COMPSCI 514: ALGORITHMS FOR DATA SCIENCE

Andrew McGregor
Lecture 10
Last Class:

- Introduced the $k$-frequent elements problem – identify all elements of a stream of $n$ elements that occur $\geq n/k$ times.
- Saw how to solve approximately using the Count-min sketch algorithm. Based on random hashing into buckets containing approximate counts.

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- Randomized methods for dimensionality reduction.
- The Johnson-Lindenstrauss Lemma.
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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.
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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\[
\text{ATAGCCGTA} \rightarrow \mathbf{x} = [1 \ 2 \ 1 \ 3 \ 4 \ 4 \ 3 \ 2 \ 1 \ 3 \ 4]
\]

\[
\begin{array}{c}
\text{5} \\
\end{array}
\rightarrow
\begin{array}{c}
x = [0 \ 0 \ 0 \ 0 \ 0 \ 1 \ 0 \ 0 \ 1 \ 1 \ 0 \ 1 \ 1 \ 1 \ldots] \\
\end{array}
\]
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 $\vec{x}_i$. 
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Many data points \( n \Rightarrow \text{tall} \). Many dimensions \( d \Rightarrow \text{wide} \).
**Dimensionality Reduction:** Compress data points so that they lie in many fewer dimensions.
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\[ \vec{x}_1, \ldots, \vec{x}_n \in \mathbb{R}^d \rightarrow \tilde{\vec{x}}_1, \ldots, \tilde{\vec{x}}_n \in \mathbb{R}^m \text{ for } m \ll d. \]

\[
\begin{align*}
x = [0 & 0 0 0 0 1 0 0 1 1 0 1 1 1 \ldots] & \Rightarrow \tilde{x} = [-5.5 & 4 3.2 -1] \\
\end{align*}
\]
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‘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 \( \tilde{\vec{x}}_i \) approximates \( \vec{x}_i \).
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 $i, j \in [n]$:

$$(1 - \epsilon)D(\vec{x}_i, \vec{x}_j) \leq \tilde{D}(\tilde{x}_i, \tilde{x}_j) \leq (1 + \epsilon)D(\vec{x}_i, \vec{x}_j).$$
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Have already seen one example in class: **MinHash**.

\[ x_A = [1 \ 0 \ 1 \ 0 \ 1 \ 0 \ 0] \quad x_B = [0 \ 1 \ 0 \ 0 \ 1 \ 1 \ 0 \ 1] \]
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MinHash

$\tilde{x}_A = [0.12] \quad \tilde{x}_B = [0.18]$
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![Diagram](image.png)
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With large enough signature size $r$, $\frac{\# \text{ matching entries in } \tilde{x}_A, \tilde{x}_B}{r} \approx J(\tilde{x}_A, \tilde{x}_B)$. 

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

- Note: here $J(\tilde{x}_A, \tilde{x}_B)$ is a similarity rather than a distance. So this is not quite low distortion embedding, but is closely related.
Euclidean Low Distortion Embedding: Given $\vec{x}_1, \ldots, \vec{x}_n \in \mathbb{R}^d$ and error parameter $\epsilon \geq 0$, find $\tilde{x}_1, \ldots, \tilde{x}_n \in \mathbb{R}^m$ (where $m \ll d$) such that for all $i, j \in [n]$:

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

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

[Diagram showing application of Pythagorean theorem to illustrate $\| \mathbf{z} \|_2 = \sqrt{z(1)^2 + z(2)^2}$.]

Can use $\tilde{x}_1, \ldots, \tilde{x}_n$ in place of $\mathbf{x}_1, \ldots, \mathbf{x}_n$ in clustering, SVM, linear classification, near neighbor search, etc.
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Can use $\tilde{x}_1, \ldots, \tilde{x}_n$ in place of $\mathbf{x}_1, \ldots, \mathbf{x}_n$ in clustering, SVM, linear classification, near neighbor search, etc.
A very easy case: Assume that $\mathbf{x}_1, \ldots, \mathbf{x}_n$ all lie on the 1\textsuperscript{st} axis in $\mathbb{R}^d$. 

![Diagram showing points on the 1\textsuperscript{st} axis in $\mathbb{R}^d$.]
A very easy case: Assume that $\tilde{x}_1, \ldots, \tilde{x}_n$ all lie on the 1st axis in $\mathbb{R}^d$.

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

- $\|\tilde{x}_i - \tilde{x}_j\|_2 = \sqrt{[\tilde{x}_i(1) - \tilde{x}_j(1)]^2} = |\tilde{x}_i(1) - \tilde{x}_j(1)| = \|\tilde{x}_i - \tilde{x}_j\|_2$. 
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- An embedding with no distortion from any \( d \) into \( m = 1 \).
A very easy case: Assume that $\mathbf{x}_1, \ldots, \mathbf{x}_n$ all lie on the $1^{st}$ axis in $\mathbb{R}^d$.

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- $\|\tilde{x}_i - \tilde{x}_j\|_2 = \sqrt{[\mathbf{x}_i(1) - \mathbf{x}_j(1)]^2} = |\mathbf{x}_i(1) - \mathbf{x}_j(1)| = \|\mathbf{x}_i - \mathbf{x}_j\|_2$.
- An embedding with no distortion from any $d$ into $m = 1$.
- More generally. there’s a no distortion embedding into $m = D$ dimensions if all the points lie is a $D$ dimensional space.
What about when we don’t make any assumptions on $\vec{x}_1, \ldots, \vec{x}_n$. I.e., they can be scattered arbitrarily around $d$-dimensional space?

• Can we find a no-distortion embedding into $m \ll d$ dimensions?
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- Can we find a no-distortion embedding into $m \ll d$ dimensions? No. Require $m = d$.
- Can we find an $\epsilon$-distortion embedding into $m \ll d$ dimensions for $\epsilon > 0$?

  For all $i, j : (1 - \epsilon)\|\vec{x}_i - \vec{x}_j\|_2 \leq \|\tilde{x}_i - \tilde{x}_j\|_2 \leq (1 + \epsilon)\|\vec{x}_i - \vec{x}_j\|_2$. 
What about when we don’t make any assumptions on $\bar{x}_1, \ldots, \bar{x}_n$. 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 $\epsilon$-distortion embedding into $m \ll d$ dimensions for $\epsilon > 0$? Yes! Always, with $m$ depending on $\epsilon$.

For all $i, j$: $(1 - \epsilon) \| \bar{x}_i - \bar{x}_j \|_2 \leq \| \tilde{x}_i - \tilde{x}_j \|_2 \leq (1 + \epsilon) \| \bar{x}_i - \bar{x}_j \|_2$. 
Johnson-Lindenstrauss Lemma: For any set of points $\mathbf{x}_1, \ldots, \mathbf{x}_n \in \mathbb{R}^d$ and $\epsilon > 0$ there exists a linear map $\Pi : \mathbb{R}^d \rightarrow \mathbb{R}^m$ such that $m = O \left( \frac{\log n}{\epsilon^2} \right)$ and letting $\tilde{\mathbf{x}}_i = \Pi \mathbf{x}_i$:

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Further, if $\Pi \in \mathbb{R}^{m \times d}$ has each entry chosen i.i.d. from $\mathcal{N}(0, 1/m)$, it satisfies the guarantee with high probability.
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Further, if $\Pi \in \mathbb{R}^{m \times d}$ 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 $n = 100,000$, $m \approx 6600$. 
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 \( \tilde{x}_i = \Pi \vec{x}_i \):

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

For all $i, j$:

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$m \times d$

$.01 \ -1.2 \ .34 \ .67 \ .10 \ -0.49 \ldots$

$.45 \ .7 \ .14 \ .18 \ -0.65 \ .76 \ldots$

$m \times 1$

$x_i$

$\tilde{x}_i$

random linear transformation (random projection)

input point (high dimensions)

compressed output point (low dimensions)

$m = O \left( \frac{\log n}{\epsilon^2} \right)$
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\(\Pi\) is known as a random projection. It is a random linear function, mapping length $d$ vectors to length $m$ vectors.
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- \( \Pi \) is known as a random projection. It is a random linear function, mapping length \( d \) vectors to length \( m \) vectors.
- \( \Pi \) 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 \( x_i = \prod \vec{x}_i \).
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• Data oblivious property means that once \( \Pi \) is chosen, \( x_1, \ldots, x_n \) can be computed in a stream with little memory.

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• When new data points are added, can be easily compressed, without updating existing points.
Compression operation is $\mathbf{x}_i = \Pi \vec{x}_i$, so for any $j$,

$$\mathbf{x}_i(j) = \langle \Pi(j), \vec{x}_i \rangle = \sum_{k=1}^{d} \Pi(j, k) \cdot \vec{x}_i(k).$$

$\Pi(j)$ is a vector with independent random Gaussian entries.

$\vec{x}_1, \ldots, \vec{x}_n$: original points ($d$ dims.), $\mathbf{x}_1, \ldots, \mathbf{x}_n$: compressed points ($m < d$ dims.), $\Pi \in \mathbb{R}^{m \times d}$: random projection (embedding function)
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$$x_i(j) = \langle \Pi(j), \vec{x}_i \rangle = \sum_{k=1}^{d} \Pi(j, k) \cdot \vec{x}_i(k).$$

$\Pi(j)$ is a vector with independent random Gaussian entries.

$\vec{x}_1, \ldots, \vec{x}_n$: original points ($d$ dims.), $x_1, \ldots, x_n$: compressed points ($m < d$ dims.), $\Pi \in \mathbb{R}^{m \times d}$: random projection (embedding function)
Compression operation is \( \mathbf{x}_i = \Pi \vec{x}_i \), so for any \( j \),

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\mathbf{x}_i(j) = \langle \Pi(j), \vec{x}_i \rangle = \sum_{k=1}^{d} \Pi(j, k) \cdot \vec{x}_i(k).
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\( \Pi(j) \) is a vector with independent random Gaussian entries.

Points with high cosine similarity have similar random projections.

Computing a length \( m \) SimHash signature \( SH_1(\vec{x}_i), \ldots, SH_m(\vec{x}_i) \) is identical to computing \( \mathbf{x}_i = \Pi \vec{x}_i \) and then taking \( \text{sign}(\mathbf{x}_i) \).
The Johnson-Lindenstrauss Lemma is a direct consequence of a closely related lemma:

**Distributional JL Lemma:** Let $\Pi \in \mathbb{R}^{m \times d}$ have each entry chosen i.i.d. as $\mathcal{N}(0, 1/m)$. If we set $m = O\left(\frac{\log(1/\delta)}{\epsilon^2}\right)$, then for any $\vec{y} \in \mathbb{R}^d$, with probability $\geq 1 - \delta$

$$(1 - \epsilon)\|\vec{y}\|_2 \leq \|\Pi \vec{y}\|_2 \leq (1 + \epsilon)\|\vec{y}\|_2$$

**\(\Pi \in \mathbb{R}^{m \times d}\):** random projection matrix. **\(d\):** original dimension. **\(m\):** compressed dimension, **\(\epsilon\):** embedding error, **\(\delta\):** embedding failure prob.
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Applying a random matrix $\Pi$ to any vector $\vec{y}$ preserves $\vec{y}$’s norm with high probability.

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Applying a random matrix \( \Pi \) to any vector \( \vec{y} \) preserves \( \vec{y} \)'s norm with high probability.

- Like a low-distortion embedding, but for the length of a compressed vector rather than distances between vectors.
- Can be proven from first principles. Will see next class.

**Symbols**:
- \( \Pi \in \mathbb{R}^{m \times d} \): random projection matrix.
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Distributional JL Lemma $\implies$ JL Lemma: Distributional JL show that a random projection $\Pi$ preserves the norm of any $y$. The main JL Lemma says that $\Pi$ preserves distances between vectors.

$\vec{x}_1, \ldots, \vec{x}_n$: original points, $\vec{x}_1, \ldots, \vec{x}_n$: compressed points, $\Pi \in \mathbb{R}^{m \times d}$: random projection matrix. $d$: original dimension. $m$: compressed dimension, $\epsilon$: embedding error, $\delta$: embedding failure prob.
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Proof: Given $\vec{x}_1, \ldots, \vec{x}_n$, define $\binom{n}{2}$ vectors $\vec{y}_{ij}$ where $\vec{y}_{ij} = \vec{x}_i - \vec{x}_j$. 

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**Proof:** Given $\bar{x}_1, \ldots, \bar{x}_n$, define $\left(\begin{array}{c} n \\ 2 \end{array}\right)$ vectors $\bar{y}_{ij}$ where $\bar{y}_{ij} = \bar{x}_i - \bar{x}_j$.

- If we choose $\Pi$ with $m = O\left(\frac{\log 1/\delta}{\epsilon^2}\right)$, for each $\bar{y}_{ij}$ with probability $\geq 1 - \delta$ we have:

$$
(1 - \epsilon)\|\bar{y}_{ij}\|_2 \leq \|\Pi \bar{y}_{ij}\|_2 \leq (1 + \epsilon)\|\bar{y}_{ij}\|_2
$$

---

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\[
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- If we choose $\Pi$ with $m = O\left(\log \frac{1}{\delta} \epsilon^2\right)$, for each $y_{ij}$ with probability $\geq 1 - \delta$ we have:

$$\left(1 - \epsilon\right)\|\bar{x}_i - \bar{x}_j\|_2 \leq \|x_i - x_j\|_2 \leq \left(1 + \epsilon\right)\|\bar{x}_i - \bar{x}_j\|_2$$

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Claim: If we choose \( \Pi \) with i.i.d. \( \mathcal{N}(0, 1/m) \) entries and 
\[ m = O \left( \frac{\log(1/\delta')}{\epsilon^2} \right) \]
letting \( \tilde{x}_i = \Pi \tilde{x}_i \), for each pair \( \tilde{x}_i, \tilde{x}_j \) with probability 
\( \geq 1 - \delta' \) we have:
\[ (1 - \epsilon) \| \tilde{x}_i - \tilde{x}_j \|_2 \leq \| x_i - x_j \|_2 \leq (1 + \epsilon) \| \tilde{x}_i - \tilde{x}_j \|_2. \]

\( \tilde{x}_1, \ldots, \tilde{x}_n \): original points, \( x_1, \ldots, x_n \): compressed points, \( \Pi \in \mathbb{R}^{m \times d} \): random projection matrix. \( d \): original dimension. \( m \): compressed dimension, \( \epsilon \): embedding error, \( \delta \): embedding failure prob.
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With what probability are all pairwise distances preserved?
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With what probability are all pairwise distances preserved?

**Union bound:** With probability $\geq 1 - \binom{n}{2} \cdot \delta'$ all pairwise distances are preserved.

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Apply the claim with $\delta' = \delta/\binom{n}{2}$.

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With what probability are all pairwise distances preserved?

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Apply the claim with \( \delta' = \delta/(\binom{n}{2}) \). \( \Rightarrow \) for \( m = O \left( \frac{\log(1/\delta')}{\epsilon'^2} \right) \), all pairwise distances are preserved with probability \( \geq 1 - \delta \).

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Claim: If we choose $\Pi$ with i.i.d. $N(0, 1/m)$ entries and $m = O\left(\frac{\log(1/\delta')}{\epsilon^2}\right)$, letting $x_i = \Pi \tilde{x}_i$, for each pair $\tilde{x}_i, \tilde{x}_j$ with probability $\geq 1 - \delta'$ we have:

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\[
m = O \left( \frac{\log(1/\delta')}{\epsilon^2} \right) = O \left( \frac{\log(\binom{n}{2}/\delta)}{\epsilon^2} \right) = O \left( \frac{\log(n^2/\delta)}{\epsilon^2} \right) = O \left( \frac{\log(n/\delta)}{\epsilon^2} \right)
\]

Yields the JL lemma.