

## Classification using knn algorithm in R (Predicting cancer results)

```
> getwd()
[1] "/home/brajesh"
> setwd("/home/brajesh/machine-learning/class-knn-r")
> getwd()
[1] "/home/brajesh/machine-learning/class-knn-r"
> wbcd<-read.csv("wisc_bc_data.csv",stringsAsFactors = FALSE)
> str(wbcd)
'data.frame':   569 obs. of  32 variables:
 $ id          : int  87139402 8910251 905520 868871 9012568 906539 925291 87880
862989 89827 ...
 $ diagnosis    : chr   "B" "B" "B" "B" ...
 $ radius_mean  : num   12.3 10.6 11 11.3 15.2 ...
 $ texture_mean : num   12.4 18.9 16.8 13.4 13.2 ...
 $ perimeter_mean : num   78.8 69.3 70.9 73 97.7 ...
 $ area_mean    : num   464 346 373 385 712 ...
 $ smoothness_mean : num   0.1028 0.0969 0.1077 0.1164 0.0796 ...
> wbcd
      id diagnosis radius_mean texture_mean
1  87139402      B      12.320      12.39
2   8910251      B      10.600      18.95
3   905520     B      11.040      16.83
4   868871      B      11.280      13.39
5   9012568      B      15.190      13.21
6   906539      B      11.570      19.04
7   925291      B      11.510      23.93
8    87880      M      13.810      23.75
9   862989      B      10.490      19.29
10  89827      B      11.060      14.96
11  91485      M      20.590      21.24
> wbcd<-wbcd[,-1]
> wbcd
      diagnosis radius_mean texture_mean perimeter_mean
1           B      12.320      12.39      78.85
2           B      10.600      18.95      69.28
3           B      11.040      16.83      70.92
4           B      11.280      13.39      73.00
5           B      15.190      13.21      97.65
6           B      11.570      19.04      74.20
7           B      11.510      23.93      74.52
8           M      13.810      23.75      91.56
9           B      10.490      19.29      67.41
10          B      11.060      14.96      71.49
11          M      20.590      21.24     137.80
> str(wbcd)
'data.frame':   569 obs. of  31 variables:
 $ diagnosis    : chr   "B" "B" "B" "B" ...
 $ radius_mean  : num   12.3 10.6 11 11.3 15.2 ...
 $ texture_mean : num   12.4 18.9 16.8 13.4 13.2 ...
 $ perimeter_mean : num   78.8 69.3 70.9 73 97.7 ...
 $ area_mean    : num   464 346 373 385 712 ...
 $ smoothness_mean : num   0.1028 0.0969 0.1077 0.1164 0.0796 ...
> table(wbcd$diagnosis)

  B    M
357 212
> bm<-table(wbcd$diagnosis)
> prop.table(bm)

      B          M
0.6274165 0.3725835
> prop.table(bm)*100

      B          M
62.74165 37.25835
> wbcd$diagnosis<-factor(wbcd$diagnosis, levels = c("B","M"), labels =
c("Benign","Malignant"))
```

```
> round(prop.table(table(wbcd$diagnosis))*100, digits = 1)

      Benign Malignant
      62.7      37.3
> summary(wbcd[c("radius_mean", "area_mean", "smoothness_mean")])
      radius_mean      area_mean      smoothness_mean
Min.   : 6.981   Min.   : 143.5   Min.   :0.05263
1st Qu.:11.700   1st Qu.: 420.3   1st Qu.:0.08637
Median :13.370   Median : 551.1   Median :0.09587
Mean   :14.127   Mean   : 654.9   Mean   :0.09636
3rd Qu.:15.780   3rd Qu.: 782.7   3rd Qu.:0.10530
Max.   :28.110   Max.   :2501.0   Max.   :0.16340
> normalize<-function(x){return((x-min(x))/(max(x)-min(x)))}
> wbcd_n<-as.data.frame(lapply(wbcd[2:31], normalize))
> wbcd_train<-wbcd_n[1:469,]
> wbcd_test<-wbcd_n[470:569,]
> wbcd_train_labels<-wbcd[1:469,1]
> wbcd_test_labels<-wbcd[470:569,1]
> install.packages("class")
Installing package into '/home/brajesh/R/x86_64-pc-linux-gnu-library/3.4'
> library(class)
> wbcd_test_pred<-knn(train = wbcd_train, test = wbcd_test, cl=wbcd_train_labels, k=21)
> install.packages("gmodels")
Installing package into '/home/brajesh/R/x86_64-pc-linux-gnu-library/3.4'
> library(gmodels)
> CrossTable(x=wbcd_test_labels, y=wbcd_test_pred, prop.chisq=FALSE)
```

#### Cell Contents

		N
N / Row Total		
N / Col Total		
N / Table Total		

Total Observations in Table: 100

wbcd_test_labels	wbcd_test_pred		Row Total
	Benign	Malignant	
Benign	61	0	61
	1.000	0.000	0.610
	0.968	0.000	
	0.610	0.000	
Malignant	2	37	39
	0.051	0.949	0.390
	0.032	1.000	
	0.020	0.370	
Column Total	63	37	100
	0.630	0.370	

```

> wbcd_z<-as.data.frame(scale(wbcd[-1]))
> wbcd_train<-wbcd_z[1:469,]
> wbcd_test<-wbcd_z[470:569,]
> wbcd_test_pred<-knn(train = wbcd_train, test = wbcd_test, cl=wbcd_train_labels, k=21)
> CrossTable(x=wbcd_test_labels, y=wbcd_test_pred, prop.chisq = FALSE)

```

#### Cell Contents

		N
N / Row Total		
N / Col Total		
N / Table Total		

Total Observations in Table: 100

wbcd_test_labels	wbcd_test_pred		Row Total
	Benign	Malignant	
Benign	61	0	61
	1.000	0.000	0.610
	0.924	0.000	
	0.610	0.000	
Malignant	5	34	39
	0.128	0.872	0.390
	0.076	1.000	
	0.050	0.340	
Column Total	66	34	100
	0.660	0.340	