Classifing Fish

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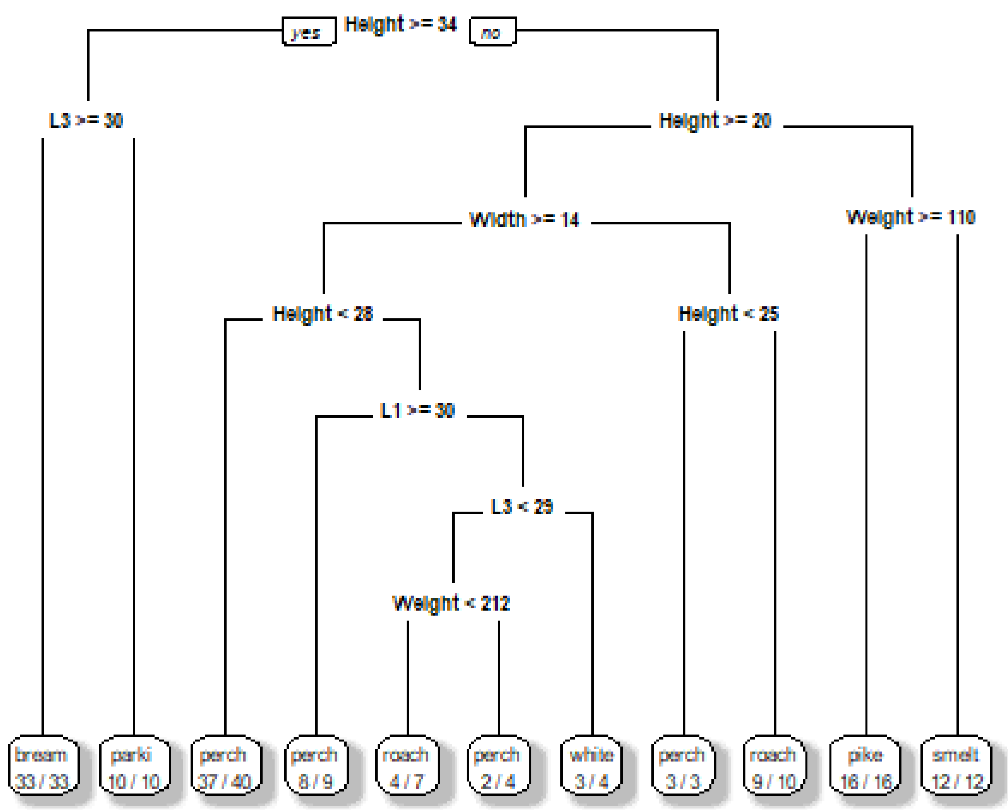
Classification Tree

```
fish <- read.table("file:///C:/Users/Asus/Documents/GitHub/classifng_fish/fish.data.txt", header
= T)
library(rpart)
require(rpart.plot)

## Loading required package: rpart.plot

fish.control <- rpart.control(minisplit = 10, minbucket = 3, xval = 0)
fish.treeorig <- rpart(Species~Weight+L1+L2+L3+Height+Width,data=fish,method="class",con
trol=fish.control)
#Let’s now plot the tree:
plot(fish.treeorig)
text(fish.treeorig)

prp(fish.treeorig,      # 模型
   faclen=0,           # 呈現的變數不要縮寫
   fallen.leaves=TRUE, # 讓樹枝以垂直方式呈現
   shadow.col="gray",  # 最下面的節點塗上陰影
   extra=2 )           # number of correct classifications / number of observations in that node
```



```
#Also check out the complexity parameter (CP):
printcp(fish.treeorig)

##
## Classification tree:
## rpart(formula = Species ~ Weight + L1 + L2 + L3 + Height + Width,
##     data = fish, method = "class", control = fish.control)
##
## Variables actually used in tree construction:
## [1] Height L1     L3     Weight Width
##
## Root node error: 94/148 = 0.63514
##
## n= 148
##
##         CP nsplit rel error
## 1 0.351064      0   1.00000
## 2 0.170213      1   0.64894
## 3 0.127660      2   0.47872
## 4 0.106383      3   0.35106
## 5 0.053191      4   0.24468
## 6 0.031915      5   0.19149
## 7 0.010638      6   0.15957
## 8 0.010000     10   0.11702


summary(fish.treeorig)

## Call:
## rpart(formula = Species ~ Weight + L1 + L2 + L3 + Height + Width,
##     data = fish, method = "class", control = fish.control)
##   n= 148
##
##           CP nsplit rel error
## 1 0.35106383      0 1.0000000
## 2 0.17021277      1 0.6489362
## 3 0.12765957      2 0.4787234
## 4 0.10638298      3 0.3510638
## 5 0.05319149      4 0.2446809
## 6 0.03191489      5 0.1914894
## 7 0.01063830      6 0.1595745
## 8 0.01000000     10 0.1170213
##
## Variable importance
## Height     L3     L2     L1 Weight  Width
##     26     16     15     15     15     13
##
## Node number 1: 148 observations,    complexity param=0.3510638
##   predicted class=perch  expected loss=0.6351351  P(node) =1
##     class counts:    33    10    54    16    18    12     5
```

```
##    probabilities: 0.223 0.068 0.365 0.108 0.122 0.081 0.034
##   left son=2 (43 obs) right son=3 (105 obs)
##   Primary splits:
##       Height < 33.9   to the right, improve=29.75863, (0 missing)
##       Width  < 11.85  to the right, improve=17.98385, (0 missing)
##       L3     < 29.7   to the right, improve=13.80398, (0 missing)
##       L2     < 28.85  to the right, improve=12.96300, (0 missing)
##       L1     < 26.1   to the right, improve=12.56245, (0 missing)
##
## Node number 2: 43 observations,    complexity param=0.106383
##   predicted class=bream  expected loss=0.2325581  P(node) =0.2905405
##     class counts:    33    10     0     0     0     0     0
##    probabilities: 0.767 0.233 0.000 0.000 0.000 0.000 0.000
##   left son=4 (33 obs) right son=5 (10 obs)
##   Primary splits:
##       L3     < 29.5   to the right, improve=15.348840, (0 missing)
##       L2     < 26.15  to the right, improve=13.530660, (0 missing)
##       L1     < 23.1   to the right, improve=13.407660, (0 missing)
##       Weight < 331.5  to the right, improve=12.015500, (0 missing)
##       Width  < 14.85  to the right, improve= 1.063123, (0 missing)
##   Surrogate splits:
##       L1     < 23.1   to the right, agree=0.977, adj=0.9, (0 split)
##       L2     < 25.2   to the right, agree=0.977, adj=0.9, (0 split)
##       Weight < 221    to the right, agree=0.953, adj=0.8, (0 split)
##
## Node number 3: 105 observations,    complexity param=0.1702128
##   predicted class=perch  expected loss=0.4857143  P(node) =0.7094595
##     class counts:     0     0    54    16    18    12     5
##    probabilities: 0.000 0.000 0.514 0.152 0.171 0.114 0.048
##   left son=6 (77 obs) right son=7 (28 obs)
##   Primary splits:
##       Height < 20.1   to the right, improve=21.78355, (0 missing)
##       Width  < 12.45  to the right, improve=20.93000, (0 missing)
##       Weight < 25.95  to the right, improve=13.35778, (0 missing)
##       L3     < 15.6   to the right, improve=10.68888, (0 missing)
##       L1     < 12.3   to the right, improve=10.63876, (0 missing)
##   Surrogate splits:
##       Width  < 12.45  to the right, agree=0.990, adj=0.964, (0 split)
##       Weight < 25.95  to the right, agree=0.838, adj=0.393, (0 split)
##       L1     < 12.3   to the right, agree=0.819, adj=0.321, (0 split)
##       L2     < 13.35  to the right, agree=0.819, adj=0.321, (0 split)
##       L3     < 14.25  to the right, agree=0.819, adj=0.321, (0 split)
##
## Node number 4: 33 observations
##   predicted class=bream  expected loss=0  P(node) =0.222973
##     class counts:    33     0     0     0     0     0     0
##    probabilities: 1.000 0.000 0.000 0.000 0.000 0.000 0.000
##
## Node number 5: 10 observations
##   predicted class=parki  expected loss=0  P(node) =0.06756757
```

```
##     class counts:     0    10     0     0     0     0     0
##    probabilities: 0.000 1.000 0.000 0.000 0.000 0.000 0.000
##
## Node number 6: 77 observations,    complexity param=0.05319149
##   predicted class=perch  expected loss=0.2987013  P(node) =0.5202703
##     class counts:     0     0    54     0    18     0     5
##    probabilities: 0.000 0.000 0.701 0.000 0.234 0.000 0.065
##   left son=12 (64 obs) right son=13 (13 obs)
##   Primary splits:
##       Width  < 14.4   to the right, improve=5.777691, (0 missing)
##       Height < 25.25  to the left,  improve=4.275974, (0 missing)
##       L1     < 25.1   to the right, improve=2.872913, (0 missing)
##       L2     < 27.15  to the right, improve=2.872913, (0 missing)
##       Weight < 548    to the right, improve=2.448383, (0 missing)
##   Surrogate splits:
##       L1 < 13.35  to the right, agree=0.844, adj=0.077, (0 split)
##       L2 < 14.55  to the right, agree=0.844, adj=0.077, (0 split)
##
## Node number 7: 28 observations,    complexity param=0.1276596
##   predicted class=pike   expected loss=0.4285714  P(node) =0.1891892
##     class counts:     0     0     0    16     0    12     0
##    probabilities: 0.000 0.000 0.000 0.571 0.000 0.429 0.000
##   left son=14 (16 obs) right son=15 (12 obs)
##   Primary splits:
##       Weight < 109.95 to the right, improve=13.714290, (0 missing)
##       L1     < 21.9   to the right, improve=13.714290, (0 missing)
##       L2     < 23.65  to the right, improve=13.714290, (0 missing)
##       L3     < 25.5   to the right, improve=13.714290, (0 missing)
##       Height < 16.05  to the left,  improve= 4.571429, (0 missing)
##   Surrogate splits:
##       L1     < 21.9   to the right, agree=1.000, adj=1.000, (0 split)
##       L2     < 23.65  to the right, agree=1.000, adj=1.000, (0 split)
##       L3     < 25.5   to the right, agree=1.000, adj=1.000, (0 split)
##       Height < 16.05  to the left,  agree=0.786, adj=0.500, (0 split)
##       Width  < 9.45   to the right, agree=0.714, adj=0.333, (0 split)
##
## Node number 12: 64 observations,    complexity param=0.0106383
##   predicted class=perch  expected loss=0.21875  P(node) =0.4324324
##     class counts:     0     0    50     0     9     0     5
##    probabilities: 0.000 0.000 0.781 0.000 0.141 0.000 0.078
##   left son=24 (40 obs) right son=25 (24 obs)
##   Primary splits:
##       Height < 27.55  to the left,  improve=3.314583, (0 missing)
##       Width  < 15.65  to the right, improve=1.557526, (0 missing)
##       L1     < 30     to the right, improve=1.174970, (0 missing)
##       L2     < 32.25  to the right, improve=1.174970, (0 missing)
##       Weight < 548    to the right, improve=1.058472, (0 missing)
##   Surrogate splits:
##       Width  < 17.4   to the left,  agree=0.719, adj=0.250, (0 split)
##       Weight < 267.5  to the left,  agree=0.688, adj=0.167, (0 split)
```

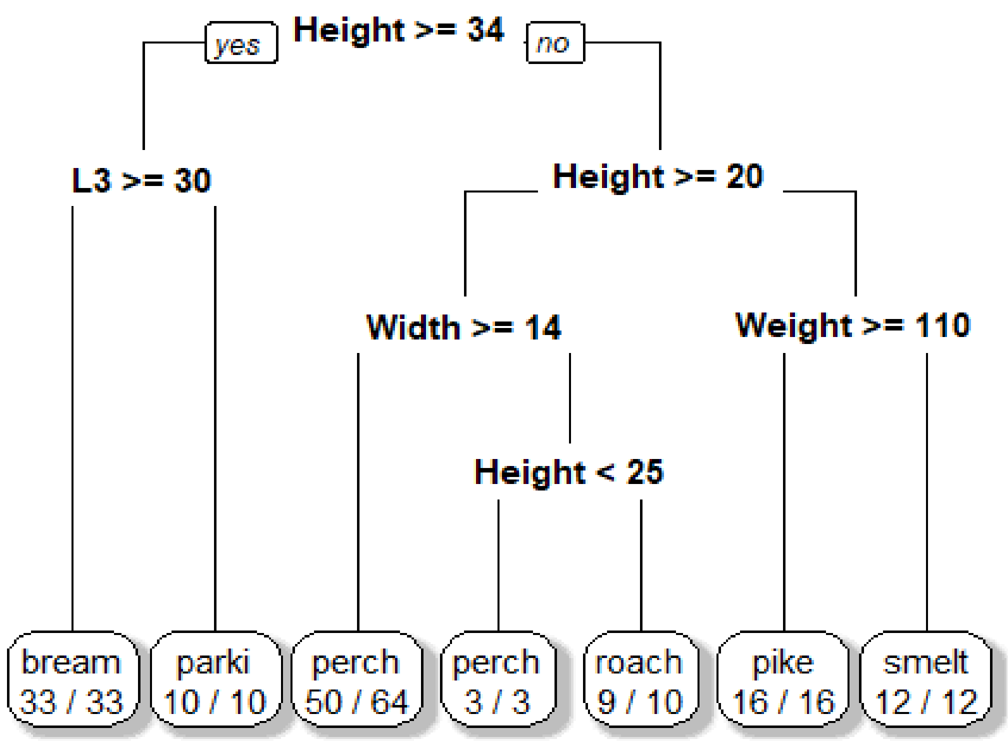
```
##       L3     < 29.05  to the left,  agree=0.656, adj=0.083, (0 split)
##
## Node number 13: 13 observations,    complexity param=0.03191489
##   predicted class=roach  expected loss=0.3076923  P(node) =0.08783784
##     class counts:     0     0     4     0     9     0     0
##    probabilities: 0.000 0.000 0.308 0.000 0.692 0.000 0.000
##   left son=26 (3 obs) right son=27 (10 obs)
##   Primary splits:
##       Height < 24.8   to the left,  improve=3.7384620, (0 missing)
##       Weight < 174.5  to the right, improve=1.0051280, (0 missing)
##       L1     < 22.5   to the right, improve=1.0051280, (0 missing)
##       L2     < 24.5   to the right, improve=1.0051280, (0 missing)
##       L3     < 21.1   to the left,  improve=0.4273504, (0 missing)
##
## Node number 14: 16 observations
##   predicted class=pike   expected loss=0  P(node) =0.1081081
##     class counts:     0     0     0    16     0     0     0
##    probabilities: 0.000 0.000 0.000 1.000 0.000 0.000 0.000
##
## Node number 15: 12 observations
##   predicted class=smelt  expected loss=0  P(node) =0.08108108
##     class counts:     0     0     0     0     0    12     0
##    probabilities: 0.000 0.000 0.000 0.000 0.000 1.000 0.000
##
## Node number 24: 40 observations
##   predicted class=perch  expected loss=0.075  P(node) =0.2702703
##     class counts:     0     0    37     0     3     0     0
##    probabilities: 0.000 0.000 0.925 0.000 0.075 0.000 0.000
##
## Node number 25: 24 observations,    complexity param=0.0106383
##   predicted class=perch  expected loss=0.4583333  P(node) =0.1621622
##     class counts:     0     0    13     0     6     0     5
##    probabilities: 0.000 0.000 0.542 0.000 0.250 0.000 0.208
##   left son=50 (9 obs) right son=51 (15 obs)
##   Primary splits:
##       L1     < 29.5   to the right, improve=2.772222, (0 missing)
##       L2     < 31.9   to the right, improve=2.772222, (0 missing)
##       Width  < 16.45  to the right, improve=2.772222, (0 missing)
##       Weight < 295    to the right, improve=2.583333, (0 missing)
##       L3     < 32.4   to the right, improve=2.216667, (0 missing)
##   Surrogate splits:
##       L2     < 31.9   to the right, agree=1.000, adj=1.000, (0 split)
##       Weight < 410    to the right, agree=0.958, adj=0.889, (0 split)
##       L3     < 32.4   to the right, agree=0.958, adj=0.889, (0 split)
##       Width  < 16.45  to the right, agree=0.833, adj=0.556, (0 split)
##       Height < 29.35  to the right, agree=0.667, adj=0.111, (0 split)
##
## Node number 26: 3 observations
##   predicted class=perch  expected loss=0  P(node) =0.02027027
##     class counts:     0     0     3     0     0     0     0
```

```
##    probabilities: 0.000 0.000 1.000 0.000 0.000 0.000 0.000
##
## Node number 27: 10 observations
##   predicted class=roach  expected loss=0.1  P(node) =0.06756757
##     class counts:     0     0     1     0     9     0     0
##    probabilities: 0.000 0.000 0.100 0.000 0.900 0.000 0.000
##
## Node number 50: 9 observations
##   predicted class=perch  expected loss=0.1111111  P(node) =0.06081081
##     class counts:     0     0     8     0     0     0     1
##    probabilities: 0.000 0.000 0.889 0.000 0.000 0.000 0.111
##
## Node number 51: 15 observations,    complexity param=0.0106383
##   predicted class=roach  expected loss=0.6  P(node) =0.1013514
##     class counts:     0     0     5     0     6     0     4
##    probabilities: 0.000 0.000 0.333 0.000 0.400 0.000 0.267
##   left son=102 (11 obs) right son=103 (4 obs)
##   Primary splits:
##       L3     < 29.25  to the left,  improve=2.003030, (0 missing)
##       Weight < 247.5  to the left,  improve=1.866667, (0 missing)
##       L1     < 22.85  to the left,  improve=1.866667, (0 missing)
##       L2     < 25     to the left,  improve=1.866667, (0 missing)
##       Height < 28.45  to the left,  improve=1.088889, (0 missing)
##   Surrogate splits:
##       L1     < 24.05  to the left,  agree=0.933, adj=0.75, (0 split)
##       L2     < 26.25  to the left,  agree=0.933, adj=0.75, (0 split)
##       Weight < 303    to the left,  agree=0.867, adj=0.50, (0 split)
##
## Node number 102: 11 observations,    complexity param=0.0106383
##   predicted class=perch  expected loss=0.5454545  P(node) =0.07432432
##     class counts:     0     0     5     0     5     0     1
##    probabilities: 0.000 0.000 0.455 0.000 0.455 0.000 0.091
##   left son=204 (7 obs) right son=205 (4 obs)
##   Primary splits:
##       Weight < 212.5  to the left,  improve=0.4350649, (0 missing)
##       L1     < 22.05  to the left,  improve=0.4350649, (0 missing)
##       L2     < 23.75  to the left,  improve=0.4350649, (0 missing)
##       L3     < 26.15  to the left,  improve=0.4350649, (0 missing)
##       Height < 28.5   to the left,  improve=0.4350649, (0 missing)
##   Surrogate splits:
##       L2     < 23.75  to the left,  agree=1.000, adj=1.00, (0 split)
##       Height < 28.5   to the left,  agree=1.000, adj=1.00, (0 split)
##       L1     < 21.25  to the left,  agree=0.909, adj=0.75, (0 split)
##       L3     < 25.4   to the left,  agree=0.909, adj=0.75, (0 split)
##       Width  < 14.95  to the right, agree=0.727, adj=0.25, (0 split)
##
## Node number 103: 4 observations
##   predicted class=white  expected loss=0.25  P(node) =0.02702703
##     class counts:     0     0     0     0     1     0     3
##    probabilities: 0.000 0.000 0.000 0.000 0.250 0.000 0.750
```

```
##
## Node number 204: 7 observations
##   predicted class=roach  expected loss=0.4285714  P(node) =0.0472973
##     class counts:     0     0     3     0     4     0     0
##    probabilities: 0.000 0.000 0.429 0.000 0.571 0.000 0.000
##
## Node number 205: 4 observations
##   predicted class=perch  expected loss=0.5  P(node) =0.02702703
##     class counts:     0     0     2     0     1     0     1
##    probabilities: 0.000 0.000 0.500 0.000 0.250 0.000 0.250

fish.prunetree <- prune.rpart(fish.treeorig,cp=0.02)
plot(fish.prunetree)
text(fish.prunetree)

prp(fish.prunetree,     # 模型
    faclen=0,           # 呈現的變數不要縮寫
    fallen.leaves=TRUE, # 讓樹枝以垂直方式呈現
    shadow.col="gray",  # 最下面的節點塗上陰影
    extra=2 )           # number of correct classifications / number of observations in that node
```

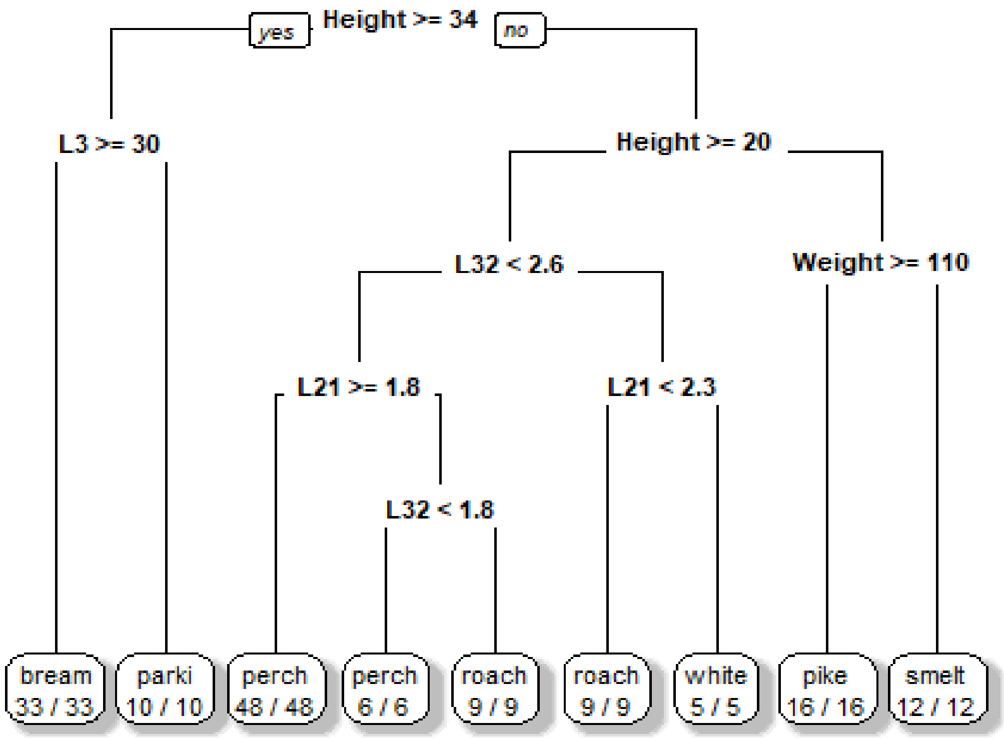


```
L21<-fish$L2-fish$L1
L32<-fish$L3-fish$L2
L31<-fish$L3-fish$L1
newfish<-cbind(fish,L21,L32,L31)
newfish.treenew<-rpart(Species~., data=newfish,method="class",parms=list(split="information
"),control=fish.control)
printcp(newfish.treenew)
```

```
##
## Classification tree:
## rpart(formula = Species ~ ., data = newfish, method = "class",
##     parms = list(split = "information"), control = fish.control)
##
## Variables actually used in tree construction:
## [1] Height L21    L3     L32    Weight
##
## Root node error: 94/148 = 0.63514
##
## n= 148
##
##         CP nsplit rel error
## 1 0.351064      0  1.000000
## 2 0.170213      1  0.648936
## 3 0.127660      2  0.478723
## 4 0.106383      3  0.351064
## 5 0.095745      4  0.244681
## 6 0.053191      5  0.148936
## 7 0.047872      6  0.095745
## 8 0.010000      8  0.000000
```

```
plot(newfish.treenew)
text(newfish.treenew)
```

```
prp(newfish.treenew,    # 模型
    faclen=0,           # 呈現的變數不要縮寫
    fallen.leaves=TRUE, # 讓樹枝以垂直方式呈現
    shadow.col="gray",  # 最下面的節點塗上陰影
    extra=2 )           # number of correct classifications / number of observations in that node
```




```
#分的有點完美(有點過度配適)
fish.control <- rpart.control(minbucket=3,minsplit=10,xval=148)
newfish.treenewcv <- rpart(Species~., data=newfish,method="class",parms=list(split="information"),control=fish.control)
printcp(newfish.treenewcv)

##
## Classification tree:
## rpart(formula = Species ~ ., data = newfish, method = "class",
##     parms = list(split = "information"), control = fish.control)
##
## Variables actually used in tree construction:
## [1] Height L21    L3     L32    Weight
##
## Root node error: 94/148 = 0.63514
##
## n= 148
##
##         CP nsplit rel error   xerror     xstd
## 1 0.351064      0  1.000000 1.000000 0.062302
## 2 0.170213      1  0.648936 0.648936 0.063704
## 3 0.127660      2  0.478723 0.478723 0.059534
## 4 0.106383      3  0.351064 0.351064 0.053870
## 5 0.095745      4  0.244681 0.361702 0.054442
```

```
## 6 0.053191      5  0.148936 0.170213 0.040187
## 7 0.047872      6  0.095745 0.180851 0.041267
## 8 0.010000      8  0.000000 0.031915 0.018238
```

```
newfish.test<-read.table("file:///C:/Users/Asus/Documents/GitHub/classifng_fish/fish_test.data.txt",h=T)
L31<-newfish.test$L3- newfish.test$L1
L32<-newfish.test$L3- newfish.test$L2
L21<-newfish.test$L2- newfish.test$L1
newfish.test<-cbind(newfish.test,L21,L32,L31)
newfish.tpred<-predict(newfish.treenewcv,newfish.test)
newfish.tpred
```

```
##    bream parki perch pike roach smelt white
## 1      1     0     0    0     0     0     0
## 2      1     0     0    0     0     0     0
## 3      0     0     1    0     0     0     0
## 4      0     0     1    0     0     0     0
## 5      0     0     0    1     0     0     0
## 6      0     0     0    0     0     1     0
## 7      0     0     0    0     0     1     0
## 8      0     1     0    0     0     0     0
## 9      0     0     0    0     1     0     0
## 10     0     0     0    0     1     0     0
## 11     0     0     0    0     0     0     1
```

Linear Discriminant Analysis

```
library(MASS)
newfish
```

```
##     Species Weight   L1   L2   L3 Height Width L21 L32 L31
## 1     bream  242.0 23.2 25.4 30.0   38.4  13.4 2.2 4.6 6.8
## 2     bream  290.0 24.0 26.3 31.2   40.0  13.8 2.3 4.9 7.2
## 3     bream  363.0 26.3 29.0 33.5   38.0  13.3 2.7 4.5 7.2
## 4     bream  430.0 26.5 29.0 34.0   36.6  15.1 2.5 5.0 7.5
## 5     bream  500.0 26.8 29.7 34.5   41.1  15.3 2.9 4.8 7.7
## 6     bream  390.0 27.6 30.0 35.0   36.2  13.4 2.4 5.0 7.4
## 7     bream  450.0 27.6 30.0 35.1   39.9  13.8 2.4 5.1 7.5
## 8     bream  500.0 28.5 30.7 36.2   39.3  13.7 2.2 5.5 7.7
## 9     bream  475.0 28.4 31.0 36.2   39.4  14.1 2.6 5.2 7.8
## 10    bream  500.0 28.7 31.0 36.2   39.7  13.3 2.3 5.2 7.5
## 11    bream  500.0 29.1 31.5 36.4   37.8  12.0 2.4 4.9 7.3
## 12    bream  500.0 29.5 32.0 37.3   37.3  13.6 2.5 5.3 7.8
## 13    bream  600.0 29.4 32.0 37.2   40.2  13.9 2.6 5.2 7.8
## 14    bream  600.0 29.4 32.0 37.2   41.5  15.0 2.6 5.2 7.8
## 15    bream  700.0 30.4 33.0 38.3   38.8  13.8 2.6 5.3 7.9
## 16    bream  700.0 30.4 33.0 38.5   38.8  13.5 2.6 5.5 8.1
## 17    bream  610.0 30.9 33.5 38.6   40.5  13.3 2.6 5.1 7.7
## 18    bream  650.0 31.0 33.5 38.7   37.4  14.8 2.5 5.2 7.7
## 19    bream  575.0 31.3 34.0 39.5   38.3  14.1 2.7 5.5 8.2
## 20    bream  685.0 31.4 34.0 39.2   40.8  13.7 2.6 5.2 7.8
## 21    bream  620.0 31.5 34.5 39.7   39.1  13.3 3.0 5.2 8.2
## 22    bream  680.0 31.8 35.0 40.6   38.1  15.1 3.2 5.6 8.8
## 23    bream  700.0 31.9 35.0 40.5   40.1  13.8 3.1 5.5 8.6
## 24    bream  725.0 31.8 35.0 40.9   40.0  14.8 3.2 5.9 9.1
## 25    bream  720.0 32.0 35.0 40.6   40.3  15.0 3.0 5.6 8.6
## 26    bream  714.0 32.7 36.0 41.5   39.8  14.1 3.3 5.5 8.8
## 27    bream  850.0 32.8 36.0 41.6   40.6  14.9 3.2 5.6 8.8
## 28    bream 1000.0 33.5 37.0 42.6   44.5  15.5 3.5 5.6 9.1
## 29    bream  920.0 35.0 38.5 44.1   40.9  14.3 3.5 5.6 9.1
## 30    bream  955.0 35.0 38.5 44.0   41.1  14.3 3.5 5.5 9.0
## 31    bream  925.0 36.2 39.5 45.3   41.4  14.9 3.3 5.8 9.1
## 32    bream  975.0 37.4 41.0 45.9   40.6  14.7 3.6 4.9 8.5
## 33    bream  950.0 38.0 41.0 46.5   37.9  13.7 3.0 5.5 8.5
## 34    white  270.0 23.6 26.0 28.7   29.2  14.8 2.4 2.7 5.1
## 35    white  270.0 24.1 26.5 29.3   27.8  14.5 2.4 2.8 5.2
## 36    white  306.0 25.6 28.0 30.8   28.5  15.2 2.4 2.8 5.2
## 37    white  540.0 28.5 31.0 34.0   31.6  19.3 2.5 3.0 5.5
## 38    white 1000.0 37.3 40.0 43.5   28.4  15.0 2.7 3.5 6.2
## 39    roach   40.0 12.9 14.1 16.2   25.6  14.0 1.2 2.1 3.3
## 40    roach   69.0 16.5 18.2 20.3   26.1  13.9 1.7 2.1 3.8
## 41    roach   78.0 17.5 18.8 21.2   26.3  13.7 1.3 2.4 3.7
## 42    roach   87.0 18.2 19.8 22.2   25.3  14.3 1.6 2.4 4.0
## 43    roach  120.0 18.6 20.0 22.2   28.0  16.1 1.4 2.2 3.6
## 44    roach  118.0 19.0 20.5 22.8   28.4  14.7 1.5 2.3 3.8
## 45    roach  110.0 19.1 20.8 23.1   26.7  14.7 1.7 2.3 4.0
```

```
## 46    roach  120.0 19.4 21.0 23.7   25.8  13.9 1.6 2.7 4.3
## 47    roach  160.0 20.5 22.5 25.3   27.8  15.1 2.0 2.8 4.8
## 48    roach  140.0 21.0 22.5 25.0   26.2  13.3 1.5 2.5 4.0
## 49    roach  160.0 21.1 22.5 25.0   25.6  15.2 1.4 2.5 3.9
## 50    roach  169.0 22.0 24.0 27.2   27.7  14.1 2.0 3.2 5.2
## 51    roach  161.0 22.0 23.4 26.7   25.9  13.6 1.4 3.3 4.7
## 52    roach  200.0 22.1 23.5 26.8   27.6  15.4 1.4 3.3 4.7
## 53    roach  180.0 23.6 25.2 27.9   25.4  14.0 1.6 2.7 4.3
## 54    roach  290.0 24.0 26.0 29.2   30.4  15.4 2.0 3.2 5.2
## 55    roach  272.0 25.0 27.0 30.6   28.0  15.6 2.0 3.6 5.6
## 56    roach  390.0 29.5 31.7 35.0   27.1  15.3 2.2 3.3 5.5
## 57    parki   55.0 13.5 14.7 16.5   41.5  14.1 1.2 1.8 3.0
## 58    parki   60.0 14.3 15.5 17.4   37.8  13.3 1.2 1.9 3.1
## 59    parki   90.0 16.3 17.7 19.8   37.4  13.5 1.4 2.1 3.5
## 60    parki  120.0 17.5 19.0 21.3   39.4  13.7 1.5 2.3 3.8
## 61    parki  150.0 18.4 20.0 22.4   39.7  14.7 1.6 2.4 4.0
## 62    parki  140.0 19.0 20.7 23.2   36.8  14.2 1.7 2.5 4.2
## 63    parki  170.0 19.0 20.7 23.2   40.5  14.7 1.7 2.5 4.2
## 64    parki  200.0 21.2 23.0 25.8   40.1  14.2 1.8 2.8 4.6
## 65    parki  273.0 23.0 25.0 28.0   39.6  14.8 2.0 3.0 5.0
## 66    parki  300.0 24.0 26.0 29.0   39.2  14.6 2.0 3.0 5.0
## 67    smelt    6.7  9.3  9.8 10.8   16.1   9.7 0.5 1.0 1.5
## 68    smelt    7.5 10.0 10.5 11.6   17.0  10.0 0.5 1.1 1.6
## 69    smelt    7.0 10.1 10.6 11.6   14.9   9.9 0.5 1.0 1.5
## 70    smelt    9.7 10.4 11.0 12.0   18.3  11.5 0.6 1.0 1.6
## 71    smelt   10.0 11.3 11.8 13.1   16.9   9.8 0.5 1.3 1.8
## 72    smelt    9.9 11.3 11.8 13.1   16.9   8.9 0.5 1.3 1.8
## 73    smelt    9.8 11.4 12.0 13.2   16.7   8.7 0.6 1.2 1.8
## 74    smelt   12.2 11.5 12.2 13.4   15.6  10.4 0.7 1.2 1.9
## 75    smelt   13.4 11.7 12.4 13.5   18.0   9.4 0.7 1.1 1.8
## 76    smelt   12.2 12.1 13.0 13.8   16.5   9.1 0.9 0.8 1.7
## 77    smelt   19.7 13.2 14.3 15.2   18.9  13.6 1.1 0.9 2.0
## 78    smelt   19.9 13.8 15.0 16.2   18.1  11.6 1.2 1.2 2.4
## 79     pike  200.0 30.0 32.3 34.8   16.0   9.7 2.3 2.5 4.8
## 80     pike  300.0 31.7 34.0 37.8   15.1  11.0 2.3 3.8 6.1
## 81     pike  300.0 32.7 35.0 38.8   15.3  11.3 2.3 3.8 6.1
## 82     pike  300.0 34.8 37.3 39.8   15.8  10.1 2.5 2.5 5.0
## 83     pike  430.0 35.5 38.0 40.5   18.0  11.3 2.5 2.5 5.0
## 84     pike  456.0 40.0 42.5 45.5   16.0   9.5 2.5 3.0 5.5
## 85     pike  510.0 40.0 42.5 45.5   15.0   9.8 2.5 3.0 5.5
## 86     pike  540.0 40.1 43.0 45.8   17.0  11.2 2.9 2.8 5.7
## 87     pike  500.0 42.0 45.0 48.0   14.5  10.2 3.0 3.0 6.0
## 88     pike  567.0 43.2 46.0 48.7   16.0  10.0 2.8 2.7 5.5
## 89     pike  770.0 44.8 48.0 51.2   15.0  10.5 3.2 3.2 6.4
## 90     pike  950.0 48.3 51.7 55.1   16.2  11.2 3.4 3.4 6.8
## 91     pike 1250.0 52.0 56.0 59.7   17.9  11.7 4.0 3.7 7.7
## 92     pike 1600.0 56.0 60.0 64.0   15.0   9.6 4.0 4.0 8.0
## 93     pike 1550.0 56.0 60.0 64.0   15.0   9.6 4.0 4.0 8.0
## 94     pike 1650.0 59.0 63.4 68.0   15.9  11.0 4.4 4.6 9.0
## 95    perch    5.9  7.5  8.4  8.8   24.0  16.0 0.9 0.4 1.3
```

```
## 96    perch   32.0 12.5 13.7 14.7   24.0  13.6 1.2 1.0 2.2
## 97    perch   40.0 13.8 15.0 16.0   23.9  15.2 1.2 1.0 2.2
## 98    perch   51.5 15.0 16.2 17.2   26.7  15.3 1.2 1.0 2.2
## 99    perch   70.0 15.7 17.4 18.5   24.8  15.9 1.7 1.1 2.8
## 100   perch  100.0 16.2 18.0 19.2   27.2  17.3 1.8 1.2 3.0
## 101   perch   78.0 16.8 18.7 19.4   26.8  16.1 1.9 0.7 2.6
## 102   perch   80.0 17.2 19.0 20.2   27.9  15.1 1.8 1.2 3.0
## 103   perch   85.0 17.8 19.6 20.8   24.7  14.6 1.8 1.2 3.0
## 104   perch   85.0 18.2 20.0 21.0   24.2  13.2 1.8 1.0 2.8
## 105   perch  110.0 19.0 21.0 22.5   25.3  15.8 2.0 1.5 3.5
## 106   perch  115.0 19.0 21.0 22.5   26.3  14.7 2.0 1.5 3.5
## 107   perch  125.0 19.0 21.0 22.5   25.3  16.3 2.0 1.5 3.5
## 108   perch  130.0 19.3 21.3 22.8   28.0  15.5 2.0 1.5 3.5
## 109   perch  120.0 20.0 22.0 23.5   26.0  14.5 2.0 1.5 3.5
## 110   perch  120.0 20.0 22.0 23.5   24.0  15.0 2.0 1.5 3.5
## 111   perch  130.0 20.0 22.0 23.5   26.0  15.0 2.0 1.5 3.5
## 112   perch  135.0 20.0 22.0 23.5   25.0  15.0 2.0 1.5 3.5
## 113   perch  110.0 20.0 22.0 23.5   23.5  17.0 2.0 1.5 3.5
## 114   perch  130.0 20.5 22.5 24.0   24.4  15.1 2.0 1.5 3.5
## 115   perch  150.0 20.5 22.5 24.0   28.3  15.1 2.0 1.5 3.5
## 116   perch  145.0 20.7 22.7 24.2   24.6  15.0 2.0 1.5 3.5
## 117   perch  150.0 21.0 23.0 24.5   21.3  14.8 2.0 1.5 3.5
## 118   perch  170.0 21.5 23.5 25.0   25.1  14.9 2.0 1.5 3.5
## 119   perch  225.0 22.0 24.0 25.5   28.6  14.6 2.0 1.5 3.5
## 120   perch  145.0 22.0 24.0 25.5   25.0  15.0 2.0 1.5 3.5
## 121   perch  188.0 22.6 24.6 26.2   25.7  15.9 2.0 1.6 3.6
## 122   perch  180.0 23.0 25.0 26.5   24.3  13.9 2.0 1.5 3.5
## 123   perch  197.0 23.5 25.6 27.0   24.3  15.7 2.1 1.4 3.5
## 124   perch  218.0 25.0 26.5 28.0   25.6  14.8 1.5 1.5 3.0
## 125   perch  300.0 25.2 27.3 28.7   29.0  17.9 2.1 1.4 3.5
## 126   perch  260.0 25.4 27.5 28.9   24.8  15.0 2.1 1.4 3.5
## 127   perch  265.0 25.4 27.5 28.9   24.4  15.0 2.1 1.4 3.5
## 128   perch  250.0 25.4 27.5 28.9   25.2  15.8 2.1 1.4 3.5
## 129   perch  250.0 25.9 28.0 29.4   26.6  14.3 2.1 1.4 3.5
## 130   perch  300.0 26.9 28.7 30.1   25.2  15.4 1.8 1.4 3.2
## 131   perch  320.0 27.8 30.0 31.6   24.1  15.1 2.2 1.6 3.8
## 132   perch  514.0 30.5 32.8 34.0   29.5  17.7 2.3 1.2 3.5
## 133   perch  556.0 32.0 34.5 36.5   28.1  17.5 2.5 2.0 4.5
## 134   perch  840.0 32.5 35.0 37.3   30.8  20.9 2.5 2.3 4.8
## 135   perch  685.0 34.0 36.5 39.0   27.9  17.6 2.5 2.5 5.0
## 136   perch  700.0 34.0 36.0 38.3   27.7  17.6 2.0 2.3 4.3
## 137   perch  700.0 34.5 37.0 39.4   27.5  15.9 2.5 2.4 4.9
## 138   perch  690.0 34.6 37.0 39.3   26.9  16.2 2.4 2.3 4.7
## 139   perch  900.0 36.5 39.0 41.4   26.9  18.1 2.5 2.4 4.9
## 140   perch  650.0 36.5 39.0 41.4   26.9  14.5 2.5 2.4 4.9
## 141   perch  820.0 36.6 39.0 41.3   30.1  17.8 2.4 2.3 4.7
## 142   perch  850.0 36.9 40.0 42.3   28.2  16.8 3.1 2.3 5.4
## 143   perch  820.0 37.1 40.0 42.5   26.2  15.6 2.9 2.5 5.4
## 144   perch 1100.0 39.0 42.0 44.6   28.7  15.4 3.0 2.6 5.6
## 145   perch 1000.0 39.8 43.0 45.2   26.4  16.1 3.2 2.2 5.4
```

```
## 146   perch 1100.0 40.1 43.0 45.5   27.5  16.3 2.9 2.5 5.4
## 147   perch 1000.0 40.2 43.5 46.0   27.4  17.7 3.3 2.5 5.8
## 148   perch 1000.0 41.1 44.0 46.6   26.8  16.3 2.9 2.6 5.5

newfish.lda<-lda(Species~.,data=newfish)

## Warning in lda.default(x, grouping, ...): variables are collinear

newfish.lda<-lda(Species~Weight+L1+Height+Width+L21+L32,data=newfish)
newfish.lda

## Call:
## lda(Species ~ Weight + L1 + Height + Width + L21 + L32, data = newfish)
##
## Prior probabilities of groups:
##      bream      parki      perch       pike      roach      smelt
## 0.22297297 0.06756757 0.36486486 0.10810811 0.12162162 0.08108108
##      white
## 0.03378378
##
## Group means:
##         Weight       L1   Height    Width       L21      L32
## bream 636.1818 30.60606 39.52727 14.10000 2.8060606 5.272727
## parki 155.8000 18.62000 39.20000 14.18000 1.6100000 2.430000
## perch 360.9333 25.31852 26.17778 15.78519 2.1259259 1.650000
## pike  742.0625 42.88125 15.85625 10.48125 3.0375000 3.281250
## roach 159.1111 20.66667 26.88333 14.57222 1.6388889 2.716667
## smelt  11.5000 11.34167 16.99167 10.21667 0.6916667 1.091667
## white 477.2000 27.82000 29.10000 15.76000 2.4800000 2.960000
##
## Coefficients of linear discriminants:
##                 LD1          LD2          LD3          LD4          LD5
## Weight  0.000911022 -0.002710071  0.007553399  0.001688806  0.006182751
## L1      0.132200166  0.036926540 -0.259794107 -0.235599786 -0.330471903
## Height -0.618519868 -0.332732865 -0.053863042 -0.330737436 -0.029226039
## Width   0.464670922 -0.341184928 -0.353062958  0.842951264 -0.201141743
## L21    -0.114071841  0.712452136 -2.278059990  0.277900320  2.700516892
## L32    -2.311243186  2.141452146  0.539501848  1.803654269 -0.461925634
##                 LD6
## Weight -0.003600115
## L1     -0.119589009
## Height -0.019796935
## Width  -0.159484049
## L21     2.813216431
## L32    -0.080912628
##
## Proportion of trace:
##    LD1    LD2    LD3    LD4    LD5    LD6
## 0.7998 0.1327 0.0473 0.0167 0.0035 0.0000
```

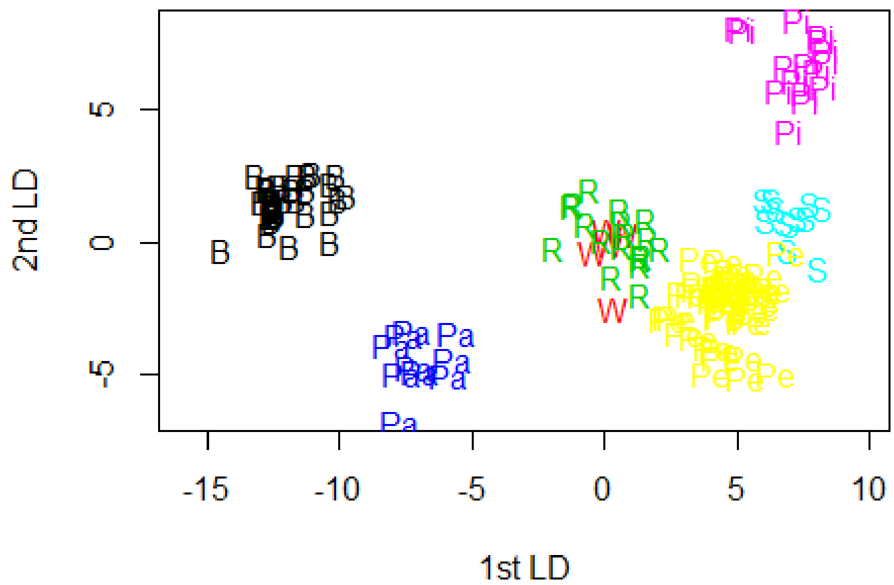
```
newfish.ldapred<-predict(newfish.lda,newfish[,-1])
table(newfish$Species,newfish.ldapred$class)

##
##         bream parki perch pike roach smelt white
##   bream    33     0     0    0     0     0     0
##   parki     0    10     0    0     0     0     0
##   perch     0     0    54    0     0     0     0
##   pike      0     0     0   16     0     0     0
##   roach     0     0     0    0    18     0     0
##   smelt     0     0     0    0     0    12     0
##   white     0     0     0    0     1     0     4

newfish.ldacv<-lda(Species~Weight+L1+Height+Width+L21+L32,data=newfish,CV=T)
table(newfish$Species,newfish.ldacv$class)

##
##         bream parki perch pike roach smelt white
##   bream    33     0     0    0     0     0     0
##   parki     0    10     0    0     0     0     0
##   perch     0     0    54    0     0     0     0
##   pike      0     0     0   16     0     0     0
##   roach     0     0     0    0    18     0     0
##   smelt     0     0     0    0     0    12     0
##   white     0     0     0    0     1     0     4

# The true error rate remains to be 0.6%
eqscplot(newfish.ldapred$x,type="n",xlab="1st LD",ylab="2nd LD")
fish.species <- c(rep("B",33),rep("W",5),rep("R",18),rep("Pa",10),rep("S",12),rep("Pi",16),rep
("Pe",54))
fish.colors <- c(rep(1,33),rep(2,5),rep(3,18),rep(4,10),rep(5,12),rep(6,16),rep(7,54))
text(newfish.ldapred$x[,1:2],fish.species,col=fish.colors)
```




```
#To predict the class identities of the new data points we use:
newfish.ldatest<-predict(newfish.lda,newfish.test)
newfish.ldatest$class

## [1] bream bream perch perch pike  smelt smelt parki roach roach white
## Levels: bream parki perch pike roach smelt white

#We see that the results agree with those obtained from the classification tree.
#Let us examine how to apply QDA to this dataset.
```

Quadratic Discriminant Analysis

```
#newfish.qda<-qda(Species~.,data=newfish)
newfish.q<-read.table("file:///C:/Users/Asus/Documents/GitHub/classifng_fish/newfish.qdata.txt
",h=T)
library(MVN)

## sROC 0.1-2 loaded

#Running (i) Mardia's; (ii) Henze-Zirkler's and (iii) Royston's Multivariate
#Normality Test:
mvn(data = newfish.q[,-c(1,8,9,10)], mvnTest = "ma")

## $multivariateNormality
##              Test        Statistic             p value Result
## 1 Mardia Skewness 426.417978948719 2.01256215659792e-58     NO
## 2 Mardia Kurtosis 1.58569973539399    0.112807439232689    YES
## 3             MVN             <NA>                 <NA>     NO
##
## $univariateNormality
##           Test  Variable Statistic   p value Normality
## 1 Shapiro-Wilk  Weight      0.8780  <0.001      NO
## 2 Shapiro-Wilk    L1        0.9679  0.0019      NO
## 3 Shapiro-Wilk    L2        0.9702  0.0033      NO
## 4 Shapiro-Wilk    L3        0.9703  0.0033      NO
## 5 Shapiro-Wilk  Height      0.9125  <0.001      NO
## 6 Shapiro-Wilk   Width      0.9344  <0.001      NO
##
## $Descriptives
##          n      Mean   Std.Dev Median  Min    Max   25th  75th       Skew
## Weight 143 398.02378 360.51374  272.0  5.9 1650.0 120.00 650.0  1.1175913
## L1     143  26.27692  10.16502   25.2  7.5   59.0  19.00  32.6  0.6215598
## L2     143  28.44406  10.88848   27.3  8.4   63.4  20.90  35.0  0.5796666
## L3     143  31.25455  11.82529   29.2  8.8   68.0  22.80  39.6  0.4306508
## Height 143  28.33217   8.39113   26.8 14.5   44.5  24.25  37.8  0.1335468
## Width  143  14.07063   2.23310   14.6  8.7   20.9  13.40  15.3 -0.4962807
##           Kurtosis
## Weight  0.89652958
## L1      0.35891664
## L2      0.32535350
## L3     -0.02200252
## Height -1.07931595
## Width   0.27826140

mvn(data = newfish.q[,-c(1,8,9,10)], mvnTest = "hz")

## $multivariateNormality
##           Test       HZ p value MVN
## 1 Henze-Zirkler 4.496681       0  NO
##
## $univariateNormality
##           Test  Variable Statistic   p value Normality
```

```
## 1 Shapiro-Wilk  Weight     0.8780  <0.001      NO
## 2 Shapiro-Wilk    L1       0.9679  0.0019      NO
## 3 Shapiro-Wilk    L2       0.9702  0.0033      NO
## 4 Shapiro-Wilk    L3       0.9703  0.0033      NO
## 5 Shapiro-Wilk  Height     0.9125  <0.001      NO
## 6 Shapiro-Wilk   Width     0.9344  <0.001      NO
##
## $Descriptives
##          n      Mean   Std.Dev Median  Min    Max   25th  75th       Skew
## Weight 143 398.02378 360.51374  272.0  5.9 1650.0 120.00 650.0  1.1175913
## L1     143  26.27692  10.16502   25.2  7.5   59.0  19.00  32.6  0.6215598
## L2     143  28.44406  10.88848   27.3  8.4   63.4  20.90  35.0  0.5796666
## L3     143  31.25455  11.82529   29.2  8.8   68.0  22.80  39.6  0.4306508
## Height 143  28.33217   8.39113   26.8 14.5   44.5  24.25  37.8  0.1335468
## Width  143  14.07063   2.23310   14.6  8.7   20.9  13.40  15.3 -0.4962807
##           Kurtosis
## Weight  0.89652958
## L1      0.35891664
## L2      0.32535350
## L3     -0.02200252
## Height -1.07931595
## Width   0.27826140
```

```
mvn(data = newfish.q[,-c(1,8,9,10)], mvnTest = "royston")
```

```
## $multivariateNormality
##      Test        H      p value MVN
## 1 Royston 46.25164 2.211833e-10  NO
##
## $univariateNormality
##           Test  Variable Statistic   p value Normality
## 1 Shapiro-Wilk  Weight     0.8780  <0.001      NO
## 2 Shapiro-Wilk    L1       0.9679  0.0019      NO
## 3 Shapiro-Wilk    L2       0.9702  0.0033      NO
## 4 Shapiro-Wilk    L3       0.9703  0.0033      NO
## 5 Shapiro-Wilk  Height     0.9125  <0.001      NO
## 6 Shapiro-Wilk   Width     0.9344  <0.001      NO
##
## $Descriptives
##          n      Mean   Std.Dev Median  Min    Max   25th  75th       Skew
## Weight 143 398.02378 360.51374  272.0  5.9 1650.0 120.00 650.0  1.1175913
## L1     143  26.27692  10.16502   25.2  7.5   59.0  19.00  32.6  0.6215598
## L2     143  28.44406  10.88848   27.3  8.4   63.4  20.90  35.0  0.5796666
## L3     143  31.25455  11.82529   29.2  8.8   68.0  22.80  39.6  0.4306508
## Height 143  28.33217   8.39113   26.8 14.5   44.5  24.25  37.8  0.1335468
## Width  143  14.07063   2.23310   14.6  8.7   20.9  13.40  15.3 -0.4962807
##           Kurtosis
## Weight  0.89652958
## L1      0.35891664
## L2      0.32535350
## L3     -0.02200252
```

```
## Height -1.07931595
## Width   0.27826140

#資料不是多元常態
#newfish.qda<-qda(Species~.,data=newfish.q)
newfish.qda<-qda(Species~Weight+L1+Height+Width+L21+L32,data=newfish.q)
newfish.qdapred<-predict(newfish.qda,newfish.q)
predict(newfish.qda,newfish.test)$class

##  [1] bream bream perch perch pike  smelt smelt parki roach roach perch
## Levels: bream parki perch pike roach smelt

newfish.qda<-qda(Species~Weight+L1+Height+Width+L21+L32,data=newfish.q,CV=T)
table(newfish.q$Species,newfish.qda$class)

##        
##         bream parki perch pike roach smelt
##   bream    33     0     0    0     0     0
##   parki     0    10     0    0     0     0
##   perch     0     0    54    0     0     0
##   pike      0     0     0   16     0     0
##   roach     0     0     1    0    17     0
##   smelt     0     0     1    0     0    11
```

Nearest Neighbor Methods

```
library(class)
newfish.knn <- knn(newfish[,2:10],newfish[,2:10],newfish[,"Species"],k=3,prob=T)
table(newfish$Species,newfish.knn)

##        newfish.knn
##         bream parki perch pike roach smelt white
##   bream    30     1     2    0     0     0     0
##   parki     1     6     1    0     2     0     0
##   perch     3     0    47    0     2     1     1
##   pike      1     0     3   11     1     0     0
##   roach     1     0     8    0     8     0     1
##   smelt     0     0     0    0     0    12     0
##   white     0     0     2    1     0     0     2

#We see that the apparent error rate for k = 3 is about 21%. For k = 2, we have:
newfish.knn<-knn(newfish[,2:10],newfish[,2:10],newfish[,"Species"],k=2,prob=T)
table(newfish$Species,newfish.knn)

##        newfish.knn
##         bream parki perch pike roach smelt white
##   bream    27     0     3    0     2     0     1
##   parki     1     7     0    0     2     0     0
##   perch     3     0    45    0     4     1     1
##   pike      1     0     2   13     0     0     0
##   roach     0     0     8    0     9     0     1
```

```
##   smelt     0     0     0    0     0    12     0
##   white     0     0     2    0     0     0     3

#k=1
newfish.knn <- knn(newfish[,2:10],newfish[,2:10],newfish[,"Species"],k=1,prob=T)
table(newfish$Species,newfish.knn)

##        newfish.knn
##         bream parki perch pike roach smelt white
##   bream    33     0     0    0     0     0     0
##   parki     0    10     0    0     0     0     0
##   perch     0     0    54    0     0     0     0
##   pike      0     0     0   16     0     0     0
##   roach     0     0     0    0    18     0     0
##   smelt     0     0     0    0     0    12     0
##   white     0     0     0    0     0     0     5

newfish1 <- newfish[,c(1,2,3,6,8,9)]
newfish.knncv <- knn.cv(newfish1[,2:6],newfish1[,"Species"],k=1,prob=T)
table(newfish1$Species,newfish.knncv)

##        newfish.knncv
##         bream parki perch pike roach smelt white
##   bream    26     0     4    0     2     0     1
##   parki     1     4     0    0     4     0     1
##   perch     3     0    37    0    11     1     2
##   pike      2     0     4    9     0     0     1
##   roach     2     0    10    0     5     0     1
##   smelt     0     0     0    0     0    12     0
##   white     0     0     3    0     0     0     2

newfish1.test<-newfish.test[,c(1,2,5,7,8)]
newfish.knntest<-knn(newfish1[,2:6],newfish1.test,newfish1[,"Species"],k=1,prob=T)
newfish.knntest

##  [1] bream bream perch white perch smelt smelt parki perch perch perch
## attr(,"prob")
##  [1] 1 1 1 1 1 1 1 1 1 1 1
## Levels: bream parki perch pike roach smelt white
```

Logistic Discrimination

```
library(nnet)
newfish.logd<-multinom(Species~.,data=newfish,maxit=250)

## # weights:  77 (60 variable)
## initial  value 287.994702
## iter  10 value 189.100680
## iter  20 value 82.739762
## iter  30 value 15.668415
## iter  40 value 0.165377
## iter  50 value 0.003851
## final  value 0.000000
## converged

newfish.logd

## Call:
## multinom(formula = Species ~ ., data = newfish, maxit = 250)
##
## Coefficients:
##       (Intercept)      Weight        L1          L2        L3     Height
## parki   -29.45533  0.02917110   6.349592  17.8259067 -23.500970   9.645257
## perch   -80.11405  0.16021628   3.267803  56.6489218 -53.765483   6.684178
## pike     15.22567 -0.05874368   8.093673   0.9753102  -3.095179 -13.084687
## roach  -277.16410 -0.51539078  54.195310 -43.6844449   4.362472  -2.952463
## smelt   455.64639  0.18459382  29.363751 -20.5072505 -10.290211 -13.228223
## white   -57.01255  0.19991067 -17.467222  31.7667561 -20.454096  -4.118171
##           Width       L21         L32        L31
## parki  3.247584  11.476314  -41.326877 -29.850563
## perch 21.052273  53.381119 -110.414404 -57.033286
## pike  21.652958  -7.118363   -4.070489 -11.188852
## roach 40.080837 -97.879755   48.046917 -49.832838
## smelt 18.368009 -49.871001   10.217040 -39.653961
## white 26.549555  49.233978  -52.220852  -2.986874
##
## Residual Deviance: 2.009681e-11
## AIC: 84

table(newfish$Species,predict(newfish.logd,newfish))

##
##         bream parki perch pike roach smelt white
##   bream    33     0     0    0     0     0     0
##   parki     0    10     0    0     0     0     0
##   perch     0     0    54    0     0     0     0
##   pike      0     0     0   16     0     0     0
##   roach     0     0     0    0    18     0     0
##   smelt     0     0     0    0     0    12     0
##   white     0     0     0    0     0     0     5

library(glmnet)
```

```
## Loading required package: Matrix

## Loading required package: foreach

## Loaded glmnet 2.0-16

x <- as.matrix(newfish[,-1])
y <- newfish$Species
cvfit <- cv.glmnet(x, y, family="multinomial", type.measure="class", nfolds=148)
predict.value <- predict(cvfit, x, s = "lambda.min", type = "class")
table(predict.value,newfish$Species)

##
## predict.value bream parki perch pike roach smelt white
##         bream    33     0     0    0     0     0     0
##         parki     0    10     0    0     0     0     0
##         perch     0     0    54    0     0     0     0
##         pike      0     0     0   16     0     0     0
##         roach     0     0     0    0    18     0     0
##         smelt     0     0     0    0     0    12     0
##         white     0     0     0    0     0     0     5

predict(newfish.logd,newfish.test)

##  [1] bream bream perch perch pike  smelt smelt parki roach roach white
## Levels: bream parki perch pike roach smelt white
```

Github: https://github.com/CaoCharles/classifng_fish