

Statistical Machine Learning

Pier Francesco Palamara

Department of Statistics

University of Oxford

Slide credits and other course material can be found at:

http://www.stats.ox.ac.uk/~palamara/SML_BDI.html

Unsupervised Learning: Visualisation and Dimensionality Reduction

Unsupervised Learning

Goals:

- Find the variables that summarise the data / capture relevant information.
- Discover informative ways to visualise the data.
- Discover the subgroups among the observations.

It is often much easier to obtain unlabeled data than labeled data!

Exploratory Data Analysis

Notation

- Data consists of p variables (features/attributes/dimensions) on n examples (items/observations).
- $\mathbf{X} = (x_{ij})$ is a $n \times p$ -matrix with $x_{ij} :=$ the j -th variable for the i -th example

$$\mathbf{X} = \begin{bmatrix} x_{11} & x_{12} & \dots & x_{1j} & \dots & x_{1p} \\ x_{21} & x_{22} & \dots & x_{2j} & \dots & x_{2p} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots \\ x_{i1} & x_{i2} & \dots & x_{ij} & \dots & x_{ip} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots \\ x_{n1} & x_{n2} & \dots & x_{nj} & \dots & x_{np} \end{bmatrix}.$$

- Denote the i -th data item by $x_i \in \mathbb{R}^p$ (we will treat it as a column vector: it is the transpose of the i -th row of \mathbf{X}).
- Assume x_1, \dots, x_n are **independently and identically distributed** samples of a **random vector** X over \mathbb{R}^p . The j -th dimension of X will be denoted $X^{(j)}$.

Crabs Data ($n = 200$, $p = 5$)

Campbell (1974) studied rock crabs of the genus **leptograpsus**. One species, **L. variegatus**, had been split into two new species according to their colour: orange and blue. Preserved specimens lose their colour, so it was hoped that morphological differences would enable museum material to be classified.

Data are available on 50 specimens of each sex of each species. Each specimen has measurements on:

- the width of the frontal lobe FL ,
- the rear width RW ,
- the length along the carapace midline CL ,
- the maximum width CW of the carapace,
and
- the body depth BD in mm.

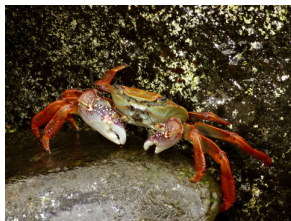


photo from: inaturalist.org

in addition to colour/species and sex (we will later view these as labels, but will ignore for now).

Crabs Data

```
## load package MASS containing the data
library(MASS)

## extract variables we will look at
varnames<-c("FL", "RW", "CL", "CW", "BD")
Crabs <- crabs[,varnames]

## look at raw data
Crabs
```

Crabs Data

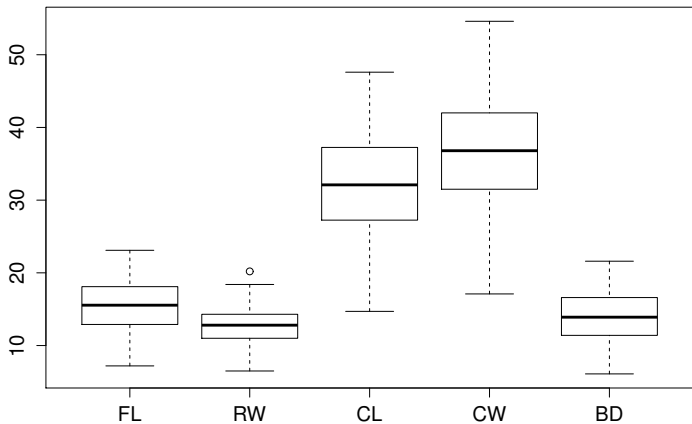
```
## look at raw data
```

```
Crabs
```

| | FL | RW | CL | CW | BD |
|----|------|------|------|------|------|
| 1 | 8.1 | 6.7 | 16.1 | 19.0 | 7.0 |
| 2 | 8.8 | 7.7 | 18.1 | 20.8 | 7.4 |
| 3 | 9.2 | 7.8 | 19.0 | 22.4 | 7.7 |
| 4 | 9.6 | 7.9 | 20.1 | 23.1 | 8.2 |
| 5 | 9.8 | 8.0 | 20.3 | 23.0 | 8.2 |
| 6 | 10.8 | 9.0 | 23.0 | 26.5 | 9.8 |
| 7 | 11.1 | 9.9 | 23.8 | 27.1 | 9.8 |
| 8 | 11.6 | 9.1 | 24.5 | 28.4 | 10.4 |
| 9 | 11.8 | 9.6 | 24.2 | 27.8 | 9.7 |
| 10 | 11.8 | 10.5 | 25.2 | 29.3 | 10.3 |
| 11 | 12.2 | 10.8 | 27.3 | 31.6 | 10.9 |
| 12 | 12.3 | 11.0 | 26.8 | 31.5 | 11.4 |
| 13 | 12.6 | 10.0 | 27.7 | 31.7 | 11.4 |
| 14 | 12.8 | 10.2 | 27.2 | 31.8 | 10.9 |
| 15 | 12.8 | 10.9 | 27.4 | 31.5 | 11.0 |
| 16 | 12.9 | 11.0 | 26.8 | 30.9 | 11.4 |
| 17 | 13.1 | 10.6 | 28.2 | 32.3 | 11.0 |
| 18 | 13.1 | 10.9 | 28.3 | 32.4 | 11.2 |
| 19 | 13.3 | 11.1 | 27.8 | 32.3 | 11.3 |
| 20 | 13.9 | 11.1 | 29.2 | 33.3 | 12.1 |

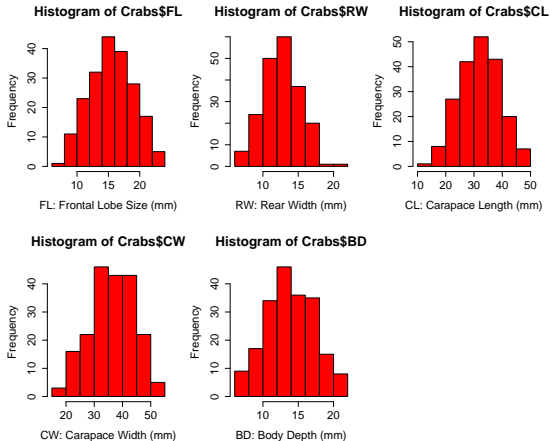
Univariate Boxplots

```
boxplot (Crabs)
```



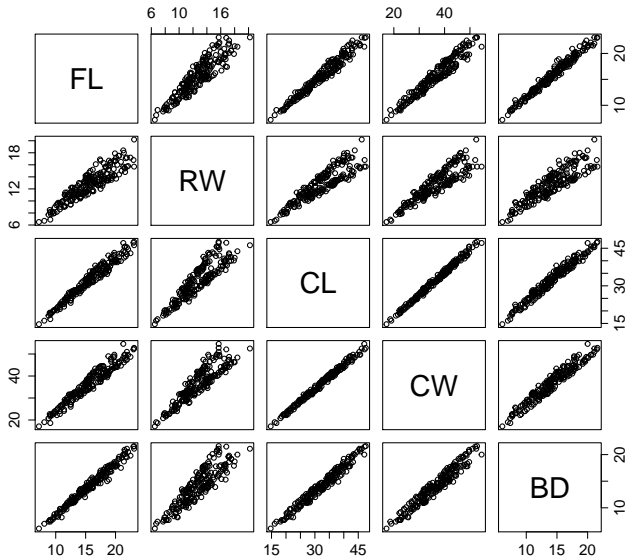
Univariate Histograms

```
par(mfrow=c(2,3))  
hist(Crabs$FL,col="red",xlab="FL: Frontal Lobe Size (mm) ")  
hist(Crabs$RW,col="red",xlab="RW: Rear Width (mm) ")  
hist(Crabs$CL,col="red",xlab="CL: Carapace Length (mm) ")  
hist(Crabs$CW,col="red",xlab="CW: Carapace Width (mm) ")  
hist(Crabs$BD,col="red",xlab="BD: Body Depth (mm) ")
```



Simple Pairwise Scatterplots

```
pairs(Crabs)
```



Visualisation and Dimensionality Reduction

The summary plots are useful, but limited use if the dimensionality p is high (a few dozens or even thousands).

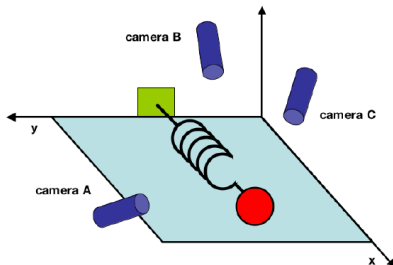
- Constrained to view data in 2 or 3 dimensions
- Approach: look for 'interesting' projections of \mathbf{X} into lower dimensions
- Hope that even though p is large, considering only carefully selected $k \ll p$ dimensions is just as informative.

Dimensionality reduction

- For each data item $x_i \in \mathbb{R}^p$, find its lower dimensional representation $z_i \in \mathbb{R}^k$ with $k \ll p$.
- Map $x \mapsto z$ should preserve the **interesting statistical properties** in data.

Dimensionality reduction

- deceptively many variables to measure, many of them redundant / correlated to each other (large p)
- often, there is a simple but unknown underlying relationship hiding
- example: ball on a frictionless spring recorded by three different cameras
 - our imperfect measurements obfuscate the true underlying dynamics
 - are our coordinates meaningful or do they simply reflect the method of data gathering?

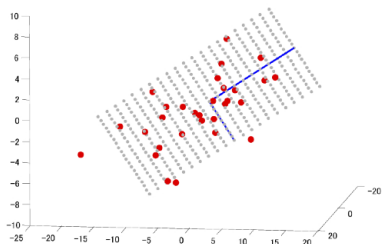


Principal Components Analysis (PCA)

- PCA considers interesting directions to be those with greatest **variance**.
- A **linear** dimensionality reduction technique: looks for a **new basis** to represent a noisy dataset.
- Workhorse for many different types of data analysis (often used for data preprocessing before supervised techniques are applied).
- Often the first thing to run on high-dimensional data.

Principal Components Analysis (PCA)

- For simplicity, we will assume from now on that our dataset is centred, i.e., we subtract the average \bar{x} from each x_i .



PCA

Find an orthogonal basis v_1, v_2, \dots, v_p for the data space such that:

- The first principal component (PC) v_1 is the **direction of greatest variance** of data.
- The j -th PC v_j (also called **loading vector**) is the **direction orthogonal to v_1, v_2, \dots, v_{j-1} of greatest variance**, for $j = 2, \dots, p$.

Principal Components Analysis (PCA)

- The k -dimensional representation of data item x_i is the vector of projections of x_i onto first k PCs:

$$z_i = V_{1:k}^\top x_i = [v_1^\top x_i, \dots, v_k^\top x_i]^\top \in \mathbb{R}^k,$$

where $V_{1:k} = [v_1, \dots, v_k]$

- Reconstruction of x_i :

$$\hat{x}_i = V_{1:k} V_{1:k}^\top x_i.$$

- PCA gives the **optimal linear reconstruction** of the original data based on a k -dimensional compression (problem sheets).

Principal Components Analysis (PCA)

- Our data set is an i.i.d. sample $\{x_i\}_{i=1}^n$ of a random vector $X = [X^{(1)} \dots X^{(p)}]^\top$.
- For the 1st PC, we seek a derived scalar variable of the form

$$Z^{(1)} = v_1^\top X = v_{11}X^{(1)} + v_{12}X^{(2)} + \dots + v_{1p}X^{(p)}$$

where $v_1 = [v_{11}, \dots, v_{1p}]^\top \in \mathbb{R}^p$ are chosen to maximise

$$\text{Var}(Z^{(1)}).$$

- The 2nd PC is chosen to be orthogonal with the 1st and is computed in a similar way. It will have the largest variance in the remaining $p - 1$ dimensions, etc.

Deriving the First Principal Component

- for any fixed v_1 ,

$$\text{Var}(Z^{(1)}) = \text{Var}(v_1^\top X) = v_1^\top \text{Cov}(X)v_1.$$

- we do not know the **true** covariance matrix $\text{Cov}(X)$, so need to replace with the sample covariance matrix, i.e.

$$S = \frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x})(x_i - \bar{x})^\top = \frac{1}{n-1} \sum_{i=1}^n x_i x_i^\top = \frac{1}{n-1} \mathbf{X}^\top \mathbf{X}.$$

- with no restriction on the norm of v_1 , $\text{Var}(Z^{(1)})$ grows without a bound: need constraint $v_1^\top v_1 = 1$, giving

$$\max_{v_1} v_1^\top S v_1$$

$$\text{subject to: } v_1^\top v_1 = 1.$$

Deriving the First Principal Component

- Lagrangian of the problem is given by:

$$\mathcal{L}(v_1, \lambda_1) = v_1^\top S v_1 - \lambda_1 (v_1^\top v_1 - 1).$$

- The corresponding vector of partial derivatives is

$$\frac{\partial \mathcal{L}(v_1, \lambda_1)}{\partial v_1} = 2Sv_1 - 2\lambda_1 v_1.$$

- Setting this to zero gives $Sv_1 = \lambda_1 v_1$. Recognize the eigenvector equation, i.e. v_1 must be an eigenvector of S and the dual variable λ_1 is the corresponding eigenvalue.
- Since $v_1^\top Sv_1 = \lambda_1 v_1^\top v_1 = \lambda_1$, the first PC must be the eigenvector associated with the largest eigenvalue of S .

PCA as eigendecomposition of the covariance matrix

- The eigenvalue decomposition of S is given by

$$S = V\Lambda V^T$$

where Λ is a diagonal matrix with eigenvalues

$$\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_p \geq 0$$

and V is a $p \times p$ orthogonal matrix whose columns are the p eigenvectors of S , i.e. the principal components v_1, \dots, v_p .

Properties of the Principal Components

- Derived scalar variable (projection to the j -th principal component)
 $Z^{(j)} = v_j^\top X$ has sample variance λ_j , for $j = 1, \dots, p$
- S is a real symmetric matrix, so eigenvectors (principal components) are orthogonal.
- Projections to principal components are **uncorrelated**:
 $\text{Cov}(Z^{(i)}, Z^{(j)}) \approx v_i^\top S v_j = \lambda_j v_i^\top v_j = 0$, for $i \neq j$.
- The **total sample variance** is given by $\sum_{i=1}^p S_{ii} = \lambda_1 + \dots + \lambda_p$, so the **proportion of total variance explained** by the j^{th} PC is $\frac{\lambda_j}{\lambda_1 + \lambda_2 + \dots + \lambda_p}$

R code

This is what we have had before:

```
> library(MASS)
> varnames<-c('FL','RW','CL','CW','BD')
> Crabs <- crabs[,varnames]
```

Now perform PCA with function `princomp`.
(Alternatively, solve for the PCs yourself using `eigen` or `svd`)

```
> Crabs.pca <- princomp(Crabs)
```

Exploring PCA output

```
> Crabs.pca <- princomp(Crabs)
> summary(Crabs.pca)
```

Importance of components:

| | Comp.1 | Comp.2 | Comp.3 | Comp.4 | Comp.5 |
|------------------------|------------|-------------|-------------|--------------|--------------|
| Standard deviation | 11.8322521 | 1.135936870 | 0.997631086 | 0.3669098284 | 0.2784325016 |
| Proportion of Variance | 0.9824718 | 0.009055108 | 0.006984337 | 0.0009447218 | 0.0005440328 |
| Cumulative Proportion | 0.9824718 | 0.991526908 | 0.998511245 | 0.9994559672 | 1.0000000000 |

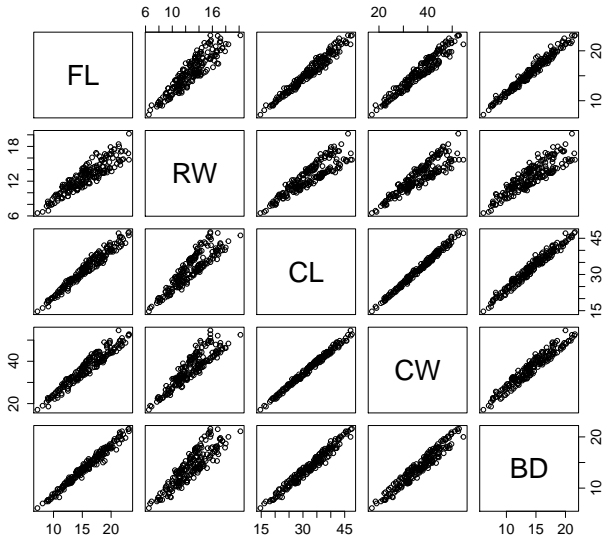
```
> loadings(Crabs.pca)
```

Loadings:

| | Comp.1 | Comp.2 | Comp.3 | Comp.4 | Comp.5 |
|----|--------|--------|--------|--------|--------|
| FL | -0.289 | -0.323 | 0.507 | 0.734 | 0.125 |
| RW | -0.197 | -0.865 | -0.414 | -0.148 | -0.141 |
| CL | -0.599 | 0.198 | 0.175 | -0.144 | -0.742 |
| CW | -0.662 | 0.288 | -0.491 | 0.126 | 0.471 |
| BD | -0.284 | -0.160 | 0.547 | -0.634 | 0.439 |

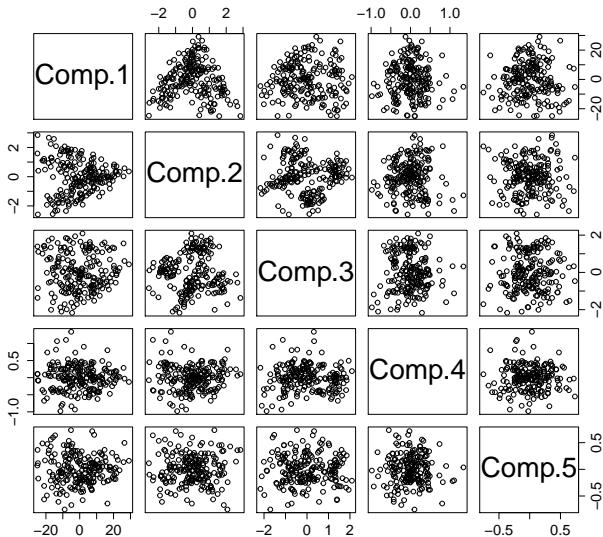
Raw Crabs Data

```
> pairs(Crabs)
```



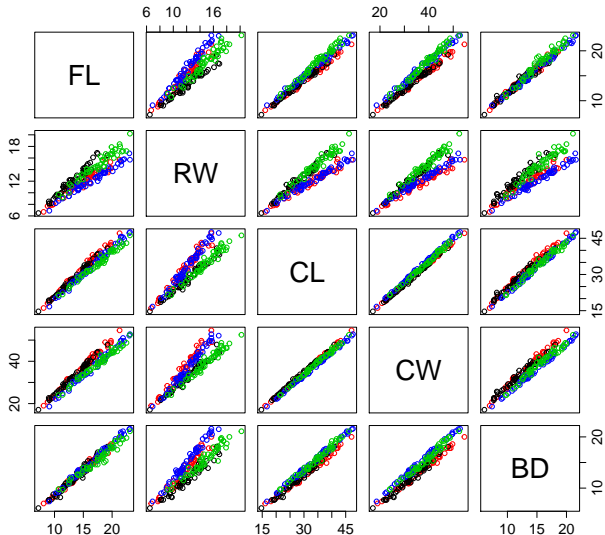
PCA of Crabs Data

```
> Crabs.pca <- princomp(Crabs)
> pairs(predict(Crabs.pca))
```



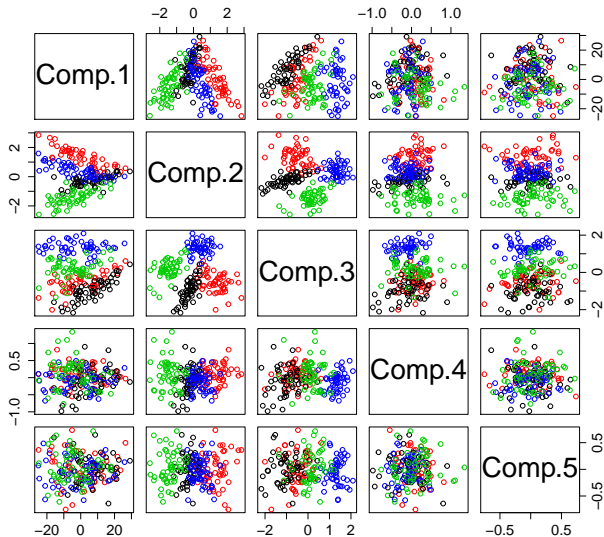
Raw Crabs Data - with labels

```
> pairs(Crabs,col=unclass(Crabs.class))
```



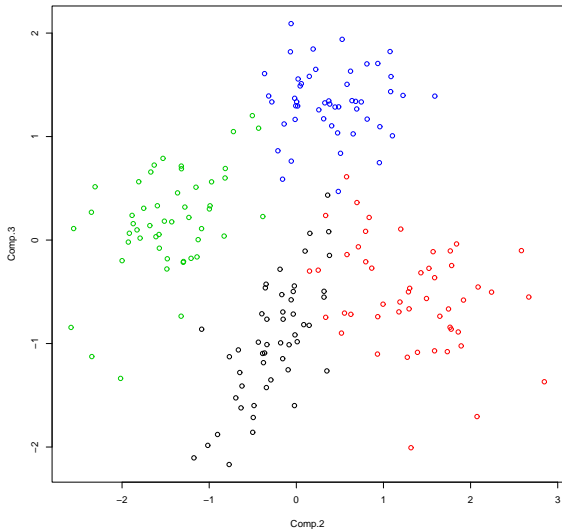
PCA of Crabs Data - with labels

```
> Crabs.pca <- princomp(Crabs)
> pairs(predict(Crabs.pca), col=unclass(Crabs.class))
```

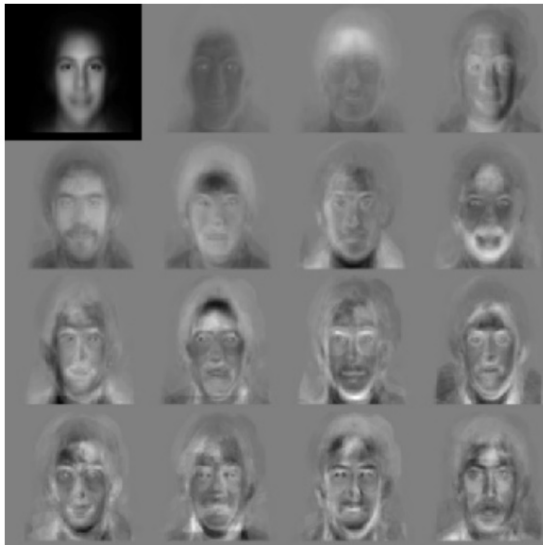


PC 2 vs PC 3

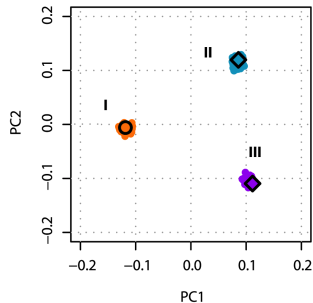
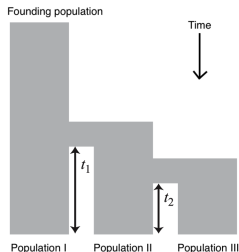
```
> Z<-predict(Crabs.pca)
> plot(Comp.3~Comp.2, data=Z, col=unclass(Crabs.class))
```



PCA on face images: Eigenfaces

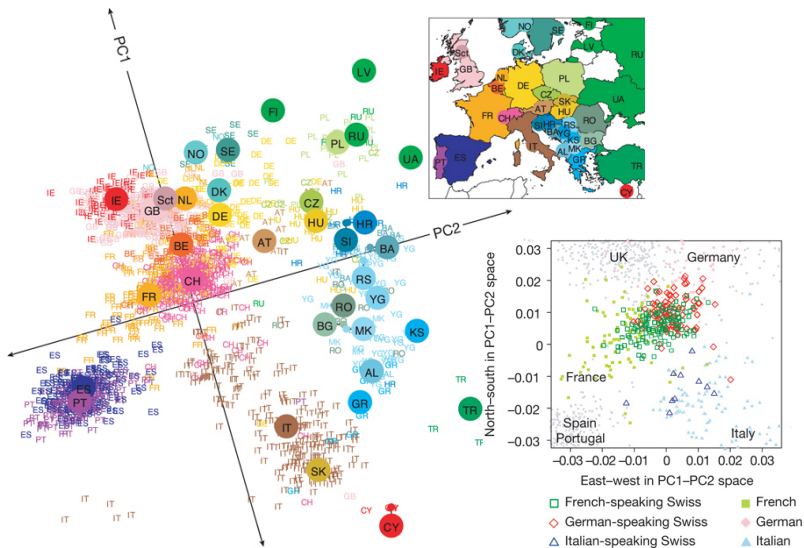


PCA on genetic data



- This experiment simulated genomes from a population. A sub-population is created at time t_1 , and a second sub-population is created at time t_2 . Individuals only reproduce and evolve within each sub-population.
- Sampling the genome of individuals from the present time (here p is the many thousands of mutations found in the genomes) and performing PCA (right) reveals the underlying low-dimensional structure of genetic variation, which reflects the model on the left.

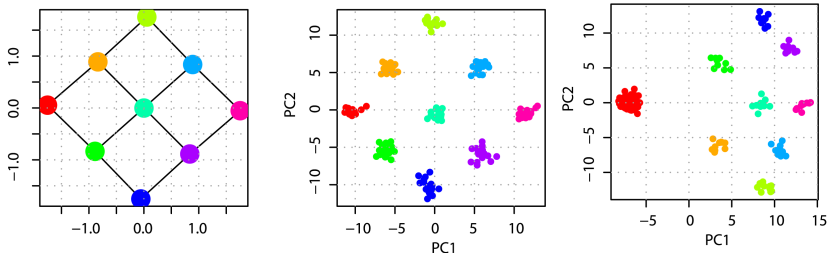
PCA on real genomes: European genetic variation



Comments on the use of PCA

- PCA commonly used to project data X onto the first k PCs giving the k -dimensional view of the data that best preserves **the first two moments**.
- Although PCs are uncorrelated, scatterplots sometimes reveal structures in the data other than linear correlation.
- Emphasis on variance is where the weaknesses of PCA stem from:
 - Assuming large variances are meaningful (high signal-to-noise ratio)
 - The PCs depend heavily on the units measurement. Where the data matrix contains measurements of vastly differing orders of magnitude, the PC will be greatly biased in the direction of larger measurement. In these cases, it is recommended to calculate PCs from $\text{Corr}(X)$ instead of $\text{Cov}(X)$ (`cor=True` in the call of `princomp`).
 - Lack of robustness to outliers: variance is affected by outliers and so are PCs.
 - Sample size (e.g. the number of crabs collected for each sub-species) will have an effect on the PCs.

PCA on genetic data: uneven sampling



- This experiment simulates the genomes of 9 sub-groups of individuals from a map (left). Individuals reproduce and evolve within each sub-group, and occasionally migrate to a neighboring sub-group with a small probability.
- Sampling an equal number of genomes from each sub-group and performing PCA (center) recovers the underlying geographic structure.
- If the same experiment is performed, this time sampling more individuals from one of the sub-groups (e.g. red sub-group, right figure), resulting PCs are affected.