

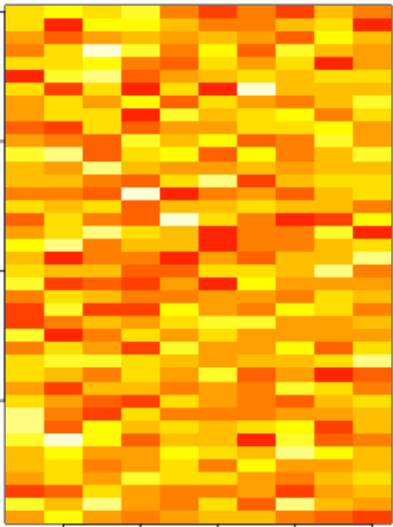


# Principal Components Analysis and Singular Value Decomposition

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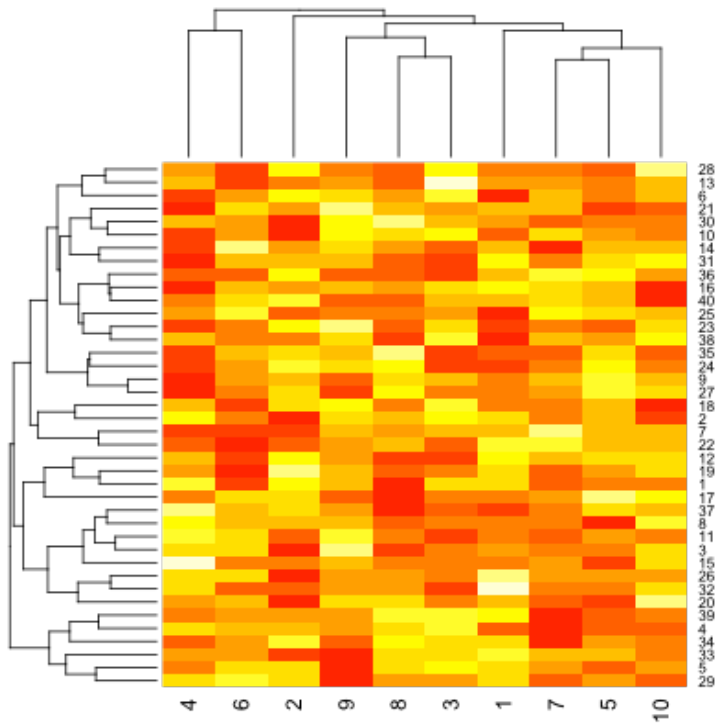
# Matrix data

```
set.seed(12345)
par(mar = rep(0.2, 4))
dataMatrix <- matrix(rnorm(400), nrow = 40)
image(1:10, 1:40, t(dataMatrix)[, nrow(dataMatrix):1])
```



# Cluster the data

```
par(mar = rep(0.2, 4))  
heatmap(dataMatrix)
```

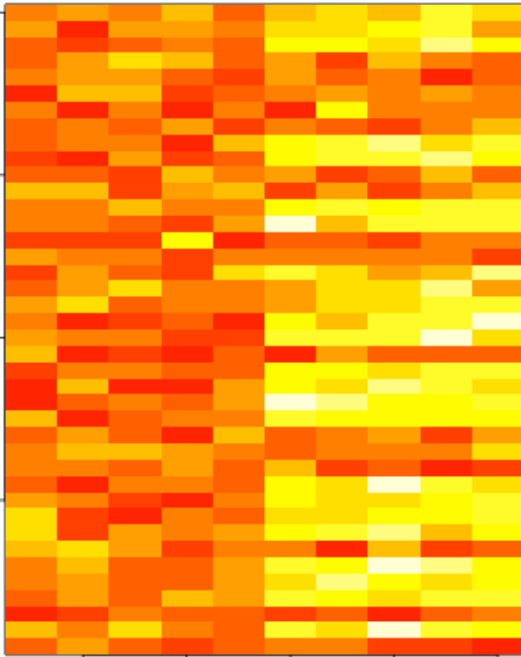


# What if we add a pattern?

```
set.seed(678910)
for (i in 1:40) {
  # flip a coin
  coinFlip <- rbinom(1, size = 1, prob = 0.5)
  # if coin is heads add a common pattern to that row
  if (coinFlip) {
    dataMatrix[i, ] <- dataMatrix[i, ] + rep(c(0, 3), each = 5)
  }
}
```

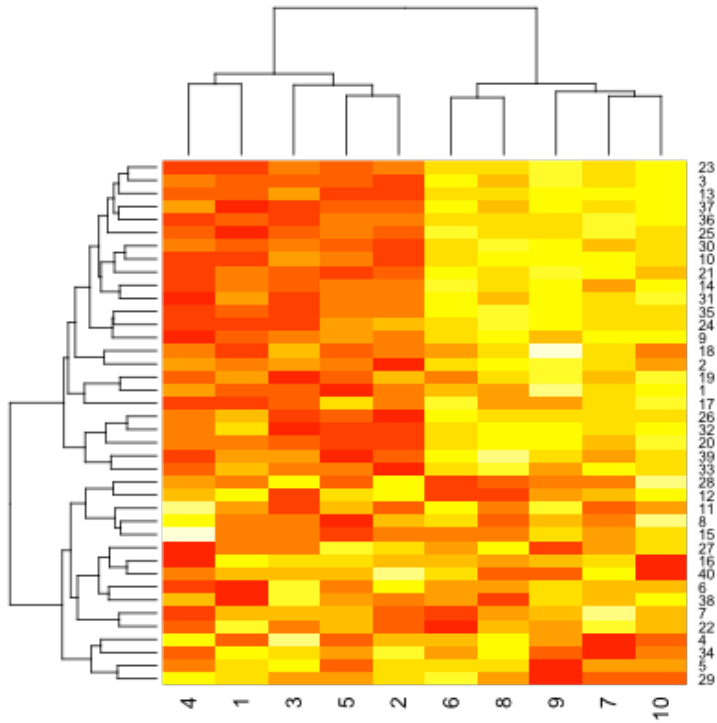
# What if we add a pattern? - the data

```
par(mar = rep(0.2, 4))  
image(1:10, 1:40, t(dataMatrix)[, nrow(dataMatrix):1])
```



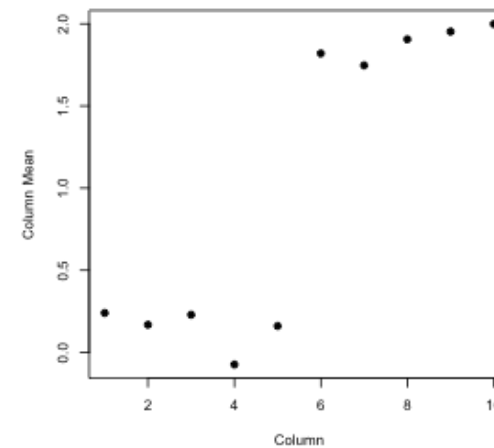
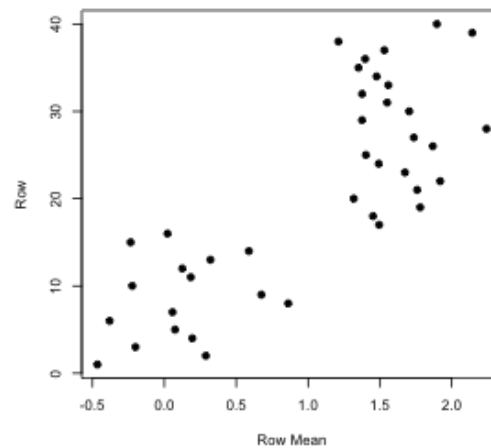
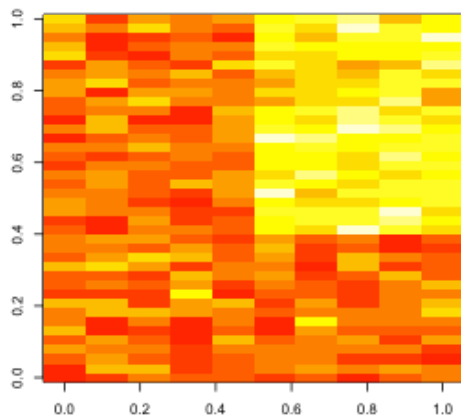
# What if we add a pattern? - the clustered data

```
par(mar = rep(0.2, 4))  
heatmap(dataMatrix)
```



# Patterns in rows and columns

```
hh <- hclust(dist(dataMatrix))  
dataMatrixOrdered <- dataMatrix[hh$order, ]  
par(mfrow = c(1, 3))  
image(t(dataMatrixOrdered)[, nrow(dataMatrixOrdered):1])  
plot(rowMeans(dataMatrixOrdered), 40:1, , xlab = "Row Mean", ylab = "Row", pch = 19)  
plot(colMeans(dataMatrixOrdered), xlab = "Column", ylab = "Column Mean", pch = 19)
```



# Related problems

You have multivariate variables  $X_1, \dots, X_n$  so  $X_1 = (X_{11}, \dots, X_{1m})$

- Find a new set of multivariate variables that are uncorrelated and explain as much variance as possible.
- If you put all the variables together in one matrix, find the best matrix created with fewer variables (lower rank) that explains the original data.

The first goal is **statistical** and the second goal is **data compression**.



# Related solutions - PCA/SVD

## SVD

If  $X$  is a matrix with each variable in a column and each observation in a row then the SVD is a "matrix decomposition"

$$X = UDV^T$$

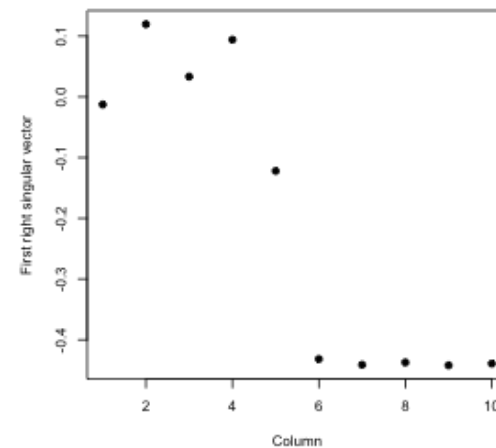
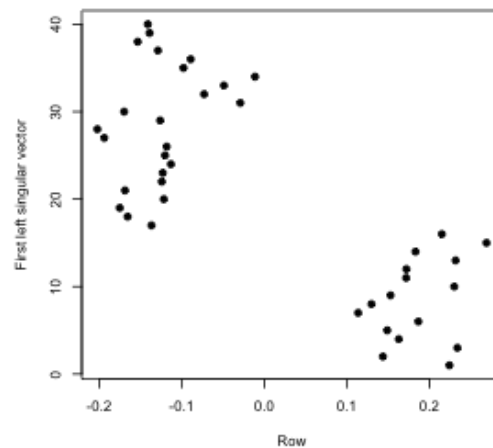
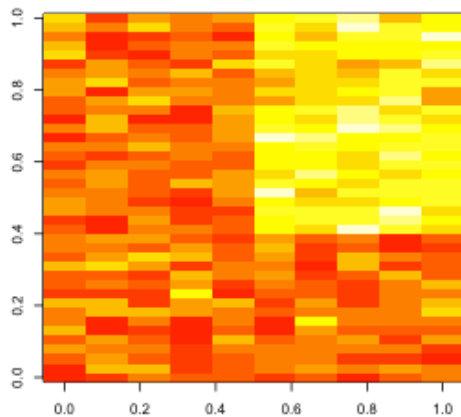
where the columns of  $U$  are orthogonal (left singular vectors), the columns of  $V$  are orthogonal (right singular vectors) and  $D$  is a diagonal matrix (singular values).

## PCA

The principal components are equal to the right singular values if you first scale (subtract the mean, divide by the standard deviation) the variables.

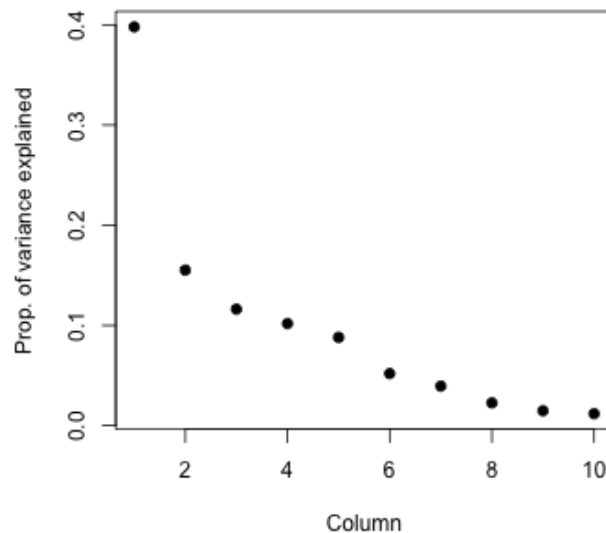
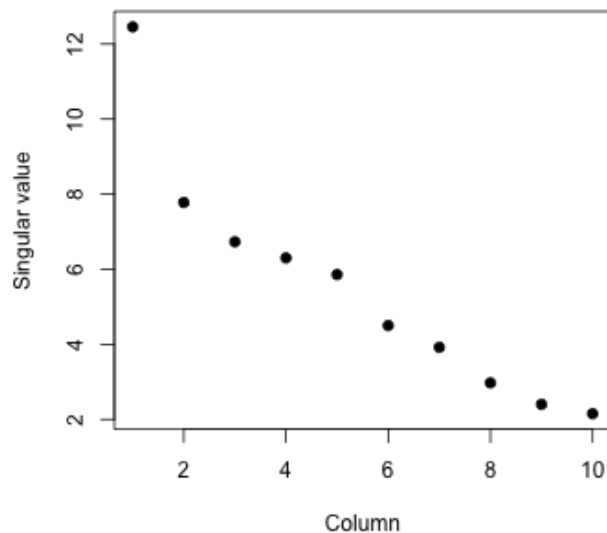
# Components of the SVD - $u$ and $v$

```
svd1 <- svd(scale(dataMatrixOrdered))  
par(mfrow = c(1, 3))  
image(t(dataMatrixOrdered)[, nrow(dataMatrixOrdered):1])  
plot(svd1$u[, 1], 40:1, , xlab = "Row", ylab = "First left singular vector",  
     pch = 19)  
plot(svd1$v[, 1], xlab = "Column", ylab = "First right singular vector", pch = 19)
```



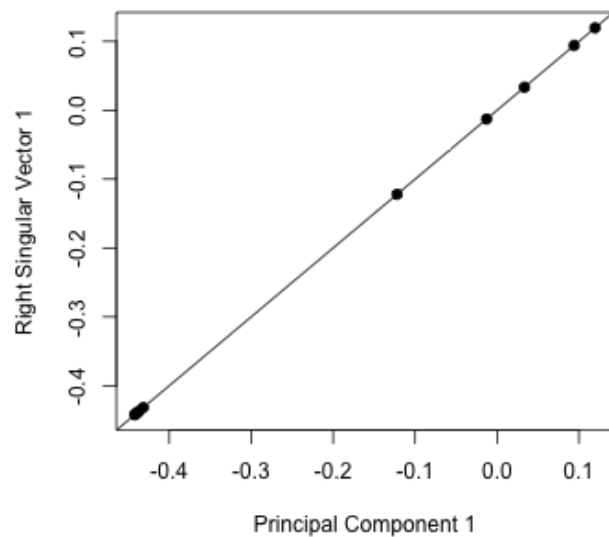
# Components of the SVD - Variance explained

```
par(mfrow = c(1, 2))  
plot(svd1$d, xlab = "Column", ylab = "Singular value", pch = 19)  
plot(svd1$d^2/sum(svd1$d^2), xlab = "Column", ylab = "Prop. of variance explained",  
     pch = 19)
```



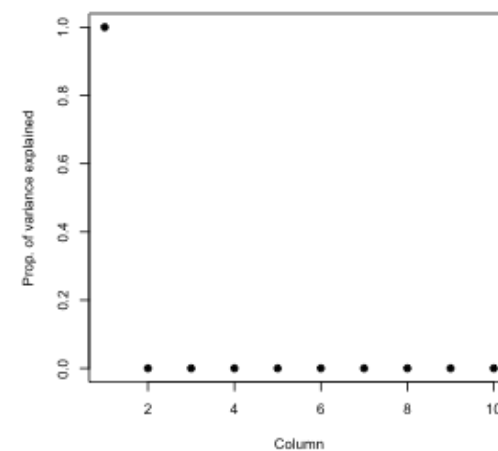
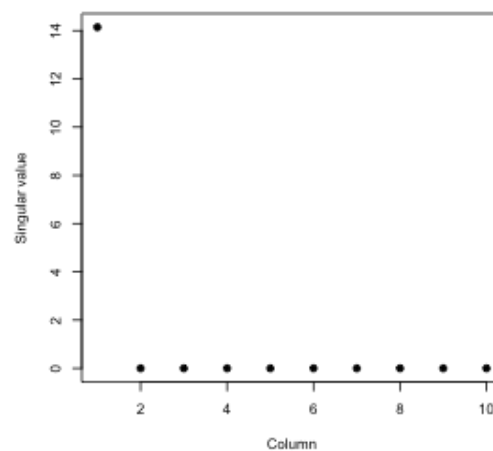
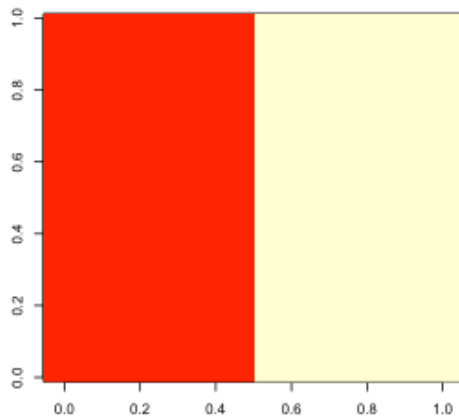
# Relationship to principal components

```
svd1 <- svd(scale(dataMatrixOrdered))  
pca1 <- prcomp(dataMatrixOrdered, scale = TRUE)  
plot(pca1$rotation[, 1], svd1$v[, 1], pch = 19, xlab = "Principal Component 1",  
      ylab = "Right Singular Vector 1")  
abline(c(0, 1))
```



# Components of the SVD - variance explained

```
constantMatrix <- dataMatrixOrdered*0
for(i in 1:dim(dataMatrixOrdered)[1]){constantMatrix[i,] <- rep(c(0,1),each=5)}
svd1 <- svd(constantMatrix)
par(mfrow=c(1,3))
image(t(constantMatrix)[,nrow(constantMatrix):1])
plot(svd1$d,xlab="Column",ylab="Singular value",pch=19)
plot(svd1$d^2/sum(svd1$d^2),xlab="Column",ylab="Prop. of variance explained",pch=19)
```

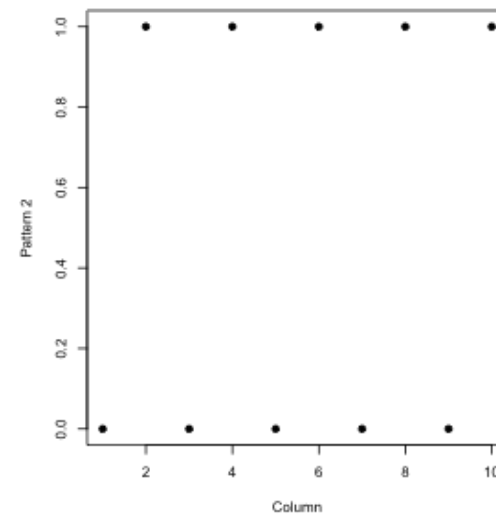
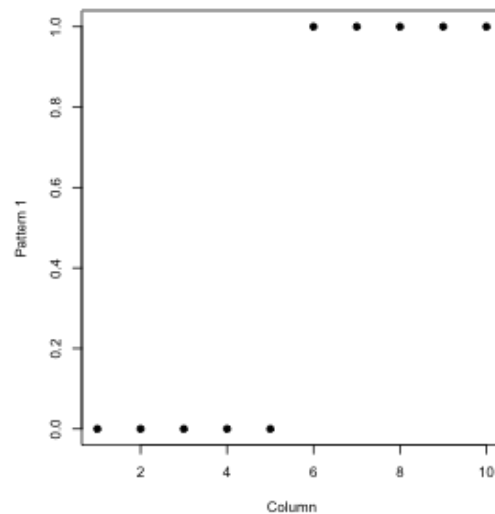
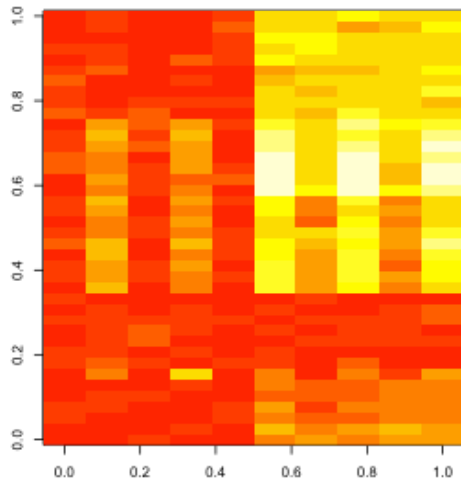


# What if we add a second pattern?

```
set.seed(678910)
for (i in 1:40) {
  # flip a coin
  coinFlip1 <- rbinom(1, size = 1, prob = 0.5)
  coinFlip2 <- rbinom(1, size = 1, prob = 0.5)
  # if coin is heads add a common pattern to that row
  if (coinFlip1) {
    dataMatrix[i, ] <- dataMatrix[i, ] + rep(c(0, 5), each = 5)
  }
  if (coinFlip2) {
    dataMatrix[i, ] <- dataMatrix[i, ] + rep(c(0, 5), 5)
  }
}
hh <- hclust(dist(dataMatrix))
dataMatrixOrdered <- dataMatrix[hh$order, ]
```

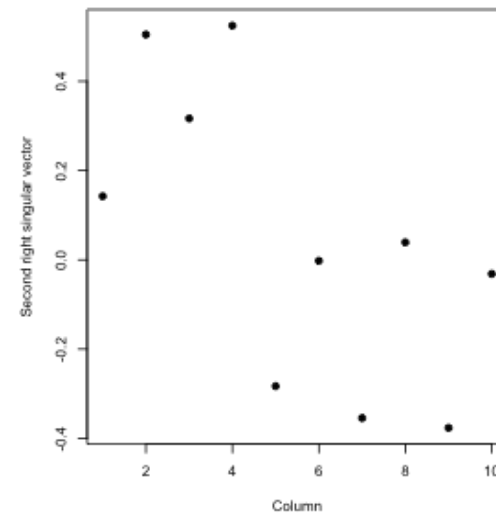
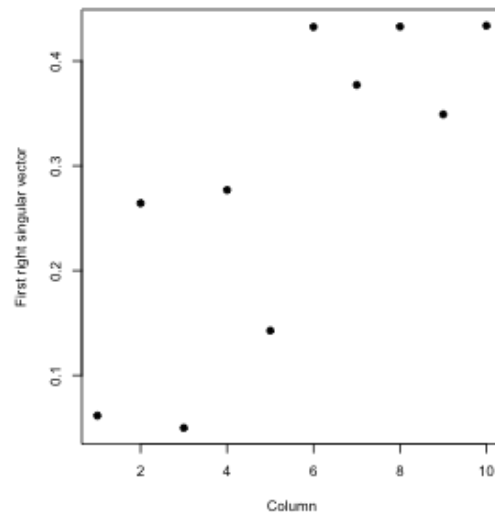
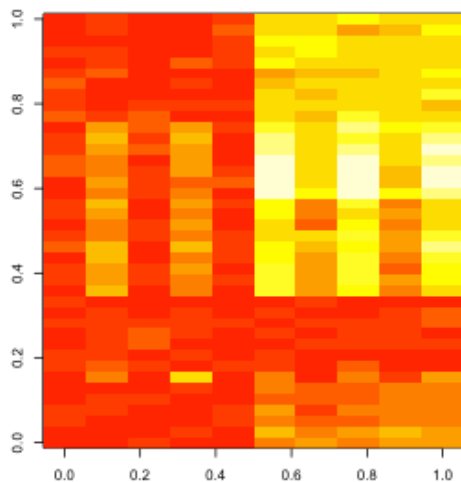
# Singular value decomposition - true patterns

```
svd2 <- svd(scale(dataMatrixOrdered))  
par(mfrow = c(1, 3))  
image(t(dataMatrixOrdered)[, nrow(dataMatrixOrdered):1])  
plot(rep(c(0, 1), each = 5), pch = 19, xlab = "Column", ylab = "Pattern 1")  
plot(rep(c(0, 1), 5), pch = 19, xlab = "Column", ylab = "Pattern 2")
```



# $v$ and patterns of variance in rows

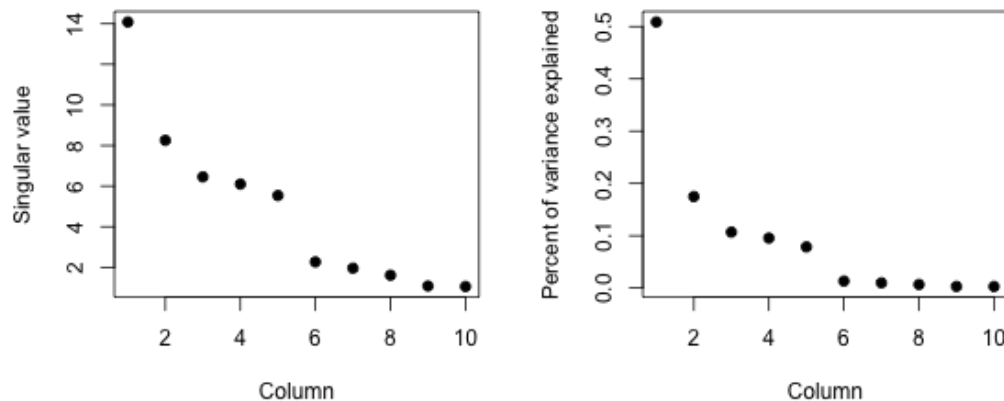
```
svd2 <- svd(scale(dataMatrixOrdered))  
par(mfrow = c(1, 3))  
image(t(dataMatrixOrdered)[, nrow(dataMatrixOrdered):1])  
plot(svd2$v[, 1], pch = 19, xlab = "Column", ylab = "First right singular vector")  
plot(svd2$v[, 2], pch = 19, xlab = "Column", ylab = "Second right singular vector")
```





# $d$ and variance explained

```
svd1 <- svd(scale(dataMatrixOrdered))  
par(mfrow = c(1, 2))  
plot(svd1$d, xlab = "Column", ylab = "Singular value", pch = 19)  
plot(svd1$d^2/sum(svd1$d^2), xlab = "Column", ylab = "Percent of variance explained",  
     pch = 19)
```



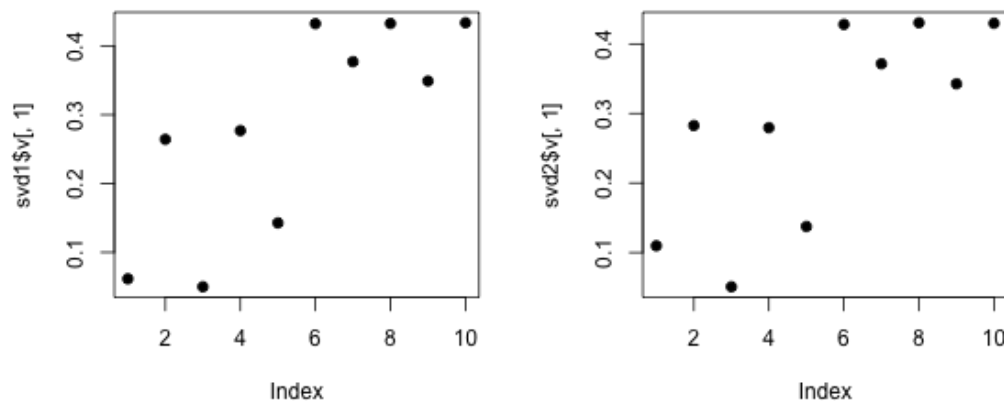
# Missing values

```
dataMatrix2 <- dataMatrixOrdered
## Randomly insert some missing data
dataMatrix2[sample(1:100, size = 40, replace = FALSE)] <- NA
svd1 <- svd(scale(dataMatrix2)) ## Doesn't work!
```

```
## Error: infinite or missing values in 'x'
```

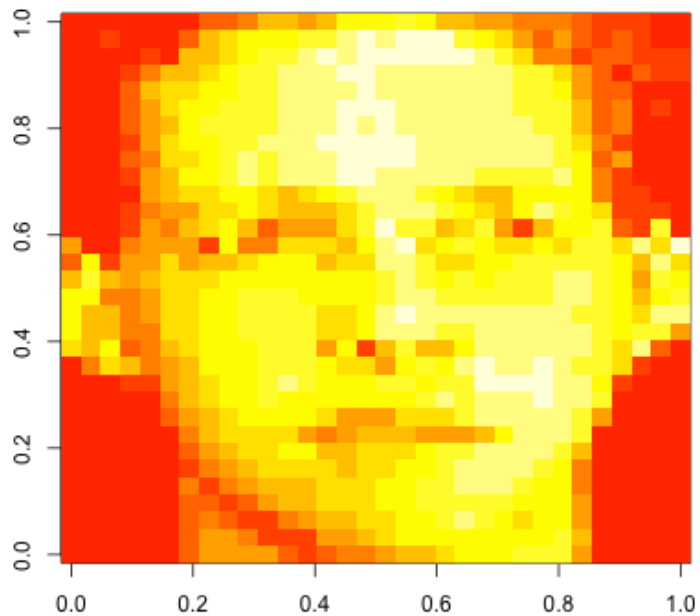
# Imputing {impute}

```
library(impute) ## Available from http://bioconductor.org
dataMatrix2 <- dataMatrixOrdered
dataMatrix2[sample(1:100,size=40,replace=FALSE)] <- NA
dataMatrix2 <- impute.knn(dataMatrix2)$data
svd1 <- svd(scale(dataMatrixOrdered)); svd2 <- svd(scale(dataMatrix2))
par(mfrow=c(1,2)); plot(svd1$v[,1],pch=19); plot(svd2$v[,1],pch=19)
```



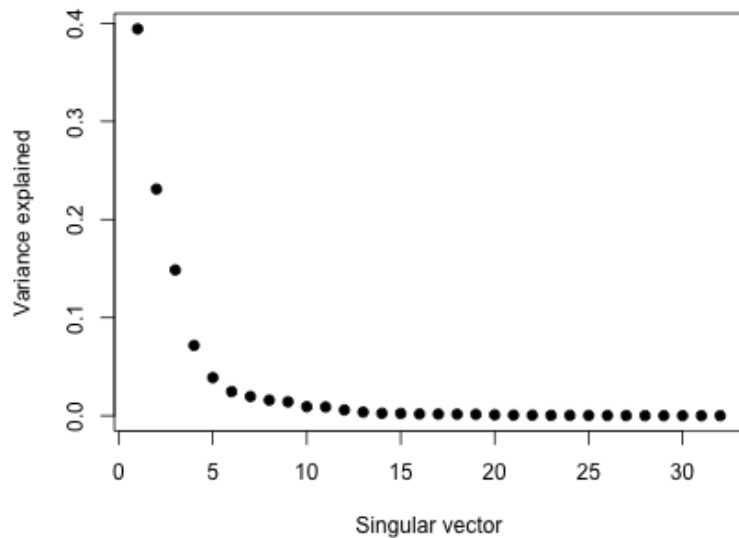
# Face example

```
load("data/face.rda")  
image(t(faceData)[, nrow(faceData):1])
```



# Face example - variance explained

```
svd1 <- svd(scale(faceData))  
plot(svd1$d^2/sum(svd1$d^2), pch = 19, xlab = "Singular vector", ylab = "Variance explained")
```

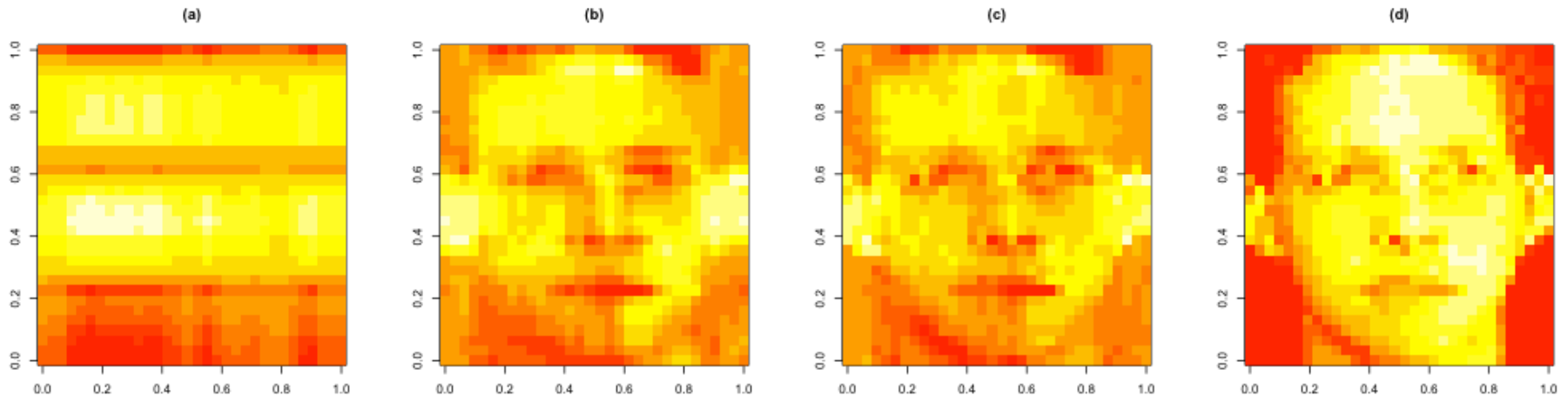


# Face example - create approximations

```
svd1 <- svd(scale(faceData))  
## Note that %*% is matrix multiplication  
  
# Here svd1$d[1] is a constant  
approx1 <- svd1$u[, 1] %*% t(svd1$v[, 1]) * svd1$d[1]  
  
# In these examples we need to make the diagonal matrix out of d  
approx5 <- svd1$u[, 1:5] %*% diag(svd1$d[1:5]) %*% t(svd1$v[, 1:5])  
approx10 <- svd1$u[, 1:10] %*% diag(svd1$d[1:10]) %*% t(svd1$v[, 1:10])
```

# Face example - plot approximations

```
par(mfrow = c(1, 4))  
image(t(approx1)[, nrow(approx1):1], main = "(a)")  
image(t(approx5)[, nrow(approx5):1], main = "(b)")  
image(t(approx10)[, nrow(approx10):1], main = "(c)")  
image(t(faceData)[, nrow(faceData):1], main = "(d)") ## Original data
```



# Notes and further resources

- **Scale matters**
- PC's/SV's may mix real patterns
- Can be computationally intensive
- [Advanced data analysis from an elementary point of view](#)
- [Elements of statistical learning](#)
- Alternatives
  - [Factor analysis](#)
  - [Independent components analysis](#)
  - [Latent semantic analysis](#)