# R Code: Multinomial logit model

Thyroid <- read.csv("C:/MA 299/R/Thyroid\_323.csv")

library(nnet)

library(MASS)

model1 <- multinom(Y ~ X17,data = Thyroid)

summary(model1)

#Test the significance (z stat)

z <- summary(model1)$coefficients/summary(model1)$standard.errors

z

# p-value

p <- (1 - pnorm(abs(z), 0, 1)) \* 2

p

# Accuracy

table1 <- data.frame(predict=predict(model1, Thyroid[1:3772,], type = "class"));

table1$predictn <- as.factor(table1$predict)

table1$aclass = as.factor(Thyroid$Y)

con1<-table(table1$predictn,table1$aclass)

con1

model2 <- multinom(Y ~ X1+X17+X18+X19+X20+X21,data = Thyroid)

summary(model2)

#Test the significance (z stat)

z2 <- summary(model2)$coefficients/summary(model2)$standard.errors

z2

# p-value

p2 <- (1 - pnorm(abs(z2), 0, 1)) \* 2

p2

#Accuracy

table2 <- data.frame(predict=predict(model2, Thyroid[1:3772,], type = "class"));

table2$predictn <- as.factor(table2$predict)

table2$aclass = as.factor(Thyroid$Y)

con2<-table(table2$predictn,table2$aclass)

con2

model3 <- multinom(Y ~ X1+factor(X2)+factor(X3)+factor(X4)+

factor(X5)+factor(X6)+factor(X7)+

factor(X8)+factor(X9)+factor(X10)+

factor(X11)+factor(X12)+factor(X13)+

factor(X14)+factor(X15)+factor(X16)+

X17+X18+X19+X20+X21,data = Thyroid)

summary(model3)

model4 <- stepAIC(model3, direction="backward")

step$anova # display results

summary(model4) # show results

#Test the significance (z stat)

z4 <- summary(model4)$coefficients/summary(model4)$standard.errors

z4

# p-value

p4 <- (1 - pnorm(abs(z4), 0, 1)) \* 2

p4

table4 <- data.frame(predict=predict(model4, Thyroid[1:3772,], type = "class"));

table4$predictn <- as.factor(table4$predict)

table4$aclass = as.factor(Thyroid$Y)

con4<-table(table4$predictn,table4$aclass)

con4

#k-fold CV for multinomial logit model

#multinomreg.cv(y, x, folds = NULL, nfolds = 10, stratified = TRUE,

#seed = FALSE, pred.ret = FALSE)

install.packages("Rfast2")

install.packages("Rcpp")

library(Rcpp)

library(Rfast2)

Thyroid$Y = as.factor(Thyroid$Y)

x1 <- as.matrix(Thyroid$X17)

model1.cv <- multinomreg.cv(Thyroid$Y, x1, nfolds = 3)

model1.cv

x2 <- as.matrix(Thyroid$X1,Thyroid$X17,Thyroid$X18,Thyroid$X19,

Thyroid$X20,Thyroid$X21)

model2.cv <- multinomreg.cv(Thyroid$Y, x2, nfolds = 3)

model2.cv

Thyroid$X2 = as.factor(Thyroid$X2)

Thyroid$X3 = as.factor(Thyroid$X3)

Thyroid$X8 = as.factor(Thyroid$X8)

Thyroid$X11 = as.factor(Thyroid$X11)

x4 <- as.matrix(Thyroid$X2,Thyroid$X3,Thyroid$X8,Thyroid$X11,

Thyroid$X17,Thyroid$X18,Thyroid$X21)

model4.cv <- multinomreg.cv(Thyroid$Y, x4, nfolds = 3)

model4.cv

##====================================================

##Classification Tree

library(rpart)

# read data

Thyroid <- read.csv("C:/MA 299/R/Thyroid\_323.csv")

# grow tree (default minsplit = 20 and xval = 10 fold cross validation)

fit <- rpart(Y ~ X1+factor(X2)+factor(X3)+factor(X4)+

factor(X5)+factor(X6)+factor(X7)+

factor(X8)+factor(X9)+factor(X10)+

factor(X11)+factor(X12)+factor(X13)+

factor(X14)+factor(X15)+factor(X16)+

X17+X18+X19+X20+X21,

method="class", data=Thyroid, control=rpart.control(minsplit = 1, xval = 3))

# show result

printcp(fit) # display the results

plotcp(fit) # visualize cross-validation results

summary(fit) # detailed summary of splits

# plot tree

plot(fit, uniform=TRUE,

main="Classification Tree for mower")

text(fit, use.n=TRUE, all=TRUE, cex=.8)

# create a postscript plot of tree

# You need to install postscript viewer.

# Go to http://download.cnet.com/Postscript-Viewer/3000-2094\_4-10845650.html.

post(fit, file = "c:/MA 299/R/Thyroid\_323.ps",

title = "Classification Tree for Thyroid")

## Prune Tree

# prune the tree

pfit<- prune(fit, cp= fit$cptable[which.min(fit$cptable[,"xerror"]),"CP"])

# show result

printcp(pfit) # display the results

# plot the pruned tree

plot(pfit, uniform=TRUE,

main="Pruned Classification Tree for Mower")

text(pfit, use.n=TRUE, all=TRUE, cex=.8)

# create a postscript plot of tree

post(pfit, file = "c:/MA 299/R/pruneThyroid\_323.ps",

title = "Pruned Classification Tree for Thyroid")