Assessment 4

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Complete all **Exercises**, and submit answers to **VtopBeta**

Datasets

```
### load packages
library(caret)
```

```
## Loading required package: lattice
```

```
## Loading required package: ggplot2
```

```
library(knitr)
```

Iris dataset for training and testing

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa

Split it into training set and testing set and validation set

```
ir_data=iris
set.seed(100)
head(ir_data)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

```
intrain <- createDataPartition(y = ir_data$Species, p= 0.7, list = FALSE)
training<-iris[intrain,]
testing<-ir_data[-intrain,]
dim(training);dim(testing)
```

```
## [1] 105   5
```

```
## [1] 45  5
```

```
summary(ir_data)
```

```
##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width   
##  Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100  
##  1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300  
##  Median :5.800   Median :3.000   Median :4.350   Median :1.300  
##  Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199  
##  3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800  
##  Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500  
##        Species  
##  setosa    :50  
##  versicolor:50  
##  virginica :50  
##                 
##                 
## 
```

```
training[["Species"]] = factor(training[["Species"]])
trctrl <- trainControl(method = "repeatedcv", number = 10, repeats = 3)
```

The results of confusion matrix show that this time the accuracy on the test set is **95.56%**.

using e1071

```
library(e1071)
model <- naiveBayes(Species ~., data = training)
class(model)
```

```
## [1] "naiveBayes"
```

```
summary(model)
```

```
##         Length Class  Mode     
## apriori 3      table  numeric  
## tables  4      -none- list     
## levels  3      -none- character
## call    4      -none- call
```

```
print(model)
```

```
##
## Naive Bayes Classifier for Discrete Predictors
##
## Call:
## naiveBayes.default(x = X, y = Y, laplace = laplace)
##
## A-priori probabilities:
## Y
##     setosa versicolor  virginica
##  0.3333333  0.3333333  0.3333333
##
## Conditional probabilities:
##             Sepal.Length
## Y                [,1]      [,2]
##   setosa     5.071429 0.3409083
##   versicolor 5.825714 0.4667427
##   virginica  6.540000 0.6611932
##
##             Sepal.Width
## Y                [,1]      [,2]
##   setosa     3.517143 0.3416962
##   versicolor 2.748571 0.2974118
##   virginica  2.962857 0.3263756
##
##             Petal.Length
## Y                [,1]      [,2]
##   setosa     1.471429 0.1856173
##   versicolor 4.182857 0.4712223
##   virginica  5.525714 0.5653437
##
##             Petal.Width
## Y                 [,1]      [,2]
##   setosa     0.2514286 0.1039554
##   versicolor 1.3114286 0.1794951
##   virginica  1.9885714 0.2857101
```

```
preds <- predict(model, newdata = training)
table(preds,training$Species)
```

```
##
## preds        setosa versicolor virginica
##   setosa         35          0         0
##   versicolor      0         33         3
##   virginica       0          2        32
```

```
(35+33+32)/(35+33+2+32+3)#change this according to the diagonal element of the previous statement result
```

```
## [1] 0.952381
```

Accuracy is **95.2381%**.

Using mlbench

```
library(mlbench)
data("HouseVotes84")
data(HouseVotes84, package = "mlbench")
model <- naiveBayes(Class ~ ., data = HouseVotes84)
predict(model, HouseVotes84[1:10,])
```

```
##  [1] republican republican republican democrat   democrat   democrat
##  [7] republican republican republican democrat
## Levels: democrat republican
```

```
predict(model, HouseVotes84[1:10,], type = "raw")
```

```
##           democrat   republican
##  [1,] 1.029209e-07 9.999999e-01
##  [2,] 5.820415e-08 9.999999e-01
##  [3,] 5.684937e-03 9.943151e-01
##  [4,] 9.985798e-01 1.420152e-03
##  [5,] 9.666720e-01 3.332802e-02
##  [6,] 8.121430e-01 1.878570e-01
##  [7,] 1.751512e-04 9.998248e-01
##  [8,] 8.300100e-06 9.999917e-01
##  [9,] 8.277705e-08 9.999999e-01
## [10,] 1.000000e+00 5.029425e-11
```

```
pred <- predict(model, HouseVotes84)
table(pred, HouseVotes84$Class)
```

```
## 
## pred         democrat republican
##   democrat        238         13
##   republican       29        155
```

```
(238+155)/(238+155+29+13)
```

```
## [1] 0.9034483
```

Accuracy is **90.34483%**.

```
## using laplace smoothing:
model <- naiveBayes(Class ~ ., data = HouseVotes84, laplace = 3)
pred <- predict(model, HouseVotes84[,-1])
table(pred, HouseVotes84$Class)
```

```
## 
## pred         democrat republican
##   democrat        237         12
##   republican       30        156
```

```
(237+156)/(237+156+12+30)
```

```
## [1] 0.9034483
```

Accuracy is still **90.34483%**.

Using a contingency table

```
data(Titanic)
m <- naiveBayes(Survived ~ ., data = Titanic)
m
```

```
## 
## Naive Bayes Classifier for Discrete Predictors
## 
## Call:
## naiveBayes.formula(formula = Survived ~ ., data = Titanic)
## 
## A-priori probabilities:
## Survived
##       No      Yes 
## 0.676965 0.323035 
## 
## Conditional probabilities:
##         Class
## Survived        1st        2nd        3rd       Crew
##      No  0.08187919 0.11208054 0.35436242 0.45167785
##      Yes 0.28551336 0.16596343 0.25035162 0.29817159
## 
##         Sex
## Survived       Male     Female
##      No  0.91543624 0.08456376
##      Yes 0.51617440 0.48382560
## 
##         Age
## Survived      Child      Adult
##      No  0.03489933 0.96510067
##      Yes 0.08016878 0.91983122
```

```
predict(m, as.data.frame(Titanic))
```

```
##  [1] Yes No  No  No  Yes Yes Yes Yes No  No  No  No  Yes Yes Yes Yes Yes
## [18] No  No  No  Yes Yes Yes Yes No  No  No  No  Yes Yes Yes Yes
## Levels: No Yes
```

Cervical Cancer

```
cancer <- read.csv("risk_factors_cervical_cancer.csv")
cancer[cancer=='?'] <- NA
cancer[["Dx.Cancer"]] = factor(cancer[["Dx.Cancer"]],ordered = TRUE)

#Splitting Dataset
intrain <- createDataPartition(y = cancer$Dx.Cancer, p = 0.7, list = FALSE)
training<-cancer[intrain,]
testing<-cancer[-intrain,]
dim(training);dim(testing)
```

```
## [1] 601  36
```

```
## [1] 257  36
```

```
summary(cancer)
```

```
##       Age        Number.of.sexual.partners First.sexual.intercourse
##  Min.   :13.00   2.0    :272               15.0   :163             
##  1st Qu.:20.00   3.0    :208               17.0   :151             
##  Median :25.00   1.0    :206               18.0   :137             
##  Mean   :26.82   4.0    : 78               16.0   :121             
##  3rd Qu.:32.00   5.0    : 44               14.0   : 79             
##  Max.   :84.00   (Other): 24               (Other):200             
##                  NA's   : 26               NA's   :  7             
##  Num.of.pregnancies  Smokes         Smokes..years.   Smokes..packs.year.
##  1.0    :270        ?   :  0    0.0         :722    0.0         :722    
##  2.0    :240        0.0 :722    1.266972909: 15    0.5132021277: 18    
##  3.0    :139        1.0 :123    5.0        :  9    1.0         :  6    
##  4.0    : 74        NA's: 13    9.0        :  9    3.0         :  5    
##  5.0    : 35                    1.0        :  8    0.05        :  4    
##  (Other): 44                    (Other)    : 82    (Other)     : 90    
```

```
##  NA's   : 56                   NA's       : 13    NA's        : 13
##  Hormonal.Contraceptives Hormonal.Contraceptives..years.   IUD
##  ?   :  0                0.0    :269                      ?   :  0
##  0.0 :269                1.0    : 77                      0.0 :658
##  1.0 :481                0.25   : 41                      1.0 : 83
##  NA's:108                2.0    : 40                      NA's:117
##                          3.0    : 39
##                          (Other):284
##                          NA's   :108
##   IUD..years.    STDs     STDs..number. STDs.condylomatosis
##  0.0    :658   ?   :  0   ?   :  0      ?   :  0
##  3.0    : 11   0.0 :674   0.0 :674      0.0 :709
##  2.0    : 10   1.0 : 79   1.0 : 34      1.0 : 44
##  5.0    :  9   NA's:105   2.0 : 37      NA's:105
##  1.0    :  8              3.0 :  7
##  (Other): 45              4.0 :  1
##  NA's   :117              NA's:105
##  STDs.cervical.condylomatosis STDs.vaginal.condylomatosis
##  ?   :  0                     ?   :  0
##  0.0 :753                     0.0 :749
##  NA's:105                     1.0 :  4
##                               NA's:105
##
##
##
##  STDs.vulvo.perineal.condylomatosis STDs.syphilis
##  ?   :  0                           ?   :  0
##  0.0 :710                           0.0 :735
##  1.0 : 43                           1.0 : 18
##  NA's:105                           NA's:105
##
##
##
##  STDs.pelvic.inflammatory.disease STDs.genital.herpes
##  ?   :  0                         ?   :  0
##  0.0 :752                         0.0 :752
##  1.0 :  1                         1.0 :  1
##  NA's:105                         NA's:105
##
##
##
##  STDs.molluscum.contagiosum STDs.AIDS  STDs.HIV   STDs.Hepatitis.B
##  ?   :  0                   ?   :  0   ?   :  0   ?   :  0
##  0.0 :752                   0.0 :753   0.0 :735   0.0 :752
##  1.0 :  1                   NA's:105   1.0 : 18   1.0 :  1
##  NA's:105                              NA's:105   NA's:105
##
##
##
##  STDs.HPV   STDs..Number.of.diagnosis STDs..Time.since.first.diagnosis
##  ?   :  0   Min.   :0.00000          1.0    : 15
##  0.0 :751   1st Qu.:0.00000          3.0    : 10
##  1.0 :  2   Median :0.00000          2.0    :  9
##  NA's:105   Mean   :0.08741          4.0    :  6
##             3rd Qu.:0.00000          7.0    :  5
##             Max.   :3.00000          (Other): 26
##                                      NA's   :787
##  STDs..Time.since.last.diagnosis Dx.Cancer     Dx.CIN
##  1.0    : 17                     0:840     Min.   :0.00000
##  2.0    : 10                     1: 18     1st Qu.:0.00000
##  3.0    :  9                               Median :0.00000
##  4.0    :  6                               Mean   :0.01049
##  7.0    :  5                               3rd Qu.:0.00000
##  (Other): 24                               Max.   :1.00000
##  NA's   :787
##      Dx.HPV               Dx             Hinselmann         Schiller
##  Min.   :0.00000   Min.   :0.00000   Min.   :0.00000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.00000
##  Median :0.00000   Median :0.00000   Median :0.00000   Median :0.00000
##  Mean   :0.02098   Mean   :0.02797   Mean   :0.04079   Mean   :0.08625
##  3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.00000   Max.   :1.00000   Max.   :1.00000
##
```

```
##     Citology          Biopsy
##  Min.   :0.00000   Min.   :0.0000
##  1st Qu.:0.00000   1st Qu.:0.0000
##  Median :0.00000   Median :0.0000
##  Mean   :0.05128   Mean   :0.0641
##  3rd Qu.:0.00000   3rd Qu.:0.0000
##  Max.   :1.00000   Max.   :1.0000
##
```

```r
trctrl <- trainControl(method = "repeatedcv", number = 2, repeats = 3)

#Training Model
model <- naiveBayes(Dx.Cancer ~ ., data = training)
class(model)
```

```
## [1] "naiveBayes"
```

```r
summary(model)
```

```
##         Length Class  Mode
## apriori  2     table  numeric
## tables  35     -none- list
## levels   2     -none- character
## call     4     -none- call
```

```r
print(model)
```

```
##
## Naive Bayes Classifier for Discrete Predictors
##
## Call:
## naiveBayes.default(x = X, y = Y, laplace = laplace)
##
## A-priori probabilities:
## Y
##          0          1
## 0.97836938 0.02163062
##
## Conditional probabilities:
##    Age
## Y       [,1]     [,2]
##   0 26.46088 8.100950
##   1 33.84615 7.787235
##
##    Number.of.sexual.partners
## Y             ?         1.0        10.0        15.0         2.0
##   0 0.000000000 0.256183746 0.001766784 0.000000000 0.330388693
##   1 0.000000000 0.076923077 0.000000000 0.000000000 0.307692308
##    Number.of.sexual.partners
## Y          28.0         3.0         4.0         5.0         6.0
##   0 0.001766784 0.233215548 0.098939929 0.047703180 0.008833922
##   1 0.000000000 0.461538462 0.000000000 0.153846154 0.000000000
##    Number.of.sexual.partners
## Y           7.0         8.0         9.0
##   0 0.012367491 0.007067138 0.001766784
##   1 0.000000000 0.000000000 0.000000000
##
##    First.sexual.intercourse
## Y             ?        10.0        11.0        12.0        13.0
##   0 0.000000000 0.001718213 0.000000000 0.008591065 0.032646048
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    First.sexual.intercourse
## Y          14.0        15.0        16.0        17.0        18.0
##   0 0.097938144 0.199312715 0.158075601 0.173539519 0.147766323
##   1 0.076923077 0.076923077 0.076923077 0.000000000 0.230769231
##    First.sexual.intercourse
## Y          19.0        20.0        21.0        22.0        23.0
##   0 0.065292096 0.034364261 0.024054983 0.008591065 0.010309278
##   1 0.384615385 0.153846154 0.000000000 0.000000000 0.000000000
```

```
##   1 0.384615385 0.153846154 0.000000000 0.000000000 0.000000000
##    First.sexual.intercourse
## Y          24.0        25.0        26.0        27.0        28.0
##   0 0.006872852 0.001718213 0.006872852 0.006872852 0.005154639
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    First.sexual.intercourse
## Y          29.0        32.0
##   0 0.008591065 0.001718213
##   1 0.000000000 0.000000000
## 
##    Num.of.pregnancies
## Y             ?         0.0         1.0        10.0        11.0
##   0 0.000000000 0.025179856 0.327338129 0.001798561 0.000000000
##   1 0.000000000 0.000000000 0.230769231 0.000000000 0.000000000
##    Num.of.pregnancies
## Y           2.0         3.0         4.0         5.0         6.0
##   0 0.318345324 0.163669065 0.091726619 0.035971223 0.025179856
##   1 0.307692308 0.230769231 0.153846154 0.076923077 0.000000000
##    Num.of.pregnancies
## Y           7.0         8.0
##   0 0.007194245 0.003597122
##   1 0.000000000 0.000000000
## 
##    Smokes
## Y           ?       0.0       1.0
##   0 0.0000000 0.8603448 0.1396552
##   1 0.0000000 0.8461538 0.1538462
## 
##    Smokes..years.
## Y             ?         0.0        0.16         0.5         1.0
##   0 0.000000000 0.860344828 0.001724138 0.005172414 0.006896552
##   1 0.000000000 0.846153846 0.000000000 0.000000000 0.000000000
##    Smokes..years.
## Y   1.266972909        10.0        11.0        12.0        13.0
##   0 0.020689655 0.005172414 0.005172414 0.005172414 0.001724138
##   1 0.000000000 0.000000000 0.076923077 0.000000000 0.000000000
##    Smokes..years.
## Y          14.0        15.0        16.0        18.0        19.0
##   0 0.005172414 0.003448276 0.006896552 0.001724138 0.005172414
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..years.
## Y           2.0        20.0        21.0        22.0        24.0
##   0 0.005172414 0.000000000 0.000000000 0.003448276 0.000000000
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..years.
## Y          28.0         3.0        32.0        34.0        37.0
##   0 0.001724138 0.008620690 0.000000000 0.000000000 0.000000000
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.076923077
##    Smokes..years.
## Y           4.0         5.0         6.0         7.0         8.0
##   0 0.006896552 0.010344828 0.003448276 0.008620690 0.008620690
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..years.
## Y           9.0
##   0 0.008620690
##   1 0.000000000
## 
##    Smokes..packs.year.
## Y             ?         0.0       0.001       0.003       0.025
##   0 0.000000000 0.860344828 0.001724138 0.000000000 0.001724138
##   1 0.000000000 0.846153846 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y          0.04        0.05         0.1        0.15        0.16
##   0 0.001724138 0.005172414 0.000000000 0.001724138 0.001724138
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.076923077
##    Smokes..packs.year.
## Y           0.2        0.25         0.3        0.32        0.37
##   0 0.005172414 0.001724138 0.001724138 0.000000000 0.000000000
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y           0.4        0.45         0.5 0.5132021277         0.7
##   0 0.001724138 0.000000000 0.000000000  0.025862069 0.000000000
##   1 0.000000000 0.000000000 0.000000000  0.000000000 0.000000000
```

```
##    Smokes..packs.year.
## Y          0.75         0.8         0.9         1.0         1.2
##   0 0.005172414 0.001724138 0.000000000 0.005172414 0.003448276
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y          1.25         1.3        1.35         1.4         1.6
##   0 0.000000000 0.001724138 0.001724138 0.003448276 0.001724138
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y          1.65        12.0        15.0        19.0         2.0
##   0 0.000000000 0.005172414 0.000000000 0.001724138 0.003448276
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y           2.1         2.2        2.25         2.4         2.5
##   0 0.001724138 0.001724138 0.000000000 0.003448276 0.001724138
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y           2.6         2.7        2.75         2.8        21.0
##   0 0.000000000 0.001724138 0.001724138 0.001724138 0.000000000
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y          22.0         3.0         3.3         3.4         3.5
##   0 0.001724138 0.008620690 0.001724138 0.000000000 0.001724138
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y          37.0         4.0         4.5         4.8         5.0
##   0 0.000000000 0.001724138 0.001724138 0.000000000 0.003448276
##   1 0.076923077 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y           5.5         5.7         6.0         7.0         7.5
##   0 0.001724138 0.001724138 0.005172414 0.003448276 0.001724138
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Smokes..packs.year.
## Y           7.6         8.0         9.0
##   0 0.001724138 0.001724138 0.003448276
##   1 0.000000000 0.000000000 0.000000000
##
##    Hormonal.Contraceptives
## Y           ?       0.0       1.0
##   0 0.0000000 0.3517787 0.6482213
##   1 0.0000000 0.1538462 0.8461538
##
##    Hormonal.Contraceptives..years.
## Y             ?         0.0        0.08        0.16        0.17
##   0 0.000000000 0.351778656 0.027667984 0.017786561 0.001976285
##   1 0.000000000 0.153846154 0.076923077 0.076923077 0.000000000
##    Hormonal.Contraceptives..years.
## Y          0.25        0.33        0.41        0.42         0.5
##   0 0.059288538 0.013833992 0.001976285 0.005928854 0.033596838
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Hormonal.Contraceptives..years.
## Y          0.58        0.66        0.67        0.75         1.0
##   0 0.007905138 0.007905138 0.001976285 0.005928854 0.110671937
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.153846154
##    Hormonal.Contraceptives..years.
## Y           1.5        10.0        11.0        12.0        13.0
##   0 0.003952569 0.015810277 0.003952569 0.003952569 0.003952569
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Hormonal.Contraceptives..years.
## Y          14.0        15.0        16.0        17.0        19.0
##   0 0.001976285 0.005928854 0.001976285 0.001976285 0.003952569
##   1 0.000000000 0.076923077 0.076923077 0.000000000 0.000000000
##    Hormonal.Contraceptives..years.
## Y           2.0 2.282200521         2.5        20.0        22.0
##   0 0.051383399 0.003952569 0.001976285 0.005928854 0.000000000
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    Hormonal.Contraceptives..years.
## Y           3.0         3.5        30.0         4.0         4.5
##   0 0.055335968 0.001976285 0.001976285 0.041501976 0.001976285
##   1 0.153846154 0.000000000 0.000000000 0.000000000 0.000000000
##    Hormonal.Contraceptives..years.
## Y           5.0         6.0         6.5         7.0         8.0
##   0 0.047430830 0.031620553 0.001976285 0.023715415 0.021739130
```

```
##   1 0.000000000 0.153846154 0.000000000 0.000000000 0.000000000
##    Hormonal.Contraceptives..years.
## Y          9.0
##   0 0.011857708
##   1 0.076923077
##
##    IUD
## Y            ?        0.0        1.0
##   0 0.00000000 0.90039841 0.09960159
##   1 0.00000000 0.61538462 0.38461538
##
##    IUD..years.
## Y             ?         0.0        0.08        0.16        0.17
##   0 0.000000000 0.900398406 0.003984064 0.001992032 0.001992032
##   1 0.000000000 0.615384615 0.000000000 0.000000000 0.000000000
##    IUD..years.
## Y          0.25        0.33        0.41         0.5        0.58
##   0 0.000000000 0.001992032 0.000000000 0.001992032 0.000000000
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    IUD..years.
## Y          0.91         1.0         1.5        10.0        11.0
##   0 0.000000000 0.011952191 0.000000000 0.000000000 0.003984064
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    IUD..years.
## Y          12.0        15.0        17.0        19.0         2.0
##   0 0.001992032 0.000000000 0.001992032 0.001992032 0.013944223
##   1 0.000000000 0.000000000 0.000000000 0.000000000 0.000000000
##    IUD..years.
## Y           3.0         4.0         5.0         6.0         7.0
##   0 0.009960159 0.007968127 0.011952191 0.003984064 0.005976096
##   1 0.153846154 0.076923077 0.000000000 0.000000000 0.076923077
##    IUD..years.
## Y           8.0         9.0
##   0 0.009960159 0.001992032
##   1 0.076923077 0.000000000
##
##    STDs
## Y           ?       0.0       1.0
##   0 0.0000000 0.8954635 0.1045365
##   1 0.0000000 0.8461538 0.1538462
##
##    STDs..number.
## Y             ?         0.0         1.0         2.0         3.0
##   0 0.000000000 0.895463511 0.043392505 0.051282051 0.007889546
##   1 0.000000000 0.846153846 0.153846154 0.000000000 0.000000000
##    STDs..number.
## Y           4.0
##   0 0.001972387
##   1 0.000000000
##
##    STDs.condylomatosis
## Y           ?       0.0       1.0
##   0 0.0000000 0.9408284 0.0591716
##   1 0.0000000 1.0000000 0.0000000
##
##    STDs.cervical.condylomatosis
## Y   ? 0.0
##   0 0   1
##   1 0   1
##
##    STDs.vaginal.condylomatosis
## Y            ?        0.0        1.0
##   0 0.00000000 0.99408284 0.00591716
##   1 0.00000000 1.00000000 0.00000000
##
##    STDs.vulvo.perineal.condylomatosis
## Y            ?        0.0        1.0
##   0 0.00000000 0.94280079 0.05719921
##   1 0.00000000 1.00000000 0.00000000
##
##    STDs.syphilis
## Y            ?        0.0        1.0
##   0 0.00000000 0.97633136 0.02366864
```

```
##    0 0.00000000 0.97633136 0.02366864
##    1 0.00000000 1.00000000 0.00000000
##
##     STDs.pelvic.inflammatory.disease
## Y             ?         0.0         1.0
##    0 0.000000000 0.998027613 0.001972387
##    1 0.000000000 1.000000000 0.000000000
##
##     STDs.genital.herpes
## Y             ?         0.0         1.0
##    0 0.000000000 0.998027613 0.001972387
##    1 0.000000000 1.000000000 0.000000000
##
##     STDs.molluscum.contagiosum
## Y             ?         0.0         1.0
##    0 0.000000000 0.998027613 0.001972387
##    1 0.000000000 1.000000000 0.000000000
##
##     STDs.AIDS
## Y   ? 0.0
##    0 0   1
##    1 0   1
##
##     STDs.HIV
## Y            ?        0.0        1.0
##    0 0.00000000 0.97633136 0.02366864
##    1 0.00000000 1.00000000 0.00000000
##
##     STDs.Hepatitis.B
## Y             ?         0.0         1.0
##    0 0.000000000 0.998027613 0.001972387
##    1 0.000000000 1.000000000 0.000000000
##
##     STDs.HPV
## Y           ?       0.0       1.0
##    0 0.0000000 1.0000000 0.0000000
##    1 0.0000000 0.8461538 0.1538462
##
##     STDs..Number.of.diagnosis
## Y         [,1]      [,2]
##    0 0.08843537 0.3072141
##    1 0.07692308 0.2773501
##
##     STDs..Time.since.first.diagnosis
## Y            ?        1.0       10.0       11.0       12.0       15.0
##    0 0.00000000 0.20408163 0.02040816 0.04081633 0.00000000 0.02040816
##    1 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
##     STDs..Time.since.first.diagnosis
## Y         16.0       18.0       19.0        2.0       21.0       22.0
##    0 0.04081633 0.02040816 0.04081633 0.14285714 0.04081633 0.02040816
##    1 1.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
##     STDs..Time.since.first.diagnosis
## Y          3.0        4.0        5.0        6.0        7.0        8.0
##    0 0.14285714 0.08163265 0.04081633 0.02040816 0.06122449 0.04081633
##    1 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
##     STDs..Time.since.first.diagnosis
## Y          9.0
##    0 0.02040816
##    1 0.00000000
##
##     STDs..Time.since.last.diagnosis
## Y            ?        1.0       10.0       11.0       12.0       15.0
##    0 0.00000000 0.24489796 0.02040816 0.04081633 0.00000000 0.02040816
##    1 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
##     STDs..Time.since.last.diagnosis
## Y         16.0       18.0       19.0        2.0       21.0       22.0
##    0 0.04081633 0.02040816 0.02040816 0.14285714 0.04081633 0.02040816
##    1 1.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
##     STDs..Time.since.last.diagnosis
## Y          3.0        4.0        5.0        6.0        7.0        8.0
##    0 0.12244898 0.08163265 0.04081633 0.02040816 0.06122449 0.04081633
##    1 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
##     STDs..Time.since.last.diagnosis
```

```
## Y          9.0
##   0 0.02040816
##   1 0.00000000
##
##    Dx.CIN
## Y          [,1]      [,2]
##   0 0.01020408 0.1005841
##   1 0.00000000 0.0000000
##
##    Dx.HPV
## Y          [,1]      [,2]
##   0 0.00170068 0.0412393
##   1 0.84615385 0.3755338
##
##    Dx
## Y          [,1]      [,2]
##   0 0.01020408 0.1005841
##   1 0.69230769 0.4803845
##
##    Hinselmann
## Y          [,1]      [,2]
##   0 0.03061224 0.1724114
##   1 0.23076923 0.4385290
##
##    Schiller
## Y          [,1]      [,2]
##   0 0.06632653 0.2490639
##   1 0.30769231 0.4803845
##
##    Citology
## Y          [,1]      [,2]
##   0 0.04251701 0.2019373
##   1 0.15384615 0.3755338
##
##    Biopsy
## Y          [,1]      [,2]
##   0 0.05102041 0.2202267
##   1 0.30769231 0.4803845
```

```r
#Testing Model
preds <- predict(model, newdata = testing)

#Confusion Matrix
conmat <- table(preds,testing$Dx.Cancer)

#Accuracy
accuracy <- (conmat[1]+conmat[4])/(conmat[1]+conmat[2]+conmat[3]+conmat[4])*100
accuracy
```

```
## [1] 91.43969
```

```r
#ROC
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
library(rowr)
prediction <- rev(seq_along(cancer$Dx.Cancer))
prediction[1:len(preds)] <- mean(as.numeric(preds))
roc_obj <- roc(cancer$Dx.Cancer,prediction)
auc(roc_obj)
```

```
## Area under the curve: 0.6005
```

Sentiment Analysis of Movie Reviews

```
# Load additional libraries
library(tm)
```

```
## Loading required package: NLP
```

```
##
## Attaching package: 'NLP'
```

```
## The following object is masked from 'package:ggplot2':
##
##     annotate
```

```
library(RTextTools)
```

```
## Loading required package: SparseM
```

```
##
## Attaching package: 'SparseM'
```

```
## The following object is masked from 'package:base':
##
##     backsolve
```

```
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 3.5.1
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:rowr':
##
##     coalesce, count
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
# Library for parallel processing
library(doMC)
```

```
## Loading required package: foreach
```

```
## Loading required package: iterators
```

```
## Loading required package: parallel
```

```
registerDoMC(cores=detectCores())  # Use all available cores
```

Reading the data

```
df<- read.csv("movie-pang02.csv", stringsAsFactors = FALSE)
glimpse(df)
```

```
## Observations: 2,000
## Variables: 2
## $ class <chr> "Pos", "Pos", "Pos", "Pos", "Pos", "Pos", "Pos", "Pos", ...
## $ text  <chr> " films adapted from comic books have had plenty of succ...
```

```
# Randomize the dataset
set.seed(1)
df <- df[sample(nrow(df)), ]
df <- df[sample(nrow(df)), ]
glimpse(df)
```

```
## Observations: 2,000
## Variables: 2
## $ class <chr> "Neg", "Pos", "Neg", "Neg", "Neg", "Neg", "Neg", "Neg", ...
## $ text  <chr> " frank detorri s   bill murray   a single dad who lives...
```

```
# Convert the 'class' variable from character to factor.
df$class <- as.factor(df$class)
```

Bag of Words Tokenisation

```
corpus <- Corpus(VectorSource(df$text))
corpus
```

```
## <<SimpleCorpus>>
## Metadata:  corpus specific: 1, document level (indexed): 0
## Content:  documents: 2000
```

```
inspect(corpus[1:3])
```

```
## <<SimpleCorpus>>
## Metadata:  corpus specific: 1, document level (indexed): 0
## Content:  documents: 3
##
## [1]  frank detorri s   bill murray   a single dad who lives on beer and junk food with no apparent unders
tanding of sanitation or hygiene   much to the dismay of his preteen daughter shane   elena franklin     wh
en he uses the  10 second rule  to retrieve a hard boiled egg from a chimp s cage at the zoo and downs it
he introduces a lethal bacteria into his system    inside his skin   the city of frank is in turmoil thanks
to the vote pandering of mayor phlegmming   voice of william shatner     so it s up to one frank pd white bl
ood cell   voice of chris rock   to save the day in peter and bobby farrelly s   osmosis jones      the city
of frank is a brightly animated   animation directed by piet kroon and tom sito   cellular municipality wher
e osmosis jones is a typical rogue cop looking for another chance    he s inadvertently teamed up with drix
voice of david hyde pierce   tv s   frasier      a cold capsule with 12 hours worth of painkillers to dispe
nse    this quarrelling duo are about to go on a   fantastic voyage   in order to hunt down thrax   voice of
laurence fishburne     the virus intent on shutting down frank    while the animation is certainly colorful
to look at   osmosis jones  story is a hackneyed one    the story cries out for puny puns   but we only get
occasional sprinklings of wit or bodily humor   drix graduated phi beta capsule    he departs on a bus headed
for bladder      neither the hero or villain is particularly interesting   thrax looks like an animated   pr
edator      although hyde pierce is a delightful sidekick    adults can desperately keep their eyes peeled
for small amusements the animators dot along the landscape    meanwhile   back in live action land   bill mu
rray is reduced to nothing more than a walking gross out joke    there s no particular enjoyment to be found
watching him vomit on molly shannon   she plays shane s teacher   mrs   boyd   or hoisting his ingrown toena
il onto a restaurant table    one must wonder how the climatic flatlining of a child s father will play to t
he family audience as well    rest assured   the whole enchilada is wrapped up with a fart joke    while far
```

```
less offensive than the farrelly s last effort   me   myself and irene     that film at least spiked some co
mic highs with jim carrey s hijinx       osmosis jones   will probably be ok for the kids   but the farrelly
s playing for the family audience is like watching marilyn manson croon a phil collins tune

## [2]  synopsis   in phantom menace the galaxy is divided into power groups whose interests will inevitably
collide in later sequels    there is an overarching galactic united nations type organization called the sen
ate presided by a weak chancellor    within the senate two camps are at odds   a bickering   isolationist al
liance called the republic and their aggressive rival the trade federation    preserving law and order are a
council of jedi knights who are meanwhile searching for a prophesied chosen one of virgin birth    manipulat
ing events behind the scenes is a dangerous   reemerging clan called the dark lords of sith   so shadowy and
secretive that they comprise a   phantom   menace    jedi knight qui gon jinn   liam neeson   and his appren
tice obi wan kenobi   ewan mcgregor   witness an invasion of teenage queen amidala s home planet naboo and b
efriend a gungan named jar jar   ahmed best      on the desert planet of tatooine the two jedi   jar jar   a
nd amidala   natalie portman   attend a lengthy drag race involving the young boy anakin skywalker   jake ll
oyd      the five protagonists try to solicit help for freeing naboo by visiting the city planet of coruscan
t where a lot of debate and political maneuvering takes place    can they free amidala s helpless planet
opinion   on tv last night i watched young   wannabe celebs pay $400 a ticket and come running out of theate
rs to bask in front of news cameras   gushing with testimonials of the phantom menace s greatness in exchang
e for a few seconds of being on national television    given this kind of media mania i wondered if phantom
menace   the most anticipated movie of 1999   could possibly live up to the extraordinary hype that preceded
it    does phantom menace match the exaggerated hype    director george lucas answers     it s only a movie
to me   any movie with russian sounding accents for bad guys   jamaican accents for good guys   and middle e
astern sounding accents for seedy gamblers accents can be expected to be more tongue in cheek than profound
visually   star wars   episode i   the phantom menace   1999   is a kid show where parents can take their yo
ung ones to marvel at child friendly cgi characters and wondrous backdrops even if the character dialogue
mostly geopolitics   is beyond the level of children    it is left to parents to patiently explain the conve
rsation   droid origins   family lineage   the definitions of terms like blockade   appeasement   federation
alliance   symbiosis   satellite controlled robots et cetera    at least this much is clear   there s plenty
of eye candy   and in the last few minutes it s good guys and joe camel lookalikes versus a caped   horned r
ed devil character and his mechanical hordes    weaknesses   weaknesses lie in the writing and in the perfor
mance    at first it seems like the film is to be an invasion story   but then phantom takes an hour long de
tour to cover one chariot race before returning to the invasion theme    this dilutes the central story    a
dditionally   smaller scenes seem written self consciously   as if they were added more to fill us in on ext
raneous background information for other movies rather than form an integral part of the present movie    ve
teran actors liam neeson and ewan mcgregor noticeably outperform the other acting leads    better ensemble c
hemistry between the five leads and background information that is central to a tight story line could have
made have given phantom stronger performances and storytelling punch    strengths   on the bright side phant
om menace as a big budget production is far ahead of the competition in terms of making whimsical creatures
worlds and vehicles appear real    the film boasts sophisticated   top of the line visuals and quality exoti
c costumes   a musical score entertaining enough to stand alone   and three worthwhile sequences in the seco
nd half    bottom line    seeing the film is entertaining and informative   like a visual theme park with st
ar wars filler information serving as dialogue between impressive money shots    we are bound to be complete
ly inundated by star wars publicity   music and tie ins for the next few months
## [3]  terrence malick made an excellent 90 minute film adaptation of james jones  world war ii novel    un
fortunately   he buried it within an overlong and overreaching 3 hour long pseudo epic    this is a shame be
cause the film features an outstanding performance by nick nolte    the best scene is when nick nolte s char
acter   lt   col   tall   is forced to deal with the direct refusal by capt   staros   elias koteas   to exe
cute an order    nolte s reaction and transformation may be the best work of his career    had terrence mali
ck concentrated on the great performances of nolte and koteas as well as those by sean penn   woody harrelso
n   and john cusack   he could have made a truly great film    instead   malick saddled the film with ploddi
ng pacing   unnecessary flashbacks   and a voice over narration all designed to telegraph the great philosop
hical underpinnings of the story   the narration was especially annoying as much of it sounded like very ba
d high school poetry    with a lot of editing   the core story could be transformed into a truly classic war
film    hopefully   the dvd version of this film will feature options to suppress the narration   and perhap
s will even provide for an alternate   shorter version of the film    i give this film
```

Data Cleanup

```r
# Use dplyr's  %>% (pipe) utility to do this neatly.
corpus.clean <- corpus %>%
  tm_map(content_transformer(tolower)) %>%
  tm_map(removePunctuation) %>%
  tm_map(removeNumbers) %>%
  tm_map(removeWords, stopwords(kind="en")) %>%
  tm_map(stripWhitespace)
```

```
## Warning in tm_map.SimpleCorpus(., content_transformer(tolower)):
## transformation drops documents
```

```
## Warning in tm_map.SimpleCorpus(., removePunctuation): transformation drops
## documents
```

```
## Warning in tm_map.SimpleCorpus(., removeNumbers): transformation drops
## documents
```

```
## Warning in tm_map.SimpleCorpus(., removeWords, stopwords(kind = "en")):
## transformation drops documents
```

```
## Warning in tm_map.SimpleCorpus(., stripWhitespace): transformation drops
## documents
```

Document Term Matrix

```
dtm <- DocumentTermMatrix(corpus.clean)
inspect(dtm[40:50, 10:15])
```

```
## <<DocumentTermMatrix (documents: 11, terms: 6)>>
## Non-/sparse entries: 6/60
## Sparsity           : 91%
## Maximal term length: 8
## Weighting          : term frequency (tf)
## Sample             :
##     Terms
## Docs apparent assured audience back bacteria beer
##   40        0       0        1    1        0    0
##   41        0       0        1    0        0    0
##   42        0       0        0    0        0    0
##   43        0       0        0    0        0    0
##   44        0       0        0    1        0    0
##   45        0       0        0    0        0    0
##   46        0       0        2    0        0    0
##   47        0       0        0    0        0    0
##   48        0       0        0    0        0    0
##   50        0       0        2    0        0    0
```

Paritioning

```
df.train <- df[1:1500,]
df.test <- df[1501:2000,]

dtm.train <- dtm[1:1500,]
dtm.test <- dtm[1501:2000,]

corpus.clean.train <- corpus.clean[1:1500]
corpus.clean.test <- corpus.clean[1501:2000]
```

Feature set selection

```
dim(dtm.train)
```

```
## [1]  1500 38957
```

```
fivefreq <- findFreqTerms(dtm.train, 5)
length((fivefreq))
```

```
## [1] 12144
```

```
# Use only 5 most frequent words (fivefreq) to build the DTM
dtm.train.nb <- DocumentTermMatrix(corpus.clean.train, control=list(dictionary = fivefreq))
dim(dtm.train.nb)
```

```
## [1]  1500 12144
```

```
dtm.test.nb <- DocumentTermMatrix(corpus.clean.test, control=list(dictionary = fivefreq))
dim(dtm.train.nb)
```

```
## [1]  1500 12144
```

Boolean feature Multinomial Naive Bayes

```
# Function to convert the word frequencies to yes (presence) and no (absence) labels
convert_count <- function(x) {
  y <- ifelse(x > 0, 1,0)
  y <- factor(y, levels=c(0,1), labels=c("No", "Yes"))
  y
}

# Apply the convert_count function to get final training and testing DTMs
trainNB <- apply(dtm.train.nb, 2, convert_count)
testNB <- apply(dtm.test.nb, 2, convert_count)

# Train the classifier
system.time( classifier <- naiveBayes(trainNB, df.train$class, laplace = 1) )
```

```
##    user  system elapsed
##   8.922   0.821  13.442
```

```
# Use the NB classifier we built to make predictions on the test set.
system.time( pred <- predict(classifier, newdata=testNB) )
```

```
##    user  system elapsed
## 220.774   5.494 262.348
```

```
# Create a truth table by tabulating the predicted class labels with the actual class labels
table("Predictions"= pred,  "Actual" = df.test$class )
```

```
##            Actual
## Predictions Neg Pos
##         Neg 224  54
##         Pos  41 181
```

Confusion Matrix

```
conf.mat <- confusionMatrix(pred, df.test$class)
conf.mat
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Neg Pos
##        Neg 224  54
##        Pos  41 181
##
##                Accuracy : 0.81
##                  95% CI : (0.7728, 0.8435)
##     No Information Rate : 0.53
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.6174
##  Mcnemar's Test P-Value : 0.2183
##
##             Sensitivity : 0.8453
##             Specificity : 0.7702
##          Pos Pred Value : 0.8058
##          Neg Pred Value : 0.8153
##              Prevalence : 0.5300
##          Detection Rate : 0.4480
##    Detection Prevalence : 0.5560
##       Balanced Accuracy : 0.8077
##
##        'Positive' Class : Neg
##
```

```
conf.mat$byClass
```

```
##          Sensitivity          Specificity       Pos Pred Value
##            0.8452830            0.7702128            0.8057554
##       Neg Pred Value            Precision               Recall
##            0.8153153            0.8057554            0.8452830
##                   F1           Prevalence       Detection Rate
##            0.8250460            0.5300000            0.4480000
## Detection Prevalence    Balanced Accuracy
##            0.5560000            0.8077479
```

```
conf.mat$overall
```

```
##       Accuracy          Kappa  AccuracyLower  AccuracyUpper   AccuracyNull
##   8.100000e-01   6.174291e-01   7.728180e-01   8.434678e-01   5.300000e-01
## AccuracyPValue  McnemarPValue
##   3.570547e-39   2.182578e-01
```

```
# Prediction Accuracy
conf.mat$overall['Accuracy']
```

```
## Accuracy
##     0.81
```

Apriori

```
library(arules)
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'arules'
```

```
## The following object is masked from 'package:dplyr':
##
##     recode
```

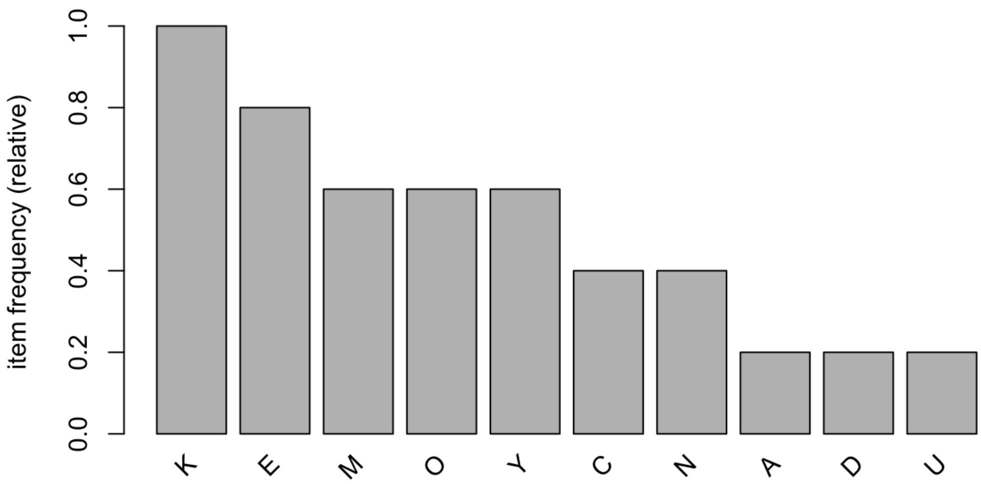
```
## The following object is masked from 'package:tm':
##
##     inspect
```

```
## The following objects are masked from 'package:base':
##
##     abbreviate, write
```

```
#Data Preprocessing
load("dataset.RData")
summary(dataset)
```

```
## transactions as itemMatrix in sparse format with
##  5 rows (elements/itemsets/transactions) and
##  10 columns (items) and a density of 0.5
##
## most frequent items:
##       K       E       M       O       Y (Other)
##       5       4       3       3       3       7
##
## element (itemset/transaction) length distribution:
## sizes
## 4 5 6
## 2 1 2
##
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##       4       4       5       5       6       6
##
## includes extended item information - examples:
##   labels
## 1      A
## 2      C
## 3      D
##
## includes extended transaction information - examples:
##   transactionID
## 1            T1
## 2            T2
## 3            T3
```

```
itemFrequencyPlot(dataset,topN=10)
```




```
#Apriori
rules <- apriori(data=dataset,parameter=list(support=0.60,confidence=0.80))
```

```
## Apriori
##
## Parameter specification:
##  confidence minval smax arem  aval originalSupport maxtime support minlen
##         0.8    0.1    1 none FALSE            TRUE       5     0.6      1
##  maxlen target   ext
##      10  rules FALSE
##
## Algorithmic control:
##  filter tree heap memopt load sort verbose
##     0.1 TRUE TRUE  FALSE TRUE    2    TRUE
##
## Absolute minimum support count: 3
##
## set item appearances ...[0 item(s)] done [0.00s].
## set transactions ...[10 item(s), 5 transaction(s)] done [0.00s].
## sorting and recoding items ... [5 item(s)] done [0.00s].
## creating transaction tree ... done [0.00s].
## checking subsets of size 1 2 3 done [0.00s].
## writing ... [10 rule(s)] done [0.00s].
## creating S4 object  ... done [0.00s].
```

```
summary(rules)
```

```
## set of 10 rules
##
## rule length distribution (lhs + rhs):sizes
## 1 2 3
## 2 6 2
##
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##       1       2       2       2       2       3
##
## summary of quality measures:
##     support       confidence         lift           count
##  Min.   :0.6   Min.   :0.80   Min.   :1.00   Min.   :3.0
##  1st Qu.:0.6   1st Qu.:1.00   1st Qu.:1.00   1st Qu.:3.0
##  Median :0.6   Median :1.00   Median :1.00   Median :3.0
##  Mean   :0.7   Mean   :0.96   Mean   :1.05   Mean   :3.5
##  3rd Qu.:0.8   3rd Qu.:1.00   3rd Qu.:1.00   3rd Qu.:4.0
##  Max.   :1.0   Max.   :1.00   Max.   :1.25   Max.   :5.0
##
## mining info:
##     data ntransactions support confidence
##  dataset             5     0.6        0.8
```

```
#Data Visualization
inspect(sort(rules,by='lift')[1:10])
```

```
##      lhs      rhs support confidence lift count
## [1]  {O}   => {E} 0.6     1.0        1.25 3
## [2]  {K,O} => {E} 0.6     1.0        1.25 3
## [3]  {}    => {E} 0.8     0.8        1.00 4
## [4]  {}    => {K} 1.0     1.0        1.00 5
## [5]  {M}   => {K} 0.6     1.0        1.00 3
## [6]  {O}   => {K} 0.6     1.0        1.00 3
## [7]  {Y}   => {K} 0.6     1.0        1.00 3
## [8]  {E}   => {K} 0.8     1.0        1.00 4
## [9]  {K}   => {E} 0.8     0.8        1.00 4
## [10] {E,O} => {K} 0.6     1.0        1.00 3
```

K-means

```r
library(ggplot2)
set.seed(20)
irisCluster <- kmeans(iris[,3:4],3,nstart=20)
irisCluster
```

```
## K-means clustering with 3 clusters of sizes 50, 52, 48
##
## Cluster means:
##   Petal.Length Petal.Width
## 1     1.462000    0.246000
## 2     4.269231    1.342308
## 3     5.595833    2.037500
##
## Clustering vector:
##   [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##  [36] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
##  [71] 2 2 2 2 2 2 2 3 2 2 2 2 2 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3
## [106] 3 2 3 3 3 3 3 3 3 3 3 3 3 2 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 2 3
## [141] 3 3 3 3 3 3 3 3 3 3
##
## Within cluster sum of squares by cluster:
## [1]  2.02200 13.05769 16.29167
##  (between_SS / total_SS =  94.3 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
## [5] "tot.withinss" "betweenss"    "size"         "iter"
## [9] "ifault"
```

```r
#Comparing clusters with the species
table(irisCluster$cluster, iris$Species)
```

```
##
##     setosa versicolor virginica
##   1     50          0         0
##   2      0         48         4
##   3      0          2        46
```

```r
irisCluster$cluster <- as.factor(irisCluster$cluster)
ggplot(iris, aes(Petal.Length, Petal.Width, color = irisCluster$cluster)) + geom_point()
```