

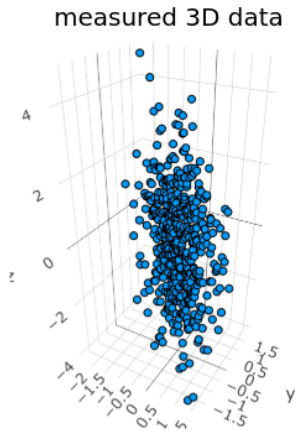
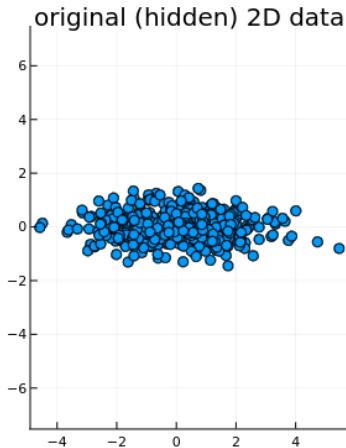
Principal Component Analysis

Johanni Brea

Introduction à l'apprentissage automatique

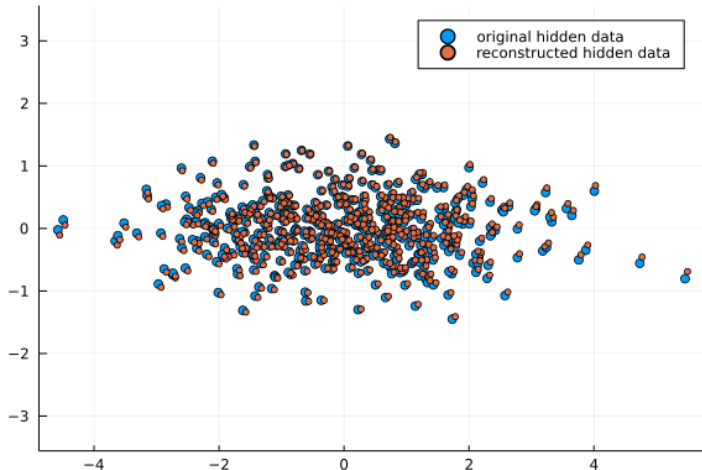
GYMINF 2021

Reconstructing a Generative Model with PCA



- ▶ Assume low-dimensional points are generated by some process, but we do not directly measure this.
- ▶ Instead we measure a linear projection to a higher dimensional space.
- ▶ Goal: Uncover the original data.

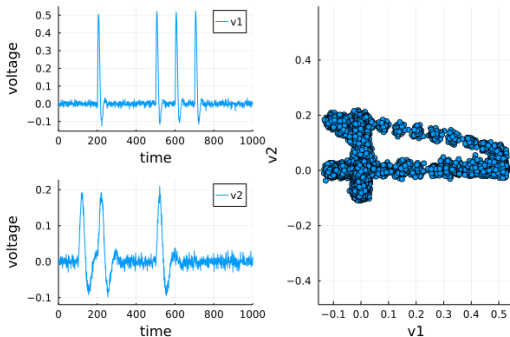
Reconstructing a Generative Model with PCA



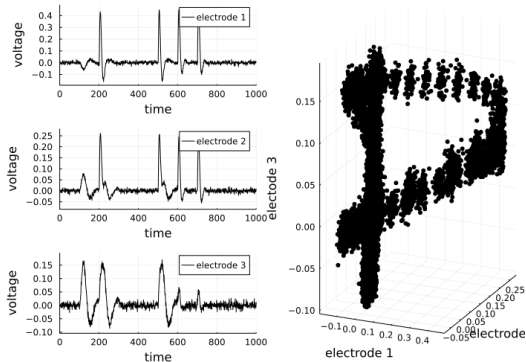
PCA can reconstruct the original data by finding lower-dimensional spaces that are as close as possible to the data.

Reconstructing Neural Activity from Electrode Recordings

Actual neuronal voltages (hidden)

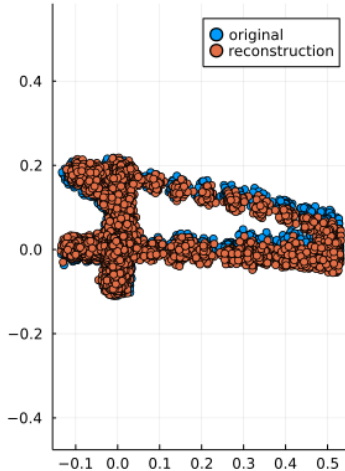
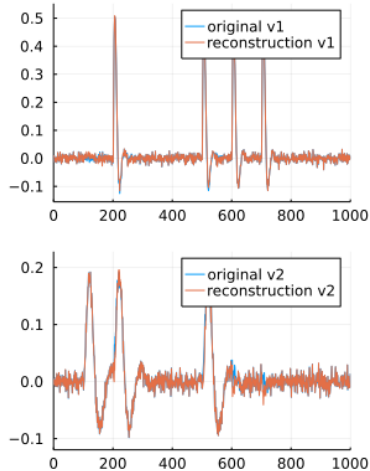


Voltages measured at the electrodes



This is artificially generated data.

Reconstructing Neural Activity from Electrode Recordings



- ▶ PCA can reconstruct the original signal for this artificial data.
- ▶ In practice, related methods like Independent Component Analysis (ICA; not covered in this course) work better.

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First Principal Component

Given x_{ij} for $i = 1, \dots, n, j = 1, \dots, p$
column-wise zero mean $\bar{x}_j = \frac{1}{n} \sum_{i=1}^n x_{ij} = 0$.

First Principal Component

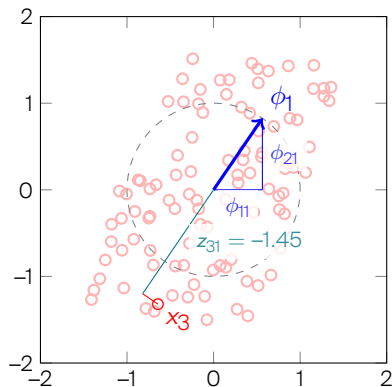
Find the direction onto which the projection of the data has the highest variance.

(projection) **scores** $z_{i1} = \langle \phi_1, x_i \rangle = \sum_{j=1}^p x_{ij} \phi_{j1}$

Find **loadings** $\phi_{11}, \phi_{21}, \dots, \phi_{p1}$ that

$$\underset{\phi_{11}, \dots, \phi_{p1}}{\text{maximize}} \frac{1}{n} \sum_{i=1}^n z_{i1}^2$$

under the constraint $\sum_{j=1}^p \phi_{j1}^2 = 1$.

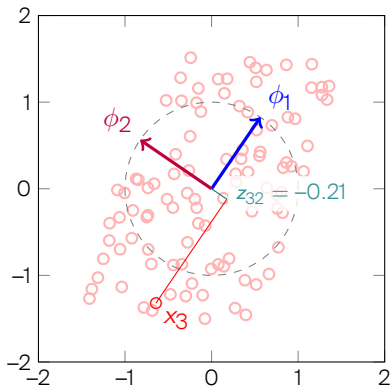


Principal Component Analysis

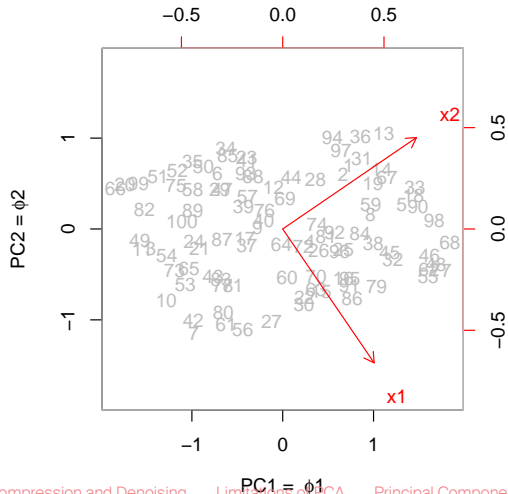
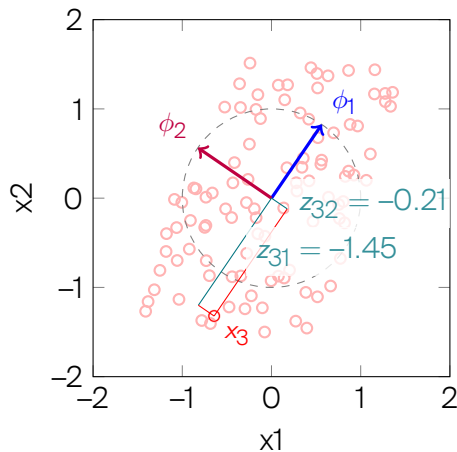
Second Principal Component

Find the direction onto which the projection of the data has the highest variance under the constraint that it is orthogonal to the first PC.

k-th Principal Component Find the direction onto which the projection of the data has the highest variance under the constraint that it is orthogonal to the first $k - 1$ PCs.



Biplots: Visualizing Scores and Loadings Simultaneously



First Principal Component Rewritten in Matrix Notation

$$z_1 = X\phi_1$$

data	X	$n \times p$ matrix	row i contains observation i
loadings	ϕ_1	$p \times 1$ column vector	first PC
scores	z_1	$n \times 1$ column vector	first PC scores of all observation

Find ϕ_1 that maximizes $\frac{1}{n} z_1^T z_1 = \text{maximizes} \frac{1}{n} \phi_1^T X^T X \phi_1$
 $\|\phi_1\|=1$ $\|\phi_1\|=1$

The solution of this optimization problem is the eigenvector of the largest eigenvalue of the covariance matrix $X^T X$.

PCA in Matrix Notation and Relation to SVD

$$Z = X\Phi$$

data	X	$n \times p$ matrix	row i contains observation i
loadings	Φ	$p \times p$ matrix	column j contains PC j
scores	Z	$n \times p$ matrix	column j = scores of PC j for all observations

The columns of the loading matrix Φ are eigenvectors of $X^T X$.

PCA is closely linked to **Singular Value Decomposition** $X = U\Sigma V^T$ where U and V are unitary matrices and Σ is a diagonal matrix. One can show that (see exercises)

$$Z = U\Sigma \quad \text{and} \quad \Phi = V$$

Quiz

Correct or wrong?

- ▶ The scores $z_{11} \approx -1.1$ and $z_{12} \approx 0.1$.
- ▶ The data has the highest variance in direction $\phi_1 \approx (0.65, -0.55, 0.5)$.
- ▶ The two-dimensional linear subspace that is closest to the data is parallel to the X1-X2-plane.

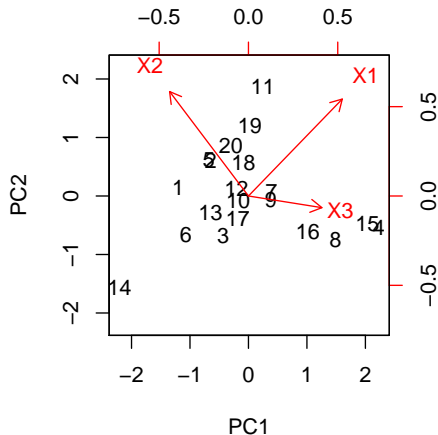
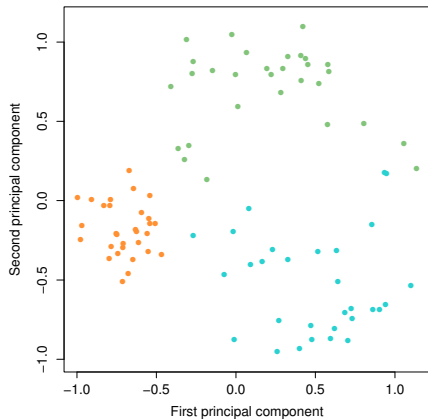
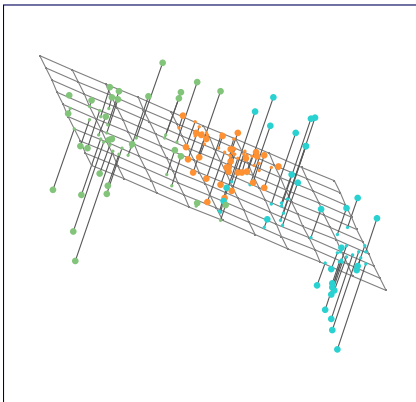


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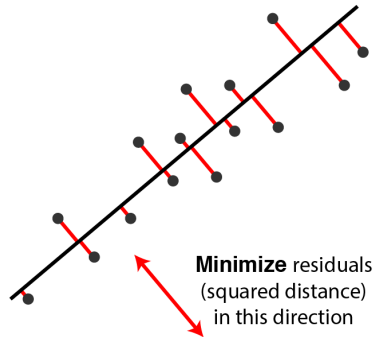
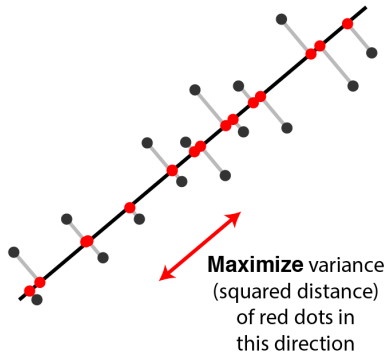
1. PCA: Directions of Largest Variance
- 2. PCA: Linear Subspaces Closest to the Data**
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PCA Provides Linear Subspaces Closest to the Data



The data varies more within the plane than perpendicular to the plane.

Connection Between the Two Interpretations of PCA



Reinterpretation of Loadings and Scores

Lossless transformation: change of basis

standard basis	\mathbb{I}	$p \times p$	columns are standard basis vectors
data	X	$n \times p$	rows are coordinates of points in standard basis
loadings	Φ	$p \times p$	columns are new basis vectors
scores	$Z = X\Phi$	$n \times p$	rows are coordinates of points in new basis
reconstruction	$X = Z\Phi^T$	$n \times p$	rows are coordinates of points in standard basis

Lossy transformation: projection to lower-dimensional space

loadings	Φ_L	$p \times L$	$L = 1, \dots, p$ first columns of Φ are new basis vectors
scores	$Z_L = X\Phi_L$	$n \times L$	rows are coordinates of points in new basis
reconstruction	$X_L = Z_L\Phi_L^T$	$n \times p$	reconstructed coordinates in standard basis

$$\Phi_L \text{ minimizes } \|X - X\Phi_L\Phi_L^T\|_2^2.$$

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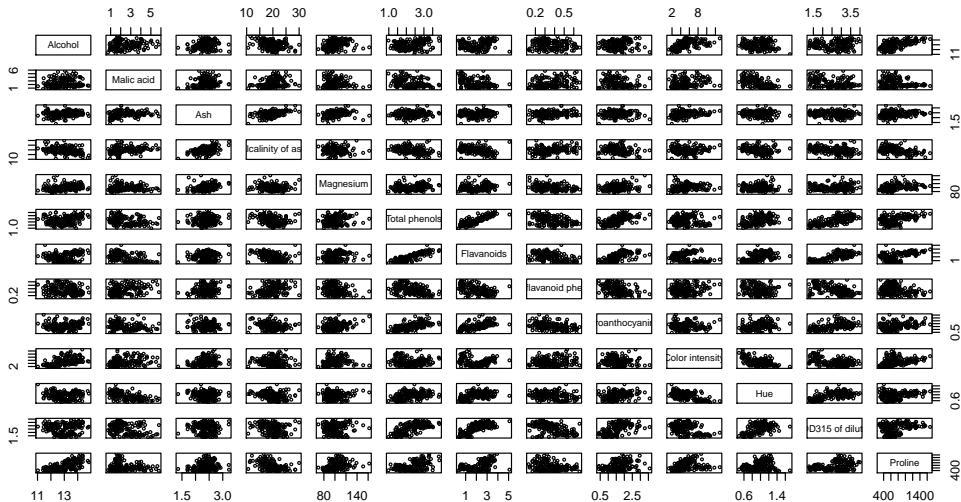
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Exploring the Wine Dataset



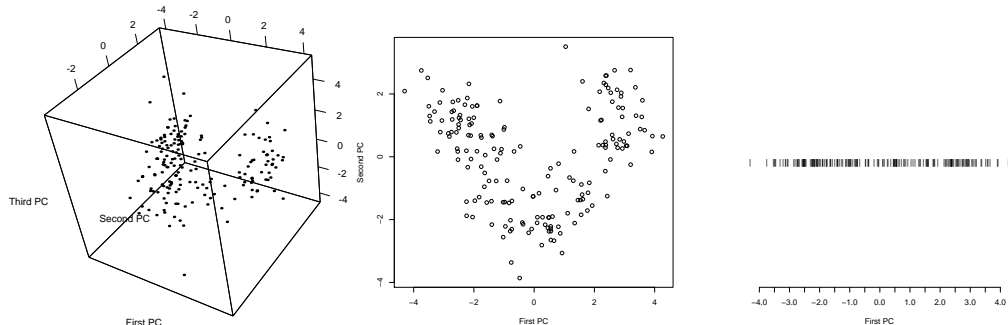
- ▶ 178 different wines from the same region in Italy were chemically analyzed.
- ▶ 13 different measurements per wine: 1) Alcohol 2) Malic acid 3) Ash 4) Alcalinity of ash 5) Magnesium 6) Total phenols 7) Flavanoids 8) Nonflavanoid phenols 9) Proanthocyanins 10) Color intensity 11) Hue 12) OD280/OD315 of diluted wines 13) Proline

Exploring the Wine Dataset



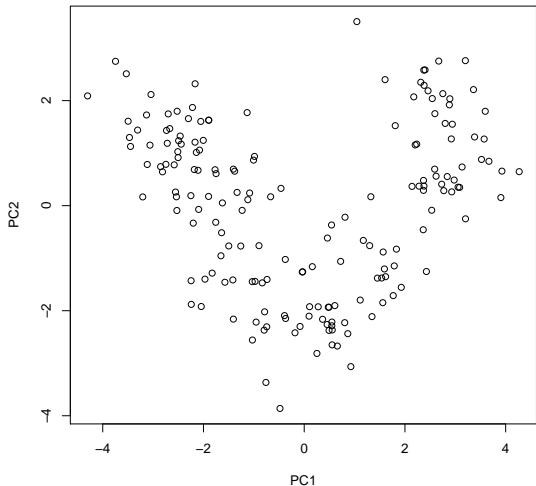
Data: $n = 178$, $p = 13$

Linear Subspaces in the Wine Data



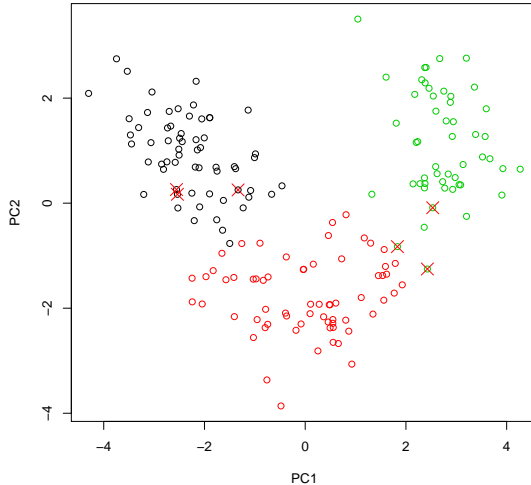
The 3D plot is obtained by projecting the 13D data onto the linear 3D subspace that is closest to the data. From there onwards we project onto the 2D and 1D subspaces closest to the data to obtain the 2D and 1D plots.

Exploring the Wine Dataset



- ▶ PCA seeks a small number of dimensions that are as interesting as possible, where the concept of *interesting* is measured by the amount that the observations vary along each dimension.
- ▶ Projecting the wine data onto the first two Principal Components PC1 and PC2 reveals some structure. Maybe three clusters?

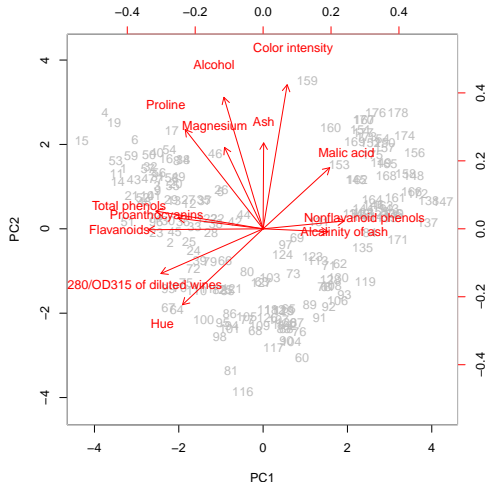
Clustering the Wine Dataset



K-means clustering

- ▶ The colors on in the image on the left indicate the classes found by 3-means clustering.
- ▶ The data actually came from wines of 3 different cultivars. The red crosses indicate data points that actually came from the red wine cultivar. All other observations were “correctly” clustered (without having seen a single class label in the training set!)

A Biplot of the Wine Data



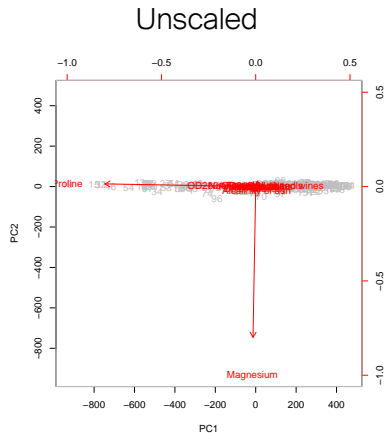
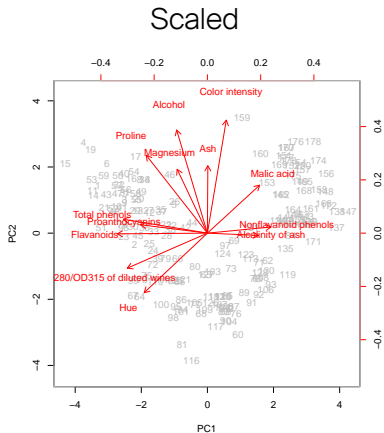
PC1, PC2 scores of all observations in grey.

Loadings in red (axis and the top and right).

The first PC corresponds roughly to the total level of phenols (with subtypes Flavanoids, Non-Flavanoids and Proanthocyanins). The Alkalinity of the ash is strongly correlated.

The second PC corresponds roughly to the amount of ash, with e.g. the color intensity strongly correlated.

Scaling Matters



The direction of highest variance may depend on the choice of units (meters versus millimeters). It is common to preprocess each predictor to have mean 0 and variance 1.

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PCA Decorrelates

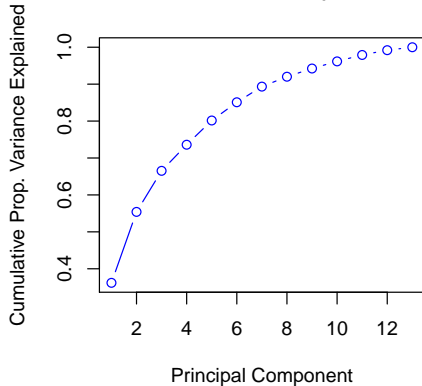
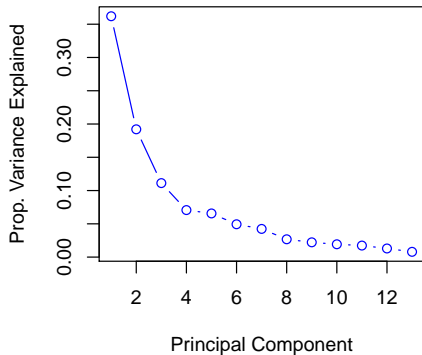
The covariance matrix of the scores is given by the diagonal matrix Λ with the eigenvalues $\lambda_1, \dots, \lambda_p$ of the covariance matrix $X^T X$ on the diagonal (sorted from largest to smallest).

$$Z^T Z = \Phi^T X^T X \Phi = \Phi^T \Lambda \Phi = \Lambda$$

This means
$$\sum_{i=1}^n z_{im} z_{in} = \begin{cases} 0 & m \neq n \\ \lambda_m & m = n \end{cases}$$

How Many Principal Components Matter?

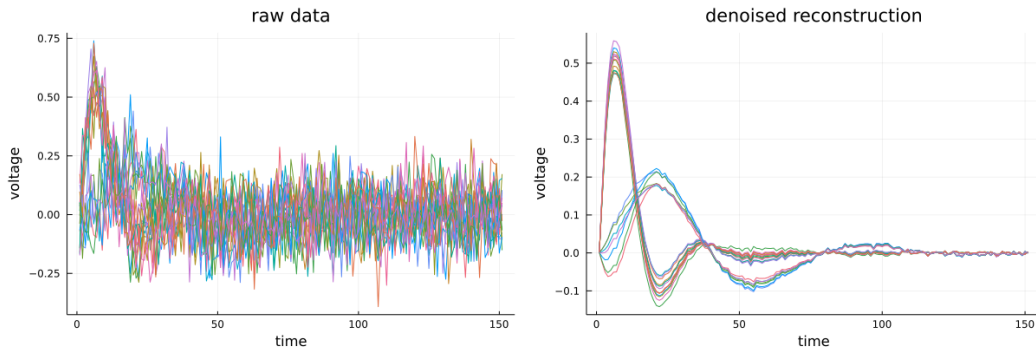
Proportion of Variance Explained (PVE) of PC m :
$$\text{PVE}_m = \frac{\lambda_m}{\sum_{j=1}^p \lambda_j} = \frac{\sum_{i=1}^n z_{im}^2}{\sum_{i=1}^n \sum_{j=1}^p x_{ij}^2}$$



How Many Principal Components Matter?

- ▶ The Proportion of Variance Explained is decreasing, i.e. $PVE_m \geq PVE_{m+1}$.
- ▶ Sometimes the first k components reach a cumulative proportion of variance explained close to 1 and all the other components do not add much anymore.
- ▶ The question of how many principal components matter is not well defined.
- ▶ In practice, we tend to look at the first few components in order to find interesting patterns in the data.
- ▶ If the signal is along the first few principal components and the noise orthogonal to that, we can use this for compression and denoising.

Denoising



This is an artificial dataset with noise. For the reconstruction we assume that the variance along the first to principal components is the signal and the rest is noise, i.e. for the reconstruction we use $L = 2$ and $X_L = Z_L \Phi_L^T$.

Lossy Image Compression with PCA



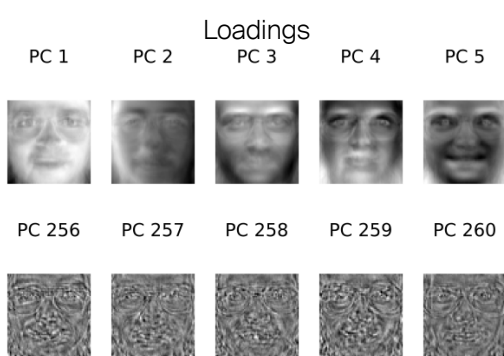
Idea: take each image as a $64 \times 64 = 4096$ dimensional vector, compute the first few principal components Φ_L and scores Z_L and store the data in this format.

If $L = 200$ is sufficient, we store $4096 \times 200 + 400 \times 200 = 899'200$ values. This corresponds to a compression factor of $\frac{1'638'400}{899'200}$. If needed, we can reconstruct the images $X_L = Z_L \Phi_L^T$.

A dataset with $n = 400$ grayscale images of faces with $p = 64 \times 64$ pixels. This corresponds to $400 \times 64^2 = 1'638'400$ pixel values.

In general the compression ratio is
$$\frac{n \times p}{(p + n) \times L}.$$

Lossy Image Compression with PCA



Original and Reconstruction with $L = 200$

original reconstruction

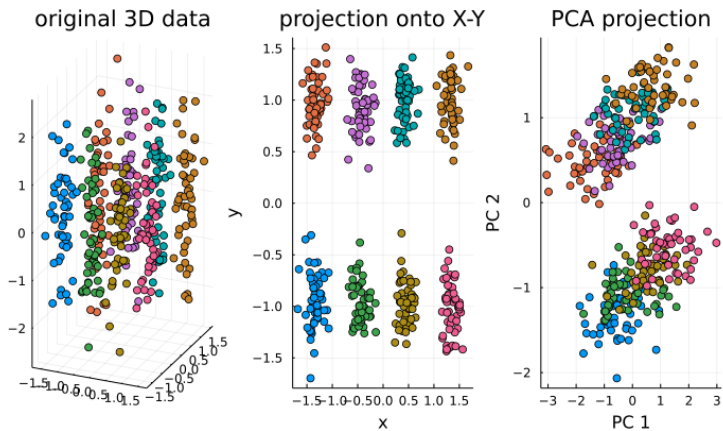


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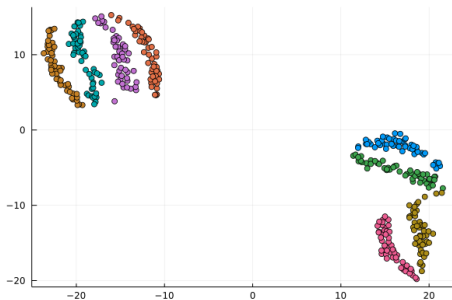
Limitations of PCA

Neighbourhood-relationships can get lost in PCA due to projections.



Alternative: t-SNE

t-Distributed Stochastic Neighbor Embedding (t-SNE)

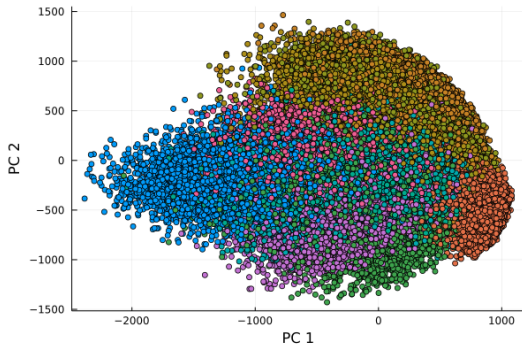


- ▶ t-SNE tries to preserve local neighbourhood-relationships, but the global structure disappears.
- ▶ t-SNE is a gradient descent procedure to find low-dimensional coordinates with the property that the probabilities of being neighbours in the low-dimensional space roughly match the probabilities of being neighbours in the high-dimensional space.
- ▶ Details can be found here:
<https://lvdmaaten.github.io/tsne> and
<https://distill.pub/2016/misread-tsne>

Limitations of PCA

Also in real data there may be clusters that cannot be seen in the first few PCs.

PCA on MNIST images



t-SNE on MNIST images

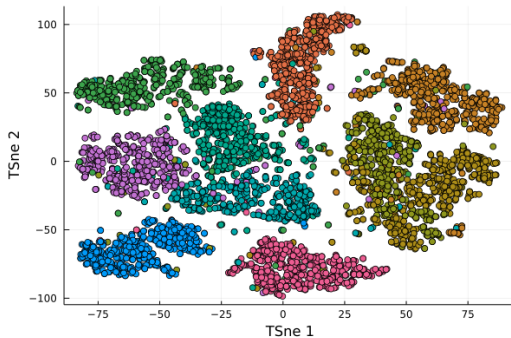


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Principal Component Regression

Unsupervised Feature Learning

PCA can be used to reduce the dimensionality of the data before supervised learning.

Instead of fitting $y_i = \beta_0 + \beta_1 x_{i1} + \dots + \beta_p x_{ip}$ fit

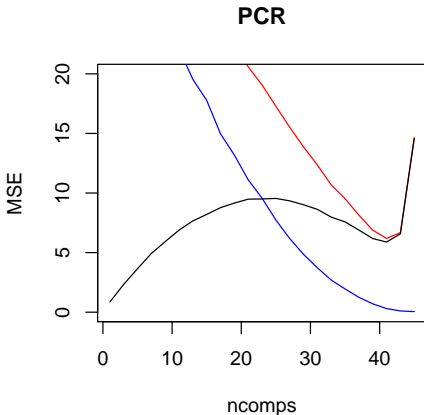
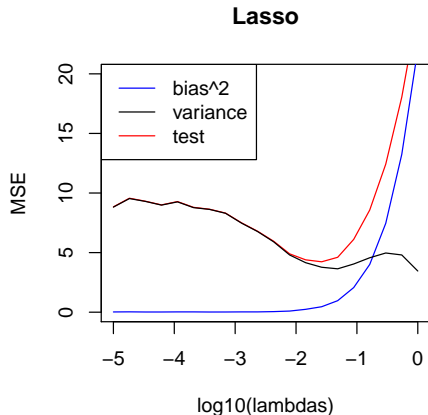
$$y_i = \beta_0 + \beta_1 z_{i1} + \dots + \beta_m z_{im}$$

with $m < p$.

In this case we can choose m with cross-validation.

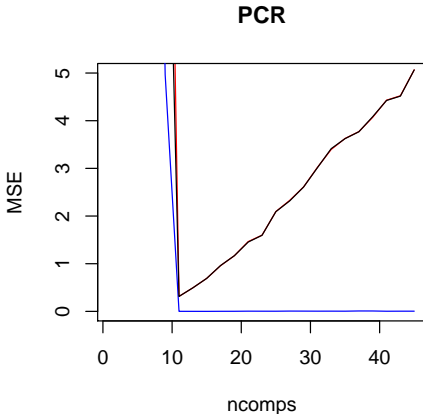
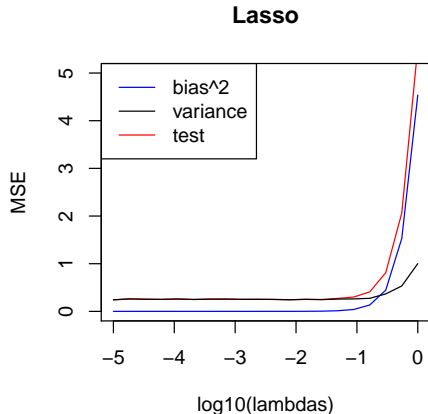
Choosing the Number of PCs in PCR

Choosing a small number of PCs in PCR acts as a regularizer that reduces the variance but may increase the bias



PCR versus Ridge Regression and the Lasso

Typically the Lasso (L1) or Ridge Regression (L2) are at least as good as PCR.



Summary

- ▶ Principal component analysis can be seen as
 1. finding the directions of largest variance in the data,
 2. finding linear subspaces that are closest to the data.
- ▶ The scores and loadings of PCA can be computed with Singular Value Decomposition or by finding the eigenvectors of the covariance matrix.
- ▶ Data with different units should be rescaled before applying PCA.
- ▶ The covariance matrix of the scores is diagonal.
- ▶ The (cumulative) proportion of variance explained can be used to see roughly how many PCs matter.
- ▶ PCA can fail to represent clusters faithfully; t-SNE may be more useful in this case.
- ▶ PCA can be used to reduce the dimensionality of a supervised learning problem, with the number of PCs acting as a regularization tuning parameter.