Chapter 03: Toward NaiveBayes: Multiclass Classifier

Multivariate (MV) Probability

In a univariate scenario where Y and X are some vector, joint and conditional probabilities may be written as
P(x,y)=P(x|y)P(y) where P(x,y), P(x|y) and p(y) are the Joint, conditional and the marginal probabilities.
Note that a univaritate solution may not be applicable to model probability for a classification task most of the time because there is always more than one predictor.
Mostly, we want to determine P(class|data) and data is almost always multivariate (MV) not univariate.
P(class|data)P(data)=P(class,data) and P(data,class)=P(data|class)P(class)
Since P(c,d)=P(d,c), P(class|data)P(data)= P(data|class)P(class)
or P(class|data)= P(data|class)P(class)/P(data)

Now for a Bayesian Classifier, given a new observation, we compute the class probabilities conditioned on data, we assign the class with the highest probability. Thus, exact value of the posterior P(class|data) is not necessary, all we need is the ratio. We can avoid the cost of computing P(data) as it is the same for all the classes.

P(class|data)= P(data|class)P(class)

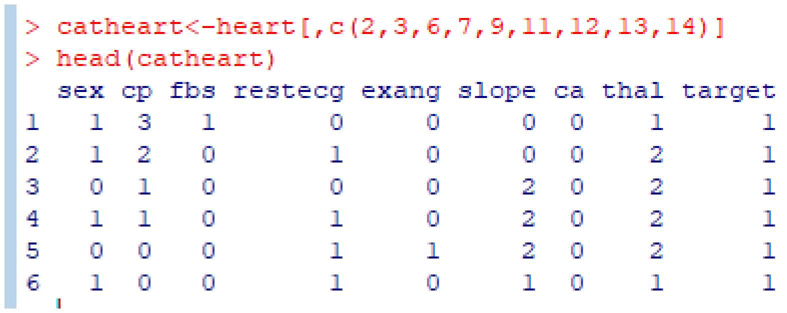
When data is conditionally independent, and there are n predictors,
we can write the first term ***P(data|class)*** above as a product,

P(data|class)=P(x_1|class)P(x_2|class)..P(x_n|class)

NaïveBayes makes this assumption that the predictors are conditionally independent.

Let us say there are two classes c_1 and c_2 and three predictors x_1,x_2,x_3, then
$P(c_1|x_1,x_2,x_3)=P(x_1|c_1)P(x_2|c_1)P(x_3|c_1)P(c_1)$ for class C_1
$P(c_2|x_1,x_2,x_3)=P(x_1|c_2)P(x_2|c_2)P(x_3|c_2)P(c_2)$ for class C_2

We can compute the numerator and assign the class with the higher value. $P(c_1)$ and $P(x|c_2)$ are easily calculated.

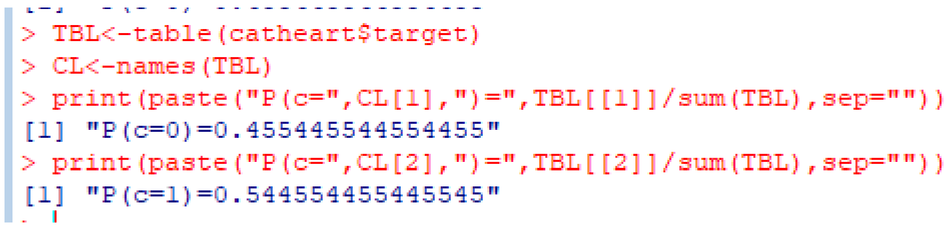


```
> catheart<-heart[,c(2,3,6,7,9,11,12,13,14)]
> head(catheart)
  sex cp fbs restecg exang slope ca thal target
1   1  3   1       0     0     0  0    1      1
2   1  2   0       1     0     0  0    2      1
3   0  1   0       0     0     2  0    2      1
4   1  1   0       1     0     2  0    2      1
5   0  0   0       1     1     2  0    2      1
6   1  0   0       1     0     1  0    1      1
```

heart<-read.csv('C:/Users/rkannan/rk/data/heart.csv',head=T,sep=',', stringsAsFactors=F)
catheart<-heart[,c(2,3,6,7,9,11,12,13,14)]

$P(c_1)$=proportion of c_1=Number of occurrences of C_1/Total Occurrences in the dataset

```
        TBL<-table(catheart$target)
CL<-names(TBL)
print(paste("P(c=",CL[1],")=",TBL[[1]]/sum(TBL),sep=""))
print(paste("P(c=",CL[2],")=",TBL[[2]]/sum(TBL),sep=""))
```



```
> TBL<-table(catheart$target)
> CL<-names(TBL)
> print(paste("P(c=",CL[1],")=",TBL[[1]]/sum(TBL),sep=""))
[1] "P(c=0)=0.455445544554455"
> print(paste("P(c=",CL[2],")=",TBL[[2]]/sum(TBL),sep=""))
[1] "P(c=1)=0.544554455445545"
```

These are the prior class probabilities.

Let us write a function to calculate,

```
        nb_likelihood<-function(df,label,class,feature,val)
        {nrow(df[df[[feature]]==val&df[[label]]==class,])/nrow(df[df[[label]]==class,])}
```

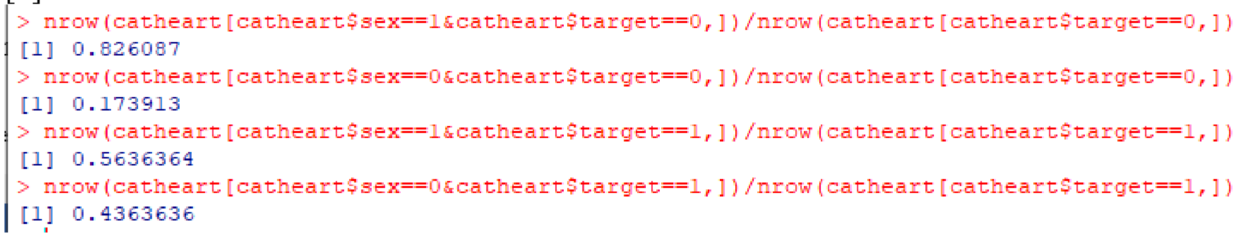
Here, df[df[[feature]]==val&df[[label]]==class,] subsets the df by the rows that satisfy the specified condition. nrow() returns the number of rows. So nb_likelihood function returns the proportion of the records for a specified class.

```
        tstidx<-sample(1:nrow(catheart),0.3*nrow(catheart),replace=F)
        trcatheart<-heart[-tstidx,]
        nb_likelihood(trcatheart,'target',0,'cp',2)
[1] 0.1318681
> nb_likelihood(trcatheart,'target',1,'cp',2)
[1] 0.4380165
```

If we were to classify using this single feature cp, when cp==2, that instance belongs to class 1, because the probability is higher

```
> nb_likelihood(trcatheart,'target',0,'cp',0)
[1] 0.7582418
> nb_likelihood(trcatheart,'target',1,'cp',0)
[1] 0.214876
> nb_likelihood(trcatheart,'target',0,'cp',3)
[1] 0.05494505
> nb_likelihood(trcatheart,'target',1,'cp',3)
[1] 0.107438
> nb_likelihood(trcatheart,'target',0,'cp',1)
[1] 0.05494505
> nb_likelihood(trcatheart,'target',1,'cp',1)
[1] 0.2396694
nrow(catheart[catheart$sex==1&catheart$target==0,])/nrow(catheart[catheart$target==0,])
[1] 0.826087
nrow(catheart[catheart$sex==0&catheart$target==0,])/nrow(catheart[catheart$target==0,])
[1] 0.173913
nrow(catheart[catheart$sex==1&catheart$target==1,])/nrow(catheart[catheart$target==1,])
[1] 0.5636364
nrow(catheart[catheart$sex==0&catheart$target==1,])/nrow(catheart[catheart$target==1,])
```

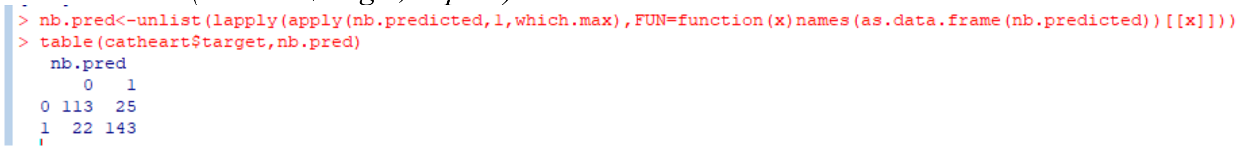
[1] 0.4363636



```
> nrow(catheart[catheart$sex==1&catheart$target==0,])/nrow(catheart[catheart$target==0,])
[1] 0.826087
> nrow(catheart[catheart$sex==0&catheart$target==0,])/nrow(catheart[catheart$target==0,])
[1] 0.173913
> nrow(catheart[catheart$sex==1&catheart$target==1,])/nrow(catheart[catheart$target==1,])
[1] 0.5636364
> nrow(catheart[catheart$sex==0&catheart$target==1,])/nrow(catheart[catheart$target==1,])
[1] 0.4363636
```

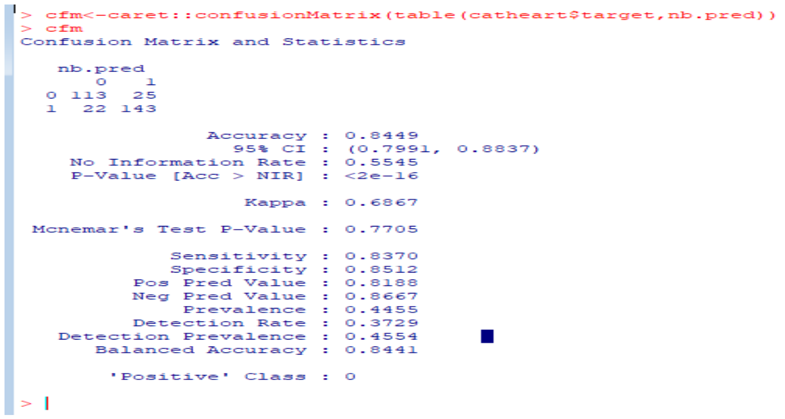
nrow(trcatheart[trcatheart$sex==1&trcatheart$target==0,])/nrow(trcatheart[trcatheart$target==0,])
nrow(trcatheart[trcatheart$sex==0&trcatheart$target==0,])/nrow(trcatheart[trcatheart$target==0,])
nrow(trcatheart[trcatheart$sex==1&trcatheart$target==1,])/nrow(trcatheart[trcatheart$target==1,])
nrow(trcatheart[trcatheart$sex==0&trcatheart$target==1,])/nrow(trcatheart[trcatheart$target==1,])

```
table(catheart[catheart$sex&catheart$target==0,c('sex','target')])/
dim(catheart[catheart$target==0,c('sex','target')])[1]
library(e1071)
nbmodel<-naiveBayes(target~.,data=catheart)
nb.predicted<-predict(nbmodel,catheart[,-which(names(catheart)=='target')],type='raw')
nb.pred<-unlist(lapply(apply(nb.predicted,1,which.max),
                FUN=function(x)names(as.data.frame(nb.predicted))[[x]]))
> table(catheart$target,nb.pred)
```



```
> nb.pred<-unlist(lapply(apply(nb.predicted,1,which.max),FUN=function(x)names(as.data.frame(nb.predicted))[[x]]))
> table(catheart$target,nb.pred)
   nb.pred
      0   1
  0 113  25
  1  22 143
```

cfm<-caret::confusionMatrix(table(catheart$target,nb.pred))
cfm

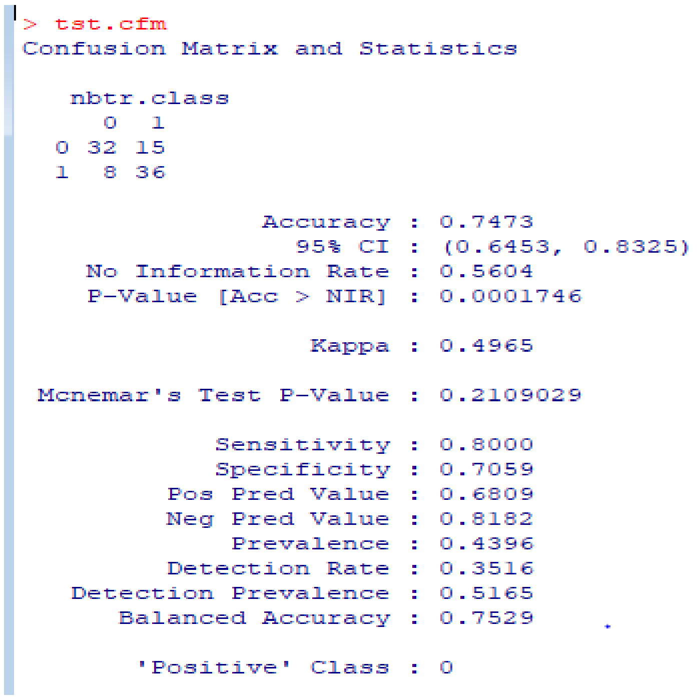


```
> cfm<-caret::confusionMatrix(table(catheart$target,nb.pred))
> cfm
Confusion Matrix and Statistics

   nb.pred
      0   1
  0 113  25
  1  22 143

               Accuracy : 0.8449
                 95% CI : (0.7991, 0.8837)
    No Information Rate : 0.5545
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.6867

 Mcnemar's Test P-Value : 0.7705

            Sensitivity : 0.8370
            Specificity : 0.8512
         Pos Pred Value : 0.8188
         Neg Pred Value : 0.8667
             Prevalence : 0.4455
         Detection Rate : 0.3729
   Detection Prevalence : 0.4554
      Balanced Accuracy : 0.8441

       'Positive' Class : 0

> 
```

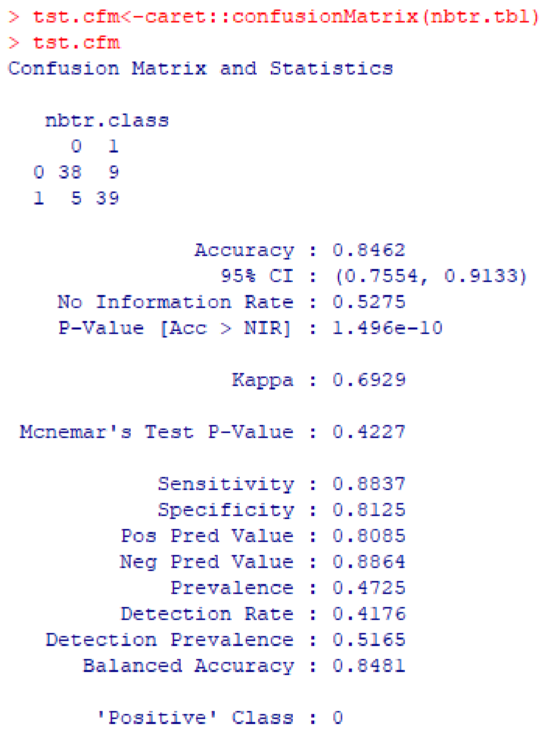
Now let us split the data into training/test sets and

```
set.seed(43)
trdidx<-sample(1:nrow(heart.df),0.7*nrow(heart.df),replace=F)
trheart.df<-heart.df[trdidx,]
tstheart.df<-heart.df[-trdidx,]
nbtr.model<-naiveBayes(target~.,data=trheart.df)
nbtr.pred<-predict(nbtr.model,tstheart.df[,-c(6)],type='raw')
nbtr.class<-unlist(apply(round(nbtr.pred),1,which.max))-1
nbtr.tbl<-table(tstheart.df[[6]], nbtr.class)
stst.cfm<-caret::confusionMatrix(nbtr.tbl)
tr.cfm
```

nbtr.pred<-predict(nbtr.model,tstcatheart[,-c(9)],type='raw')
nbtr.class<-unlist(apply(round(nbtr.pred),1,which.max))-1
nbtr.tbl<-table(tstcatheart[[9]], nbtr.class)
tst.cfm<-caret::confusionMatrix(nbtr.tbl)
tst.cfm



```
> tst.cfm
Confusion Matrix and Statistics

   nbtr.class
     0  1
  0 32 15
  1  8 36

               Accuracy : 0.7473
                 95% CI : (0.6453, 0.8325)
    No Information Rate : 0.5604
    P-Value [Acc > NIR] : 0.0001746

                  Kappa : 0.4965

 Mcnemar's Test P-Value : 0.2109029

            Sensitivity : 0.8000
            Specificity : 0.7059
         Pos Pred Value : 0.6809
         Neg Pred Value : 0.8182
             Prevalence : 0.4396
         Detection Rate : 0.3516
   Detection Prevalence : 0.5165
      Balanced Accuracy : 0.7529

       'Positive' Class : 0
```



```
> tst.cfm<-caret::confusionMatrix(nbtr.tbl)
> tst.cfm
Confusion Matrix and Statistics

   nbtr.class
     0  1
  0 38  9
  1  5 39

               Accuracy : 0.8462
                 95% CI : (0.7554, 0.9133)
    No Information Rate : 0.5275
    P-Value [Acc > NIR] : 1.496e-10

                  Kappa : 0.6929

 Mcnemar's Test P-Value : 0.4227

            Sensitivity : 0.8837
            Specificity : 0.8125
         Pos Pred Value : 0.8085
         Neg Pred Value : 0.8864
             Prevalence : 0.4725
         Detection Rate : 0.4176
   Detection Prevalence : 0.5165
      Balanced Accuracy : 0.8481

       'Positive' Class : 0
```

catheart<-heart[,c(2,3,6,7,9,11,12,13,14)]
head(catheart)
table(catheart$target)
sum(table(catheart$target))
set.seed(43)
trdidx<-sample(1:nrow(catheart),
*0.7*nrow(catheart),replace=F)*
trcatheart<-catheart[trdidx,]
tstcatheart<-catheart[-trdidx,]
nbtr.model<-naiveBayes(target~.,data=trcatheart)
nblearning.pred<-predict(nbtr.model,trcatheart[,-c(9)],type="raw")
nblearning.class<-unlist(apply(round(
nblearning.pred),1,which.max))-1
nblearning.tbl<-table(trcatheart[,c(9)],nblearning.class)
tr.cfm<-caret::confusionMatrix(nblearning.tbl)

In R,iterative computations can be vectorized as follows
------------------formatt correcting--- vectorized R solution--------------------
do.call('rbind',
lapply(c("sex","cp","fbs","restecg","exang","slope","ca","thal"),
FUN=function(d,df=catheart,cl='target') {

```
classvalues=unique(df[[cl]])
do.call('rbind',
lapply(classvalues,FUN=function(clv,feature=d,dataset=df,target=cl) {
featurevalues=unique(dataset[[feature]])
do.call('rbind',
lapply(featurevalues,FUN=function(fv,cvalue=clv,f=feature,dset=dataset,cl=target) {
c(clvar=cl,clval=clv,predictor=f,predval=fv,class_cond_prob=
nb_likelihood(df=dset,label=cl,class=cvalue,feature=f,val=fv))
} )
)#do.call
})
)#dp.call
})#lapply
)#do.call
```

[TODO] We still have to validate our implementation against standard implementation by evaluating the class probabilities for a few test data observations.