> mushroom <- read.csv(file.choose(),header = TRUE)

> str(mushroom)

> mushroom <- mutate\_if(mushroom,is.character,as.factor)

> table(mushroom[,1])

> table(mushroom[,2])

> table(mushroom[,3])

> table(mushroom[,17]) #only p-cases!

> mushroom <- mushroom[,-17] # delete colume veil\_type

> table(mushroom$type,mushroom$odor)

> # data splicing

> set.seed(12345)

> s <- sample(1:nrow(mushroom), size = ceiling(0.80 \* nrow(mushroom)), replace = FALSE)

> head(s)

> #training set

> mushroom\_train <- mushroom[s,]

> #Test set

> mushroom\_test <- mushroom[-s,]

> library(party)

> # building the classification tree with ctree()

> partyTree <- ctree(type~.,data=mushroom\_train)

> testPred<- predict(partyTree,newdata=mushroom\_test)

> T<-table(actual=mushroom\_test$type,predicted=testPred)

> T

> sum(diag(T)/sum(T))

> partyTree