Big Data Analysis Application and Practice (XAI605)

Other Linear Dimensionality Reduction Methods

2023 Spring

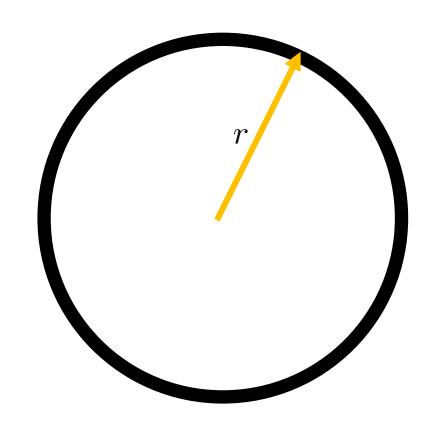
Instructor: Sejun Park

Counter intuitive property in high dim.

Volume of a sphere of radius r

$$\operatorname{Vol}(\mathbb{B}_n(r)) = rac{\pi^{n/2} r^n}{\Gamma(1+n/2)}$$

 Γ : gamma function



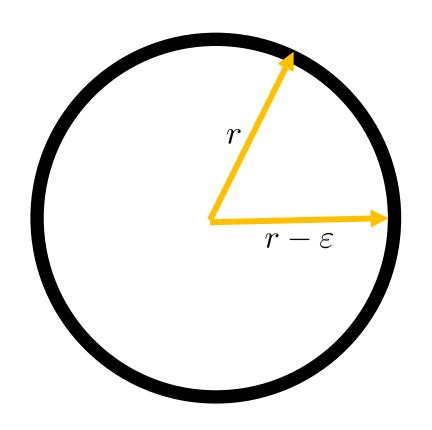
Counter intuitive property in high dim.

Region around the shell occupies most volume of a sphere

$$\mathsf{Vol}(\mathbb{B}_n(r)) = rac{\pi^{n/2} r^n}{\Gamma(1+n/2)}$$

$$\frac{\operatorname{Vol}(\mathbb{B}_n(r)) - \operatorname{Vol}(\mathbb{B}_n(r-\varepsilon))}{\operatorname{Vol}(\mathbb{B}_n(r))}$$

$$= 1 - \frac{(r-\varepsilon)^n}{r^n}$$



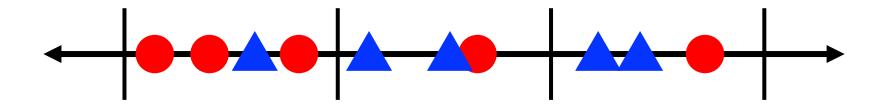
- Curse of dimensionality: problems in data analysis that occurs as the dimensionality increases
 - Typically, under the setup: #samples = n dimension

- Statistical aspects
 - In high-dimensional data, it becomes more likely to find spurious or random correlations between unrelated features
 - This is often called "overfitting"

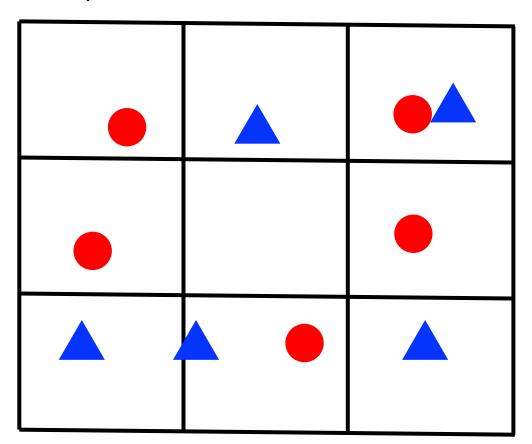
- Curse of dimensionality: problems in data analysis that occurs as the dimensionality increases
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- Computational aspects
 - Sampling from continuous/discrete distribution requires FLOPS at least exponential to the parameter dimension (until now), i.e., NP-hard

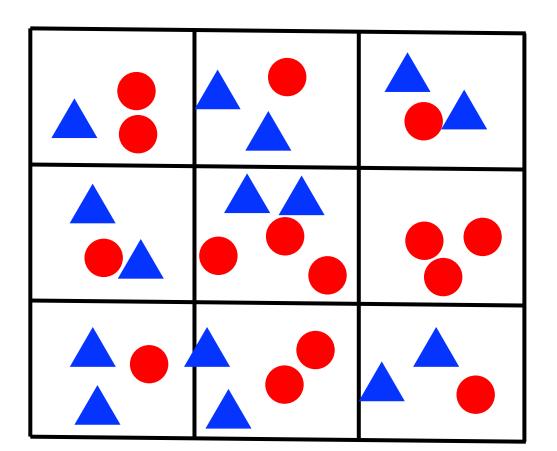
- Consider a simple classification problem:
 - This is similar to the k-NN algorithm
 - First, split the state space (say a unit cube) by cubes of equal side length
 - Estimate the label of a new sample by the majority labels of training data in the cube containing the sample
- For low-dimensional data, this can be a good estimator of the true distribution



- As the dimensionality of data increases, #samples in each cube decreases exponentially fast
 - Under fixed #sample



 To have preserve the density of samples in each cube, we need exponentially many samples



High-dimensional data

- With big data embedded in bigger dimensional space, can we efficiently do dimension reduction?
 - e.g., we want to preserve the pairwise distance between data (MDS)

- We may use PCA (or equivalently MDS) for small k
 - Finding basis requires O(#dim x #data x #data) FLOPS
 - For both SVD & power iteration under assuming naïve matrix multiplication
 - In addition, we need to perform additional matrix product for projecting original data to the found subspace

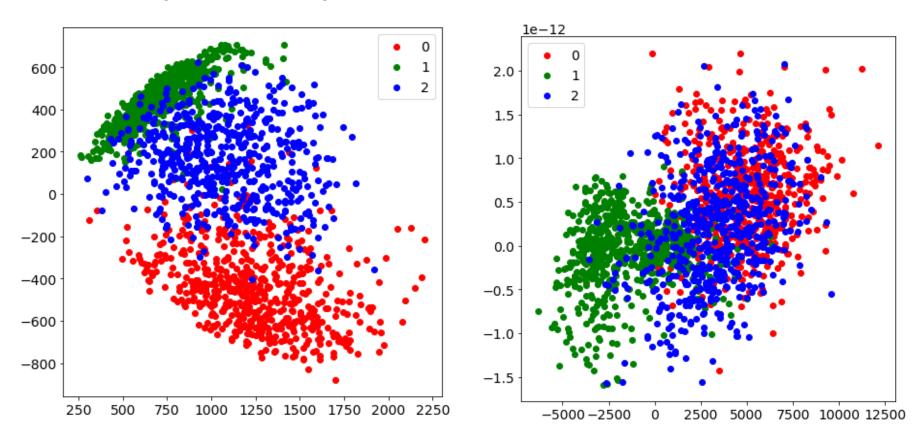
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 - For both SVD & power iteration under assuming naïve matrix multiplication
 - In addition, we need to perform additional matrix product for projecting original data to the found subspace
- Can we do this more efficiently?

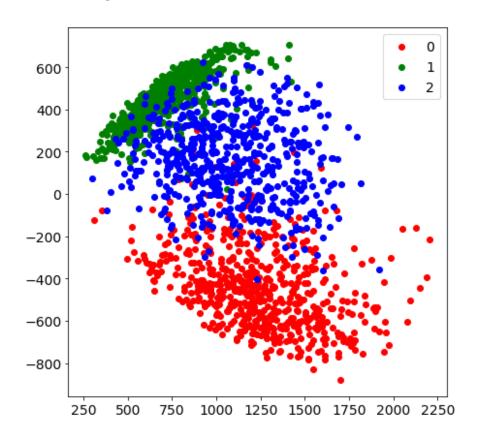
Naïve idea

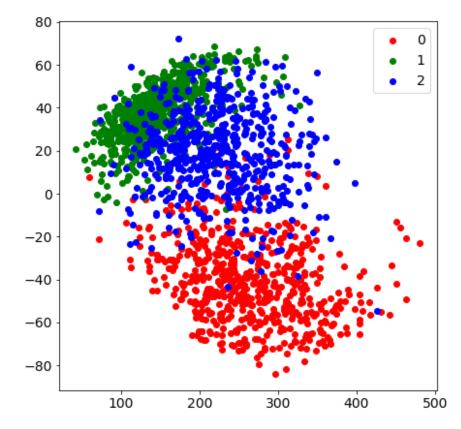
- We can choose random subspace and project data
 - Subsampled MNIST data with labels 0, 1, 2 (#samples ~ 1900)
 - Left: original PCA, Right: projection to random subspace (dim=2)



Naïve idea

- We can also do random projection first, and apply PCA
 - Left: original PCA (dim=28x28=784 -> 2)
 - Right: PCA after random projection (dim=784 -> 78 -> 2)





Johnson-Lindenstrauss lemma

- Why such a naïve idea works?
 - Mathematical explanation: Johnson-Lindenstrauss lemma

For any $\varepsilon > 0$, $x_1, \ldots, x_n \in \mathbb{R}^p$, and an integer $k > (8 \log n)/\varepsilon^2$, there exists a linear map $f : \mathbb{R}^p \to \mathbb{R}^k$ such that for any i, j

$$||(1-\varepsilon)||x_i - x_j|| \le ||f(x_i) - f(x_j)|| \le (1+\varepsilon)||x_i - x_j||$$

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- If n=1900, then $8\log n\approx 26.23\Longrightarrow \varepsilon\leq 1.725$ with k=78
- Theory often provides a vacuous bound but this bound is indeed tight up to a constant multiplicative factor!

Proof sketch

Lemma. Let $x \in \mathbb{R}^p$ and M be a $k \times p$ random matrix whose entries are i.i.d. N(0,1). Then,

$$\mathbb{P}\left((1-\varepsilon)\|x\|^2 \le \left\|\frac{1}{\sqrt{k}}Mx\right\|^2 \le (1+\varepsilon)\|x\|^2\right) \ge 1 - 2e^{-k(\varepsilon^2 - \varepsilon^3)/4}$$

Proof sketch

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Proof sketch. This is from standard concentration inequality (i.e., law of large numbers) with the following observation

$$\mathbb{E}\left[\left\|\frac{1}{\sqrt{k}}Mx\right\|\right] = \frac{1}{k} \sum_{i=1}^{k} \sum_{j=1}^{p} \mathbb{E}\left[(M_{ij}x_{j})^{2}\right] = \frac{1}{k} \sum_{i=1}^{k} \sum_{j=1}^{p} (x_{j})^{2}$$
$$= \frac{1}{k} \sum_{i=1}^{k} \|x\|^{2} = \|x\|^{2}$$

Proof sketch

Proof sketch of JL lemma. Let $N=M/\sqrt{k}$ and assume $\varepsilon<\frac{1}{2}$

$$\mathbb{P}\left(\exists i, j \text{ s.t. } \|N(x_i - x_j)\|^2 \notin (1 \pm \varepsilon) \|x_i - x_j\|^2\right)$$

$$\leq \sum_{i>j} \mathbb{P}\left(\|N(x_i - x_j)\|^2 \notin (1 \pm \varepsilon) \|x_i - x_j\|^2\right)$$

$$\leq \frac{n(n-1)}{2} \cdot 2e^{-k(\varepsilon^2 - \varepsilon^3)/4}$$

$$< n^2 e^{-k\varepsilon^2/8}$$

$$\leq 1 \text{ under } k \geq \frac{16 \log n}{\varepsilon^2}$$

Johnson-Lindenstrauss transform

JL lemma only guarantees the existence of good linear maps

- Q. Can we find such a good linear map?
- A. Yes (with high probability)
 - Choose a realization of the random matrix used in the proof!

$$x \mapsto \frac{1}{\sqrt{k}} Mx$$

Complexity of random projection

 Random projection (JL transformation) requires one matrix multiplication (matrix size: k x p, p x n)

 This is extremely fast: even if we find basis (subspace) via some optimization procedure (e.g. PCA), we still need such a projection step

And as we observed before, RP can be done before PCA

Fast Johnson-Lindenstrauss transform

- Computational complexity of random projection?
 - Naïve matrix-vector product requires O(kp) FLOPS

Fast Johnson-Lindenstrauss transform

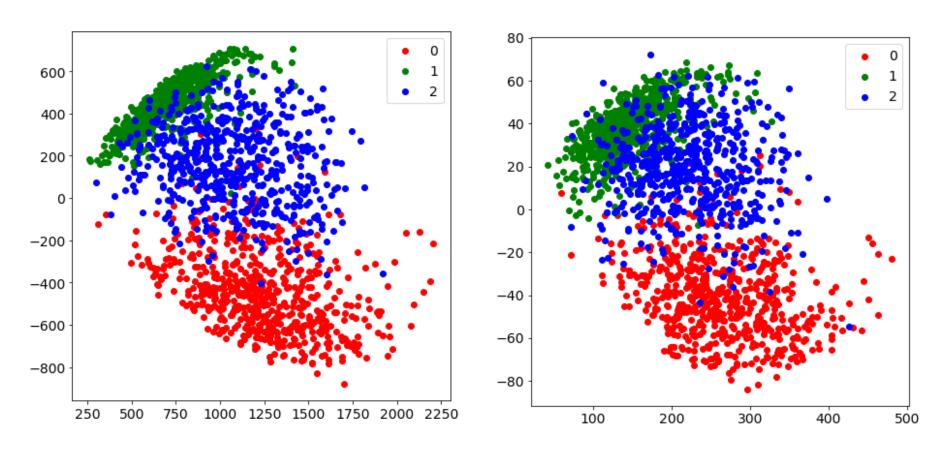
- Computational complexity of random projection?
 - Naïve matrix-vector product requires O(kp) FLOPS

- Q. Can we do this even faster?
- A. Yes (with different random matrix)
 - This requires only $O(p \log p + k \log^2 n)$ FLOPS

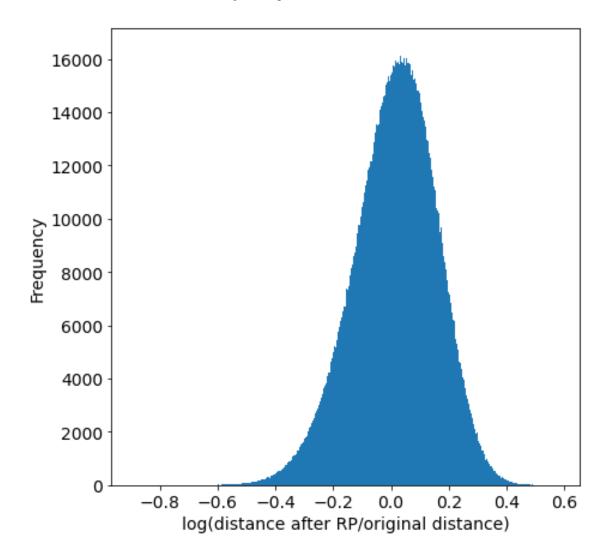
$$x \mapsto PHDx$$

- $D \in \mathbb{R}^{p \times p}$: diagonal matrix
- $H \in \mathbb{R}^{p \times p}$: matrix encoding FFT (FFT can be done in $O(p \log p)$ FLOPS)
- $P \in \mathbb{R}^{k \times p}$: sparse matrix containing $\Theta(k \log^2 n)$ non-zero entries

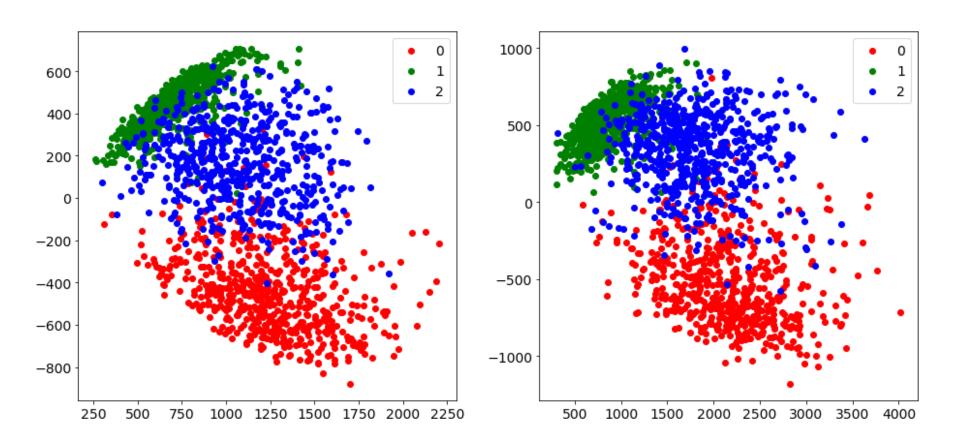
- #sample~1900, random projection from dim=784 to dim=74
 - Left: original PCA, Right: PCA after RP



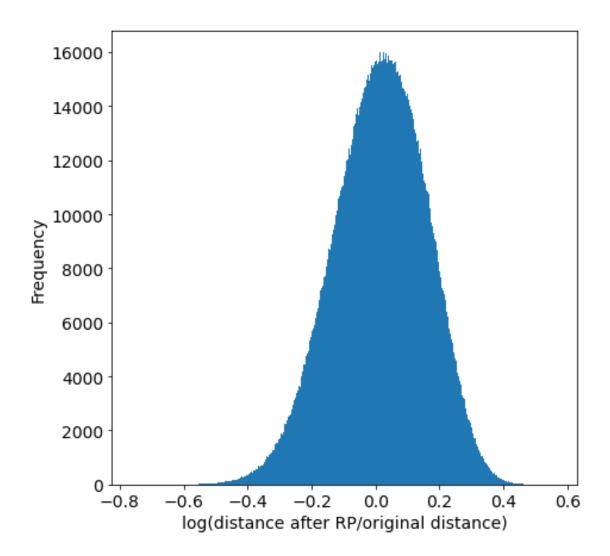
#sample~1900, random projection from dim=784 to dim=74



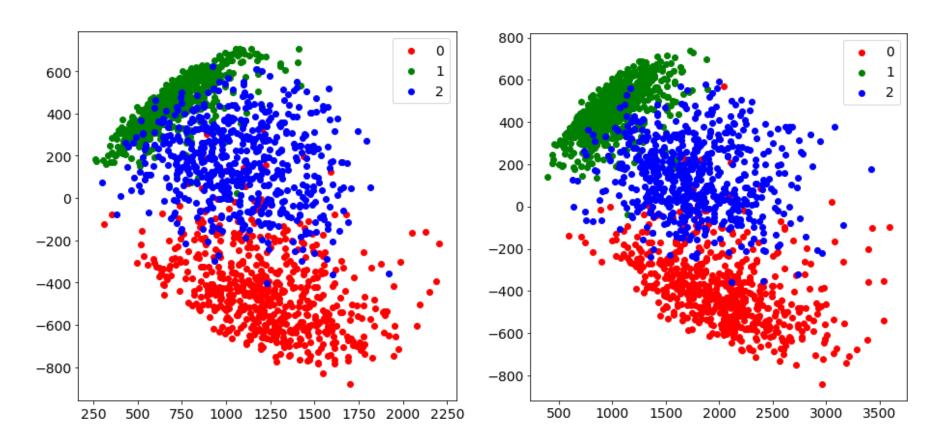
- #sample~1900, random projection from dim=784 to dim=100
 - Left: original PCA, Right: PCA after RP



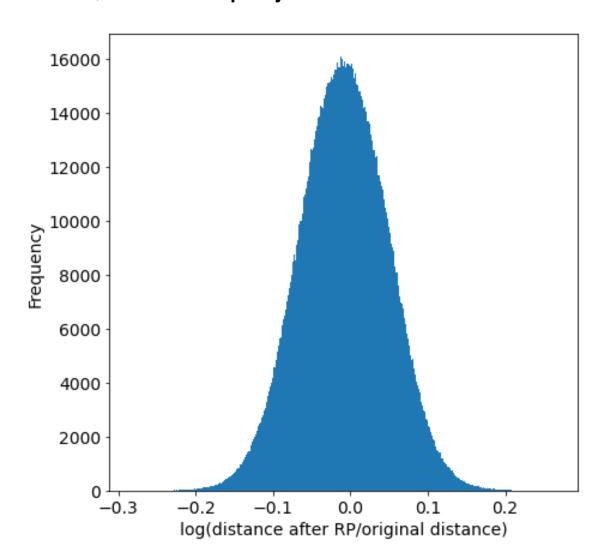
#sample~1900, random projection from dim=784 to dim=100



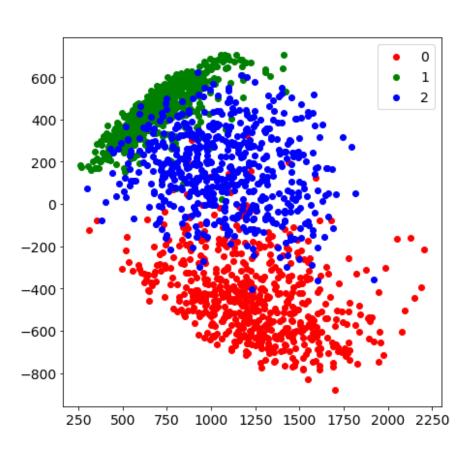
- #sample~1900, random projection from dim=784 to dim=500
 - Left: original PCA, Right: PCA after RP

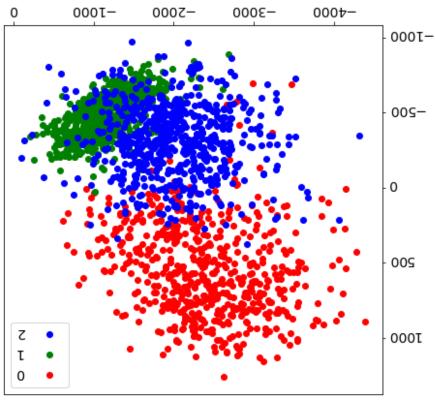


#sample~1900, random projection from dim=784 to dim=500

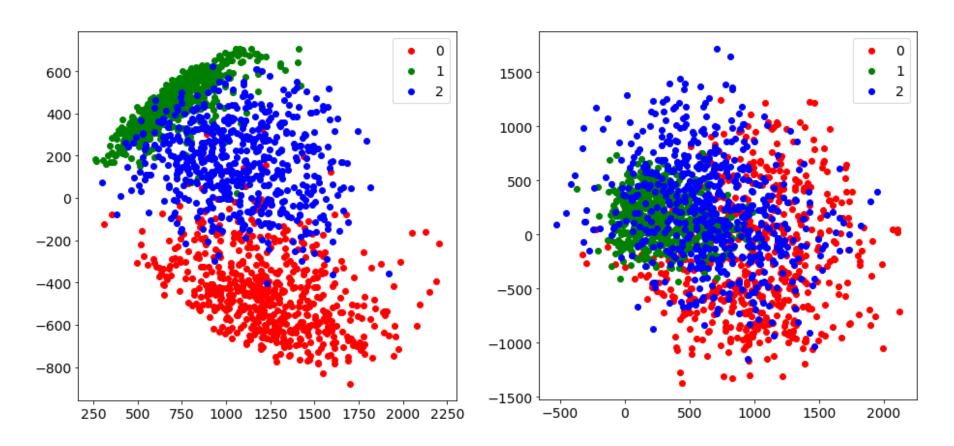


- #sample~1900, random projection from dim=784 to dim=30
 - Left: original PCA, Right: PCA after RP





- #sample~1900, random projection from dim=784 to dim=10
 - Left: original PCA, Right: PCA after RP

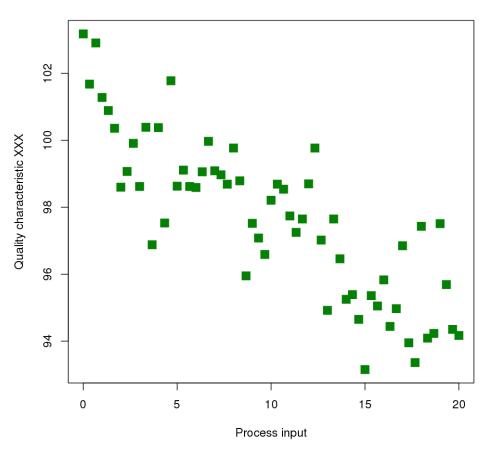


Linear dimensionality reduction with labeled data

Labeled data

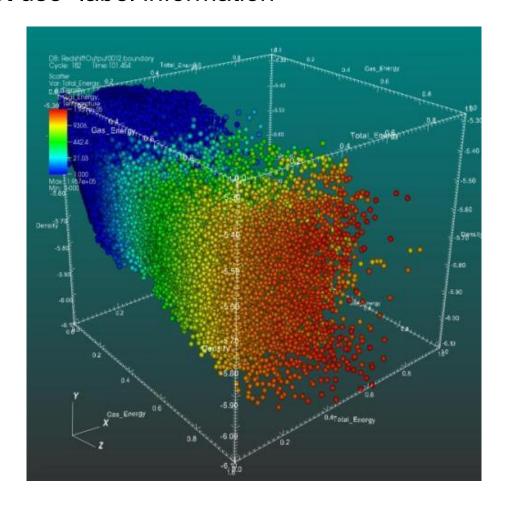
- Given labeled data, can we see a good scatter plot via PCA?
 - PCA does not use "label information"

Scatterplot for quality characteristic XXX



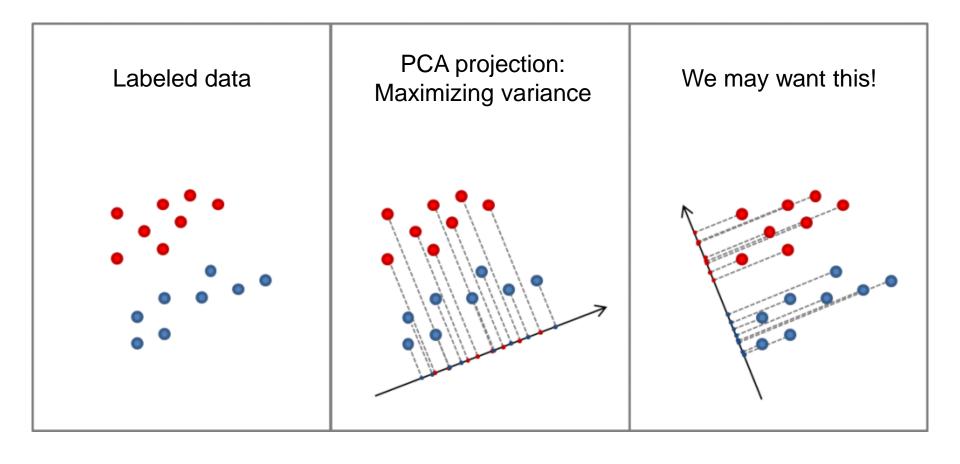
Labeled data

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Labeled data

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Sufficient dimension reduction

 Dimensionality reduction method considering classification and regression setups

- Goal: find the best low-dimensional representation of inputs preserving information of data
 - In PCA, we aim to minimize the error between the original data and reconstructed data from low-dimensional representation

Sufficient dimension reduction

- As in typical classical methods, we first consider
 - Linear transformation
 - Linear model in both classification and regression setups
 - Gaussian noise

Sufficient dimension reduction

- As in typical classical methods, we first consider
 - Linear transformation
 - Linear model in both classification and regression setups
 - Gaussian noise

- Suppose that input can be represented by low-dimensional representation without label information loss
 - X: input RV, Y: label RV, P: projection matrix

$$Y \perp X \mid P^{\top}X$$

Uniqueness of projection matrix

- Such a projection matrix P is not unique in general
 - We can use a different basis for the column space of P
 - i.e., for any invertible matrix M

$$Y \perp X \mid P^{\top}X \iff Y \perp X \mid MP^{\top}X$$

Uniqueness of projection matrix

- Such a projection matrix P is not unique in general
 - We can use a different basis for the column space of P

$$Y \perp X \mid P^{\top}X \Longleftrightarrow Y \perp X \mid Q^{\top}X$$

 So we may consider the subspace spanned by the column space of P

$$\mathcal{S}(P) = \operatorname{span}(p_1, \dots, p_k)$$

 $P = [p_1, \dots, p_k] \in \mathbb{R}^{p \times k}$

Dimension reduction subspace

• S is a dimension reduction subspace if its basis b_1, \ldots, b_k satisfies

$$Y \perp X \mid b_1^{\top} X, \dots b_k^{\top} X$$

We are particularly interested in minimum DRS (DRS with minimum dim.)

Dimension reduction subspace

• S is a dimension reduction subspace if its basis b_1, \ldots, b_k satisfies

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• We are particularly interested in minimum DRS (DRS with minimum dim.)

- Minimum DRS may not be unique
 - X follows uniform distribution on $\{(x_1, x_2) \in \mathbb{R}^2 : x_1^2 + x_2^2 = 1\}$
 - $y|x = x_1^2 + \varepsilon$

$$Y \perp X \mid x_1^2, \ Y \perp X \mid x_2^2$$

Dimension reduction subspace

• S is a dimension reduction subspace if its basis b_1, \ldots, b_k satisfies

$$Y \perp X \mid b_1^{\top} X, \dots b_k^{\top} X$$

We are particularly interested in minimum DRS (DRS with minimum dim.)

 A unique minimum DRS exists (called central subspace) if the support of X is open and convex

We want to approximate the central subspace

- Now, consider the following inverse model
 - Want to estimate an input given a label
 - $\mu \in \mathbb{R}^p, U \in \mathbb{R}^{p \times k}, \beta_y \in \mathbb{R}^k, \varepsilon \sim N(0, I)$
 - Assume $\sum_y \beta_y = 0$ and columns of U are orthonormal $(U^\top U = I)$

$$(X|Y=y) = \mu + U\beta_y + \varepsilon$$

• Observe the distribution of Y|X

$$f_{Y|X}(y|x) \propto f_{X|Y}(x|y)f_Y(y)$$

$$\propto \exp\left(-\frac{1}{2}\|x - \mu - U\beta_y\|^2\right)f_Y(y)$$

$$\propto \exp\left(-\frac{1}{2}(\beta_y^\top \beta_y - 2\beta_y^\top U^\top (x - \mu))\right)f_Y(y)$$

• Observe the distribution of $Y|U^{\top}X$

$$f_{Y|X}(y|U^{\top}x) \propto f_{U^{\top}X|Y}(U^{\top}x|y)f_{Y}(y)$$

$$\propto \exp\left(-\frac{1}{2}\|U^{\top}x - U^{\top}\mu - \beta_{y}\|^{2}\right)f_{Y}(y)$$

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- This implies that there is no information loss in the projection
 - Under this specific model at least, i.e., $Y \perp X \mid U^{\top}X$

- Now, consider a more general setup
 - ε : noise independent of X (e.g., additive Gaussian)

$$Y = g(v_1^{\top} X, \dots, v_k^{\top} X, \varepsilon)$$

Here, we want to estimate the central subspace

$$\mathsf{span}(v_1,\ldots,v_k)$$

- We make one assumption
 - Inverse regression model satisfies this assumption

Assumption. For any $b \in \mathbb{R}^p$, $\mathbb{E}[b^\top x | v_1^\top x, \dots, v_k^\top x]$ is linear in $v_1^\top x, \dots, v_k^\top x$, i.e., there exist c_0, \dots, c_k such that

$$\mathbb{E}[b^{\top}x|v_1^{\top}x,\dots,v_k^{\top}x] = c_0 + c_1v_1^{\top}x + \dots + v_k^{\top}x$$

- Under the assumption, it holds that
 - See [Sliced Inverse Regression for Dimension Reduction (Li, 1991)]

$$\mathbb{E}[X|Y=y] - \mathbb{E}[X] = \mu_y - \mu \in \mathsf{span}(\Sigma v_1, \dots, \Sigma v_k)$$

- This can be interpreted in a different way
 - For $Z = \Sigma^{-1/2}(X \mu)$, i.e., whitened data

$$\mathbb{E}[Z|Y=y] \in \mathsf{span}(\Sigma^{1/2}v_1,\ldots,\Sigma^{1/2}v_k)$$

- This implies that eigenvectors of $Cov(\mathbb{E}[Z|Y])$ is in the span
 - And vectors orthogonal to the span cannot be the eigenvectors

- Sliced inverse regression
 - Compute $\hat{\mu} = \frac{1}{n} \sum_{i=1}^{n} x_i, \ \hat{\Sigma} = \frac{1}{n} \sum_{i=1}^{n} (x_i \hat{\mu})(x_i \hat{\mu})^{\top}$
 - Whiten data: $z_i = \hat{\Sigma}^{-1/2}(x_i \hat{\mu})$
 - Choose c disjoint intervals $\mathcal{I}_1, \ldots, \mathcal{I}_c$ of the support of y
 - n_j : #samples in \mathcal{I}_j
 - Compute $\hat{\nu}_j = \frac{1}{n_i} \sum_{i:x_i \in \mathcal{I}_j} x_i$, $\hat{\Phi} = \frac{1}{n} \sum_{j=1}^c n_j \hat{\nu}_j \hat{\nu}_j^\top$
 - Compute top-k eigenvectors u_1', \ldots, u_k' of $\hat{\Phi}$
 - Compute $\hat{U}_k = [\Sigma^{-1/2}u_1', \dots, \Sigma^{-1/2}u_k']$

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 - Compute $\hat{U}_k = [\Sigma^{-1/2}u_1', \dots, \Sigma^{-1/2}u_k']$

Remark

- the sliced inverse regression can only approximate a subspace of the central subspace
- Typical choices of slices $\mathcal{I}_1, \dots, \mathcal{I}_c$ are intervals containing a similar #samples

- Now, consider the binary classification setup: y = 1, 2
 - n_j : #sample of class j

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- Objective of Fisher's linear discriminant analysis

$$\arg \max_{u:\|u\|=1} \frac{u^{\top}(\hat{\mu}_1 - \hat{\mu}_2)}{u^{\top}\hat{\Sigma}_1 u + u^{\top}\hat{\Sigma}_2 u}$$

$$\hat{\mu}_j = \frac{1}{n_j} \sum_{i:y_i = j} x_i, \ \frac{1}{n_j} \sum_{i:y_i = j} (x_i - \hat{\mu}_j) (x_i - \hat{\mu}_j)^{\top}$$

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• Solution: $u \propto (\hat{\Sigma}_1 + \hat{\Sigma}_2)^{-1}(\hat{\mu}_1 - \hat{\mu}_2)$

- Extension to general classification setup: y = 1, ..., c
 - n_j : #sample of class j
- Objective

$$\arg\max_{u:\|u\|=1} \frac{u^{\top} \Sigma_B u}{u^{\top} \hat{\Sigma} u}$$

$$\hat{\Sigma}_B = \frac{1}{c} \sum_{j=1}^{c} (\hat{\mu}_j - \hat{\mu}) (\hat{\mu}_j - \hat{\mu})^{\top}$$

- Extension to general classification setup: y = 1, ..., c
 - n_j : #sample of class j

Objective

$$\arg\max_{u:\|u\|=1} \frac{u^{\top} \Sigma_B u}{u^{\top} \hat{\Sigma} u} \Longleftrightarrow \arg\max_{v:\|v\|=1} \frac{v^{\top} \Sigma^{-1/2} \Sigma_B \Sigma^{-1/2} v}{v^{\top} \hat{\Sigma}^{-1/2} \hat{\Sigma} \hat{\Sigma}^{-1/2} v}$$

$$= \arg\max_{v:\|v\|=1} v^{\top} \Sigma^{-1/2} \Sigma_B \Sigma^{-1/2} v$$

$$= \arg\max_{v:\|v\|=1} v^{\top} \hat{\Phi} v$$

$$\hat{\Phi} = \frac{1}{c} \sum_{i=1}^{c} \left(\Sigma^{-1/2} (\hat{\mu}_j - \hat{\mu}) \right) \left(\Sigma^{-1/2} (\hat{\mu}_j - \hat{\mu}) \right)^{\top}$$

 Multiclass LDA reduces to sliced inverse regression with the same #sample for all classes

•
$$n_j = n_{j'}$$

 Hence, it also generalizes for choosing a subspace rather than a single vector in the vanilla FDA for binary classification