

# Index Construction and Advanced Queries

COMP90042 LECTURE 19, THE UNIVERSITY OF MELBOURNE

by

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# Today

1. Inverted index construction.
2. Phrase searching and other advanced query types.

# Inverted Index construction

# Inverted Index construction

## Static scenario:

1. Static collection of documents
2. Offline construction
3. Fixed at query time (no delete or append)

## Real world scenario:

1. Document collection grows over time
2. Documents arrive at a given rate (1000 docs/second)
3. Documents should be searchable immediately
4. Might want to delete or update documents

# Static construction

## Constraints:

1. Static collection of documents (e.g. 1TB webcrawl)
2. Offline construction (only query after construction)
3. Fixed at query time (no modify or append)

## Constraints and Properties:

1. Fixed amount of memory available
2. Dataset will not fit in memory
3. Final index small compared to dataset

# Static construction - Algorithm

## Algorithm:

Split document collection into blocks (X documents per block) and construct inverted indexes for each block. Merge blocks at the end.

```
1 def ConstructStatic ( Collection ) :
2     n = 0
3     vocab = {} # map term to term_id
4     # split collection into fixed size batches
5     for batch in Collection :
6         # invert each batch
7         B = InvertBatch ( batch , vocab )
8         storeToDisk ( B )
9         n = n + 1
10    # merge all inverted batches
11    MergeAllInvertedBatches ( B0 , B1 ... , Bn )
```

# Static construction - InvertBatch

## Invert one batch:

1. Process documents in batch
2. Use global vocabulary to map terms to term ids
3. Create inverted index for all docs in batch
4. Can already compress postings lists (vbyte)

## Stored on disk:

Term-ID	Compressed size	Compressed posting
5	52	<vbyte>
7	454	<vbyte>
9	432	<vbyte>
12	5324	<vbyte>

# Static construction - MergeBatches

Merge batches:

1. Open all  $n$  files containing batches on disk
2. Read one term (or a few) from each file
3. Perform  $n$ -way merge, merging terms with same ids
4. Merge equivalent to appending bytes as document ids are increasing
5. Read the next terms

Note: In a way this is a form of map and reduce which is used for distributed index construction.



# Static construction - MergeBatches

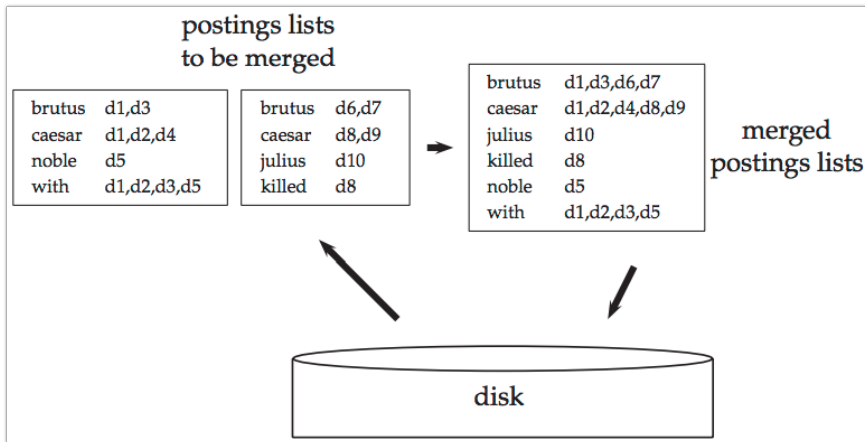


Figure 4.3., Intro to Information Retrieval, Manning et al.

# From static to incremental indexing

## Auxiliary Index

1. One static large static index on disk
2. As new documents arrive keep them in-memory in second index
3. If second index becomes too big, merge with static index
4. Query both indexes and merge results

# From static to incremental indexing

## Problem

1. After one year our index has  $N = 10$  billion postings
2. At each time we have an inverted index in memory which is merged it has more than  $n = 1$  million postings
3. Total merges =  $N/n$ . At each merge we look at all existing postings.

Thus,

$$totalcost = n + 2n + 3n + 4n + \dots + (N/n)n = O(N^2/n)$$

Example:  $N = 10$  billion,  $n = 1$  million =  
 $N^2/n = 10B^2/1M = 100$  trillion I/Os

# Incremental, logarithmic indexing

## Idea

1. Use a logarithmic number ( $\log N$ ) of indexes. At each level  $i$ , store index of size  $2^i \times n$
2. Query all  $\log N$  indexes at the same time and merge results
3. Construction cost:  $N \log(N/n)$

Lets look at this “in action”:

<http://blog.mikemccandless.com/2011/02/visualizing-lucenes-segment-merges.html>

# Incremental construction

Lucene (Open Source Search Engine):

1. Add over 650GB/hour worth of documents to the index on modern hardware
2. Incremental indexing as fast as batch indexing.

Lucene Code:

```
EnglishAnalyzer sa = new EnglishAnalyzer();
IndexWriterConfig iwc = new IndexWriterConfig(sa);
iwc.setSimilarity(new BM25Similarity());
IndexWriter writer = new IndexWriter(indexDir, iwc);

docContent = "This is a test";
Document document = new Document();
document.add(new Field(FIELD_BODY, docContent));
writer.addDocument(document);
```

# Distributed Index Construction

- Search engines such as Elasticsearch support distributed indexes
- Break documents into shards which are spread across processing nodes
- Balance shards such as indexing and search is evenly distributed (hard problem!)
- Search: Query each shard and merge results (hard problem!)

# Index Construction - Summary

- Block based processing of large collections
- Merge blocks to larger indexes
- Logarithmic merging reduces I/O costs
- Query multiple indexes at once
- When dealing with large amounts of data, careful engineering of construction algorithms is required to make things “work”

# Phrase searching and advanced queries



# Advanced queries

Users sometime want to look for:

- Exact phrases such as “the University of Melbourne”
- Arbitrary patterns in non-tokenized text such as “AGCTAGCAGAA” in genome databases
- Documents/sentences that are similar to an existing example.

# Phrase queries

What is a phrase query?

1. Seek to identify documents that contain a specific phrase “the who”
2. Combination of individual known terms that occur sequentially in documents
3. Two or more terms possible - “the president of the united states”

Approaches

1. Inverted Index based
2. String matching indexes (Suffix Arrays)

# Phrase queries - Inverted Index

## Hack

Find the top-K most frequent phrases in your query log and add them as a token to your dictionary. Probably solves 90% of all incoming queries.

## Positional Inverted Index

- In addition to document ids and frequencies, store the **positions** of each term in the document.
- Perform intersection to find phrases
- Index size dramatically increased

# Positional Inverted Index

term $t$	$f_t$	Postings list for $t$ (docids,freqs)
and	6	$\langle 1, 6, 7, 8, 9, 12 \rangle, \langle 1, 2, 3, 3, 1, 2 \rangle$
big	3	$\langle 2, 5, 42 \rangle, \langle 1, 1, 1 \rangle$
old	1	$\langle 32 \rangle, \langle 4 \rangle$
in	7	$\langle 2, 3, 5, 6, 8, 14, 25 \rangle, \langle 1, 1, 4, 1, 5, 3, 1 \rangle$
the	52	$\langle 1, 2, 3, 4, 5, 7, 8, 9, \dots \rangle, \langle 10, 21, 10, 42, 12, 14, 12, 4, \dots \rangle$
night	4	$\langle 1, 12, 13, 14 \rangle, \langle 2, 2, 1, 3 \rangle$
house	5	$\langle 6, 21, 32, 33, 43 \rangle, \langle 2, 3, 4, 2, 1 \rangle$
sleep	3	$\langle 1, 51, 53 \rangle, \langle 1, 2, 3 \rangle$
where	4	$\langle 1, 3, 4, 6 \rangle, \langle 1, 1, 2, 1 \rangle$

# Positional Inverted Index

term $t$	$f_t$	Postings list for $t$ (docids,freqs,positions)
and	6	$\langle 1, 6, 7, \dots \rangle, \langle 1, 2, 3, \dots \rangle, \langle \langle 5 \rangle, \langle 12, 43 \rangle, \langle 6, 45, 212 \rangle, \dots \rangle$
big	3	$\langle 2, 5, 42 \rangle, \langle 1, 1, 1 \rangle, \langle \langle 8 \rangle, \langle 43 \rangle, \langle 65 \rangle \rangle$
old	1	$\langle 32 \rangle, \langle 4 \rangle, \langle \langle 6, 34, 56, 59 \rangle \rangle$
$\vdots$	$\vdots$	$\vdots$

# Positional Index - Search

## Phrase Search Algorithm

- Intersect document ids of phrase terms
- For the documents containing all terms, intersect position lists
- Perform ranking on result set

## Problems

- Slow when phrase terms occur in many documents in the collection (“the who”)
- Slow when terms occur often in documents but not as phrase (“the president of the united states”)

# Positional Index - Intersection

## Small-vs-Small

To intersect  $n$  lists, pick the smallest and intersect with the second smallest. Use result of the intersection to keep intersecting.

5	6	13	53	234
---	---	----	----	-----

2	4	6	12	53	434	545	656
---	---	---	----	----	-----	-----	-----

1	3	4	6	9	10	11	12	13	14	18
---	---	---	---	---	----	----	----	----	----	----

1	2	3	4	6	8	9	10	13	14	15	17	19	...
---	---	---	---	---	---	---	----	----	----	----	----	----	-----

# Suffix Arrays

- Alternative search index which does not require tokenization
- Widely used in bioinformatics for exact string searches
- Gives you more runtime guarantees than an inverted index

Example: <https://www.ncbi.nlm.nih.gov/nuccore/?term=G TTCCTCAAG>



# Classical String Matching

## Problem

Given a string  $T$  and a pattern  $P$  over an alphabet  $\Sigma$  of constant size  $\sigma$ . Let  $n = |T|$  be the length of  $T$ , and  $m = |P|$  be the length of  $P$  and  $n \gg m$ .

## Example

$T = \text{abracadabrabarbara\$}$ ,  $n=18$

$P = \text{bar}$ ,  $m=3$

## Problem: String search

- Does  $P$  occur in  $T$ ? (Existence query)
- How often does  $P$  occur in  $T$ ? (Count query)
- Where does  $P$  occur in  $T$ ? (Locate query)

# Simple Solutions

- Check for each  $i$  in  $i \in \{0, \dots, n - m - 1\}$  if  $T[i..i + m - 1] = P$ .

```
for (size_t i=0; i<n; ++i){
    bool match=true;
    for (size_t j=0; j<m && match; ++j)
        match = (i+j < n && T[i+j] == P[j]);
    if (match)
        return true;
}
return false;
```

- Time complexity:  $\mathcal{O}(n \cdot m)$  comparisons

# Improved solution

- Knuth, Morris, and Pratt precomputed a table of size  $m$  which allows to shift the pattern by possibly more than one position in case of a mismatch and get complexity:  $\mathcal{O}(n + m)$
- This solution is optimal in the online scenario, in which we are not allowed to pre-process  $T$  (online scenario), but not in ...

## our scenario

We are allowed to **pre-compute an index structure**  $I$  for  $T$  and use  $I$  for the string search.

- $I$  should be small
- Time complexity of matching independent of  $n$

# Suffix Arrays - Idea

- Store all suffixes of the text
- Sort them in lexicographical order
- Each occurrence of  $P$  is a prefix of a suffix

# Suffix Arrays (1)

$i$	$SA[i]$	$T[SA[i]..n-1]T[0..SA[i]-1]$
0	18	\$abracadabrabarbara
1	17	a\$abracadabrabarbar
2	10	abarbara\$abracadabr
3	7	abrabarbara\$abracad
4	0	abracadabrabarbara\$
5	3	acadabrabarbara\$abr
6	5	adabrabarbara\$abrac
7	15	ara\$abracadabrabarb
8	12	arbara\$abracadabrab
9	14	bara\$abracadabrabar
10	11	barbara\$abracadabra
11	8	brabarbara\$abracada
12	1	bracadabrabarbara\$a
13	4	cadabrabarbara\$abra
14	6	dabrabarbara\$abraca
15	16	ra\$abracadabrabarba
16	9	rabarbara\$abracadab
17	2	racadabrabarbara\$ab
18	13	rbara\$abracadabraba

- First sort suffixes of  $T$ . (quicksort:  $\mathcal{O}(n^2 \log n)$ , best algorithms:  $\mathcal{O}(n)$ )
- Storing all suffixes takes  $n^2 \log \sigma$  bits space. Only store starting positions of suffixes in  $SA$  ( $n \log n$  bits).
- Question: How fast can we search using  $T$  and  $SA$ ?

# Suffix Arrays (2)

- The suffixes are *ordered* in SA. We can use *binary search*!
- Start with the empty string  $\epsilon$  which matches all prefixes (i.e. the interval  $[sp_0..ep_0] = [0..n - 1]$ ) of suffixes in SA.
- Then use binary search to determine the interval  $SA[sp_j..ep_j]$  in  $SA[sp_{j-1}..ep_{j-1}]$  so that all suffixes start with  $P[0..j - 1]$  for all  $j \in [1..m]$ .
- $P$  occurs in  $T$  if  $[sp_m..ep_m]$  is not empty.
- If  $P$  occurs the count query can be answered by  $ep_m - sp_m + 1$ .
- Time complexity:  $\mathcal{O}(m \cdot \log n)$ , space  $\mathcal{O}(n \log n + |T|)$

# Suffix Arrays - Example

$i$	$SA[i]$	$T[SA[i]..n-1]T[0..SA[i]-1]$
0	18	\$abracadabrabarbara
1	17	a\$abracadabrabarbar
2	10	abarbara\$abracadabr
3	7	abrabarbara\$abracad
4	0	abracadabrabarbara\$
5	3	acadabrabarbara\$abr
6	5	adabrabarbara\$abrac
7	15	ara\$abracadabrabarb
8	12	arbara\$abracadabrab
9	14	bara\$abracadabrabar
10	11	barbara\$abracadabra
11	8	brabarbara\$abracada
12	1	bracadabrabarbara\$a
13	4	cadabrabarbara\$abra
14	6	dabrabarbara\$abraca
15	16	ra\$abracadabrabarba
16	9	rabarbara\$abracadab
17	2	racadabrabarbara\$ab
18	13	rbara\$abracadabraba

■ Search for *bar*.

# Suffix Arrays - Example

$i$	$SA[i]$	$T[SA[i]..n - 1]T[0..SA[i] - 1]$
0	18	\$abracadabrabarbara
1	17	a\$abracadabrabarbar
2	10	abarbara\$abracadabr
3	7	abrabarbara\$abracad
4	0	abracadabrabarbara\$
5	3	acadabrabarbara\$abr
6	5	adabrabarbara\$abrac
7	15	ara\$abracadabrabarb
8	12	arbara\$abracadabrab
9	14	bara\$abracadabrabar
10	11	barbara\$abracadabra
11	8	brabarbara\$abracada
12	1	bracadabrabarbara\$a
13	4	cadabrabarbara\$abra
14	6	dabrabarbara\$abraca
15	16	ra\$abracadabrabarba
16	9	rabarbara\$abracadab
17	2	racadabrabarbara\$ab
18	13	rbara\$abracadabraba

- Search for *bar*.
- Step 1: *b* interval [9..12]



# Suffix Arrays - Example

$i$	$SA[i]$	$T[SA[i]..n - 1]T[0..SA[i] - 1]$
0	18	\$abracadabrabarbara
1	17	a\$abracadabrabarbar
2	10	abarbara\$abracadabr
3	7	abrabarbara\$abracad
4	0	abracadabrabarbara\$
5	3	acadabrabarbara\$abr
6	5	adabrabarbara\$abrac
7	15	ara\$abracadabrabarb
8	12	arbara\$abracadabrab
9	14	bara\$abracadabrabar
10	11	barbara\$abracadabra
11	8	brabarbara\$abracada
12	1	bracadabrabarbara\$a
13	4	cadabrabarbara\$abra
14	6	dabrabarbara\$abraca
15	16	ra\$abracadabrabarba
16	9	rabarbara\$abracadab
17	2	racadabrabarbara\$ab
18	13	rbara\$abracadabraba

- Search for *bar*.
- Step 1: *b* interval  
[9..12]
- Step 2: *ba* interval  
[9..10]

# Suffix Arrays - Example

$i$	$SA[i]$	$T[SA[i]..n - 1]T[0..SA[i] - 1]$
0	18	\$abracadabrabarbara
1	17	a\$abracadabrabarbar
2	10	ababara\$abracadabr
3	7	abrabarbara\$abracad
4	0	abracadabrabarbara\$
5	3	acadabrabarbara\$abr
6	5	adabrabarbara\$abrac
7	15	ara\$abracadabrabarb
8	12	arbara\$abracadabrab
9	14	bara\$abracadabrabar
10	11	barbara\$abracadabra
11	8	brababara\$abracada
12	1	bracadabrabarbara\$a
13	4	cadabrabarbara\$abra
14	6	dabrabarbara\$abraca
15	16	ra\$abracadabrabarba
16	9	rabarbara\$abracadab
17	2	racadabrabarbara\$ab
18	13	rbara\$abracadabraba

- Search for *bar*.
- Step 1: *b* interval [9..12]
- Step 2: *ba* interval [9..10]
- Step 2: *bar* interval [9..10]

# Suffix Arrays - State-of-the-Art

- Compressed Suffix Arrays (CSA) use space equivalent to the **compressed** size of the text. Example: 1GB text, 8GB Suffix Array, Compressed text (gzip) 200MB, CSA 150MB
- Can be constructed, parallel, space-efficiently
- Can be used to index TBs of data
- Can solve queries that are hard to solve using an inverted index
- Widely used in bioinformatics where the concept of tokens does not exist

# More advanced queries

Many more advanced queries exist

- Wildcard/misspelling queries ( Sydney vs. Sidney: query S?dney )
- Regular expression queries ( “[Jj]ohn.\*”@smith.com??? ” )
- Proximity queries ( “president” close to “obama” )

Often specialized indexing structures are required to solve those kind of queries efficiently. Generally **much slower** than regular queries.

# Phrase search - Summary

- Inverted indexes with positional information and intersection
- Use substantially more space than regular inverted index
- Suffix array is an alternative index structure to inverted indexes
- Complex queries require specialized indexes

# Further Reading

## Reading:

- Manning, Christopher D; Raghavan, Prabhakar; Schütze, Hinrich; Introduction to information retrieval, Cambridge University Press 2008. (Chapter 4)

## Additional References:

- <http://blog.mikemccandless.com/2011/02/visualizing-lucenes-segment-merges.html>
- Simon J. Puglisi, William F. Smyth, Andrew Turpin: A taxonomy of suffix array construction algorithms. ACM Comput. Surv. 39(2): 4 (2007)
- Paolo Ferragina, Rodrigo González, Gonzalo Navarro, Rossano Venturini: Compressed text indexes: From theory to practice. ACM JEA 13 (2008)