COMPSCI 514: ALGORITHMS FOR DATA SCIENCE

Cameron Musco

University of Massachusetts Amherst. Spring 2019.

Lecture 1/09

LOGISTICS

- 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.

SUMMARY

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Last Class:

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

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This Class:

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

FREQUENT ELEMENTS WITH COUNT-MIN SKETCH

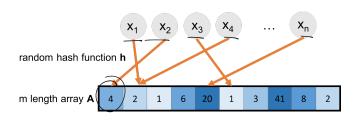
Frequent Items Problem: Identify all items with frequency

$$\geq n/k$$
 in a stream of n items. $\geq \frac{n}{k}$ $< (-\epsilon) \frac{1}{k}$

FREQUENT ELEMENTS WITH COUNT-MIN SKETCH

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

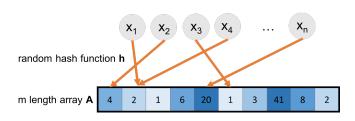
Count-Min Sketch: Bloom filter like solution using random hashing.



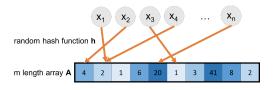
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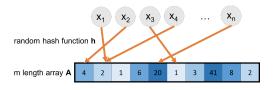


Use $A[\mathbf{h}(x)]$ to estimate f(x), the frequency of x in the stream. I.e., $|\{x_i : x_i = x\}|$.



Use A[h(x)] to estimate f(x)

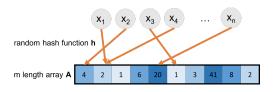
Claim 1: We always have $A[h(x)] \ge f(x)$. Why?



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· $A[\mathbf{h}(x)]$ counts the number of occurrences of any y with

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, including x itself.

$$A[h(x)] = f(x) + \sum_{y \neq x: h(y) = h(x)} f(y)$$

$$A[h(x)] = f(x) + \sum_{\substack{y \neq x: h(y) = h(x) \\ \text{error in frequency estimate}}} f(y)$$

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error in frequency estimate

Expected Error:

$$\mathbb{E}\left[\sum_{y\neq x: h(y)=h(x)} f(y)\right] = \underbrace{\sum_{y=1}^{n}}_{m} f(y)$$

$$P_{n}(h(y) = h(x)) \cdot \frac{1}{n}$$

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Expected Error:

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

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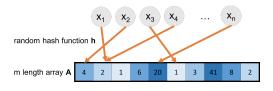
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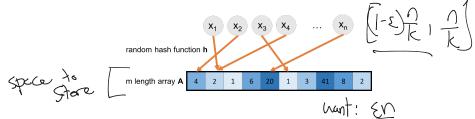
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What property of h is required to show this bound? 2-universal.



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

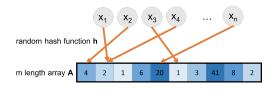
$$f(x) \le A[\mathbf{h}(x)] \le f(x) + \frac{3n}{m}.$$



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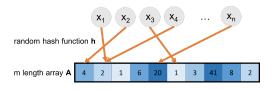
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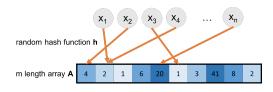
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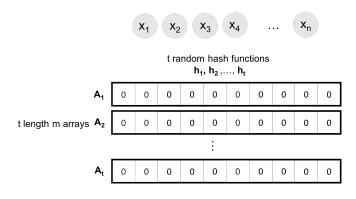
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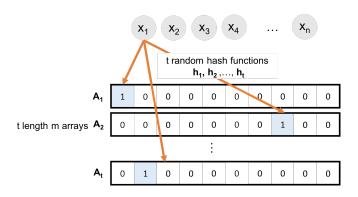


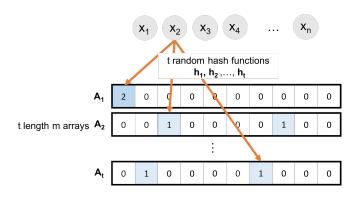
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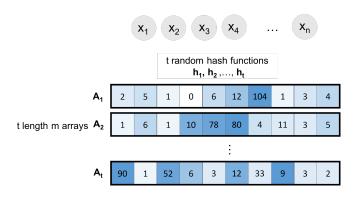
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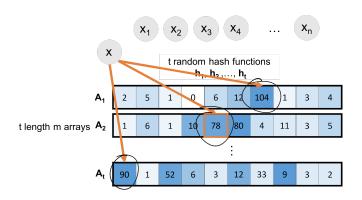
To solve the (ϵ, k) -Frequent elements problem, set $m = \frac{3k}{\epsilon}$. How can we improve the success probability? Repetition.



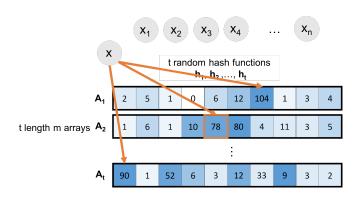




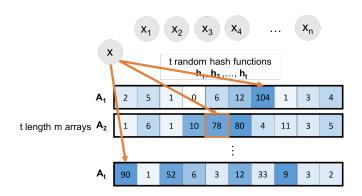




Estimate f(x) with $\tilde{f}(x) = \min_{i \in [t]} A_i[\mathbf{h}_i(x)]$. (count-min sketch)

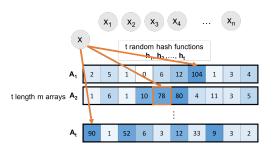


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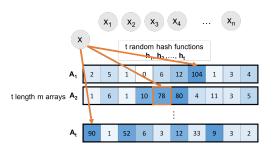


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Why min instead of mean or median? The minimum estimate is always the most accurate since they are all overestimates of the true frequency!



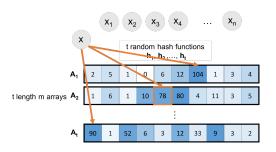
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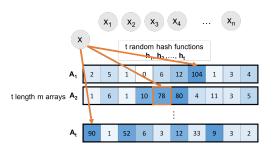


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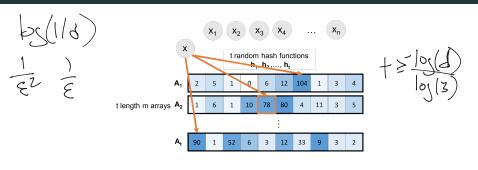
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COUNT-MIN SKETCH ANALYSIS



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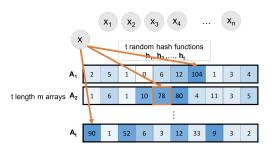
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$$|-|/3^{\dagger}| \Rightarrow |-|5|$$
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$$|-$$

• What is
$$PI_{V}(x) \le J(x) \le J(x) + \frac{1}{R}J(x) = I_{V}(x) = \frac{1}{R}J(x)$$

• To get a good estimate with probability $> 1 - \delta$ set $t = O(\log(1/\delta))$

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- 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 $t = O(\log(1/\delta))$.

COUNT-MIN SKETCH

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.

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• Accurate enough to solve the (ϵ, k) -Frequent elements problem.

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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?

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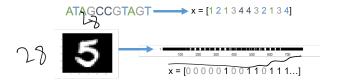
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- The human genome contains 3 billion+ base pairs. Genetic datasets often contain information on 100s of thousands+ mutations and genetic markers.

DATA AS VECTORS AND MATRICES

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.

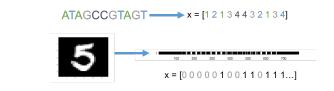
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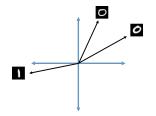
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Similarities/distances between vectors (e.g., $\langle x,y\rangle$, $||x-y||_2$) have meaning for underlying data points.

DATASETS AS VECTORS AND MATRICES

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

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

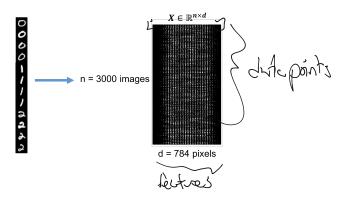
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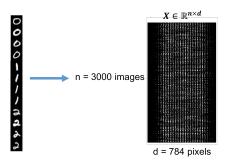


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Many data points $n \implies \text{tall.}$ Many dimensions $d \implies \text{wide.}$

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

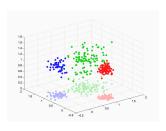
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$$\vec{x}_1, \dots, \vec{x}_n \in \mathbb{R}^d \to \tilde{x}_1, \dots, \tilde{x}_n \in \mathbb{R}^m$$
 for $m \ll d$.

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

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

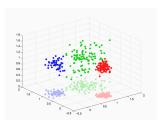


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Generally will not consider directly how well \tilde{x}_i approximates \vec{x}_i .

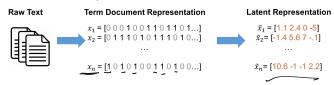
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- Autoencoders

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

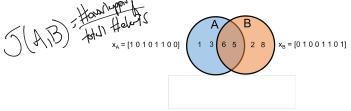
Low Distortion Embedding: Given $\vec{x}_1, \ldots, \vec{x}_n \in \mathbb{R}^d$, distance function D, and error parameter $\epsilon \geq 0$, find $\underbrace{\tilde{x}_1, \ldots, \tilde{x}_n}_{i=1} \in \mathbb{R}^m$ (where $m \ll d$) and distance function \tilde{D} such that for all $i, j \in [n]$:

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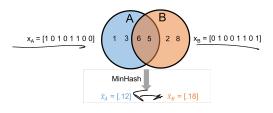
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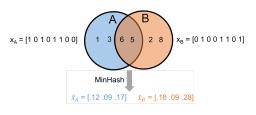
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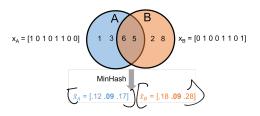
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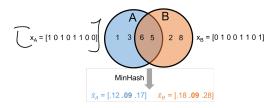


With large enough signature size r, $\frac{\# \text{ matching entries in } \vec{x}_A, \vec{x}_B}{r} \approx J(\vec{x}_A, \vec{x}_B)$.

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• 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 embedding, but is closely related.

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

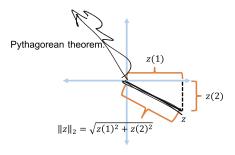
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 excliben in fine

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

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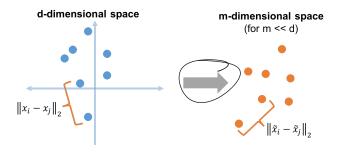
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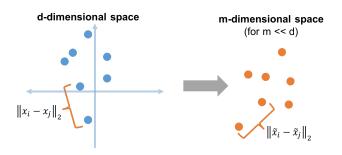
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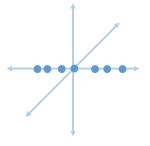
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Can use $\tilde{x}_1, \dots, \tilde{x}_n$ in place of $\vec{x}_1, \dots, \vec{x}_n$ in clustering, SVM, linear classification, near neighbor search, etc.

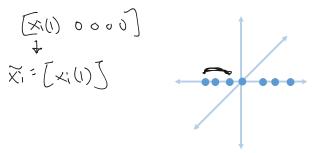
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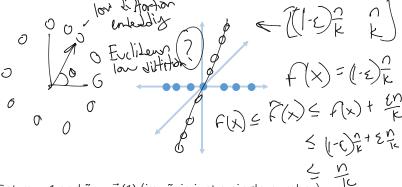


Set m=1 and $\tilde{x}_i=\vec{x}_i(1)$ (i.e., \tilde{x}_i is just a single number).

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

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