

# KNN on Oncogenic Cells

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## Description

This is solution to “R - Programming: K-Nearest Neighbour Assignment” on Topcoder.

## Problem Statement

Routine breast cancer screening allows the disease to be diagnosed and treated prior to it causing noticeable symptoms. The process of early detection involves examining the breast tissue for abnormal lumps or masses. If a lump is found, a fine-needle aspiration biopsy is performed, which uses a hollow needle to extract a small sample of cells from the mass. A clinician then examines the cells under a microscope to determine whether the mass is likely to be malignant or benign.

If machine learning could automate the identification of cancerous cells, it would provide considerable benefit to the health system. Automated processes are likely to improve the efficiency of the detection process, allowing physicians to spend less time diagnosing and more time treating the disease. An automated screening system might also provide greater detection accuracy by removing the inherently subjective human component from the process.

Apply the k-NN algorithm to perform diagnosis Benign or Malignant

## The Dataset

The dataset for the above problem was imported from [https://github.com/stedy/Machine-Learning-with-R-datasets/blob/master/wisc\\_bc\\_data.csv](https://github.com/stedy/Machine-Learning-with-R-datasets/blob/master/wisc_bc_data.csv)

s

```
data = read.csv("wisc_bc_data.csv")
str(data)
```

```
## 'data.frame':   569 obs. of  32 variables:
##  $ id                : int  842302 842517 84300903 84348301 84358402 843786 844359 84458202 844...
##  $ diagnosis         : Factor w/ 2 levels "B","M": 2 2 2 2 2 2 2 2 2 ...
##  $ radius_mean       : num  18 20.6 19.7 11.4 20.3 ...
##  $ texture_mean      : num  10.4 17.8 21.2 20.4 14.3 ...
##  $ perimeter_mean    : num  122.8 132.9 130 77.6 135.1 ...
##  $ area_mean         : num  1001 1326 1203 386 1297 ...
##  $ smoothness_mean   : num  0.1184 0.0847 0.1096 0.1425 0.1003 ...
##  $ compactness_mean  : num  0.2776 0.0786 0.1599 0.2839 0.1328 ...
##  $ concavity_mean    : num  0.3001 0.0869 0.1974 0.2414 0.198 ...
##  $ concave.points_mean : num  0.1471 0.0702 0.1279 0.1052 0.1043 ...
##  $ symmetry_mean     : num  0.242 0.181 0.207 0.26 0.181 ...
##  $ fractal_dimension_mean : num  0.0787 0.0567 0.06 0.0974 0.0588 ...
##  $ radius_se         : num  1.095 0.543 0.746 0.496 0.757 ...
##  $ texture_se        : num  0.905 0.734 0.787 1.156 0.781 ...
##  $ perimeter_se      : num  8.59 3.4 4.58 3.44 5.44 ...
##  $ area_se          : num  153.4 74.1 94 27.2 94.4 ...
```

```
## $ smoothness_se      : num  0.0064 0.00522 0.00615 0.00911 0.01149 ...
## $ compactness_se     : num  0.049 0.0131 0.0401 0.0746 0.0246 ...
## $ concavity_se       : num  0.0537 0.0186 0.0383 0.0566 0.0569 ...
## $ concave.points_se  : num  0.0159 0.0134 0.0206 0.0187 0.0188 ...
## $ symmetry_se        : num  0.03 0.0139 0.0225 0.0596 0.0176 ...
## $ fractal_dimension_se : num  0.00619 0.00353 0.00457 0.00921 0.00511 ...
## $ radius_worst       : num  25.4 25 23.6 14.9 22.5 ...
## $ texture_worst      : num  17.3 23.4 25.5 26.5 16.7 ...
## $ perimeter_worst    : num  184.6 158.8 152.5 98.9 152.2 ...
## $ area_worst         : num  2019 1956 1709 568 1575 ...
## $ smoothness_worst   : num  0.162 0.124 0.144 0.21 0.137 ...
## $ compactness_worst  : num  0.666 0.187 0.424 0.866 0.205 ...
## $ concavity_worst    : num  0.712 0.242 0.45 0.687 0.4 ...
## $ concave.points_worst : num  0.265 0.186 0.243 0.258 0.163 ...
## $ symmetry_worst     : num  0.46 0.275 0.361 0.664 0.236 ...
## $ fractal_dimension_worst: num  0.1189 0.089 0.0876 0.173 0.0768 ...

data = data[-1]    #Removal of patient indices
```

## Including Libraries

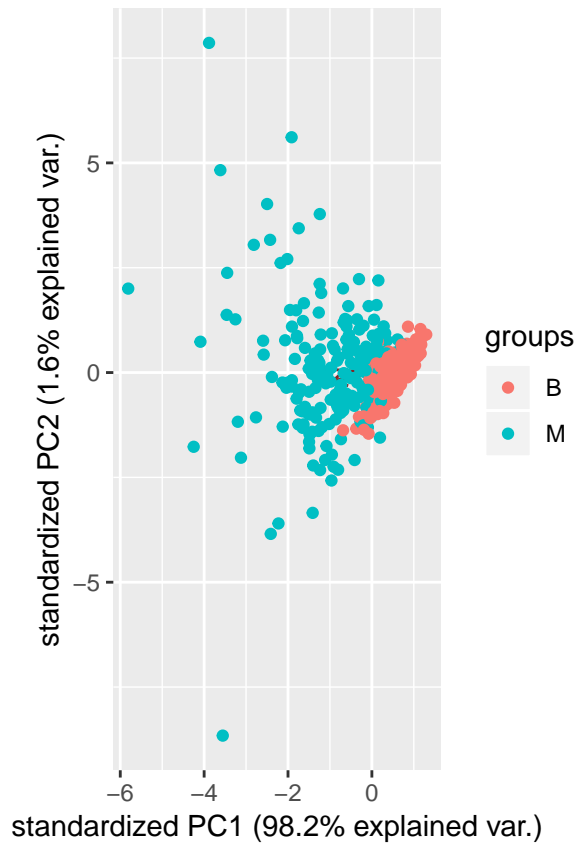
The following libraries were needed to be installed and imported for the assignment.

```
library(pca3d)
library(class)
library(gmodels)
library(ggbiplot)
```

```
## Loading required package: ggplot2
## Loading required package: plyr
## Loading required package: scales
## Loading required package: grid
```

## Principal Component Analysis

```
#pca3d(princomp(data[,c(2:31)]), group = data$diagnosis)
ggbiplot(princomp(data[,c(2:31)]), groups = data$diagnosis, varname.size = 0)
```



The graph above shows the existence of spacial separation in the euclidian space between the two tumour catgrories.

## Pre-Processing : Normalization

```
normalize <- function(x) {
  return ((x - min(x)) / (max(x) - min(x)))
}

data_n = as.data.frame(lapply(data[2:31], normalize))
summary(data_n)
```

```
##   radius_mean    texture_mean  perimeter_mean    area_mean
## Min.   :0.0000   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
## 1st Qu.:0.2233   1st Qu.:0.2185   1st Qu.:0.2168   1st Qu.:0.1174
## Median :0.3024   Median :0.3088   Median :0.2933   Median :0.1729
## Mean   :0.3382   Mean   :0.3240   Mean   :0.3329   Mean   :0.2169
## 3rd Qu.:0.4164   3rd Qu.:0.4089   3rd Qu.:0.4168   3rd Qu.:0.2711
## Max.   :1.0000   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
## smoothness_mean compactness_mean concavity_mean  concave.points_mean
## Min.   :0.0000   Min.   :0.0000   Min.   :0.00000   Min.   :0.0000
## 1st Qu.:0.3046   1st Qu.:0.1397   1st Qu.:0.06926   1st Qu.:0.1009
## Median :0.3904   Median :0.2247   Median :0.14419   Median :0.1665
## Mean   :0.3948   Mean   :0.2606   Mean   :0.20806   Mean   :0.2431
## 3rd Qu.:0.4755   3rd Qu.:0.3405   3rd Qu.:0.30623   3rd Qu.:0.3678
## Max.   :1.0000   Max.   :1.0000   Max.   :1.00000   Max.   :1.0000
```

```

## symmetry_mean fractal_dimension_mean radius_se
## Min. :0.0000 Min. :0.0000 Min. :0.00000
## 1st Qu.:0.2823 1st Qu.:0.1630 1st Qu.:0.04378
## Median :0.3697 Median :0.2439 Median :0.07702
## Mean :0.3796 Mean :0.2704 Mean :0.10635
## 3rd Qu.:0.4530 3rd Qu.:0.3404 3rd Qu.:0.13304
## Max. :1.0000 Max. :1.0000 Max. :1.00000
## texture_se perimeter_se area_se smoothness_se
## Min. :0.0000 Min. :0.00000 Min. :0.00000 Min. :0.0000
## 1st Qu.:0.1047 1st Qu.:0.04000 1st Qu.:0.02064 1st Qu.:0.1175
## Median :0.1653 Median :0.07209 Median :0.03311 Median :0.1586
## Mean :0.1893 Mean :0.09938 Mean :0.06264 Mean :0.1811
## 3rd Qu.:0.2462 3rd Qu.:0.12251 3rd Qu.:0.07170 3rd Qu.:0.2187
## Max. :1.0000 Max. :1.00000 Max. :1.00000 Max. :1.0000
## compactness_se concavity_se concave.points_se symmetry_se
## Min. :0.00000 Min. :0.00000 Min. :0.0000 Min. :0.0000
## 1st Qu.:0.08132 1st Qu.:0.03811 1st Qu.:0.1447 1st Qu.:0.1024
## Median :0.13667 Median :0.06538 Median :0.2070 Median :0.1526
## Mean :0.17444 Mean :0.08054 Mean :0.2235 Mean :0.1781
## 3rd Qu.:0.22680 3rd Qu.:0.10619 3rd Qu.:0.2787 3rd Qu.:0.2195
## Max. :1.00000 Max. :1.00000 Max. :1.0000 Max. :1.0000
## fractal_dimension_se radius_worst texture_worst perimeter_worst
## Min. :0.00000 Min. :0.0000 Min. :0.0000 Min. :0.0000
## 1st Qu.:0.04675 1st Qu.:0.1807 1st Qu.:0.2415 1st Qu.:0.1678
## Median :0.07919 Median :0.2504 Median :0.3569 Median :0.2353
## Mean :0.10019 Mean :0.2967 Mean :0.3640 Mean :0.2831
## 3rd Qu.:0.12656 3rd Qu.:0.3863 3rd Qu.:0.4717 3rd Qu.:0.3735
## Max. :1.00000 Max. :1.0000 Max. :1.0000 Max. :1.0000
## area_worst smoothness_worst compactness_worst concavity_worst
## Min. :0.00000 Min. :0.0000 Min. :0.0000 Min. :0.00000
## 1st Qu.:0.08113 1st Qu.:0.3000 1st Qu.:0.1163 1st Qu.:0.09145
## Median :0.12321 Median :0.3971 Median :0.1791 Median :0.18107
## Mean :0.17091 Mean :0.4041 Mean :0.2202 Mean :0.21740
## 3rd Qu.:0.22090 3rd Qu.:0.4942 3rd Qu.:0.3025 3rd Qu.:0.30583
## Max. :1.00000 Max. :1.0000 Max. :1.0000 Max. :1.00000
## concave.points_worst symmetry_worst fractal_dimension_worst
## Min. :0.0000 Min. :0.0000 Min. :0.0000
## 1st Qu.:0.2231 1st Qu.:0.1851 1st Qu.:0.1077
## Median :0.3434 Median :0.2478 Median :0.1640
## Mean :0.3938 Mean :0.2633 Mean :0.1896
## 3rd Qu.:0.5546 3rd Qu.:0.3182 3rd Qu.:0.2429
## Max. :1.0000 Max. :1.0000 Max. :1.0000

```

## Dividing Training and Test Data

We take `N_sample` rows as test cases and use the rest to train the classifier.

```

N_sample = 100
s_index = sample(1:569, N_sample)
data_Train = data_n[-s_index,]
data_Test = data_n[s_index,]

```

## KNN

```
N_K = 25
data_knn = knn(train = data_Train, test = data_Test, cl = data[s_index, 1], k = N_K)
```

## Accuracy Analysis

The confusion matrix is shown below.

```
CrossTable(x = data[s_index, 1], data_knn)
```

```
##
##
##   Cell Contents
## |-----|
## |                N |
## | Chi-square contribution |
## |      N / Row Total |
## |      N / Col Total |
## |      N / Table Total |
## |-----|
##
##
## Total Observations in Table:  100
##
##
##               | data_knn
## data[s_index, 1] |      B |      M | Row Total |
## -----|-----|-----|-----|
##           B |      62 |       0 |      62 |
##           |    12.555 |    22.320 |      |
##           |     1.000 |     0.000 |    0.620 |
##           |     0.969 |     0.000 |      |
##           |     0.620 |     0.000 |      |
## -----|-----|-----|-----|
##           M |       2 |      36 |      38 |
##           |    20.484 |    36.417 |      |
##           |     0.053 |     0.947 |    0.380 |
##           |     0.031 |     1.000 |      |
##           |     0.020 |     0.360 |      |
## -----|-----|-----|-----|
##   Column Total |      64 |      36 |      100 |
##           |    0.640 |    0.360 |      |
## -----|-----|-----|-----|
##
##
```