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*. http://www.rdatamining.com/docs/RDataMining.pdf

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:

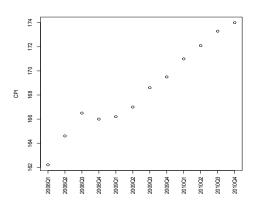
$$y = c_0 + c_1 x_1 + c_2 x_2 + \cdots + c_k x_k,$$

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

- linear regression with function Im()
- 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



Linear Regression

```
## correlation between CPI and year / quarter
cor(year, cpi)
## [1] 0.9096
cor(quarter, cpi)
## [1] 0.3738
## build a linear regression model with function lm()
fit <- lm(cpi ~ year + quarter)</pre>
fit.
##
## Call:
## lm(formula = cpi ~ year + quarter)
##
## Coefficients:
## (Intercept)
                        vear
                                  quarter
      -7644.49
                        3.89
                                      1.17
##
```

With the above linear model, CPI is calculated as

$$cpi = c_0 + c_1 * year + c_2 * quarter,$$

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

What will the CPI be in 2011?

With the above linear model, CPI is calculated as

$$cpi = c_0 + c_1 * year + c_2 * quarter,$$

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

What will the CPI be in 2011?

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"
                        "terms"
## [10] "call"
                                        "model"
##
## $class
## [1] "lm"
fit$coefficients
## (Intercept)
                     vear
                               quarter
     -7644.488
                     3.888
                                 1.167
##
```

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

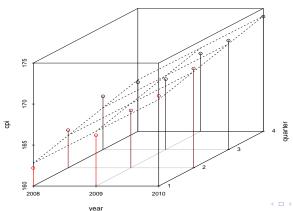
```
# differences between observed values and fitted values
residuals(fit)
## 1 2 3 4 5 6 ...
## -0.57917 0.65417 1.38750 -0.27917 -0.46667 -0.83333 -0.40...
## 8 9 10 11 12
## -0.66667 0.44583 0.37917 0.41250 -0.05417
summary(fit)
##
## Call:
## lm(formula = cpi ~ year + quarter)
##
## Residuals:
    Min 1Q Median 3Q Max
##
## -0.833 -0.495 -0.167 0.421 1.387
##
## Coefficients:
             Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) -7644.488 518.654 -14.74 1.3e-07 ***
```

year 3 888 0 258 15 06 1 1e-07 ***

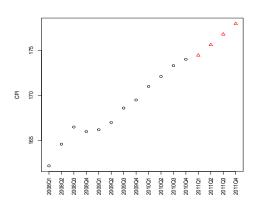
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3D Plot of the Fitted Model

```
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</pre>
```



Prediction of CPIs in 2011



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Generalized Linear Model (GLM)

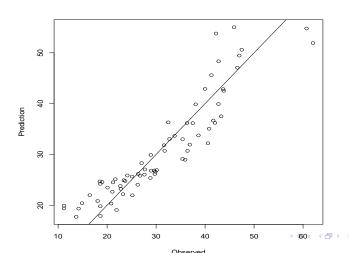
- Generalizes linear regression by allowing the linear model to be related to the response variable via a link function and allowing the magnitude of the variance of each measurement to be a function of its predicted value
- Unifies various other statistical models, including linear regression, logistic 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
## -11.569 -3.006 0.127 2.831 10.097
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) 0.73429 0.30895 2.38 0.0204 *
              0.00213 0.00145 1.47 0.1456
## age
## waistcirc 0.01049 0.00248 4.23 7.4e-05 ***
## hipcirc 0.00970 0.00323 3.00 0.0038 **
## elbowbreadth 0.00235 0.04569 0.05 0.9590
                                                           16 / 44
## kneebreadth
               0.06319
                         0.02819
                                   2.24
                                         0.0284 *
```

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)</pre>
```



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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 0.4 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

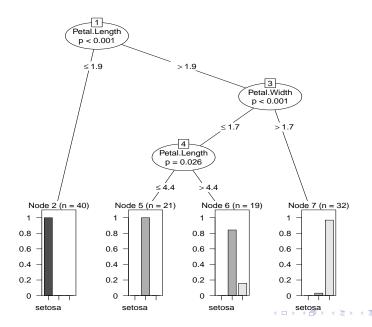
- Control the training of decision trees: MinSplit, MinBusket, MaxSurrogate and MaxDepth
- ► Target variable: Species
- ▶ Independent variables: all other variables

```
library(party)
myFormula <- Species ~ Sepal.Length + Sepal.Width + Petal.Length +
   Petal.Width
iris_ctree <- ctree(myFormula, data = train.data)</pre>
# check the prediction
table(predict(iris_ctree), train.data$Species)
##
##
                setosa versicolor virginica
##
     setosa
                    40
##
    versicolor
                                37
                                          31
##
    virginica
```

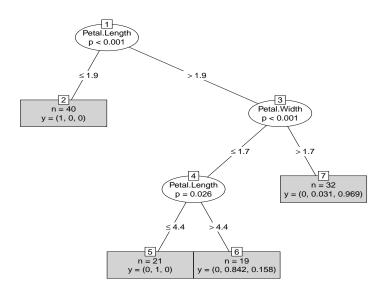
Print ctree

```
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</pre>
```

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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
                                    6.5
        43.29 99.5 116.5
                                              8.9
## 48
     65
                                    6.2
## 49
     59
        35.41 96.0 108.5
                                              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
##
                       4.50
                             6.13
## 47
       4.42
               4.95
       4.63
               5.01 4.48 6.37
## 48
## 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
```

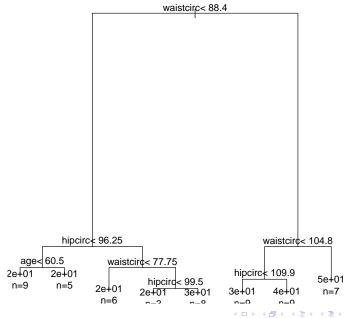
Train a Decision Tree with Package rpart

```
# 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,]</pre>
bodyfat.test <- bodyfat[ind==2,]</pre>
# train a decision tree
library(rpart)
myFormula <- DEXfat ~ age + waistcirc + hipcirc + elbowbreadth +
                       kneebreadth
bodyfat_rpart <- rpart(myFormula, data = bodyfat.train,</pre>
                        control = rpart.control(minsplit = 10))
# print(bodyfat_rpart£cptable)
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 7265,0000 30,95
##
     2) waistcirc< 88.4 31 960.5000 22.56
##
       4) hipcirc< 96.25 14 222.3000 18.41
##
         8) age< 60.5 9 66.8800 16.19 *
         9) age>=60.5 5 31.2800 22.41 *
##
##
       5) hipcirc>=96.25 17 299.6000 25.97
##
       10) waistcirc< 77.75 6 30.7300 22.32 *
##
        11) waistcirc>=77.75 11 145.7000 27.96
##
          23) hipcirc>=99.5 8 72.2900 29.54 *
##
##
     3) waistcirc>=88.4 25 1417.0000 41.35
##
       6) waistcirc< 104.8 18 330.6000 38.09
        12) hipcirc< 109.9 9 69.0000 34.38 *
##
        13) hipcirc>=109.9 9 13.0800 41.81 *
##
       7) waistcirc>=104.8 7 404.3000 49.73 *
##
```

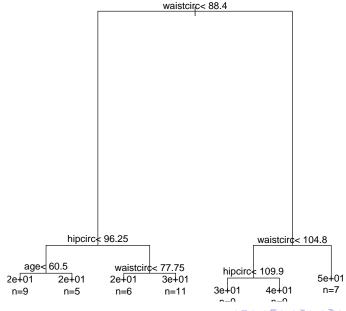
The rpart Tree



Select the Best Tree

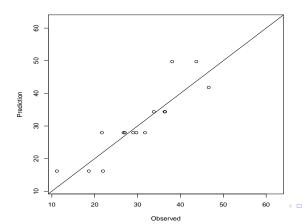
```
# select the tree with the minimum prediction error
opt <- which.min(bodyfat_rpart$cptable[, "xerror"])
cp <- bodyfat_rpart$cptable[opt, "CP"]
# prune tree
bodyfat_prune <- prune(bodyfat_rpart, cp = cp)
# plot tree
plot(bodyfat_prune)
text(bodyfat_prune, use.n = T)</pre>
```

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)</pre>
```



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R Packages for Random Forest

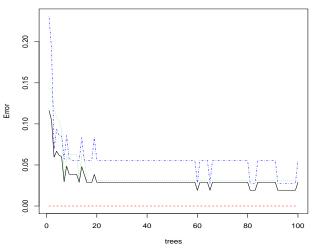
- Package randomForest
 - very fast
 - cannot handle data with missing values
 - a limit of 32 to the maximum number of levels of each categorical attribute
- Package party: cforest()
 - not limited to the above maximum levels
 - slow
 - needs more memory

Train a Random Forest

```
table(predict(rf), train.data$Species)
##
##
                setosa versicolor virginica
##
    setosa
                    36
                                0
##
    versicolor
                               31
    virginica
                                         34
##
                     0
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
                                              0.00000
## setosa
                  36
                              0
## versicolor
                             31
                                              0.03125
## virginica
                                       34
                                              0.05556
```

Error Rate of Random Forest

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



Variable Importance

```
importance(rf)

## MeanDecreaseGini

## Sepal.Length 6.914

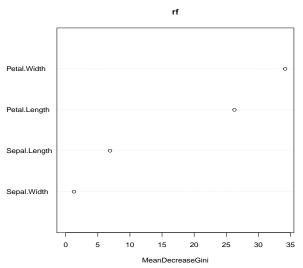
## Sepal.Width 1.283

## Petal.Length 26.267

## Petal.Width 34.164
```

Variable Importance

varImpPlot(rf)



Margin of Predictions

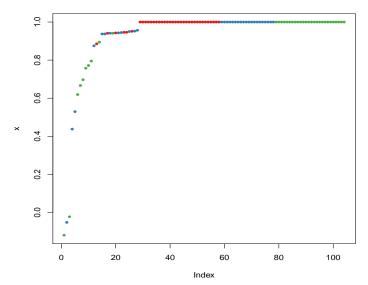
The margin of a data point is as the proportion of votes for the correct class minus maximum proportion of votes for other classes. Positive margin means correct classification.

```
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))</pre>
```

Margin of Predictions



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

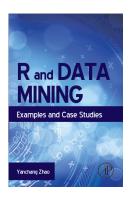
http://www.rdatamining.com/docs/RDataMining.pdf

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 http://group.rdatamining.com
- ► RDataMining on Twitter (1,800+ followers)

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The End





Thanks!

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