Finding near-duplicate documents

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Duplicate versus near duplicate documents

- Duplicate = identical?
- Near duplicate:
  small structural differences
    - not just content similarity
- define "small"
  - date change?
  - small edits?
  - metadata change?
  - other?

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Applications

- creating collection
  - indexing
- Crawling network
- Returning query results
  - cluster near duplicates; return 1
- Plagiarism

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Framework

- Algorithm to assign quantitative degree of similarity between documents
- Issues
  - What is basic token for documents?
    - character
    - word/term
  - What is threshold for "near duplicate"?
  - What are computational costs?

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Classic document comparison

- Edit distance
  - count deletions, additions, substitutions to convert Doc_1 into Doc_2
  - can each action can have different cost
  - applications
    - UNIX "diff"
    - similarity of genetic sequences
- Edit distance algorithm
  - dynamic programming
  - time O(m*n) for strings length m and n

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Edit distance for collections

- token = word
  - compare other applications
- Cost is $O(\sum_{i,j} |Doc_i|*|Doc_j|)$
- Right sense of similarity?

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Addressing computation cost

A general paradigm to find duplicates in N docs:

1. Define function *f* capturing contents of each document in one number
   "Hash function", "signature", "fingerprint"
2. Create <$f(doc_i)$, ID of doc_i> pairs
3. Sort the pairs
4. Recognize duplicate or near-duplicate documents as having the same *f* value or *f* values within a small threshold

Compare: computing a similarity score on pairs of documents

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Optimistic cost

A general paradigm to find duplicates in N docs:

1. Define function *f* capturing contents of each document in one number   O(|doc|)
   "Hash function", "signature", "fingerprint"
2. Create <$f(doc_i)$, ID of doc_i> pairs $O(\Sigma_{i=1...N} (|doc_i|))$
3. Sort the pairs $O(N \log N)$
4. Recognize duplicate or near-duplicate documents as having the same *f* value or *f* values within a small threshold $O(N)$

Compare: computing a similarity score on pairs of documents

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General paradigm: details

1. Define function *f* capturing contents of each document in one number
   "Hash function", "signature", "sketch", "fingerprint"
2. Create <$f(doc_i)$, ID of doc_i> pairs
3. Sort the pairs
4. Recognize duplicate or near-duplicate documents as having the same *f* value or *f* values within a small threshold
   - recognize exact duplicates:
     - threshold = 0
     - examine documents to verify duplicates
   - recognize near-duplicates
     Problem with "small threshold" ?

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General paradigm: details

4. Recognize duplicate or near-duplicate documents as having the same *f* value or *f* values within a small threshold
   - recognize exact duplicates:
     - threshold = 0
     - examine documents to verify duplicates
   - recognize near-duplicates
     Problem with "small threshold" ?

     How deal with

     $<1, D_1> <1.01, D_2> <1.02, D_3> \ldots <1.99, D_{100}>$

     and threshold .01 (using $\leq$ threshold) ?

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"Syntactic clustering"

We will look at this one example:

Andrei Z. Broder, Steven C. Glassman, Mark S. Manasse, and Geoffrey Zweig, Syntactic Clustering of the Web
Sixth International WWW Conference, 1997.

- "syntactic similarity" versus semantic
  Sequences of words
- Finding near duplicates
- Doc = sequence of words
  Word = Token
- Uses **sampling**
- Similarity based on **shingles**
- Does compare documents

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Shingles

- A *w*-shingle is a contiguous subsequence of *w* words
- The *w*-shingling of doc D, S(D, *w*) is the set of ***unique*** w-shingles of D

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Similarity of docs with shingles

- For **fixed *w***, resemblance of docs A and B :
  r(A, B) = |S(A) ∩ S(B)| / |S(A) U S(B)|
  Jaccard coefficient
- For **fixed *w***, containment of doc A in doc B :
  C(A, B) = |S(A) ∩ S(B)| / |S(A)|
- For **fixed *w***, resemblance distance betwn docs A and B :
  D(A, B) = 1- r(A, B)
  Is a metric (triangle inequality)

Note we are now comparing documents!

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Example

A: “a rose is red a rose is white”

4-shingles:

“a rose is red”
“rose is red a”
“is red a rose”
“red a rose is”
“a rose is white”

B: “a rose is white a rose is red”

4-shingles:

“a rose is white”
“rose is white a”
“is white a rose”
“white a rose is”
“a rose is red”

r(A, B) = 0.25

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Sample of shingles

Want to ***estimate*** r and/or c

Do this by calculating approximation on a sample of shingles **for fixed *w***

- 1-to-1 map each shingle to integer in fixed, large range R
  - 64-bit hash, R=[0, 2^{64-1}]
- Let Π be a random permutation from R to R
- For any S(D) define:
  H(D) = Set of integer hash values corresponding to shingles in S(D)
  Π(D) = Set of permuted values in H(D)
  ***x*(Π, D) = smallest integer in Π(D)**

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Sketch of shingles

- Let $\Pi_1, \ldots, \Pi_m$ be m random permutations R → R
  - text: m=20

The sketch of doc D for $\Pi_1, \ldots, \Pi_m$ is
$\psi(D) = \{x(\Pi_i, D) \mid 1 \le i \le m\}$

doc → set shingles → set integers
→ m sets permuted integers
→ m smallest integers: one per permutation

Sketch is a ***sampling***

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Approximation of resemblance

Theorem:

For random permutation Π:

r(A, B) = P (*x*(Π, A) = *x*(Π, B))

Estimate P (*x*(Π, A) = *x*(Π, B)) as

| ψ(A) ∩ ψ(B) | / m

recall m is # permutations

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Algorithm used (text’s version)

1. Calculate *sketch* $\psi(D_i)$ for every doc D_i
2. Calculate $|\psi(D_i) \cap \psi(D_j)| = ct_{ij}$ for each non-empty intersection:
   1. Produce list of <shingle value, docID> pairs for all shingle values $x(\Pi_k, D_i)$ in the sketch for each doc.
   2. Sort the list by shingle value
   3. Produce all triples <$ID(D_i)$, $ID(D_j)$, $ct_{i,j}$> for which $ct_{i,j}>0$

   This *not linear-time* for the list of docs for one shingle value
3. Build clusters of similar/almost identical docs
   Degree of similarity depends on threshold …

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Clustering

1. Define docs to be similar if approximate resemblance greater than a predetermined threshold *t:*
   $ct_{ij} / m > t$
2. Build graph of docs:
   edge between each pair of similar docs
3. The clusters of similar docs are the connected components in the graph
   – single link cluster similarity

Equivalently :

- UNION-FIND (text book)
- minimum spanning tree with edge removal
  – more info, more work?

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Revisit the original paradigm

A general paradigm to find duplicates in N docs:

1. Define function *f* capturing contents of each document in one number O(|doc|)
   "Hash function", "signature", "fingerprint"
2. Create <f(doc$_i$), ID of doc$_i$> pairs $O(\Sigma_{i=1...N} (|doc_i|))$
3. Sort the pairs O(N log N)
4. Recognize duplicate or near-duplicate documents as having the same *f* value or *f* values within a small threshold O(N)

Compare: computing a similarity score on pairs of documents

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Paradigm?

- Does compare docs, so not same as paradigm we started with, but uses ideas
- Contents of doc captured by sketch – a set of shingle values
- Similarity of docs scored by count of common shingle values for docs
- Don't look at all doc pairs, look at all doc pairs that share a shingle value
- Uses clustering by similarity threshold

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Algorithm cost

1. Calculate *sketch* $\psi(D_i)$ for every D_i $O(\Sigma_i m|D_i|)$
2. Calculate $|\psi(D_i) \cap \psi(D_j)| = ct_{ij}$ for each non-empty intersection:
   i. Produce list of <shingle value, docID> pairs for all shingle values $x(\Pi_k, D_i)$ in the sketch for each doc.
   ii. Sort the list by shingle value O(mN log (mN))
   iii. Produce all triples <ID(D_i), ID(D_j), $ct_{i,j}$> for which $ct_{i,j}$>0
   This *not linear-time* for the list of docs for one shingle value $O(mN^2)$
3. Build clusters of similar/almost identical docs
   Degree of similarity depends on threshold …

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More efficient : supershingles

"meta-sketch"

1. Sort shingle values of a sketch
2. Compute the shingling of the sequence of shingle values
   - Each original shingle value now a token
   - Gives "supershingles"
3. "meta-sketch" = set of supershingles

One supershingle in common =>
sequences of shingles in common
Documents with ≥1 supershingle in common => similar

- Each supershingle for a doc. characterizes the doc
- Sort <supershingle, docID> pairs: docs sharing a supershingle are similar => our first paradigm

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Pros and Cons of Supershingles

\+ Faster
\- Problems with small documents – not enough shingles
\- Can't do containment
  Shingles of superset that are not in subset break up sequence of shingle values

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Variations of shingling

- Can define different ways to do sampling
- Studies in original paper used modular arithmetic
  - sketch formed by taking shingle hash values mod some selected m

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Original experiments (1996) by Broder et. al.

- 30 million HTML and text docs (150GB) from Web crawl
- 10-word shingles
- 600 million shingles (3GB)
- 40-bit shingle “fingerprints”
- Sketch using 4% shingles (variation of alg. we’ve seen)
- Used count of shingles for similarity
- Using threshold *t* = 50%, found
  - 3.6 million clusters of 12.3 million docs
  - 2.1 million clusters of identical docs – 5.3 million docs
  - remaining 1.5 million clusters mixture: “exact duplicates and similar”

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