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[Instructions for use](#)

ERATO Minato project kickoff meeting@Hokkaido University

SketchSort: An Efficient Nearest Neighbor Graph Construction Method

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SketchSort: An Efficient Nearest Neighbor Graph Construction Method

- 高速な近傍グラフ構築手法の提案
 - Input: データー点の集合 Output: 距離 ϵ 以内の点ペアー
 - LSH + Multiple Sorting Method (Uno 08)
 - LSH: ベクトルデーターを距離関係を保ったまま、バイナリーの文字列に射影する
 - MSM: 文字列集合から、ハミング距離 d 以内の文字列ペアーを列挙する
- Missing Neighborの理論的な見積もり

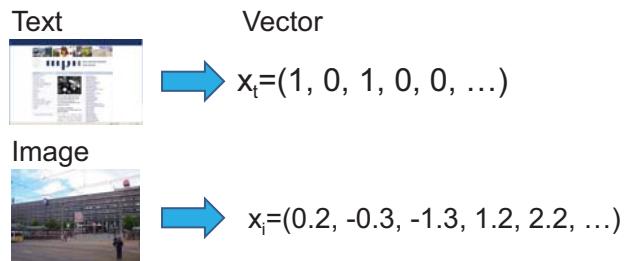
$$E \left[\frac{|F_2|}{|E^*|} \right] \leq \left(1 - \sum_{k=0}^{\lfloor d \rfloor} \binom{\ell}{k} p^k (1-p)^{\ell-k} \right)^Q,$$

・大規模画像上で既存手法と比較することにより、提案手法の有効性を示した。

Outline

- Motivation
- Method
- Experiments and Results

Data represented as vector



Chemical Compound, Protein, DNA/RNA etc

Locality Sensitive Hashing (Gionis et al,99)

- Mapping vector to binary string (sketch)
- Conserve the distance in the original space
- Enable to store gigascale data in main memory
- Speed up learning algorithms

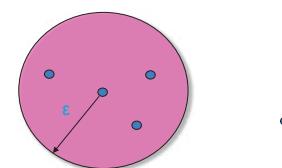
$$x = (0.2, -0.3, -1.3, 1.2, 2.2, \dots)$$



$$s = 10101011101010101$$

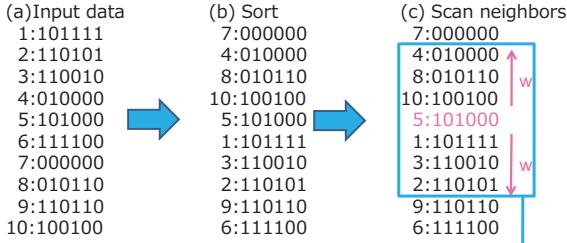
All Pairs Similarity Search

- Finding all neighbor pairs from sketches
 - Find all pairs $(i, j), i < j, \Delta(x_i, x_j) \leq \epsilon$
- Enable to build a neighborhood graph
 - semi-supervised learning, spectral clustering, ROI detection in images, retrieval of protein sequences



Single Sorting Method (SSM)

- Find neighbors by sorting sketches
- Various applications ex) google news



Drawbacks of Single Sorting

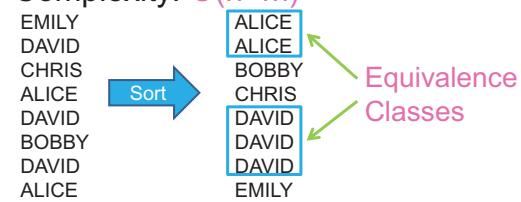
- Need a large number of distance calculation for achieving reasonable accuracy.
- Can not derive an analytic estimate of the fraction of missing neighbors.

Overview of SketchSort

- Employ the multiple sorting method (MSM) as a building block
 - Enumerate all pairs within Hamming distance d from a string pool $S = \{s_1, \dots, s_n\}$
- A number of distance calculation is significantly reduced
- A bound of the expected fraction of missing neighbors can be obtained.

Special case: Finding identical strings($d=0$)

- Radix sort, and partition the strings into equivalence classes: $O(n)$
- Build edges between all pairs in equivalent classes: $O(m)$
- Complexity: $O(n+m)$



Multiple sorting method ($d > 0$)

- Mask d characters in all possible ways
 - Perform radix sort $\binom{d}{d}$ times
 - Time exponential to d , polynomial to the string length $|s|$
 - Still linear to the number of strings!!
 - Ex) $d=2$
- | | | | | | | | | | | | |
|---------|------|------|------|--------|------|------|------|--------|------|------|------|
| 7:0000 | 0001 | 0011 | 1100 | 7:0000 | 0001 | 0011 | 1110 | 7:0000 | 0011 | 1100 | 1110 |
| 4:0100 | 0001 | 1101 | 1100 | 4:0100 | 0001 | 1101 | 1100 | 4:0100 | 0011 | 1101 | 1100 |
| 8:0100 | 1001 | 0111 | 1000 | 8:0100 | 1001 | 0111 | 1000 | 8:0100 | 0111 | 1001 | 1000 |
| 10:1000 | 0011 | 1001 | 0111 | 5:1010 | 0010 | 0010 | 1110 | 5:1010 | 0010 | 1001 | 0111 |
| 5:1010 | 0010 | 1110 | 1000 | 1:1011 | 1111 | 1101 | 1100 | 1:1011 | 0011 | 1101 | 1110 |
| 1:1011 | 1111 | 0011 | 1100 | 3:1100 | 1000 | 1101 | 1100 | 3:1100 | 1101 | 1100 | 0001 |
| 2:1100 | 0111 | 0111 | 0011 | 2:1101 | 0111 | 0111 | 0001 | 2:1101 | 0111 | 0101 | 1110 |
| 3:1100 | 1000 | 1101 | 1100 | 9:1101 | 1000 | 1101 | 1100 | 9:1101 | 1101 | 1101 | 1110 |
| 9:1101 | 1000 | 1101 | 1100 | 6:1111 | 0011 | 0011 | 1010 | 6:1111 | 0011 | 0111 | 0110 |
| 6:1111 | 0011 | 1001 | 0111 | 10:11 | 0111 | 1001 | 0111 | 10:11 | 0111 | 1101 | 1110 |

Blockwise masking

- Mask d blocks in all possible ways
- The number of sorting operations reduced
- Non-neighbors might be detected

- Filtered out by calculating actual Hamming distances

■ Ex) $d=2$

7:0000	0001	0011	1100	7:0000	0011	1100	1110	7:0000	1110	1100	1110
4:0100	0001	1101	1100	4:0100	0010	1101	1100	4:0100	0110	1001	0110
8:0100	1001	0111	1000	8:0100	0111	0111	1100	8:0100	1101	0110	0110
10:1000	0011	1001	0111	10:1001	0001	1001	1100	10:1001	0110	1010	0111
5:1010	0010	1110	1000	5:1010	0010	1110	1100	5:1010	0110	1010	1010
1:1011	1111	0011	1100	1:1011	1111	0011	1101	1:1011	0011	1101	1110
2:1101	0111	0111	0011	2:1101	0111	0111	0001	2:1101	0111	0111	0001
3:1100	1000	1101	1100	9:1101	1000	1101	1100	9:1101	1101	1101	1110
9:1100	1000	1101	1100	6:1111	0011	0011	1010	6:1111	0011	0111	0110
6:1111	0011	1001	0111	10:11	0111	1001	0111	10:11	0111	1101	1110

Recursive Algorithm

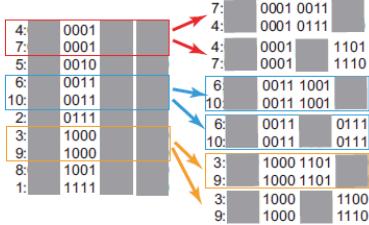


Figure 5: Updating equivalence classes in block concatenation. Strings in a block are sorted and equivalence classes (shown as square frames) are detected. A next block is concatenated to each equivalence class and sorted again.

SketchSort

- Basic idea: Map vectors to strings and apply MSM
- Not good: Create long strings and apply MSM at once
- Replication:
 - Create Q independent string pools of length $|I|$
 - apply MSM to each string pool
- Report the pairs less than a threshold ϵ

$$\Delta(x_i, x_j) \leq \epsilon$$

Duplication Checks

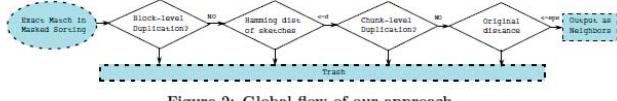


Figure 2: Global flow of our approach.

- Block-level duplication check
 - Define dictionary order of blocks, and take only minimum combinations of blocks.
ex) $d=2$
 $(1,2) < (1,3) < (1,4) < (2,3) < (2,4) < (3,4)$
- Chunk-level duplication check
 - Take only minimum chunks.

Bound of type-II error: Missing edge ratio

- Basically, type-II error is more crucial
 - type-I errors are filtered out by distance calculations
- Missing edge ratio (type-II error) is bounded as

$$E \left[\frac{|F_2|}{|E^*|} \right] \leq \left(1 - \sum_{k=0}^{\lfloor d \rfloor} \binom{\ell}{k} p^k (1-p)^{\ell-k} \right)^Q,$$

where p is an upper bound of the non-collision probability of neighbors

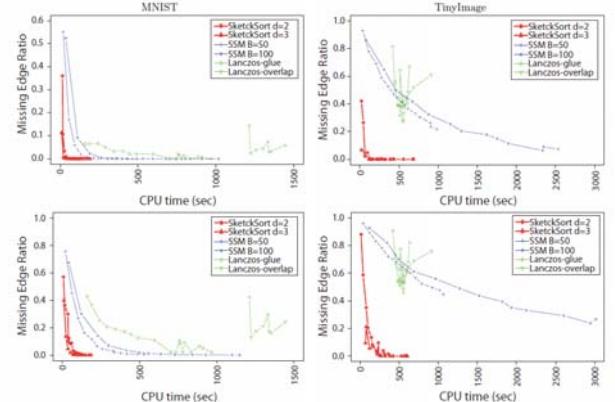
$$p = \frac{\arccos(1 - \epsilon)}{\pi}.$$

Two types of errors

- True edges E^* , Our results E
- Type-I error (false positive): A non-neighbor pair has a Hamming distance within d in at least one replicate
 $F_1 = \{(i, j) \mid (i, j) \in E, (i, j) \notin E^*\}$.
- Type II-error (false negative): A neighbor pair has a Hamming distance larger than d in all replicates
 $F_2 = \{(i, j) \mid (i, j) \notin E, (i, j) \in E^*\}$.

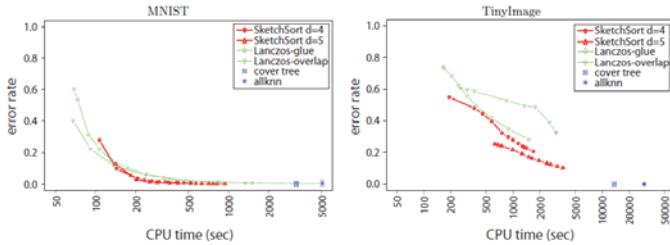
Results for All Pairs Similarity Search

Faster and more accurate than recent methods



All pairs similarity search on MNIST and TinyImage datasets for cosine distance thresholds 0.1π (top) and 0.15π (bottom).

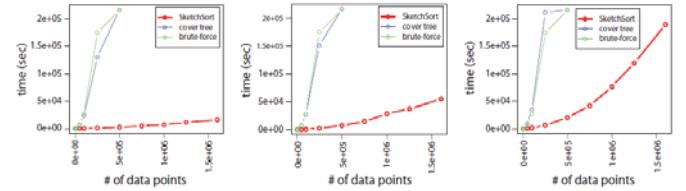
Results for 5-nearest neighbor search



Error rate for 5-nearest neighbor search on MNIST and TinyImage datasets

All Pairs Similarity Search in 1.6 Million Images

- Set parameters so as to keep missing edge ratio no more than 1.0×10^{-6}
- Enable to detect similar pairs nearly exactly
- Take only 4.3 hours for 1.6 million images



Near duplication detection in up to 1.6 million images at threshold 0.05π (left), 0.10π (middle) and 0.15π (right)

A C++ implementation of SketchSort is available from
<http://code.google.com/p/sketchsort/>

This page is under construction.

Introduction

SketchSort is a software for all pairs similarity search. It takes as an input data points and outputs approximate nearest neighbor pairs within a distance. First, the input data points are mapped to binary bit strings by locality sensitive hashing, and then nearest neighbor pairs of strings within a distance threshold are found. SketchSort is based on the locality sensitive hashing proposed in [1]. The main idea is that if the cosine distance for a nearest neighbor pair is no more than a user-specified threshold, the nearest neighbor pair is judged. One might worry about missed nearest neighbor pairs by our method. A theoretical bound of the expectation of missing edge ratio is derived. It enables us to set parameters so as to keep the empirical missing edge ratio as small as possible.

Quick Start

To compile SketchSort, please type the following:

```
tar -zxf sketchsort_0.1.0.tar.gz
cd sketchsort_0.1.0
make
./sketchsort -n 1000000 -k 10 -t 0.05 -l 1000000 -r 1000000 -c 1000000 -o sketchsort.out
```

Usage

SketchSort (optional) mode for output file

Output:

```
SketchSort (0.05) set the learning distance threshold (default: 0.05)
-n mumber (1) set the number of shards (default: 1). This k is set to d + 2 is recommended.
-k mumber (2) set the number of shards (default: 2).
-t mumber (3) set the learning distance threshold (default: 0.05)
-l mumber (4) set the number of shards (default: 1)
-c mumber (5) set the number of shards (default: 1)
```

A reader who would like to know the meanings of these options can see our original paper [2].

Format of input file

For all .dat file in the input file need to be commented #. Each line in the input file is a feature vector in which each element is separated by a space.

Elements in a lines need to be the same number. Here is an example:

```
#1 1.2 3.3 0.1 0.5
#2 4.5 2.1 0.9 0.2
#3 0.2 3.4 5.5 0.3 0.4
```