

COMPSCI 514: ALGORITHMS FOR DATA SCIENCE

Cameron Musco

University of Massachusetts Amherst. Fall 2019.

Lecture 9

- Problem Set 2 was released on 9/28. **Due Friday 10/11.**
- Problem Set 1 should be graded by the end of this week.
- Midterm on Thursday 10/17. Will cover material through this week, but not material next week (10/8 and 10/10).

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- This Thursday, will have a MAP (Midterm Assessment Process).
 - Someone from the Center for Teaching & Learning will collect feedback from you during the first 20 minutes of class.
 - Will be summarized and relayed to me anonymously, so I can make any adjustments and incorporate suggestions to help you learn the material better.

Last Class: The Frequent Elements Problem

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- Randomized algorithm: **Count-Min sketch**
- Analysis via Markov's inequality and repetition. 'Min trick' similar to median trick.

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This Class: Randomized dimensionality reduction.

- The extremely powerful **Johnson-Lindenstrauss Lemma** and random projection.
- Linear algebra warm up.

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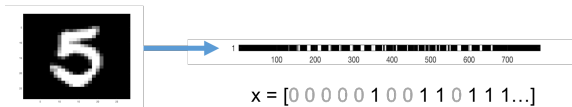
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- The human genome contains 3 billion+ base pairs. Genetic datasets often contain information on **100s of thousands+ mutations and genetic markers**.

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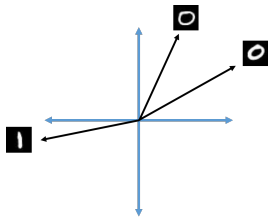
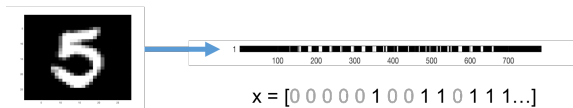
ATAGCCGTAGT \longrightarrow $x = [1\ 2\ 1\ 3\ 4\ 4\ 3\ 2\ 1\ 3\ 4]$



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

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Data Points: $x_1, x_2, \dots, x_n \in \mathbb{R}^d$

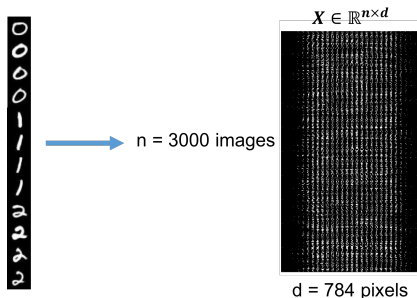
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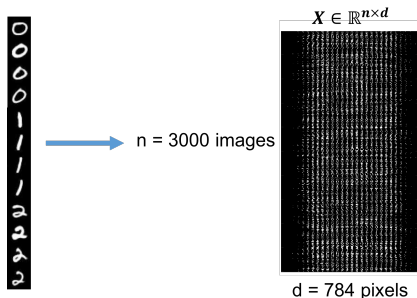


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Many data points $n \implies$ tall. Many dimensions $d \implies$ wide.

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

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‘Lossy compression’ that still preserves important information about the relationships between x_1, \dots, x_n .

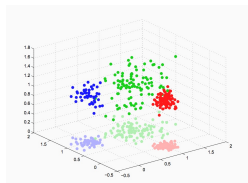
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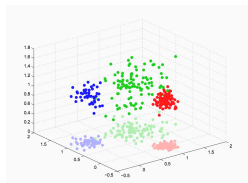
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Generally will not consider directly how well \tilde{x}_i approximates x_i .

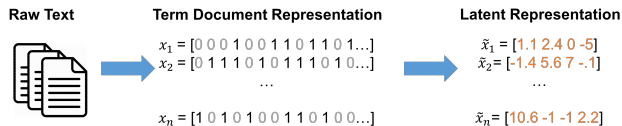
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- Principal component analysis

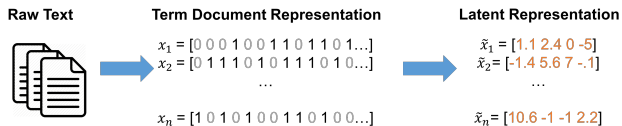
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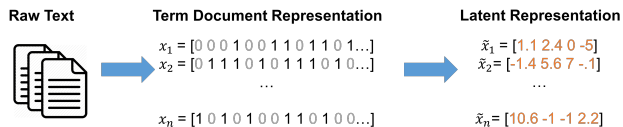
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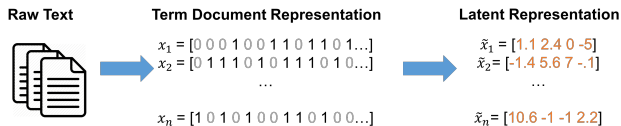
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- Autoencoders

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

Low Distortion Embedding: Given $x_1, \dots, x_n \in \mathbb{R}^d$, distance function D , and error parameter $\epsilon \geq 0$, find $\tilde{x}_1, \dots, \tilde{x}_n \in \mathbb{R}^{d'}$ (where $d' \ll d$) and distance function \tilde{D} such that for all $i, j \in [n]$:

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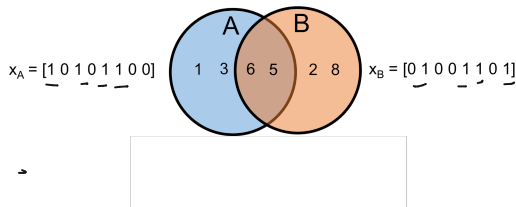
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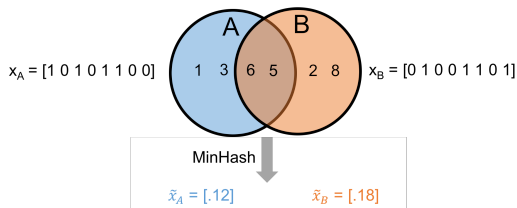


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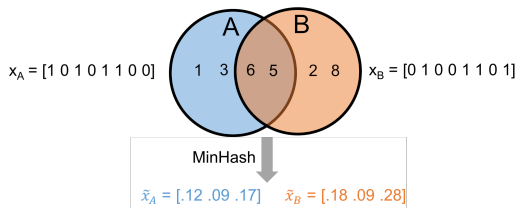


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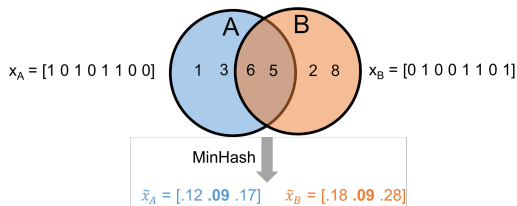


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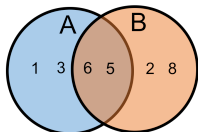
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$$D(x_A, x_B) \approx 1/3$$

$x_A = [1 0 1 0 1 1 0 0]$



$x_B = [0 1 0 0 1 1 0 1]$

$$\tilde{D}(\tilde{x}_A, \tilde{x}_B) = 1/3$$



With large enough signature size r , can argue that (# matching entries in \tilde{x}_A, \tilde{x}_B) $\approx J(x_A, x_B)$.

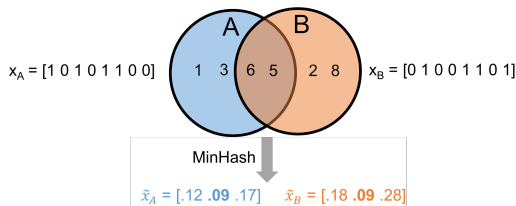
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- Reduce dimension from $d = |U|$ to r .

Low Distortion Embedding for Euclidean Space: Given $x_1, \dots, x_n \in \mathbb{R}^d$ and error parameter $\epsilon \geq 0$, find $\tilde{x}_1, \dots, \tilde{x}_n \in \mathbb{R}^{d'}$ (where $d' \ll d$) such that for all $i, j \in [n]$:

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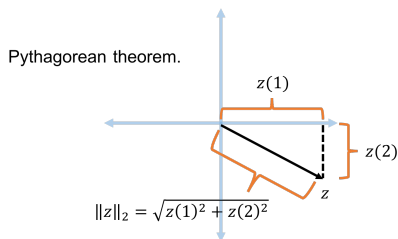
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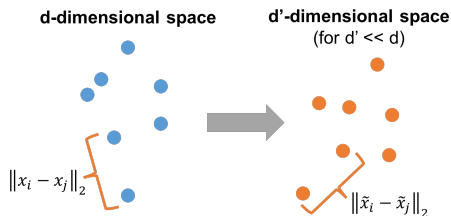
$$(1 - \epsilon)\|x_i - x_j\|_2 \leq \|\tilde{x}_i - \tilde{x}_j\|_2 \leq (1 + \epsilon)\|x_i - x_j\|_2$$

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



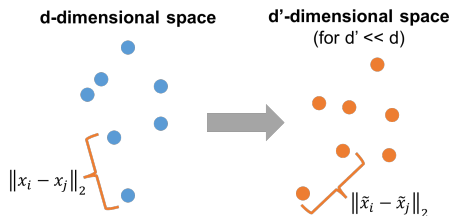
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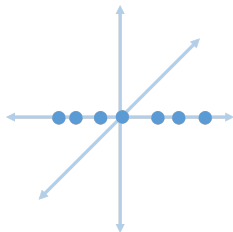
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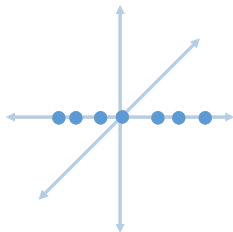
Can use $\tilde{x}_1, \dots, \tilde{x}_n$ in place of x_1, \dots, x_n in many applications: clustering, SVM, near neighbor search, etc.

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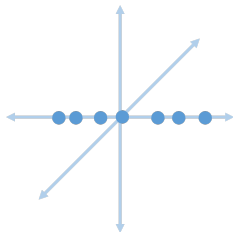


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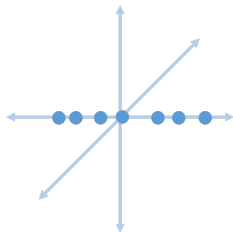


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$$\|\tilde{x}_i - \tilde{x}_j\|_2$$

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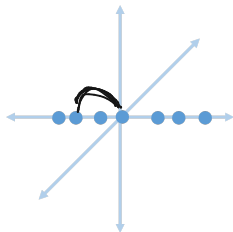


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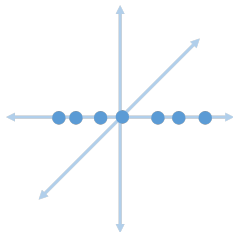


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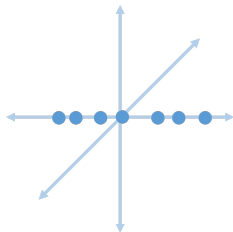


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$$\|\tilde{x}_i - \tilde{x}_j\|_2 = \sqrt{[x_i(1) - x_j(1)]^2} = |x_i(1) - x_j(1)| = \|x_i - x_j\|_2.$$

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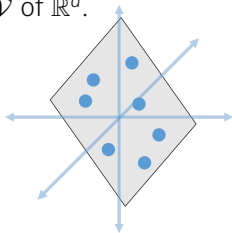
- For all i, j :

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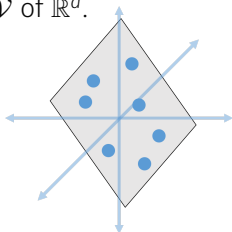
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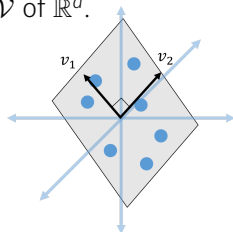


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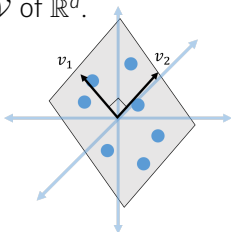
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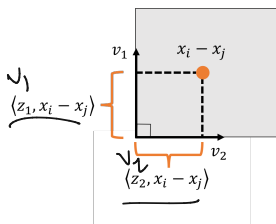
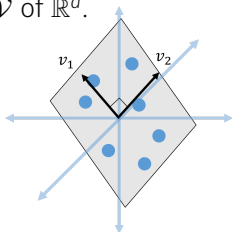


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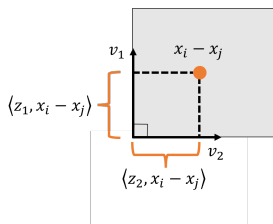
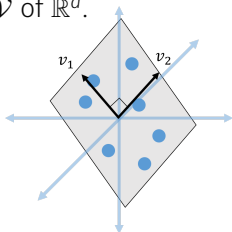


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$V_k \in \mathbb{R}^{d \times k}$

$$k \begin{bmatrix} v_1 \\ v_2 \\ \vdots \\ v_k \end{bmatrix}^T \begin{bmatrix} x_i - x_j \end{bmatrix} = \begin{bmatrix} \langle v_1, x_i - x_j \rangle \\ \langle v_2, x_i - x_j \rangle \\ \vdots \\ \langle v_k, x_i - x_j \rangle \end{bmatrix}$$

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- An embedding with **no distortion** from any d into $d' = k$.
- $\mathbf{V}^T : \mathbb{R}^d \rightarrow \mathbb{R}^k$ is a linear map giving our dimension reduction.

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

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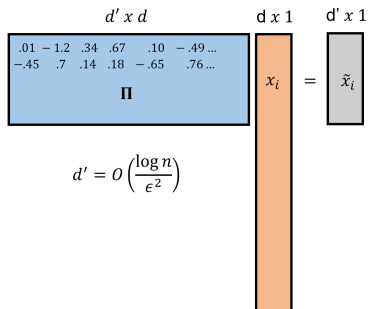
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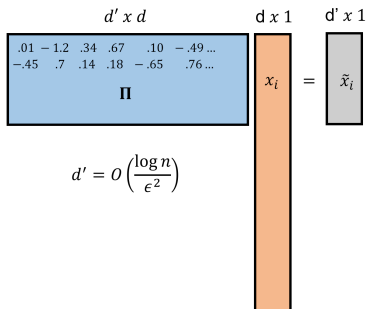
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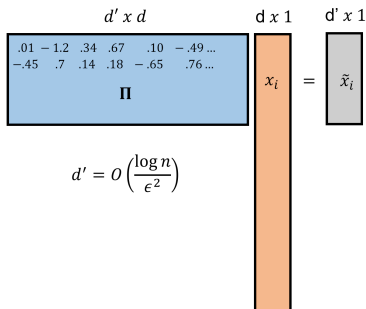


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- **Data oblivious** transformation. Stark contrast to methods like PCA.

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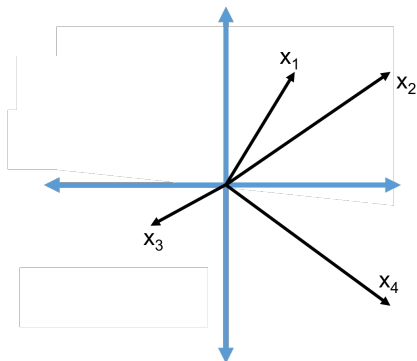
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- When new data points are added, can be easily compressed, without updating existing points.

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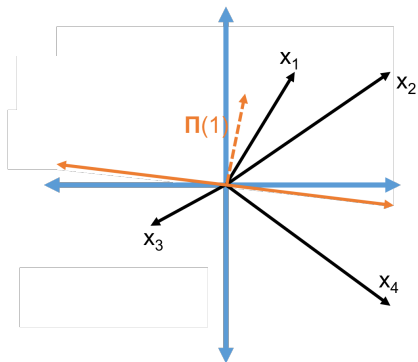
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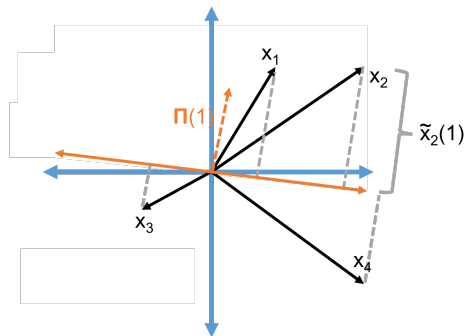
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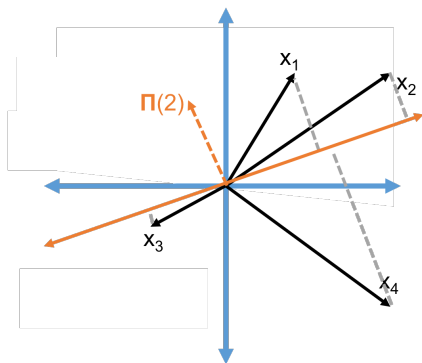
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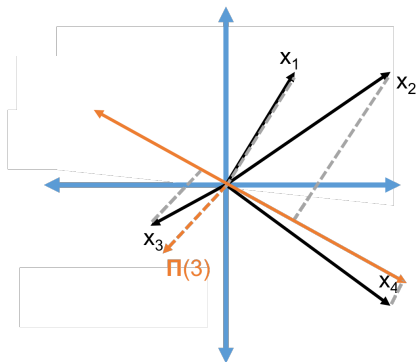
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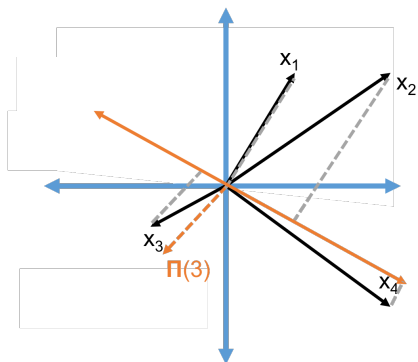
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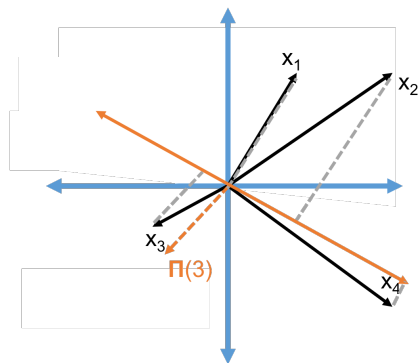
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$$\tilde{x}_i = [1.1 \ -2.4 \ 0.1 \ -5]$$



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

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Can be proven from first principles. Will see next.

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Setting δ to any fixed constant yields the JL lemma.

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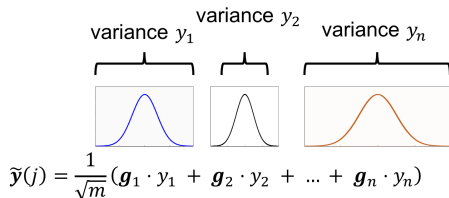
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Stability is another explanation for the **central limit theorem**.

So far: Letting $\mathbf{\Pi} \in \mathbb{R}^{d \times m}$ have each entry chosen i.i.d. as $\frac{1}{\sqrt{m}} \cdot \mathcal{N}(0, 1)$, for any $y \in \mathbb{R}^d$, letting $\tilde{\mathbf{y}} = \mathbf{\Pi}y$:

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So far: Letting $\mathbf{\Pi} \in \mathbb{R}^{d \times m}$ have each entry chosen i.i.d. as $\frac{1}{\sqrt{m}} \cdot \mathcal{N}(0, 1)$, for any $y \in \mathbb{R}^d$, letting $\tilde{\mathbf{y}} = \mathbf{\Pi}y$:

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How is $\|\tilde{\mathbf{y}}\|_2^2$ distributed? Does it concentrate?

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Gives the distributional JL Lemma and thus the classic JL Lemma.

Questions?