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- Principal Component Analysis (PCA)
- Probabilistic PCA
- Independent component analysis (ICA)

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- Sometimes data depends on the variables we can not measure (hard to measure)
  - Answers on the test depend on Intelligence
  - Brain activity in the brain is measured by sensors
  - Stock prices depend on market confidence



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- Latent factor discovered → data storage may decrease a lot

- Latent factors
  - Center
  - Scaling
- Original vs compressed
  - $100 \times 100 \times 5 = 50000$
  - $100 \times 100 + 2 \times 5 + 2 \times 5 = 10020$

$$3 \mid 3 \mid 3 \mid 3 \mid 3$$

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## Principal Component Analysis (PCA)

- PCA is a technique for reducing the complexity of high dimensional data
- It can be used to approximate high dimensional data with a few dimensions (latent features) → much less data to store
- New variables might have a special interpretation

### Applications

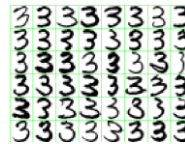
- Image recognition
- Information compression
- Subspace clustering
- ...

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## Principal Component Analysis (PCA)

- Example 1: Handwritten digits
  - Can we get a more compact summary?

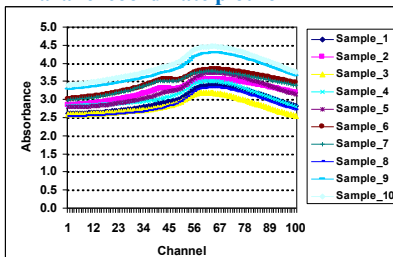


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## Absorbance records for ten samples of chopped meat

### Parallel coordinate plot for "FAT"



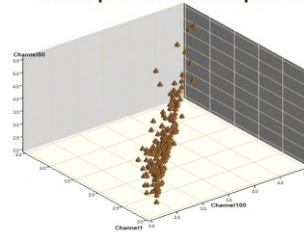
1 target (fat)  
100 features  
(absorbance at 100  
wavelengths or  
channels)  
The features are  
strongly correlated  
to each other

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## 3-D plots of absorbance records for samples of meat - channels 1, 50 and 100

### Scatterplot for three components



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## Principal components analysis

**Idea:** Introduce a new coordinate system (PC1, PC2, ...) where

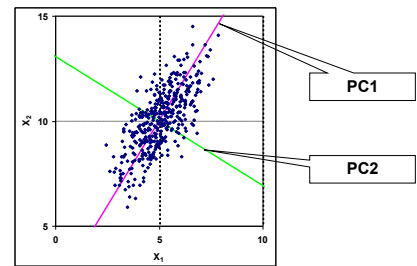
- The first principal component (PC1) is the direction that maximizes the variance of the projected data
- The second principal component (PC2) is the direction that maximizes the variance of the projected data after the variation along PC1 has been removed
- The third principal component (PC3) is the direction that maximizes the variance of the projected data after the variation along PC1 and PC2 has been removed
- ....

In the new coordinate system, coordinates corresponding to the last principal components are very small → can take away these columns

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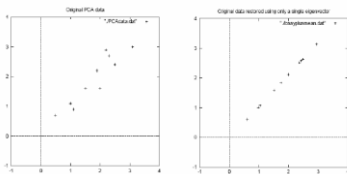
## Principal Component Analysis - two inputs



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## PCA- after reducing dimensionality



- Data became approximate (but less data to store)
- $PC_1, \dots, PC_M$  are actually **eigenvectors of sample covariance** (first largest eigenvalue, ..., Mth largest eigenvalue)

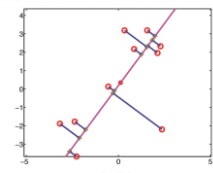
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## PCA: another view

- Aim: minimize the distance between the original and projected data

$$\min_V \sum_{i=1}^N \|x_n - \tilde{x}_n\|^2$$



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## PCA: computations

Data  $D = \begin{bmatrix} \mathbf{x}_1 & \mathbf{x}_2 & \dots & \mathbf{x}_p \end{bmatrix}$ ,  $\mathbf{x}_i = (x_{i1}, \dots, x_{in})$

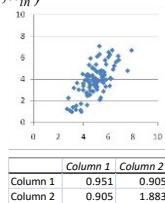
1. Centred data

$$X = \begin{bmatrix} \mathbf{x}_1 - \bar{\mathbf{x}}_1 & \mathbf{x}_2 - \bar{\mathbf{x}}_2 & \dots & \mathbf{x}_p - \bar{\mathbf{x}}_p \end{bmatrix}$$

2. Covariance matrix

$$S = \frac{1}{N} X^T X$$

3. Search for eigenvectors and eigenvalues of  $S$



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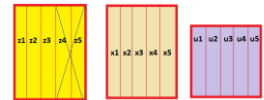
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## PCA: computations

4. Coordinates of any data point  $\mathbf{x} = (x_1, \dots, x_p)$  in the new coordinate system:

$$\mathbf{z} = (z_1, \dots, z_n), z_i = \mathbf{x}^T \mathbf{u}_i$$



Matrix form:  $\mathbf{Z} = \mathbf{X} \mathbf{U}$

5. Discard principle components after some  $M$

Store:  $N \times M + p \times M$   
instead  $N \times p$

6. New data will have dimensions  $N \times M$  instead of  $N \times p$

100\*50 vs  
100\*4+50\*4

Getting approximate original data:

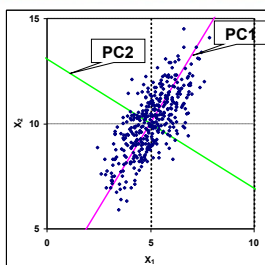
$$\mathbf{X}' = \mathbf{Z} \mathbf{U}_M^T$$

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## Principal Component Analysis



Eigenanalysis of the Covariance Matrix

Eigenvalue	2.8162	0.3835
Proportion	0.880	0.120
Cumulative	0.880	1.000

Variable	PC1	PC2
X1	0.523	0.852
X2	0.852	-0.523

Loadings (U)

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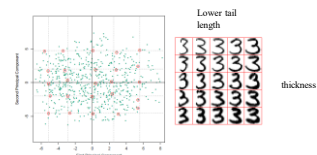
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## Principal Component Analysis

- Digits: two eigenvectors extracted

$$\mathbf{x} = \begin{bmatrix} 3 \\ 3 \end{bmatrix} + z_1 \begin{bmatrix} 3 \\ 3 \end{bmatrix} + z_2 \begin{bmatrix} 3 \\ 3 \end{bmatrix}$$

- Interpretation of eigenvectors



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## PCA in R

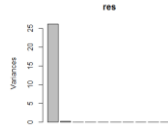
- `Prcomp()`, `biplot()`, `screplot()`

```
mydata=read.csv2("tecaton.csv")
data1=mydata
data1$fat=c()
res=prcomp(data1)
lambda=res$sdev^2
#eigenvalues
lambda
#proportion of variation
sprintf("%2.3f",lambda/sum(lambda)*100)
screplot(res)
```

[1] 2.612713e+01 2.385369e-01 7.844883e-02 3.018501e-01  
[7] 2.052212e-04 1.084213e-04 2.077326e-05 1.150359e-05

> lambda

[1] "98.679" "0.901" "0.296" "0.114" "0.006"  
[9] "0.000" "0.000" "0.000" "0.000" "0.000"



Only 1 component captures the 99% of variation!

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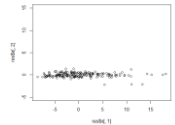
## PCA in R

- Principal component loadings (U)

```
U=res$rotation
head(U)
```

> head(U)

	PC1	PC2	PC3
Channel11	0.07938192	0.1156228	0.08073156
Channel12	0.07987445	0.1170972	0.07887873
Channel13	0.08036498	0.1185571	0.07702127
Channel14	0.08085611	0.1200006	0.07515015
Channel15	0.08135022	0.1214075	0.07323819
Channel16	0.08184806	0.1227401	0.07136048



- Data in (PC1, PC2) – scores (Z)

```
plot(res$x[,1],res$x[,2],ylim=c(-5,15))
```

Do we need second dimension?

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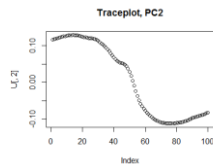
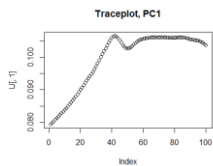
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## PCA in R

- Trace plots

```
U=loadings(res)
plot(U[,1], main="Traceplot, PC1")
plot(U[,2],main="Traceplot, PC2")
```



Which components contribute to PC1-2?

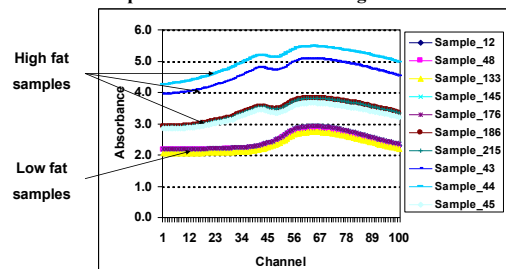
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## Absorbance records for ten samples of chopped meat

### PCA2 captures the most of remaining variation



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## PCA for high-dimensional data

- Standard PCA for  $p \gg N$ 
  - At most  $N$  eigenvalues are nonzero
  - Running time is  $O(p^3)$
- High-dimensional PCA
  1. Use  $S' = \frac{1}{N} X X^T$  (instead of  $S = \frac{1}{N} X^T X$ )
  2. Eigenvalues do not change
  3. Eigenvectors of  $S$  are  $X^T v_i$

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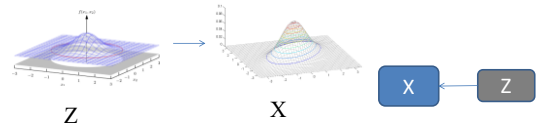
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## Probabilistic PCA

- $z_i$ -latent variables,  $x_i$ -observed variables
 
$$z \sim N(0, I)$$

$$x|z \sim N(x|Wz + \mu, \sigma^2 I)$$
- Alternatively
 
$$z \sim N(0, I), x = \mu + Wz + \epsilon, \epsilon \sim N(0, \sigma^2 I)$$
- **Interpretation:** Observed data ( $X$ ) is obtained by rotation, scaling and translation of standard normal distribution ( $Z$ ) and adding some noise.



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## Probabilistic PCA

- **Aim:** extract  $Z$  from  $X$
- Distribution of  $x$ :
 
$$x \sim N(\mu, C)$$

$$C = WW^T + \sigma^2 I$$
- Rotation invariance
  - Assume that  $x$  was generated from  $z' = Rz, RR^T = I$ ,  $p(x)$  does not change!
 
$$x|z' \sim N(x|Wz' + \mu, \sigma^2 I)$$
  - **Model will not be able to find latent factors uniquely!** ☹️
    - It does not distinguish  $z$  from  $z'$

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## Probabilistic PCA

- Estimation of parameters: ML

**Theorem.** ML estimates are given by

$$\mu_{ML} = \bar{x}$$

$$W_{ML} = U_M (L_M - \sigma_{ML}^2 I)^{\frac{1}{2}} R$$

$$\sigma_{ML}^2 = \frac{1}{p-M} \sum_{i=M+1}^p \lambda_i$$

- $U_M$  matrix of  $M$  eigenvectors
- $L_M$  diagonal matrix of  $M$  eigenvalues
- $R$  any orthogonal matrix

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## Probabilistic PCA

- Estimation of  $Z$ 
  - Use mean of posterior
$$\hat{z} = (W_{ML}^T W_{ML} + \sigma_{ML}^2 I)^{-1} W_{ML}^T (x - \mu)$$
- Connection to standard PCA
  - Assume  $R = I, \sigma^2 = 0 \rightarrow$  get standard PCA components scaled by inverse root of eigenvalues
$$Z = XUL^{-\frac{1}{2}}$$

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## Advantages of probabilistic PCA

- More settings to specify  $\rightarrow$  more flexible
- Can be faster when  $M \ll p$
- Missing values can be handled
- $M$  can be derived if a Bayesian version is used
- Probabilistic PCA can be applied to classification problems directly
- Probabilistic PCA can generate new data

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## Probabilistic PCA in R

- Use **pcaMethods** from Bioconductor
- Install
  - `source("https://bioconductor.org/biocLite.R")`
  - `biocLite("pcaMethods")`

`Ppca(data, nPcs,...)`

**Results:** scores, loadings...

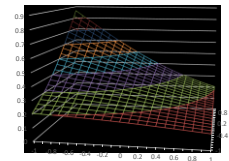
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## Independent component analysis (ICA)

- Probabilistic PCA does not capture latent factors
  - Rotation invariance
- Let's choose distribution which is not rotation invariant  $\rightarrow$  will get unique latent factors
- Choose non-Gaussian  $p_i(z) = p(z)$
- Assuming latent features are **independent**



$$p(z) = \prod_{i=1}^M p_i(z_i)$$

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## ICA

- **Model**

$$x = \mu + Wz + \epsilon, \quad \epsilon \sim \mathcal{N}(0, \Sigma)$$

- **Estimation A: Maximum likelihood** ( $V = W^{-1}$ )

- Assuming noise-free  $x$

$$\max_V \sum_{i=1}^n \sum_{j=1}^p \log(p_j(v_j^T x_i))$$

$$\text{Subject to } \|v_i\| = 1$$

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## ICA

- Setting  $G_j(z) = -\log(p_j(z))$ ,  $z_j = v_j^T x$  and assuming large sample

$$\min_V \sum_{j=1}^p E(G_j(z_j))$$

$$\text{Subject to } \|v_i\| = 1$$

- **Prewhitening**

- Use PCA:  $X' = XU$
- Computing  $z_i$ s for given  $V$ :  $Z = X'V$

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## ICA

- **Estimation B: maximize negentropy**

- ICA looks for model which is as much non-Gaussian as possible

- **Entropy**  $H(z) = -\int p(z) \log p(z) dz = E(-\log p(z))$

- **Negentropy**  $J(z_i) = H(z_i') - H(z_i)$

- $z_i' \sim \mathcal{N}(E(z_i), \text{var}(z_i))$

- **Negentropy maximization**

$$\max_V \sum_{j=1}^p J(z_j) = \min_V \sum_{j=1}^p H(z_j) = \min_V \sum_{j=1}^p E(-\log p(z_j))$$

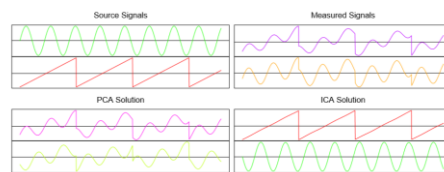
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## ICA

- **Example**



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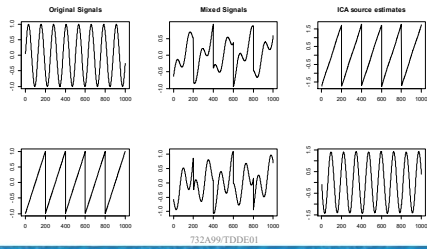
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## Independent component analysis: R

```
S <- cbind(sin((1:1000)/20), rep((((1:200)-100)/100), 5)) #Generate data
A <- matrix(c(0.291, 0.6557, -0.5439, 0.5572), 2, 2)
X <- S %*% A
a <- fastICA(X, 2, alg.typ = "parallel", fun = "logcosh", alpha = 1,
method = "R", row.norm = FALSE, maxit = 200, tol = 0.0001, verbose = TRUE) #ICA
```



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