Probabilistic Polynomials and Hamming Nearest Neighbors

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## Hamming Nearest Neighbor Problem

#### Definition (Hamming Nearest Neighbor Problem)

Given a set D of n database points in  $\{0,1\}^d$ , we wish to preprocess D so that for queries  $q \in \{0,1\}^d$ , we answer a point  $u \in D$  that differs from q in a minimum number of coordinates.

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#### Curse of Dimensionality (Barkol, Rabani '00)

All solutions require either

- $2^{\Omega(d)}$  size data structure (store all answers), or
- $\Omega(n/\operatorname{polylog}(n))$  query time (try all points).

Hamming Nearest Neighbor Problem: Past Work

Past work has gotten around this problem in a variety of ways:

- ► Approximate solutions: find a point with distance within (1 + ϵ) of the optimal
  - Lots of beautiful results and impact: hashing, dimensionality reduction, ...

"Curse of approximation": still requires n<sup>Ω(1/ε<sup>2</sup>)</sup> space.
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- 'Planted' case: All vectors are random except one pair with distance much smaller than expected; find the planted pair among the *n* vectors
  - O(n<sup>1.62</sup>) time algorithm, independent of dimension.
     [G. Valiant '12]

#### Batch Hamming Nearest Neighbor Problem

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Lower bounds no longer apply, but still best previously known solutions take either:

- $n \cdot 2^{\Omega(d)}$  time (build a table of all answers), or
- $n^2 \cdot d^{\Omega(1)}$  time (try all pairs).

#### Theorem (AW '15)

Let  $D \subseteq \{0,1\}^d$  be a database of n vectors of dimension  $d = c \log n$ , where c can be a function of n. Any batch of n Hamming nearest neighbor queries on D can be answered in randomized  $n^{2-1/O(c \log^2 c)}$  time, whp.

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- If d = O(log n), then the algorithm runs in truly subquadratic time: n<sup>2-ϵ</sup>, for some ϵ > 0.
- Improves on the trivial algorithm when d = o(log<sup>2</sup>(n)/log log<sup>2</sup>(n)).
- Algorithm technique: Compute Hamming distances using Efficiently Computable Low-Degree Probabilistic Polynomials (Very different techniques from past work)

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#### Theorem (AW '15)

Suppose there is  $\epsilon > 0$  such that for all constant *c*, Batch HNN can be solved in  $2^{o(d)} \cdot n^{2-\epsilon}$  time on a set of *n* points in  $\{0,1\}^{c \log n}$ . Then the Strong Exponential Time Hypothesis is false.

Let *R* be a ring (can be  $\mathbb{Z}_m, \mathbb{Z}, \mathbb{Q}, \mathbb{R}, ...$ ). A polynomial *p* in *n* variables over *R* computes the boolean function  $f : \{0,1\}^n \to \{0,1\}$  if for each  $x \in \{0,1\}^n$  we have p(x) = f(x).

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$$OR(x_1, x_2, \dots, x_n) = \begin{cases} 0 & \text{if } x_1 = x_2 = \dots = x_n = 0\\ 1 & \text{otherwise.} \end{cases}$$

Then,

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Note: We never need to take powers of a variable greater than 1, since  $x_i = x_i^2$  when  $x_i \in \{0, 1\}$ . (We only need to look at multilinear polynomials)

## Probabilistic Polynomial

Let  $f : \{0,1\}^n \to \{0,1\}$  be any Boolean function on *n* variables.

#### Definition (Probabilistic Polynomial)

A probabilistic polynomial over R for f with error  $\epsilon$  and degree d is a distribution  $\mathcal{D}$  of degree-d polynomials over R with the property that for each  $x \in \{0, 1\}^n$ ,

$$\Pr_{p \sim \mathcal{D}}[p(x) = f(x)] \ge 1 - \epsilon.$$

Note: The probability is only over the polynomial p, not over the input x.

[Aspnes, Beigel, Furst, Rudich '93] Set  $S_0 = \{1, 2, \dots, n\}$  and

construct subsets

$$S_0 \supseteq S_1 \supseteq S_2 \cdots \supseteq S_{\log_2(n)+1}$$

such that each element of  $S_i$  is included in  $S_{i+1}$  with probability 1/2.

Let 
$$p_i(x) = \sum_{j \in S_i} x_j$$
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Our probabilistic polynomial for OR is

$$p(x) = 1 - \prod_i (1 - p_i(x))$$

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- ► O(log(n)) degree polynomial for OR with e = 2/3.
- ► Can augment to degree O(log(n) log(1/ε)) for any ε > 0 (use the fact that the error is one-sided).

Notation: For  $x \in \{0,1\}^n$ , write  $|x| = \sum_{i=1}^n x_i$ .

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MAJORITY(x) = 1 iff  $|x| \ge n/2$ .

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Theorem (Razborov, Smolensky '87)

A probabilistic polynomial with  $\epsilon$  error for MAJORITY requires degree  $\Omega(\sqrt{n \log(1/\epsilon)})$ .

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We will actually look at the threshold function:  $TH_{\theta}(x) = 1$  iff  $|x|/n \ge \theta$ . In particular,  $MAJORITY = TH_{1/2}$ .

Two cases depending on how close |x|/n is to  $\theta$  (whether or not it is within  $\delta = \Theta(\sqrt{\log(1/\epsilon)/n})$ ):

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If |x|/n ∉ [θ − δ, θ + δ], then if we construct a new smaller vector x̃ by sampling 1/10 of the entries of x, it is likely that |x̃|/(n/10) lies on the same side of θ as |x|/n (by Chernoff-Hoeffding).

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► To decide which of the two cases we are in, we can use TH<sub>θ+δ</sub>(x̃) and TH<sub>θ-δ</sub>(x̃).

# From Probabilistic Polynomial to Hamming Distance Algorithm

Given an efficient (small number of monomials) polynomial, we can evaluate it on many points quickly:

#### Lemma (R. Williams '14)

Given a polynomial  $P(x_1, \ldots, x_d, y_1, \ldots, y_d)$  with at most  $n^{0.17}$ monomials, and two sets of n inputs  $A = \{a_1, \ldots, a_n\} \subseteq \{0, 1\}^d$ ,  $B = \{b_1, \ldots, b_n\} \subseteq \{0, 1\}^d$ , we can evaluate P on all pairs  $(a_i, b_j) \in A \times B$  in  $\tilde{O}(n^2)$  time.

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- Beats the trivial runtime of  $\Omega(n^{2.17})$  time.
- Since we want a subquadratic algorithm, we can't just let A, B be our sets of vectors.
- Instead, group our vectors into n/s groups of size s. Each element of A or B will correspond to a group.

# We will use this to solve the following sub-problem of Batch HNN: Definition (Hamming distance problem)

Given an integer k and two collections of s vectors of dimension d as input, output 1 iff there is a pair of vectors (one from each collection) with Hamming distance at most k.

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Let x<sub>1</sub>,..., x<sub>s</sub> and y<sub>1</sub>,..., y<sub>s</sub> be the two collections of vectors.
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- Let D<sub>d</sub> be the probabilistic polynomial of degree O(√d log(1/ε)) for the threshold function TH<sub>(k+1)/d</sub> on d inputs. Sample p ~ D<sub>d</sub> with error ε = 1/s<sup>3</sup>.

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- Let  $\mathcal{D}_d$  be the probabilistic polynomial of degree  $O(\sqrt{d \log(1/\epsilon)})$  for the threshold function  $TH_{(k+1)/d}$  on d inputs. Sample  $p \sim \mathcal{D}_d$  with error  $\epsilon = 1/s^3$ .

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Our polynomial is:

$$q(x_1, y_1, \ldots, x_s, y_s) := \sum_{(i,j)\in R} (1 + p(x_{i,1} + y_{j,1}, \ldots, x_{i,d} + y_{j,d})).$$

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- If all the x<sub>i</sub> and y<sub>j</sub> have Hamming distance > k, then the sum is 0. Otherwise, it is 0 or 1 with 1/2 chance each (based on our choice of R)
- Since the error is one-sided, we can amplify to get as high a success probability as we want.

# Solving Batch Hamming Nearest Neighbor

Two more steps:

- ► Hamming distance problem (is there a pair with distance ≤ k) polynomial ⇒ algorithm.
- ► Hamming distance problem algorithm ⇒ Batch Hamming nearest neighbor (for each vector, find its nearest neighbor) algorithm.

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#### Lemma

Given a threshold k, and subsets  $R, B \subseteq \{0,1\}^d$  with |R| = |B| = n and  $d = c \log n$ , we can find a  $v \in R$  and  $u \in B$  whose Hamming distance is  $\leq k$  in time  $n^{2-1/O(c \log^2 c)}$  (or determine that none exist).

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Partition each of R and B into n/s groups of size s = n<sup>1/O(c log<sup>2</sup> c)</sup>.

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- Partition each of R and B into n/s groups of size s = n<sup>1/O(c log<sup>2</sup> c)</sup>.
- Our probabilistic polynomial on each group has degree  $O(\sqrt{d \log s})$ . Hence the number of monomials is  $(\frac{2d}{\sqrt{d \log s}})$ , which is  $\leq n^{0.17}$  for a suitable choice of constants.

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- Partition each of R and B into n/s groups of size s = n<sup>1/O(c log<sup>2</sup> c)</sup>.
- Our probabilistic polynomial on each group has degree  $O(\sqrt{d \log s})$ . Hence the number of monomials is  $\binom{2d}{\sqrt{d \log s}}$ , which is  $\leq n^{0.17}$  for a suitable choice of constants.
- ► Using the fast evaluation lemma, we can evaluate on all pairs of groups in n<sup>2-1/O(c log<sup>2</sup> c)</sup> time.

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Hamming distance problem algorithm  $\Rightarrow$  Batch Hamming nearest neighbor

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If the Hamming distance problem can be solved in T(n, d) time, then the Batch Hamming nearest neighbor problem can be solved in  $O(ndT(\sqrt{n}, d))$  time.

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- Partition each of D and Q into n/s groups of size  $s = \sqrt{n}$ .
- For k from 0, 1, 2, ..., d 1:
- Call the Hamming distance problem algorithm on each pair of a group from D and a group from Q. If a pair (u, v) ∈ Q × D is found, then v is a nearest neighbor for u. Remove u from Q and continue.
- There are at most n calls that do not return a vector pair for each k, so dn total such calls.
- There are at most n calls that return a vector pair since we remove each vector from Q once we find a pair for it.

## Putting it all together

Combining our lemmas yields:

#### Theorem (AW '15)

Let  $D \subseteq \{0,1\}^d$  be a database of n vectors of dimension  $d = c \log n$ , where c can be a function of n. Any batch of n Hamming nearest neighbor queries on D can be answered in randomized  $n^{2-1/O(c \log^2 c)}$  time, whp.

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- Other ways to quickly evaluate polynomials
  - Feels strange to use matrix multiplication instead of FFT
  - That said, fast MM used here is not necessarily impractical!