## HW1

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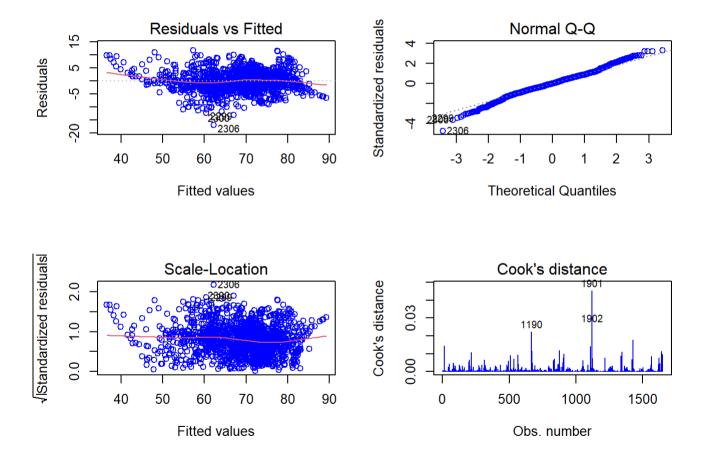
1.

```
###1
#(1)
csv1=read.csv("C://Users//张铭韬//Desktop//学业//港科大//MSDM5054机器学习//作业//hw1//Life Expectancy Data.csv")
df1=csv1[,-c(1,2)]
df1=na.omit(df1)
mod1=lm(Life.expectancy~.,data=df1)
summary(mod1)
```

```
##
## Call:
## lm(formula = Life.expectancy \sim ... data = df1)
##
## Residuals:
       Min
                 10 Median
                                   3Q
                                          Max
## -16.9597 -2.0621 -0.0147 2.2751 11.7115
## Coefficients:
                                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                                   5. 445e+01 8. 400e-01 64. 822 < 2e-16 ***
                                  -9.684e-01 3.379e-01 -2.865 0.00422 **
## StatusDeveloping
## Adult.Mortality
                                  -1.663e-02 9.494e-04 -17.517 < 2e-16 ***
## infant.deaths
                                  9.350e-02 1.065e-02
                                                         8.777 < 2e-16 ***
## Alcohol
                                  -9.140e-02 3.316e-02 -2.756 0.00592 **
                                  3.673e-04 1.801e-04
## percentage. expenditure
                                                         2.040 0.04156 *
## Hepatitis.B
                                  -6.525e-03 4.449e-03 -1.467 0.14265
## Measles
                                  -7.865e-06 1.079e-05 -0.729 0.46597
## BMI
                                  3.376e-02 5.998e-03 5.628 2.15e-08 ***
## under five deaths
                                  -7.035e-02 7.711e-03 -9.123 < 2e-16 ***
## Polio
                                  7. 935e-03 5. 152e-03
                                                       1.540 0.12370
## Total. expenditure
                                  7.586e-02 4.067e-02
                                                       1.865 0.06236.
## Diphtheria
                                  1.490e-02 5.928e-03
                                                        2.513 0.01205 *
## HIV. AIDS
                                  -4.370e-01 1.784e-02 -24.490 < 2e-16 ***
## GDP
                                  8.738e-06 2.837e-05
                                                        0.308 0.75813
## Population
                                  -6. 425e-10 1. 749e-09 -0. 367 0. 71337
## thinness..1.19.years
                                  -1.238e-02 5.300e-02 -0.234 0.81527
## thinness. 5.9. years
                                  -4. 798e-02 5. 231e-02 -0. 917 0. 35917
## Income.composition.of.resources 9.817e+00 8.321e-01 11.797 < 2e-16 ***
## Schooling
                                  8.665e-01 5.940e-02 14.587 < 2e-16 ***
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
##
## Residual standard error: 3.588 on 1629 degrees of freedom
## Multiple R-squared: 0.8356, Adjusted R-squared: 0.8336
## F-statistic: 435.7 on 19 and 1629 DF, p-value: < 2.2e-16
```

#Adult.Mortality, infant.deaths, under.five.deaths, BMI, HIV.AIDS, Income.composition.of.resources, Schooling may be the most #important variables; next are: Status, Alcohol, Diphtheria and percentage.expenditure.

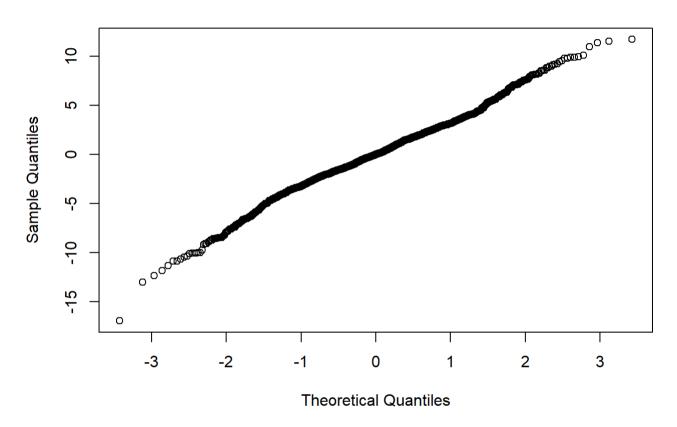
#总体检验 par(mfrow=c(2,2)) plot(mod1, which=1:4, col="blue") #独立性 library(DescTools)



DurbinWatsonTest(mod1)

```
##
## Durbin-Watson test
##
## data: mod1
## DW = 0.70551, p-value < 2.2e-16
\#\# alternative hypothesis: true autocorrelation is greater than 0
#残差正态性
1mres=residuals(mod1)
shapiro.test(1mres)
##
## Shapiro-Wilk normality test
##
## data: 1mres
## W = 0.99082, p-value = 1.159e-08
par(mfrow=c(1,1))
qqnorm(1mres)
```

## **Normal Q-Q Plot**



```
#方差齐性
library(zoo)

##
## 载入程辑包: 'zoo'

## The following objects are masked from 'package:base':
##
## as.Date, as.Date.numeric
```

```
library(lmtest)
bptest(mod1)
```

```
## studentized Breusch-Pagan test
## data: mod1
## BP = 188.24, df = 19, p-value < 2.2e-16
```

```
#(2)
confint(mod1, level=0.95)
```

```
##
                                                        97.5 %
                                           2.5 %
## (Intercept)
                                    5. 280349e+01 5. 609873e+01
## StatusDeveloping
                                   -1.631210e+00 -3.055239e-01
## Adult. Mortality
                                   -1.849399e-02 -1.476948e-02
## infant.deaths
                                    7. 260415e-02 1. 143953e-01
## Alcohol
                                   -1.564424e-01 -2.634759e-02
## percentage.expenditure
                                   1. 406977e-05 7. 206029e-04
## Hepatitis.B
                                   -1.525013e-02 2.200833e-03
## Measles
                                   -2.902123e-05 1.329036e-05
## BMI
                                    2. 199085e-02 4. 552044e-02
## under five deaths
                                   -8.547344e-02 -5.522328e-02
## Polio
                                   -2.169947e-03 1.804045e-02
## Total. expenditure
                                   -3.921521e-03 1.556380e-01
## Diphtheria
                                    3. 272244e-03 2. 652641e-02
## HIV. AIDS
                                   -4.719608e-01 -4.019673e-01
## GDP
                                   -4.690855e-05 6.438443e-05
                                   -4.072414e-09 2.787485e-09
## Population
## thinness..1.19.years
                                   -1.163427e-01 9.157275e-02
## thinness. 5.9. years
                                   -1.505946e-01 5.462745e-02
## Income.composition.of.resources 8.184423e+00 1.144872e+01
## Schooling
                                    7. 499887e-01 9. 830178e-01
```

```
#Adult.Mortality: [-1.849399e-02,-1.476948e-02]
# HIV.AIDS: [-4.719608e-01,-4.019673e-01]

#These 2 variables both pass the t-test(a=.001) so I'm confident they have negative impact on the life expectancy.

#(3)
confint(mod1,level=0.97)
```

```
##
                                                        98.5 %
                                           1.5 %
## (Intercept)
                                    5. 262661e+01 5. 627561e+01
## StatusDeveloping
                                   -1.702370e+00 -2.343631e-01
## Adult.Mortality
                                   -1.869392e-02 -1.456956e-02
## infant.deaths
                                    7. 036087e-02 1. 166385e-01
## Alcohol
                                   -1.634257e-01 -1.936430e-02
## percentage.expenditure
                                   -2.385583e-05 7.585285e-04
## Hepatitis.B
                                   -1.618687e-02 3.137574e-03
## Measles
                                   -3.129245e-05 1.556158e-05
## BMI
                                    2.072782e-02 4.678347e-02
## under five deaths
                                   -8.709722e-02 -5.359950e-02
## Polio
                                   -3.254810e-03 1.912532e-02
## Total. expenditure
                                   -1. 248643e-02 1. 642029e-01
## Diphtheria
                                    2.023997e-03 2.777466e-02
## HIV. AIDS
                                   -4.757180e-01 -3.982101e-01
## GDP
                                   -5.288259e-05 7.035846e-05
## Population
                                   -4.440643e-09 3.155714e-09
## thinness..1.19.years
                                   -1.275033e-01 1.027333e-01
## thinness. 5.9. years
                                   -1.616106e-01 6.564344e-02
## Income.composition.of.resources 8.009200e+00 1.162394e+01
## Schooling
                                    7. 374800e-01 9. 955264e-01
```

```
#Schooling:[7.374800e-01, 9.955264e-01]----→The larger the number of years of Schooling is, the longer the Life Expectancy is.

# Alcohol:[-1.634257e-01 -1.936430e-02]---→The more alcohol consumption recorded per capita (15+) is, the shorter the Life Expectancy is.

# (4)

# Adult. Mortality: < 2e-16

# infant. deaths: < 2e-16

# under. five. deaths: < 2e-16

# BMI: 2.15e-08

# HIV. AIDS: < 2e-16

# Troome. composition. of. resources: < 2e-16

# Schooling: < 2e-16

mod2=lm(Life. expectancy~Adult. Mortality+infant. deaths+under. five. deaths+BMI+HIV. AIDS+Income. composition. of. resources+Schooling, data=df1)

summary (mod2)
```

```
##
## Call:
## lm(formula = Life.expectancy ~ Adult.Mortality + infant.deaths +
      under. five. deaths + BMI + HIV. AIDS + Income. composition. of. resources +
##
      Schooling, data = df1)
##
## Residuals:
      Min
               10 Median
                                      Max
## -17.604 -2.072 -0.023
                          2. 200 12. 308
##
## Coefficients:
##
                                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                                  53.2080766 0.5361598 99.239 < 2e-16 ***
## Adult. Mortality
                                  -0.0178405 0.0009597 -18.589 < 2e-16 ***
## infant.deaths
                                   0.0910551 0.0098397 9.254 < 2e-16 ***
## under five deaths
                                  -0.0699153 0.0073116 -9.562 < 2e-16 ***
## BMI
                                   0.0366104 0.0057061 6.416 1.83e-10 ***
## HIV. AIDS
                                  -0.4337578 0.0180613 -24.016 < 2e-16 ***
## Income.composition.of.resources 10.8860992 0.8247651 13.199 < 2e-16 ***
## Schooling
                                   0.9746212 0.0555178 17.555 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '* 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.683 on 1641 degrees of freedom
## Multiple R-squared: 0.8254, Adjusted R-squared: 0.8247
## F-statistic: 1108 on 7 and 1641 DF, p-value: < 2.2e-16
```

```
#(5)
new_obs=data.frame(Adult.Mortality=125, infant.deaths=94, under.five.deaths=2, BMI=55, HIV.AIDS=0.5, Income.composition.of.resources =0.9, Schooling=18)
# create the new observation
predict(mod2, newdata=new_obs, interval="confidence", level=0.99)
```

```
## fit lwr upr
## 1 88.53472 86.15881 90.91064
```

```
#(6)
AIC (mod1)
## [1] 8914.947
AIC (mod2)
## [1] 8989.692
```

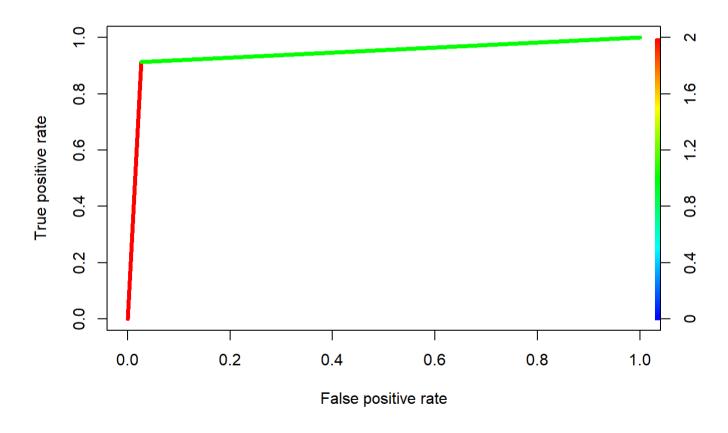
2.

#The AIC of mod1(full model) is smaller than mod2(smaller model).

```
###2
#(1)
train=read.csv("C://Users//张铭韬//Desktop//学业//港科大//MSDM5054机器学习//作业//hw1//BreastCancer train.csv")
train=train[,-1]
test=read.csv("C://Users//张铭韬//Desktop//学业//港科大//MSDM5054机器学习//作业//hw1//BreastCancer test.csv")
test=test[,-1]
train$type[which(train$Class== "benign")]=0 # benign编号为0
train$type[which(train$Class== "malignant")]=1 # malignant编号为1
test$type[which(test$Class== "benign")]=0 # benign编号为0
test$type[which(test$Class== "malignant")]=1 # malignant编号为1
train=train[,-10]
train=na.omit(train)
test=test[,-10]
test=na.omit(test)
train$type=factor(train$type)
test$type=factor(test$type)
glmod1=glm(type~., data=train, family=binomial)
summary(glmod1)
```

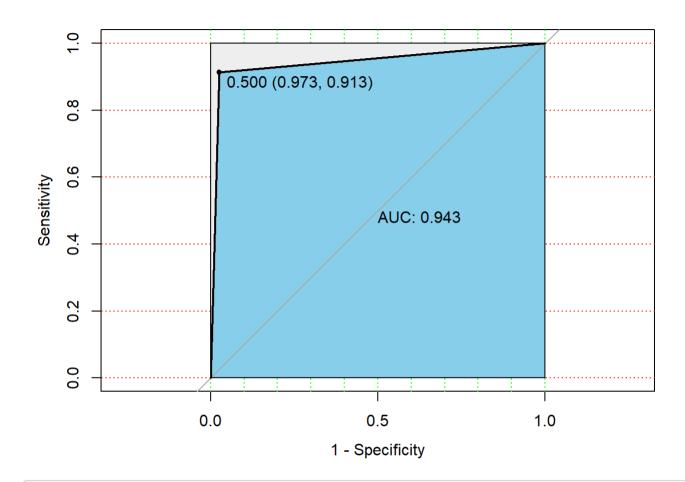
```
##
## Call:
## glm(formula = type^{\sim}., family = binomial, data = train)
##
## Deviance Residuals:
      Min
                1Q Median
                                          Max
## -3.2871 -0.0863 -0.0542
                              0.0218
                                      1.8764
## Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                  -10.5582
                               1.7131 -6.163 7.12e-10 ***
## Cl. thickness
                    0.3671
                               0.2154
                                       1.704 0.0883.
## Cell.size
                   -0.2865
                               0.2772 -1.034 0.3013
## Cell. shape
                    0.5608
                               0.3082
                                       1.820
                                               0.0688 .
## Marg. adhesion
                    0.3486
                               0.1411
                                        2.470
                                               0.0135 *
                               0.2656
## Epith.c.size
                    0.4145
                                        1.561
                                               0.1186
## Bare.nuclei
                    0.2939
                               0.1214
                                        2.420
                                               0.0155 *
## Bl.cromatin
                    0.6060
                               0.2613
                                        2.319
                                               0.0204 *
## Normal.nucleoli
                    0.1968
                               0.1635
                                        1.203
                                               0.2288
                               0.4110
                                       0.788
## Mitoses
                    0.3238
                                               0.4308
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##
      Null deviance: 506.096 on 391 degrees of freedom
## Residual deviance: 53.745 on 382 degrees of freedom
## AIC: 73.745
## Number of Fisher Scoring iterations: 8
```

```
#Marg. adhesion, Bare. nuclei and Bl. cromatin are significant variables. predl=predict(glmod1, test, interval="prediction", type="response") predl=ifelse(pred1>0.5,1,0) library(ROCR) pl=prediction(pred1, test$type) #预测值和真实值 perfl=performance(p1,"tpr","fpr") plot(perf1, colorize=TRUE, lwd=4)
```



#AUC:0.943
performance(p1, "auc")@y.values[[1]]

```
## [1] 0.9430128
#Another method:
library (pROC)
## Type 'citation("pROC")' for a citation.
## 载入程辑包: 'pROC'
## The following objects are masked from 'package:stats':
##
      cov, smooth, var
modelroc1=roc(test$type, pred1) #真实值和预测值
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
plot(modelroc1, print.auc=TRUE, auc.polygon=TRUE, legacy.axes=TRUE, grid=c(0.1, 0.2),
    grid.col=c("green", "red"), max.auc.polygon=TRUE,
    auc.polygon.col="skyblue", print.thres=TRUE)
```

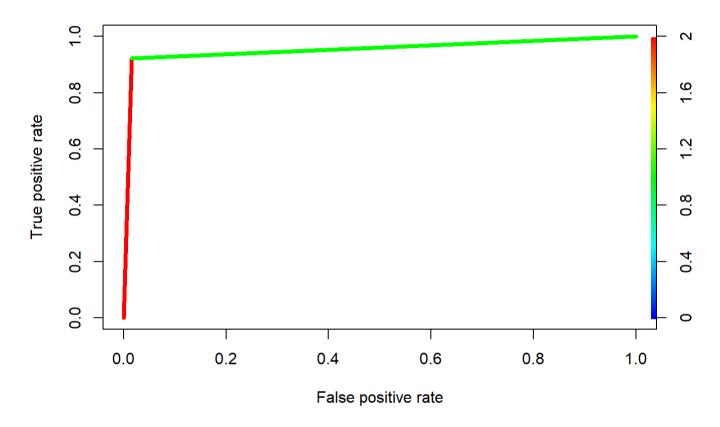


#(2) glmod2=glm(type $^{\sim}$ C1. thickness+Cell. shape+Marg. adhesion+Bare. nuclei+B1. cromatin, data=train, family=binomial) summary(glmod2)

```
##
## Call:
## glm(formula = type ~ Cl. thickness + Cell. shape + Marg. adhesion +
      Bare. nuclei + Bl. cromatin, family = binomial, data = train)
##
## Deviance Residuals:
      Min
                10 Median
                                          Max
## -3, 2350 -0, 1046 -0, 0577
                             0.0239 1.9109
## Coefficients:
                Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                 -9.7502
                             1.4970 -6.513 7.35e-11 ***
## Cl. thickness
                  0.4866
                             0.1936 2.513 0.01198 *
## Cell. shape
                  0.4915
                             0.2002
                                      2.455 0.01410 *
## Marg. adhesion 0.3515
                             0.1236
                                      2.844 0.00446 **
## Bare.nuclei
                  0.2917
                             0.1078
                                      2.707 0.00679 **
## Bl.cromatin
                  0.7599
                             0.2293
                                      3.314 0.00092 ***
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 506.096 on 391 degrees of freedom
## Residual deviance: 61.363 on 386 degrees of freedom
## AIC: 73.363
## Number of Fisher Scoring iterations: 8
```

```
pred2=predict(glmod2, test, interval="prediction", type="response")
pred2=ifelse(pred2>0.5,1,0)

p2=prediction(pred2, test$type) #预测值和真实值
perf2=performance(p2,"tpr","fpr")
plot(perf2, colorize=TRUE, lwd=4)
```

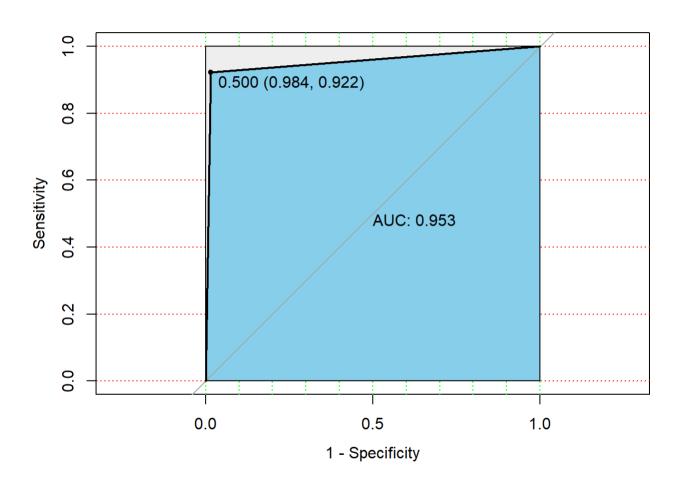


```
#AUC:0.953
performance(p2, "auc")@y.values[[1]]
```

```
## [1] 0.9531863
```

modelroc2=roc(test\$type,pred2) #真实值和预测值

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases</pre>
```

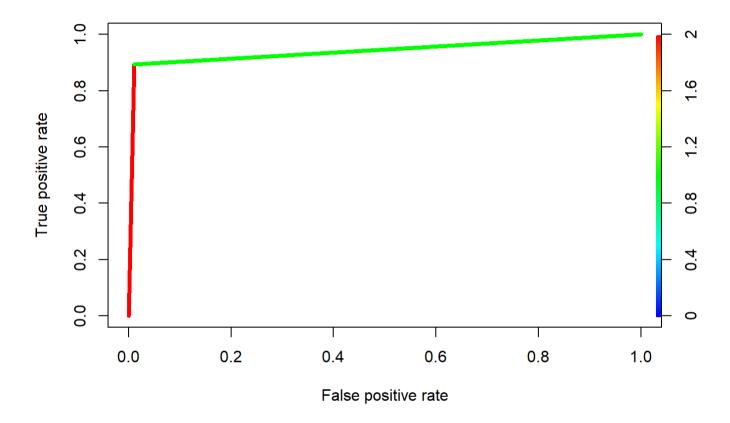


```
#The AUC of glmod2 is larger than glmod1.

#(3)
library(MASS)
lda.fit=lda(type~.,data=train)
lda.fit #Prior probabilities of groups先验概率; Coefficients of linear discriminants线性方程系数
```

```
## Call:
## lda(type ~ ., data = train)
## Prior probabilities of groups:
          0
## 0.6530612 0.3469388
## Group means:
    Cl. thickness Cell. size Cell. shape Marg. adhesion Epith. c. size Bare. nuclei
## 0
         2.878906 1.281250
                             1.382812
                                             1.304688
                                                          2.097656
                                                                      1.339844
        7. 117647 6. 669118 6. 617647
                                             5. 786765
                                                          5. 345588
                                                                      7.757353
## Bl.cromatin Normal.nucleoli Mitoses
## 0
        2.023438
                        1. 238281 1. 066406
## 1
        6. 264706
                        6. 176471 2. 786765
## Coefficients of linear discriminants:
##
                           LD1
## Cl. thickness
                    0.15467544
## Cell.size
                    0.07723506
## Cell. shape
                    0.11382233
## Marg. adhesion
                   0.08656188
## Epith.c.size
                    0.13050211
## Bare.nuclei
                    0.24893576
## Bl.cromatin
                    0.12066142
## Normal.nucleoli 0.10230580
## Mitoses
                   -0.02736122
```

```
lda.pred=predict(lda.fit, test)
lda.pred$class #预测的所属类的结果;后验概率为lda.pred$posterior
## [1] 1 1 0 0 0 1 0 0 1 0 1 0 1 0 0 0 1 1 1 1 0 1 1 0 0 0 0 0 1 0 0 0 1 0
## [38] 0 0 0 1 1 0 0 0 1 0 1 0 1 1 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 1 0 1 1 0 0 1 0 0 1
## [112] 1 1 1 0 1 1 0 1 1 1 1 1 0 1 1 0 1 1 1 1 0 1 1 0 1 1 1 1 1 0 1 0 1 0 1 0 1 0 0 0 0 1 0 1 0 0 0 1
## [260] 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0
## Levels: 0 1
tab=table(lda.pred$class, test$type) #预测值和真实值
    #混淆矩阵
tab
##
      0 1
   0 186 11
##
  1 2 92
erro=1-sum(diag(prop. table(tab)))
                         #计算误判率
erro
## [1] 0.04467354
ldap1=prediction((as.numeric(lda.pred$class)-1), test$type) #预测值和真实值
ldaperf1=performance(ldap1, "tpr", "fpr")
plot (ldaperfl, colorize=TRUE, lwd=4)
```



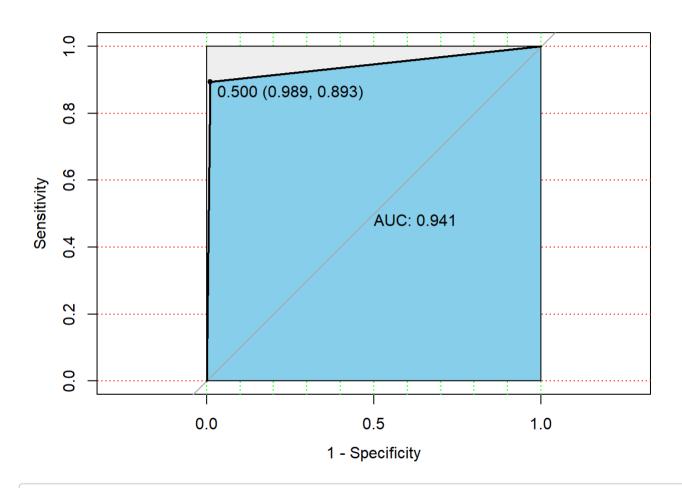
```
#AUC:0.941
performance(ldap1, "auc")@y.values[[1]]
```

```
## [1] 0.9412828
```

modelldarocl=roc(test\$type, (as. numeric(lda. pred\$class)-1)) #真实值和预测值

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases</pre>
```

```
plot(modelldaroc1, print.auc=TRUE, auc.polygon=TRUE, legacy.axes=TRUE, grid=c(0.1, 0.2), grid.col=c("green", "red"), max.auc.polygon=TRUE, auc.polygon.col="skyblue", print.thres=TRUE)
```



#(4) lda.fit2=lda(type~C1.thickness+Cell.shape+Marg.adhesion+Bare.nuclei+B1.cromatin,data=train) lda.fit2 #Prior probabilities of groups先验概率; Coefficients of linear discriminants线性方程系数

```
## Call:
## lda(type ~ Cl. thickness + Cell. shape + Marg. adhesion + Bare. nuclei +
       Bl. cromatin, data = train)
##
## Prior probabilities of groups:
##
          0
## 0.6530612 0.3469388
##
## Group means:
## Cl. thickness Cell. shape Marg. adhesion Bare. nuclei Bl. cromatin
## ()
         2.878906 1.382812
                                  1.304688
                                              1.339844
                                                           2.023438
        7. 117647 6. 617647
                                  5. 786765
                                              7.757353
                                                           6.264706
## 1
##
## Coefficients of linear discriminants:
                       LD1
## C1. thickness 0.1615430
                0.2355030
## Cell. shape
## Marg. adhesion 0.1111864
## Bare.nuclei 0.2409875
## Bl. cromatin 0.1902969
```

```
lda.pred2=predict(lda.fit2,test)
lda.pred2$class #预测的所属类的结果;后验概率为lda.pred$posterior
```

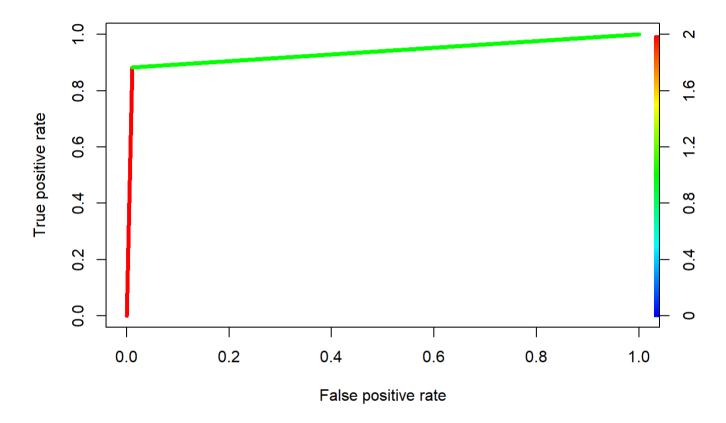
```
tab2=table(lda.pred2$class, test$type) #预测值和真实值
tab2 #混淆矩阵
```

```
##
## 0 1
## 0 186 12
## 1 2 91
```

```
erro2=1-sum(diag(prop.table(tab2))) #计算误判率
erro2
```

```
## [1] 0.04810997
```

```
ldap2=prediction((as.numeric(lda.pred2$class)-1),test$type) #预测值和真实值
ldaperf2=performance(ldap2,"tpr","fpr")
plot(ldaperf2,colorize=TRUE,lwd=4)
```



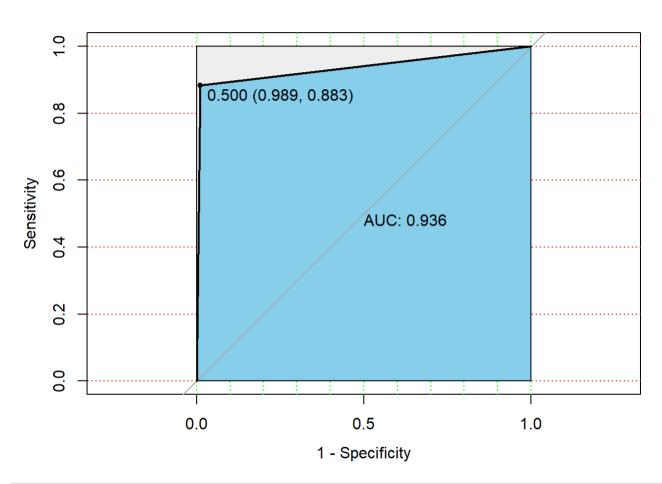
```
#AUC:0.936
performance(ldap2, "auc")@y.values[[1]]
```

```
## [1] 0.9364284
```

modelldaroc2=roc(test\$type, (as. numeric(lda.pred2\$class)-1)) #真实值和预测值

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases</pre>
```

```
plot(modelldaroc2, print.auc=TRUE, auc.polygon=TRUE, legacy.axes=TRUE, grid=c(0.1, 0.2),
    grid.col=c("green", "red"), max.auc.polygon=TRUE,
    auc.polygon.col="skyblue", print.thres=TRUE)
```



```
#(5)
qda.fit=qda(type~.,data=train)
qda.fit #Prior probabilities of groups先验概率
```

```
## Call:
## qda(type ~ ., data = train)
## Prior probabilities of groups:
          0
## 0.6530612 0.3469388
## Group means:
## C1.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size Bare.nuclei
## ()
         2.878906 1.281250 1.382812
                                           1.304688
                                                        2.097656
                                                                    1.339844
        7. 117647 6. 669118 6. 617647
                                            5. 786765
                                                        5. 345588
                                                                    7.757353
## 1
## Bl. cromatin Normal. nucleoli Mitoses
## ()
       2.023438
                       1. 238281 1. 066406
## 1
        6.264706
                       6. 176471 2. 786765
```

```
qda. pred=predict(qda. fit, test)
qda. pred$class #预测的所属类的结果;后验概率为qda. pred$posterior
```

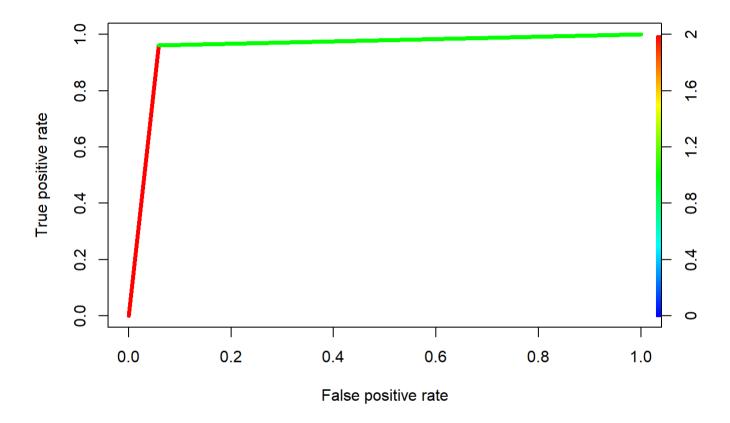
```
tabq1=table(qda.pred$class, test$type) #预测值和真实值
tabq1 #混淆矩阵
```

```
##
## 0 1
## 0 177 4
## 1 11 99
```

```
erroql=1-sum(diag(prop.table(tab))) #计算误判率
erroql
```

```
## [1] 0.04467354
```

```
qdapl=prediction((as.numeric(qda.pred$class)-1),test$type) #预测值和真实值
qdaperf1=performance(qdap1,"tpr","fpr")
plot(qdaperf1,colorize=TRUE,lwd=4)
```



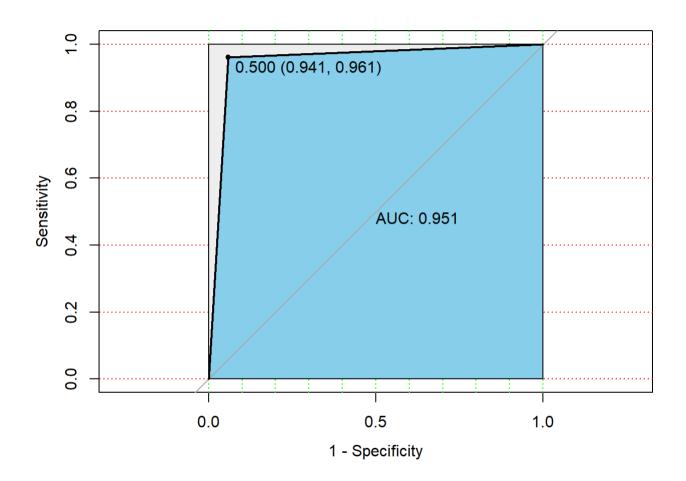
```
#AUC:0.951
performance(qdap1, "auc")@y.values[[1]]
```

```
## [1] 0.9513272
```

modelqdarocl=roc(test\$type, (as.numeric(qda.pred\$class)-1)) #真实值和预测值

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases</pre>
```

```
plot(modelqdaroc1, print.auc=TRUE, auc.polygon=TRUE, legacy.axes=TRUE, grid=c(0.1, 0.2),
    grid.col=c("green", "red"), max.auc.polygon=TRUE,
    auc.polygon.col="skyblue", print.thres=TRUE)
```



```
#(6)
# MODEL AUC
#glm full model 0.943
#glm smaller model 0.953
#LDA full model 0.941
#LDA smaller model 0.936
#QDA full model 0.951
```

3.

```
###3
#Actually I've done the homework at the exact day it's assigned.
#So I wrote this mvKNN function 2 days later when the notification announced. The result is about the same as the kknn library
function.
#But I still reserve my codes written before because maybe they will be useful in the future.
#I can write a loop for k and h for myknn function, but that's not so efficient as the knn.cv or train.kknn in libraries to cho
ose the best k and h.
#So I still choose them for searching best k and h, and use my function to do the result check, and make sure the myknn functio
n I wrote is correct.
#These are the codes for both my function and the library functions.
mvKNN Gaussian=function (trainx, trainv, testx, testv, k=9, h=2, delta=0.5) {
 M=dim(trainx)[1]
 N=dim(testx)[1]
 Xt=rbind(trainx, testx)
  Dtest=as.matrix(dist(Xt, method = "euclidean"))
 Dtest=Dtest[-c(1:M),]
  Pre=c()
  Error=c()
  for (1 in 1:N) {
    Tsort=sort(Dtest[1,1:M], index.return = TRUE)
    index=Tsort$ix[1:k]
    Weight=exp((-0.5*((Tsort$x[1:k]/h)^2))) ### you can change the kernel function here.
    Vote=trainy[Tsort$ix[1:k]]
    tent=data.frame("Weight"=Weight, "Vote"=Vote)
    tent2=aggregate(tent[, c("Weight")], list(Vote = tent$Vote), sum)
    if (\dim(\text{tent2})[1]==1) {
      if (tent2[1,1]==1) {
        if (delta==0) {
          PreY=0
        } e 1 s e {
          PreY=1
```

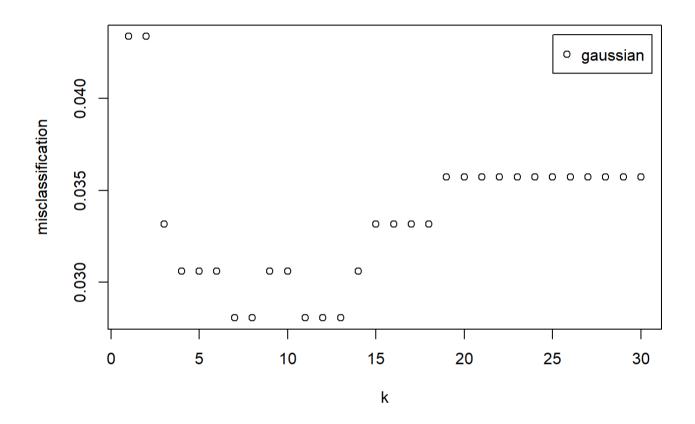
```
}e1se{
       PreY=0
   }else{
     if (tent2\$x[tent2\$Vote==0]/(tent2\$x[tent2\$Vote==0]+tent2\$x[tent2\$Vote==1])>=de1ta) \{ (tent2\$x[tent2\$Vote==0]+tent2\$x[tent2\$Vote==1])>=de1ta \} \}
       PreY=0
     }e1se{
       PreY=1
   ErrorY=PreY!=testv[1]
   Pre[1]=PreY
   Error[1]=ErrorY
 return (Pre)
#(1)&(2)
library (class)
library(kknn)
trainx=train[,1:9]#训练集
testx=test[,1:9]#测试集
trainy=train[,10]
testy=test[,10]
### Check the best k and h at the same time:
#测试不同方法, distance=2
# model.tkknn=train.kknn(type~.,train,kernel = c("rectangular","triangular","epanechnikov","biweight","triweight","cos","in
v", "gaussian", "optimal"), distance=2, scale=T, kmax=30)
# model. tkknn$MISCLASS #显示错误率;$MEAN. ABS平均绝对误差;$MEAN. SQU均方误差
```

```
# model.tkknn #输出最优参数情况
# plot(model.tkknn)

#核函数为epanechnikov时,取distance=1-4进行测试
model.tkknnl=train.kknn(type~.,train,kernel = "gaussian",distance=1,scale=T,kmax=30)
model.tkknnl #输出最优参数情况
```

```
## Call:
## train.kknn(formula = type ~ ., data = train, kmax = 30, distance = 1, kernel = "gaussian", scale = T)
##
Type of response variable: nominal
## Minimal misclassification: 0.02806122
## Best kernel: gaussian
## Best k: 7
```

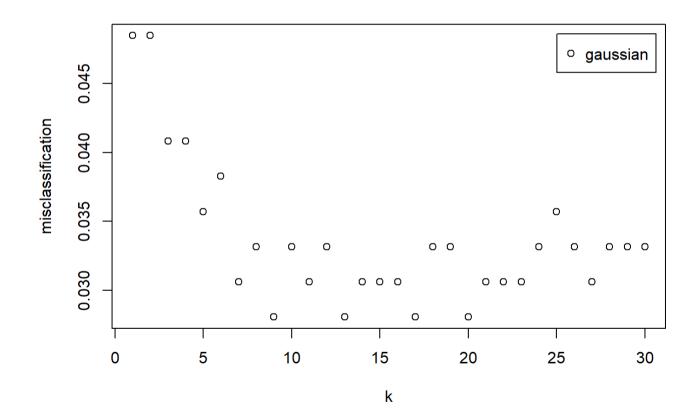
plot(model.tkknn1)



model.tkknn2=train.kknn(type~.,train,kernel = "gaussian",distance=2,scale=T,kmax=30) model.tkknn2 #输出最优参数情况

```
## Call:
## train.kknn(formula = type ~ ., data = train, kmax = 30, distance = 2, kernel = "gaussian", scale = T)
##
Type of response variable: nominal
## Minimal misclassification: 0.02806122
## Best kernel: gaussian
## Best k: 9
```

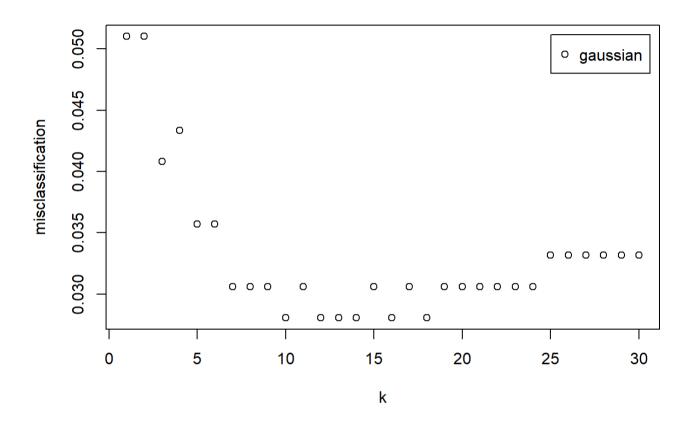
plot(model.tkknn2)



```
model.tkknn3=train.kknn(type~.,train,kernel = "gaussian",distance=3,scale=T,kmax=30)
model.tkknn3 #输出最优参数情况
```

```
## Call:
## train.kknn(formula = type ~ ., data = train, kmax = 30, distance = 3, kernel = "gaussian", scale = T)
##
Type of response variable: nominal
## Minimal misclassification: 0.02806122
## Best kernel: gaussian
## Best k: 10
```

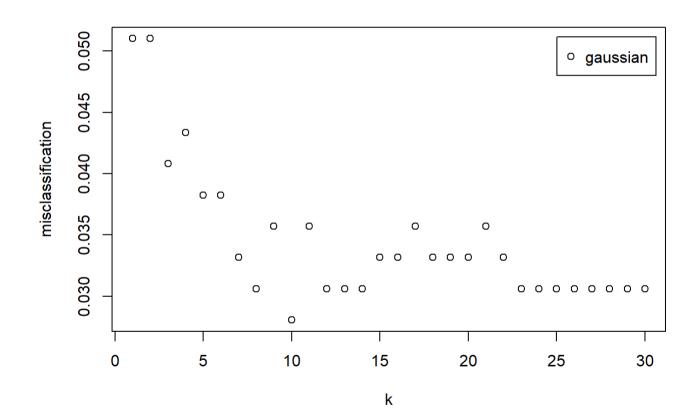
plot(model.tkknn3)



model.tkknn4=train.kknn(type~.,train,kernel = "gaussian",distance=4,scale=T,kmax=30) model.tkknn4 #输出最优参数情况

```
## Call:
## train.kknn(formula = type ~ ., data = train, kmax = 30, distance = 4, kernel = "gaussian", scale = T)
##
Type of response variable: nominal
## Minimal misclassification: 0.02806122
## Best kernel: gaussian
## Best k: 10
```

plot (model. tkknn4)



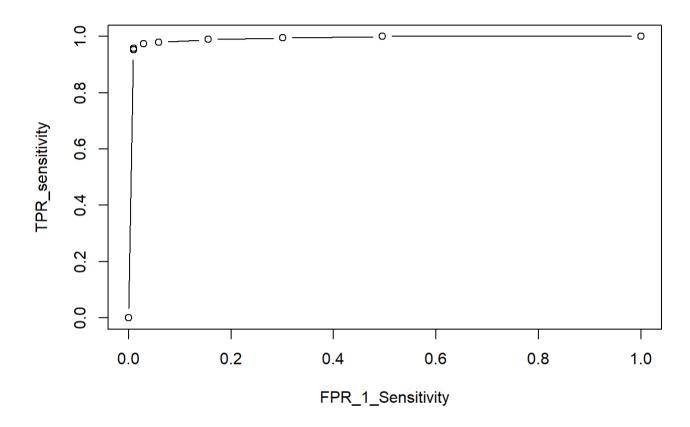
```
#There's no significant changes so we can take distance=2 and k=9
# knntab2=table(trainy, model. tkknn2$fitted. values[[9]])
# knntab2
                                  #混淆矩阵
# 1-sum(diag(prop. table(knntab2)))
                                  #计算误判率
#采用最优参数做预测
model.kknn=kknn(type~.,train,testx,k=model.tkknn2$best.parameters$k,scale=T,distance=2,kernel=model.tkknn2$best.parameters$kern
e1)
# model.kknn$C #邻居的观测值号
# train[model.kknn$C,]#杳看邻居
# model.kknn$D #邻居与它的距离
# model.kknn$W #邻居的权重
# model.kknn$CL #邻居的类别
# model.kknn$prob#预测的概率
#summary (model.kknn)
fit=fitted(model.kknn)
fit
```

knntab2=table(testy,fit)

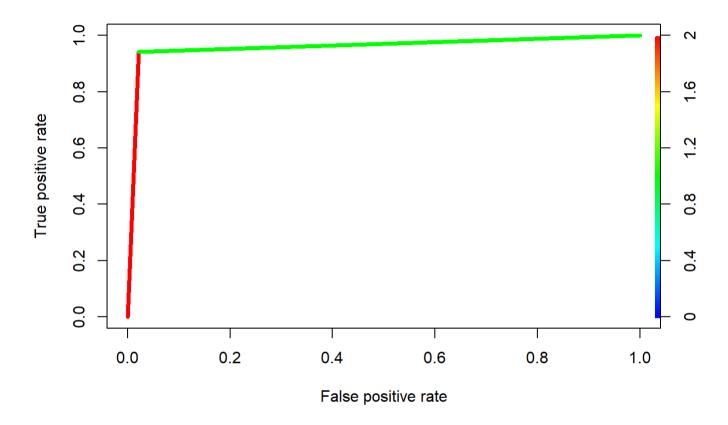
knntab2 #混淆矩阵

```
##
      fit
## testy 0 1
     0 184 4
##
    1 6 97
1-sum(diag(prop. table(knntab2))) #计算误判率
## [1] 0.03436426
starttime=Sys.time()
myfit=myKNN Gaussian(trainx, trainy, testx, testy, k=9, h=2)
knntabmy=table(testy, myfit)
                             #混淆矩阵
knntabmy
      myfit
## testy 0 1
     0 184 4
     1 6 97
1-sum(diag(prop.table(knntabmy))) #计算误判率
## [1] 0.03436426
endtime=Sys.time()
timeinterval=endtime-starttime
timeinterval
## Time difference of 0.3480692 secs
```

```
#The function I wrote is correct with the kknn function, but a bit slower.
#Then do the ROC manually and compare it with the picture in the library:
deltalist=c(0.001, 0.01, 0.02, 0.1, 0.2, 0.5, 0.8, 0.9, 0.98, 0.99, 0.999)
TPR sensitivity=c(1)
FPR 1 Sensitivity=c(1)
for (i in 1:length(deltalist)) {
 pred tent=rep("1", 291)
 pred tent[which(model.kknn$prob[,1]>deltalist[i])]="0"
 pred tent=as.numeric(pred tent)
 knntab tent=table(pred tent, testy) #预测值和真实值
 TPR sensitivity[i+1]=knntab tent[1,1]/(knntab tent[1,1]+knntab tent[2,1])
 FPR 1 Sensitivity [i+1] = knntab tent [1,2] / (knntab tent [1,2] + knntab tent [2,2])
TPR sensitivity=append (TPR sensitivity, 0)
FPR 1 Sensitivity=append (FPR 1 Sensitivity, 0)
plot(FPR 1 Sensitivity, TPR sensitivity, type="b")
```



knnp2=prediction((as.numeric(fit)-1), testy) #预测值和真实值knnperf2=performance(knnp2, "tpr", "fpr")
plot(knnperf2, colorize=TRUE, lwd=4)



```
#AUC:0.960
performance(knnp2, "auc")@y.values[[1]]
```

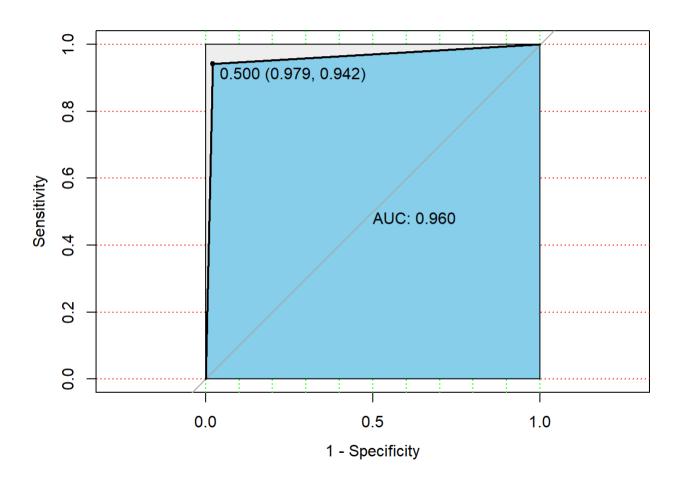
```
## [1] 0.9602355
```

```
modelknnroc2=roc(testy,(as.numeric(fit)-1)) #真实值和预测值
```

```
## Setting levels: control = 0, case = 1
```

## Setting direction: controls < cases

```
plot(modelknnroc2, print.auc=TRUE, auc.polygon=TRUE, legacy.axes=TRUE, grid=c(0.1, 0.2), grid.col=c("green", "red"), max.auc.polygon=TRUE, auc.polygon.col="skyblue", print.thres=TRUE)
```



```
## [1] 0.04846939 0.05867347 0.03316327 0.03571429 0.03061224 0.02551020

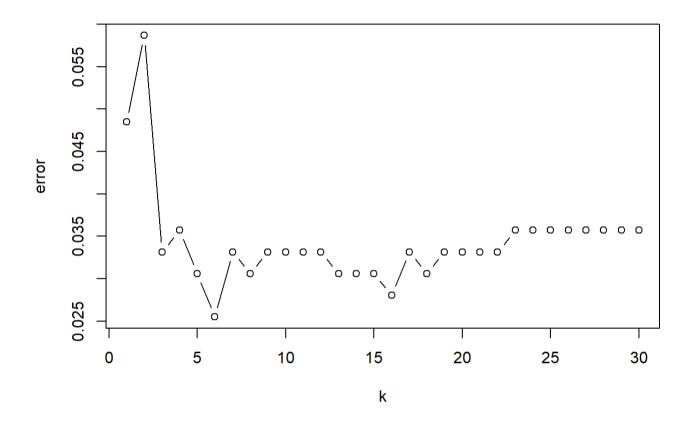
## [7] 0.03316327 0.03061224 0.03316327 0.03316327 0.03316327 0.03316327

## [13] 0.03061224 0.03061224 0.03061224 0.02806122 0.03316327 0.03061224

## [19] 0.03316327 0.03316327 0.03316327 0.03316327 0.03571429 0.03571429

## [25] 0.03571429 0.03571429 0.03571429 0.03571429 0.03571429
```

```
plot(error, type="b", xlab="k")
```



```
#the best tuned K-value is K=6

#取k=6进行预测

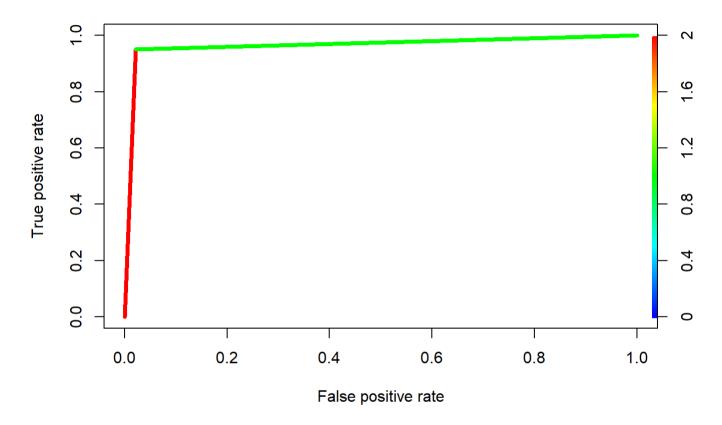
predict1=knn(trainx, testx, cl=trainy, k=6, prob=T)
knntab1=table(testy, predict1)
knntab1 #混淆矩阵
```

```
## predict1
## testy 0 1
## 0 184 4
## 1 5 98
```

```
1-sum(diag(prop.table(knntabl))) #计算误判率
```

```
## [1] 0.03092784
```

```
knnpl=prediction((as.numeric(predict1)-1),testy) #预测值和真实值
knnperfl=performance(knnpl,"tpr","fpr")
plot(knnperfl,colorize=TRUE,lwd=4)
```



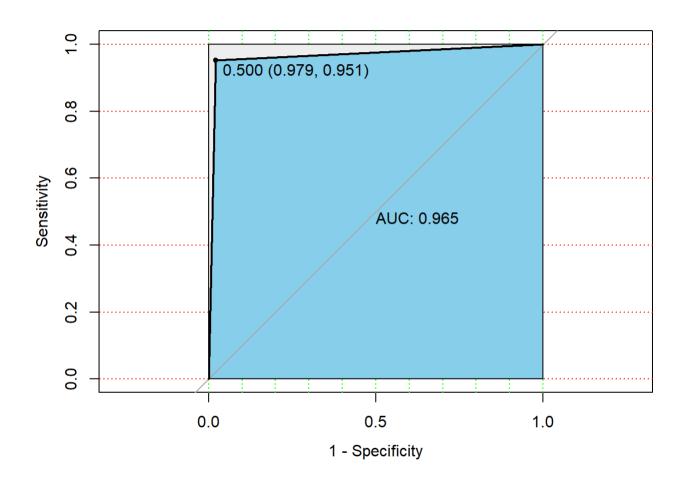
```
#AUC:0.965
performance(knnp1, "auc")@y.values[[1]]
```

```
## [1] 0.9650899
```

modelknnrocl=roc(testy, (as.numeric(predict1)-1)) #真实值和预测值

```
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases</pre>
```

```
plot(modelknnroc1, print.auc=TRUE, auc.polygon=TRUE, legacy.axes=TRUE, grid=c(0.1, 0.2),
    grid.col=c("green", "red"), max.auc.polygon=TRUE,
    auc.polygon.col="skyblue", print.thres=TRUE)
```



```
#(3)
# MODEL
                      AUC
#glm full model
                      0.943
#glm smaller model
                      0.953
#LDA full model
                      0.941
#LDA smaller model
                      0.936
#QDA full model
                      0.951
#KNN rectangular k=6
                      0.965 ***√
#KNN Gaussian h=2 k=9
                      0.960 **
```