

Regression and Classification with R*

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Outline

Introduction

Linear Regression

Generalized Linear Regression

Decision Trees with Package party

Decision Trees with Package rpart

Random Forest

Online Resources

Regression and Classification with R [†]

- ▶ build a linear regression model to predict CPI data
- ▶ build a generalized linear model (GLM)
- ▶ build decision trees with package *party* and *rpart*
- ▶ train a random forest model with package *randomForest*

[†]Chapter 4: Decision Trees and Random Forest & Chapter 5: Regression, in book *R and Data Mining: Examples and Case Studies*.

Regression

- ▶ Regression is to build a function of *independent variables* (also known as *predictors*) to predict a *dependent variable* (also called *response*).
- ▶ For example, banks assess the risk of home-loan applicants based on their age, income, expenses, occupation, number of dependents, total credit limit, etc.
- ▶ linear regression models
- ▶ generalized linear models (GLM)

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Linear Regression

- ▶ Linear regression is to predict response with a linear function of predictors as follows:

$$y = c_0 + c_1x_1 + c_2x_2 + \cdots + c_kx_k,$$

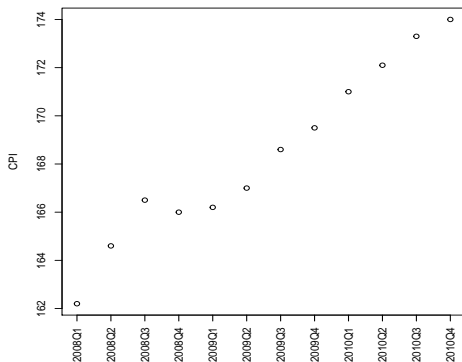
where x_1, x_2, \dots, x_k are predictors and y is the response to predict.

- ▶ linear regression with function `lm()`
- ▶ the Australian CPI (Consumer Price Index) data: quarterly CPIs from 2008 to 2010 [‡]

[‡]From Australian Bureau of Statistics, <http://www.abs.gov.au>.

The CPI Data

```
year <- rep(2008:2010, each = 4)
quarter <- rep(1:4, 3)
cpi <- c(162.2, 164.6, 166.5, 166, 166.2, 167, 168.6, 169.5, 171,
        172.1, 173.3, 174)
plot(cpi, xaxt = "n", ylab = "CPI", xlab = "")
# draw x-axis, where 'las=3' makes text vertical
axis(1, labels = paste(year, quarter, sep = "Q"), at = 1:12, las = 3)
```



Linear Regression

```
## correlation between CPI and year / quarter
cor(year, cpi)

## [1] 0.9096316

cor(quarter, cpi)

## [1] 0.3738028

## build a linear regression model with function lm()
fit <- lm(cpi ~ year + quarter)
fit

##
## Call:
## lm(formula = cpi ~ year + quarter)
##
## Coefficients:
## (Intercept)      year      quarter
##   -7644.488      3.888      1.167
```


With the above linear model, CPI is calculated as

$$\text{cpi} = c_0 + c_1 * \text{year} + c_2 * \text{quarter},$$

where c_0 , c_1 and c_2 are coefficients from model fit.

What will the CPI be in 2011?

```
cpi2011 <- fit$coefficients[[1]] +  
  fit$coefficients[[2]] * 2011 +  
  fit$coefficients[[3]] * (1:4)  
cpi2011  
  
## [1] 174.4417 175.6083 176.7750 177.9417
```

With the above linear model, CPI is calculated as

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cpi2011  
  
## [1] 174.4417 175.6083 176.7750 177.9417
```

An easier way is to use function `predict()`.

More details of the model can be obtained with the code below.

```
attributes(fit)
```

```
## $names
## [1] "coefficients" "residuals"      "effects"
## [4] "rank"          "fitted.values"  "assign"
## [7] "qr"            "df.residual"    "xlevels"
## [10] "call"          "terms"          "model"
##
## $class
## [1] "lm"
```

```
fit$coefficients
```

```
## (Intercept)          year          quarter
## -7644.487500      3.887500      1.166667
```

Function residuals(): differences between observed values and fitted values

```
# differences between observed values and fitted values  
residuals(fit)
```

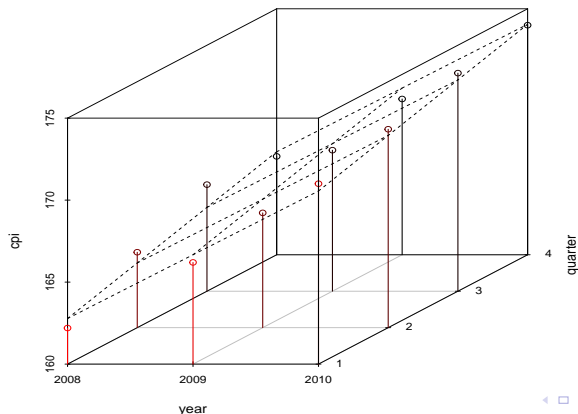
```
##           1           2           3           4           5  
## -0.57916667  0.65416667  1.38750000 -0.27916667 -0.46666667  
##           6           7           8           9          10  
## -0.83333333 -0.40000000 -0.66666667  0.44583333  0.37916667  
##          11          12  
##  0.41250000 -0.05416667
```

```
summary(fit)
```

```
##  
## Call:  
## lm(formula = cpi ~ year + quarter)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max   
## -0.8333 -0.4948 -0.1667  0.4208  1.3875   
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)
```

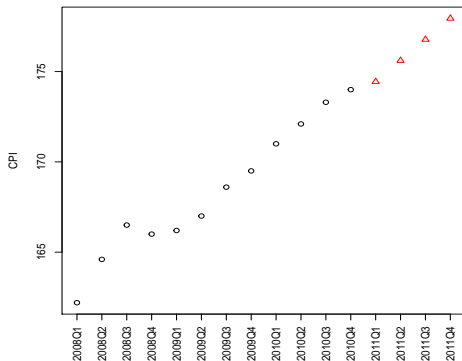
3D Plot of the Fitted Model

```
library(scatterplot3d)
s3d <- scatterplot3d(year, quarter, cpi, highlight.3d = T, type = "h",
  lab = c(2, 3)) # lab: number of tickmarks on x-/y-axes
s3d$plane3d(fit) # draws the fitted plane
```



Prediction of CPIs in 2011

```
data2011 <- data.frame(year = 2011, quarter = 1:4)
cpi2011 <- predict(fit, newdata = data2011)
style <- c(rep(1, 12), rep(2, 4))
plot(c(cpi, cpi2011), xaxt = "n", ylab = "CPI", xlab = "", pch = style,
     col = style)
axis(1, at = 1:16, las = 3, labels = c(paste(year, quarter, sep = "Q"),
    "2011Q1", "2011Q2", "2011Q3", "2011Q4"))
```



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Generalized Linear Model (GLM)

- ▶ Generalizes linear regression by allowing the linear model to be related to the response variable via a link function and allowing the magnitude of the variance of each measurement to be a function of its predicted value
- ▶ Unifies various other statistical models, including linear regression, logistic regression and Poisson regression
- ▶ Function `glm()`: fits generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution

Build a Generalized Linear Model

```
data("bodyfat", package="TH.data")
myFormula <- DEXfat ~ age + waistcirc + hipcirc + elbowbreadth +
  kneebreadth
bodyfat.glm <- glm(myFormula, family = gaussian("log"), data = bodyfat)
summary(bodyfat.glm)
```

##

Call:

glm(formula = myFormula, family = gaussian("log"), data = b...

##

Deviance Residuals:

##	Min	1Q	Median	3Q	Max
##	-11.5688	-3.0065	0.1266	2.8310	10.0966

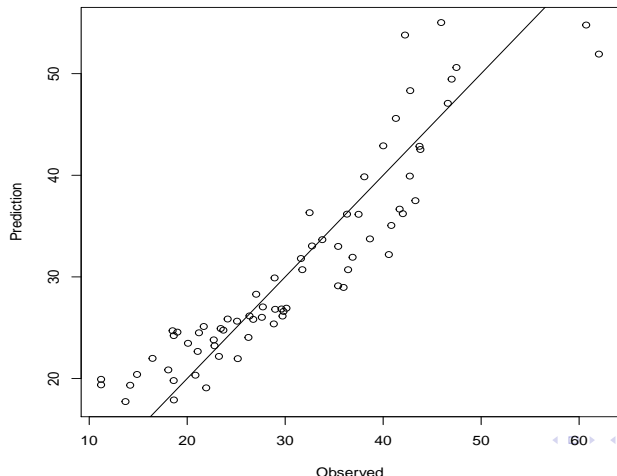
##

Coefficients:

##		Estimate	Std. Error	t value	Pr(> t)	
##	(Intercept)	0.734293	0.308949	2.377	0.02042	*
##	age	0.002129	0.001446	1.473	0.14560	
##	waistcirc	0.010489	0.002479	4.231	7.44e-05	***
##	hipcirc	0.009702	0.003231	3.003	0.00379	**
##	elbowbreadth	0.002355	0.045686	0.052	0.95905	
##	kneebreadth	0.063188	0.028193	2.241	0.02843	*

Prediction with Generalized Linear Regression Model

```
pred <- predict(bodyfat.glm, type = "response")  
plot(bodyfat$DEXfat, pred, xlab = "Observed", ylab = "Prediction")  
abline(a = 0, b = 1)
```



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The iris Data

```
str(iris)

## 'data.frame': 150 obs. of  5 variables:
## $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1...
## $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1...
## $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0...
## $ Species      : Factor w/ 3 levels "setosa","versicolor",....

# split data into two subsets: training (70%) and test (30%); set
# a fixed random seed to make results reproducible
set.seed(1234)
ind <- sample(2, nrow(iris), replace = TRUE, prob = c(0.7, 0.3))
train.data <- iris[ind == 1, ]
test.data <- iris[ind == 2, ]
```

Build a ctree

- ▶ Control the training of decision trees: MinSplit, MinBusket, MaxSurrogate and MaxDepth
- ▶ Target variable: Species
- ▶ Independent variables: all other variables

```
library(party)
myFormula <- Species ~ Sepal.Length + Sepal.Width + Petal.Length +
  Petal.Width
iris_ctree <- ctree(myFormula, data = train.data)
# check the prediction
table(predict(iris_ctree), train.data$Species)
```

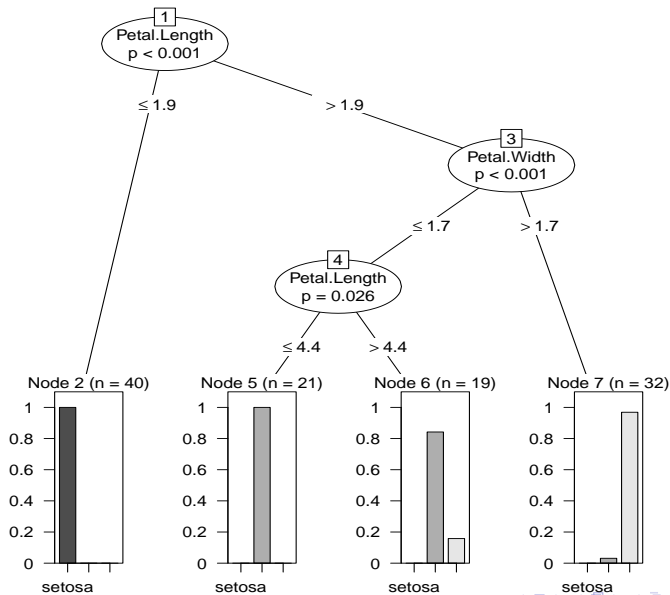
```
##
##          setosa versicolor virginica
## setosa          40           0         0
## versicolor       0          37         3
## virginica        0           1        31
```

Print ctree

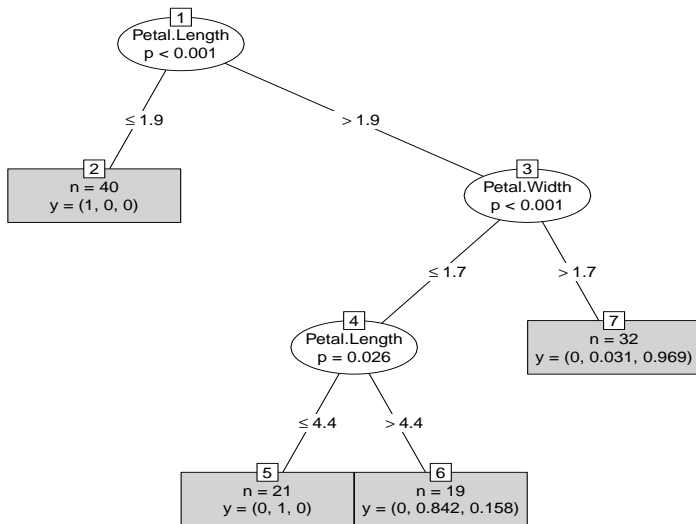
```
print(iris_ctree)

##
##   Conditional inference tree with 4 terminal nodes
##
## Response:   Species
## Inputs:   Sepal.Length, Sepal.Width, Petal.Length, Petal.Width
## Number of observations:  112
##
## 1) Petal.Length <= 1.9; criterion = 1, statistic = 104.643
##   2)* weights = 40
## 1) Petal.Length > 1.9
##   3) Petal.Width <= 1.7; criterion = 1, statistic = 48.939
##     4) Petal.Length <= 4.4; criterion = 0.974, statistic = ...
##       5)* weights = 21
##       4) Petal.Length > 4.4
##         6)* weights = 19
##     3) Petal.Width > 1.7
##       7)* weights = 32
```

```
plot(iris_ctree)
```



```
plot(iris_ctree, type = "simple")
```



Test

```
# predict on test data  
testPred <- predict(iris_ctree, newdata = test.data)  
table(testPred, test.data$Species)
```

```
##  
## testPred      setosa versicolor virginica  
##   setosa         10          0          0  
## versicolor      0         12          2  
## virginica        0          0         14
```

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The bodyfat Dataset

```
data("bodyfat", package = "TH.data")  
dim(bodyfat)
```

```
## [1] 71 10
```

```
# str(bodyfat)  
head(bodyfat, 5)
```

```
##      age DEXfat waistcirc hipcirc elbowbreadth kneebreadth  
## 47  57  41.68    100.0    112.0           7.1           9.4  
## 48  65  43.29     99.5    116.5           6.5           8.9  
## 49  59  35.41     96.0    108.5           6.2           8.9  
## 50  58  22.79     72.0     96.5           6.1           9.2  
## 51  60  36.42     89.5    100.5           7.1          10.0  
##      anthro3a anthro3b anthro3c anthro4  
## 47      4.42      4.95      4.50      6.13  
## 48      4.63      5.01      4.48      6.37  
## 49      4.12      4.74      4.60      5.82  
## 50      4.03      4.48      3.91      5.66  
## 51      4.24      4.68      4.15      5.91
```

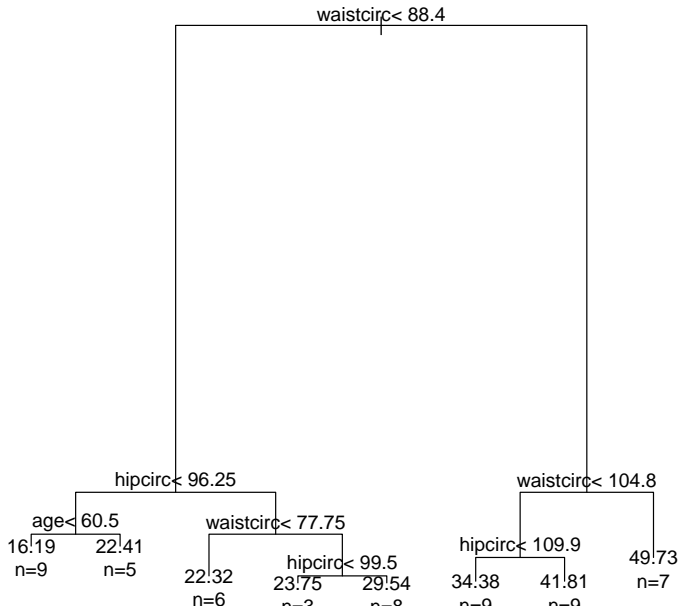
Train a Decision Tree with Package rpart

```
# split into training and test subsets
set.seed(1234)
ind <- sample(2, nrow(bodyfat), replace=TRUE, prob=c(0.7, 0.3))
bodyfat.train <- bodyfat[ind==1,]
bodyfat.test <- bodyfat[ind==2,]
# train a decision tree
library(rpart)
myFormula <- DEXfat ~ age + waistcirc + hipcirc + elbowbreadth +
               kneebreadth
bodyfat_rpart <- rpart(myFormula, data = bodyfat.train,
                      control = rpart.control(minsplit = 10))
# print(bodyfat_rpart$cpstable)
print(bodyfat_rpart)
plot(bodyfat_rpart)
text(bodyfat_rpart, use.n=T)
```

The rpart Tree

```
## n= 56
##
## node), split, n, deviance, yval
##      * denotes terminal node
##
## 1) root 56 7265.0290000 30.94589
##    2) waistcirc< 88.4 31 960.5381000 22.55645
##      4) hipcirc< 96.25 14 222.2648000 18.41143
##        8) age< 60.5 9 66.8809600 16.19222 *
##        9) age>=60.5 5 31.2769200 22.40600 *
##      5) hipcirc>=96.25 17 299.6470000 25.97000
##        10) waistcirc< 77.75 6 30.7345500 22.32500 *
##        11) waistcirc>=77.75 11 145.7148000 27.95818
##          22) hipcirc< 99.5 3 0.2568667 23.74667 *
##          23) hipcirc>=99.5 8 72.2933500 29.53750 *
##    3) waistcirc>=88.4 25 1417.1140000 41.34880
##      6) waistcirc< 104.75 18 330.5792000 38.09111
##        12) hipcirc< 109.9 9 68.9996200 34.37556 *
##        13) hipcirc>=109.9 9 13.0832000 41.80667 *
##      7) waistcirc>=104.75 7 404.3004000 49.72571 *
```

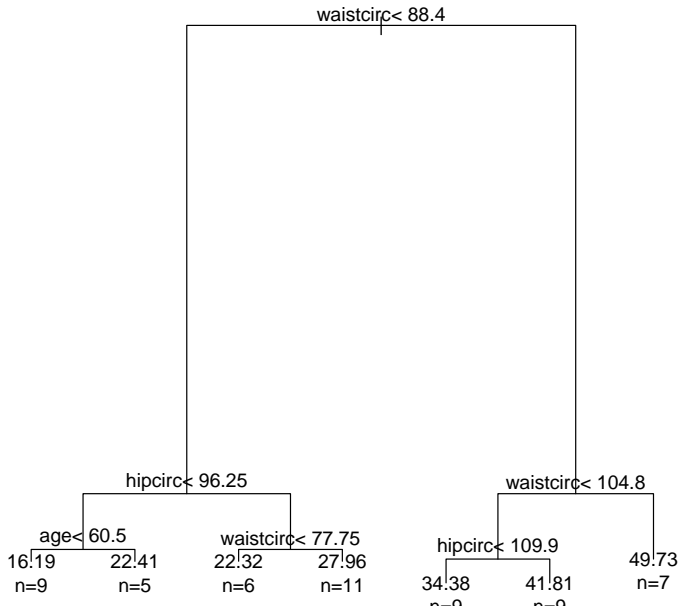
The rpart Tree



Select the Best Tree

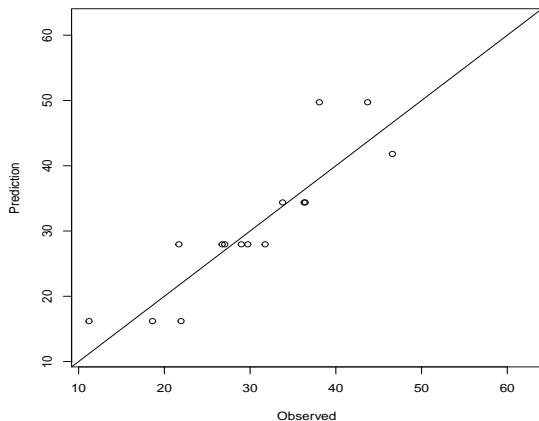
```
# select the tree with the minimum prediction error
opt <- which.min(bodyfat_rpart$cptable[, "xerror"])
cp <- bodyfat_rpart$cptable[opt, "CP"]
# prune tree
bodyfat_prune <- prune(bodyfat_rpart, cp = cp)
# plot tree
plot(bodyfat_prune)
text(bodyfat_prune, use.n = T)
```

Selected Tree



Model Evaluation

```
DEXfat_pred <- predict(bodyfat_prune, newdata = bodyfat.test)
xlim <- range(bodyfat$DEXfat)
plot(DEXfat_pred ~ DEXfat, data = bodyfat.test, xlab = "Observed",
     ylab = "Prediction", ylim = xlim, xlim = xlim)
abline(a = 0, b = 1)
```



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R Packages for Random Forest

- ▶ Package *randomForest*
 - ▶ very fast
 - ▶ cannot handle data with missing values
 - ▶ a limit of 32 to the maximum number of levels of each categorical attribute
 - ▶ extensions: *extendedForest*, *gradientForest*
- ▶ Package *party*: `cforest()`
 - ▶ not limited to the above maximum levels
 - ▶ slow
 - ▶ needs more memory

Train a Random Forest

```
# split into two subsets: training (70%) and test (30%)
ind <- sample(2, nrow(iris), replace=TRUE, prob=c(0.7, 0.3))
train.data <- iris[ind==1,]
test.data <- iris[ind==2,]
# use all other variables to predict Species
library(randomForest)
rf <- randomForest(Species ~ ., data=train.data, ntree=100,
                    proximity=T)
```

```
table(predict(rf), train.data$Species)
```

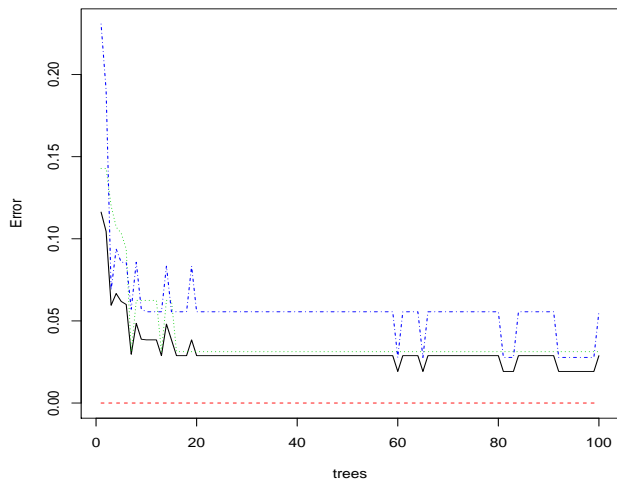
```
##
##           setosa versicolor virginica
##  setosa         36           0         0
##  versicolor     0          31         2
##  virginica       0           1        34
```

```
print(rf)
```

```
##
## Call:
##  randomForest(formula = Species ~ ., data = train.data, ntr...
##           Type of random forest: classification
##           Number of trees: 100
## No. of variables tried at each split: 2
##
##           OOB estimate of  error rate: 2.88%
## Confusion matrix:
##           setosa versicolor virginica class.error
## setosa         36           0         0 0.00000000
## versicolor     0          31         1 0.03125000
## virginica       0           2        34 0.05555556
```

Error Rate of Random Forest

```
plot(rf, main = "")
```



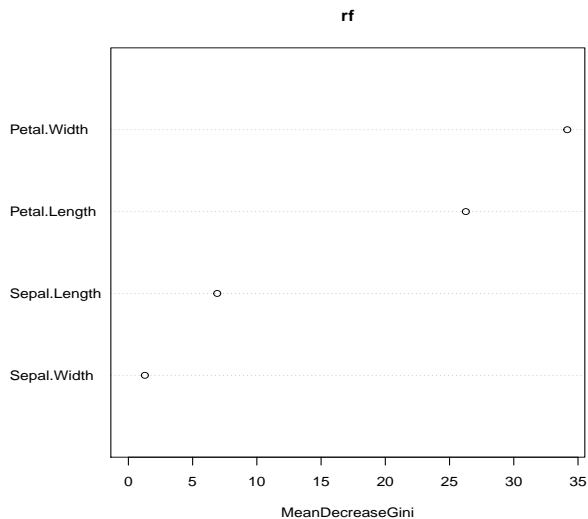
Variable Importance

```
importance(rf)
```

##	MeanDecreaseGini
## Sepal.Length	6.913882
## Sepal.Width	1.282567
## Petal.Length	26.267151
## Petal.Width	34.163836

Variable Importance

```
varImpPlot(rf)
```



Margin of Predictions

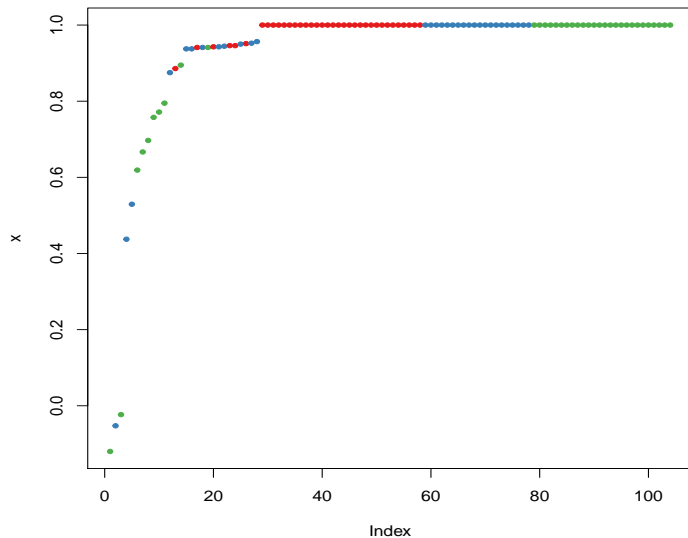
The margin of a data point is as the proportion of votes for the correct class minus maximum proportion of votes for other classes. Positive margin means correct classification.

```
irisPred <- predict(rf, newdata = test.data)
table(irisPred, test.data$Species)
```

```
##
## irisPred      setosa versicolor virginica
##   setosa      14          0          0
##   versicolor   0         17          3
##   virginica    0          1         11
```

```
plot(margin(rf, test.data$Species))
```

Margin of Predictions



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<http://www.rdatamining.com/docs/RDataMining.pdf>

- ▶ R Reference Card for Data Mining

<http://www.rdatamining.com/docs/R-refcard-data-mining.pdf>

- ▶ Free online courses and documents

<http://www.rdatamining.com/resources/>

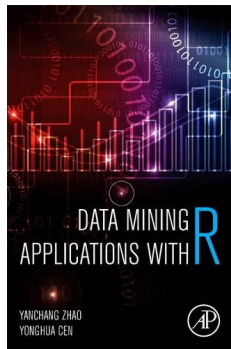
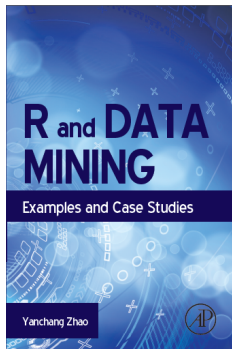
- ▶ RDataMining Group on LinkedIn (12,000+ members)

<http://group.rdatamining.com>

- ▶ RDataMining on Twitter (2,000+ followers)

@RDataMining

The End



Thanks!

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