Live-Demo in R

Workflow of a typical data analysis

A live demo

1. General note on data graphics in R
2. We demonstrate the typical workflow of an in-depth analysis
    - Data cleaning
    - Exploratory analysis
    - Statistical methods
    - Model evaluation & feature selection
3. Step-by-step demonstration

Analysis goals

1. **Analyze decisions on credit approvals**
   - From the free dataset repository of the University of California (https://archive.ics.uci.edu/ml/datasets.html)
   - Data about credit card applications
   - Contains a good mix of continuous and nominal attributes, including a few missing values
2. **Analytical questions**
   - What are driving attributes behind approvals?
   - Can we predict approvals?
   - Are there clear rules?

Methods

- Understanding the data via queries, aggregations and visualizations
- See if there is a clustering of acceptance/denial events
- Predicting the outcome of the credit card application via classification/regression
- Model evaluation

Introduction

Basic concepts of data graphics in R

An overview of data graphics in R

- There are 3 main graphics systems in R
  - built-in functionality (examples: plot(), hist(), etc.)
  - `lattice` package (e.g. scatterplot matrices)
  - `ggplot2` (implements 'The Grammar of Graphics' [Wilkinson, 2005])

Creating a data toy example (1/2)

Examplify different plotting options of R with a little toy dataset

- The following code generates our toy data
- We will skip the code for a moment to get the intuition from a few appropriate plots
- Data: Relationships between 3 price classes, product quality and customer satisfaction

```r
# Create a scaling funtion that returns values between 0 and 100(%)
scale.fun <- function(vals) {return(abs( vals / max(vals) * 100 ))}
# Assume three different quality levels
quality.levels <- factor(c(1,2,3), labels=c("low", "mid", "hi"))
# Create a vector with 100 entries for each level
qualities <- rep(quality.levels, 100)
table(qualities)
```

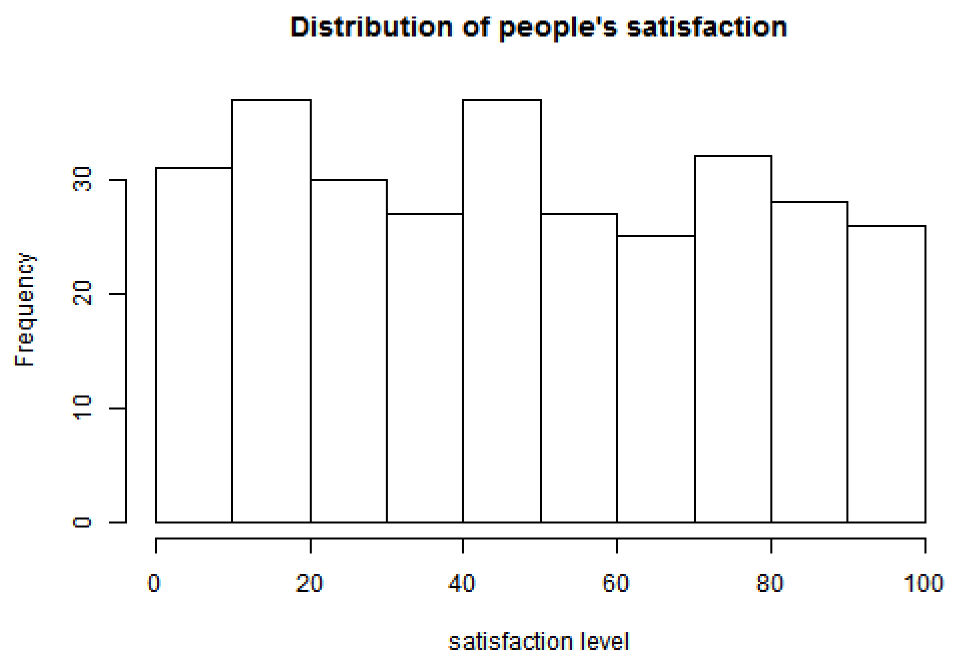
```
## qualities
## low mid  hi
## 100 100 100
```

Creating a data toy example (2/2)

```r
# Model relationship between price & customer satisfaction for different quality levels
dat <- data.frame(satisfaction=NA, price=NA, quality=qualities)

dat$price[dat$quality=="low"] <- 50:149
dat$price[dat$quality=="mid"] <- 150:249
dat$price[dat$quality=="hi"] <- 250:349

dat$satisfaction[dat$quality=="low"] <- scale.fun(0.1 * 1:100 + rnorm(100))
dat$satisfaction[dat$quality=="mid"] <- scale.fun(0.75 * 1:100 + rnorm(100))
dat$satisfaction[dat$quality=="hi"] <- scale.fun(runif(100))
```

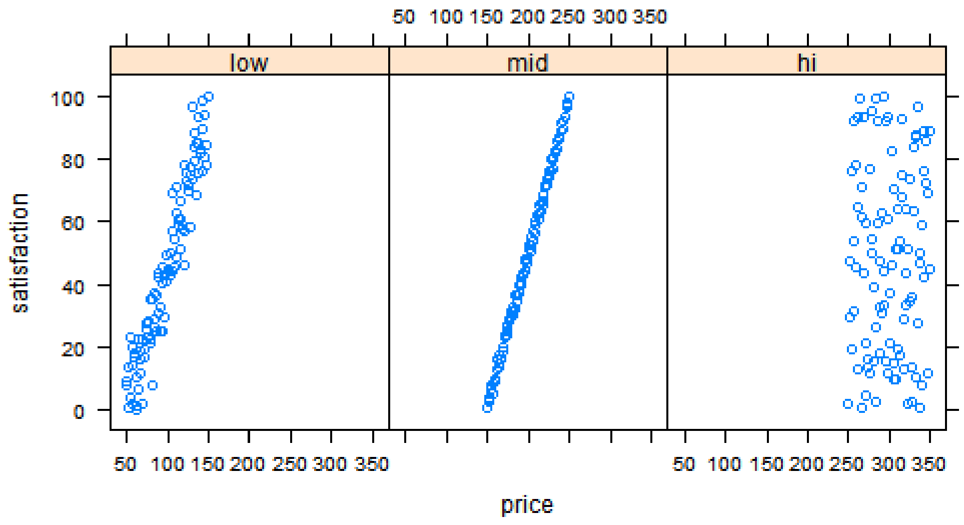
Example of a basic plot

```
# Create a histogram, suppress default label for x-axis
hist(dat$satisfaction, main="Distribution of people's satisfaction", xlab="")
# One can add things to the opened plot
title(xlab = "satisfaction level")
```



A simple `lattice` example

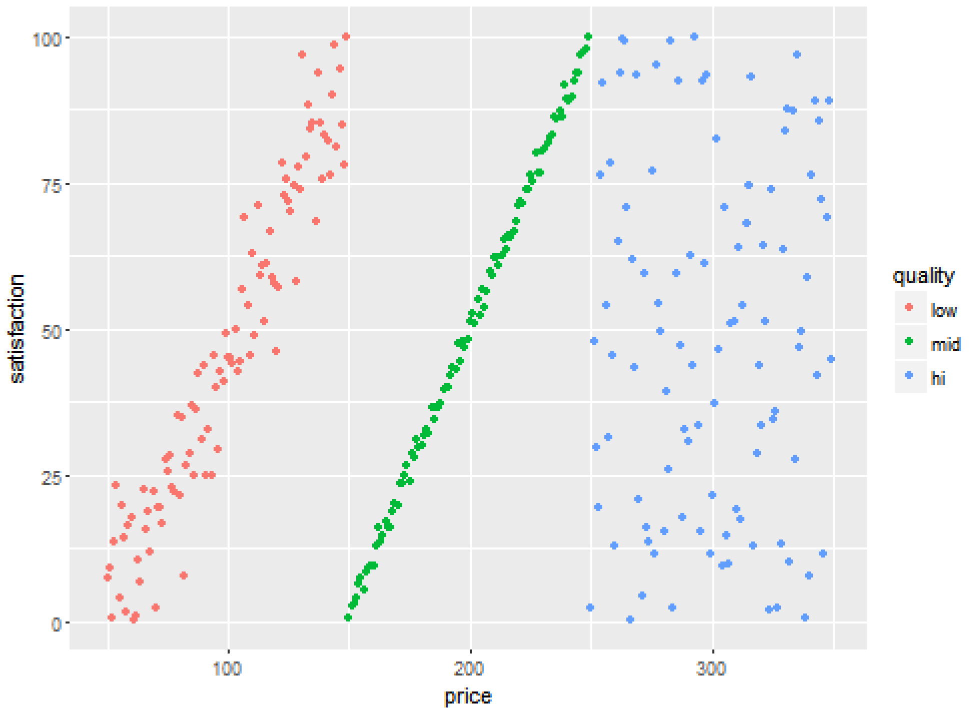
```r
require(lattice)
# Create a scatterplot for each quality level
xyplot(satisfaction ~ price | quality, data = dat)
```



Note that we can see now differing correlations between the variables.

A simple ggplot2 example

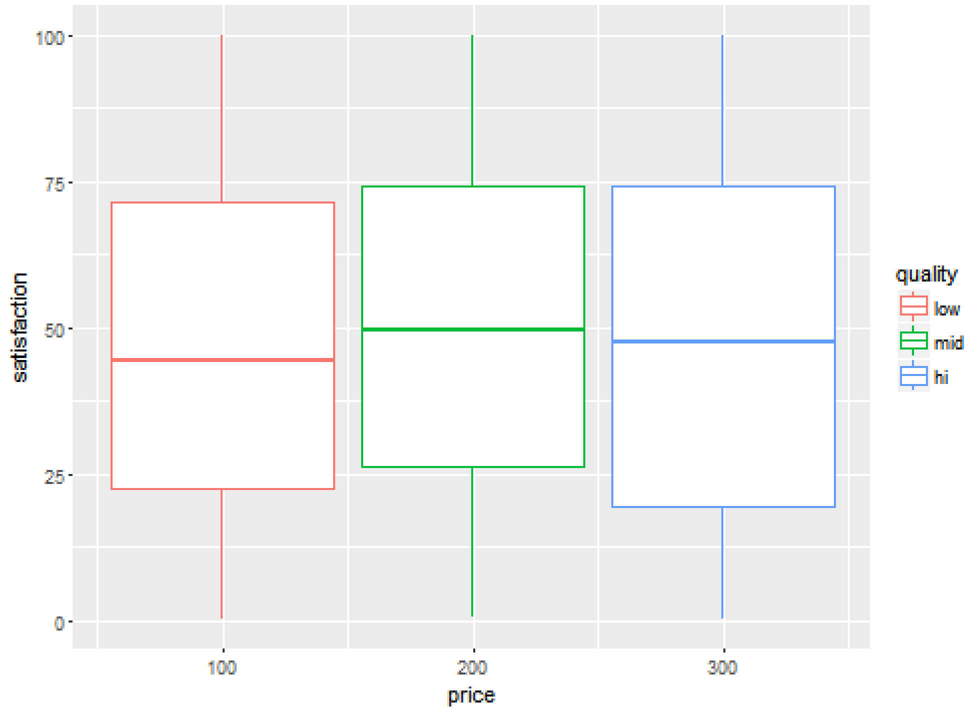
```r
require(ggplot2)
# Plot price vs. satisfaction in a colored scatterplot (Note: British spelling!)
ggplot(dat, aes(x=price, y=satisfaction, colour=quality)) + geom_point()
```



Other ggplot2 examples (1/2)

The concept of the grammar of graphs allows for easy adjustments of the visualization

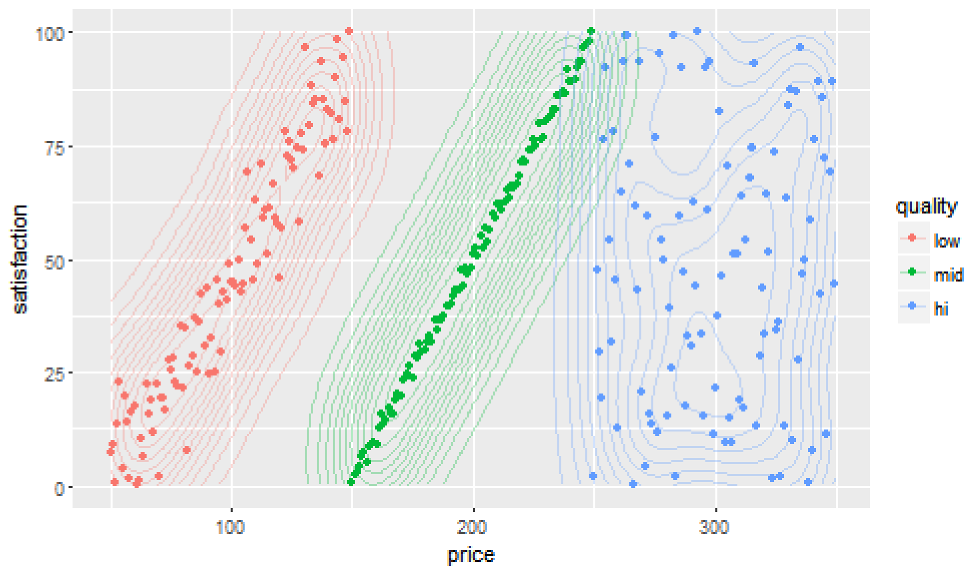
```
# Now a boxplot of the data (with a slight change of the command)
ggplot(dat, aes(x=price, y=satisfaction, colour=quality)) + geom_boxplot()
```



Other ggplot2 examples (2/2)

E.g. overlaying of several plots. For more information please have a look at: https://www.rstudio.com/wp-content/uploads/2015/03/ggplot2-cheatsheet.pdf

```
# Now a boxplot of the data (with a slight change of the command)
ggplot(dat, aes(x=price, y=satisfaction, colour=quality)) + geom_point() +
       geom_density2d(alpha=0.3)
```



Note on `ggplot2`

- The grammar of graphics formalizes a mapping of data characteristics to graphics, including:
  - geoms: Types of graphs
  - aesthetics: Dimensions of the graphs ("x-axis", "y-axis", "color")
  - and various other items

```
g <- ggplot(dat, aes(x=price, y=satisfaction, colour=quality)) + geom_point()
```

- The plus-sign is used to compose graphs
- There is also a convenience function `qplot`
- For furter information, have a look into the R Graphics Cookbook

Data Analysis - Part I

Data cleaning

Loading the data

```
# Read in the credit data from a CSV-file
raw.data <- read.csv("credit.csv", header=T, sep=",", stringsAsFactors=F)
```

The variable `raw.data` is of type data.frame.

```
# How many rows and columns? ("dimensions" of the data frame)
dim(raw.data)
```

```
## [1] 690  16
```

```
colnames(raw.data) # column names
```

```
##  [1] "A1"    "A2"    "A3"    "A4"    "A5"    "A6"    "A7"    "A8"   
##  [9] "A9"    "A10"   "A11"   "A12"   "A13"   "A14"   "A15"   "Class"
```

An initial inspection of the data

```r
# The str-function provides a quick overview
str(raw.data)
```

```
## 'data.frame':    690 obs. of  16 variables:
##  $ A1   : chr  "b" "a" "a" "b" ...
##  $ A2   : num  30.8 58.7 24.5 27.8 20.2 ...
##  $ A3   : num  0 4.46 0.5 1.54 5.62 ...
##  $ A4   : chr  "u" "u" "u" "u" ...
##  $ A5   : chr  "g" "g" "g" "g" ...
##  $ A6   : chr  "w" "q" "q" "w" ...
##  $ A7   : chr  "v" "h" "h" "v" ...
##  $ A8   : num  1.25 3.04 1.5 3.75 1.71 ...
##  $ A9   : chr  "t" "t" "t" "t" ...
##  $ A10  : chr  "t" "t" "f" "t" ...
##   [list output truncated]
```

Treatment of missing values (1/2)

```
dim(raw.data)
```

```
## [1] 690  16
```

```
# Check for missing values
any(is.na(raw.data))
```

```
## [1] TRUE
```

```
# Account for empty strings
raw.data[raw.data == ""] <- NA
```

Treatment of missing values (2/2)

```r
# Drop rows with NaN values
na.raw.inds <- which(apply(is.na(raw.data), 1, any))
length(na.raw.inds)
```

```
## [1] 37
```

```r
raw.data <- raw.data[-c(na.raw.inds),]
dim(raw.data)
```

```
## [1] 653  16
```

Inspecting a subset of the data

```
# Show a sample from the data
raw.data[c(1,5,8,353,601),]
```

```
##     A1    A2     A3 A4 A5 A6 A7   A8 A9 A10 A11 A12 A13 A14  A15 Class
## 1    b 30.83  0.000  u  g  w  v 1.25  t   t   1   f   g 202    0     +
## 5    b 20.17  5.625  u  g  w  v 1.71  t   f   0   f   s 120    0     +
## 8    a 22.92 11.585  u  g cc  v 0.04  t   f   0   f   g  80 1349     +
## 370  b 21.42  0.750  y  p  r  n 0.75  f   f   0   t   g 132    2     -
## 636  b 18.17  2.460  u  g  c  n 0.96  f   t   2   t   g 160  587     -
```

Replacements of symbolic true/false values (1/2)

```r
# We already know that the Class-column contains + and - signs
unique(raw.data$Class)
```

```
## [1] "+" "-"
```

```r
# However, what else?
head(raw.data, n=1)
```

```
##   A1    A2 A3 A4 A5 A6 A7   A8 A9 A10 A11 A12 A13 A14 A15 Class
## 1  b 30.83  0  u  g  w  v 1.25  t   t   1   f   g 202   0     +
```

Replacements of symbolic true/false values (2/2)

```
# Replace +/- values with 1/0
raw.data[raw.data$Class == "+", "Class"] <- 1.0
raw.data[raw.data$Class == "-", "Class"] <- 0.0
```

Conveniently, none of the categorical attributes contains the strings 't' of 'f', hence, we can easily substitute ...

```
# Replace t/f values with 1/0
raw.data[raw.data == "t"] <- 1.0
raw.data[raw.data == "f"] <- 0.0
```

Creating dummies for categorical variables (1/3)

Separate the sets of categorical and numerical variables

```
# (Already) numeric columns
to.keep <- c("Class", "A2", "A3", "A8", "A9", "A10", "A11","A12","A14","A15")
# Categorical columns
to.split <- c("A1", "A4", "A5", "A6", "A7", "A13")
```

```
# Separate numeric from categorical data
numeric.data <- raw.data[, to.keep]
dim(numeric.data)
```

```
## [1] 653  10
```

Creating dummies for categorical variables (2/3)

Introduce new columns with 0/1 values for categorical values

```r
ext.raw.data <- raw.data[,to.keep] # create a copy of the data frame

for (j in to.split) { # for each categorical variable

  fac <- as.factor(raw.data[,j]) # represent column as a factor
  for (categ in levels(fac)) { # handle each category ('level')

    tmp.vec <- fac == categ # creates vector of true/false values
    tmp.vec <- as.numeric(tmp.vec) # true => 1 # false => 0
    ext.raw.data <- cbind(ext.raw.data, tmp.vec) # append new column to data frame
    colnames(ext.raw.data)[ncol(ext.raw.data)] <-
      sprintf("%s(%s)", j, categ) # create useful column name
  }
}
```

Creating dummies for categorical variables (3/3)

Compare the dimensions of the data frame before and afterwards

```r
print(paste(dim(raw.data), dim(ext.raw.data), sep= " vs. "))
```

```
## [1] "653 vs. 653" "16 vs. 44"
```

Show example of new columns:

```r
lc.ind <- ncol(ext.raw.data)
str(ext.raw.data[, (lc.ind -2):lc.ind])
```

```
## 'data.frame':    653 obs. of  3 variables:
##  $ A13(g): num  1 1 1 1 0 1 1 1 1 1 ...
##  $ A13(p): num  0 0 0 0 0 0 0 0 0 0 ...
##  $ A13(s): num  0 0 0 0 1 0 0 0 0 0 ...
```

Export data to csv for inspection in an external editor

Export to csv:

```
write.table(ext.raw.data, "binarized_credit_data.csv", col.names = T,
            row.names=F, quote=F, sep=",")
```

Reading it back in:

```
ext.raw.data <- read.csv(ext.raw.data, "binarized_credit_data.csv", header=T,
                         stringsAsFactors = F, sep=",")
```

Finally, we update the name of the data frame to stay consistent

```
data <- ext.raw.data
```

Data Analysis - Part II

Exploratory analysis

Count non-zero entries (1/2)

```
# Check if all columns are numeric
all(sapply(data, is.numeric))
```

```
## [1] FALSE
```

```
# Need to convert each column of the matrix
data <- as.data.frame(apply(data, 2, as.numeric))
all(sapply(data, is.numeric))
```

```
## [1] TRUE
```

Count non-zero entries (2/2)

```
table(data[,"Class"])
```

```
##
##   0   1
## 357 296
```

```
# Count the non-zero entries of each attribute for each class
agg <- aggregate(subset(data, select = -Class), by=list(Class = data[,"Class"]),
          function(x) {length(x[x >0])})
agg[,c(1:10)]
```

```
##   Class  A2  A3  A8  A9 A10 A11 A12 A14 A15
## 1     0 357 349 311  71  84  84 157 309 190
## 2     1 296 291 282 278 203 203 145 216 188
```

Determining discriminative attributes (1/3)

We want to mark interesting attributes with high presence and strong discriminativity. This section also demonstrates the print()-function of R.

```r
agg <- subset(agg, select=-Class)
ratios <- sapply(agg, function(x) {x[2] / x[1]})
nonzeros <- colSums(agg)
inds.decreasing <- order(nonzeros, decreasing=T)

# Prepare a print-out ...
print(sprintf("% -8s % -8s (% -s)", "Attribute", "Count", "Ratio"))
print("--------------------------")
```

Determining discriminative attributes (2/3)

```r
# Do the print-out ...
for (i in inds.decreasing[1:15]) { # print out top 15 elements
  count <- nonzeros[i]
  ratio <- ratios[i]
  if (count > 10) {
    if (ratio > 2 || ratio < 0.5) {
      print(sprintf("% -8s % -8s  (%.2f)  <-- discriminates the classes well)",
                    names(ratios)[i], count, ratio))
    } else {
      print(sprintf("% -8s % -8s  (%.2f)", names(ratios)[i], count, ratio))
    }
  }
}
```

Determining discriminative attributes (3/3)

```
## [1] "Attribute Count    (Ratio)"
## [1] "---------------------------"
## [1] "A2       653       (0.83)"
## [1] "A3       640       (0.83)"
## [1] "A13(g)   598       (0.88)"
## [1] "A8       593       (0.91)"
## [1] "A14      525       (0.70)"
## [1] "A4(u)    499       (1.00)"
## [1] "A5(g)    499       (1.00)"
## [1] "A1(b)    450       (0.81)"
## [1] "A7(v)    381       (0.75)"
## [1] "A15      378       (0.99)"
## [1] "A9       349       (3.92)  <-- discriminates the classes well)"
## [1] "A12      302       (0.92)"
## [1] "A10      287       (2.42)  <-- discriminates the classes well)"
## [1] "A11      287       (2.42)  <-- discriminates the classes well)"
```

Selecting discriminative attributes by correlations

This is an alternative approach for determining single descriminative attributes. We rank attributes by their pairwise Pearson's correlations with the class labels.

```r
# Compute Pearson's correlation between attributes and the class labels
test <- cor(subset(data, select=-Class), as.numeric(data[,"Class"]))
sort(test, decreasing = T)[1:10]
```

```
##  [1] 0.7388289 0.4518657 0.4060516 0.3327282 0.2070860 0.1881173 0.1844048
##  [8] 0.1802520 0.1727660 0.1652691
```

```r
top5 <- rownames(test)[order(test, decreasing = T)][1:5]
top5
```

```
## [1] "A9"  "A10" "A11" "A8"  "A3"
```

Visualizing with a scatterplot matrix (1/4)

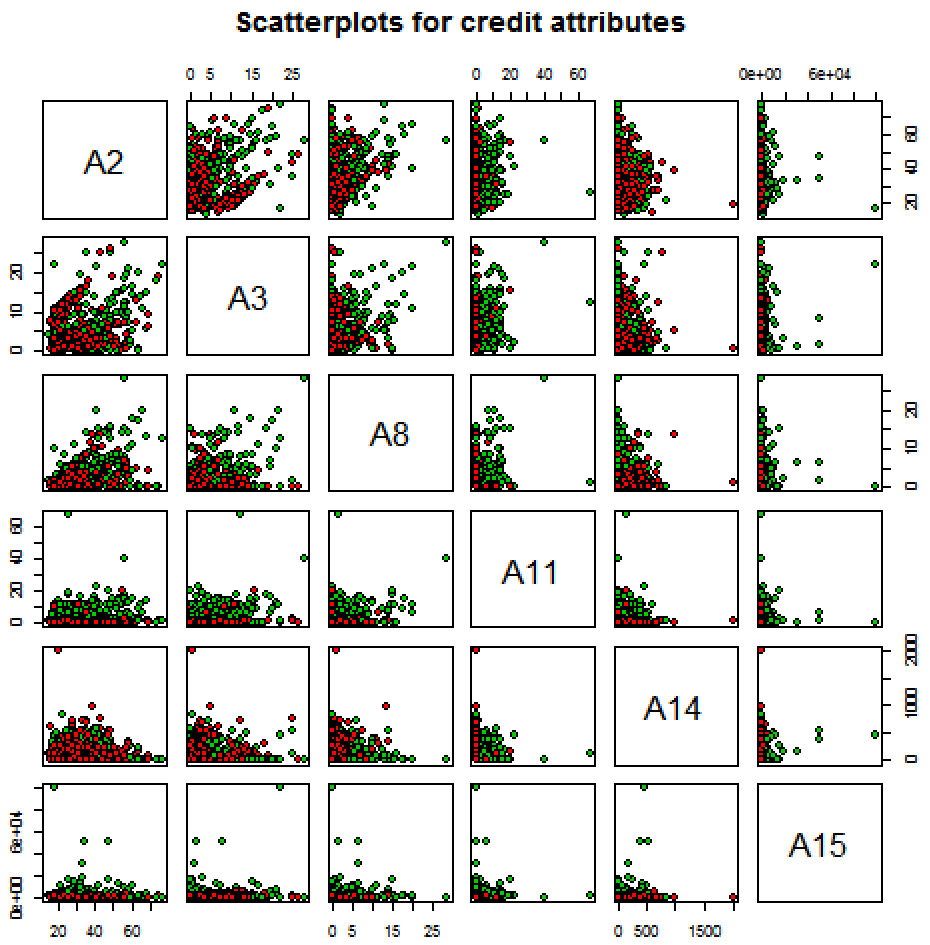
First, we need to select all non-binary columns from the data frame

```r
selection <- which(apply(data, 2, function(x) {!(all(is.element(x, c(0,1))))}))
```

Option 1: Using the built-in functionality

```r
# Builtin-function 'pairs'
pairs(data[,selection], main = "Scatterplots for credit attributes",
      pch = 21, bg = c("red", "green3")[data$Class + 1])

# Note: See plot on next slide
```

Visualizing with a scatterplot matrix (2/4)

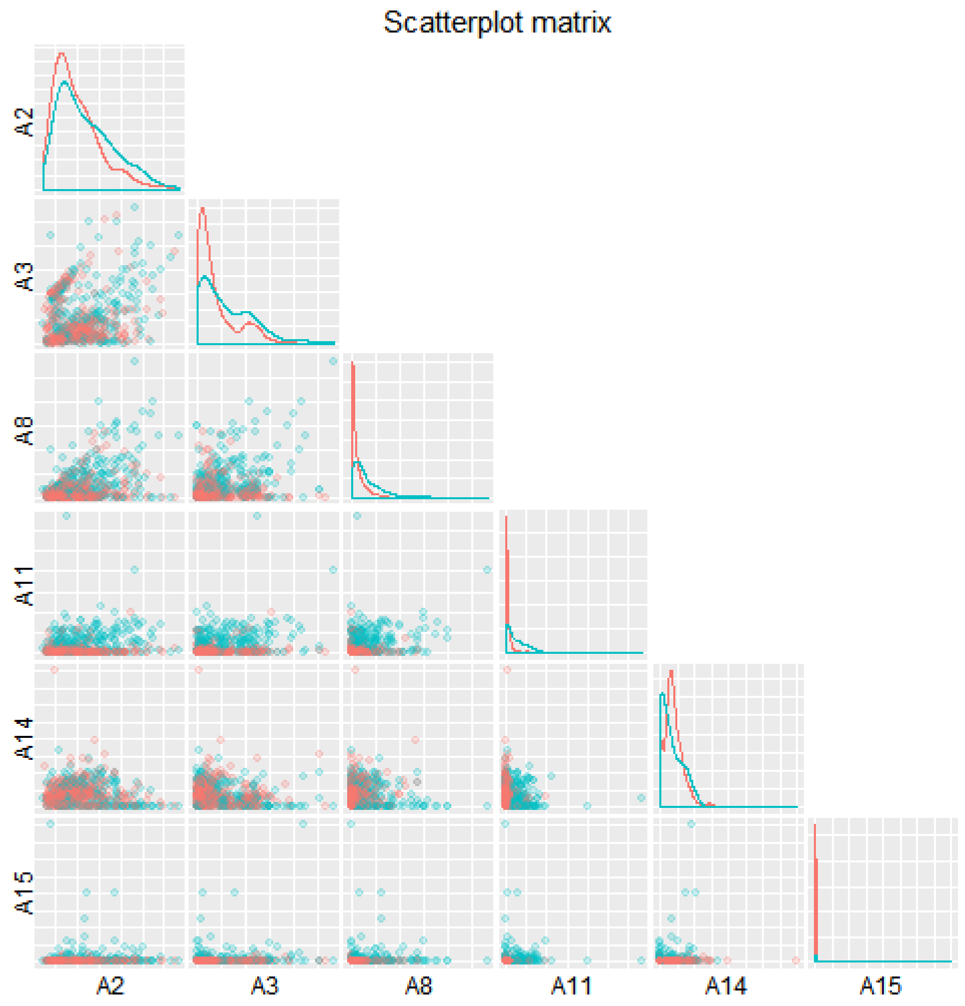


Visualizing with a scatterplot matrix (3/4)

Option 2: Using functionality from `ggplot2`

```r
# To beautify the labeling of the plots, we should convert the class into a factor
data[,"Class"] <- factor(data[,"Class"], levels = c("0","1"),
                         labels=c("denial", "approval"))

multi_colored_kde <- function(data, mapping, ...){
  ggplot(data = data, mapping=mapping) +
    geom_density(mapping = aes_string(color="Class"), fill=NA)
}

ggpairs(data, columns=selection, title= "Scatterplot matrix",
        mapping=ggplot2::aes_string(color="Class"),
        upper="blank",
        diag  = list(continuous=multi_colored_kde),
        lower = list(continuous=wrap("points", alpha=0.2)),
        axisLabels= "none") # Note: See plot on next slide
```

Visualizing with a scatterplot matrix (4/4)

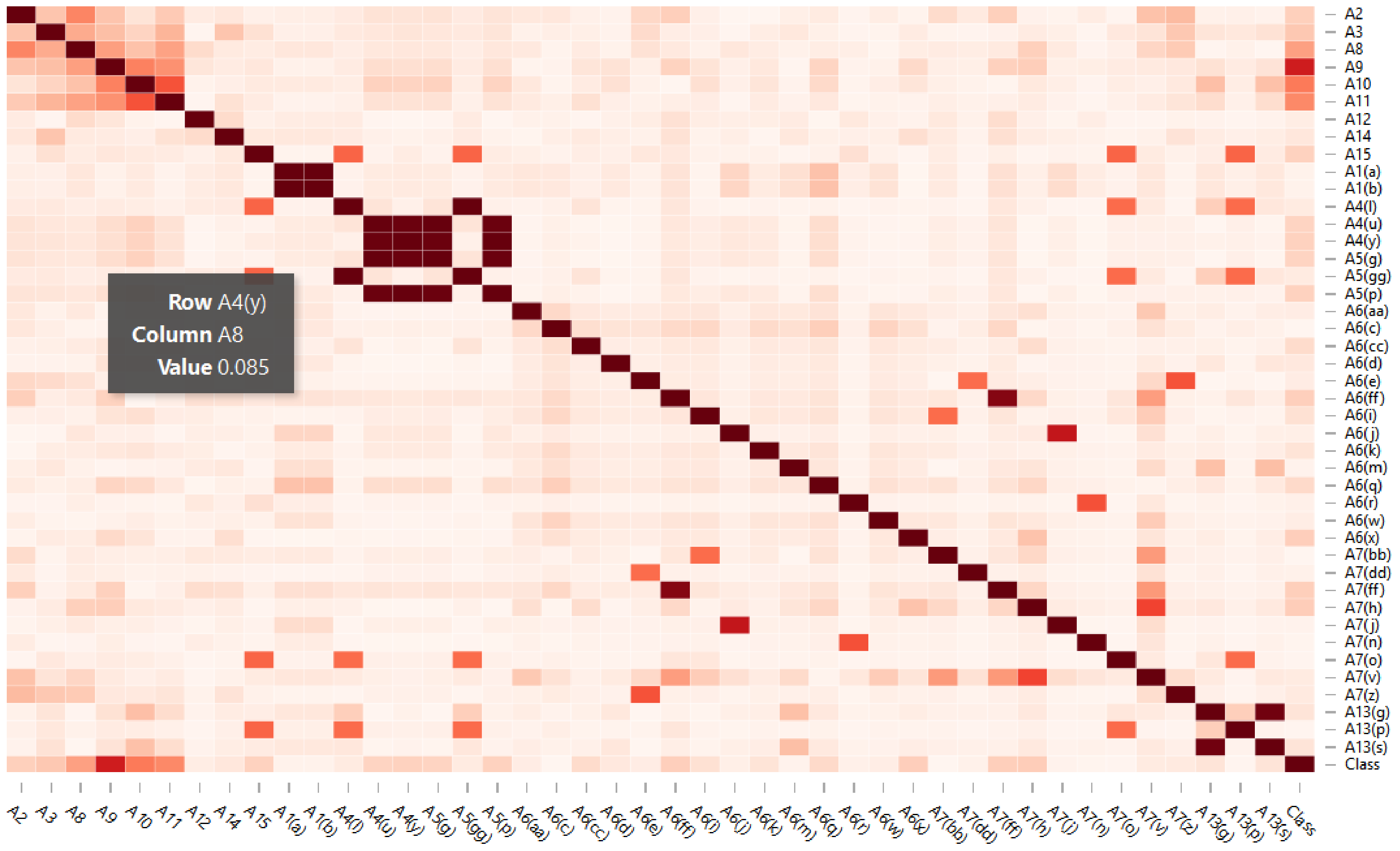


Heatmap visualization of pairwise correlations (1/3)

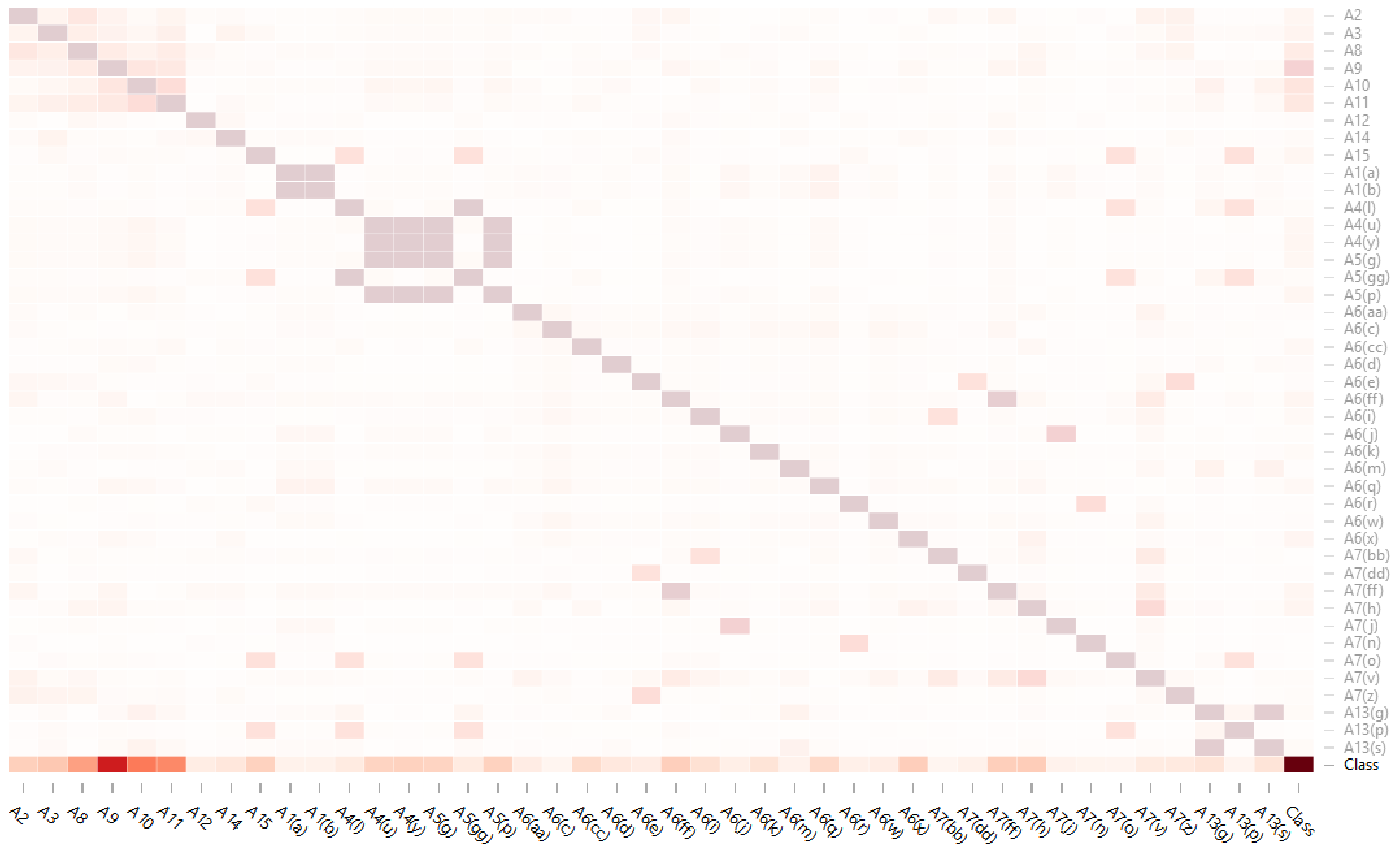
A heatmap is a colored matrix, where the color intensity of cells represents the strengths of pairwise relationships.

```r
require(d3heatmap, quietly = T) # load one of the packages for heatmaps

# To compute pairwise correlations, attributes need to be numeric
tmp <- as.matrix(sapply(subset(data, select = -Class), as.numeric))
tmp <- cbind(tmp, as.integer(as.character(data$Class) == "approval"))
colnames(tmp)[ncol(tmp)] <- "Class"
# Compute a matrix of pairwise correlations
tmp.cor <- cor(tmp)
any(is.na(tmp.cor)) # columns with very low variance may introduce NAs
tmp.cor[is.na(tmp.cor)] <- 0

d3heatmap(abs(tmp.cor),color = "Reds",dendrogram = "none")
```

Heatmap visualization of pairwise correlations (2/3)



Heatmap visualization of pairwise correlations (3/3)



Hint: Working with re-usable code snippets

You can outsource codeblocks to make them re-usable

the comand `source()` reads in and executes an R-script

```r
source('read_in_credit_data.R')
source('preprocess_credit_data.R')
source('scatter_plot_matrix.R')
```

Data Analysis - Part III

Statistical methods

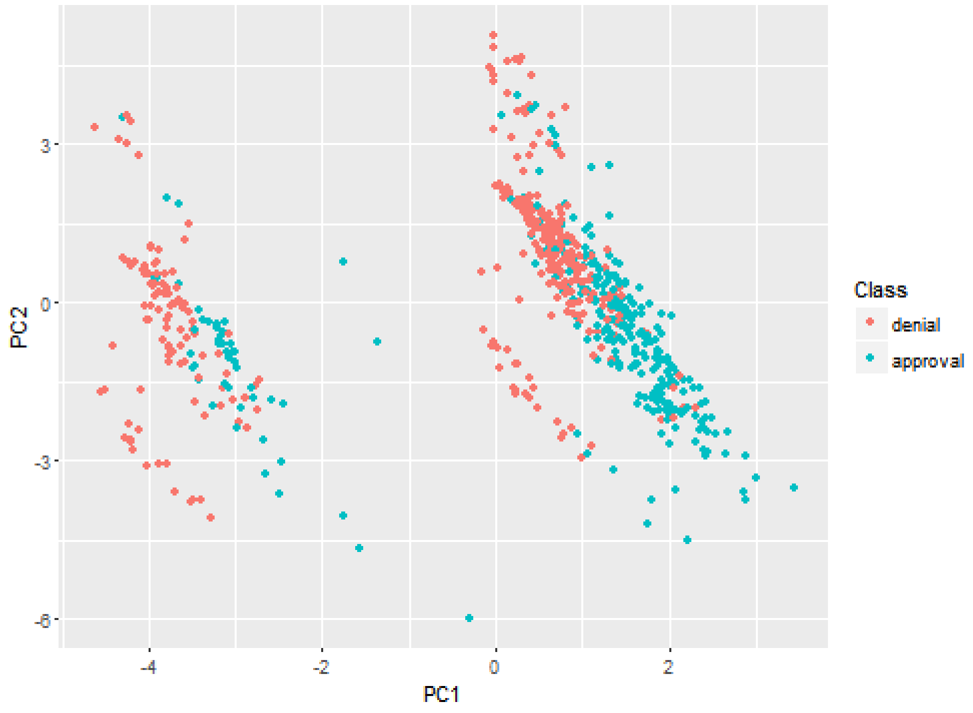
Pre-filtering of attributes

Depending on the methods, some of the following steps are necessary (e.g. for principal component analysis)

```
# Separate the class from the rest of the data
classes <- data[,"Class"]
data <- subset(data, select=-Class)

# Remove columns with little variation
require(caret)
data <- data[,-c(nearZeroVar(data))]

# Center and scale columns (necessary for some ML-methods)
data.orig <- data
data <- scale(data)
```

Compute a PCA

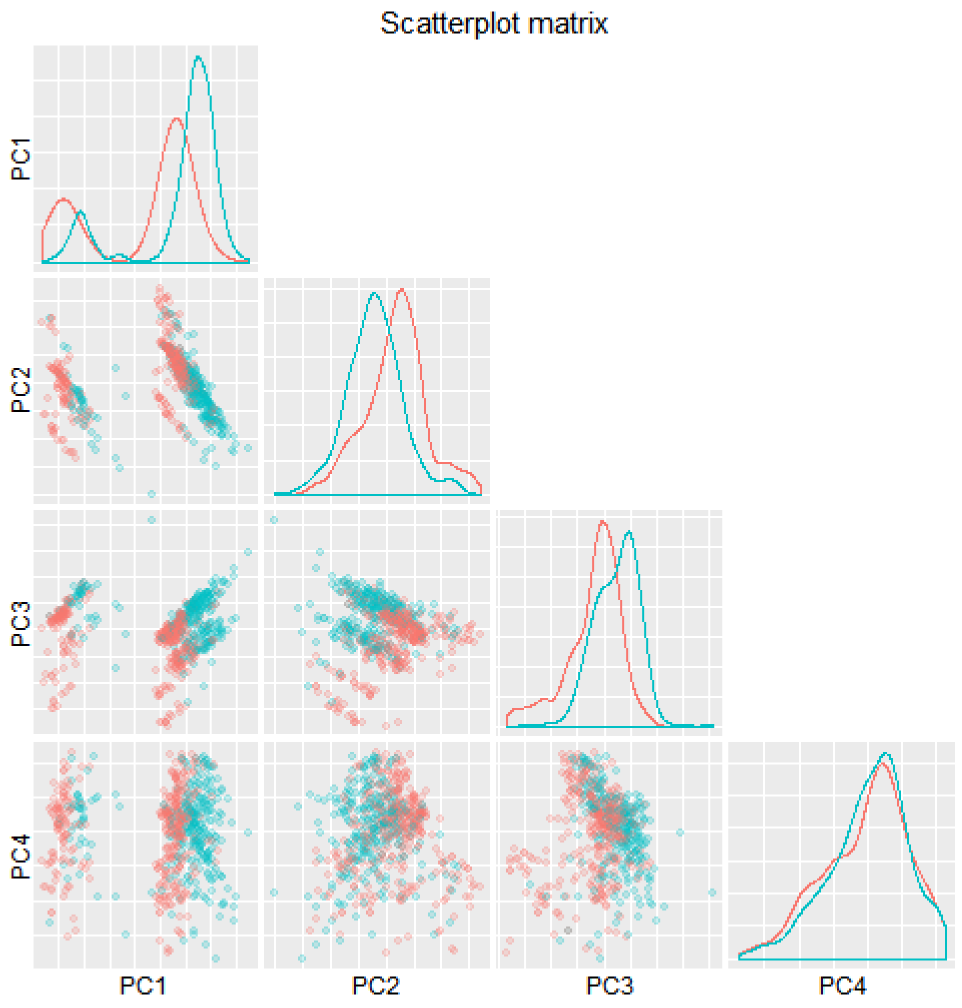
```
pca <- prcomp(data)
pca4plot <- as.data.frame(pca$x)
pca4plot[,"Class"] <- classes
ggplot(pca4plot, aes(x=PC1, y=PC2, colour=Class)) + geom_point()
```



Scatterplot matrix of a PCA (1/2)

```
ggpairs(pca4plot, columns= c(1,2,3,4), color="Class", title= "Scatterplot matrix",
        mapping=ggplot2::aes_string(color="Class"),
        upper="blank",
        diag  = list(continuous=multi_colored_kde),
        lower = list(continuous=wrap("points", alpha=0.2)),
        axisLabels= "none")

# Note: See plot on next slide
```

Scatterplot matrix of a PCA (2/2)

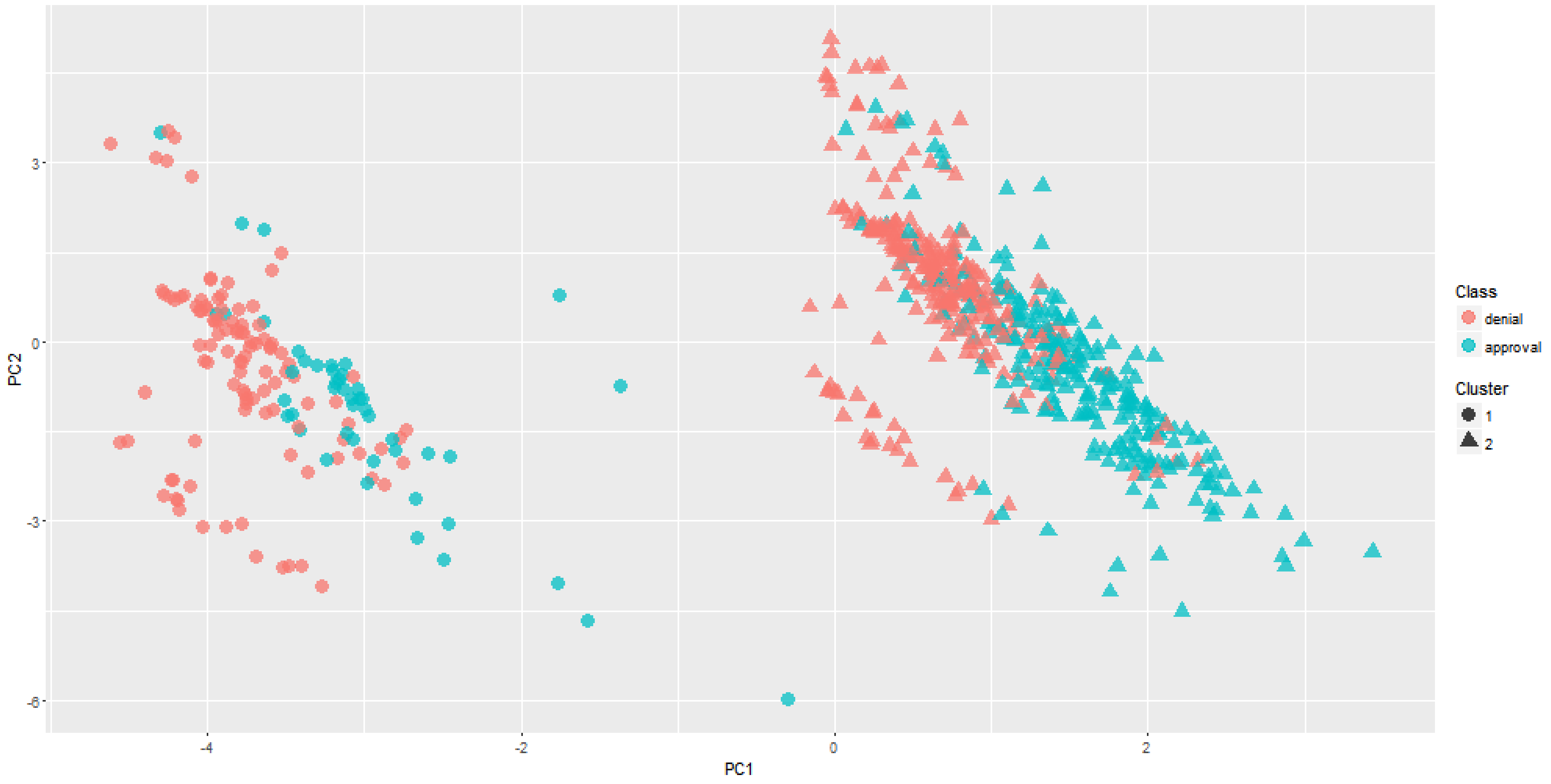


Computing kmeans-clusters (1/4)

```r
# Since k-means starts with a randomized initialization, we fix a random seed
# for reproducibility of the experiments
set.seed(10)

clustIDs <- kmeans(data, 2)$cluster
pca4plot[,"Cluster"] <- as.factor(clustIDs)
ggplot(pca4plot, aes(x=PC1, y=PC2, colour=Class, shape=Cluster))
       + geom_point(size=4, alpha=0.75)

clustIDs <- kmeans(data, 3)$cluster
pca4plot[,"Cluster"] <- as.factor(clustIDs)
ggplot(pca4plot, aes(x=PC1, y=PC2, colour=Class, shape=Cluster))
       + geom_point(size=4, alpha=0.75)

# Note: See plots on next slides
```

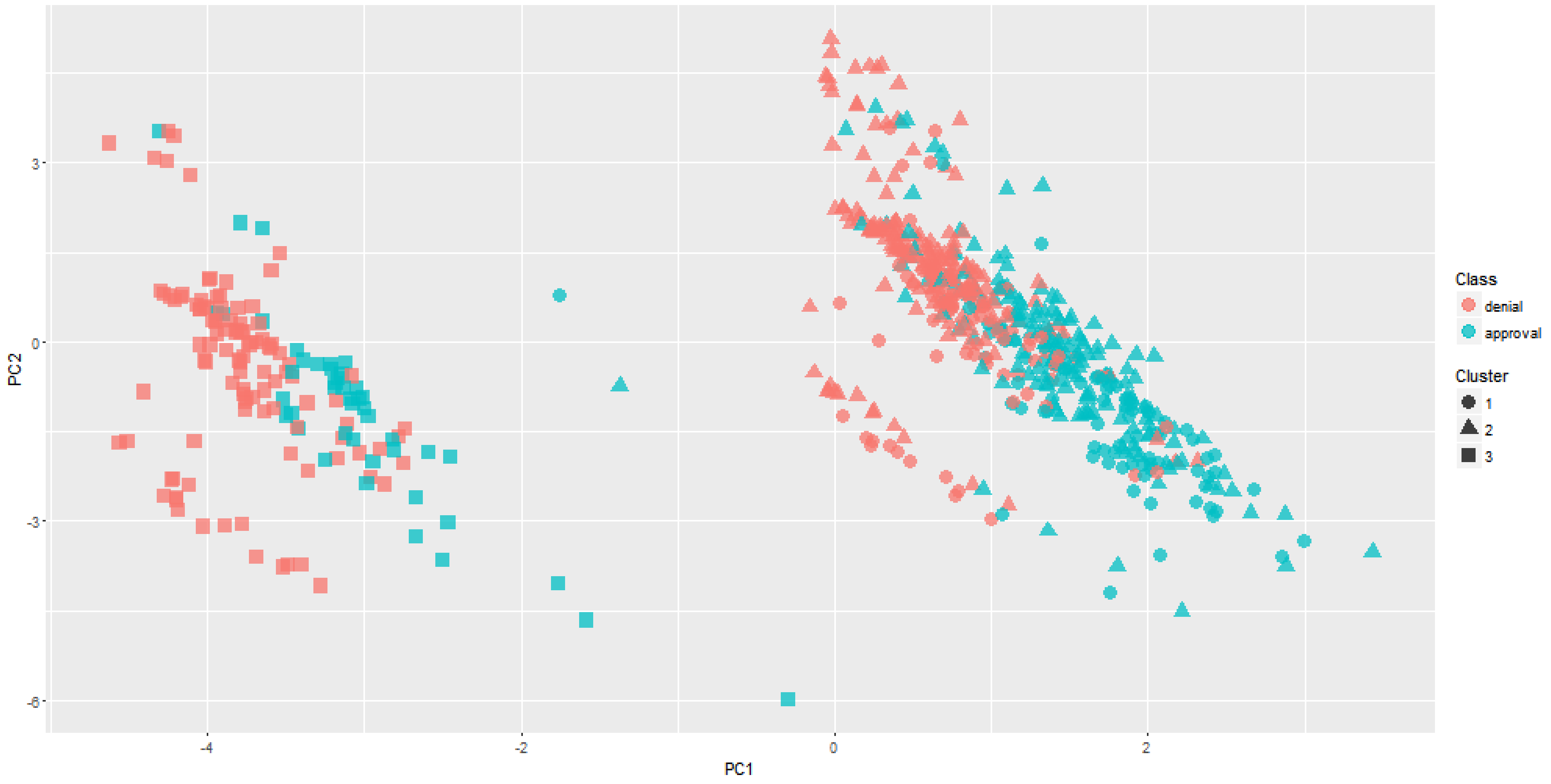
Computing kmeans-clusters (2/4)

Assuming 2 cluster centers



Computing kmeans-clusters (3/4)

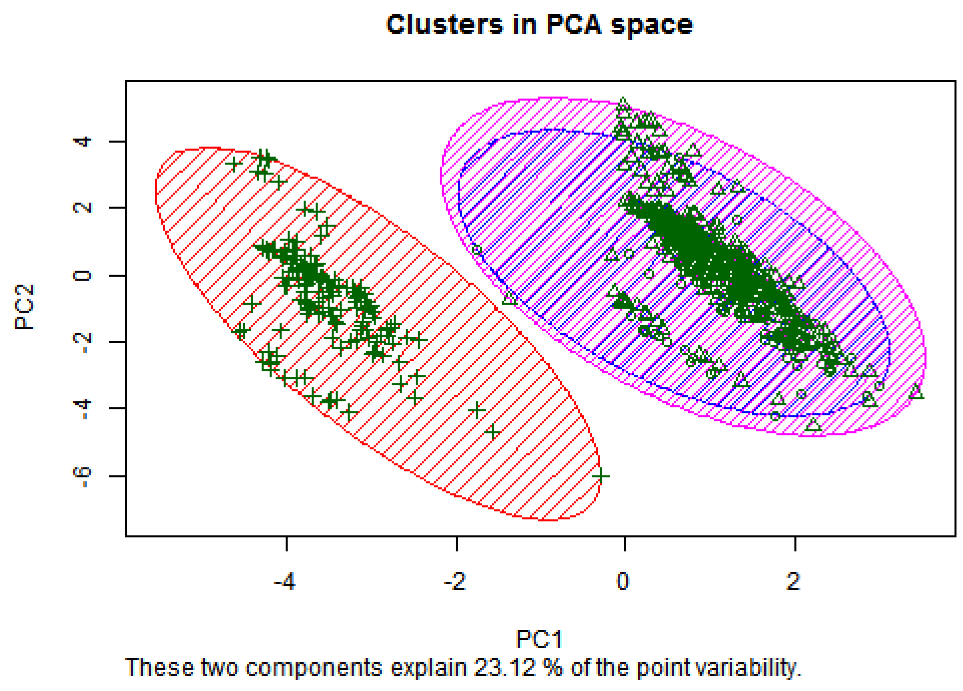
Assuming 3 cluster centers



Computing kmeans-clusters (4/4)

Use another form of visualizing

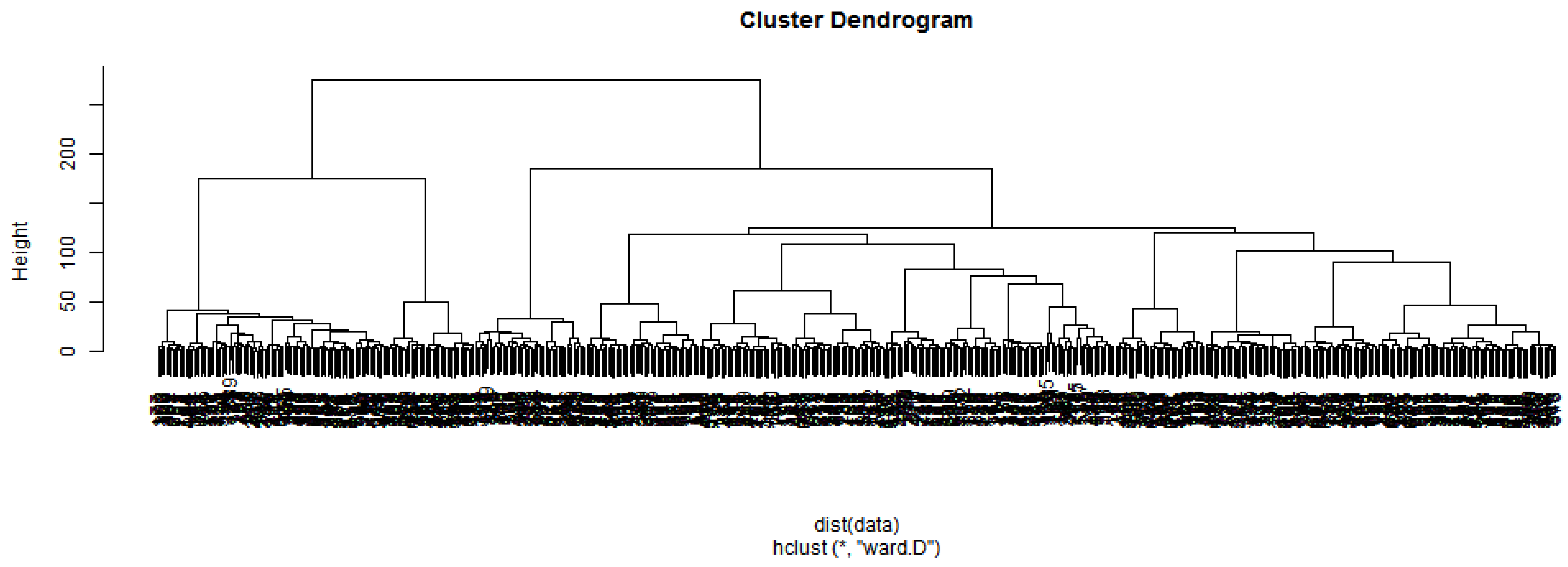
```
library(cluster)
clusplot(data, clustIDs, color=TRUE, shade=TRUE, labels=0, lines=0,
         main = "Clusters in PCA space", xlab="PC1", ylab="PC2")
```



Hierarchical clustering (1/2)

Learn a hierarchical cluster model

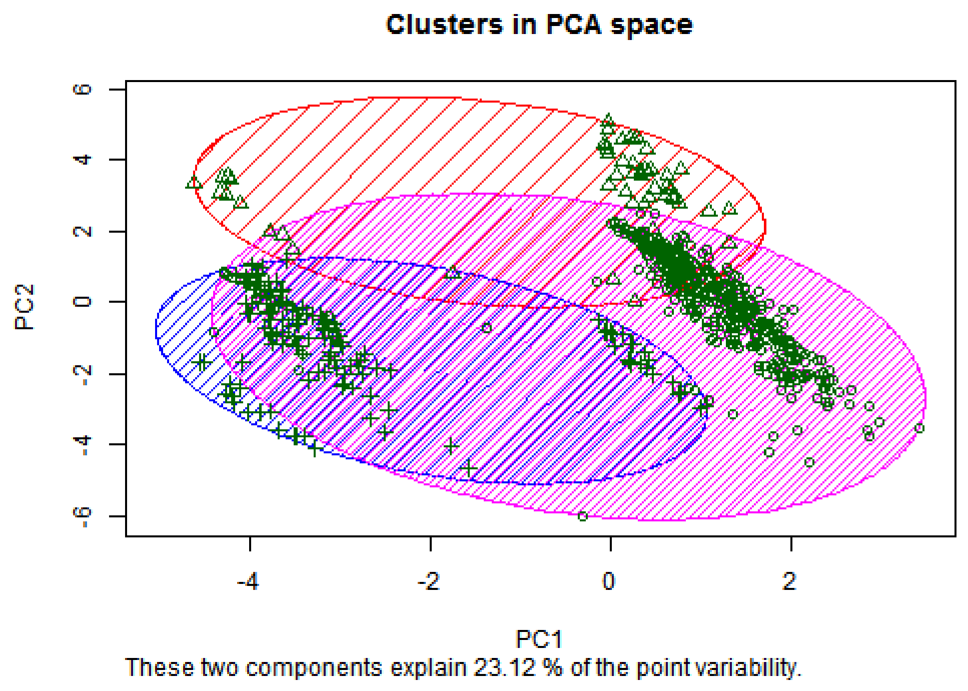
```
clusters <- hclust(dist(data), method='ward.D')
# "ward.D", "single", "complete", "average", ...
plot(clusters)
```



Hierarchical clustering (2/2)

Visualize the result for a comparison

```
clustIDs <- cutree(clusters, k=3)
clusplot(data, clustIDs, color=TRUE, shade=TRUE, labels=0, lines=0,
         main = "Clusters in PCA space", xlab="PC1", ylab="PC2")
```



Learning a decision tree model (1/5)

```r
# Make a split of the data into train and test set
set.seed(51)
train.sample <- sample(nrow(data), floor(0.75 * 653))
str(train.sample)
```

```
##  int [1:489] 507 131 195 641 141 541 487 263 627 73 ...
```

```r
d.train <- data.orig[train.sample,]
d.test <- data.orig[-train.sample,]

cl.train <- classes[train.sample]
cl.test <- classes[-train.sample]
```

Learning a decision tree model (2/5)

```
# Check statistical properties - are they comparable?
prop.table(table(classes))
## classes
##    denial  approval
## 0.5467075 0.4532925
prop.table(table(cl.train))
## cl.train
##    denial  approval
## 0.5337423 0.4662577
prop.table(table(cl.test))
## cl.test
##    denial  approval
## 0.5853659 0.4146341
```

Learning a decision tree model (3/5)

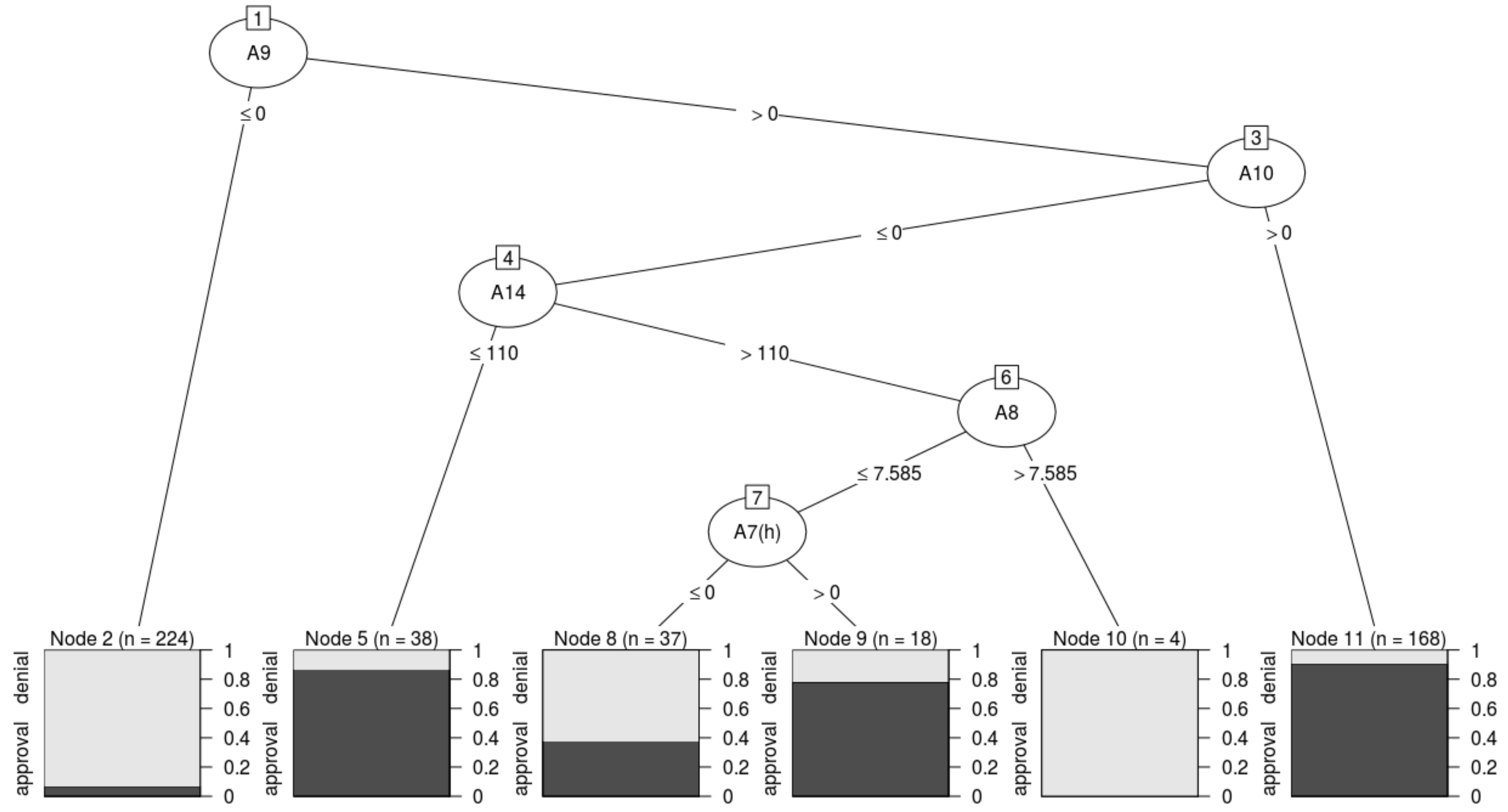
Building the model

```r
require(C50)
credit.model <- C5.0(d.train, cl.train, control=C5.0Control(minCases=10))
summary(credit.model)
```

```
Class specified by attribute `outcome'

Read 489 cases (32 attributes) from undefined.data

Decision tree:

A9 <= 0: denial (224/15)
A9 > 0:
:...A10 > 0: approval (168/16)
    A10 <= 0:
    :...A14 <= 110: approval (38/5)
        A14 > 110:
        :...A8 > 7.585: denial (4)
            A8 <= 7.585:
            :...A7(=h) <= 0: denial (37/14)
                A7(=h) > 0: approval (18/4)
```

Plotting the decision tree model (4/5)

```
plot(credit.model)
```



Learning a decision tree model (5/5)

Use the model for predictions on the test set

```r
cred.preds <- predict(credit.model, d.test)


# Make a confusion matrix for the predictions
library(gmodels)
CrossTable(cl.test, cred.preds, prop.chisq = FALSE, prop.c = FALSE,
           prop.r =F, dnn = c("actual approval","predicted approval"))
```

```
Total Observations in Table:  164


                | predicted approval 
actual approval |    denial |  approval | Row Total | 
----------------|-----------|-----------|-----------|
         denial |        85 |        11 |        96 | 
                |     0.518 |     0.067 |           | 
----------------|-----------|-----------|-----------|
       approval |        11 |        57 |        68 | 
                |     0.067 |     0.348 |           | 
----------------|-----------|-----------|-----------|
   Column Total |        96 |        68 |       164 | 
----------------|-----------|-----------|-----------|
```

Learning a linear model to classify the data (1/3)

Note that this abuses a thresholding a linear regression to classify data

```r
tmp.train.df <- as.data.frame(d.train)
tmp.train.df$Class <- as.numeric(cl.train=="approval")

linear.model <- lm(Class ~ ., data=tmp.train.df)
```

```r
# Inspect the model
summary(linear.model)

# Note: See output on the next slide
```

Learning a linear model to classify the data (2/3)

```
##
## Call:
## lm(formula = Class ~ ., data = tmp.train.df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.89906 -0.09278  0.01710  0.16663  1.05325
##
## Coefficients: (4 not defined because of singularities)
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.024e+00  3.932e-01   2.605  0.00950 **
## A2           7.750e-04  1.471e-03   0.527  0.59857
## A3          -4.744e-03  3.267e-03  -1.452  0.14713
## A8           8.039e-03  5.679e-03   1.416  0.15753
## A9           6.000e-01  3.665e-02  16.369  < 2e-16 ***
## A10          1.020e-01  3.941e-02   2.587  0.00998 **
## A11          5.730e-03  3.720e-03   1.540  0.12417
## A12         -1.051e-02  3.054e-02  -0.344  0.73086
## A14         -2.977e-04  1.007e-04  -2.957  0.00327 **
## A15          1.282e-05  5.126e-06   2.502  0.01271 *
## `A1(a)`      3.968e-03  3.386e-02   0.117  0.90677
## `A1(b)`             NA         NA      NA       NA
## `A4(u)`     -9.151e-01  3.881e-01  -2.358  0.01880 *
```

Learning a linear model to classify the data (3/3)

```r
# Make predictions on new data points
linear.preds <- as.numeric(predict(linear.model, d.test) > 0.5)
# Inspect the results
CrossTable(cl.test, linear.preds, prop.chisq = FALSE, prop.c = FALSE,
           prop.r =F, dnn = c("actual approval","predicted approval"))
```

```
Total Observations in Table:  164


                | predicted approval
actual approval |         0 |         1 | Row Total |
----------------|-----------|-----------|-----------|
              0 |        78 |        18 |        96 |
                |     0.476 |     0.110 |           |
----------------|-----------|-----------|-----------|
              1 |         2 |        66 |        68 |
                |     0.012 |     0.402 |           |
----------------|-----------|-----------|-----------|
   Column Total |        80 |        84 |       164 |
----------------|-----------|-----------|-----------|
```

Learning with a SVM (1/3)

```r
library(kernlab)

dat.train.df <- as.data.frame(d.train)
dat.train.df$Class <- cl.train

svm.classifier <- ksvm(Class ~ ., data=dat.train.df, kernel = "vanilladot")
```

Learning with a SVM (2/3)

```
svm.classifier
```

```
## Support Vector Machine object of class "ksvm"
##
## SV type: C-svc  (classification)
##  parameter : cost C = 1
##
## Linear (vanilla) kernel function.
##
## Number of Support Vectors : 207
##
## Objective Function Value : -131.0236
## Training error : 0.132924
```

Learning with a SVM (3/3)

Use the model for predictions on the test set

```
svm.preds <- predict(svm.classifier, d.test)
CrossTable(cl.test, svm.preds, prop.chisq = FALSE, prop.c = FALSE,
           prop.r =F, dnn = c("actual approval","predicted approval"))
```

```
                | predicted approval
actual approval |    denial |  approval | Row Total |
----------------|-----------|-----------|-----------|
         denial |        78 |        18 |        96 |
                |     0.476 |     0.110 |           |
----------------|-----------|-----------|-----------|
       approval |         5 |        63 |        68 |
                |     0.030 |     0.384 |           |
----------------|-----------|-----------|-----------|
   Column Total |        83 |        81 |       164 |
----------------|-----------|-----------|-----------|
```

Definitions of performance measures

```r
# Recall
recall <- function(preds, targets) {
  sum(preds & targets) / sum(targets) # TP / (TP + FN)
}
# Precision
precision <- function(preds, targets) {
  sum(preds & targets) / sum(preds) # TP / (TP + FP)
}
# Accuracy
accuracy <- function(preds, targets) {
  sum(preds == targets) / length(targets) # (TP + TN) / (TP + TN + FP + FN)
}
# R-Squared
r_squared <- function(preds, targets) {
  cor(preds, targets)^2 # R-Squared is equal to the squared Pearson's correlation
}
```

Doing k-fold cross-validation for a SVM (1/3)

```r
require(kernlab, quietly=T)

tmp.train.df <- as.data.frame(d.train)
tmp.train.df$Class <- cl.train

set.seed(15)
# Assign a random number k in c(1:10) to each data frame row
folds <- sample(rep(1:10, length=nrow(tmp.train.df)))
table(folds)
```

```
## folds
##  1  2  3  4  5  6  7  8  9 10
## 49 49 49 49 49 49 49 49 49 48
```

```r
cv.recalls <- rep(NA, 10)
cv.precisions <- rep(NA, 10)
cv.accuracies <- rep(NA, 10)
```

Doing k-fold cross-validation for a SVM (2/3)

```r
for (k in 1:10) {
  # Fit model on all data samples except those having number k assigned
  fold_k.fit <- ksvm(Class ~ ., data=tmp.train.df[folds!=k,], kernel = "vanilladot")
  # Use model to predict labels for all data samples having number k assigned
  fold_k.preds <- predict(fold_k.fit, subset(tmp.train.df[folds==k,], select=-Class))

  cv.recalls[k] <- recall(fold_k.preds=="approval", cl.train[folds==k]=="approval")
  cv.precisions[k] <- precision(fold_k.preds=="approval", cl.train[folds==k]=="approval")
  cv.accuracies[k] <- accuracy(fold_k.preds=="approval", cl.train[folds==k]=="approval")
}
```

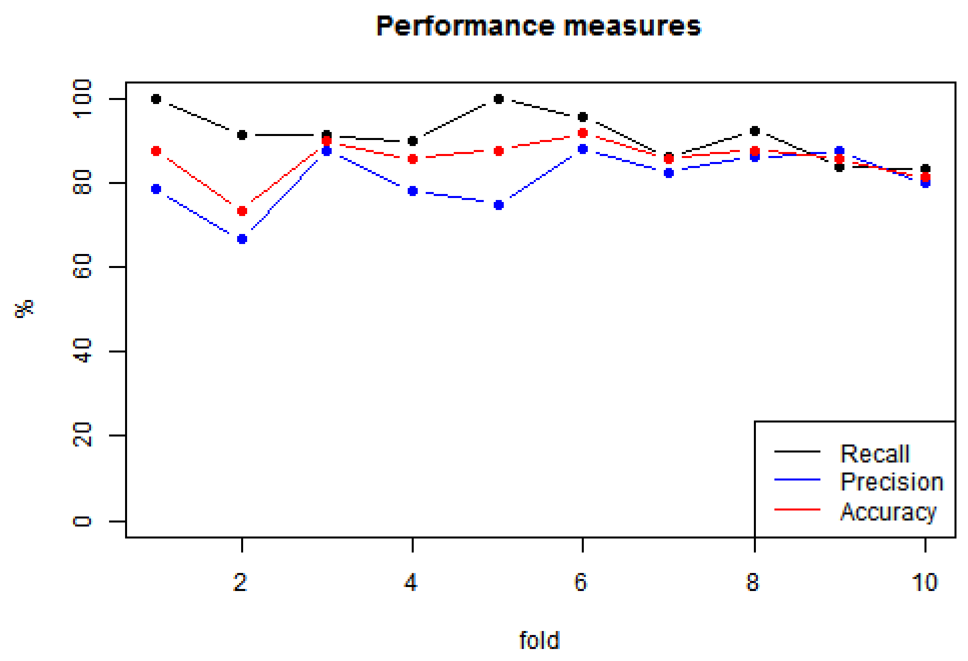
```r
summary(cv.accuracies)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
## 0.7347  0.8571  0.8673  0.8568  0.8776  0.9184
```

Doing k-fold cross-validation for a SVM (3/3)

Let's also plot the results of the individual folds.

```
plot(cv.recalls * 100, pch=19, type="b", ylim=c(0,100), main = "Performance measures", xlab="fold", yla
points(cv.precisions * 100, pch=19, type="b", col="blue")
points(cv.accuracies * 100, pch=19, type="b", col="red")
legend("bottomright", c("Recall", "Precision", "Accuracy"), col=c("black", "blue", "red"), lty=1)
```



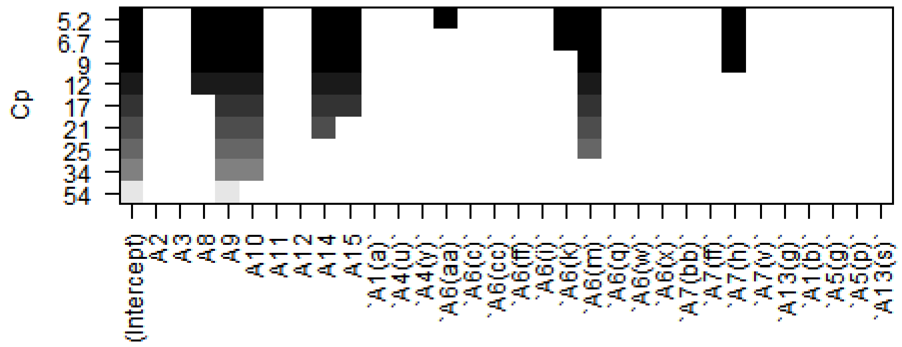
Feature selection with a regression model (1/3)

```r
require(leaps)

# Prepare data frame
tmp.train.df <- as.data.frame(d.train)
tmp.train.df$Class <- as.numeric(cl.train=="approval")

# We can specify the linear model as a string
formel <- "Class ~ ."

# Apply forward selection on the attributes
subsets.fit <- regsubsets(as.formula(formel), data=tmp.train.df, method="forward")
```

```
## Reordering variables and trying again:
```

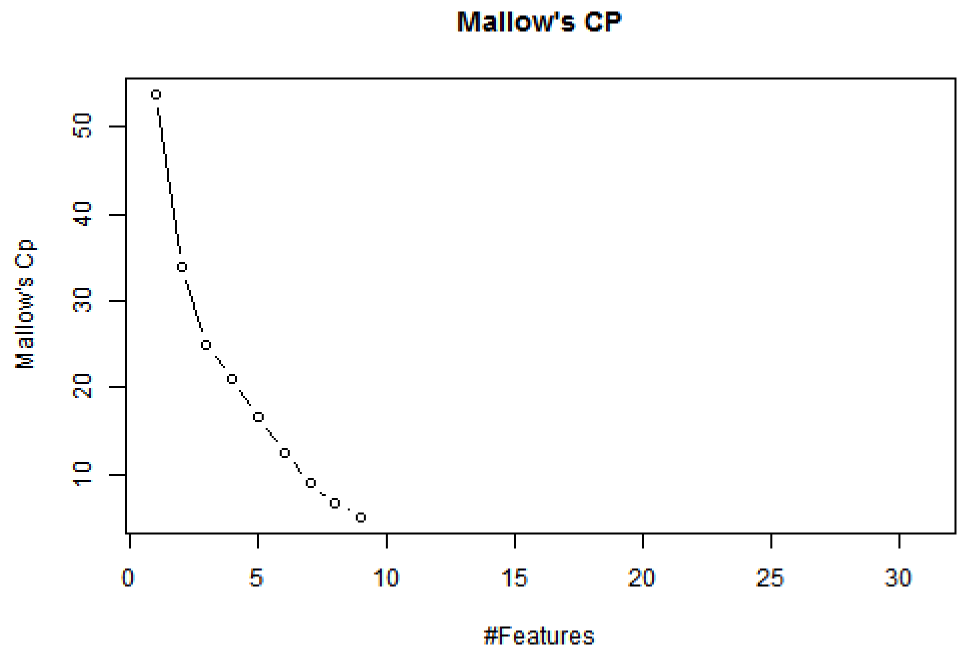
Feature selection with a regression model (2/3)

```
fit.summary <- summary(subsets.fit)

# Note: "Mallow's Cp is a measure for a model's performance, taking into account its complexity"
plot(subsets.fit, scale="Cp")
```



Feature selection with a regression model (3/3)

```
# Make a plot of model complexity' vs. Mallow's Cp
# Note: The lower, the better
plot(fit.summary$cp, type="b", main="Mallow's CP", xlab="#Features", ylab="Mallow's Cp", xlim=c(1,(ncol
```



Summary

- Addressed the core parts of data analysis
  - Data preparation
  - Data modelling
  - Data visualization
  - Model evaluation
- Remember:
  - Data analysis is an iterative process (CRISP)
  - Each step will give you insights for the next one