COMPSCI 514: ALGORITHMS FOR DATA SCIENCE

Andrew McGregor

Lecture 11

HIGH DIMENSIONAL DATA

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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.

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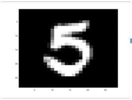

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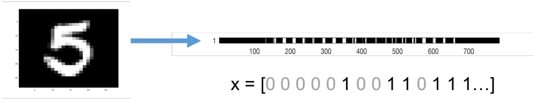

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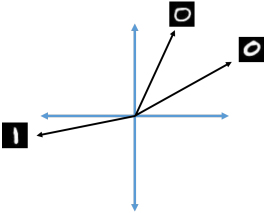

Similarities/distances between vectors (e.g., $\langle x, y \rangle$, $\|x - y\|_2$) have meaning for underlying data points.

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

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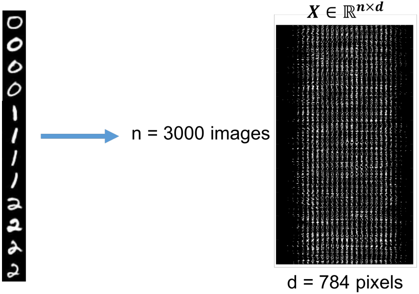

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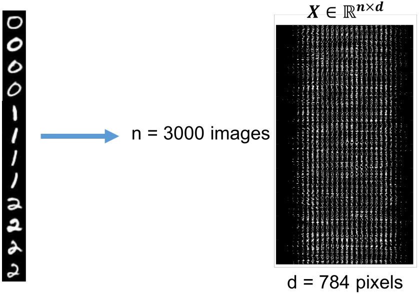

Many data points $n \implies$ tall. Many dimensions $d \implies$ wide.

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$\rightarrow$ x = [0 0 0 0 0 1 0 0 1 1 0 1 1 1…] $\rightarrow$ $\tilde{x}$ = [-5.5 4 3.2 -1]

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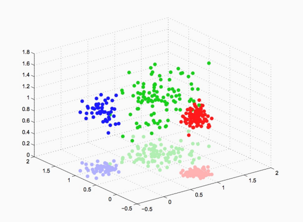
'Lossy compression' that still preserves important information about the relationships between $\vec{x}_1, \ldots, \vec{x}_n$.



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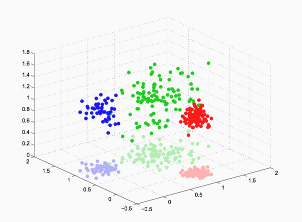

Generally will not consider directly how well $\tilde{x}_i$ approximates $\vec{x}_i$.

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 $i, j \in [n]$:

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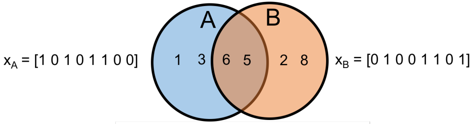

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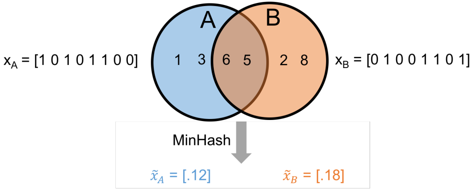

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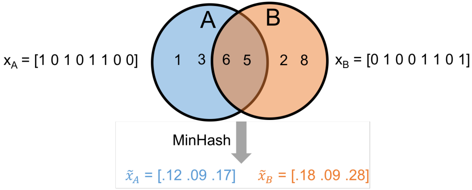

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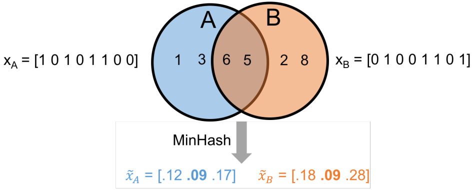

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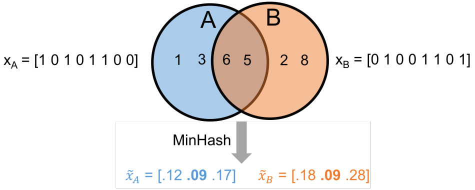

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- Note: here $J(\vec{x}_A, \vec{x}_B)$ is a similarity rather than a distance. So this is not quite low distortion embedding, but is closely related.

Euclidean Low Distortion Embedding: Given $\vec{x}_1, \ldots, \vec{x}_n \in \mathbb{R}^d$ 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 $i, j \in [n]$:

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

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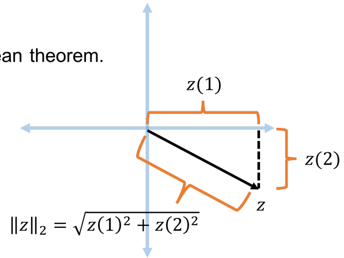
Pythagorean theorem.



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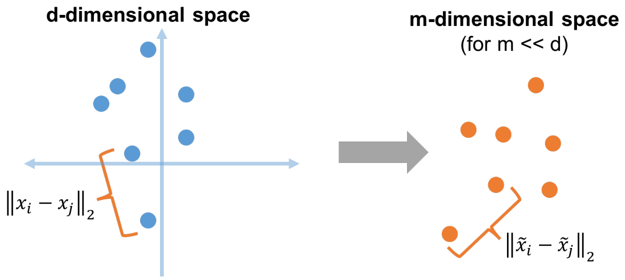

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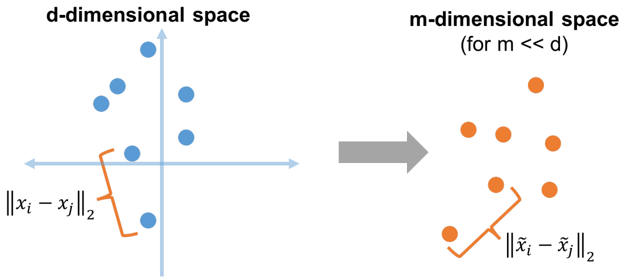
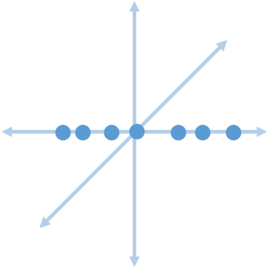


Can use $\tilde{x}_1, \ldots, \tilde{x}_n$ in place of $\vec{x}_1, \ldots, \vec{x}_n$ in clustering, SVM, linear classification, near neighbor search, etc.

A very easy case: Assume that $\vec{x}_1, \ldots, \vec{x}_n$ all lie on the 1^{st} axis in $\mathbb{R}^d$.



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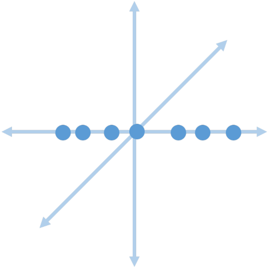

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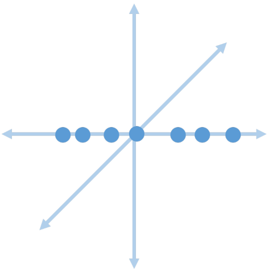

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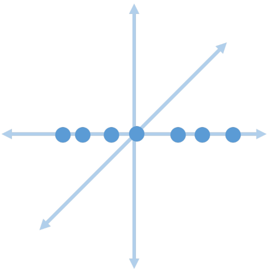

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- An embedding with no distortion from any d into $m = 1$.
- More generally. there's a no distortion embedding into $m = D$ dimensions if all the points lie is a D dimensional space.

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- Can we find an ϵ-distortion embedding into $m \ll d$ dimensions for $\epsilon > 0$? Yes! Always, with m depending on ϵ.

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

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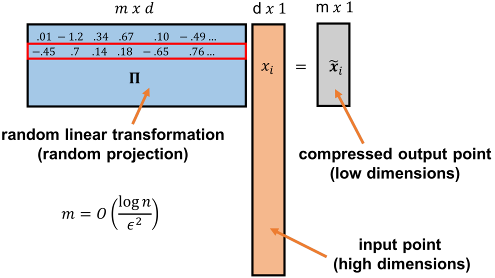

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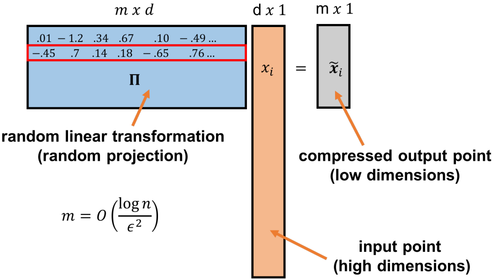

- $\mathbf{\Pi}$ is known as a random projection. It is a random linear function, mapping length d vectors to length m vectors.

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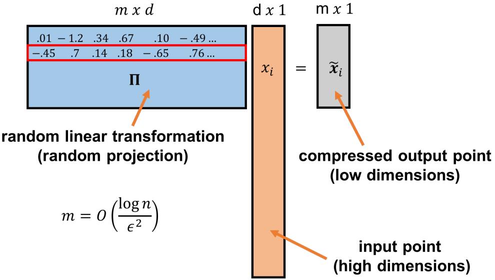
For all i, j : $(1-\epsilon)\|\vec{x}_i - \vec{x}_j\|_2 \le \|\mathbf{x}_i - \mathbf{x}_j\|_2 \le (1+\epsilon)\|\vec{x}_i - \vec{x}_j\|_2$.



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

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- Compression can be performed in parallel on different servers.
- When new data points are added, can be easily compressed, without updating existing points.

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 $\geq 1 - \delta$

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

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

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- Like a low-distortion embedding, but for the length of a compressed vector rather than distances between vectors.

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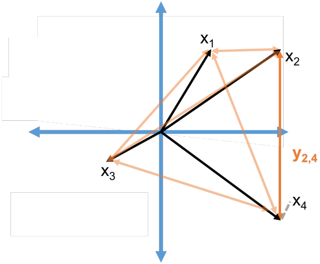

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Yields the JL lemma.