

# CS 260: Foundations of Data Science

Prof. Sara Mathieson

Spring 2025



**HVERFORD**  
COLLEGE

- Reminder: **pair work is required** for the final project – find a partner ASAP or email me!
- **Lab 7 and project proposal** (both short)
  - Due Wednesday

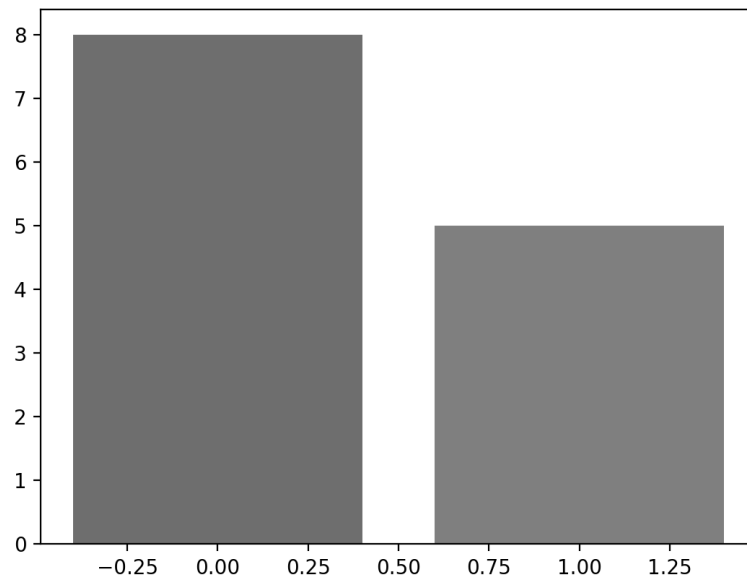
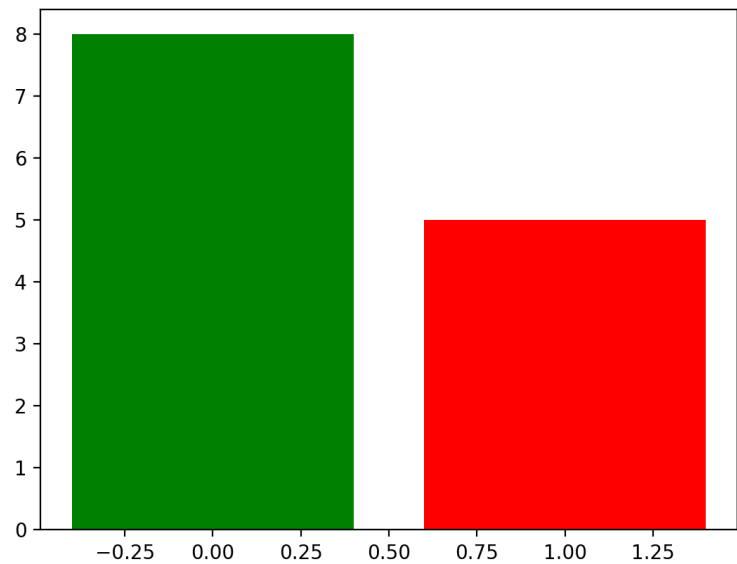
# Outline

- Finish data visualization intro
- Dimensionality reduction
- PCA for data visualization

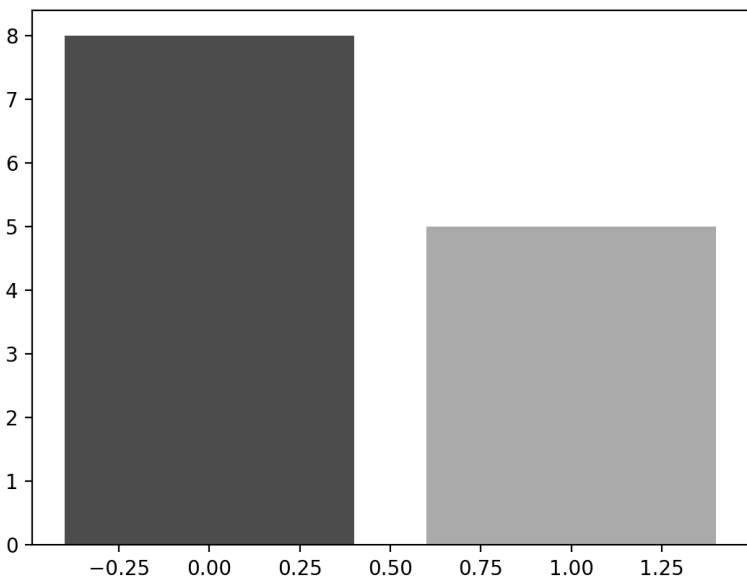
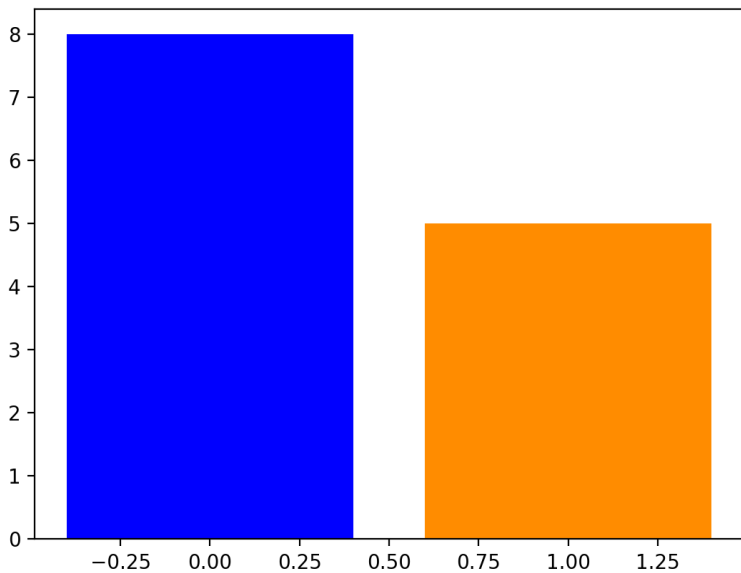
# Outline

- Finish data visualization intro
- Dimensionality reduction
- PCA for data visualization

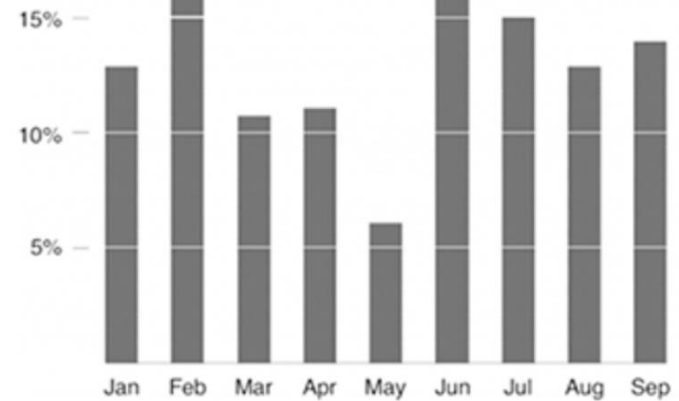
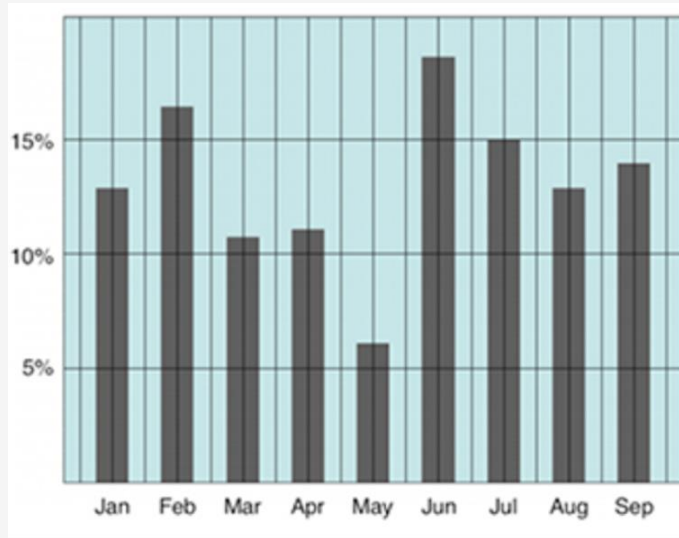
# Red/green vs. blue/orange



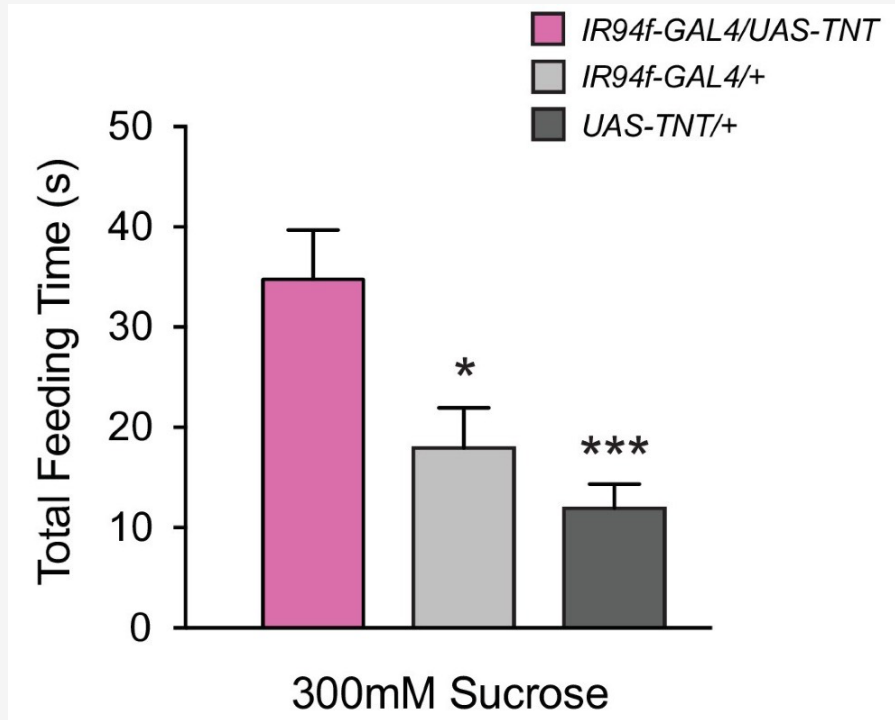
To black  
and white



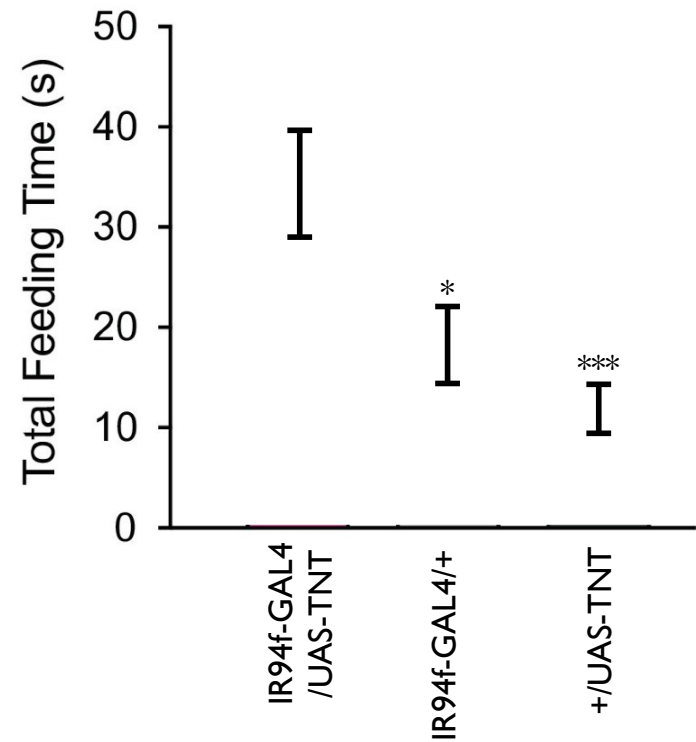
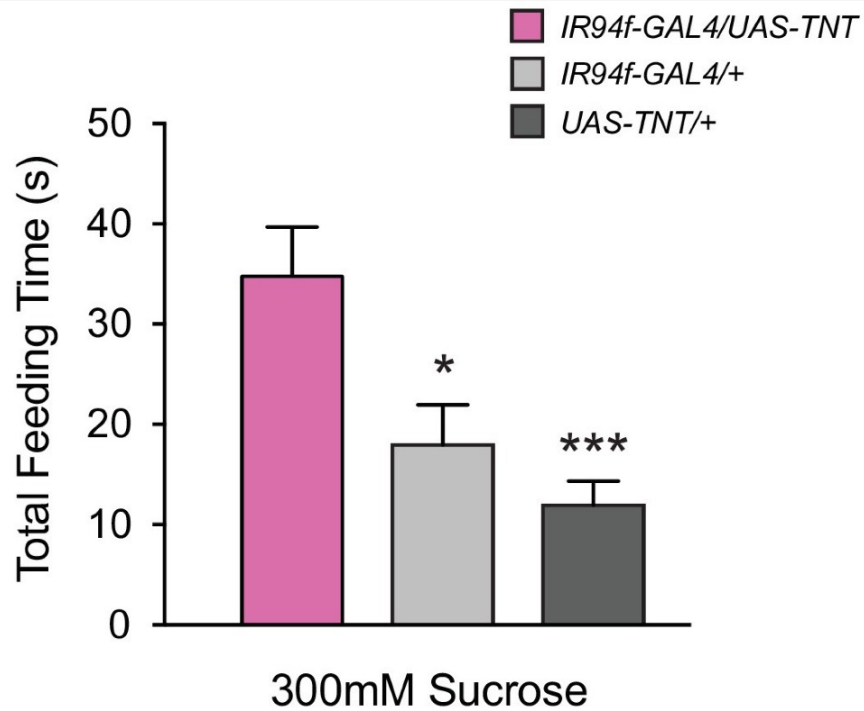
# Data::Ink



# Data::Ink

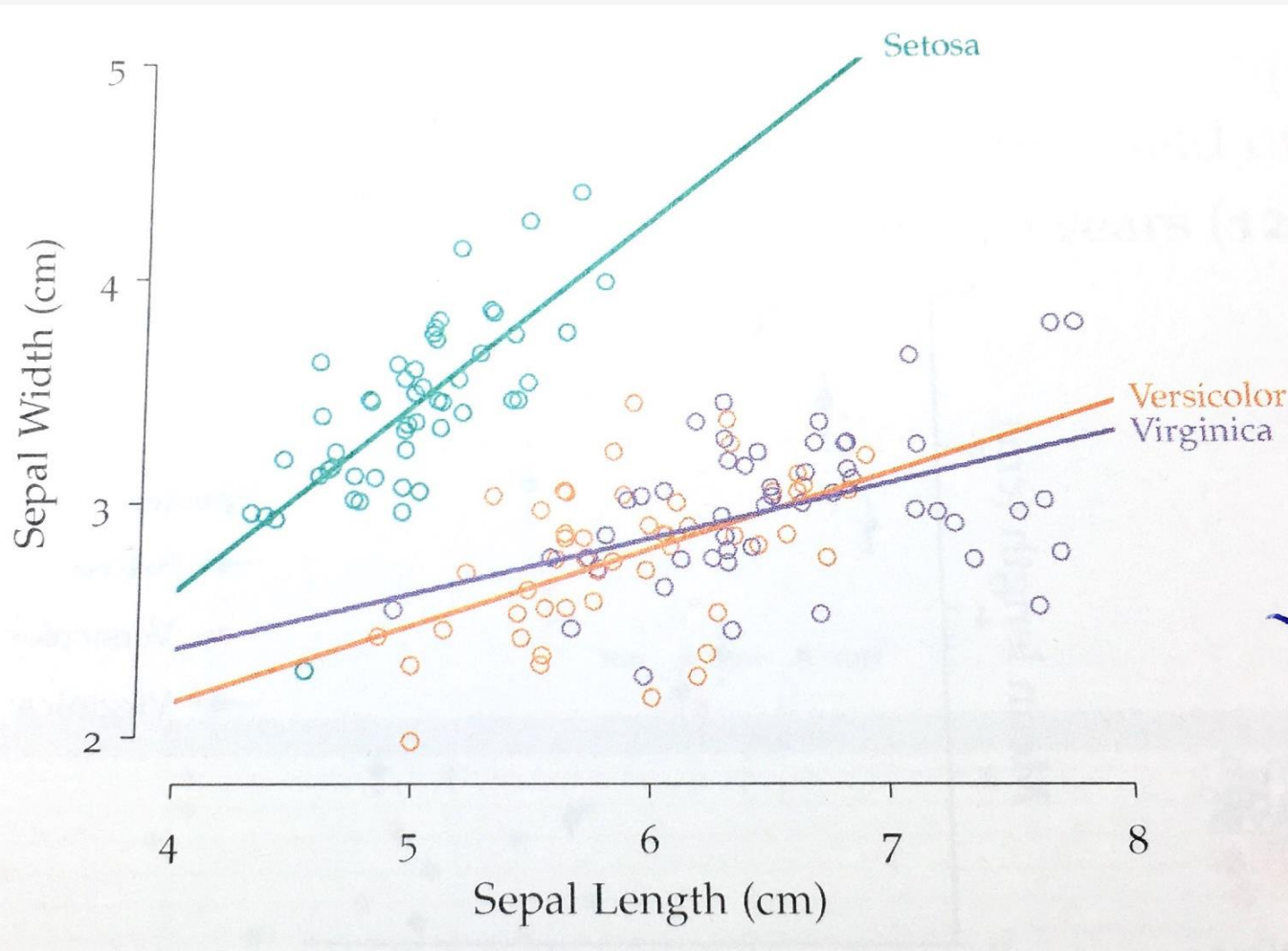


# Data::Ink





# Data::Ink



Where is the legend?

# Data::Ink

---

- Remove excess ink
- Show distributions, instead of bars
- Can you remove the legend?
- Remove double encodings
- Is a log scale appropriate?
- What do the 'error bars' represent?

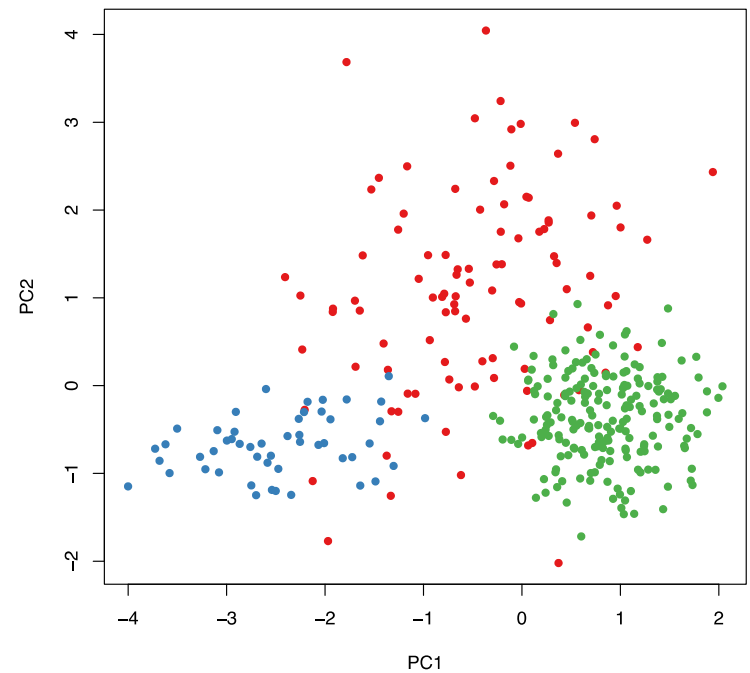
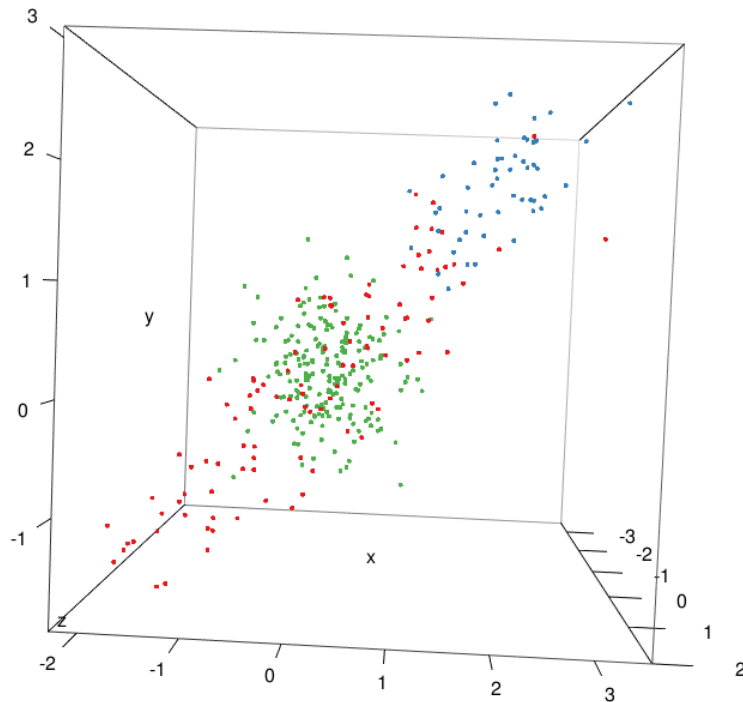
# Outline

- Finish data visualization intro
- Dimensionality reduction
- PCA for data visualization

# Principal Components Analysis (PCA)

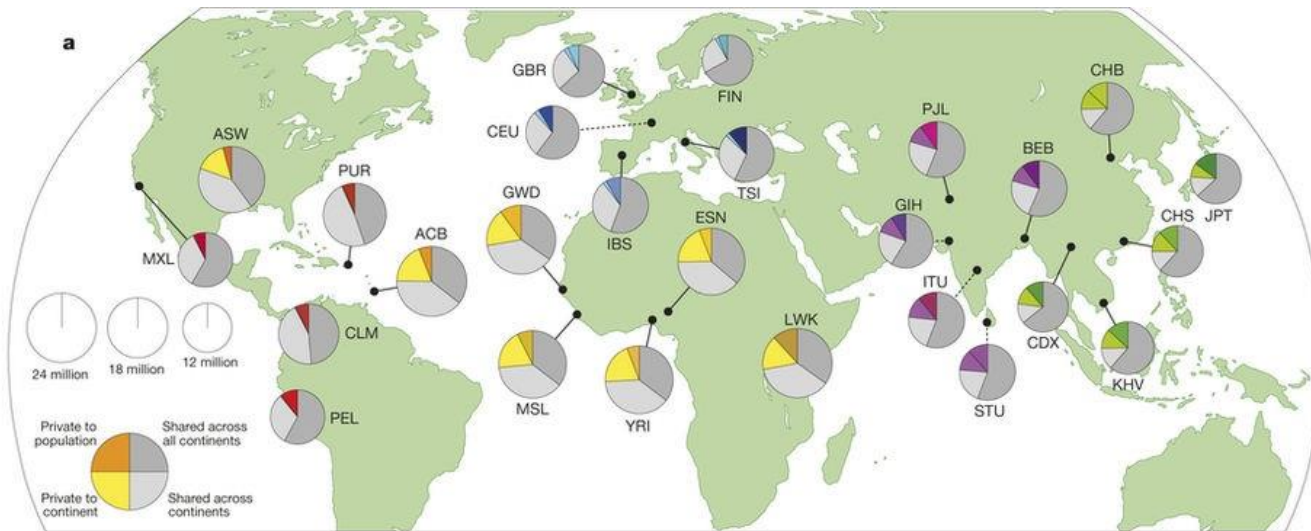
- Transforms  $p$ -dimensional data so that the new first dimension explains as much of the variation as possible, the new second explains as much of the remaining variation as possible, and so on
- Typically, we look at the first few dimensions of the transformed data and use as a means of dimensionality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

# Principal component analysis



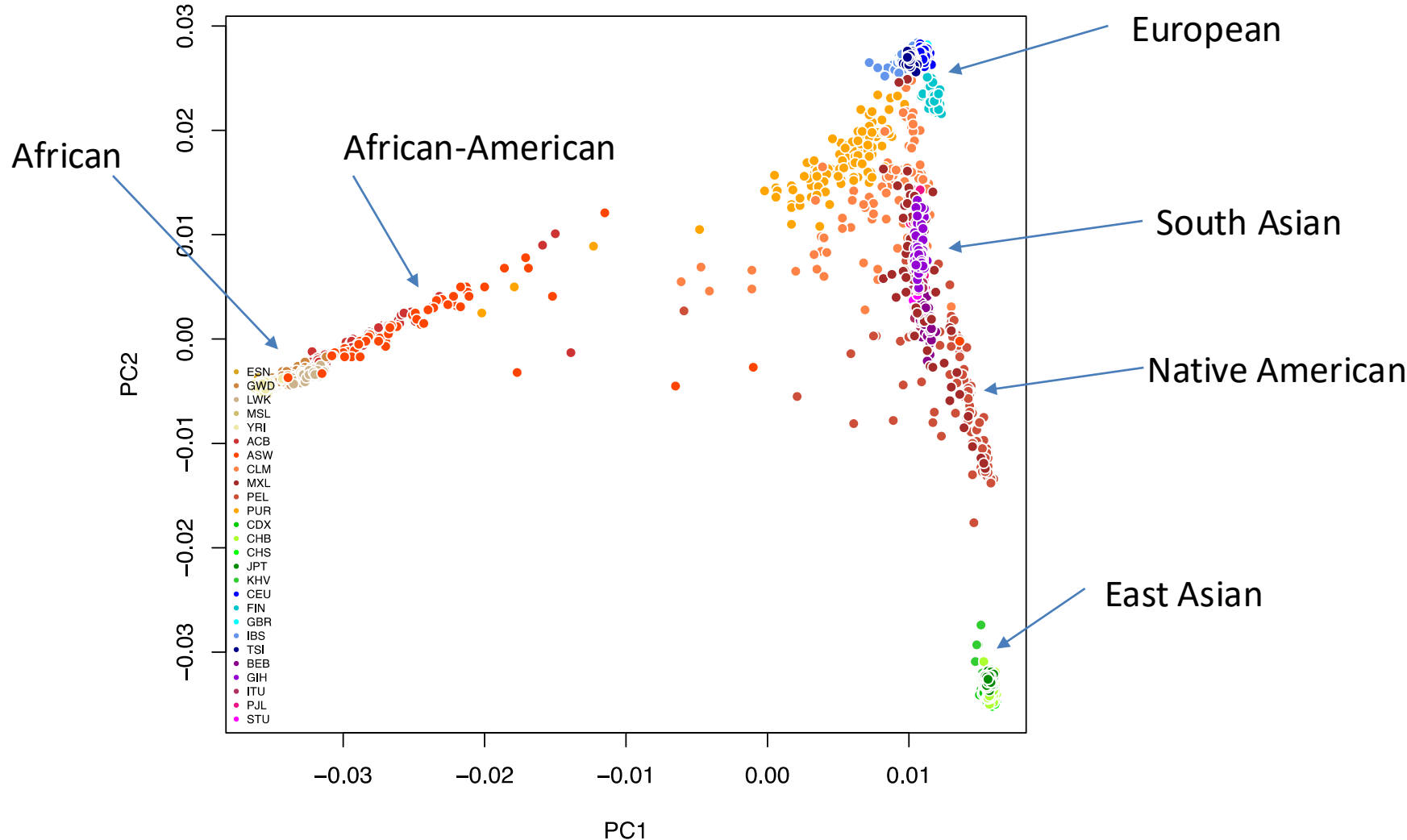
# The 1000 Genomes project

- 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/>



```
##ALT=<ID=CN120,Description="Copy number allele: 120 copies">
##ALT=<ID=CN121,Description="Copy number allele: 121 copies">
##ALT=<ID=CN122,Description="Copy number allele: 122 copies">
##ALT=<ID=CN123,Description="Copy number allele: 123 copies">
##ALT=<ID=CN124,Description="Copy number allele: 124 copies">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##bcftools_annotateVersion=1.6+htslib-1.6
```

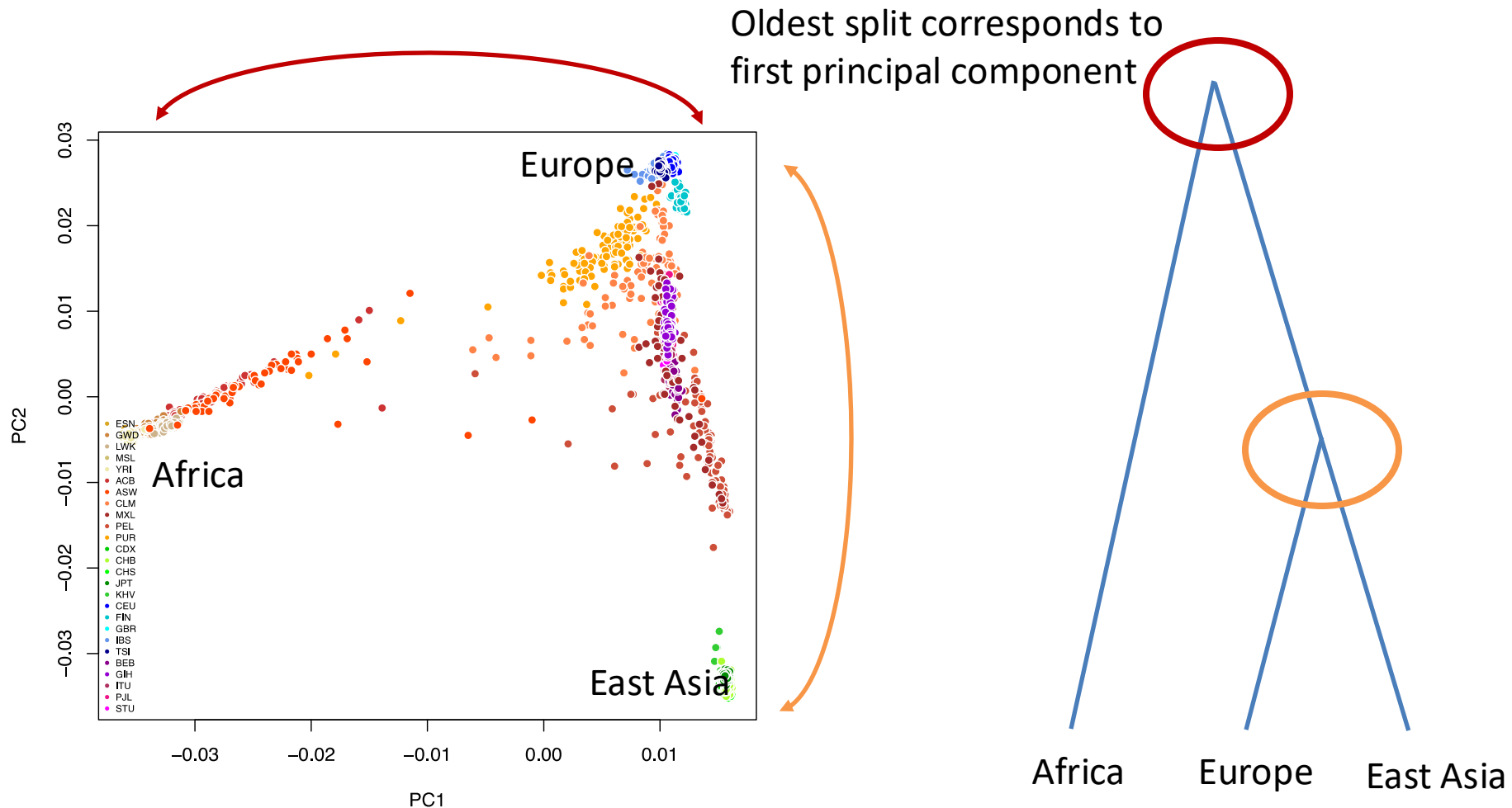
# Global population structure





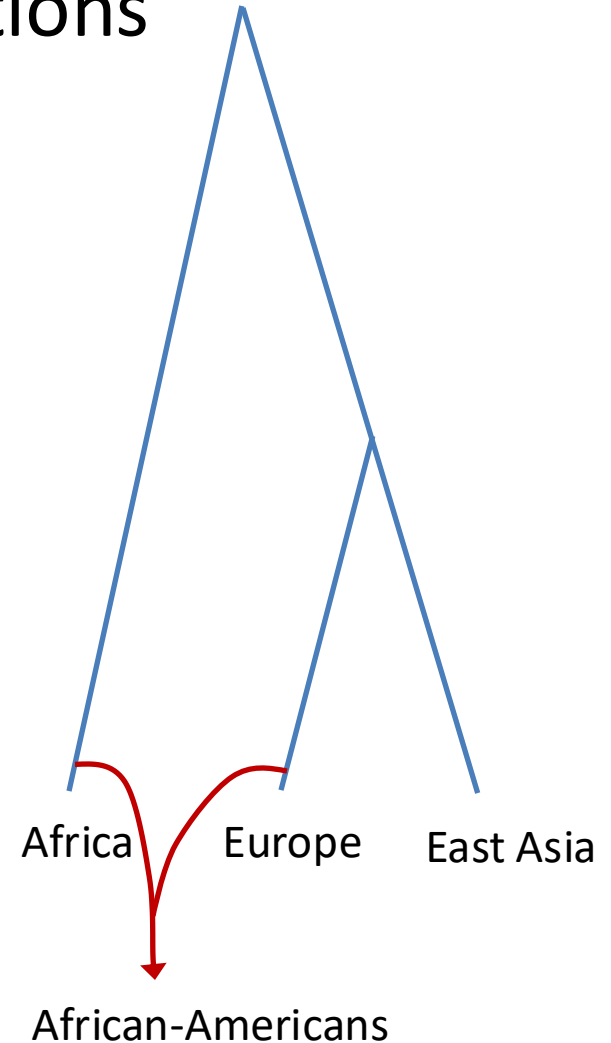
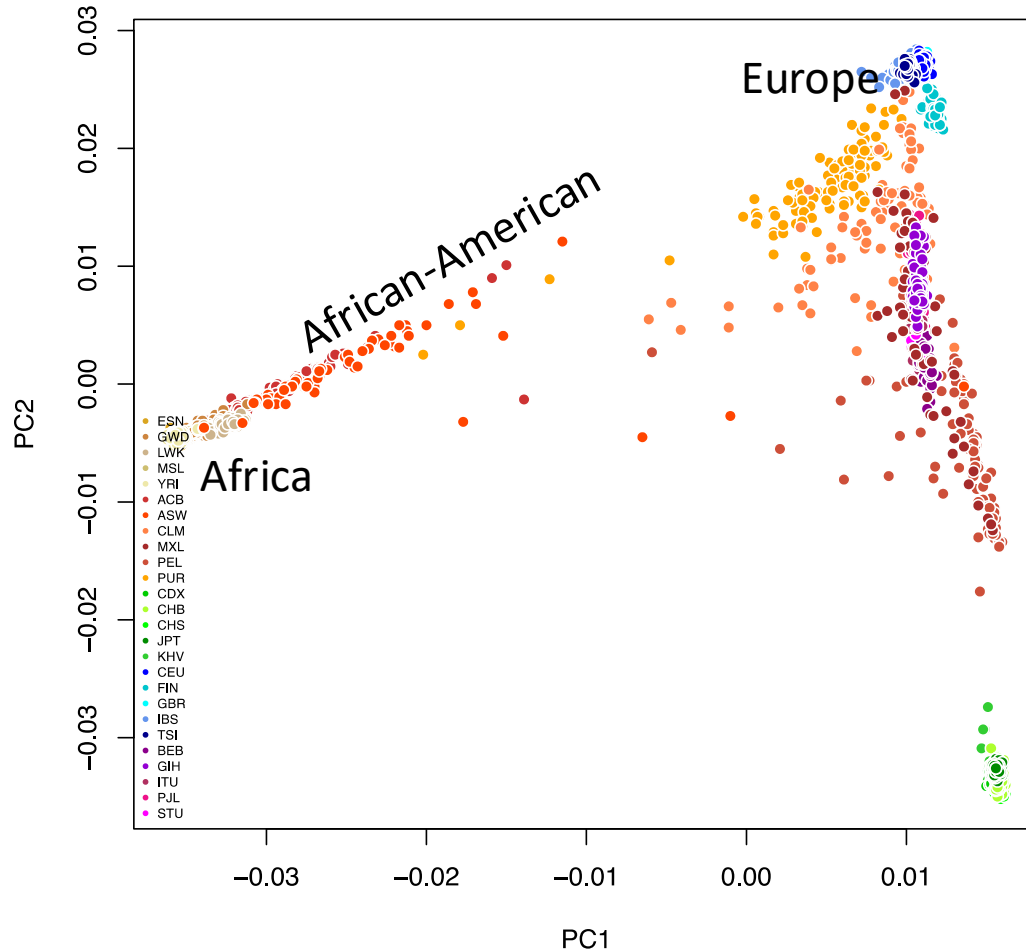
# What causes these patterns?

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

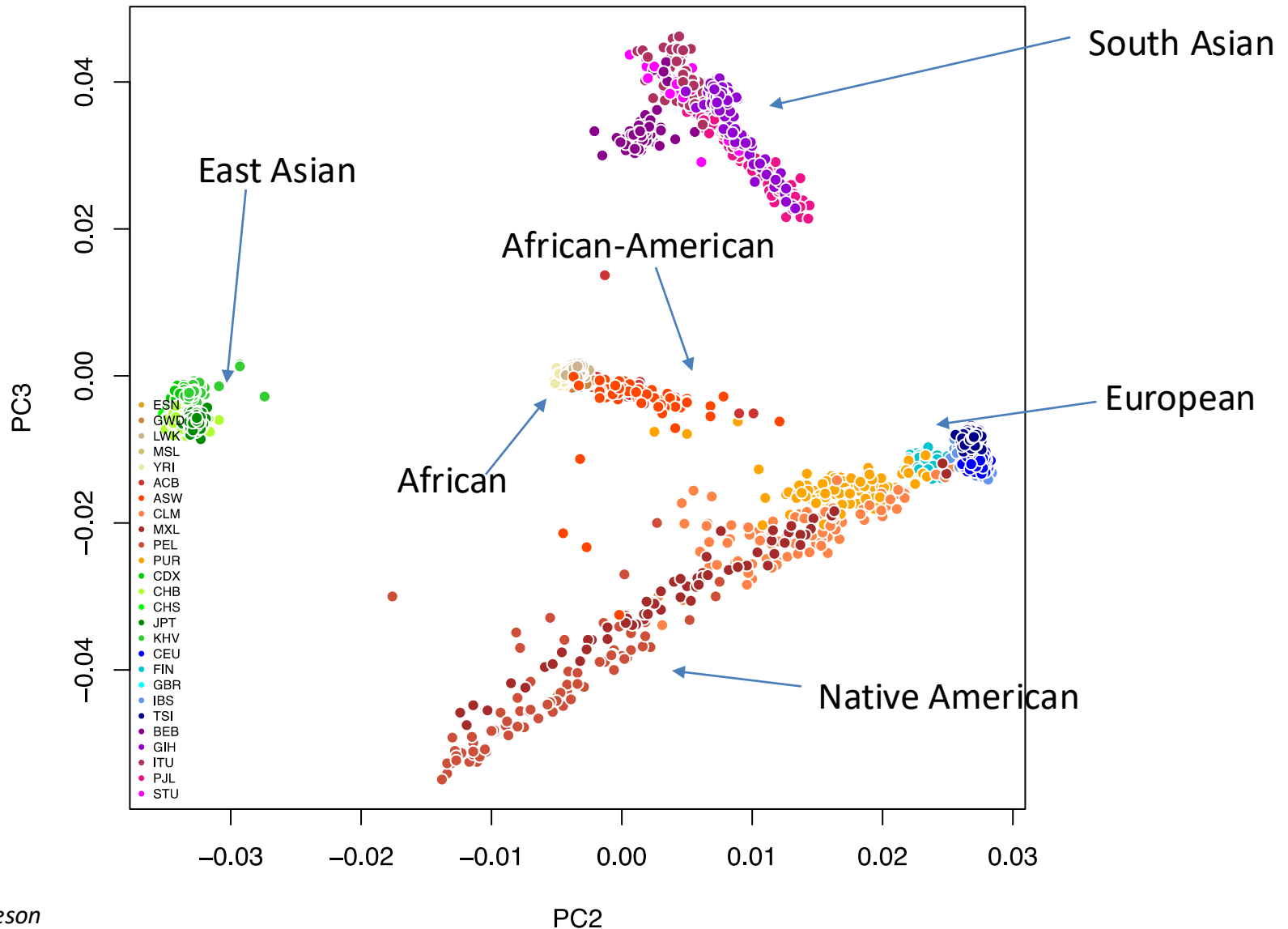


# What causes these patterns?

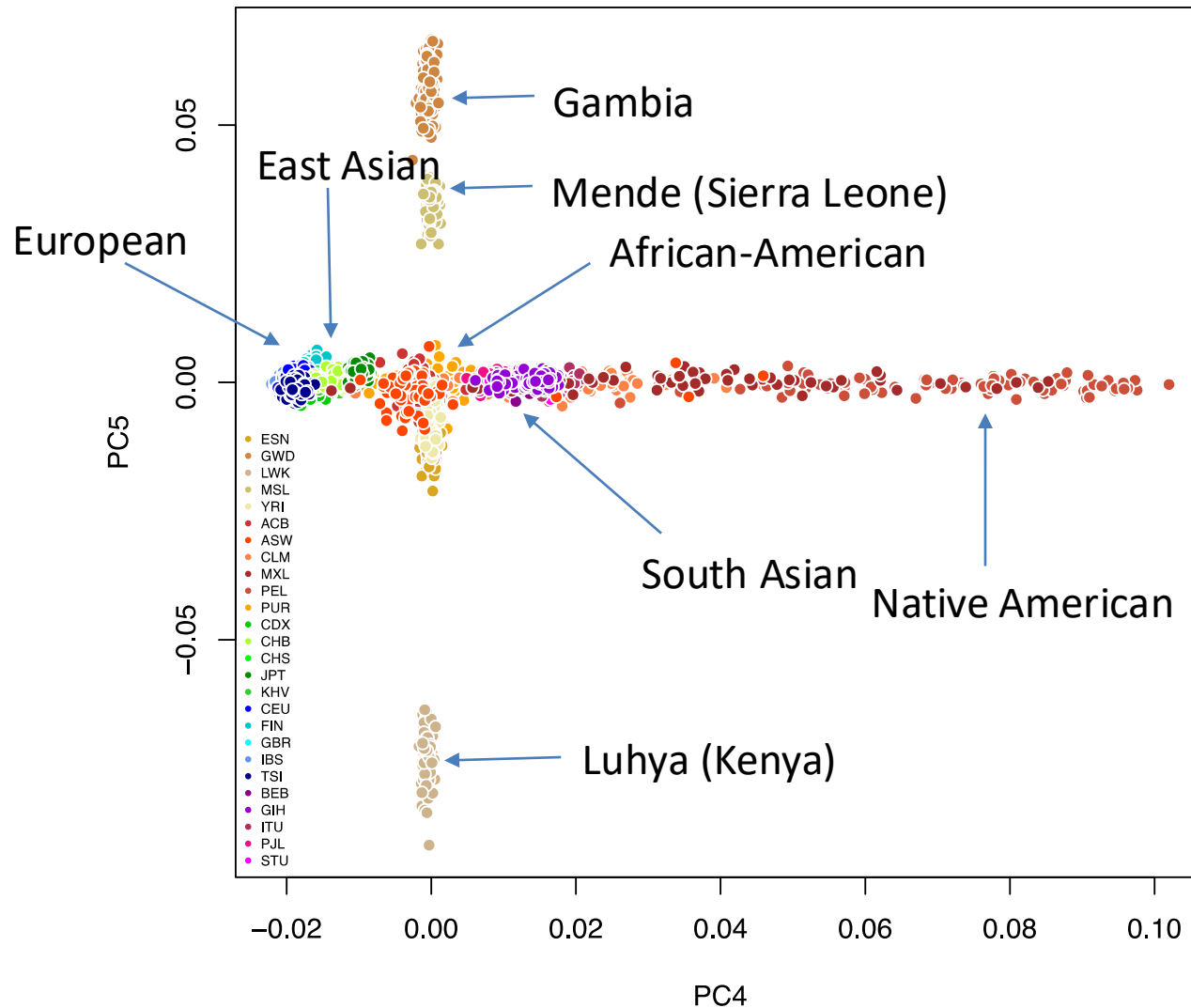
## 2. **Admixture** merges populations




# Global population structure



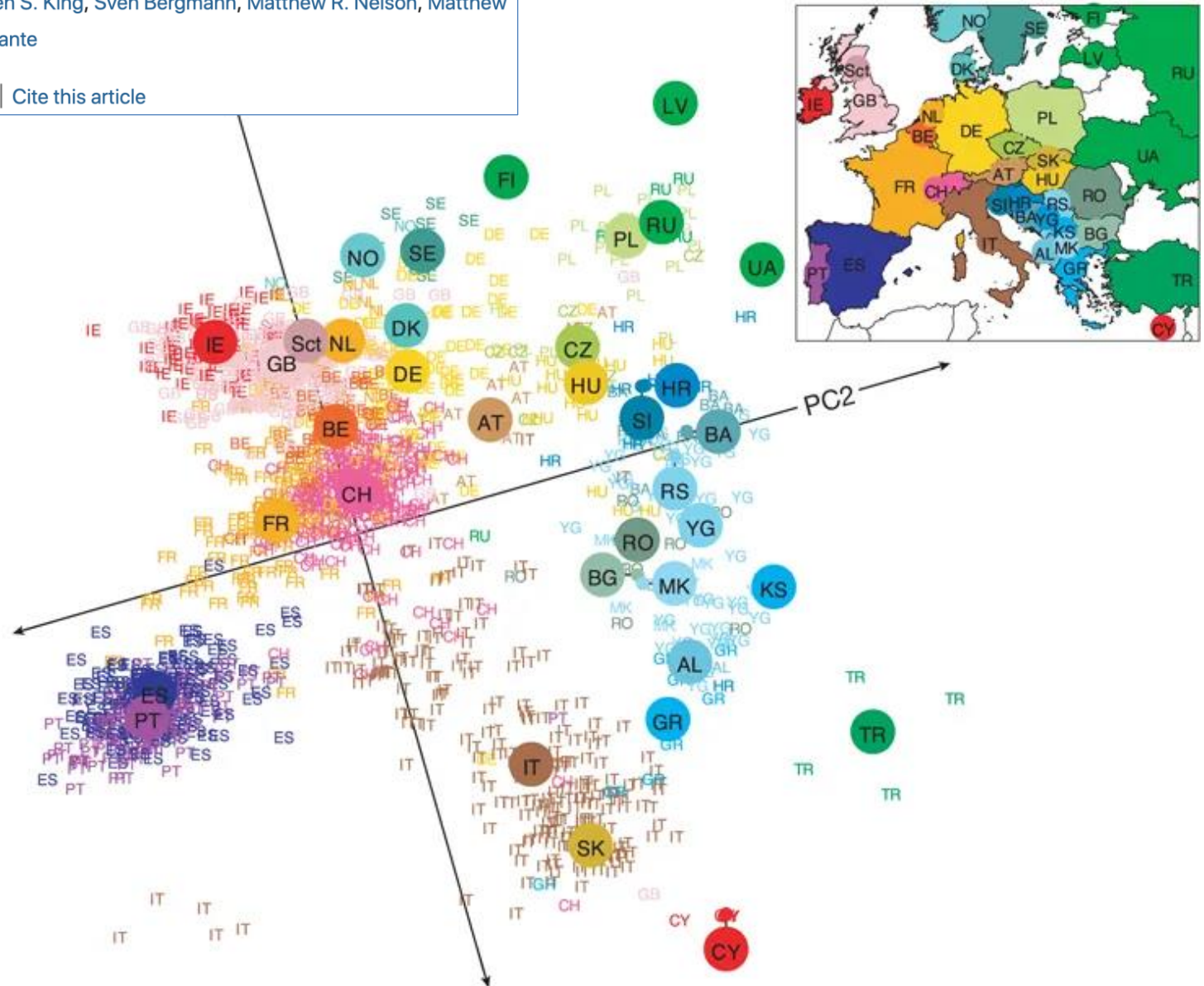
# Global population structure



# 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](#)



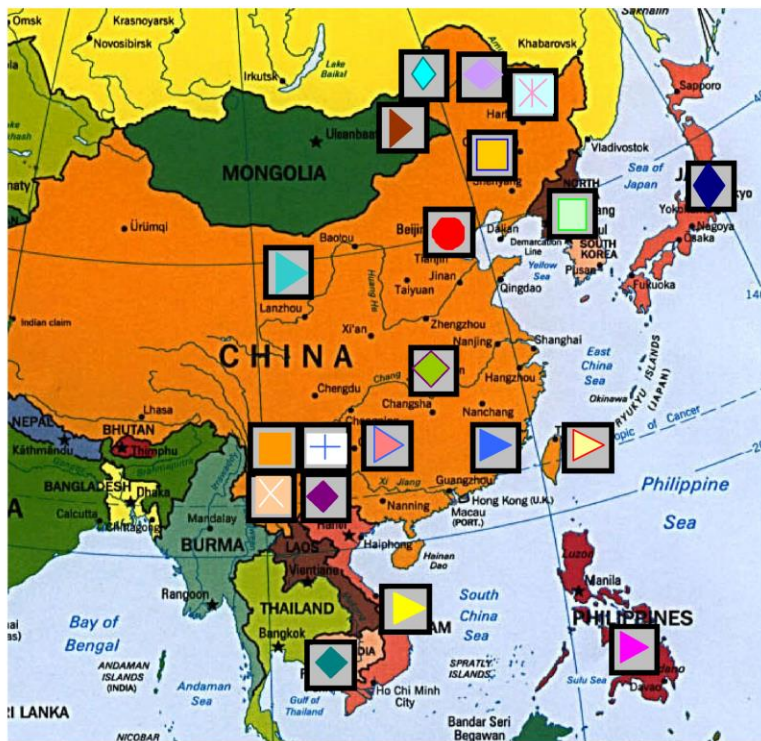
# Analysis of East Asia Genetic Substructure Using Genome-Wide SNP Arrays

Chao Tian, Roman Kosoy, Annette Lee, Michael Ransom, John W. Belmont, Peter K. Gregersen, Michael F. Seldin 

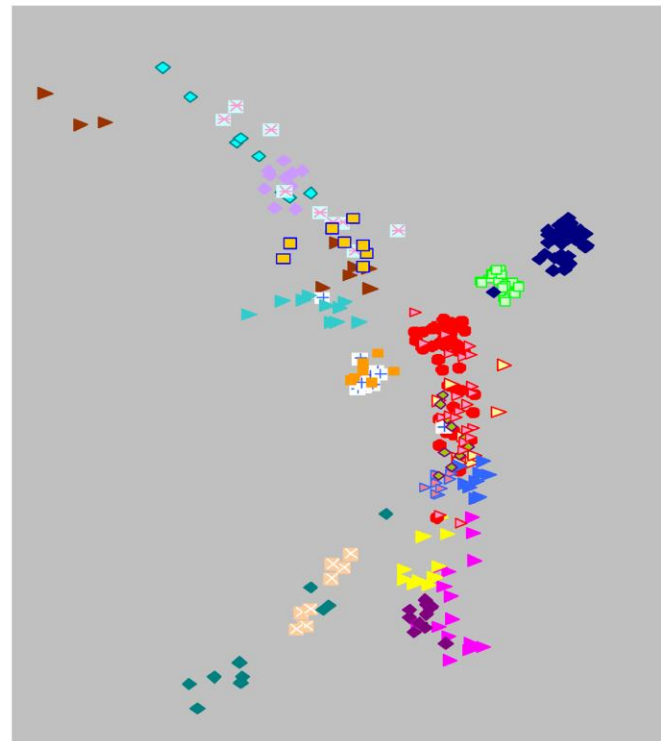
Published: December 5, 2008 • <https://doi.org/10.1371/journal.pone.0003862>

-  FIL
-  VIET
-  LAHU
-  DAI
-  CAMB
-  CHB
-  MGL
-  ORQ
-  DAUR
-  KOR
-  TWN
-  YI
-  HEZ
-  MIAO
-  NAXI
-  SHE
-  TU
-  TUJ
-  XIBO
-  CHA
-  JPT
-  YAK

C



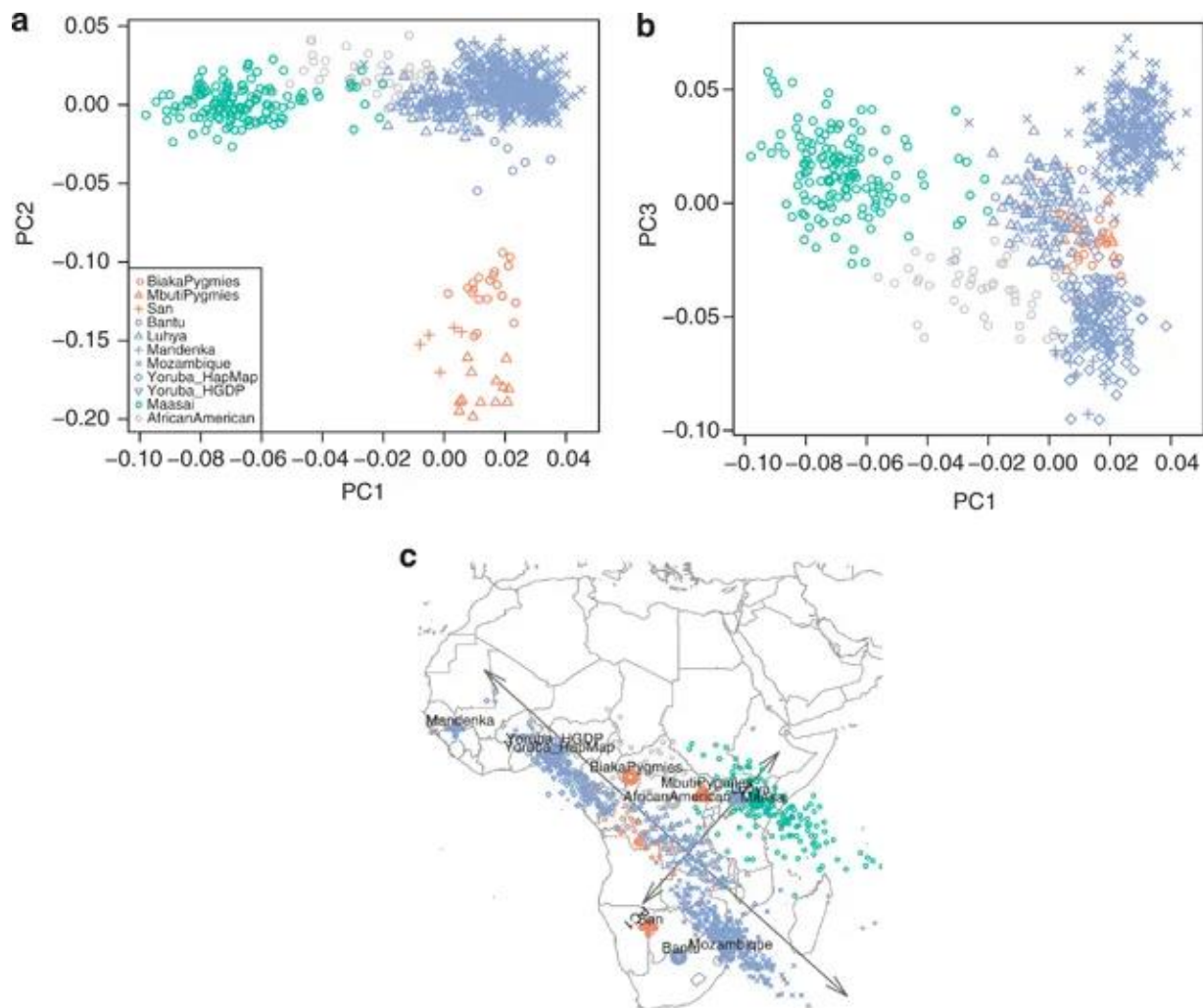
D





# A genomic analysis identifies a novel component in the genetic structure of sub-Saharan African populations

Martin Sikora, Hafid Laayouni, Francesc Calafell, David Comas & Jaume Bertranpetit 



# Outline

- Finish data visualization intro
- Dimensionality reduction
- PCA for data visualization



# Principal Component Analysis

**Step 1**

input data

$X_{orig}$

$X_{orig} =$

$n$  examples

$f_1$

$f_2$

not just taking best 2!

2!

$p$  features

$n \times p$

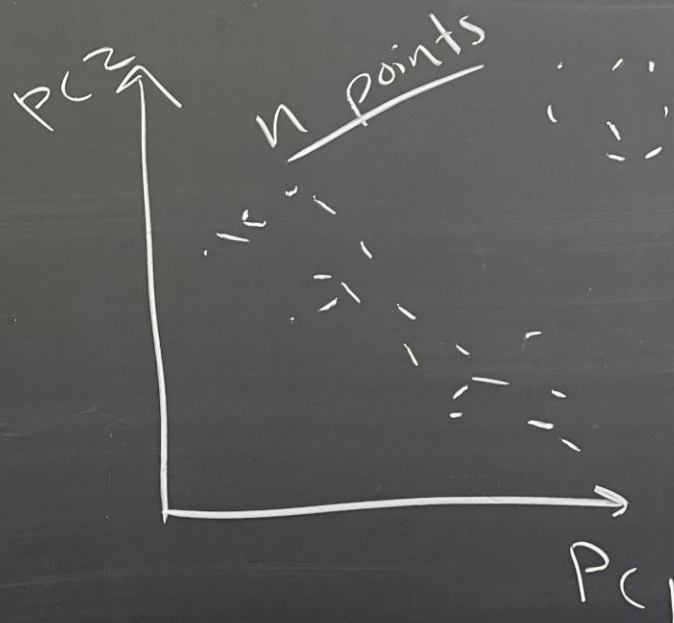
**$p \gg n$**

Sometimes!

(PCA)

goal: create  $n \times r$  matrix for visualization

$$r = z \text{ (often)}$$



no labels! (i.e.  $\vec{y}$ )

unsupervised

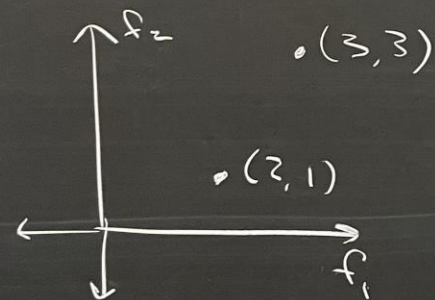


Step 2 Subtract of column-wise mean

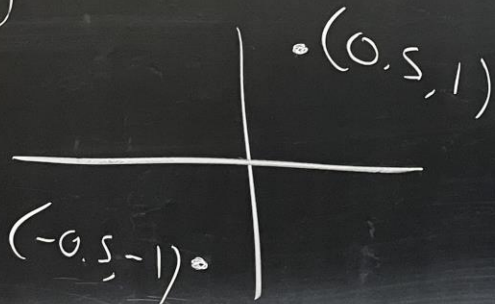
$$X_{\text{orig}} = \begin{bmatrix} f_1 & f_2 \\ 2 & 1 \\ 3 & 3 \end{bmatrix}$$

$$\bar{f}_1 = 2.5$$

$$\bar{f}_2 = 2$$



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



Step 3 Compute covariance matrix A

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

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

(n-1 to make unbiased)

for 2 features

$A^T = A$   
Symmetric

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

**Step 4**

compute eigenvalues & eigenvectors of  $A$

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

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

Solve for  $\lambda$

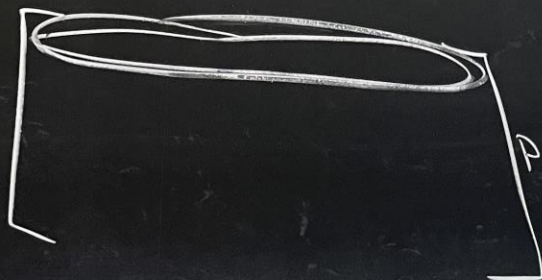
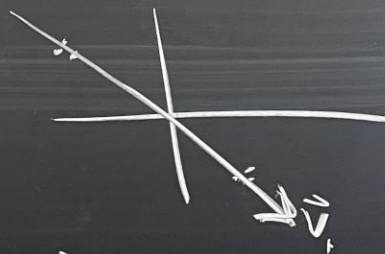
identity

$$I = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$

$p=2$

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

plug back in



$$= \begin{bmatrix} p_1 & p_2 \\ \square & \square \end{bmatrix}_n$$



Step 5

$$W = \begin{bmatrix} | & | & | \\ \vec{v}_1 & \vec{v}_2 & \dots & \vec{v}_r \\ | & | & | \\ \lambda_1 & \lambda_2 & \dots & \lambda_r \end{bmatrix}$$

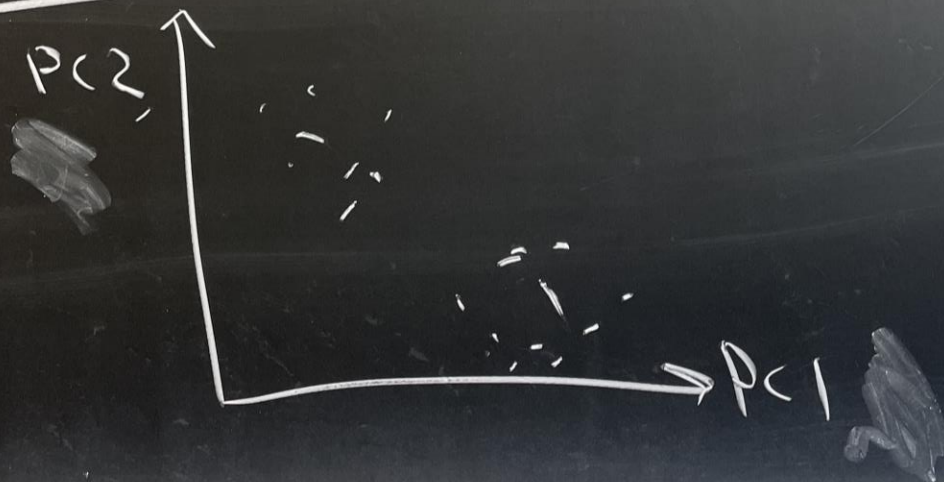
matrix of eigenvectors

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

transformed data

Step 6

plot to visualize!



# Handout 16

Step 1

$$X_{orig} = \begin{bmatrix} 0 & 1 \\ 0 & 1 \\ 0 & 1 \\ 1 & 0 \\ 1 & 0 \\ 1 & 0 \\ 1 & 0 \end{bmatrix} \quad \leftarrow \bar{f}_{1,orig} = \frac{1}{2}, \bar{f}_{2,orig} = \frac{1}{2}$$

Step 2

$$X = \begin{bmatrix} \textcircled{f_1} & \textcircled{f_2} \\ -1/2 & 1/2 \\ -1/2 & 1/2 \\ -1/2 & 1/2 \\ 1/2 & -1/2 \\ 1/2 & -1/2 \\ 1/2 & -1/2 \end{bmatrix} \quad \bar{f}_1 = 0, \bar{f}_2 = 0$$

Step 3

$$\text{var}(f_1) = \frac{1}{6-1} \left( \left(-\frac{1}{2}\right) \left(-\frac{1}{2}\right) \cdot 6 \right) = \frac{1}{5} \cdot \frac{1}{4} \cdot 6$$

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

$$\text{cov}(f_1, f_2) = \frac{1}{5} \left( -\frac{1}{2} \right) \left( \frac{1}{2} \right) \cdot 6 = -\frac{3}{10}$$

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



Step 4

$$\det \left( \begin{bmatrix} 3/10 & -3/10 \\ -3/10 & 3/10 \end{bmatrix} - \overbrace{\begin{bmatrix} \lambda & 0 \\ 0 & \lambda \end{bmatrix}}^{\lambda I} \right) = 0$$

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

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

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

→  $\lambda^2$   
 $\lambda \left( \lambda - \frac{3}{5} \right) = 0$   
 Sort by high → low magnitude

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

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

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

Sort by high → low magnitude

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



$$W = \begin{bmatrix} \vec{v}_1 & \vec{v}_2 \end{bmatrix} = \begin{bmatrix} 1 & 1 \\ -1 & 1 \end{bmatrix}$$

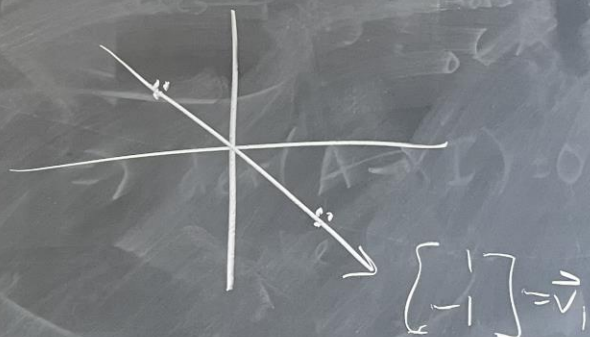
$\uparrow \quad \quad \uparrow$   
 $\lambda_1 = \frac{3}{5} \quad \lambda_2 = 0$

$$T_2 = X W_2 = \begin{bmatrix} -\frac{1}{2} & \frac{1}{2} \\ \vdots & \vdots \\ \frac{1}{2} & -\frac{1}{2} \\ \vdots & \vdots \end{bmatrix}$$

dot product

$$\begin{bmatrix} \vec{p}_1 & \vec{p}_2 \end{bmatrix} = \begin{bmatrix} 1 & 1 \\ -1 & 1 \end{bmatrix} = \begin{bmatrix} -1 & 0 \\ -1 & 0 \\ -1 & 0 \\ -1 & 0 \\ -1 & 0 \end{bmatrix}$$

$\uparrow \quad \quad \uparrow$   
 $\vec{p}_1 \quad \vec{p}_2$



Step 6

PC2

↑ no variation

PC1

