COMPSCI 514: ALGORITHMS FOR DATA SCIENCE

Andrew McGregor Lecture 10

(ϵ, k) -frequent items problem

Given stream of n items x_1, \ldots, x_n where each $x_i \in U$. Return a set F, such that for every $x \in U$:

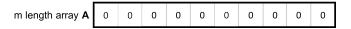
- 1. If $f(x) \ge n/k$ then $x \in F$
- 2. If $f(x) < (1 \epsilon)n/k$ then $x \notin F$

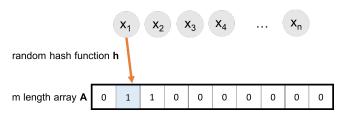
where f(x) is the number of times x appears in the stream.

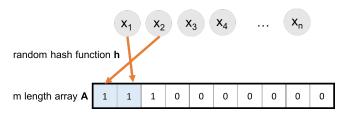
Count-Min Sketch: A random hashing based method closely related to bloom filters.

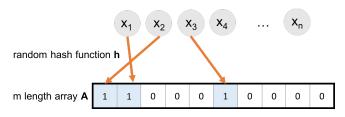


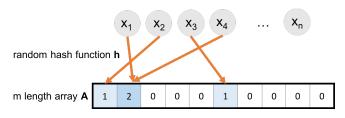
random hash function h

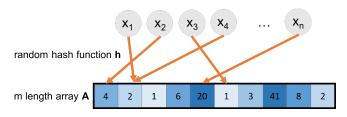




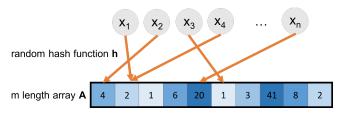








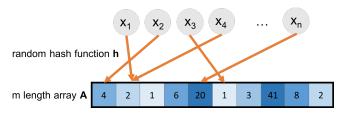
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Use $A[\mathbf{h}(x)]$ to estimate f(x), the frequency of x in the stream.

- Claim: $A[\mathbf{h}(x)] \geq f(x)$.
- Claim: $A[\mathbf{h}(x)] \le f(x) + 2n/m$ with probability at least 1/2.

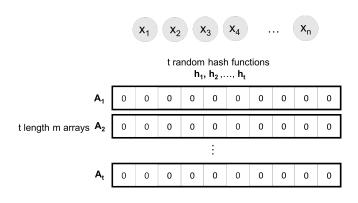
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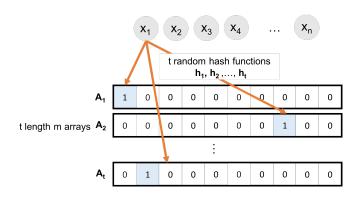


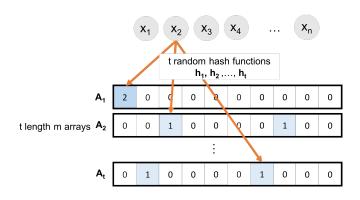
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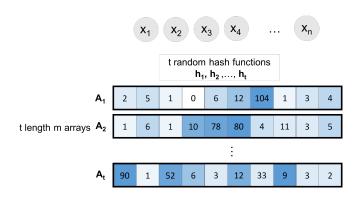
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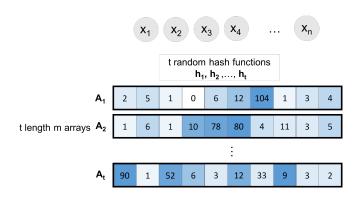
How can we increase this probability to $1 - \delta$ for arbitrary $\delta > 0$?

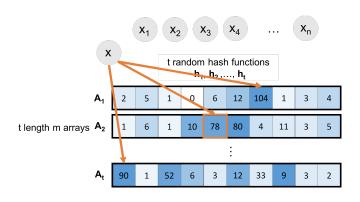


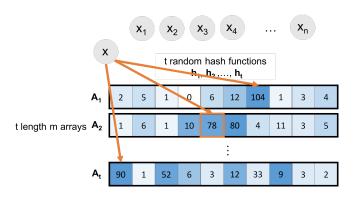




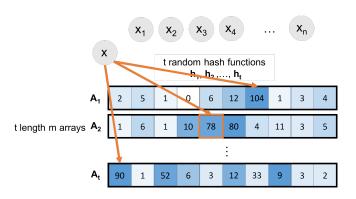




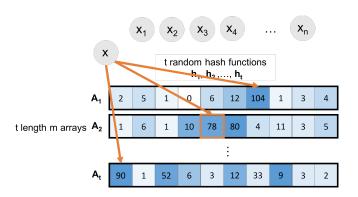




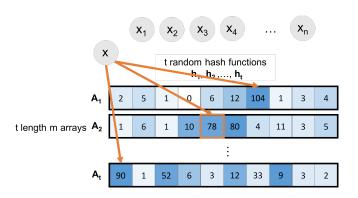
• Estimate f(x) with $\tilde{f}(x) = \min_{i \in [t]} A_i[\mathbf{h}_i(x)]$.



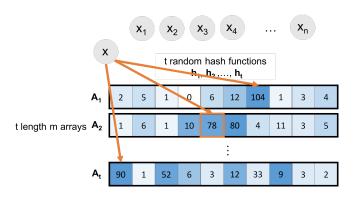
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- Setting $t = \log(1/\delta)$ ensures probability is at least 1δ .
- Setting $m = 2k/\epsilon$ ensures the error 2n/m is $\epsilon n/k$ and this is enough to determine whether we need to output the element.

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 $O\left(\log(1/\delta)\cdot k/\epsilon\right)$ space.

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- How should we set δ if we want a good estimate for all items at once, with 99% probability? $\delta=0.01/|U|$ ensures

 $Pr[there\ exists\ x\in U\ with\ a\ bad\ estimate]$

$$\leq \sum_{x \in U} \Pr[\text{estimate for } x \text{ is bad}] \leq \sum_{x \in U} 0.01/|U| = 0.01$$

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One approach:

- Maintain a set F while processing the stream:
- At step *i*:
 - Add ith stream element to F if it's estimated frequency is ≥ i/k and it isn't already in F.
 - Remove any element from F whose estimated frequency is < i/k.
- Store at most k items at once and have all items with frequency $\geq n/k$ stored at the end of the stream.

Questions on Frequent Elements?

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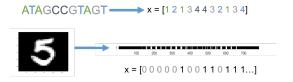
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- The human genome contains 3 billion+ base pairs. Genetic datasets often contain information on 100s of thousands+ mutations and genetic markers.

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.

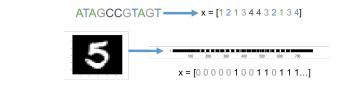
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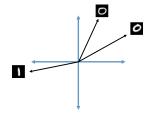
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Similarities/distances between vectors (e.g., $\langle x, y \rangle$, $\|x - y\|_2$) have meaning for underlying data points.

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

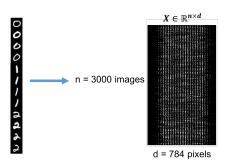
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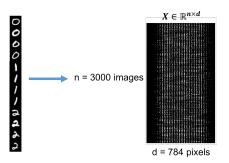


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Many data points $n \implies \text{tall.}$ Many dimensions $d \implies \text{wide.}$

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 for $m \ll d$.

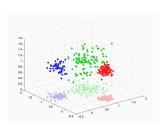
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$$\longrightarrow x = [0\ 0\ 0\ 0\ 0\ 1\ 0\ 0\ 1\ 1\ 1\ 1\ ...] \longrightarrow \tilde{x} = [-5.5\ 4\ 3.2\ -1]$$

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

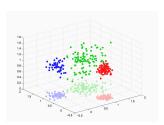


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Generally will not consider directly how well \tilde{x}_i approximates \vec{x}_i .

LOW DISTORTION EMBEDDING

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 $\tilde{x_1}, \ldots, \tilde{x_n} \in \mathbb{R}^m$ (where $m \ll d$) and distance function \tilde{D} such that for all $i, j \in [n]$:

$$(1-\epsilon)D(\vec{x_i},\vec{x_j}) \leq \tilde{D}(\tilde{x_i},\tilde{x_j}) \leq (1+\epsilon)D(\vec{x_i},\vec{x_j}).$$

We'll focus on the case where D and \tilde{D} are Euclidean distances. I.e., the distance between two vectors x and y is defined as

$$\|\vec{x} - \vec{y}\|_2 = \sqrt{\sum_i (\vec{x}(i) - \vec{y}(i))^2}$$

This is related to the Euclidean norm, $\|\vec{z}\|_2 = \sqrt{\sum_{i=1}^n \vec{z}(i)^2}$.

THE JOHNSON-LINDENSTRAUSS LEMMA

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 $\mathbf{M} : \mathbb{R}^d \to \mathbb{R}^m$ such that $m = O\left(\frac{\log n}{\epsilon^2}\right)$ and letting $\tilde{x}_i = \mathbf{M}\vec{x}_i$:

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