

# Principal Component Analysis II

PCA: An alternate technique for EDA and feature generation.

# Today's Roadmap

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PCA Review  
Interpreting PCA  
Applications of PCA

# PCA Review

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## PCA Review

Interpreting PCA

Applications of PCA

## [Recap] How to obtain Principal Components

a. Compute SVD on **centered  $X$** :

$$X = U\Sigma V^T$$

b. Take the first  $k$  columns of  $XV$  or  $U\Sigma$



These are the first  $k$  **principal components**.

c. If we wanted to get a **rank- $k$  approximation** of  $X$ :  
( $\sigma_j$ : j-th singular value,  $u_j$ : j-th col of U,  $v_j$ : j-th col of V)

This effectively gives us  $k$  "features" from our  $d$  original features.

```
U[:, 0:k] @ np.diag(S[0:k]) @ Vt[0:k, :]
```

$$X_p = \sum_{j=1}^p \sigma_j u_j v_j^T$$

The diagram shows the rank- $k$  approximation  $X_p = U \Sigma V^T$ . Matrix  $U$  is highlighted with a yellow border. The product  $\Sigma V^T$  is highlighted with an orange border.

For most applications, we directly analyze the principal components themselves.

## [Recap] How much variance is captured

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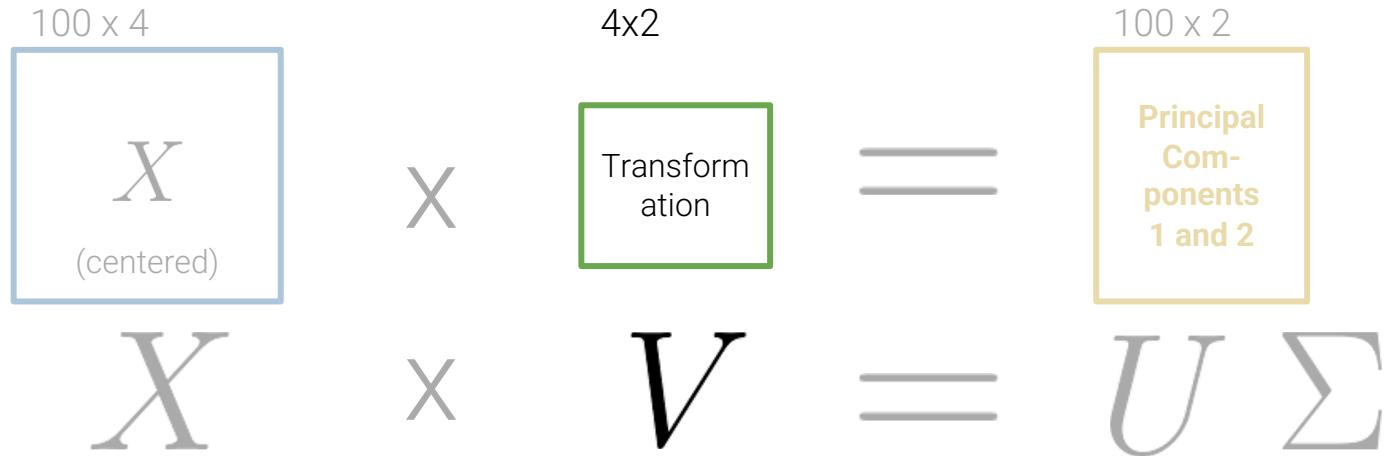
- The principal components are a low-dimension representation that capture as much of the original data's **total variance** as possible.
- **Component scores** tell us how much variance each principal component captures:

$$\frac{\text{i-th component score}}{n} = \frac{(\text{i-th singular value})^2}{\text{total variance}}$$

- The component scores sum to total variance if we **center our data**.

## PCA with SVD

To get the first **two principal components**, first find the SVD  $X = U\Sigma V^T$ .



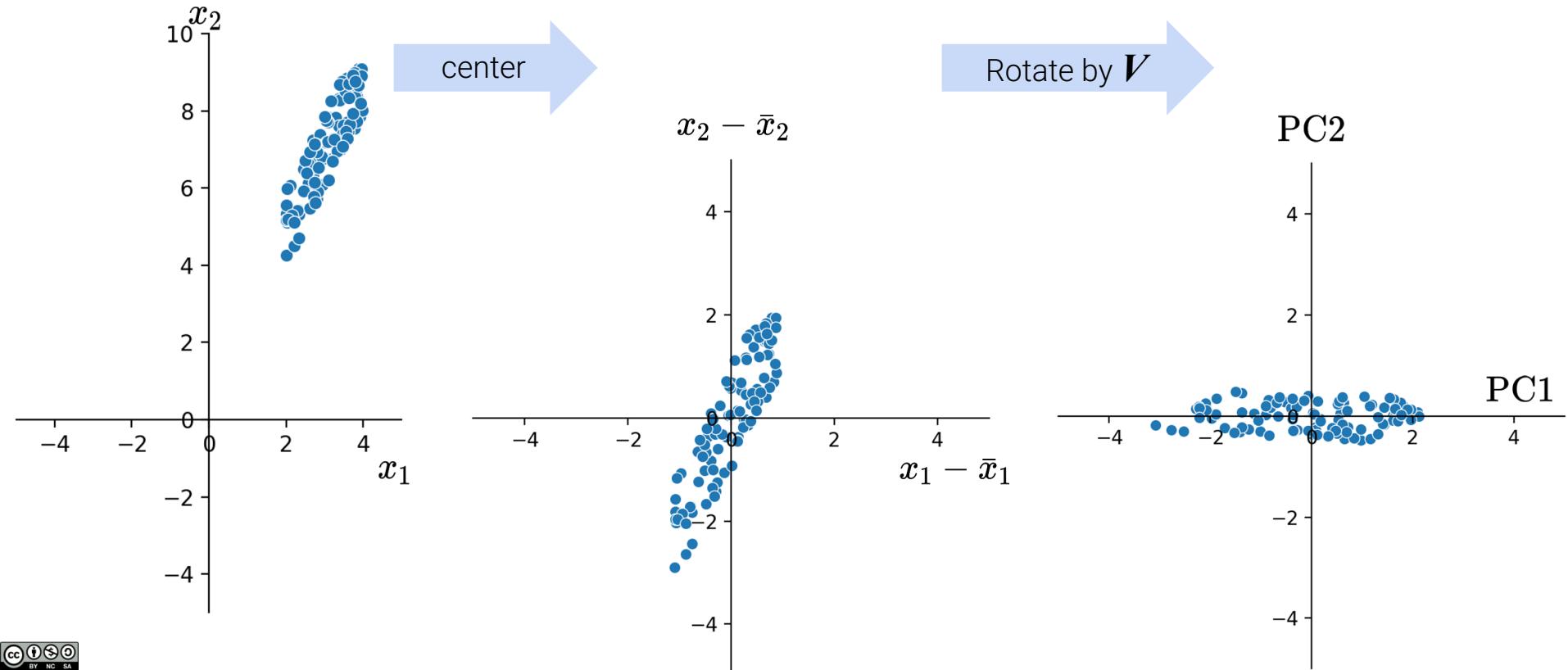
Take the first 2 **columns of  $U\Sigma$**  (or  $XV$ ). These are PC1 and PC2.

why?

The first  $n$  **rows of  $V^T$**  are **directions** for the  $n$  principal components.

## How PCA transforms data, visually

PCA first centers the data matrix, then rotates it such that the direction with the most variation (i.e. the direction that's the most spread-out) is aligned with the x-axis.



## Columns of $V$ are the directions

$$X \in \mathbb{R}^{n \times d}$$
$$V \in \mathbb{R}^{d \times d}$$
$$XV = \begin{bmatrix} | & & | \\ \vdots & \vdots & \vdots \\ x_1 & \dots & x_j & \dots & x_d \\ \vdots & & \vdots & & \vdots \\ | & & | & & | \end{bmatrix} \begin{bmatrix} v_{11} & & & & \\ \vdots & & & & \\ v_{j1} & \dots & v_k & \dots & v_d \\ \vdots & & | & & | \\ v_{d1} & & & & \end{bmatrix}$$

transformation

$$\text{scalar 1} \cdot \begin{bmatrix} | \\ \vdots \\ x_1 \\ \vdots \\ | \end{bmatrix} + \dots + v_{j1} \cdot \begin{bmatrix} | \\ \vdots \\ x_j \\ \vdots \\ | \end{bmatrix} + \dots + v_{d1} \cdot \begin{bmatrix} | \\ \vdots \\ x_d \\ \vdots \\ | \end{bmatrix} = \text{PC1}$$

feature 1

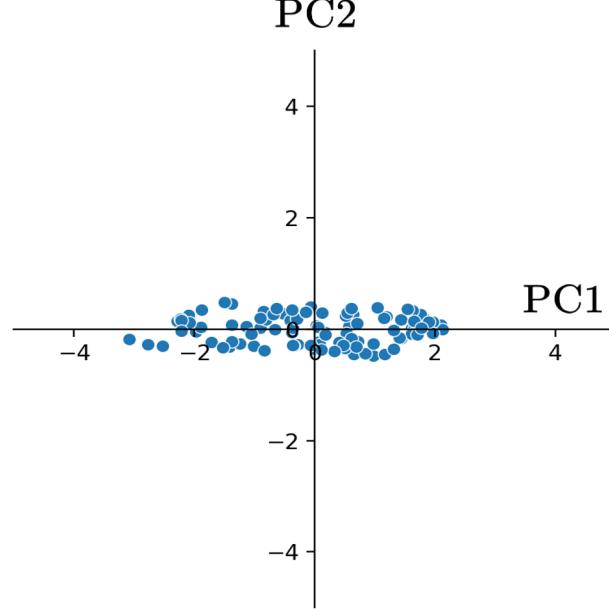
The elements of each **column of  $V$  (row of  $V^T$ )** **rotate** the original feature vectors into a principal component.

The first column of  $V$  indicates **how each feature contributes** (e.g., positively, negatively, etc.) to PC1.

# Principal Components

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- Principal components are all **orthogonal** to each other
  - Why? Recall that columns of  $U$  are orthonormal!
- Principal Components are **axis-aligned**
  - If we plot two PCs on a 2D plane, one will lie on the x-axis, the other on the y-axis
- Principal Components are **linear combinations** of columns in our data  $\mathbf{X}$



# Interpreting PCA

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PCA Review

**Interpreting PCA**

Applications of PCA

## [From last time] Why perform PCA?

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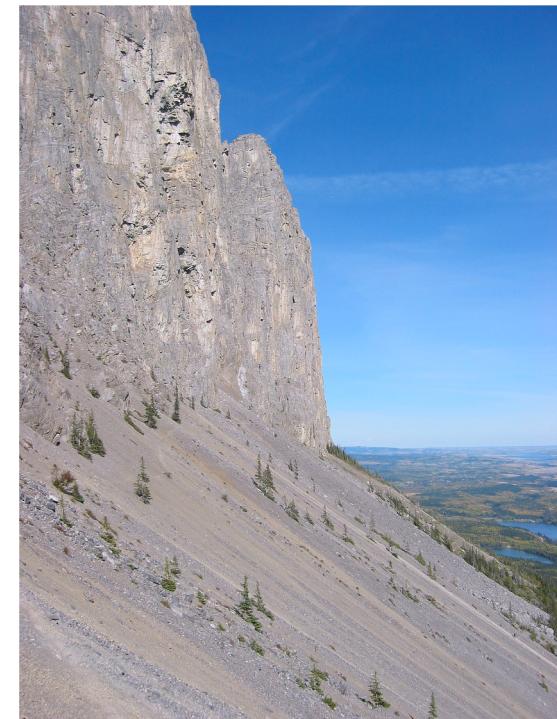
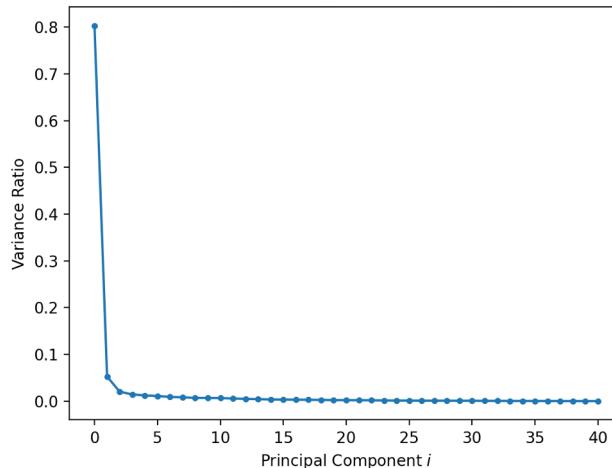
We often perform PCA during the Exploratory Data Analysis (EDA) stage of our data science lifecycle (if we already know what to model, we probably don't need PCA); it helps us with

- Visually identifying **clusters** of similar observations in high dimensions.
- Removing irrelevant dimensions if we suspect that the dataset is inherently low rank. For example, if the columns are **collinear**: there are many attributes but only a few mostly determine the rest through linear associations.
- Finding a small basis for representing variations in complex things, e.g., images, genes.
- Reducing the number of dimensions to make some computation cheaper.

# Scree Plot

If the first two singular values are large and all others are small, then **two dimensions are enough** to describe most of what distinguishes one observation from another. If not, then a PCA scatter plot is omitting lots of information.

A **scree plot** shows the variance ratio captured by each principal component, largest first.



Scree [[wikipedia](#)]

## Biplot

$$v_{11} \cdot \begin{bmatrix} | \\ \vdots \\ x_1 \\ \vdots \\ | \end{bmatrix} + \cdots + v_{j1} \cdot \begin{bmatrix} | \\ \vdots \\ x_j \\ \vdots \\ | \end{bmatrix} + \cdots + v_{d1} \cdot \begin{bmatrix} | \\ \vdots \\ x_d \\ \vdots \\ | \end{bmatrix} = \text{PC1}$$

scalar 1

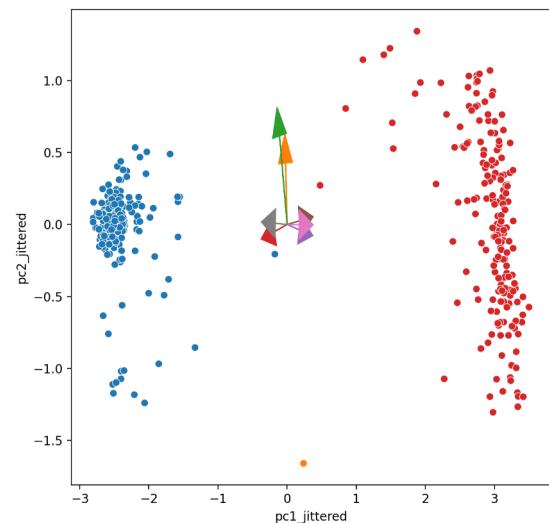
The  $i$ -th column of  $V$  indicates **how each feature contributes** to PC  $i$ .

Biplots superimpose the **directions** onto the plot of PC1 vs. PC2.

Vector  $j$  corresponds to the direction for feature  $j$ , e.g.,  $(v_{1j}, v_{2j})$ .

- There are several ways to scale biplots vectors; in this course we plot the direction itself.
- For other scalings, which can lead to more interpretable directions/loadings, see [[SAS biplots](#)].

Through biplots, we can interpret how features correlate with the principal components shown: positively, negatively, or not much at all.

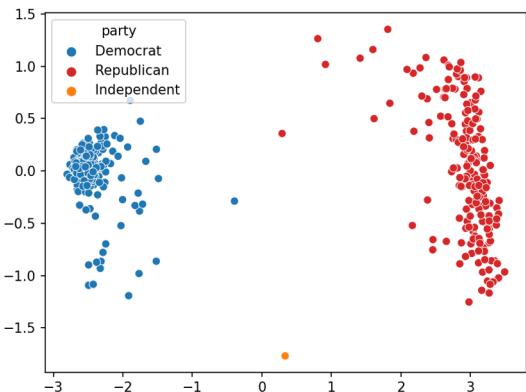


# Summary: Plots based on PCA

## PCA Plot

Scatter plot of PC1 against PC2

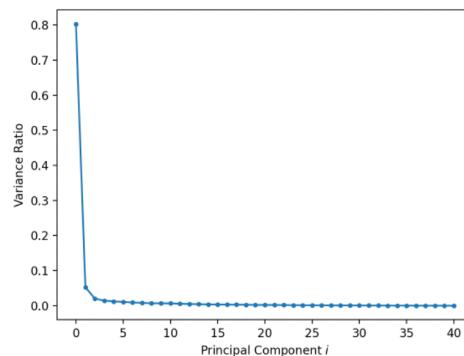
- Helps us assess similarities between our data points and if there are any clusters in our dataset.



## Scree Plot

Line plot showing the **variance ratio** captured by each principal component, largest first.

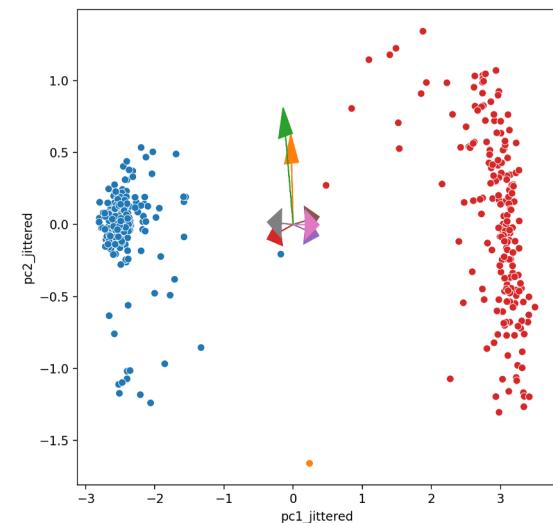
- If first two is large enough, we know PCA plot is good representation of data
- “Elbow” method to assess how many PCs to use



## Biplot

PCA plot + **directions** of feature importance for PC1 and PC2

- All benefits from PCA plot, and
- Shows how much some features contribute to PC1/2



# Applications of PCA

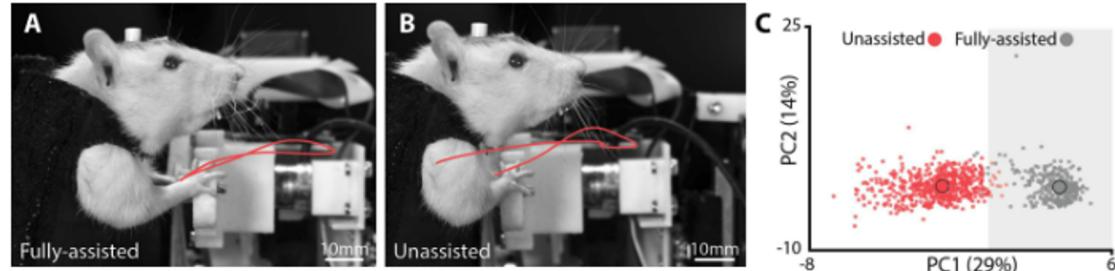
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PCA Review  
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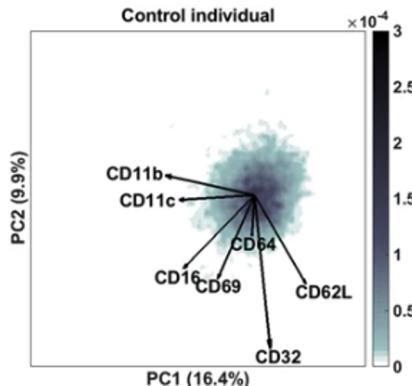
# PCA in Biology

PCA is commonly used in biomedical contexts, which have many named variables!

1. To cluster data ([Paper 1](#), [Paper 2](#))



2. To identify correlated variables ([interpret](#) rows of  $V^T$  as linear coefficients) ([Paper 3](#)). Uses [biplots](#).



## Why perform PCA?

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We often perform PCA during the **Exploratory Data Analysis** (EDA) stage of our data science lifecycle (if we already know what to model, we probably don't need PCA); it helps us with

- Visually identifying clusters of similar observations in high dimensions.
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# Image Classification

Fashion-MNIST: a Novel Image Dataset for Benchmarking Machine Learning Algorithms. Han Xiao, Kashif Rasul, Roland Vollgraf. arXiv:1708.07747

<https://github.com/zalandoresearch/fashion-mnist>



In **machine learning**, PCA is often used as a **preprocessing step** prior to training a supervised model..

## Demo

Lecture 23

# Principal Component Analysis II

Content credit: [Acknowledgments](#)

