COMPSCI 514: Algorithms for Data Science

Cameron Musco University of Massachusetts Amherst. Fall 2023. Lecture 12

Logistics

- The midterm exam is next Tuesday in class.
- · This Thursday we will do exam review in class.
- I will also hold extra office hours Thursday 11am-12:45pm in LGRC A112.
- · No quiz this week.
- If you need extended time on the exam, email me by Wednesday to let me know.

Summary

Last Class: Frequent Elements and Count-Min Sketch

- The frequent elements problem in data streams.
- · Count-min sketch for frequency estimation via random hashing.
- Full analysis via Markov's inequality and repetition.

This Class: Randomized Compression of High Dimensional Data

- Low-distortion embeddings and the Johnson-Lindenstraus (JL)
 Lemma.
- · Proof the IL Lemma.
- Example application to clustering.

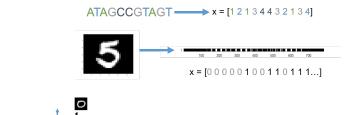
High Dimensional Data

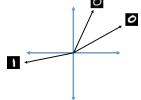
'Big Data' means not just many data points, but many measurements per data point. I.e., very high dimensional data.

- Twitter has 321 million active monthly users. Records (tens of)
 thousands of measurements per user: who they follow, who
 follows them, when they last visited the site, timestamps for
 specific interactions, how many tweets they have sent, the text
 of those tweets, etc.
- A 3 minute Youtube clip with a resolution of 500 × 500 pixels at 15 frames/second with 3 color channels is a recording of ≥ 2 billion pixel values. Even a 500 × 500 pixel color image has 750,000 pixel values.
- 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.





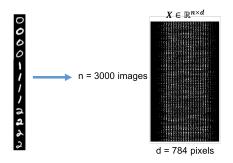
Similarities/distances between vectors (e.g., $\langle x, y \rangle$, $\|x - y\|_2$) have meaning for underlying data points.

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

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



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

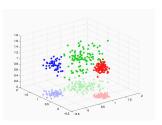
Dimensionality Reduction

Dimensionality Reduction: Compress data points so that they lie in many fewer dimensions.

$$\vec{x}_1, \dots, \vec{x}_n \in \mathbb{R}^d \to \tilde{x}_1, \dots, \tilde{x}_n \in \mathbb{R}^m$$
 for $m \ll d$.

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

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

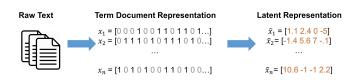


Generally will not consider directly how well \tilde{x}_i approximates \vec{x}_i .

Dimensionality Reduction

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

- · Principal component analysis
- · Latent semantic analysis (LSA)



- · Linear discriminant analysis
- Autoencoders

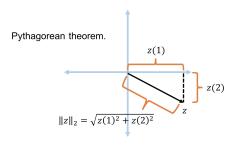
Compressing data makes it more efficient to work with. May also remove extraneous information/noise.

Embeddings for Euclidean Space

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

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

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



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

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

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

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.

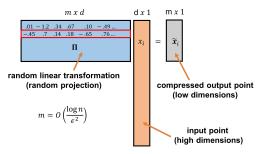
For d=1 trillion, $\epsilon=.05$, and n=100,000, $m\approx 6600$.

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 $\vec{x}_1, \dots, \vec{x}_n$ 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 $\tilde{\mathbf{x}}_i = \Pi \vec{x}_i$:

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



- •
 • In is known as a random projection. It is a random linear function, mapping length d vectors to length m vectors.
- •
 • I is data oblivious. Stark contrast to methods like PCA.

Algorithmic Considerations

- Many alternative constructions: ± 1 entries, sparse (most entries 0), Fourier structured, etc. \Longrightarrow more efficient computation of $\tilde{\mathbf{x}}_i = \mathbf{\Pi} \vec{\mathbf{x}}_i$.
- Data oblivious property means that once Π is chosen, $\tilde{\mathbf{x}}_1, \dots, \tilde{\mathbf{x}}_n$ can be computed in a stream with little memory.
- 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.

Distributional JL

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

Applying a random matrix Π 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.

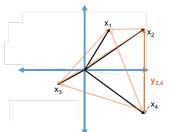
 $\Pi \in \mathbb{R}^{m \times d}$: random projection matrix. d: original dimension. m: compressed dimension, ϵ : embedding error, δ : embedding failure prob.

Distributional JL \implies JL

Distributional JL Lemma \Longrightarrow **JL Lemma:** Distributional JL show that a random projection Π preserves the norm of any y. The main JL Lemma says that Π preserves distances between vectors.

Since Π is linear these are the same thing!

Proof: Given $\vec{x}_1, \dots, \vec{x}_n$, define $\binom{n}{2}$ vectors \vec{y}_{ij} where $\vec{y}_{ij} = \vec{x}_i - \vec{x}_j$.



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

$$(1 \quad c) \| \vec{\sigma} \vec{\nabla} \quad \vec{\nabla} \| = c \| \mathbf{n} \vec{\sigma} \cdot \mathbf{n} (\vec{\nabla} \quad \vec{\nabla}) \vec{\nabla} \quad \vec{\nabla} \| = c (1 + c) \| \vec{\sigma} \cdot \vec{\nabla} \quad \vec{\nabla} \|$$

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Distributional $JL \implies JL$

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

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

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

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

Yields the JL lemma.