COMPSCI 514: Algorithms for Data Science

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University of Massachusetts Amherst. Fall 2026.

Lecture 13

Logistics

- Midterm 1 grades have been posted.
- Median around an 88%, which is quite good.
- If you are worried about your grade, feel free to email me and set up a time to chat.
- Problem Set 2 is nearly done with grading, and we will post grades shortly.
- Online quiz this week
  + in class quiz on Monday

Summary

Last Few Classes:

- Approximate nearest neighbor search and solution via LSH.
- Guest lecture on solution via greedy search on ‘navigable’ graphs.

Today:

- Finish up analysis of LSH repetitions.
- Start on spectral methods unit: linear algebraic techniques for working with large and high dimensional datasets.
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If you feel shaky on your linear algebra background, you'll want to start doing some review. See the reading material for resources.

LSH Wrap Up

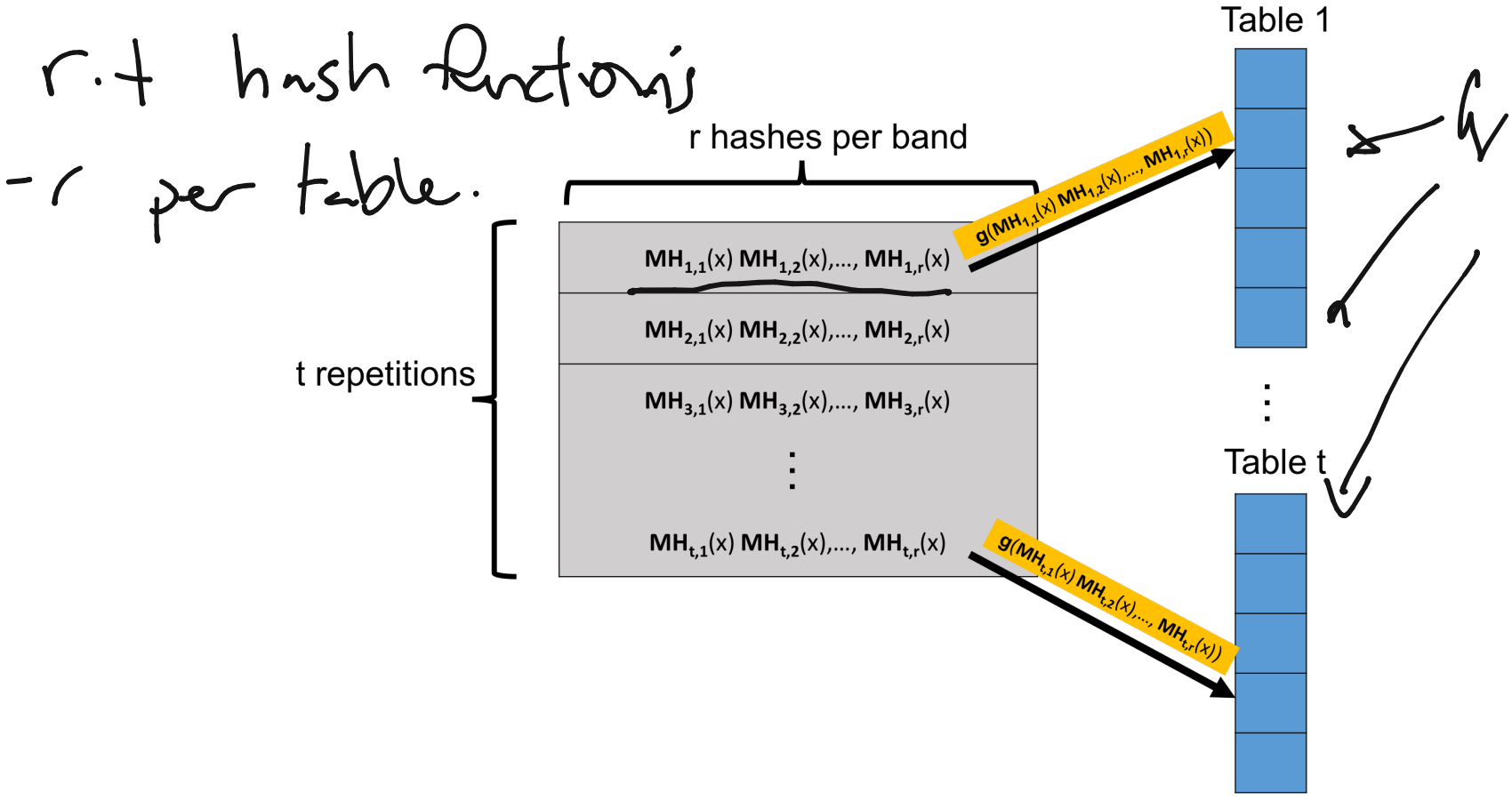
Balancing Hit Rate and Query Time

We want to balance a small probability of false negatives (a high hit rate) with a small probability of false positives (a small query time.)



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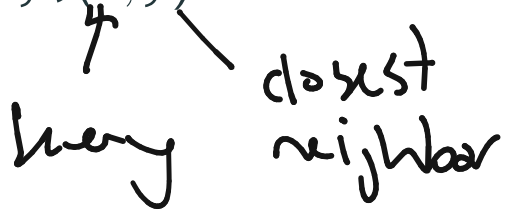
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Create *t* hash tables. Each is indexed into not with a single MinHash value, but with *r* values, appended together. A length *r* signature.

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$$\Pr[MH_{i,1}(x) = MH_{i,1}(y) \cap \ldots \cap MH_{i,r}(x) = MH_{i,r}(y)]$$
$$= s \cdot s \cdot s = s^r$$

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- Probability that x and y match in at least one repetition:
  (i.e. land in same bucket at least once)

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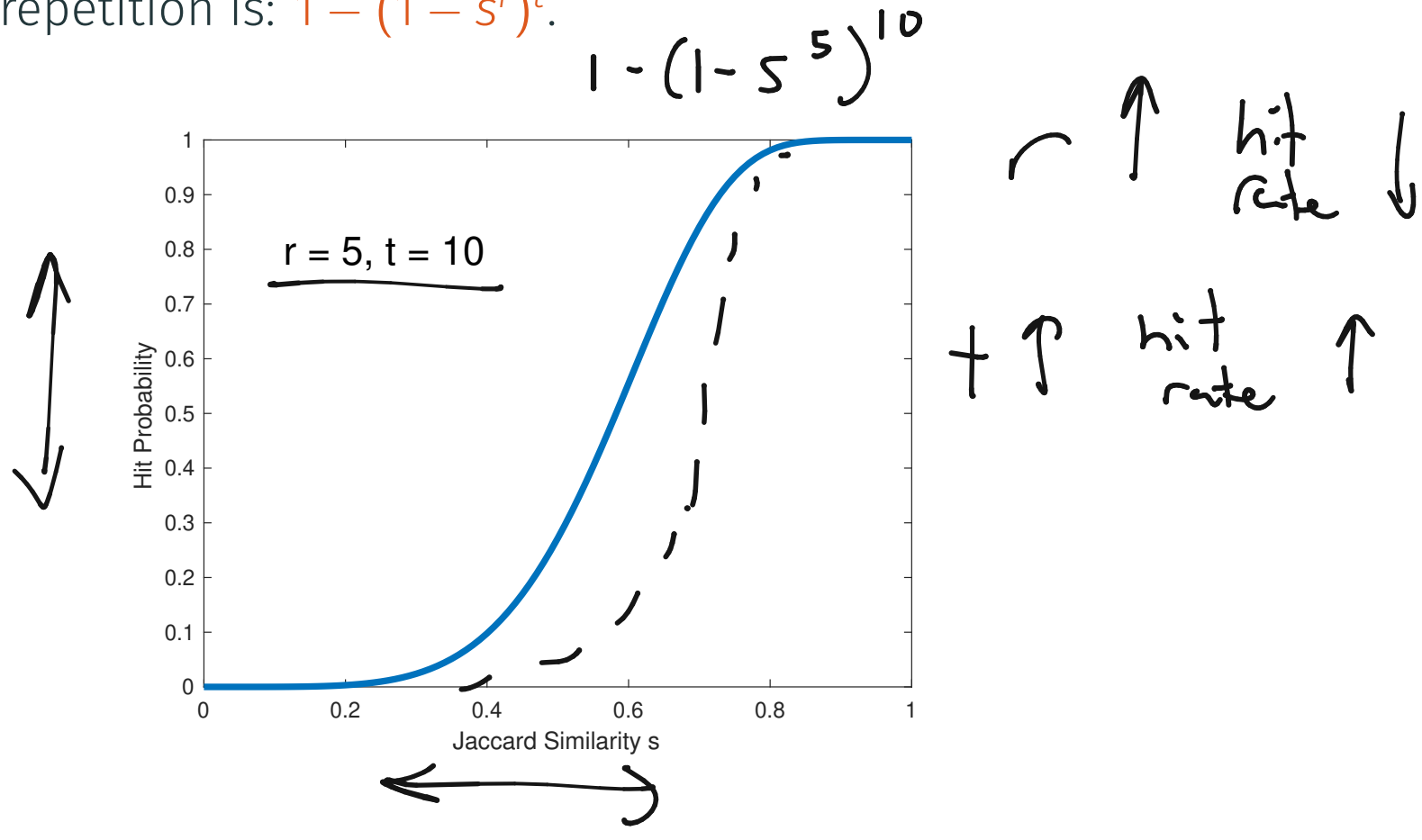
$$\text{Hit Probability: } 1 - (1 - s^r)^t.$$

The s-curve

Using t repetitions each with a signature of r MinHash values, the probability that x and y with Jaccard similarity $J(x, y) = s$ match in at least one repetition is: $1 - (1 - s^r)^t$.

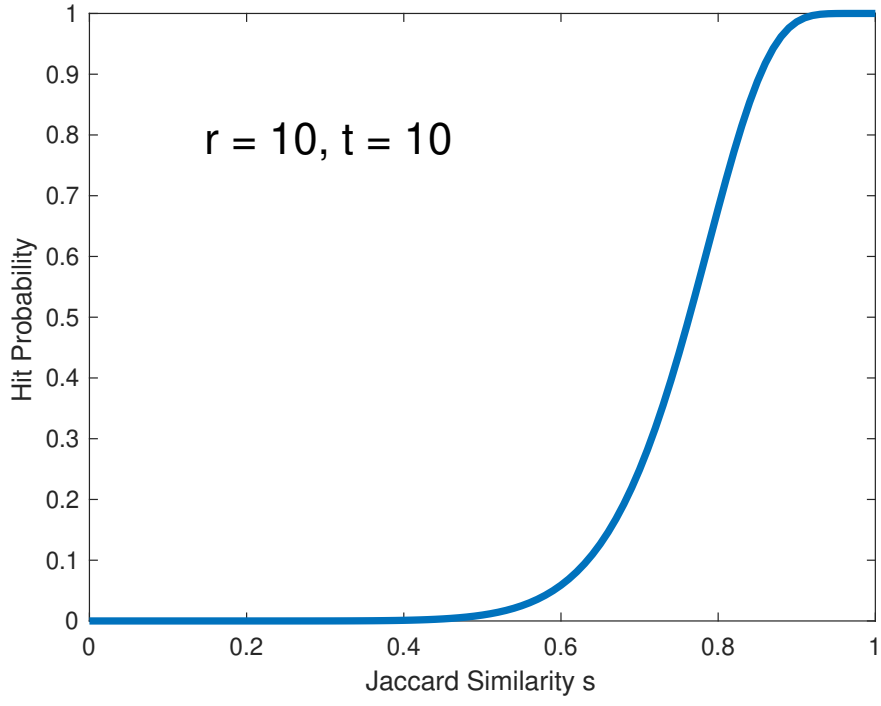
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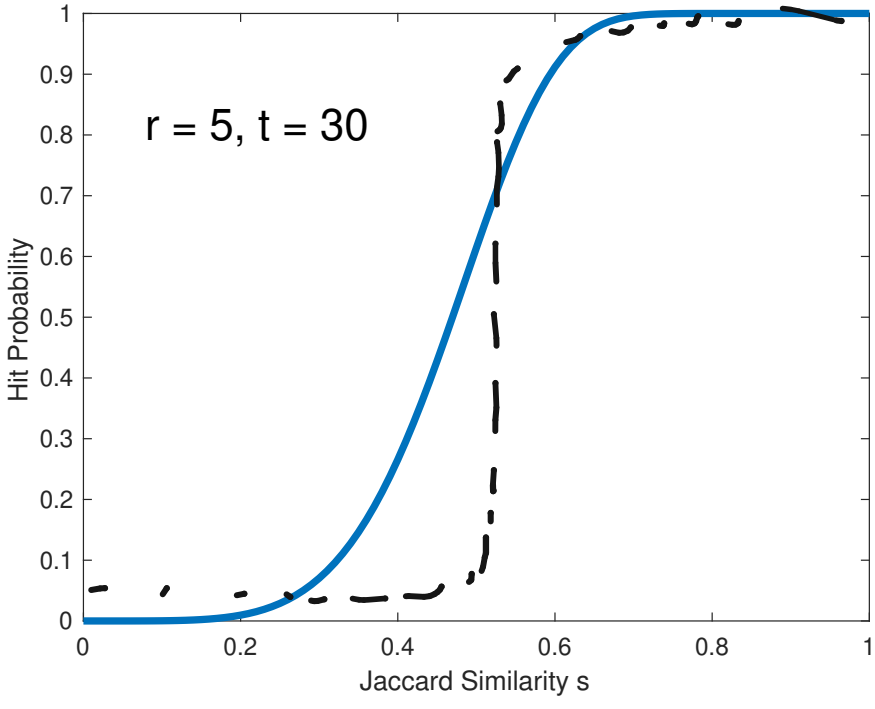
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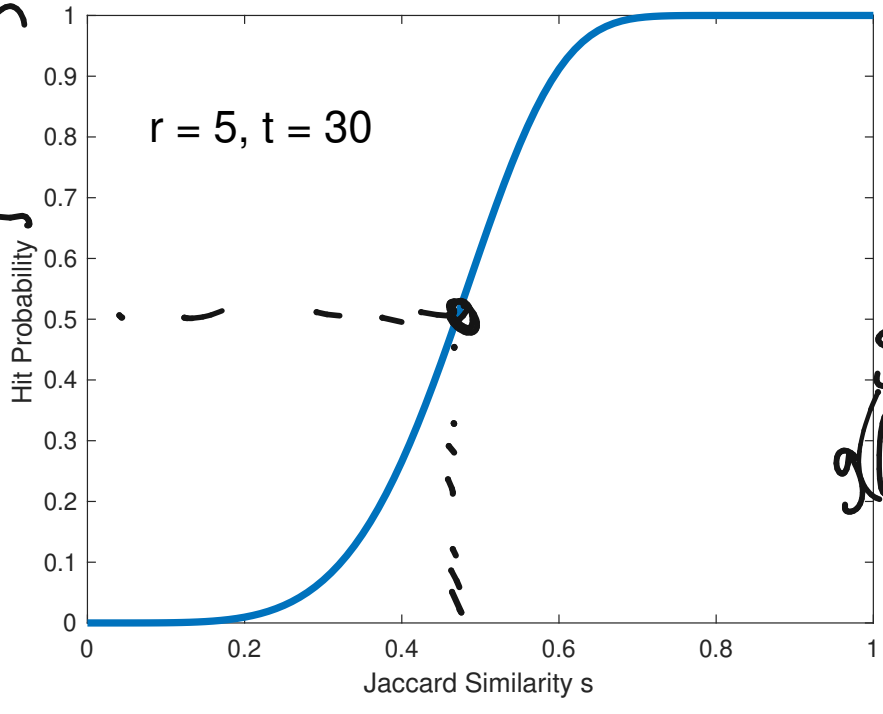
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$r, t \to \infty$

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r and t are tuned depending on application. 'Threshold' when hit probability is 1/2 is $\approx (1/t)^{1/r}$. E.g., $\approx (1/30)^{1/5} = .51$ in this case.

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$10,000,000 - 10010$ "fun items"

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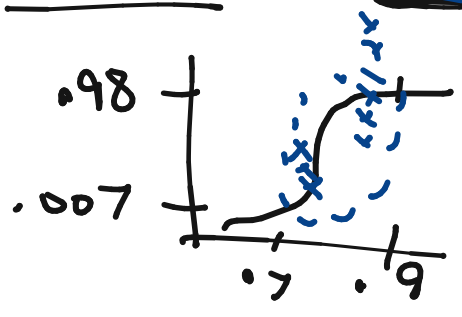
goal: return something with similarity $\geq .7$

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(actual close neighbors)

- Hit probability for $J(x, y) \geq .9$ is $\geq 1 - (1 - .9^{25})^{50} \approx .98$
- Hit probability for $J(x, y) \in [.7, .9]$ is $\leq 1 - (1 - .9^{25})^{50} \approx .98$
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Expected Number of Items Scanned: (proportional to query time)

$$\leq 10 + .98 * 10,000 + .007 * 9,989,990 \approx 80,000$$

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if $J(x,y) \in [.7,.9]$
$.007 \leq$ hit prob $\leq .98$

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Compressing High-Dimensional Data and the Johnson-Lindenstrauss Lemma

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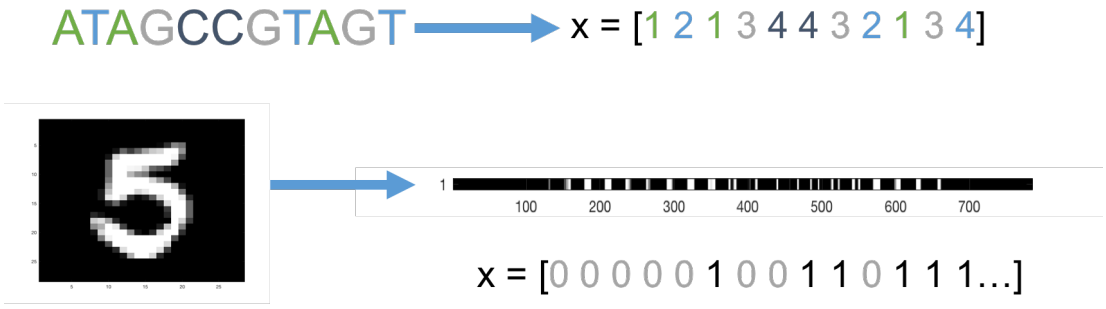
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- The human genome contains 3 billion+ base pairs. Genetic datasets often contain information on 100s of thousands+ mutations and genetic markers.

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.

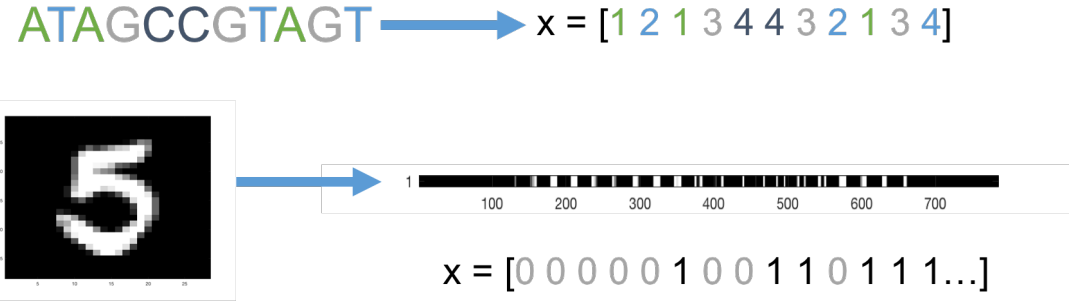
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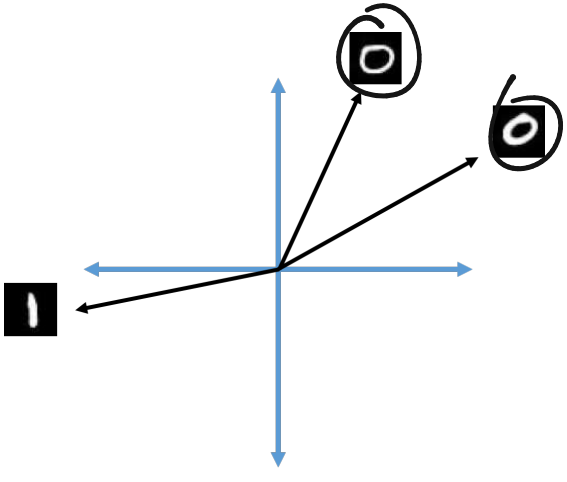
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Similarities/distances between vectors (e.g., $\langle x, y \rangle$, $\|x - y\|_2$) have meaning for underlying data points.

often after transformation
e.g., with neural network

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

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

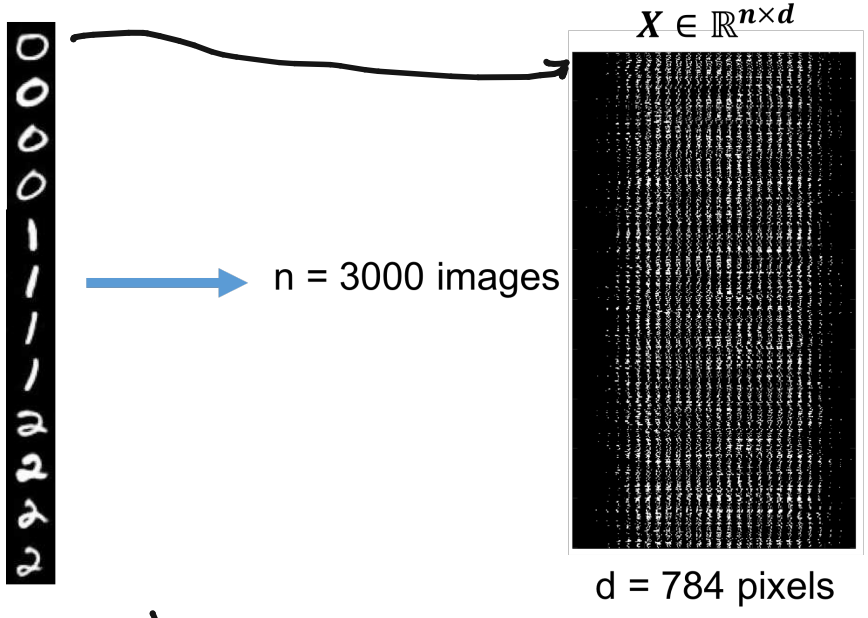
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transpose $X_i^T = \begin{bmatrix} \vdots \\ \vdots \end{bmatrix}$



n = # data points

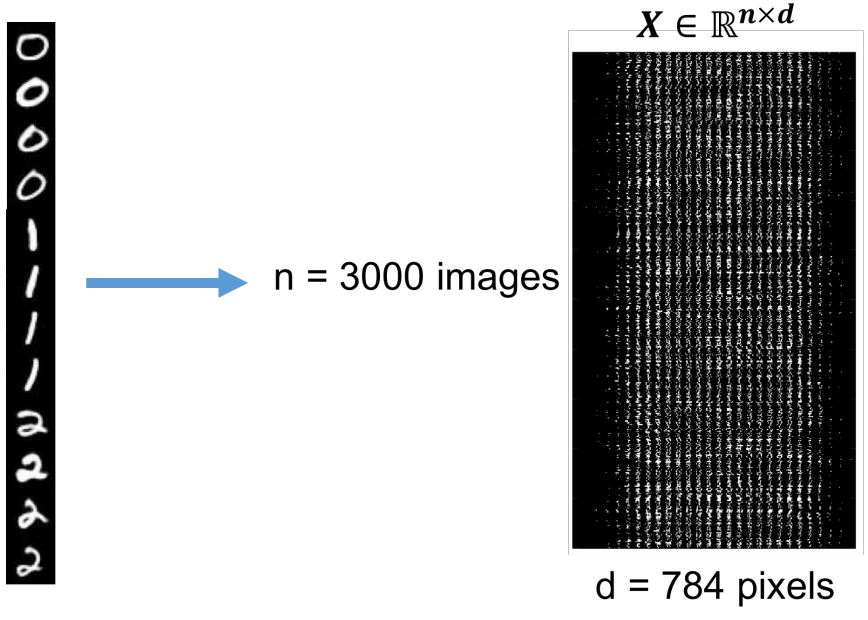
d = dimension.

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

Dimensionality Reduction

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



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

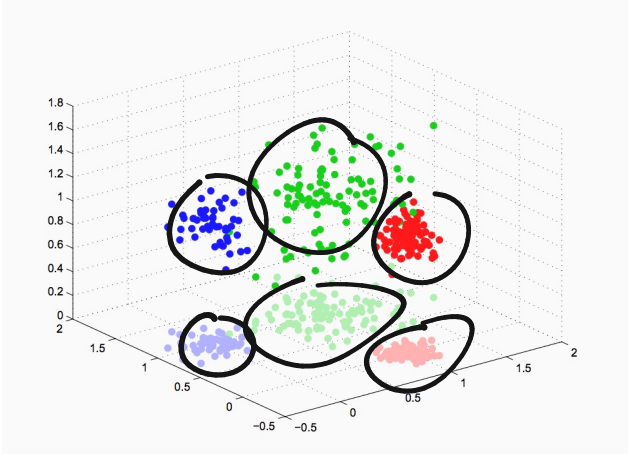
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'Lossy compression' that still preserves important information about the relationships between $\vec{x}_1, \ldots, \vec{x}_n$.



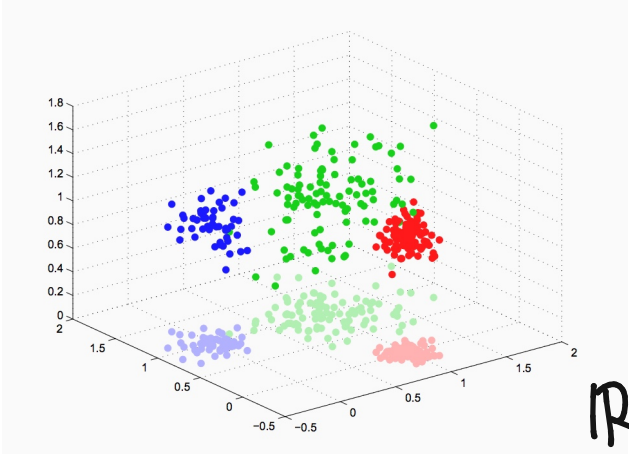
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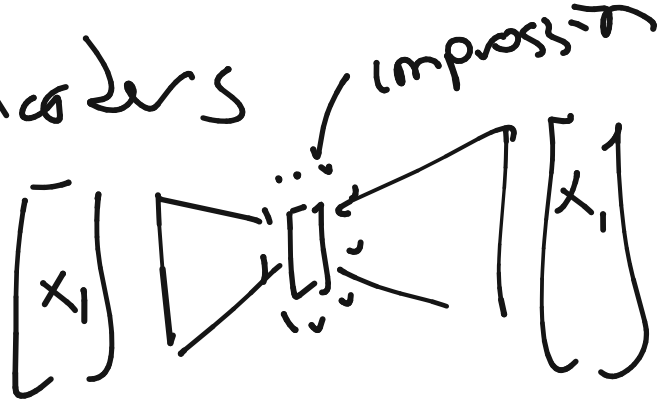
$\mathbb{R}^m$ $\mathbb{R}^2$

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

Dimensionality Reduction

Dimensionality reduction is one of the most important techniques in data science. What methods have you heard of?

- PCA (SVD) (principal component analysis)
- TSNE (often used for visualization)
- LDA
- autoencoders

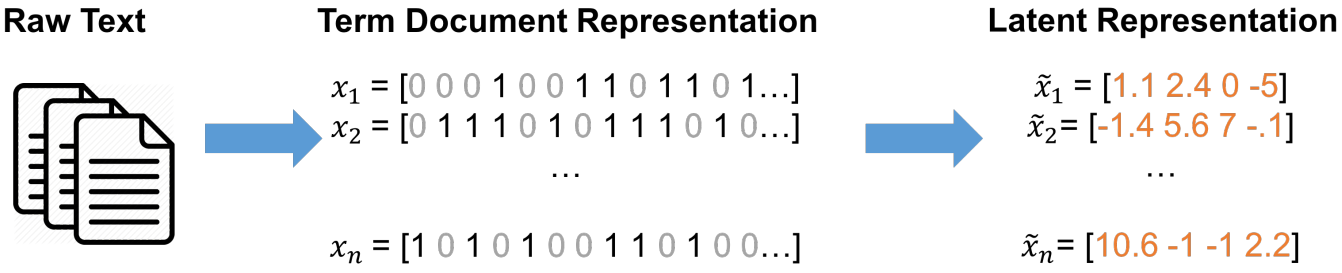


- Isomap, LLE, etc. (spectral graph theory)

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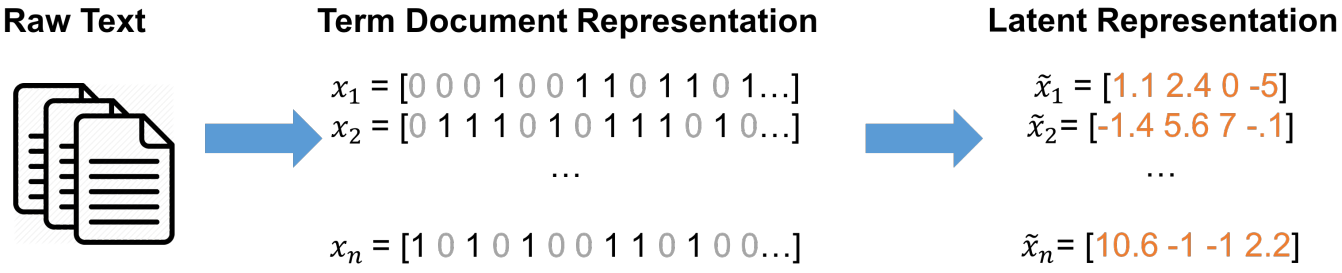


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Compressing data makes it more efficient to work with. May also remove extraneous information/noise.

Embeddings for Euclidean Space

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 $i, j \in [n]$:

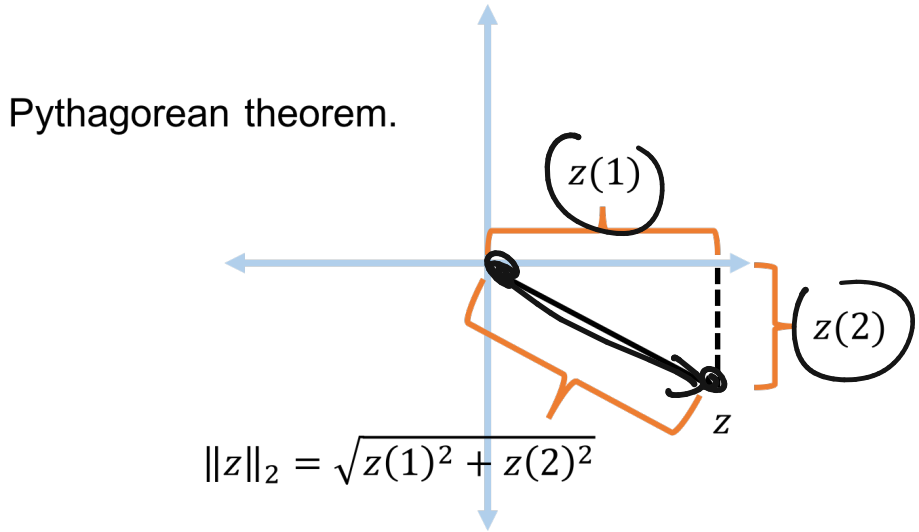
$$(1-\epsilon)\|\vec{x}_i - \vec{x}_j\|_2 \leq \|\tilde{x}_i - \tilde{x}_j\|_2 \leq (1+\epsilon)\|\vec{x}_i - \vec{x}_j\|_2.$$

Embeddings for Euclidean Space

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 $i, j \in [n]$:

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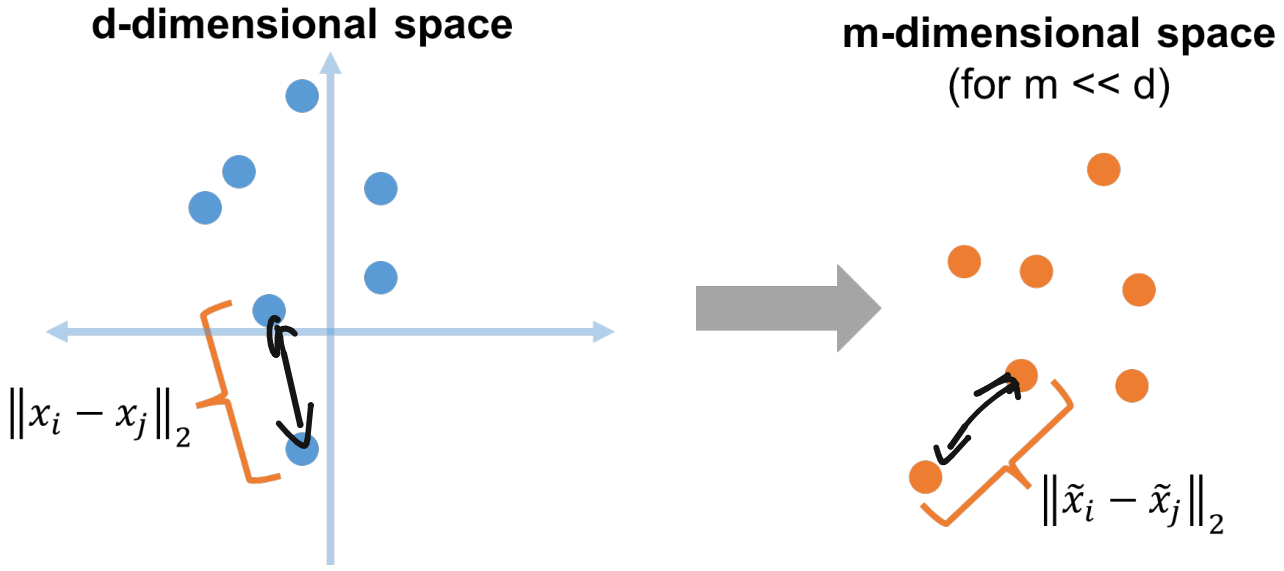
Recall that for $\vec{z} \in \mathbb{R}^n$, $\|\vec{z}\|_2 = \sqrt{\sum_{i=1}^{n} \vec{z}(i)^2}$.



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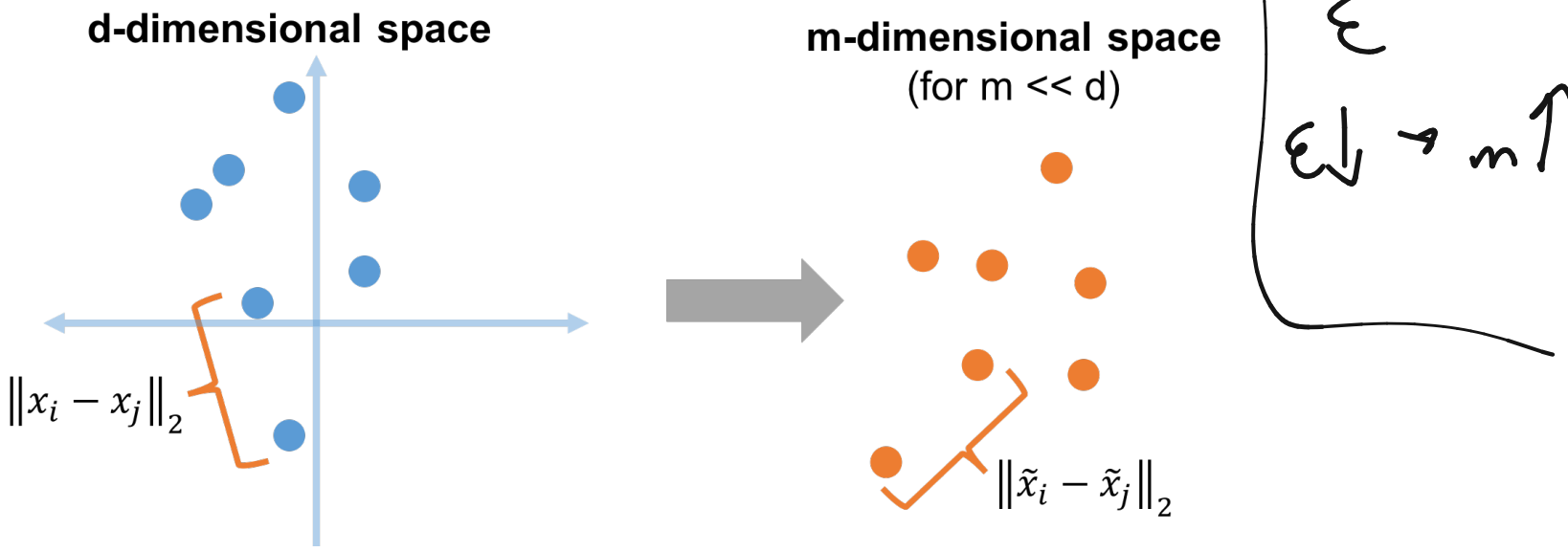
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Can use $\tilde{x}_1, \ldots, \tilde{x}_n$ in place of $\vec{x}_1, \ldots, \vec{x}_n$ in clustering, SVM, linear classification, near neighbor search, etc.

The Johnson-Lindenstrauss Lemma

The Johnson-Lindenstrauss Lemma tells us that for any set of points $\vec{x}_1, \ldots, \vec{x}_n \in \mathbb{R}^d$ and any $\epsilon > 0$, we can find an ϵ-distortion embedding into m dimensions, where m depends only on the error parameter ϵ and the number of points n, but not the original dimension d.

The Johnson-Lindenstrauss Lemma

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

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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.

Π : $\mathbb{R}^d \to \mathbb{R}^m$, $\{x_i\}_d = \{\tilde{x}_i\}_m$

easy to construct.

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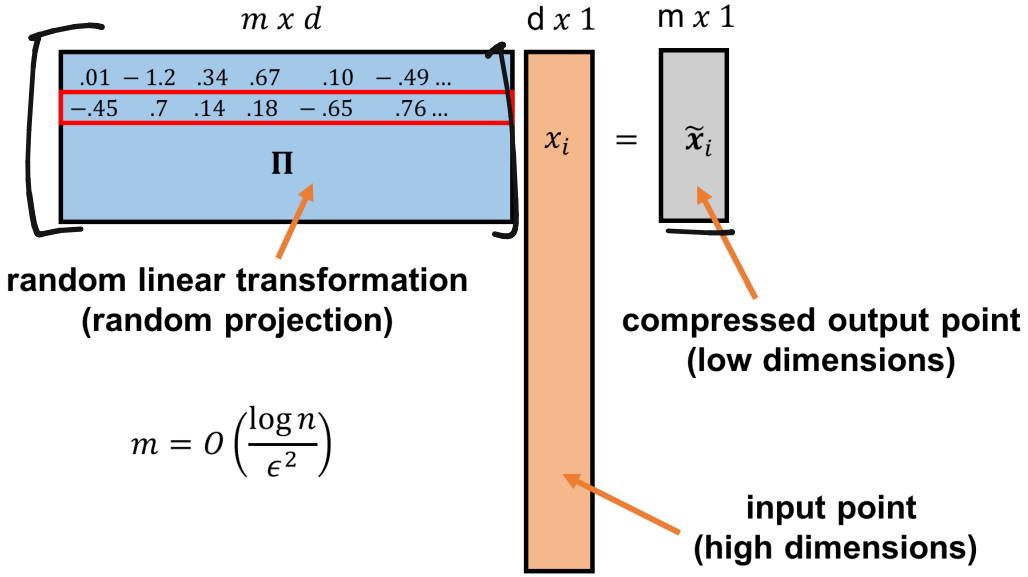
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Very surprising! Powerful result with a simple construction: applying a random linear transformation to a set of points preserves distances between all those points with high probability.

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 $\tilde{\mathbf{x}}_i = \mathbf{\Pi}\vec{x}_i$:

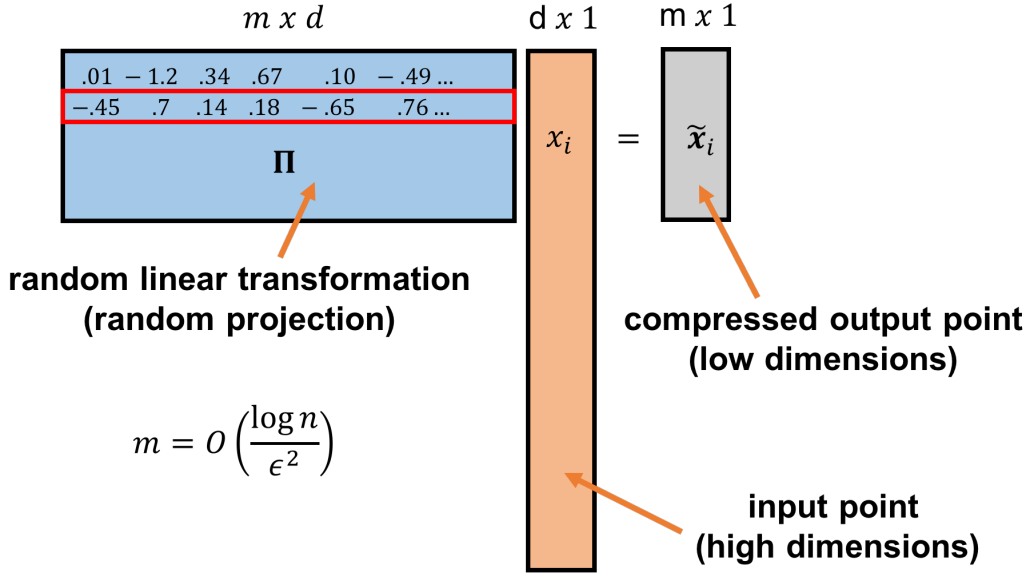
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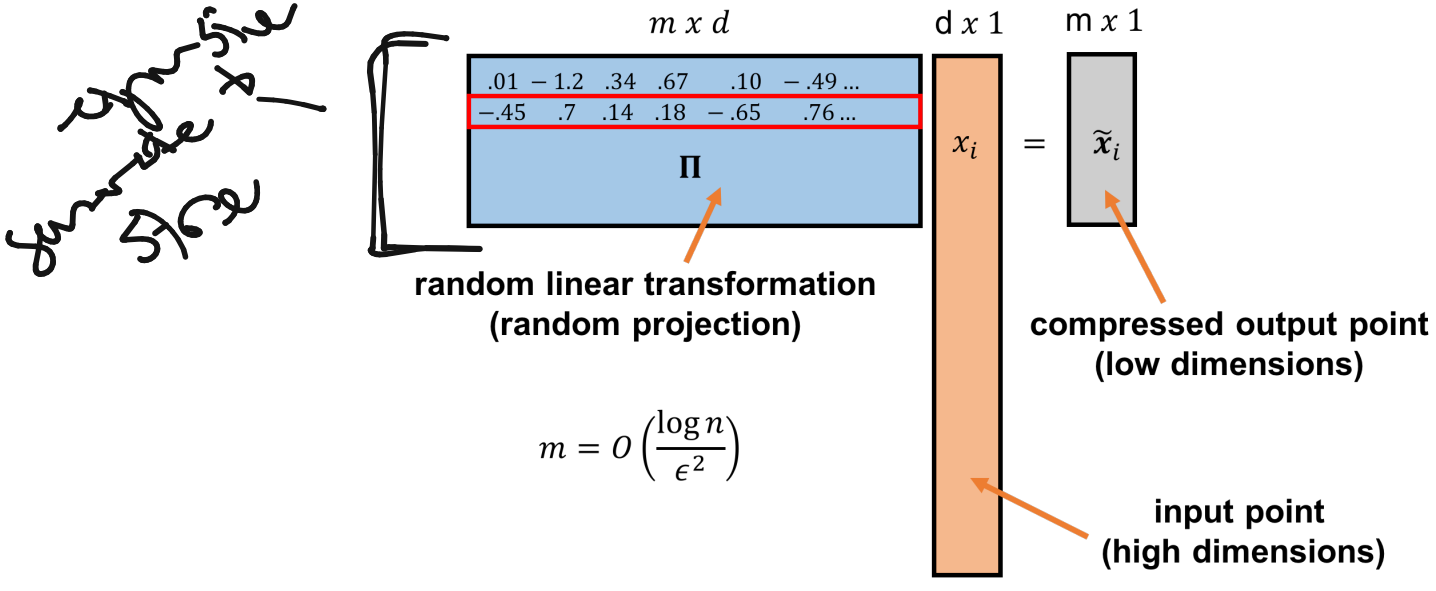


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- $\mathbf{\Pi}$ is data oblivious. Stark contrast to methods like PCA.

Algorithmic Considerations

- Many alternative constructions: ± 1 entries, sparse (most entries 0), Fourier structured, etc. $\implies$ more efficient computation of $\tilde{\mathbf{x}}_i = \mathbf{\Pi}\vec{x}_i$.

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- 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.

Johnson-Lindenstrauss Lemma Proof

Distributional JL

The Johnson-Lindenstrauss Lemma is a direct consequence of a closely related lemma:

Distributional JL Lemma: Let $\mathbf{\Pi} \in \mathbb{R}^{m \times d}$ 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 $\geq 1 - \delta$

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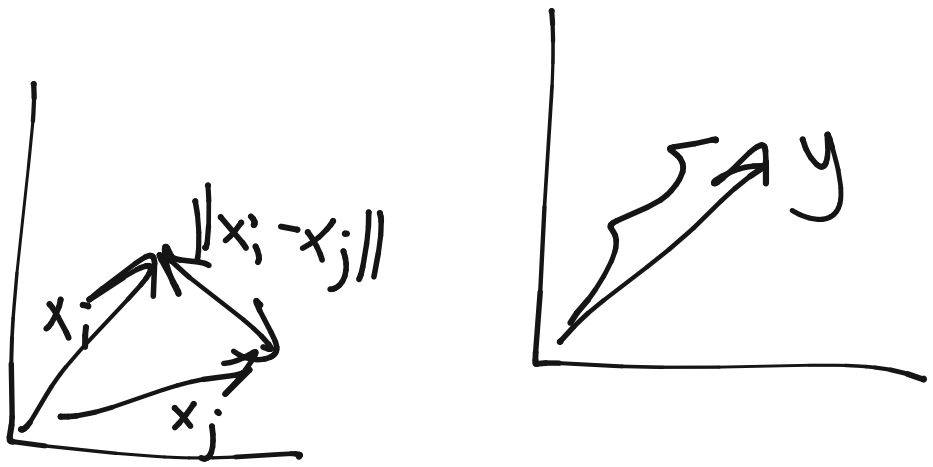
Applying a random matrix $\mathbf{\Pi}$ to any vector $\vec{y}$ preserves $\vec{y}$'s norm with high probability.

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

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Distributional JL $\implies$ JL

Distributional JL Lemma $\implies$ **JL Lemma:** Distributional JL show that a random projection $\mathbf{\Pi}$ preserves the norm of any y. The main JL Lemma says that $\mathbf{\Pi}$ preserves distances between vectors.



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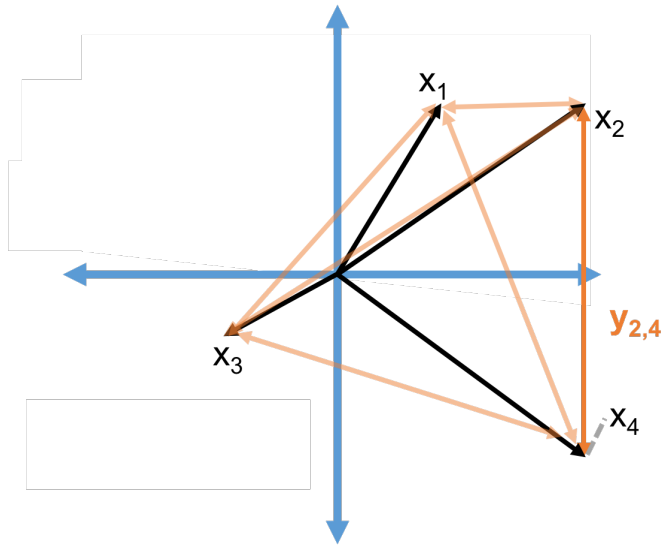
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$$m = O\left(\frac{\log(1/\delta')}{\epsilon^2}\right)$$

$\vec{x}_1, \ldots, \vec{x}_n$: original points, $\tilde{\mathbf{x}}_1, \ldots, \tilde{\mathbf{x}}_n$: compressed points, $\mathbf{\Pi} \in \mathbb{R}^{m \times d}$: random projection matrix. d: original dimension. m: compressed dimension, ϵ: embedding error, δ: embedding failure prob.

Distributional JL $\implies$ JL

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

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

With what probability are all pairwise distances preserved?

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

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

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

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$\log(n^2) = 2\log n$

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$O\left(\frac{\log n}{\epsilon^2}\right)$

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

Yields the JL lemma.