Faster and Accurate Similarity Evaluations via Sampling

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Introduction

- There are many applications that involve making a huge number of distance/similarity evaluations between complex objects
- For example:
 - Locate the best match for a song or image
 - Find the best match for some DNA sample in a crime scene
 - Cluster data into groups
 - Facial recognition
 - Reconstruct a phylogenetic tree
 - ...

Introduction

Several different (and often complementary) approaches to reduce the computational cost

- Reduce the number of distance evaluations organizing the data (vp-trees, Burkhard-Keller trees, GHTs, GNATs, ...) exploiting triangle inequality
- **2** Filter with a simpler distance function δ' : $\delta'(A, B) > r' \implies \delta(A, B) > r$
- Reduce the "dimensionality" using a simpler distance function with approximation guarantees

Introduction

We focus here in distance/similarity measures between sets and multisets

- In many applications we can modellize our complex object as a set or multiset
- For example,
 - from a long DNA sequence we can extract the set/multiset of k-mers
 - from a textual document we can extract the *vocabulary*, the set of distinct words (or stems) in the document
 - ...

Similarity measures

Consider two sets A and B.

Jaccard's index	$\frac{ A \cap B }{ A \cup B }$
Otsuka-Ochiai (a.k.a. Cosine)	$\frac{ A \cap B }{\sqrt{ A \cdot B }}$
Sørensen-Dice	$2\frac{ A \cap B }{ A + B }$
Kulczynski 1	$\frac{ A \cap B }{ A \triangle B }$
Kulczynski 2	$\frac{1}{2} \left(\frac{ A \cap B }{ A } + \frac{ A \cap B }{ B } \right)$
Simpson	$\frac{ A \cap B }{\min(A , B)}$
Braun-Blanquet	$\frac{ A \cap B }{\max(A , B)}$
Correlation	$\cos^2(A,B) = \frac{ A \cap B ^2}{ A \cdot B }$

Estimating Similarity

Let S_A and S_B two random samples of A and B, resp., and σ a similarity measure.

- Does $\sigma(S_A, S_B)$ give us an unbiased estimation of $\sigma(A, B)$?
- If not, can we find an unbiased estimator for σ(A, B) from the information in the samples?
- How accurate are these estimations? How do they depend on the size of the samples? should lead to more accurate estimates but computationally more costly!

Sampling

procedure DISTINCTSAMPLING(k, 2)

fill S with the first ${\bf k}$ distinct elements (and hash values) of the stream ${\mathfrak Z}$

for all $z \in \mathcal{Z}$ do

if HASH(z) < min hash value in S then

Discard *z*; **continue**

 \triangleright HASH(z) > min hash value in S

if $z \in S$ then

Update z stats

else \triangleright replace elem of min. hash with z

 $S \leftarrow S \setminus \{\text{elem. with min. hash in } S \} \cup \{z\}$

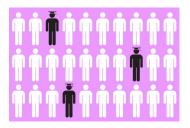
return S

Distinct Sampling

- The algorithm draws a random sample of k distinct elements (each one has prob. 1/n of being drawn, n = number of distinct elements), by keeping in the sample the k elements with the largest hash values seen so far¹
- If we use uniform random numbers in (0, 1) instead of hash values (and don't check if z ∈ S) ⇒ Reservoir Sampling

¹Pragmatic assumptions: hash values uniformly distributed; probability of collisions negligible

Affirmative Sampling (Lumbroso & M., 2019)



- The larger the cardinality (n) the larger the samples ⇒ samples better represent diversity
- All distinct elements have the same opportunity to be sampled

```
procedure AFFIRMATIVESAMPLING(k, \mathcal{Z})
    fill S with the first k distinct elements (and hash values)
    of the stream 2.
    for all z \in S do
        if HASH(z) < min hash value in S then
            Discard z: continue
        \triangleright HASH(z) > min hash value in S
        if z \in S then
            Update z stats
        else if HASH(z) > k-th largest hash value in S then
            S \leftarrow S \cup \{z\}
        else \triangleright replace elem of min. hash with z
            S \leftarrow S \setminus \{\text{elem. with min. hash in } S \} \cup \{z\}
    return S
```

- The size of the sample S is a random variable = the number of k-records in a random permutation of size n
- The sample does not contain the k-records, but the |S| elements with the largest hash values seen so far ⇒ S is a random sample
- If x ∈ S then x has been added to S in its very first occurrence and it has remained in S ever since ⇒ can collect exact stats (e.g. frequency counts) for x

• Properties of |S| are very well understood; in particular

 $\mathbb{E}\left\{|S|\right\} = k \ln(n/k) + \text{l.o.t.}$

The exact and asymptotic distribution of R, moments, ... is known (e.g., Helmi, M., Panholzer, 2014)

• Estimating cardinality (**RECORDINALITY**, Helmi, Lumbroso, M., Viola, 2012)

$$\mathbb{E}\left\{k\left(1+\frac{1}{k}\right)^{|S|-k+1}-1\right\}=n$$

 We also understand fairly well F = number of times an element substitutes another in the sample (not a k-record, but larger than some k-record):

 $\mathbb{E}\left\{F_{n}\right\} = k \ln^{2}(n/k) + \text{l.o.t.}$

Expected cost of Affirmative Sampling

$$\mathbb{E} \{ C \} = \Theta(N + (\mathbb{E} \{ |S| \} + \mathbb{E} \{ F \}) \log \mathbb{E} \{ |S| \})$$
$$= \Theta(N + (\log^2 n) \cdot (\log \log n))$$

using hashing for membership and a couple of priority queues (one of fixed size k, the other of size |S| - k)

Estimating Proportions

Let P some property.

- n = # of distinct elements
- $n_P = #$ of distinct elements that satisfy P
- S = size of the sample \leftarrow in general, a r.v., assume $2 \leqslant S \leqslant n$
- $S_P = #$ of elements in the sample that satisfy P

Theorem

$$\mathbb{E}\left\{\frac{S_{P}}{S}\right\} = \frac{n_{P}}{n}$$

$$\mathbb{E}\left\{\frac{S_{P}}{S}\right\} \sim \frac{n_{p}}{n} \cdot \left(1 - \frac{n_{p}}{n}\right) \cdot \mathbb{E}\left\{\frac{1}{S}\right\}$$

For affirmative sampling $\mathbb{E}\left\{1/S\right\} \sim 1/\mathbb{E}\left\{S\right\} = 1/(k \ln(n/k))$

Estimating the Jaccard similarity

- S_A and S_B random samples from A and B, resp.
- For any set X let $\tau_X = \min\{hash(x) | x \in X\}$ and $X^{\geq \tau} = \{x \in X | hash(x) \geq \tau\}$

• Let
$$\tau = \max\{\tau_{S_A}, \tau_{S_B}\}$$
. Then
• $S_A^{\geqslant \tau} \cup S_B^{\geqslant \tau} = (S_A \cup S_B)^{\geqslant \tau}$ is a random sample of $A \cup B$
• $(S_A^{\geqslant \tau} \cup S_B^{\geqslant \tau}) \cap (A \cap B) = (S_A^{\geqslant \tau} \cap S_B^{\geqslant \tau}) = (S_A \cap S_B)^{\geqslant \tau} = (S_A \cap S_B)$

Estimating the Jaccard similarity

Theorem
1
$$\mathbb{E}\left\{J(S_{A}^{\geq \tau}, S_{B}^{\geq \tau})\right\} = J(A, B) = \frac{|A \cap B|}{|A \cup B|}$$

2 $\mathbb{V}\left\{J(S_{A}^{\geq \tau}, S_{B}^{\geq \tau})\right\} \sim \frac{J(A, B) \cdot (1 - J(A, B))}{k \ln(|A \cup B|/k)}$

Estimating the size of the intersection

Moreover we can estimate the size of the intersection with:

$$\begin{aligned} Z_1 &= \frac{|S_A \cap S_B|}{|S_A|} \cdot \left(k \left(1 + \frac{1}{k} \right)^{|S_A| - k + 1} - 1 \right) \\ Z_2 &= \frac{|S_A \cap S_B|}{|S_A|} \cdot \frac{|S_A| - 1}{1 - \tau_{S_A}} \end{aligned}$$

$$\mathbb{E}\left\{Z_{1}\right\} = \mathbb{E}\left\{Z_{2}\right\} = |A \cap B|$$

N.B. No need to "filter" the sample S_A

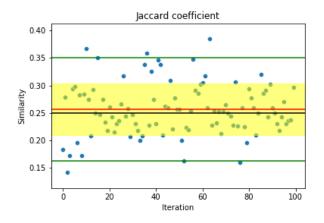
Estimating other similarity measures

The same proof that works for Jaccard's similarity also works for:

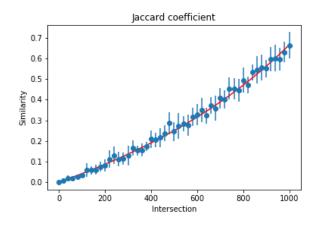
- Containment: $c(A, B) = |A \cap B|/|A|$ (this index is 1 if $A \subseteq B$); $\mathbb{E} \{ c(S_A, S_B) \} = c(A, B)$
- If σ is any of Jaccard, Simpson, Braun-Blanquet, Kulczynski 2 or Sørensen-Dice:

$$\mathbb{E}\left\{\sigma(S_A',S_B')\right\} = \sigma(A,B)$$

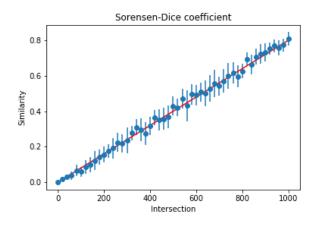
We conjecture this also holds (asymptotically) for cosine, correlation and Kulczynski 1



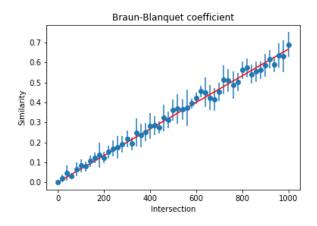
|A| = 1000, |B| = 1500, J(A, B) = 0.25red line = avg. of 100 experiments yellow band = avg \pm std. deviation green lines = 95% of observations



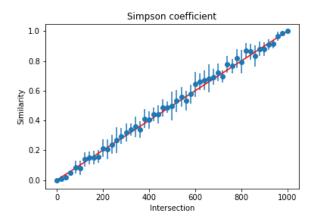
$$\begin{split} |A| &= 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\} \\ \text{red line} = J(A, B) = |A \cap B| / |A \cup B| \end{split}$$



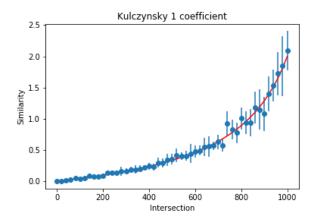
$$\begin{split} |A| &= 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\} \\ \text{red line} &= S \\ \texttt{ørensen-Dice}(A, B) = 2 |A \cap B / (|A| + |B|) \end{split}$$



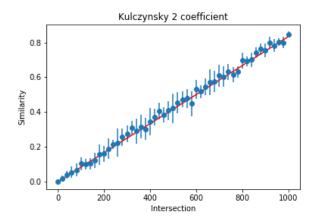
 $|A| = 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\}$ red line = Braun-Blanquet $(A, B) = |A \cap B| / max(|A|, |B|)$



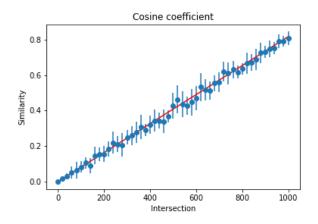
 $|A| = 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\}$ red line = Simpson $(A, B) = |A \cap B| / min((|A|, |B|))$



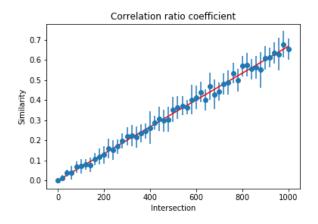
$$\begin{split} |A| &= 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\} \\ \text{red line} = K_1(A, B) = |A \cap B| / |A \triangle B| \end{split}$$



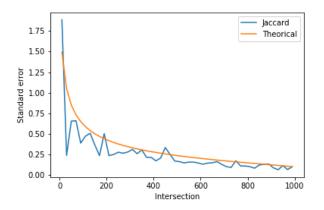
$$\begin{split} |A| &= 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\}\\ \text{red line} = K_2(A, B) &= \frac{1}{2} \left(|A \cap B| / |A| + |A \cap B| / |B|\right) \end{split}$$



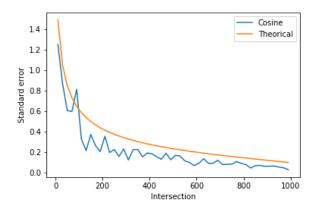
$$\begin{split} |A| &= 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\} \\ \text{red line} &= \cos(A, B) = |A \cap B| / \sqrt{|A| \cdot |B|} \end{split}$$



$$\begin{split} |A| &= 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\} \\ \text{red line} &= \text{Corr}(A, B) = |A \cap B|^2 / (|A| \cdot |B|) \end{split}$$



$$\begin{split} |A| &= 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\} \\ \text{blue line = sample standard error for } J(A, B) \\ \text{red line = SE}_n \left[\hat{\sigma} \right] &= \sqrt{\mathbb{V}\left\{ \hat{\sigma} \right\}} / \sigma \end{split}$$



$$\begin{split} |A| &= 1000, |B| = 1500, |A \cap B| \in \{0, 10, \dots, 1000\} \\ \text{blue line} = \text{sample standard error for } \cos(A, B) \\ \text{red line} = \text{SE}_n \left[\hat{\sigma} \right] &= \sqrt{\mathbb{V}\left\{ \hat{\sigma} \right\}} / \sigma \end{split}$$

Some final remarks

Experiments suggest that the standar error of all similarity estimators $\hat{\sigma}$ behave in all cases as

$$\mathsf{SE}_n\left[\hat{\sigma}\right] = \frac{\sqrt{\mathbb{V}\left\{\hat{\sigma}\right\}}}{\mathbb{E}\left\{\hat{\sigma}\right\}} \sim \frac{1}{\sqrt{\sigma \cdot |S|}},$$

not only for Jaccard.

N.B. We can make $|S| \rightarrow \infty$ as $|A|, |B| \rightarrow \infty$ using affirmative sampling, without commiting to a fixed large value of k, but making the standard error go to 0 (albeit slowly).

Some final remarks

- Prove the conjecture about unbiased estimation of the similarity measures: cosine, correlation, Kulczynski 1
- Prove the conjecture about the standard error for the different studied similarity measures
- Extend our work to other similarity/distance measures: we are aware of almost 80 similarity/distance measures—however many are not interesting in this context as they count also *negative matches* (the number of elements neither in A nor in B)
- Carry out the analysis of similarity measures for multisets: on-going work, works for Jaccard similarity—however, we need to sample items according to their frequencies, we have not to use distinct sampling