COMPSCI 514: ALGORITHMS FOR DATA SCIENCE

Cameron Musco University of Massachusetts Amherst. Spring 2019. Lecture 9

- Problem Set 2 was released Sunday night and is due Sunday 3/8.
- Please make sure to mark all teammates in the GradeScope submission (don't just write names on the document).
- The Midterm will be on Thursday 3/12. Will cover material through this week.
- Study guide/practice questions to be released soon.

Last Class:

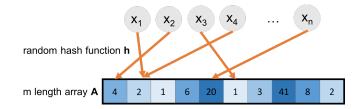
- Continued on the frequent elements problem.
- Misra-Greis summaries (deterministic method).
- \cdot Started on Count-Min Sketch (randomized method).

This Class:

- Finish up Count-Min Sketch analysis.
- \cdot Start on randomized methods for dimensionality reduction.
- The Johnson-Lindenstrauss Lemma.

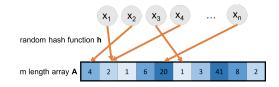
Frequent Items Problem: Identify all items with frequency $\geq n/k$ in a stream of *n* items.

Count-Min Sketch: Bloom filter like solution using random hashing.



Use $A[\mathbf{h}(x)]$ to estimate f(x), the frequency of x in the stream. I.e., $|\{x_i : x_i = x\}|$.

COUNT-MIN SKETCH ACCURACY



Use $A[\mathbf{h}(x)]$ to estimate f(x)

Claim 1: We always have $A[h(x)] \ge f(x)$. Why?

- $A[\mathbf{h}(x)]$ counts the number of occurrences of any y with $\mathbf{h}(y) = \mathbf{h}(x)$, including x itself.
- $A[\mathbf{h}(x)] = f(x) + \sum_{y \neq x: \mathbf{h}(y) = \mathbf{h}(x)} f(y).$

f(x): frequency of x in the stream (i.e., number of items equal to x). h: random hash function. m: size of count-min sketch array.

Α

$$[\mathbf{h}(x)] = f(x) + \sum_{\substack{y \neq x: \mathbf{h}(y) = \mathbf{h}(x)}} f(y) \quad .$$

Expected Error:

error in frequency estimate

$$\mathbb{E}\left[\sum_{y \neq x: h(y)=h(x)} f(y)\right] = \sum_{y \neq x} \Pr(h(y) = h(x)) \cdot f(y)$$
$$= \sum_{y \neq x} \frac{1}{m} \cdot f(y) = \frac{1}{m} \cdot (n - f(x)) \le \frac{n}{m}$$

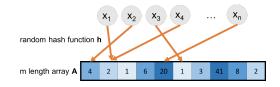
What is a bound on probability that the error is $\geq \frac{3n}{m}$?

Markov's inequality: $\Pr\left[\sum_{y \neq x:h(y)=h(x)} f(y) \ge \frac{3n}{m}\right] \le \frac{1}{3}$.

What property of h is required to show this bound? 2-universal.

f(x): frequency of x in the stream (i.e., number of items equal to x). h: random hash function. m: size of count-min sketch array.

COUNT-MIN SKETCH ACCURACY

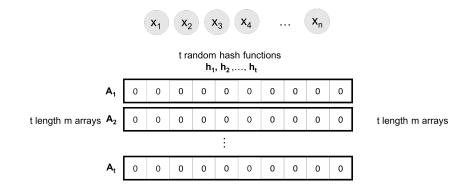


Claim: For any x, with probability at least 2/3,

$$f(x) \le A[\mathbf{h}(x)] \le f(x) + \frac{3n}{m} \cdot \frac{\epsilon n}{k}$$

To solve the (ϵ, k) -Frequent elements problem, set $m = \frac{3k}{\epsilon}$. How can we improve the success probability? Repetition.

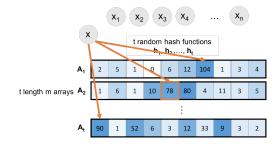
f(x): frequency of x in the stream (i.e., number of items equal to x). h: random hash function. m: size of count-min sketch array.



Estimate f(x) with $\tilde{f}(x) = \min_{i \in [t]} A_i[\mathbf{h}_i(x)]$. (count-min sketch)

Why min instead of mean or median? The minimum estimate is always the most accurate since they are all overestimates of the true frequency!

COUNT-MIN SKETCH ANALYSIS



Estimate f(x) by $\tilde{f}(x) = \min_{i \in [t]} A_i[\mathbf{h}_i(x)]$

• For every x and $i \in [t]$, we know that for $m = O(k/\epsilon)$, with probability $\geq 2/3$:

$$f(x) \leq A_i[\mathbf{h}_i(x)] \leq f(x) + \frac{\epsilon n}{k}.$$

- What is $\Pr[f(x) \le \tilde{f}(x) \le f(x) + \frac{\epsilon n}{k}]$? $1 1/3^t$.
- To get a good estimate with probability $\geq 1 \delta$, set $t = O(\log(1/\delta))$.

Upshot: Count-min sketch lets us estimate the frequency of every item in a stream up to error $\frac{\epsilon n}{k}$ with probability $\geq 1 - \delta$ in $O(\log(1/\delta) \cdot k/\epsilon)$ space.

- Accurate enough to solve the (ϵ, k) -Frequent elements problem.
- Actually identifying the frequent elements quickly requires a little bit of further work.

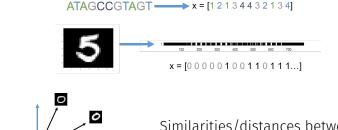
One approach: Separately store a list of potential frequent elements as they come in. At step *i*, keep any elements whose estimated frequency is $\geq i/k$. List contains at most O(k) items at any step and has all items with frequency $\geq n/k$ stored at the end of the stream.

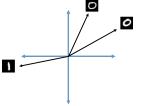
Questions on Frequent Elements?

'Big Data' means not just many data points, but many measurements per data point. I.e., very high dimensional data.

- Twitter has 321 million active monthly users. Records (tens of) thousands of measurements per user: who they follow, who follows them, when they last visited the site, timestamps for specific interactions, how many tweets they have sent, the text of those tweets, etc.
- A 3 minute Youtube clip with a resolution of 500×500 pixels at 15 frames/second with 3 color channels is a recording of \geq 2 billion pixel values. Even a 500 \times 500 pixel color image has 750,000 pixel values.
- The human genome contains 3 billion+ base pairs. Genetic datasets often contain information on 100s of thousands+ mutations and genetic markers.

In data analysis and machine learning, data points with many attributes are often stored, processed, and interpreted as high dimensional vectors, with real valued entries.



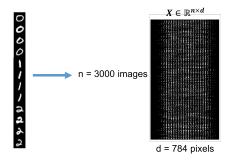


Similarities/distances between vectors (e.g., $\langle x, y \rangle$, $||x - y||_2$) have meaning for underlying data points.

Data points are interpreted as high dimensional vectors, with real valued entries. Data set is interpreted as a matrix.

Data Points: $\vec{x}_1, \vec{x}_2, \ldots, \vec{x}_n \in \mathbb{R}^d$.

Data Set: $X \in \mathbb{R}^{n \times d}$ with *i*th rows equal to \vec{x}_i .



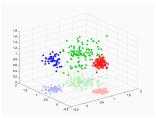
Many data points $n \implies$ tall. Many dimensions $d \implies$ wide.

Dimensionality Reduction: Compress data points so that they lie in many fewer dimensions.

$$\vec{x}_1, \ldots, \vec{x}_n \in \mathbb{R}^d \to \tilde{x}_1, \ldots, \tilde{x}_n \in \mathbb{R}^m$$
 for $m \ll d$.

5
$$\longrightarrow$$
 $x = [0 0 0 0 0 1 0 0 1 1 0 1 1 1...] $\longrightarrow \tilde{x} = [-5.5 4 3.2 - 1]$$

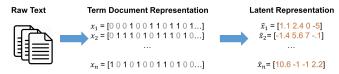
'Lossy compression' that still preserves important information about the relationships between $\vec{x}_1, \ldots, \vec{x}_n$.



Generally will not consider directly how well \tilde{x}_i approximates \vec{x}_i .

Dimensionality reduction is one of the most important techniques in data science.

- Principal component analysis
- Latent semantic analysis (LSA)



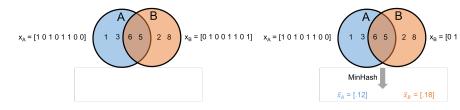
- Linear discriminant analysis
- Autoencoders

Compressing data makes it more efficient to work with. May also remove extraneous information/noise.

Low Distortion Embedding: Given $\vec{x}_1, \ldots, \vec{x}_n \in \mathbb{R}^d$, distance function D, and error parameter $\epsilon \ge 0$, find $\tilde{x}_1, \ldots, \tilde{x}_n \in \mathbb{R}^m$ (where $m \ll d$) and distance function \tilde{D} such that for all $i, j \in [n]$:

$$(1-\epsilon)D(\vec{x}_i,\vec{x}_j) \leq \tilde{D}(\tilde{x}_i,\tilde{x}_j) \leq (1+\epsilon)D(\vec{x}_i,\vec{x}_j).$$

Have already seen one example in class: MinHash.



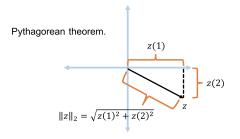
With large enough signature size r, $\frac{\# \text{ matching entries in } \tilde{x}_A, \tilde{x}_B}{r} \approx J(\vec{x}_A, \vec{x}_B).$

• Reduce dimension from d = |U| to r. Note: here $J(\vec{x}_A, \vec{x}_B)$ is a similarity rather than a distance. So this is not quite low distortion ¹⁶

Euclidean Low Distortion Embedding: Given $\vec{x}_1, \ldots, \vec{x}_n \in \mathbb{R}^d$ and error parameter $\epsilon \ge 0$, find $\tilde{x}_1, \ldots, \tilde{x}_n \in \mathbb{R}^m$ (where $m \ll d$) such that for all $i, j \in [n]$:

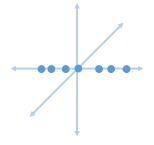
$$(1-\epsilon)\|\vec{x}_i - \vec{x}_j\|_2 \le \|\tilde{x}_i - \tilde{x}_j\|_2 \le (1+\epsilon)\|\vec{x}_i - \vec{x}_j\|_2.$$

Recall that for $\vec{z} \in \mathbb{R}^n$, $\|\vec{z}\|_2 = \sqrt{\sum_{i=1}^n \vec{z}(i)^2}$.





m-dimensional space (for m << d) A very easy case: Assume that $\vec{x}_1, \ldots, \vec{x}_n$ all lie on the 1st axis in \mathbb{R}^d .

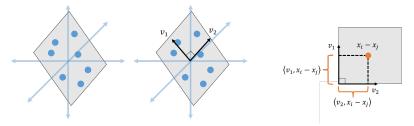


Set m = 1 and $\tilde{x}_i = \vec{x}_i(1)$ (i.e., \tilde{x}_i is just a single number).

$$\cdot \|\tilde{x}_i - \tilde{x}_j\|_2 = \sqrt{[\vec{x}_i(1) - \vec{x}_j(1)]^2} = |\vec{x}_i(1) - \vec{x}_j(1)| = \|\vec{x}_i - \vec{x}_j\|_2.$$

• An embedding with no distortion from any d into m = 1.

A pretty easy case: Assume that $\vec{x}_1, \ldots, \vec{x}_n$ lie in any *k*-dimensional subspace \mathcal{V} of \mathbb{R}^d .



- Let $\vec{v}_1, \vec{v}_2, \dots, \vec{v}_k$ be an orthonormal basis for \mathcal{V} and let $\mathbf{V} \in \mathbb{R}^{d \times k}$ be the matrix with these vectors as its columns.
- For all i, j we have $\vec{x}_i \vec{x}_j \in \mathcal{V}$ and (a good exercise!):

$$\|\vec{x}_i - \vec{x}_j\|_2 = \sqrt{\sum_{\ell=1}^k \langle v_\ell, \vec{x}_i - \vec{x}_j \rangle^2} = \|\mathbf{V}^{\mathsf{T}}(\vec{x}_i - \vec{x}_j)\|_2.$$

What about when we don't make any assumptions on $\vec{x}_1, \dots, \vec{x}_n$. I.e., they can be scattered arbitrarily around *d*-dimensional space?

- Can we find a no-distortion embedding into $m \ll d$ dimensions? No. Require m = d.
- Can we find an ϵ -distortion embedding into $m \ll d$ dimensions for $\epsilon > 0$? Yes! Always, with m depending on ϵ .

For all $i, j : (1 - \epsilon) \|\vec{x}_i - \vec{x}_j\|_2 \le \|\tilde{x}_i - \tilde{x}_j\|_2 \le (1 + \epsilon) \|\vec{x}_i - \vec{x}_j\|_2$.

Johnson-Lindenstrauss Lemma: For any set of points $\vec{x}_1, \ldots, \vec{x}_n \in \mathbb{R}^d$ and $\epsilon > 0$ there exists a linear map $\Pi : \mathbb{R}^d \to \mathbb{R}^m$ such that $m = O\left(\frac{\log n}{\epsilon^2}\right)$ and letting $\tilde{x}_i = \Pi x_i$:

For all
$$i, j: (1 - \epsilon) \|\vec{x}_i - \vec{x}_j\|_2 \le \|\tilde{x}_i - \tilde{x}_j\|_2 \le (1 + \epsilon) \|\vec{x}_i - \vec{x}_j\|_2$$
.

Further, if $\mathbf{\Pi} \in \mathbb{R}^{m \times d}$ has each entry chosen i.i.d. from $\mathcal{N}(0, 1/m)$, it satisfies the guarantee with high probability.

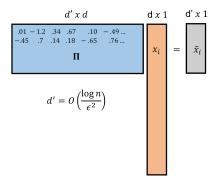
For d = 1 trillion, $\epsilon = .05$, and n = 100,000, $m \approx 6600$.

Very surprising! Powerful result with a simple construction: applying a random linear transformation to a set of points preserves distances between all those points with high probability.

RANDOM PROJECTION

For any $\vec{x}_1, \ldots, \vec{x}_n$ and $\mathbf{\Pi} \in \mathbb{R}^{m \times d}$ with each entry chosen i.i.d. from $\mathcal{N}(0, 1/m)$, with high probability, letting $\tilde{x}_i = \mathbf{\Pi} \vec{x}_i$:

For all $i, j: (1 - \epsilon) \|\vec{x}_i - \vec{x}_j\|_2 \le \|\tilde{x}_i - \tilde{x}_j\|_2 \le (1 + \epsilon) \|\vec{x}_i - \vec{x}_j\|_2.$



- **П** is known as a random projection.
- **П** is data oblivious. Stark contrast to methods like PCA.

- Many alternative constructions: ± 1 entries, sparse (most entries 0), Fourier structured, etc. \implies more efficient computation of $\tilde{x}_i = \mathbf{\Pi} \vec{x}_i$.
- Data oblivious property means that once $\mathbf{\Pi}$ is chosen, $\tilde{x}_1, \ldots, \tilde{x}_n$ can be computed in a stream with little memory.
- Memory needed is just O(d + nm) vs. O(nd) to store the full data set.
- Compression can also be easily performed in parallel on different servers.
- When new data points are added, can be easily compressed, without updating existing points.