

APPROXIMATE NEAREST NEIGHBOR SEARCH VIA GROUP TESTING

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CS754: ADVANCED IMAGE PROCESSING UNDER PROF. AJIT RAJWADE

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Locality Sensitiv

Distance-Sensitive Bloom

Algorithm

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Nearest Neighbor Search



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Introduction

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- Nearest neighbor search is a fundamental problem with many applications in machine learning systems.
- Task: Given a dataset $D = \{x_1, x_2, \dots, x_N\}$, the goal is to build a data structure that can be queried with any point q to obtain a small set of points $x_i \in D$ that have high similarity (low distance) to the query. This structure is called an index.
- Such tasks frequently arise in genomics, web-scale data mining, machine learning, and other large-scale applications.

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Group Testing



Approximate Nearest Neighbor Search via Group Testing

Introduction

• The paper uses a doubly regular design: Each item appears in an equal number of tests; each test has an equal number of

• We are given a set D of N items, with k positives ("hits") and N-k negatives ("misses").

- Goal: Identify all positive items using fewer than N group tests.
- A group test is positive iff at least one item in the group is positive.
- **Testing Variants:** Can be *noisy* (with false positives/negatives), adaptive (tests depend on previous results), or non-adaptive (all tests run in parallel).
- items.

Formal Problem Statement



• (R, c)-Approximate Near Neighbor: Given a dataset D, if there exists a point within distance R of a query y, return some point within distance $c \cdot R$, with high probability.

- \bullet R is the distance threshold (radius).
- c > 1 is the approximation factor.
- ullet Any algorithm that solves the randomized nearest neighbor problem also solves the approximate near neighbor problem with c=1 and any R> distance to the nearest neighbor.
- (Definition) Randomized Nearest neighbor: Given a dataset D and a distance metric $d(\cdot,\cdot)$ and a failure probability $\delta \in [0,1]$, construct a data structure which, given a query point y reports the point $x \in D$ with the smallest distance d(x,y) with probability greater than $1-\delta$.

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Locality Sensitive Hashing



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A hash function $h(x) \to \{1, \dots, R\}$ is a function that maps an input x to an integer in the range [1, R]. The two points x and y are said to collide if h(x) = h(y).

$$s(x,y) = Pr_H(h(x) = h(y))$$

For now, we will assume that s(x,y) = sim(x,y).

For any positive integer L, we may transform an LSH family H with collision probability s(x,y) into a new family having $s(x,y)^L$ by sampling L hash functions from H and concatenating the values to obtain a new hash code $[h_1(x),h_2(x),...,h_L(x)]$. If the original hash family had the range [1,R], the new hash family has the range $[1,R^L]$.

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Locality Sensitive Hashing



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- Locality Sensitive Hashing (LSH) algorithms use an LSH function to partition the dataset into buckets.
- The hash function is selected so that the distance between points in the same bucket is likely to be small.
- To find the near neighbors of a query, we hash the query and compute the distance to every point in the corresponding bucket.
- Count-Based LSH identifies neighbors by simply counting how many times two points land in the same hash bucket across multiple hash functions.

Distance-Sensitive Bloom Filters



• (Definition) Approximate Set Membership: Given a set D of N points and similarity thresholds S_L and S_H , construct a data structure which, given a query point y, has: True Positive Rate: If there is $x \in D$ with $sim(x,y) > S_H$, the structure returns true w.p. $\geq p$ False Positive Rate: If there is no $x \in D$ with $sim(x,y) > S_L$, the structure returns true w.p. < q

ullet The distance-sensitive Bloom filter solves this problem using LSH functions and a 2D bit array. The structure consists of m binary arrays that are each indexed by an LSH function. There are threeparameters: the number of arrays m, a positive threshold $t \leq m$, and the number of concatenated hash functions L used within each array.

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- To construct the filter, we insert elements $x \in D$ by setting the bit located at array index $[m, h_m(x)]$ to 1.
- To query the filter, we determine the m hash values of the query y. If at least t of the corresponding bits are set, we return true.
 Otherwise, we return false.
- ullet (Theorem) Assuming the existence of an LSH family with collision probability s(x,y)=sim(x,y), the distance-sensitive Bloom filter solves the approximate membership query problem with

$$p \ge 1 - \exp\left(-2m(-t + S_H^L)^2\right)$$
$$q \le \exp\left(-2m(-t + NS_L^L)^2\right)$$

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Index Construction



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Input: Dataset D of size N, positive integers B and R, similarity threshold S

Output: A FLINNG search index consisting of membership sets $M_{r,b}$ and group tests $C_{r,b}$

- For r = 0 to R 1:
 - ullet Let $\pi(D)$ be a random permutation of D
 - For b = 0 to B 1:
 - Define $M_{r,b} = \{\pi(D)_i \mid i \bmod B = b\}$
- For r = 0 to R 1:
 - For b = 0 to B 1:
 - \bullet Construct a classifier $C_{r,b}$ for membership set $M_{r,b}$ with true positive rate p and false positive rate q

Index Construction



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- If we apply a similarity threshold to the dataset, we obtain a near neighbor set $K = \{x \in D | sim(x, y) \ge S\}$. We consider K to be the set of "positives" in the group testing problem.
- In order to do so, we split the dataset D into a set of groups, which we visualize as a $B \times R$ grid of cells. Each cell has a group of items $M_{r,b}$ and a corresponding group test $C_{r,b}$. To assign items to cells, we evenly distribute the N points among the B cells in each column of the grid, and we independently repeat this assignment process R times.

Index Query



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Input: A FLINNG index and a query y

Output: Approximate set K of neighbors with similarity greater than the threshold S

- Initialize $\hat{K} = \{1, \dots, N\}$
- For r = 0 to R 1:
 - Initialize $Y = \emptyset$
 - For b = 0 to B 1:
 - If $C_{r,b}(y) = 1$ then: $Y = Y \cup M_{r,b}$
 - $\hat{K} = \hat{K} \cap Y$

Index Query



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- To query the index with a point y, we begin by querying each classifier. If $C_{r,b}(y)=1$, then at least one of the points in $M_{r,b}$ has high similarity to y. We collect all of these "candidate points" by taking the union of the $M_{r,b}$ sets for which $C_{r,b}(y)=1$.
- We repeat this process for each of the R repetitions to obtain R candidate sets, one for each column in the grid.
- With high probability, each candidate set contains the true neighbors, but it may also have some non-neighbors that were included in $M_{r,b}$ by chance. To filter out these points, we intersect the candidate sets to obtain our approximate near neighbor set \hat{K} .

Group Testing: Runtime and Accuracy



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Lemma: Suppose we have a dataset D of points, where a subset $K\subseteq D$ is "positive" and the rest are "negative". Construct a $B\times R$ grid of tests, where each test has i.i.d true positive rate p and false negative rate q. Then the algorithm reports points as "positive" with probability:

$$Pr(\mathsf{Report}\ x\mid x\in K)\geq p^R$$

$$\begin{split} \Pr(\mathsf{Report}\ x \mid x \notin K) & \leq \left[q \left(\frac{eN(B-1)}{B(N-1)} \right)^{|K|} + \right. \\ & \left. p \left(1 - \left(\frac{N(B-1)}{eB(N-1)} \right)^{|K|} \right) \right]^R \end{split}$$

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Group Testing: Runtime and Accuracy



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The cost of group testing inference includes the cost to do all $B \times R$ tests, plus the cost of intersecting the positive groups.

Theorem: Under the assumptions in the previous lemma, let us suppose that each test runs in $\mathcal{O}(T)$. Then with probability $1 - \delta$:

$$t_{\mathsf{query}} = \mathcal{O}\left(BRT + \frac{RN}{B}(p|K| + qB)log(\frac{1}{\delta})logN\right)$$

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Bounding the Test Cost



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To distinguish between the |K| nearest neighbors and the rest of the dataset:

$$S_H = sim(x_{|K|}, y) = s_{|K|}$$

$$S_L = sim(x_{|K|+1}, y) = s_{|K|+1}$$

(Definition) γ -Stable query: We say that the query is γ -stable if $\frac{log(s_{|K|})}{log(s_{|K|})-log(s_{|K|})} \leq \gamma$

Theorem: Given a true positive rate p, false negative rate qand stability parameter γ , it is possible to choose m, L and t so that the resulting distance-sensitive Bloom filter has true positive rate p and false negative rate q for all γ -stable queries. The query time is

$$\mathcal{O}(mL) = \mathcal{O}(-log(min(q, 1-p))N\gamma log(N))$$

Query Time Analysis



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