt
 2 ../proceedings/papers/1504.txt
 2 ../proceedings/papers/1464.txt
 2 ../proceedings/papers/1303.txt
 2 ../proceedings/papers/1298.txt
 ...
```

Exercise I

Download Exercise 1 from

http://www.smiffy.de/dbkda-2018/IR-exercise-1.pdf

with solutions:

http://www.smiffy.de/dbkda-2018/IR-exercise-1-solution.pdf

Online Search - Discussion

- Good for small and medium size datasets
- No additional datastructure/tools/systems needed
- Disadvantage: Speed to perform online search, if document base is big

- Alternate Approach:
  - Build an appropriate datastructure for fast retrieval (offline)
  - Query the datastructure

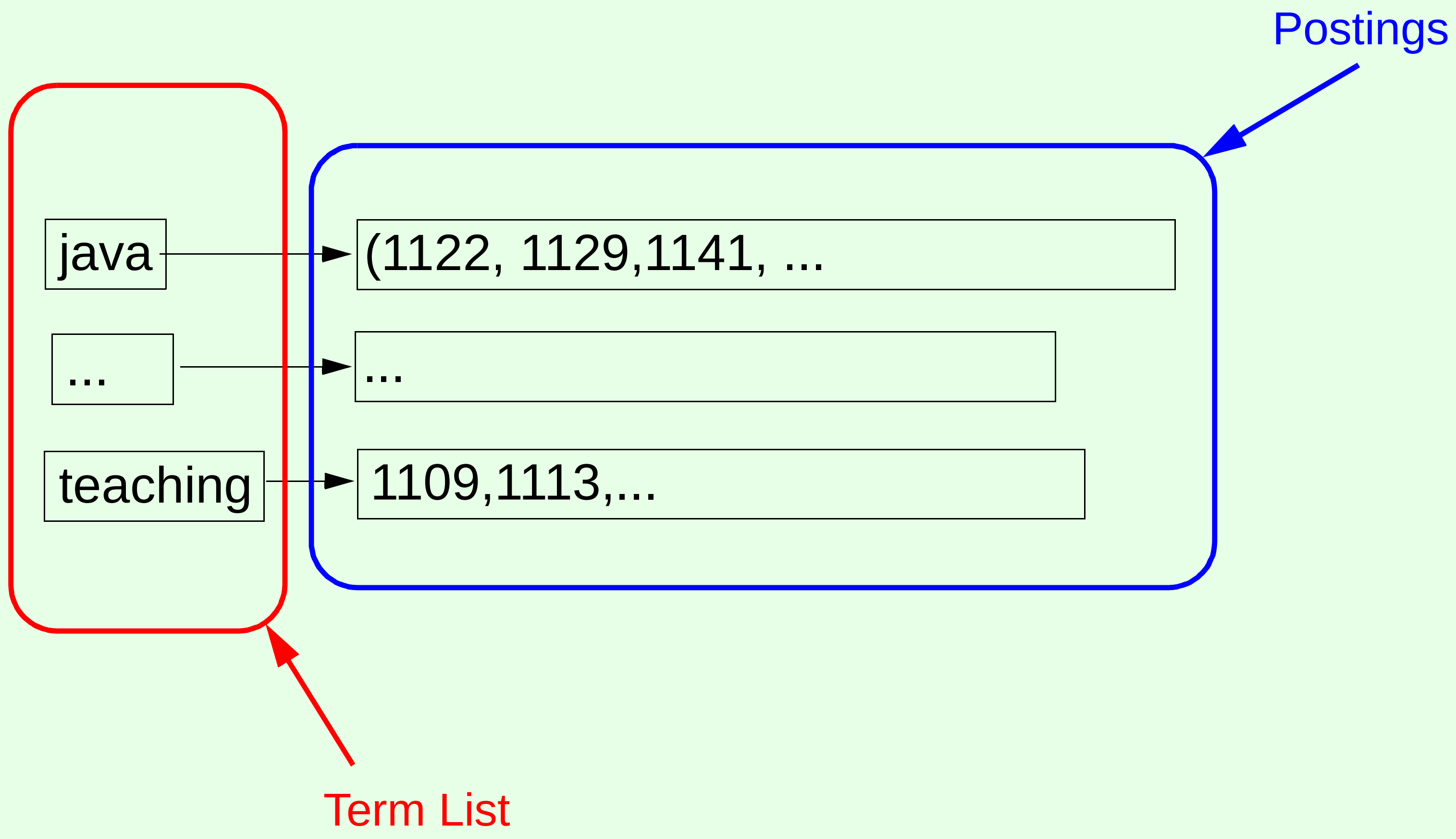
Inverted Index

- Document-set datastructure:

```
...
document_n   -> (sorted list of words in document_n)
document_n+1 -> (sorted list of words in document_n+1)
...
```

- Needed: Alternate datastructure, to store information, in which documents a word appears
- General structure (words sorted alphabetically):

```
...
word_n   -> (sorted list of documents containing word_n)
word_n+1 -> (sorted list of documents containing word_n+1)
...
```


Postings
java
(1122, 1129,1141, ...
...
...
teaching
1109,1113,...
Term List

Principles

- Each document is considered as a set of words
- Typically, the term list is stored in memory with a link to the document list (postings) on disk
- term list and posting list are stored sorted
- Disadvantage: No ranking possible

some statistics ...

- Conference Proceedings (IEEE EDUCON 2018)
- 300 papers
- 1473809 words alltogether
- 47288 different words (without stemming)
- 38033 different words (with stemming)
- avg: ~ 4913 words/paper
- avg: ~ 1139 different words/paper (without stemming)
- avg: ~7.5 documents per word

- Compare the amount of memory to be read using grep and using an inverted index
  - grep: 1,920,421 bytes
  - Inverted Index: Access word list + 7.5 document identifiers (on average)

General Indexer Principle
(Blocked, Sort-Based Indexing)

- For performance reason, each document-path is assigned a numeric ID, which is then used during the previously described process

- Collect all document-term pairs
- Sort pairs by their term (first criteria) and document identifier (second criteria)
- Collect all pairs (term, document) with the same term into a single entry of the inverted list.

Modeling an Inverted Index using Files

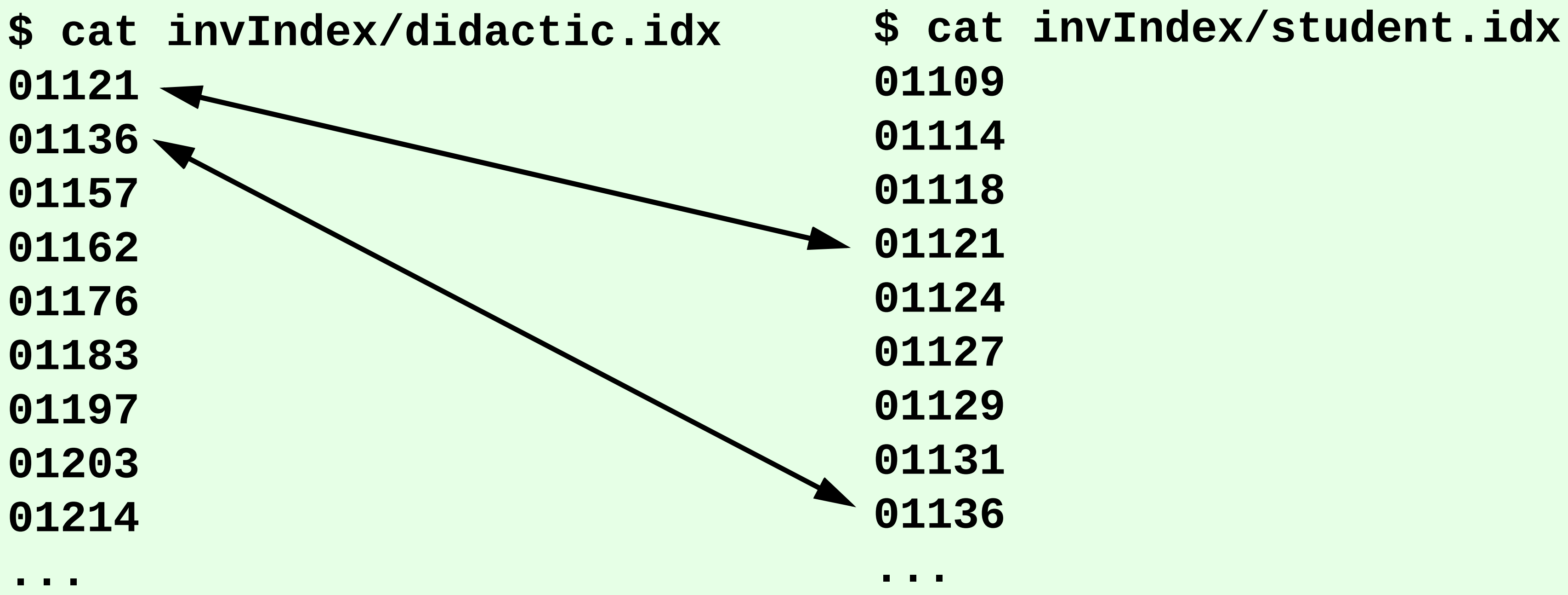
- Entries (words) represent files
- Postings (document IDs) are represented by the content (one document-ID per line)
- Postings are sorted by ID
- Example:

```
$ cat invIndex/drivers.txt
01207
01226
01234
01242
01279
01363
...
```

- Eventually using subfolders to keep number of files per directory small

How to Process a Query

- Example: Search for documents containing the word didactic and student



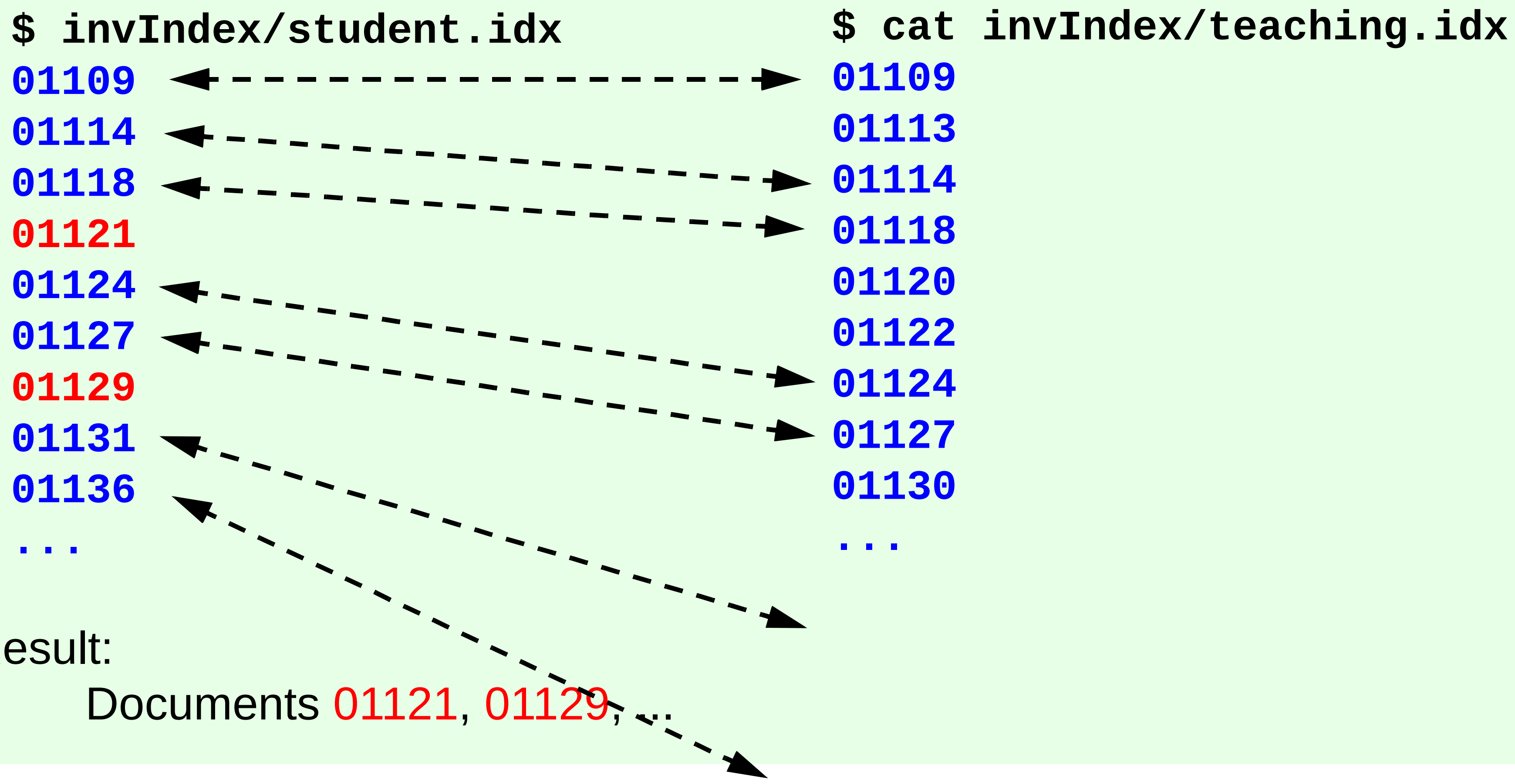
```
$ cat invIndex/didactic.idx
01121
01136
01157
01162
01176
01183
01197
01203
01214
...
```

```
$ cat invIndex/student.idx
01109
01114
01118
01121
01124
01127
01129
01131
01136
...
```

- Result:

  Documents 01121, 01136, ...

- Example: Search for documents containing the word student, but not teaching



```
$ invIndex/student.idx          $ cat invIndex/teaching.idx
01109                           01109
01114                           01113
01118                           01114
01121                           01118
01124                           01120
01127                           01122
01129                           01124
01131                           01127
01136                           01130
...                             ...
```

- Result:

  Documents 01121, 01129, ...

Step 1: Transform all PDF-Documents to Text Format

```
# We assume, that we have a number of pdf documents to index.
# In this case, we use xpdf [1]

export XPDF=c:/Programme/xpdf-3.0/bin64/pdftotext.exe
export PDF_DOCS=papers/*.pdf

#!/usr/bin/bash
for f in $PDF_DOCS; do
      $XPDF $f;
done

# Result: For every pdf document, a txt-document with the same
# name is generated in the same directory
```

[1] https://www.xpdfreader.com/

Step 2: Assign each File a Unique Document ID

- List all documents and add a line number

```
ls papers/*.txt| cat -n
     1  papers/1109.txt
     2  papers/1112.txt
     3  papers/1113.txt
     4  papers/1114.txt
     ...
```

- Format the output

```
ls papers/*.txt| cat -n | awk '{printf "%04d:%s\n", $1, $2}' \
    > file-id.map
0001    papers/1109.txt
0002    papers/1112.txt
0003    papers/1113.txt
0004    papers/1114.txt
...
```

Step 3: Extract different words from a Document

```
# Tokenize the text document.
# We look for the regex-pattern [A-Za-z]+ (1-n characters) and
# print them to STDOUT. With the -o option, we only print the
# matching part. Because multiple files are given, grep adds the
filename in front of each word.
#
$ grep -o -E '[A-Za-z]+' papers/*.txt
papers/1109.txt:The
papers/1109.txt:influence
papers/1109.txt:of
papers/1109.txt:class
papers/1109.txt:attendance
papers/1109.txt:on
papers/1109.txt:the
papers/1109.txt:throughput
...
```

Step 4: Lowercase all, sort by term

- Lowercase everything

```
grep -o -E '[A-Za-z]+' papers/*.txt| tr 'A-Z' 'a-z' > doc-term.txt
papers/1109.txt:the
papers/1109.txt:influence
papers/1109.txt:of
papers/1109.txt:class
papers/1109.txt:attendance
...
```

- Sort by term (first criteria) and by filename (second criteria)

```
sort -t: -k2,2 -k1,1 doc-term.txt
papers/1109.txt:a
papers/1109.txt:a
...
papers/1112.txt:a
papers/1112.txt:a
...
```

Step 5: Remove Duplicates

- Remove Duplicates

```
sort -t: -k2,2 -k1,1 doc-term.txt |uniq > term-file.txt
papers/1109.txt:a
papers/1112.txt:a
papers/1113.txt:a
papers/1114.txt:a
...
papers/247.txt:a
papers/1236.txt:aaai
papers/1330.txt:aaai
...
```

Step 6: Replace document-name by ID

```
$ sort -t: term-file.txt|head -n5
papers/1109.txt:a
papers/1109.txt:about
papers/1109.txt:absenteeism
papers/1109.txt:abstract
papers/1109.txt:ac
```

```
$ head -n5 file-id.map
0001:papers/1109.txt
0002:papers/1112.txt
0003:papers/1113.txt
0004:papers/1114.txt
0005:papers/1118.txt
```

```
$ sort -t: term-file.txt |  join -11 -22 -t: - file-id.map -o1.2,2.1
a:0001
about:0001
absenteeism:0001
abstract:0001
ac:0001
academia:0001
academic:0001
```

join-columns

column
separator

output columns

- Sort byTerm

```
$ sort -t: term-file.txt |  join -11 -22 -t: - file-id.map \
  -o1.2,2.1|sort -t: -k1,2 | tee invIndex.idx
a:0001
a:0002
...
a:0299
a:0300
aaai:0086
aaai:0140
aaai:0143
...
```

Next step:

- Write all entries with same term in a single file

awk-Intro needed

Generate file-based entry

- File: write-inverted-index-to-file.awk

```
{
  if ($1 != last) {
     print $2 > DIR"/"$1".txt"
     last = $1
  } else {
     print $2 >> DIR"/"$1".txt"
  }
}
```

create a new file

append to file

- Execution:

```
awk -F: -v DIR=d:/data/invIndex \
    -f write-inverted-index-to-file.awk invIndex.idx
```

Generated Inverted Index:

```
$ invIndex/teaching.txt
0001
0003
0004
0005
0006
0007
...
```

```
$ ls invIndex/tea*
d:/data/invIndex/tea.txt
d:/data/invIndex/teach.txt
d:/data/invIndex/teachable.txt
d:/data/invIndex/teacher.txt
d:/data/invIndex/teachercentered.txt
d:/data/invIndex/teacherfocused.txt
d:/data/invIndex/teacherled.txt
...
```

Example Query:

- Search for documents, containing the keywords, teaching and students

```
$  comm -1 -2 ./teaching.txt ./students.txt | \
   join -11 -21 - file-id.map -t: -o2.2
papers/1109.txt
papers/1113.txt
papers/1114.txt
papers/1118.txt
papers/1121.txt
...
```

Boolean Search - Discussion

- Advantages/Disadvantages
  - + Easy to implement
  - - Small index (fast)
  - - No ranking possible

Ranking of Results

- Possible criteria:
  - The number of times, a word appears in a text
  - The relevance of the word ('whatever' vs. 'cambridge')
- Approach:
  - Store for each word, the number of times it appears in a document (Term Frequency - $tf_{term, doc}$)
  - Store for each word, in how many document it appears (Document Frequency - df_t)
- Ranking:
  - If a term appears more often in document A than in document B, document A is considered more relevant for the query
  - Terms which appears in a smaller number of documents have a higher weight

tf*idf (TFIDF)

- term frequency–inverse document frequency
- Measure how important a word for a document is
- $tf_{t,d}$: Measure, how many times a term t appears inside a document d (typically normalized)
- idf_t: Measure to distinguish important from unimportant terms
- Definition:

  df_t: In how many documents of the collection D does term t appear

  $idf_t = \log(N/df_t)$ # high for rare terms, low for frequent terms

  N: Number of documents in collection D
- Composite weight for each term in each document:

  $tfidf_{t,D} = tf_{t,d} * idf_t$

tf*idf (TFIDF)

- Score of a document with respect to a query with terms q (q_1, ..., q_n).

  score (q,d) = sum $_{t \text{ in } q}$**: tfidf**$_{t,doc}$

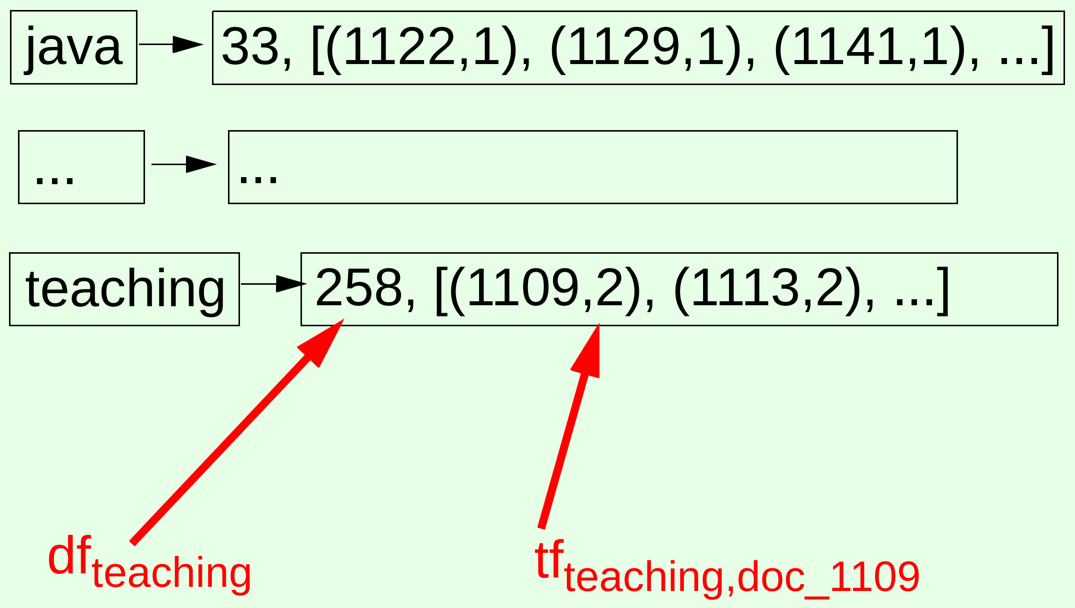
- Vector Space model
- Idea: Represent each document as a vector *V* in a n-dimensional vector space
- Dimensions are spanned by terms in the document collection
- Similarity of two documents is calculated by the angle between vector representation of each document

  sim(d_1, d_2) = V(d_1)/|V(d_1)| * V(d_2)/|V(d_2)|
  Dot product: V(d_1)*V(d_2) = sum $_{i=1..M}$ **(** $d_{1i}*d_{2i}$**)**
  Euclidian length: |V(d_1)| = sum $_{i=1..M}$ **(**v_i*v_i**)**

- Query is also a vector ...

Index Structure

- **Resume:** We have to store additional information in our index



- tf-idxIndex/java.txt

```
# occurence: 33 docs
papers/1122.txt:1
papers/1129.txt:1
papers/1141.txt:1
...
```

- ...

- tf-idxIndex/teaching.txt

```
# occurence: 238 docs
papers/1109.txt:2
papers/1113.txt:2
papers/1114.txt:121
papers/1118.txt:27
...
```

- Sort by term (first criteria) and by filename (second criteria)

```
sort -t: -k2,2 -k1,1 doc-term.txt
papers/1109.txt:a
papers/1109.txt:a
...
papers/1112.txt:a
papers/1112.txt:a
```

- Remove duplicates and count them

```
$ sort -t: -k2,2 -k1,1 doc-term.txt |uniq -c|head
     69 papers/1109.txt:a
    631 papers/1112.txt:a
     42 papers/1113.txt:a
    125 papers/1114.txt:a
    119 papers/1118.txt:a
     66 papers/1121.txt:a
```

count

number of times, each term appears inside a document

- Minor formatting issues ...

```
$ sort -t: -k2,2 -k1,1 doc-term.txt |uniq -c| \
   awk -F' ' '{printf "%s:%d\n", $2, $1}'> invIndexTfIdf.idx
papers/1109.txt:a:69
papers/1112.txt:a:631
papers/1113.txt:a:42
papers/1114.txt:a:125
papers/1118.txt:a:119
papers/1121.txt:a:66
papers/1122.txt:a:279
papers/1124.txt:a:138
papers/1126.txt:a:177
papers/1127.txt:a:100


# replace document name by ID is ommited here (see boolean search)
```

Distribute in Multiple Files (One File per Term)

```
$ awk -F: -v DIR=d:/data/tfIdfInvIndex \
          -f write-inverted-tfidf-index-to-file.awk \
    invIndexTfIdf.idx
```

- write-inverted-tfidf-index-to-file.awk

```
{
  if ($1 != last) {
        print $2":"$3 > DIR"/"$1".idx"
     last = $1
  } else {
     print $2":"$3 >> DIR"/"$1".idx"
  }
}
```

- ... and what's about the Document Frequency (df_{term}) ?

- Improve write-inverted-tfidf-index-to-file.awk to also write out the Document Frequency df_{term}

Extended awk-script (document frequency)

```
{
  if ($1 != last) {
     if (last!="")
        print count > DIR"/"last".df"
     print $2":"$3 > DIR"/"$1".idx"
     last = $1
     count = 1
  } else {
     print $2":"$3 >> DIR"/"$1".idx"
     count++
  }
}
END {
  print $2":"$3 > DIR"/"last".df"
}
```

for the last entry in file

Show Index:

```
$ head tfIdfInvIndex/java.idx
papers/1122.txt:1
papers/1129.txt:1
papers/1141.txt:1
papers/1149.txt:4
papers/1171.txt:6
papers/1191.txt:4
papers/1203.txt:1
papers/1218.txt:8
papers/1346.txt:1
papers/1359.txt:1


$ head tfIdfInvIndex/java.df
33
```

```
$ head tfIdfInvIndex2/java.idx
0007:1
0011:1
0018:1
0024:4
0039:6
0053:4
0060:1
0069:8
0147:1
0153:1


$ head tfIdfInvIndex2/java.df
33
```

Example Query:

```
export DF_JAVA=$(cat d:/data/tfIDFInvIndex/java.df)
export DF_PHP=$(cat d:/data/tfIDFInvIndex/php.df)
export N=$(ls papers/*.txt| wc -l)
join -11 -21 -t:    d:/data/tfIdfInvIndex/php.idx \
      -o1.1,1.2,2.2 d:/data/tfIdfInvIndex/java.idx > result.txt
export LC_ALL=C && awk -F: -v DF1=$DF_JAVA -v DF2=$DF_PHP -v N=$N \
                           -f ranking.awk result.txt | \
    sort -t: -k2,2nr
papers/1587.txt:66.5875
papers/1441.txt:44.4532
papers/1218.txt:33.3553
papers/1466.txt:20.1116
papers/1149.txt:11.1595
papers/1517.txt:6.68337
papers/1457.txt:6.6526
...
```

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Calculation of tf*idf values

- ranking.awk

```
{
   tf1 = $2
   tf2 = $3
   idf1 = log(N/DF1)*tf1
   idf2 = log(N/DF2)*tf2
   print $1":"idf1+idf2
}
```

file identifier

Exercise II

Download Exercise 2 from

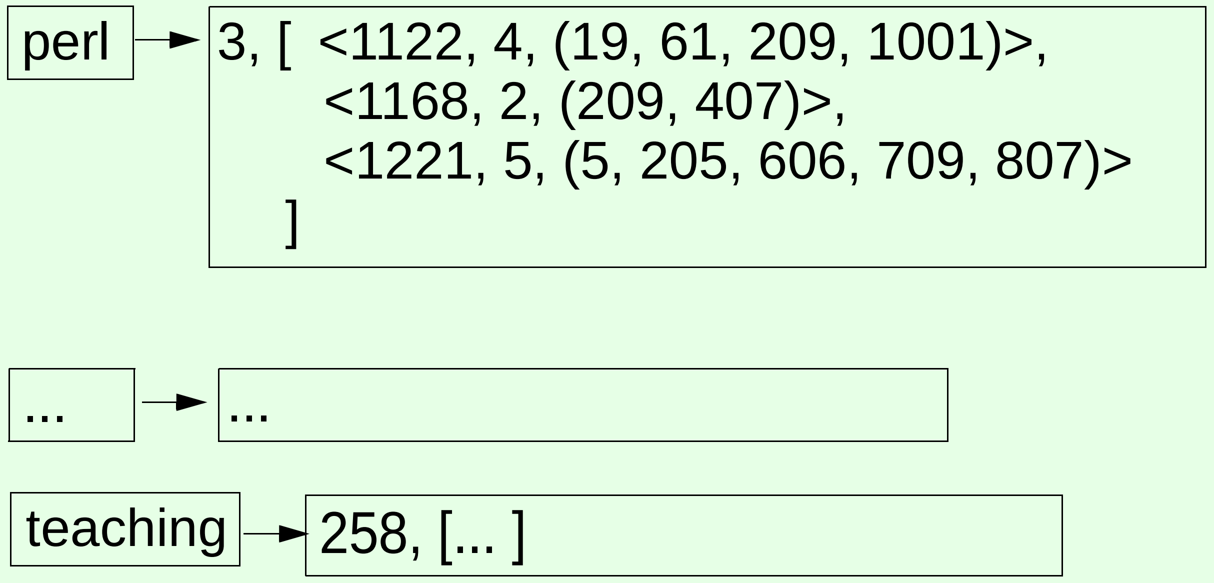
http://www.smiffy.de/dbkda-2018/IR-exercise-2.pdf

with solutions:

http://www.smiffy.de/dbkda-2018/IR-exercise-2-solution.pdf

Phrase Match - Positional Indexes

- For phrase queries such like „Dead men don't wear plaid“ we also need information about the position of a word in a file



Numerating the Words Inside a Document

include filename

```
grep -H -E -a -o '[A-Za-z]+' papers/1587.txt| tr 'A-Z' 'a-z'|cat -n
     1  papers/1587.txt:a
     2  papers/1587.txt:practical
     3  papers/1587.txt:approach
     4  papers/1587.txt:for
     5  papers/1587.txt:teaching
     6  papers/1587.txt:model
     7  papers/1587.txt:driven
     8  papers/1587.txt:software
     9  papers/1587.txt:development
    10  papers/1587.txt:a
    11  papers/1587.txt:plea
    12  papers/1587.txt:for
    ...
```

numerize,starting from 1

Remove Leading spaces, replace : with <tab>

```
$ grep -H -E -a -o '[A-Za-z]+' papers/1587.txt| tr 'A-Z' 'a-z'| cat -n|\
  sed 's#^ *##;s#:#\t#'
1       papers/1587.txt a
2       papers/1587.txt practical
3       papers/1587.txt approach
4       papers/1587.txt for
5       papers/1587.txt teaching
6       papers/1587.txt model
7       papers/1587.txt driven
8       papers/1587.txt software
9       papers/1587.txt development
10      papers/1587.txt a
11      papers/1587.txt plea
12      papers/1587.txt for
13      papers/1587.txt the
...
```

Loop Over Document Collection

```
rm -f position.Index
for f in papers/*.txt; do
    grep -H -E -a -o '[A-Za-z]+' $f | tr 'A-Z' 'a-z'| cat -n| \
       sed 's#^ *##;s#:#\t#' >> position.Index ;
done
less position.Index
1       papers/1580.txt gamification
2       papers/1580.txt technique
3       papers/1580.txt for
...
3465    papers/1580.txt page
1       papers/1581.txt traffic
2       papers/1581.txt lights
3       papers/1581.txt through
...
```

Sort by Term, File, Position

```
                 numeric sort

sort -k3 -k2 -k1n position.Index | tee sortedPosition.Index
84      papers/1580.txt a
88      papers/1580.txt a
103     papers/1580.txt a
139     papers/1580.txt a
...
3441    papers/1580.txt a
97      papers/1581.txt a
110     papers/1581.txt a
119     papers/1581.txt a
...
```

Distribution to Multiple Files

- Target Format:

```
$ ls invPosIndex/wo*.idx
invPosIndex/women.idx
invPosIndex/word.idx
invPosIndex/wordpress.idx
invPosIndex/work.idx
invPosIndex/workbench.idx
invPosIndex/worked.idx
...

$ cat invPosIndex/women.idx
papers/1582.txt 2274,2482,2505,2541,2975
papers/1588.txt 751,783,806,2480,2503,2539,2979,3338
...
```

awk-script

```
# Format : 208   papers/1151.txt   about
#    sort order: col3, col2 , col1            new term
{                                                    end current line
  if ($3 != last_term) {
    if (last_term != "")
      printf "\n" >> DIR"/invPosIndex/"last_term".idx"
    printf "%s\t%d", $2, $1 > DIR"/invPosIndex/"$3".idx"
    last_term = $3
    last_file = $2                            new document (same term)
  } else {
    if ($2!=last_file) {
      printf "\n%s\t%d", $2, $1 >> DIR"/invPosIndex/"$3".idx"
      last_file = $2
    } else                       next position (same document & term)
      printf ",%d", $1 >> DIR"/invPosIndex/"$3".idx"
  }
```

Index Structure

```
$ head -15 invPosIndex/bachelor.idx
...
papers/1170.txt 1026,1513,1593,1841
papers/1172.txt 1294
papers/1189.txt 1946,1955,2614
papers/1190.txt 395
papers/1191.txt 62,293,415,1637
papers/1198.txt 95,704,1592
...
```

```
$ head invPosIndex/degree.idx
...
papers/1173.txt 1747,1919
papers/1176.txt 1813,5481,5597
papers/1189.txt 1397,1573,1947,1956,5234
papers/1190.txt 60,97,119,376,396,413,435, ...
papers/1191.txt 63,70,88,294,416,1638,2528
papers/1196.txt 2143
...
```

- Which documents contain the phrase „bachelor degree“
  - Both terms must appear
  - „bachelor“ must appear directly before „degree“

Index Structure

```
$ head -15 invPosIndex/bachelor.idx
...
papers/1170.txt 1026,1513,1593,1841
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papers/1189.txt 1946,1955,2614
papers/1190.txt 395
papers/1191.txt 62,293,415,1637
papers/1198.txt 95,704,1592
...
```

```
$ head invPosIndex/degree.idx
...
papers/1173.txt 1747,1919
papers/1176.txt 1813,5481,5597
papers/1189.txt 1397,1573,1947,1956,5234
papers/1190.txt 60,97,119,376,396,413,435, ...
papers/1191.txt 63,70,88,294,416,1638,2528
papers/1196.txt 2143
...
```

- Which documents contain the phrase „bachelor degree“
  - Both terms must appear in a document
  - „bachelor“ must appear directly before „degree“

Query Execution

```
   $ join -11 -21  $(DIR)/invPosIndex/bachelor.idx \
                   $(DIR)/invPosIndex/degree.idx -o1.1,1.2,2.2 | \
     awk -F' ' -f phraseMatch.awk | sort -k2,2nr
```

document

positionlist
for „bachelor“

find documents which
contain both terms

positionlist
for „degree“

look for cases, in which the term
„bachelor“ appears directly befor „degree“

Example Query

- phraseMatch.awk

positions at which „bachelor“ appear

```
{
    num_matches = 0
    num_elem = split($0,a," ")
    num_fw = split(a[2], fw, ",")
    num_sw = split(a[3], sw, ",")
    i=1
    j=1
    do {
        if (fw[i]>sw[j]) {
            j++
        } else if (fw[i]+1==sw[j]) {
            i++
            j++
            num_matches++
       } else
            i++
    } while (i <num_fw && j < num_sw)
    if (num_matches > 0)
       print $1" "num_matches
```

positions at which „degree“ appear

here, we have a match

print number of matches for each document containing a match

Topics not Covered

- Stemming & Lemmatisation
- Vector Space Model
- Compression

Summary

- What was the purpose of this tutorial?

- Unix Tools like `grep, tr, sed, uniq, comm, sort, join` are very powerful tools for data scientists
- `awk` can be seen as a programming language with perfect fit to the previous mentioned tools
- Alternatives to awk are `python`, `perl`, `ruby`, `php`, ... (depends on own preferences)
- There are a number of other tools not covered in this tutorial like `paste`, `cut`, `zgrep`, `zcat`, `wget`, ... which are also worth to get discovered
- To glue all commands together, risk a look at `make`

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thanks for your audience

&

enjoy dbkda 2018