

# CS 260: Foundations of Data Science

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HAVERFORD  
COLLEGE

# Lab 7 notes

Logistic regression cost function:

$$J(\vec{w}) = - \sum_{i=1}^n [y_i \log(h_{\vec{w}}(\vec{x}_i)) + (1 - y_i) \log(1 - h_{\vec{w}}(\vec{x}_i))]$$

if  $h_{\vec{w}}(\vec{x}_i) = 0$  or  $1 - h_{\vec{w}}(\vec{x}_i) = 0 \rightarrow$  skip  $\log(0)$  or add 0

# Outline for today

- Dimensionality reduction
- PCA for data visualization

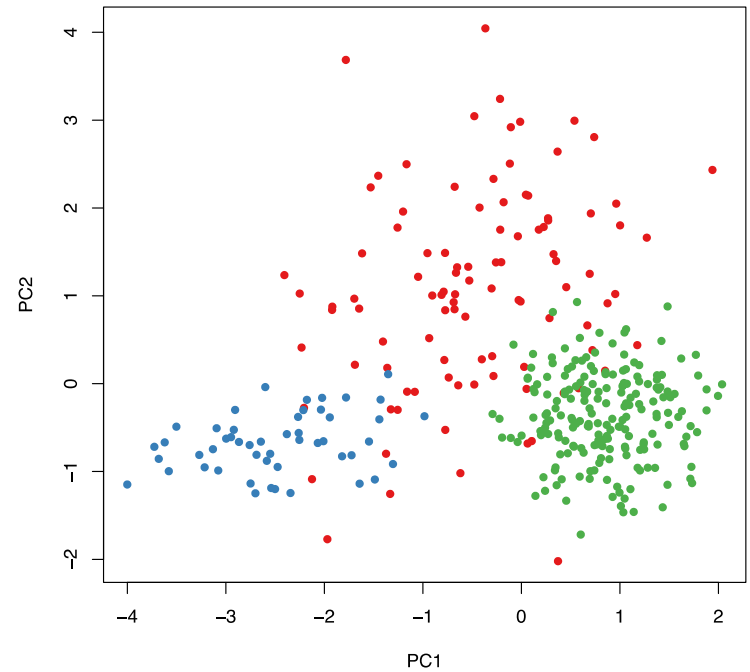
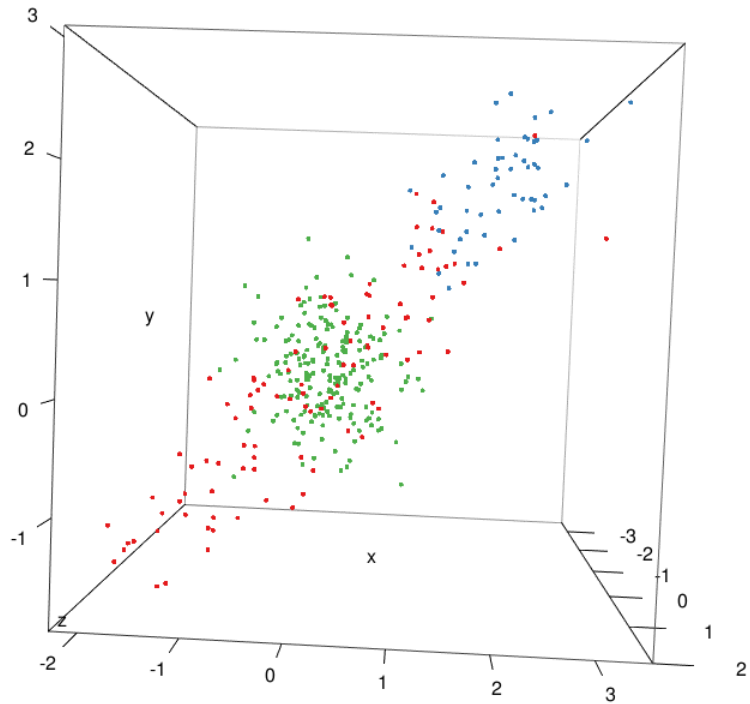
# Outline for today

- Dimensionality reduction
- PCA for data visualization

# Principal Component Analysis (PCA)

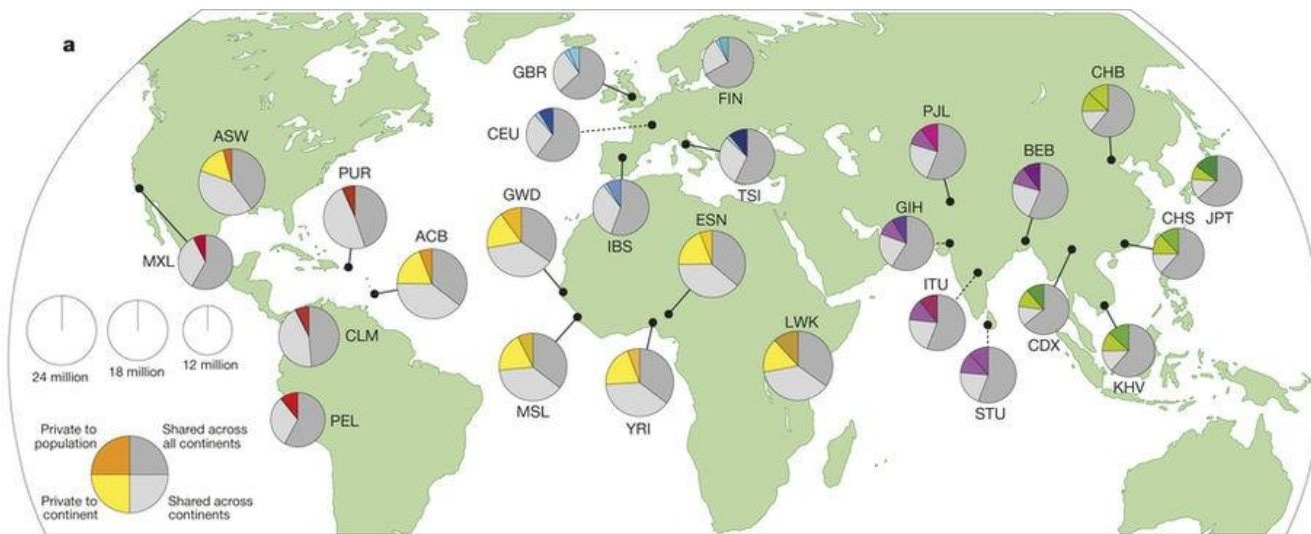
- Transforms  $p$ -dimensional data so that the new first dimension explains as much of the variation as possible, the new second explains as much of the remaining variation as possible, and so on
- PCA is a linear transformation
- Typically, we look at the first few dimensions of the transformed data as a means of dimensionality reduction and visualization
- PCA is often used for:
  - Data visualization
  - Infer qualitative relationships between groups

# PCA Example



# The 1000 Genomes project

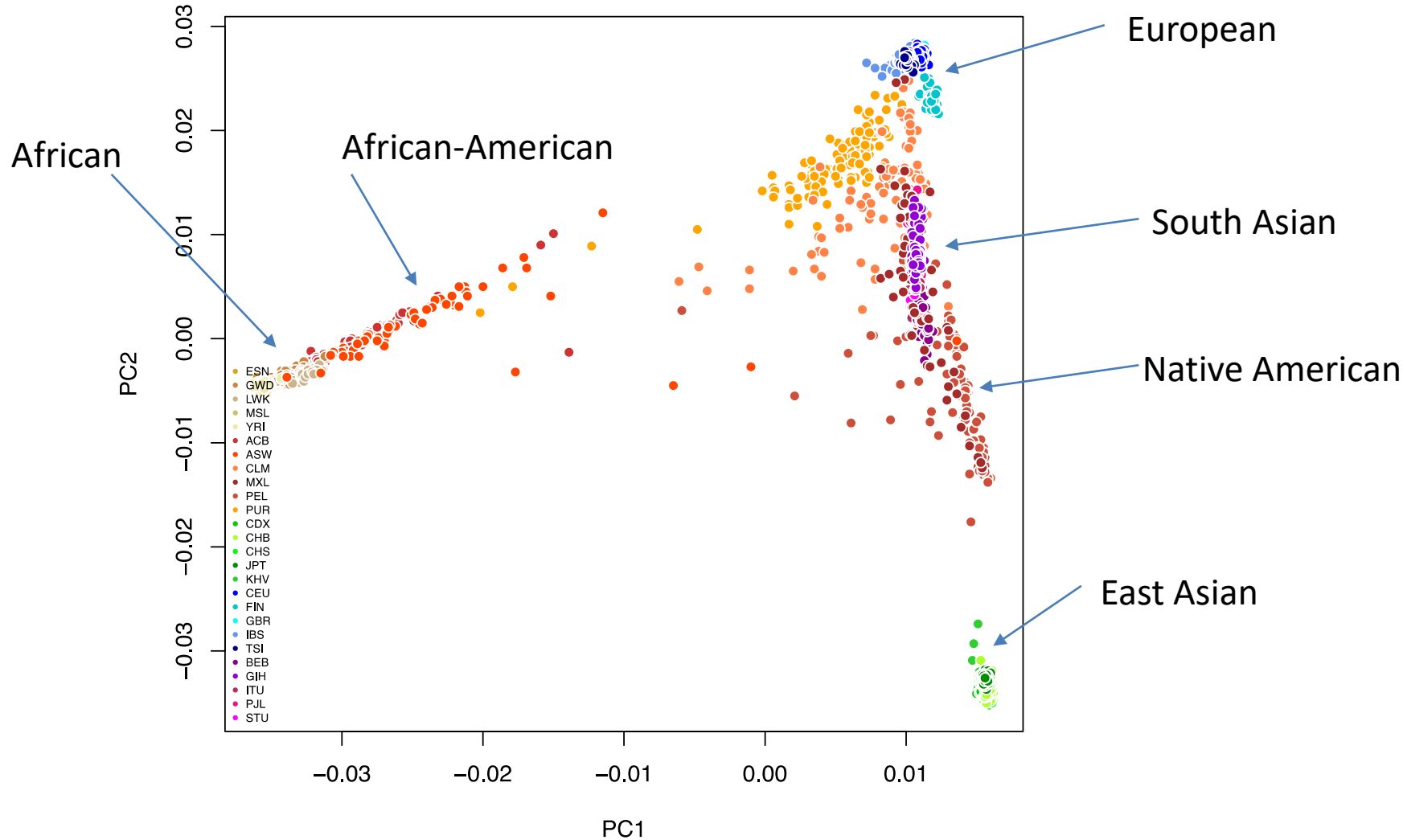
- Whole-genome **sequence data** from 2504 individuals from 26 populations
- A catalog of human genetic variation, useful as a reference or **imputation** panel
- Completely public. Download from <ftp://ftp-trace.ncbi.nih.gov/1000genomes/>



#bcftools annotateCommand=annotate -x INFO 20130502_phase3_final/ALL.chr20.phase3_shapeit2_mvncall_integrated_v5.20130502.genotypes.vcf.gz; Date=Fri Jan 19 19:20:16 2018																						
#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	HG00096	HG00097	HG00099	HG00100	HG00101	HG00102	HG00103	HG00105	HG00106	HG00107	HG00108	HG00109	HG00110	HG00111
20	60343	.	G	A	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60419	.	A	G	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60479	rs149529999		T	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60522	rs150241001		T	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60568	.	A	C	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60571	rs116145529		C	A	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60579	.	G	A	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60649	.	A	G	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60778	.	A	G	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60795	rs184056664		G	C	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60808	.	G	A	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60810	.	G	GA	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60826	.	A	G	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60828	rs187713677		T	G	100	PASS	.	GT	0 0	0 0	0 1	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60864	.	G	A	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60895	.	A	G	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	60916	.	G	T	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	61044	.	C	A	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	61070	.	C	T	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	61098	rs6078030		C	T	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 1	0 0	1 0	0 0	0 0	0 0	0 0	0 1	0 0
20	61118	.	A	G	100	PASS	.	GT	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0
20	61138	rs140305189		C	CT	100	PASS	.	GT	0 0	0 1	0 0	0 0	0 1	0 0	0 0	0 1	0 0	0 0			

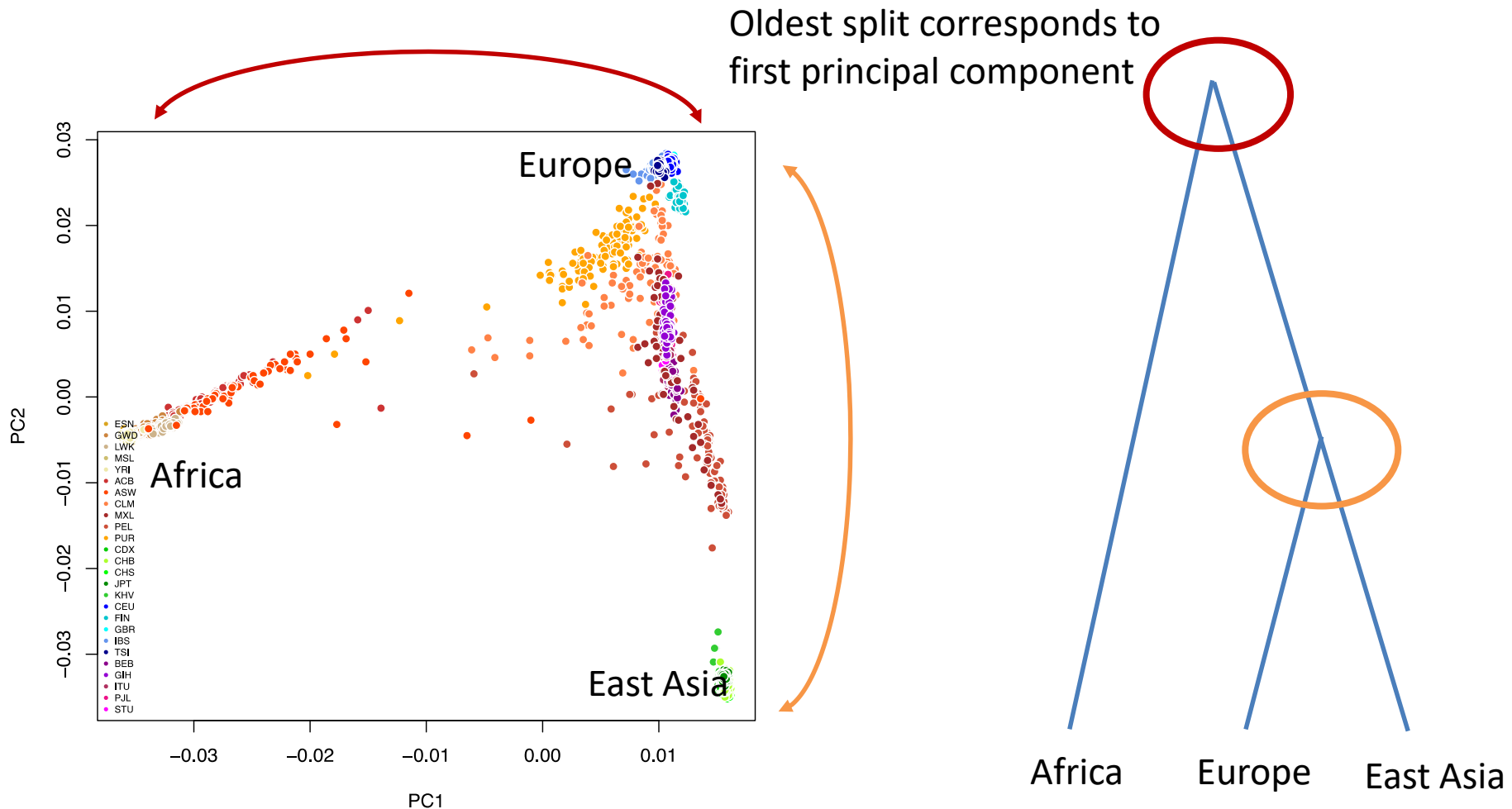


# Global population structure



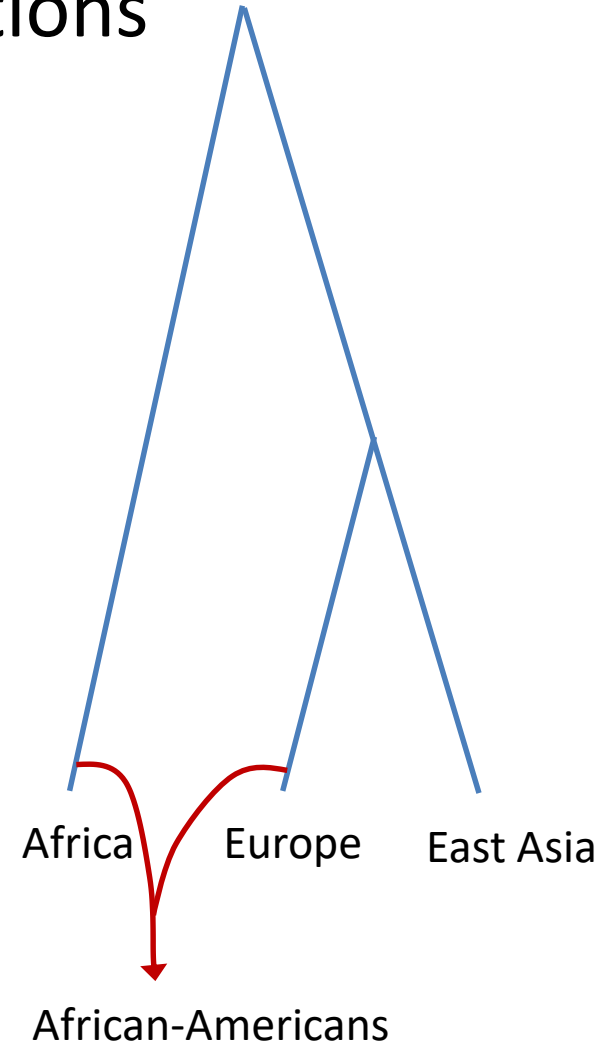
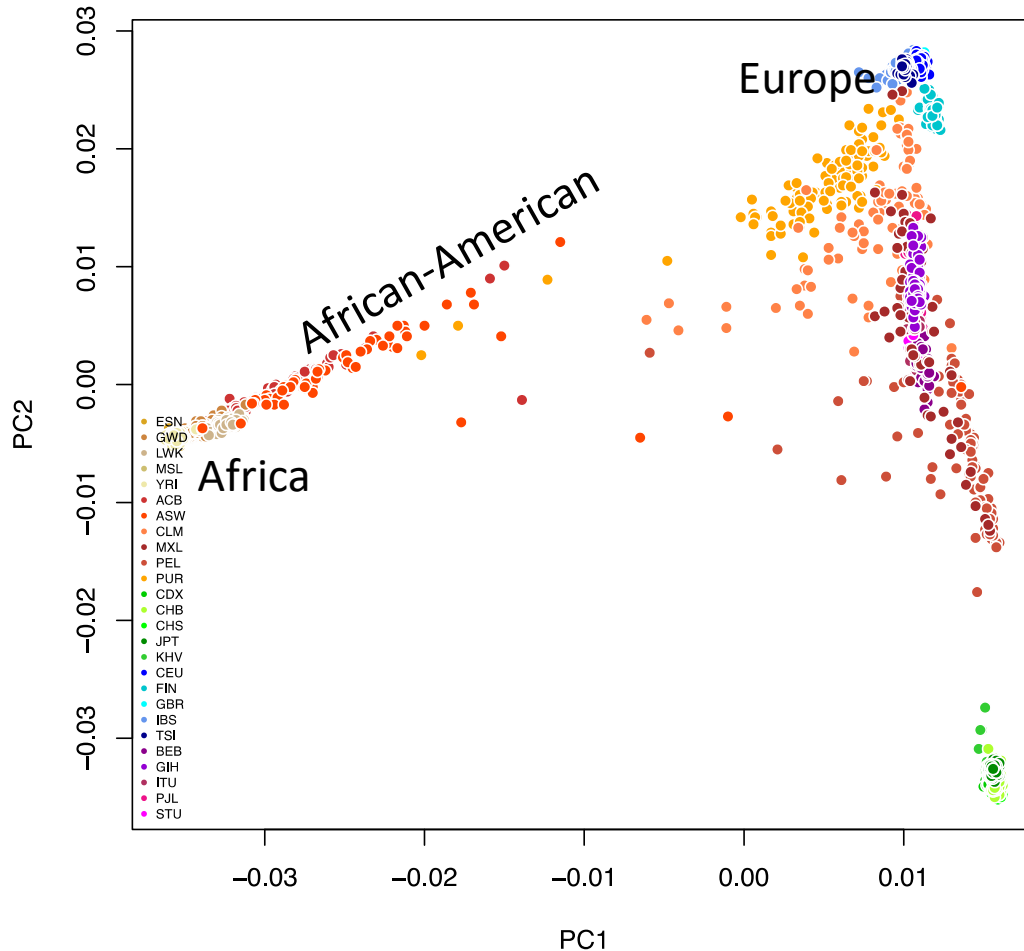
# What causes these patterns?

## 1. Populations **splits** separate populations

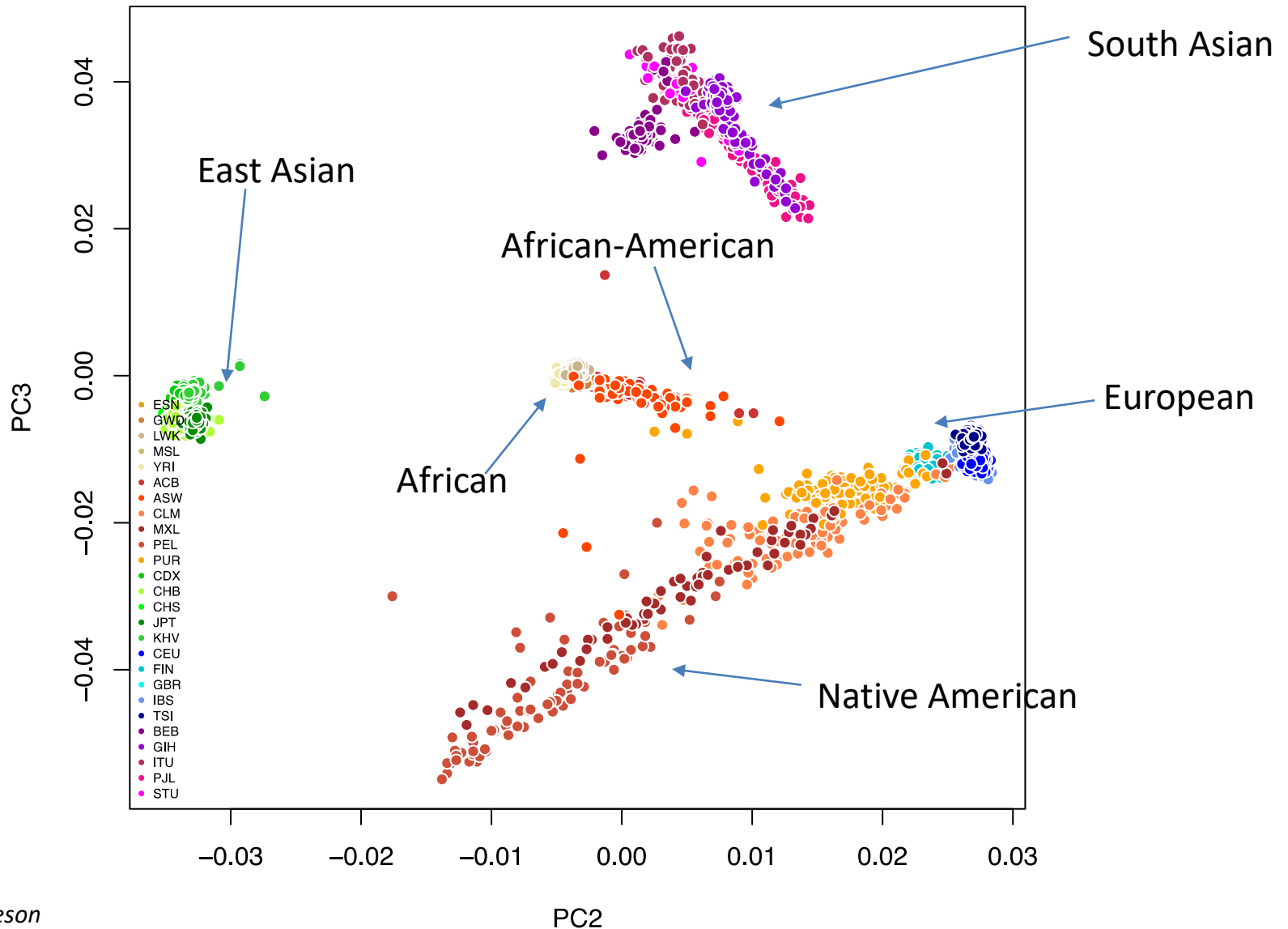


# What causes these patterns?


## 2. **Admixture** merges populations



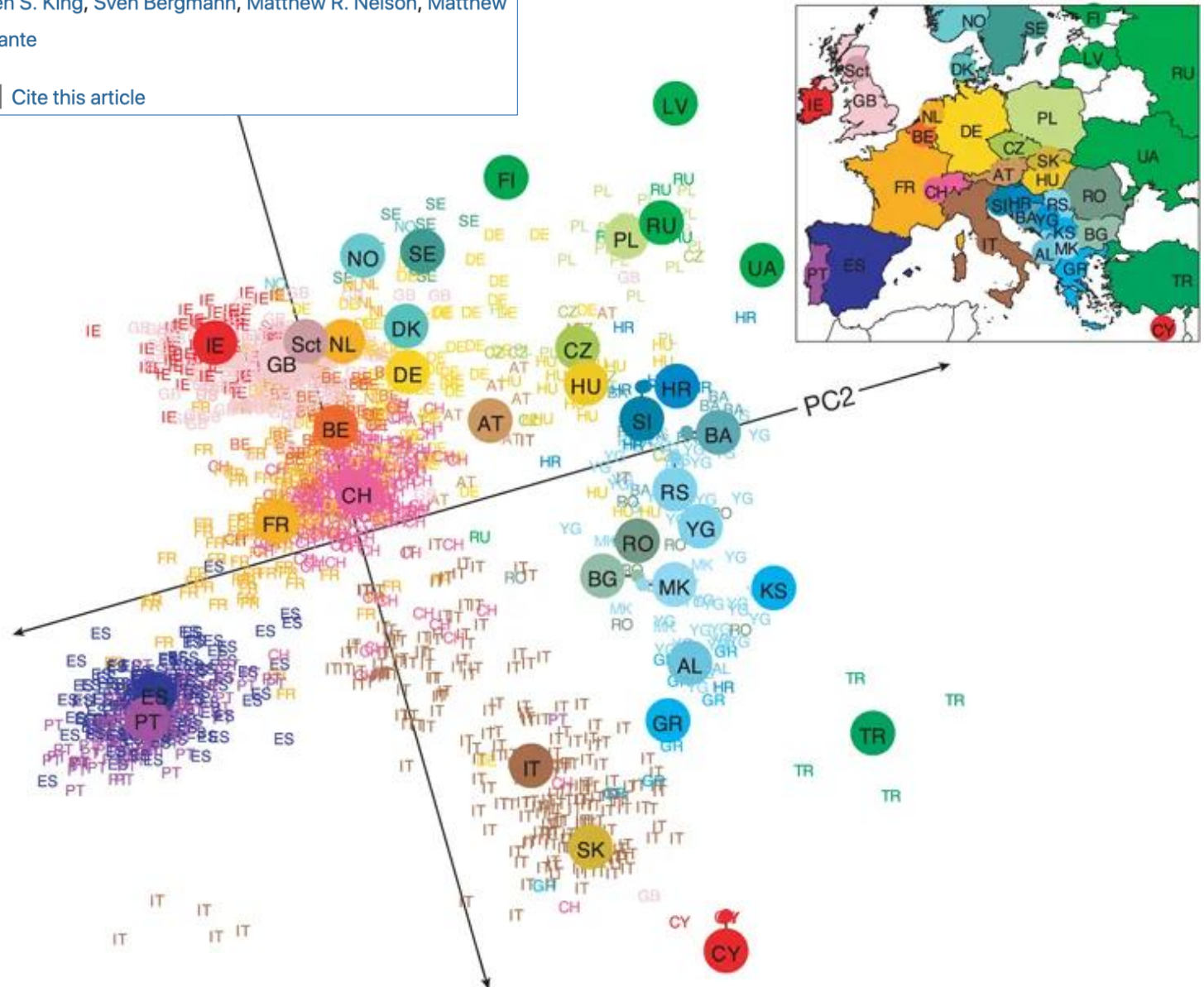
# Global population structure



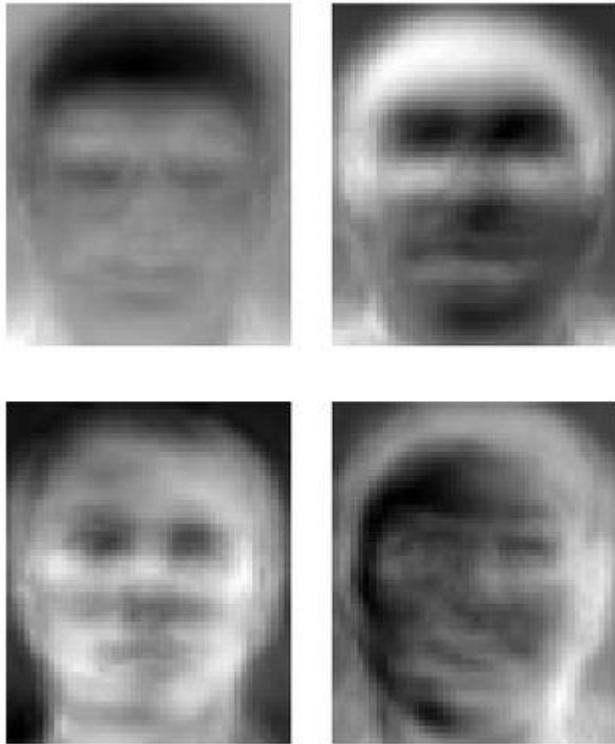
# Genes mirror geography within Europe

John Novembre , Toby Johnson, Katarzyna Bryc, Zoltán Kutalik, Adam R. Boyko, Adam Auton, Amit Indap, Karen S. King, Sven Bergmann, Matthew R. Nelson, Matthew Stephens & Carlos D. Bustamante

*Nature* **456**, 98–101(2008) | [Cite this article](#)



# PCA application: Eigenfaces



- Low-dimensional representation of face images
- Used for face recognition/classification

*Wikipedia*

# Outline for today

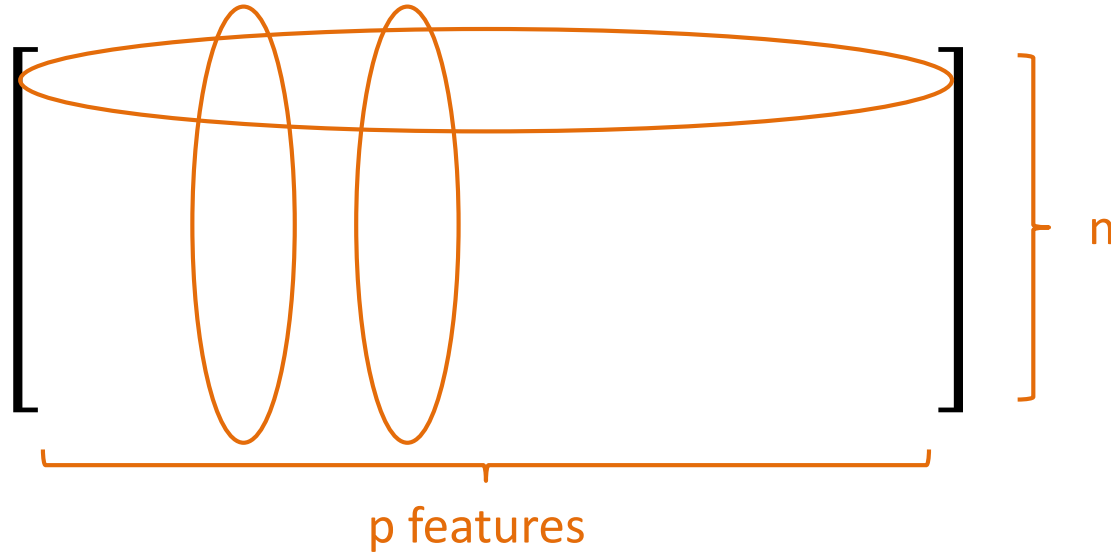
- Dimensionality reduction
- PCA for data visualization

# PCA Algorithm

## Step 1:

$$X_{orig} =$$

p >> n




## Goal: Create nx2 matrix for visualization



# PCA Algorithm

Step 2: Subtract off column-wise mean

$$X_{orig} = \begin{bmatrix} 2 & 1 \\ 3 & 3 \end{bmatrix}$$



$\overline{x_1} = 2.5$        $\overline{x_2} = 2$

$$X = \begin{bmatrix} -0.5 & -1 \\ 0.5 & 1 \end{bmatrix}$$

# PCA Algorithm

Step 3: Compute covariance matrix A

$$A = \begin{bmatrix} \text{cov}(f, f) & \text{cov}(f, g) \\ \text{cov}(g, f) & \text{cov}(g, g) \end{bmatrix}$$

↓  
square & symmetric

2 features f, g

Runtime  $O(np^2)$

$$\text{cov}(f, g) = \frac{1}{n-1} \sum_{i=1}^n (f_i - \bar{f})(g_i - \bar{g})$$

$$\text{cov}(f, f) = \text{var}(f) = \frac{1}{n-1} \sum_{i=1}^n (f_i - \bar{f})^2$$

Handout 15, page 1

Handout 16

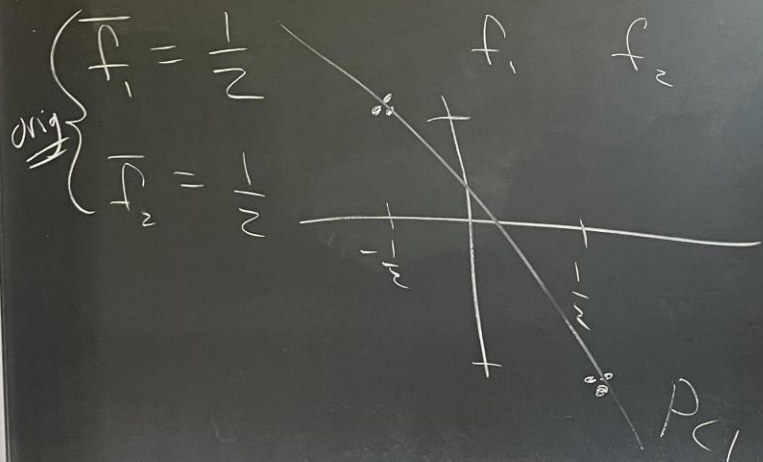
Step 1  
4  
2

X =

$$\begin{bmatrix} -1/2 & 1/2 \\ -1/2 & 1/2 \\ -1/2 & 1/2 \\ 1/2 & -1/2 \\ 1/2 & -1/2 \\ 1/2 & -1/2 \end{bmatrix}$$

$f_1$

$f_2$



Step 3

$$A = \begin{bmatrix} \text{var}(f_1) & \text{cov}(f_1, f_2) \\ \text{cov}(f_2, f_1) & \text{var}(f_2) \end{bmatrix}$$

$$\bar{f}_1 = 0$$

$$\bar{f}_2 = 0$$

$$\text{cov}(f_1, f_2) = \frac{1}{6-1} \left( -\frac{1}{2} \cdot \frac{1}{2} \right) \cdot 6$$

$$= -\frac{3}{10}$$

$$\Rightarrow A = \begin{bmatrix} 3/10 & -3/10 \\ -3/10 & 3/10 \end{bmatrix}$$

# PCA Algorithm

Step 4: Compute eigenvalues and eigenvectors of A

$$A\vec{v} = \lambda\vec{v}$$

eigenvalue

eigenvector


$$\det(A - \lambda I) = 0$$

Solve for  $\lambda$  and plug into first equation to solve for  $\vec{v}$

# PCA Algorithm

Step 5: Sort eigenvectors by eigenvalues (high->low)

$$W = \begin{bmatrix} \overset{\lambda_1}{\vdots} & \overset{\lambda_2}{\vdots} & \dots & \vdots \\ \overrightarrow{v_1} & \overrightarrow{v_2} & \dots & \overrightarrow{v_r} \\ \vdots & \vdots & \dots & \vdots \end{bmatrix}$$

 first eigenvector

$p \times r$   
usually  $r = 2$

And compute the transformed data:

$$T_{n \times r} = X_{n \times p} W_{p \times r}$$

Handout 15, page 2

Step 4

$$\det(A - \lambda I) = 0$$

$$\begin{bmatrix} 3/10 & -3/10 \\ -3/10 & 3/10 \end{bmatrix} - \lambda \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} = 0$$

6

$$\det \begin{pmatrix} 3/10 - \lambda & -3/10 \\ -3/10 & 3/10 - \lambda \end{pmatrix} = 0$$

$$\left(\frac{3}{10} - \lambda\right)^2 - \left(\frac{3}{10}\right)^2 = 0$$
$$\cancel{\left(\frac{3}{10}\right)^2} - 2 \cdot \frac{3}{10} \lambda + \lambda^2 - \cancel{\left(\frac{3}{10}\right)^2} = 0$$

$$\det \begin{bmatrix} a & b \\ c & d \end{bmatrix} = ad - bc$$

$$\lambda^2 - \frac{3}{5} \lambda = 0$$

$$\lambda \left( \lambda - \frac{3}{5} \right) = 0 \Rightarrow$$

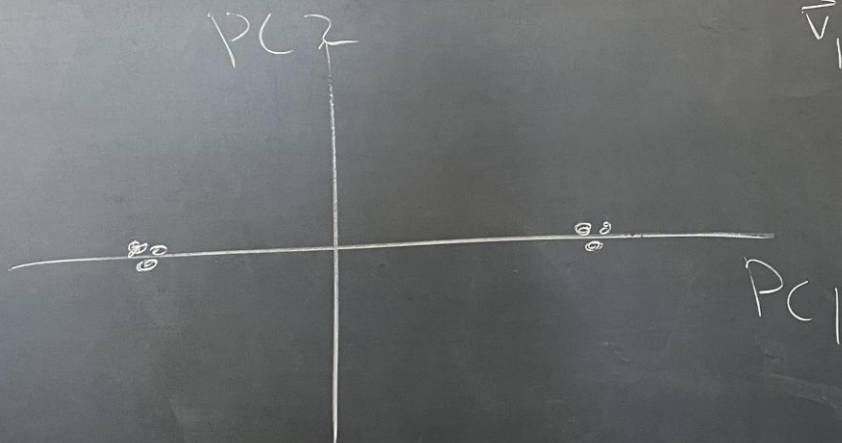
$$\lambda_1 = \frac{3}{5}$$
$$\lambda_2 = 0$$

$$A\vec{v} = \lambda \vec{v}$$

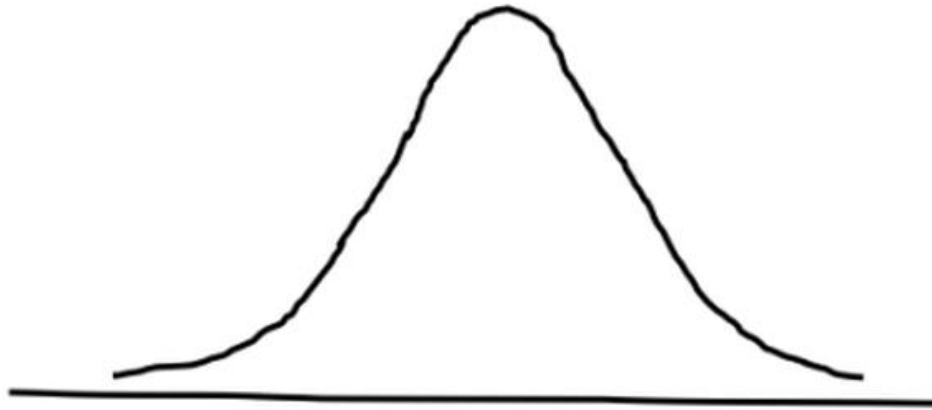


$$T_2 = XW_2 = \begin{bmatrix} -1/2 & 1/2 \\ -1/2 & 1/2 \\ -1/2 & 1/2 \\ 1/2 & -1/2 \\ 1/2 & -1/2 \\ 1/2 & -1/2 \end{bmatrix} \begin{bmatrix} 1 \\ -1 \end{bmatrix} \begin{bmatrix} 1 \\ 1 \end{bmatrix} = \begin{bmatrix} -1 & 0 \\ -1 & 0 \\ -1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 1 & 0 \end{bmatrix}$$

$\lambda_1 = 3/5 \quad \lambda_2 = 0$   
 $\vec{v}_1 \quad \vec{v}_2$



# Looking ahead: Statistics next week!



Normal Distribution



Paranormal Distribution