Lab 8

#Breast Cancer Project Today we are going to explore some data from the Univeristy of Wisconsin Cancer Center on Breast biosy data.

```
wisc.data <-read.csv("/Users/JoshTran/Desktop/BIMM 143/Week 5/WisconsinCancer.csv", row.n
head(wisc.data)
```

```
         diagnosis radius_mean texture_mean perimeter_mean area_mean
842302           M       17.99        10.38         122.80    1001.0
842517           M       20.57        17.77         132.90    1326.0
84300903         M       19.69        21.25         130.00    1203.0
84348301         M       11.42        20.38          77.58     386.1
84358402         M       20.29        14.34         135.10    1297.0
843786           M       12.45        15.70          82.57     477.1
         smoothness_mean compactness_mean concavity_mean concave.points_mean
842302           0.11840          0.27760         0.3001             0.14710
842517           0.08474          0.07864         0.0869             0.07017
84300903         0.10960          0.15990         0.1974             0.12790
84348301         0.14250          0.28390         0.2414             0.10520
84358402         0.10030          0.13280         0.1980             0.10430
843786           0.12780          0.17000         0.1578             0.08089
         symmetry_mean fractal_dimension_mean radius_se texture_se perimeter_se
842302          0.2419                0.07871    1.0950     0.9053        8.589
842517          0.1812                0.05667    0.5435     0.7339        3.398
84300903        0.2069                0.05999    0.7456     0.7869        4.585
84348301        0.2597                0.09744    0.4956     1.1560        3.445
84358402        0.1809                0.05883    0.7572     0.7813        5.438
843786          0.2087                0.07613    0.3345     0.8902        2.217
         area_se smoothness_se compactness_se concavity_se concave.points_se
842302    153.40      0.006399        0.04904      0.05373           0.01587
842517     74.08      0.005225        0.01308      0.01860           0.01340
84300903   94.03      0.006150        0.04006      0.03832           0.02058
84348301   27.23      0.009110        0.07458      0.05661           0.01867
84358402   94.44      0.011490        0.02461      0.05688           0.01885
843786     27.19      0.007510        0.03345      0.03672           0.01137
         symmetry_se fractal_dimension_se radius_worst texture_worst
842302       0.03003             0.006193        25.38         17.33
842517       0.01389             0.003532        24.99         23.41
84300903     0.02250             0.004571        23.57         25.53
84348301     0.05963             0.009208        14.91         26.50
84358402     0.01756             0.005115        22.54         16.67
843786       0.02165             0.005082        15.47         23.75
         perimeter_worst area_worst smoothness_worst compactness_worst
842302            184.60     2019.0           0.1622            0.6656
842517            158.80     1956.0           0.1238            0.1866
84300903          152.50     1709.0           0.1444            0.4245
84348301           98.87      567.7           0.2098            0.8663
84358402          152.20     1575.0           0.1374            0.2050
```

```
843786          103.40      741.6           0.1791            0.5249
         concavity_worst concave.points_worst symmetry_worst
842302           0.7119               0.2654         0.4601
842517           0.2416               0.1860         0.2750
84300903         0.4504               0.2430         0.3613
84348301         0.6869               0.2575         0.6638
84358402         0.4000               0.1625         0.2364
843786           0.5355               0.1741         0.3985
         fractal_dimension_worst
842302                  0.11890
842517                  0.08902
84300903                0.08758
84348301                0.17300
84358402                0.07678
843786                  0.12440
```

> Q1. How many patients samples are in this dataset?

```
nrow(wisc.data)
```

```
[1] 569
```

There are 569 patients in this data set.

> Q2. How many cancer (M) and non cancer (B) samples are there?

```
table(wisc.data$diagnosis)
```

```

  B   M 
357 212 
```

```
head(wisc.data)
```

```
         diagnosis radius_mean texture_mean perimeter_mean area_mean
842302           M       17.99        10.38         122.80    1001.0
842517           M       20.57        17.77         132.90    1326.0
84300903         M       19.69        21.25         130.00    1203.0
84348301         M       11.42        20.38          77.58     386.1
84358402         M       20.29        14.34         135.10    1297.0
843786           M       12.45        15.70          82.57     477.1
         smoothness_mean compactness_mean concavity_mean concave.points_mean
842302           0.11840          0.27760         0.3001             0.14710
842517           0.08474          0.07864         0.0869             0.07017
84300903         0.10960          0.15990         0.1974             0.12790
84348301         0.14250          0.28390         0.2414             0.10520
84358402         0.10030          0.13280         0.1980             0.10430
843786           0.12780          0.17000         0.1578             0.08089
```

```
         symmetry_mean fractal_dimension_mean radius_se texture_se perimeter_se
842302          0.2419                0.07871    1.0950     0.9053        8.589
842517          0.1812                0.05667    0.5435     0.7339        3.398
84300903        0.2069                0.05999    0.7456     0.7869        4.585
84348301        0.2597                0.09744    0.4956     1.1560        3.445
84358402        0.1809                0.05883    0.7572     0.7813        5.438
843786          0.2087                0.07613    0.3345     0.8902        2.217
         area_se smoothness_se compactness_se concavity_se concave.points_se
842302    153.40      0.006399        0.04904      0.05373           0.01587
842517     74.08      0.005225        0.01308      0.01860           0.01340
84300903   94.03      0.006150        0.04006      0.03832           0.02058
84348301   27.23      0.009110        0.07458      0.05661           0.01867
84358402   94.44      0.011490        0.02461      0.05688           0.01885
843786     27.19      0.007510        0.03345      0.03672           0.01137
         symmetry_se fractal_dimension_se radius_worst texture_worst
842302       0.03003             0.006193        25.38         17.33
842517       0.01389             0.003532        24.99         23.41
84300903     0.02250             0.004571        23.57         25.53
84348301     0.05963             0.009208        14.91         26.50
84358402     0.01756             0.005115        22.54         16.67
843786       0.02165             0.005082        15.47         23.75
         perimeter_worst area_worst smoothness_worst compactness_worst
842302            184.60     2019.0           0.1622            0.6656
842517            158.80     1956.0           0.1238            0.1866
84300903          152.50     1709.0           0.1444            0.4245
84348301           98.87      567.7           0.2098            0.8663
84358402          152.20     1575.0           0.1374            0.2050
843786            103.40      741.6           0.1791            0.5249
         concavity_worst concave.points_worst symmetry_worst
842302            0.7119               0.2654         0.4601
842517            0.2416               0.1860         0.2750
84300903          0.4504               0.2430         0.3613
84348301          0.6869               0.2575         0.6638
84358402          0.4000               0.1625         0.2364
843786            0.5355               0.1741         0.3985
         fractal_dimension_worst
842302                   0.11890
842517                   0.08902
84300903                 0.08758
84348301                 0.17300
84358402                 0.07678
843786                   0.12440
```

```r
diagnosis <- as.factor(wisc.data$diagnosis)
#diagnosis
```

```r
head(diagnosis)
```

```
[1] M M M M M M
Levels: B M
```

Now exclude the diagnosis cloumn from the data

```
wisc.data <- wisc.data[,-1]
```

> Q3. How many “dimensions”,“Variables”, “columns”, are in this dataset?

```
ncol(wisc.data)
```

```
[1] 30
```

#Principal Component Analysis (PCA)

To perform PCA in R we can use `prcomp()` function. it takes as input a numeric dataset and optional `scale = FALSE/TRUE` argument.

We generally always want to set the `scale=TRUE` but lets make sure by checking if the mean and standard deviation values are different across these 30 columns.

```
round(colMeans(wisc.data) )
```

```
            radius_mean            texture_mean          perimeter_mean 
                     14                      19                      92 
              area_mean         smoothness_mean        compactness_mean 
                    655                       0                       0 
         concavity_mean     concave.points_mean           symmetry_mean 
                      0                       0                       0 
 fractal_dimension_mean               radius_se              texture_se 
                      0                       0                       1 
           perimeter_se                 area_se           smoothness_se 
                      3                      40                       0 
         compactness_se            concavity_se       concave.points_se 
                      0                       0                       0 
            symmetry_se    fractal_dimension_se            radius_worst 
                      0                       0                      16 
          texture_worst         perimeter_worst              area_worst 
                     26                     107                     881 
       smoothness_worst       compactness_worst         concavity_worst 
                      0                       0                       0 
   concave.points_worst          symmetry_worst fractal_dimension_worst 
                      0                       0                       0 
```

```
pca <- prcomp(wisc.data, scale = TRUE)
summary(pca)
```

```
Importance of components:
                          PC1    PC2     PC3     PC4     PC5     PC6     PC7
Standard deviation     3.6444 2.3857 1.67867 1.40735 1.28403 1.09880 0.82172
Proportion of Variance 0.4427 0.1897 0.09393 0.06602 0.05496 0.04025 0.02251
Cumulative Proportion  0.4427 0.6324 0.72636 0.79239 0.84734 0.88759 0.91010
                           PC8    PC9    PC10   PC11    PC12    PC13    PC14
Standard deviation     0.69037 0.6457 0.59219 0.5421 0.51104 0.49128 0.39624
Proportion of Variance 0.01589 0.0139 0.01169 0.0098 0.00871 0.00805 0.00523
Cumulative Proportion  0.92598 0.9399 0.95157 0.9614 0.97007 0.97812 0.98335
                          PC15    PC16    PC17    PC18    PC19    PC20   PC21
Standard deviation     0.30681 0.28260 0.24372 0.22939 0.22244 0.17652 0.1731
Proportion of Variance 0.00314 0.00266 0.00198 0.00175 0.00165 0.00104 0.0010
Cumulative Proportion  0.98649 0.98915 0.99113 0.99288 0.99453 0.99557 0.9966
                          PC22    PC23   PC24    PC25    PC26    PC27    PC28
Standard deviation     0.16565 0.15602 0.1344 0.12442 0.09043 0.08307 0.03987
Proportion of Variance 0.00091 0.00081 0.0006 0.00052 0.00027 0.00023 0.00005
Cumulative Proportion  0.99749 0.99830 0.9989 0.99942 0.99969 0.99992 0.99997
                          PC29    PC30
Standard deviation     0.02736 0.01153
Proportion of Variance 0.00002 0.00000
Cumulative Proportion  1.00000 1.00000
```

> Q4. From your results, what proportion of the original variance is captured by the first principal components (PC1)? 0.4427

> Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data? 0.72636

> Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data? PC7

```r
attributes(pca$x)
```

```
$dim
[1] 569  30

$dimnames
$dimnames[[1]]
  [1] "842302"    "842517"    "84300903"  "84348301"  "84358402"  "843786"
  [7] "844359"    "84458202"  "844981"    "84501001"  "845636"    "84610002"
 [13] "846226"    "846381"    "84667401"  "84799002"  "848406"    "84862001"
 [19] "849014"    "8510426"   "8510653"   "8510824"   "8511133"   "851509"
 [25] "852552"    "852631"    "852763"    "852781"    "852973"    "853201"
 [31] "853401"    "853612"    "85382601"  "854002"    "854039"    "854253"
 [37] "854268"    "854941"    "855133"    "855138"    "855167"    "855563"
 [43] "855625"    "856106"    "85638502"  "857010"    "85713702"  "85715"
 [49] "857155"    "857156"    "857343"    "857373"    "857374"    "857392"
 [55] "857438"    "85759902"  "857637"    "857793"    "857810"    "858477"
```

```
 [61] "858970"    "858981"    "858986"    "859196"    "85922302"  "859283"   
 [67] "859464"    "859465"    "859471"    "859487"    "859575"    "859711"   
 [73] "859717"    "859983"    "8610175"   "8610404"   "8610629"   "8610637"  
 [79] "8610862"   "8610908"   "861103"    "8611161"   "8611555"   "8611792"  
 [85] "8612080"   "8612399"   "86135501"  "86135502"  "861597"    "861598"   
 [91] "861648"    "861799"    "861853"    "862009"    "862028"    "86208"    
 [97] "86211"     "862261"    "862485"    "862548"    "862717"    "862722"   
[103] "862965"    "862980"    "862989"    "863030"    "863031"    "863270"   
[109] "86355"     "864018"    "864033"    "86408"     "86409"     "864292"   
[115] "864496"    "864685"    "864726"    "864729"    "864877"    "865128"   
[121] "865137"    "86517"     "865423"    "865432"    "865468"    "86561"    
[127] "866083"    "866203"    "866458"    "866674"    "866714"    "8670"     
[133] "86730502"  "867387"    "867739"    "868202"    "868223"    "868682"   
[139] "868826"    "868871"    "868999"    "869104"    "869218"    "869224"   
[145] "869254"    "869476"    "869691"    "86973701"  "86973702"  "869931"   
[151] "871001501" "871001502" "8710441"   "87106"     "8711002"   "8711003"  
[157] "8711202"   "8711216"   "871122"    "871149"    "8711561"   "8711803"  
[163] "871201"    "8712064"   "8712289"   "8712291"   "87127"     "8712729"  
[169] "8712766"   "8712853"   "87139402"  "87163"     "87164"     "871641"   
[175] "871642"    "872113"    "872608"    "87281702"  "873357"    "873586"   
[181] "873592"    "873593"    "873701"    "873843"    "873885"    "874158"   
[187] "874217"    "874373"    "874662"    "874839"    "874858"    "875093"   
[193] "875099"    "875263"    "87556202"  "875878"    "875938"    "877159"   
[199] "877486"    "877500"    "877501"    "877989"    "878796"    "87880"    
[205] "87930"     "879523"    "879804"    "879830"    "8810158"   "8810436"  
[211] "881046502" "8810528"   "8810703"   "881094802" "8810955"   "8810987"  
[217] "8811523"   "8811779"   "8811842"   "88119002"  "8812816"   "8812818"  
[223] "8812844"   "8812877"   "8813129"   "88143502"  "88147101"  "88147102" 
[229] "88147202"  "881861"    "881972"    "88199202"  "88203002"  "88206102" 
[235] "882488"    "88249602"  "88299702"  "883263"    "883270"    "88330202" 
[241] "88350402"  "883539"    "883852"    "88411702"  "884180"    "884437"   
[247] "884448"    "884626"    "88466802"  "884689"    "884948"    "88518501" 
[253] "885429"    "8860702"   "886226"    "886452"    "88649001"  "886776"   
[259] "887181"    "88725602"  "887549"    "888264"    "888570"    "889403"   
[265] "889719"    "88995002"  "8910251"   "8910499"   "8910506"   "8910720"  
[271] "8910721"   "8910748"   "8910988"   "8910996"   "8911163"   "8911164"  
[277] "8911230"   "8911670"   "8911800"   "8911834"   "8912049"   "8912055"  
[283] "89122"     "8912280"   "8912284"   "8912521"   "8912909"   "8913"     
[289] "8913049"   "89143601"  "89143602"  "8915"      "891670"    "891703"   
[295] "891716"    "891923"    "891936"    "892189"    "892214"    "892399"   
[301] "892438"    "892604"    "89263202"  "892657"    "89296"     "893061"   
[307] "89344"     "89346"     "893526"    "893548"    "893783"    "89382601" 
[313] "89382602"  "893988"    "894047"    "894089"    "894090"    "894326"   
[319] "894329"    "894335"    "894604"    "894618"    "894855"    "895100"   
[325] "89511501"  "89511502"  "89524"     "895299"    "8953902"   "895633"   
[331] "896839"    "896864"    "897132"    "897137"    "897374"    "89742801" 
[337] "897604"    "897630"    "897880"    "89812"     "89813"     "898143"   
[343] "89827"     "898431"    "89864002"  "898677"    "898678"    "89869"    
[349] "898690"    "899147"    "899187"    "899667"    "899987"    "9010018"  
[355] "901011"    "9010258"   "9010259"   "901028"    "9010333"   "901034301"
[361] "901034302" "901041"    "9010598"   "9010872"   "9010877"   "901088"   
```

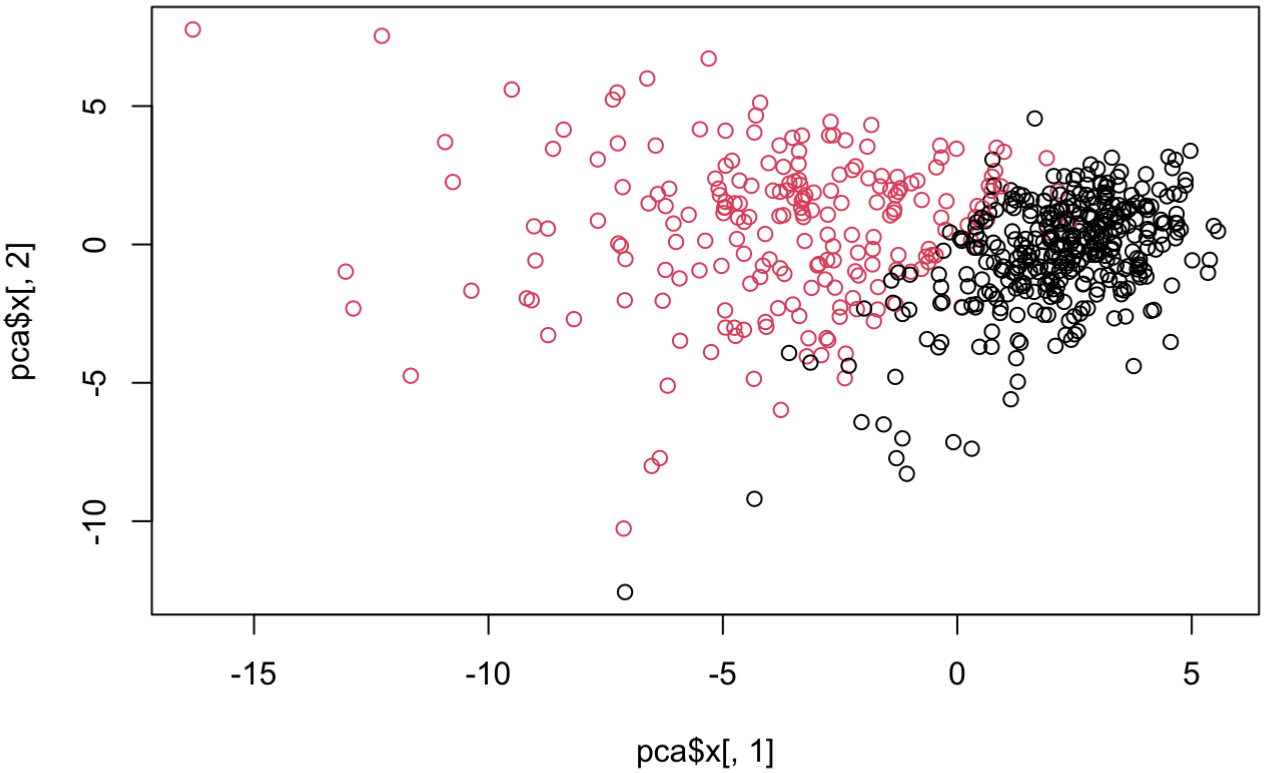
```
[367] "9011494"   "9011495"   "9011971"   "9012000"   "9012315"   "9012568"  
[373] "9012795"   "901288"    "9013005"   "901303"    "901315"    "9013579"  
[379] "9013594"   "9013838"   "901549"    "901836"    "90250"     "90251"    
[385] "902727"    "90291"     "902975"    "902976"    "903011"    "90312"    
[391] "90317302"  "903483"    "903507"    "903516"    "903554"    "903811"   
[397] "90401601"  "90401602"  "904302"    "904357"    "90439701"  "904647"   
[403] "904689"    "9047"      "904969"    "904971"    "905189"    "905190"   
[409] "90524101"  "905501"    "905502"    "905520"    "905539"    "905557"   
[415] "905680"    "905686"    "905978"    "90602302"  "906024"    "906290"   
[421] "906539"    "906564"    "906616"    "906878"    "907145"    "907367"   
[427] "907409"    "90745"     "90769601"  "90769602"  "907914"    "907915"   
[433] "908194"    "908445"    "908469"    "908489"    "908916"    "909220"   
[439] "909231"    "909410"    "909411"    "909445"    "90944601"  "909777"   
[445] "9110127"   "9110720"   "9110732"   "9110944"   "911150"    "911157302"
[451] "9111596"   "9111805"   "9111843"   "911201"    "911202"    "9112085"  
[457] "9112366"   "9112367"   "9112594"   "9112712"   "911296201" "911296202"
[463] "9113156"   "911320501" "911320502" "9113239"   "9113455"   "9113514"  
[469] "9113538"   "911366"    "9113778"   "9113816"   "911384"    "9113846"  
[475] "911391"    "911408"    "911654"    "911673"    "911685"    "911916"   
[481] "912193"    "91227"     "912519"    "912558"    "912600"    "913063"   
[487] "913102"    "913505"    "913512"    "913535"    "91376701"  "91376702" 
[493] "914062"    "914101"    "914102"    "914333"    "914366"    "914580"   
[499] "914769"    "91485"     "914862"    "91504"     "91505"     "915143"   
[505] "915186"    "915276"    "91544001"  "91544002"  "915452"    "915460"   
[511] "91550"     "915664"    "915691"    "915940"    "91594602"  "916221"   
[517] "916799"    "916838"    "917062"    "917080"    "917092"    "91762702" 
[523] "91789"     "917896"    "917897"    "91805"     "91813701"  "91813702" 
[529] "918192"    "918465"    "91858"     "91903901"  "91903902"  "91930402" 
[535] "919537"    "919555"    "91979701"  "919812"    "921092"    "921362"   
[541] "921385"    "921386"    "921644"    "922296"    "922297"    "922576"   
[547] "922577"    "922840"    "923169"    "923465"    "923748"    "923780"   
[553] "924084"    "924342"    "924632"    "924934"    "924964"    "925236"   
[559] "925277"    "925291"    "925292"    "925311"    "925622"    "926125"   
[565] "926424"    "926682"    "926954"    "927241"    "92751"    

$dimnames[[2]]
 [1] "PC1"  "PC2"  "PC3"  "PC4"  "PC5"  "PC6"  "PC7"  "PC8"  "PC9"  "PC10"
[11] "PC11" "PC12" "PC13" "PC14" "PC15" "PC16" "PC17" "PC18" "PC19" "PC20"
[21] "PC21" "PC22" "PC23" "PC24" "PC25" "PC26" "PC27" "PC28" "PC29" "PC30"
```

> Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why?

This is a hot mess of a plot and we will need to generate our own plots to make sense of this PCA result.

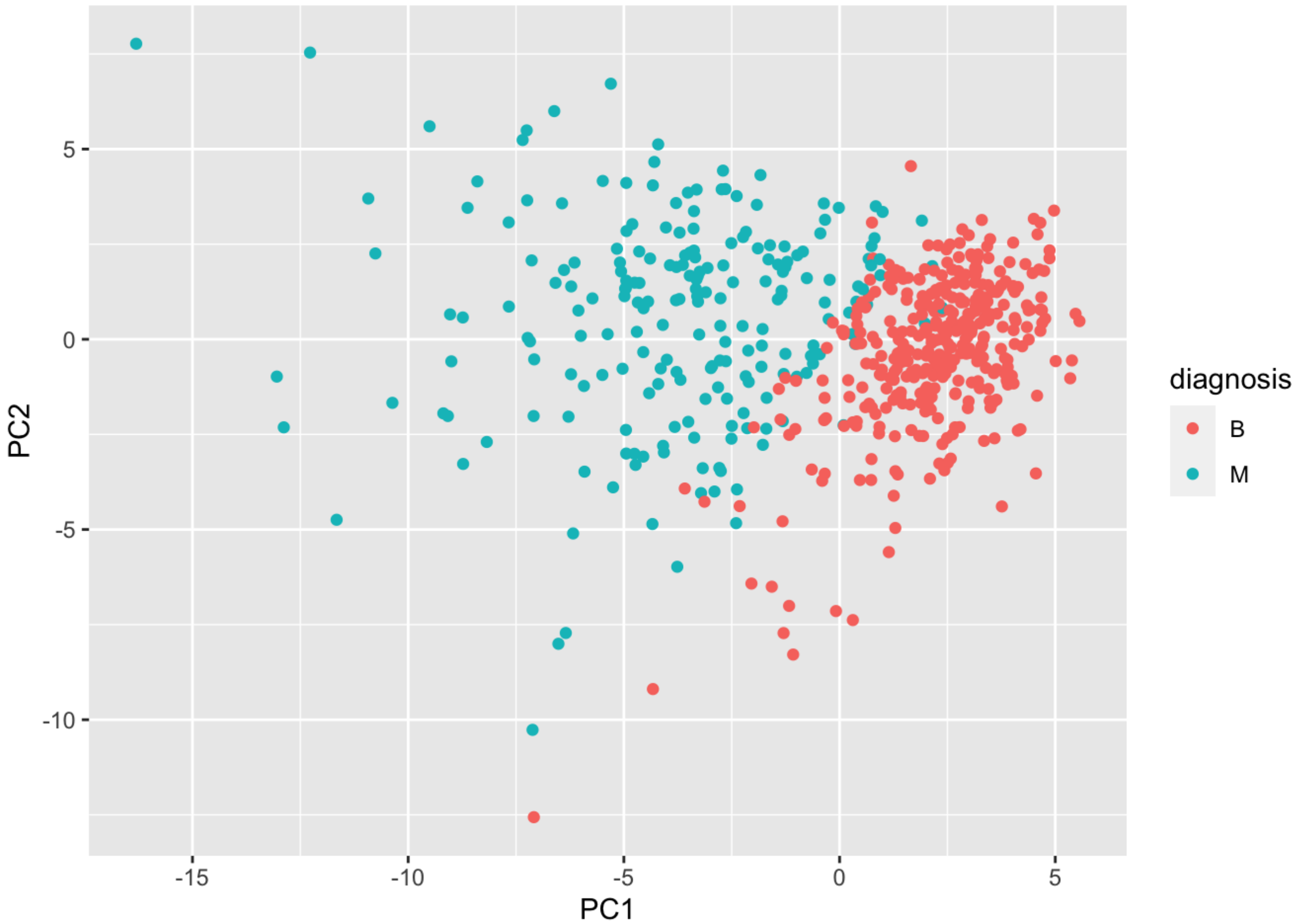
```
plot(pca$x[,1], pca$x[,2], col= diagnosis)
```




```r
# Create a data.frame for ggplot
df <- as.data.frame(pca$x)
df$diagnosis <- diagnosis

# Load the ggplot2 package
library(ggplot2)

# Make a scatter plot colored by diagnosis
ggplot(df) +
  aes(PC1, PC2, col= diagnosis) +
  geom_point()
```



> Q8. How much variance is captured in the top 3 PCs.

They capture 72.636% of the total variance.

> Q9. For the first principal component, what is the component of the loading vector (i.e. wisc.pr$rotation[,1]) for the feature concave.points_mean?

This tells us how much this original feature contributes to the first PC.

```
pca$rotation["concave.points_mean",1]
```

```
[1] -0.2608538
```

```
attributes(pca)
```

```
$names
[1] "sdev"     "rotation" "center"   "scale"    "x"

$class
[1] "prcomp"
```

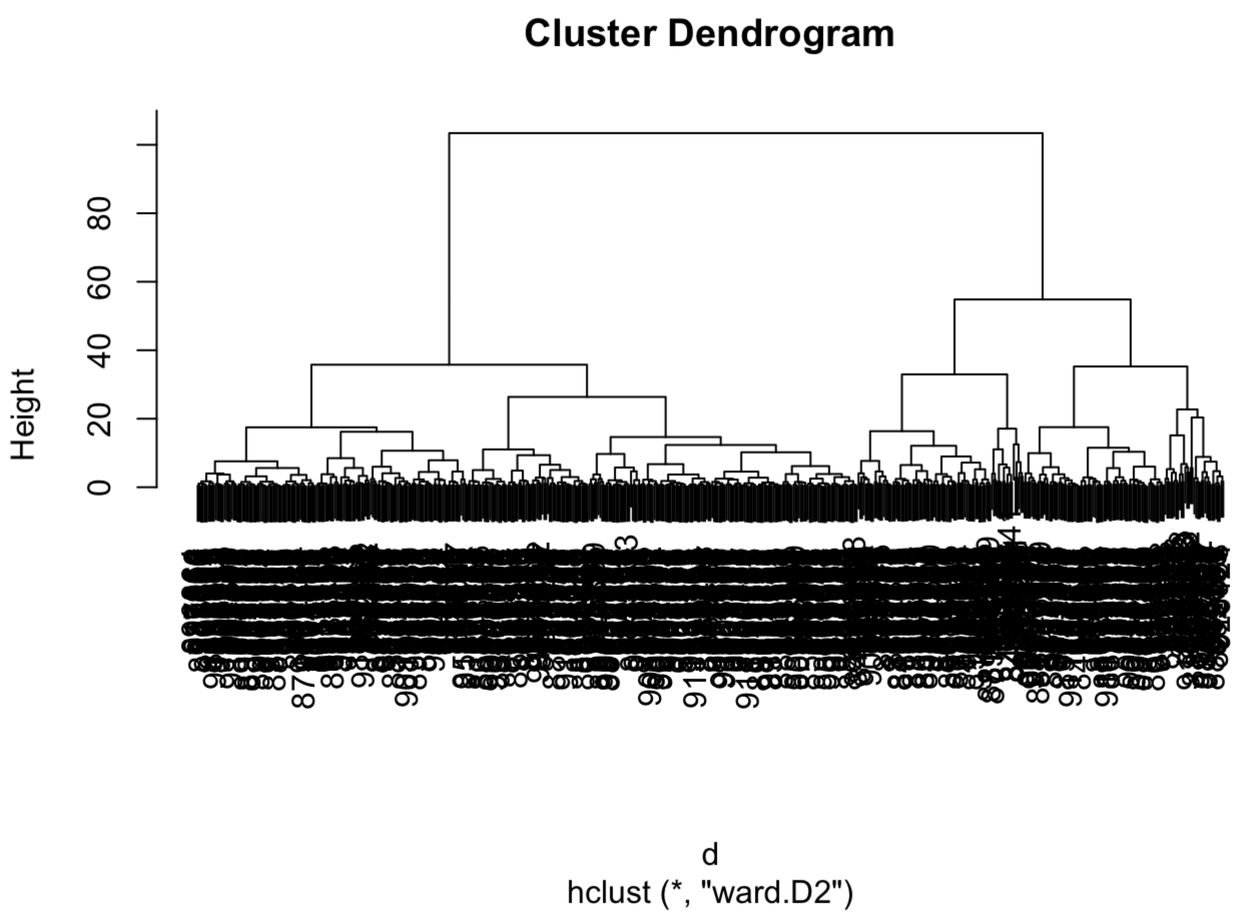
#Combine PCA results with clustering

We can use our new PCA variables (i.e the scores along the PCs contained in R `pca$x`) as input for other methods such as clustering

```
#Hclust needs a distance matrix as input

d <- dist(pca$x [,1:3] )

hc <- hclust(d, method="ward.D2")
plot(hc)
```



> Q11. Using the plot() and abline() functions, what is the height at which the clustering model has 4 clusters?

h = 35.5

To get our cluster membership vector we can use the `cutree()` function and specify a height (`h`) or number of groups(`k`).

```
grps <- cutree(hc, h=35.5)
table(grps)
```

```
grps
  1   2   3   4
```

```
111  92 216 150
```

I want to find out how many diagnosis "M" and "B" are in each grp?

```
table(diagnosis)
```

```
diagnosis
  B   M 
357 212 
```

> Q12. Can you find a better cluster vs diagnoses match by cutting into a different number of clusters between 2 and 10?

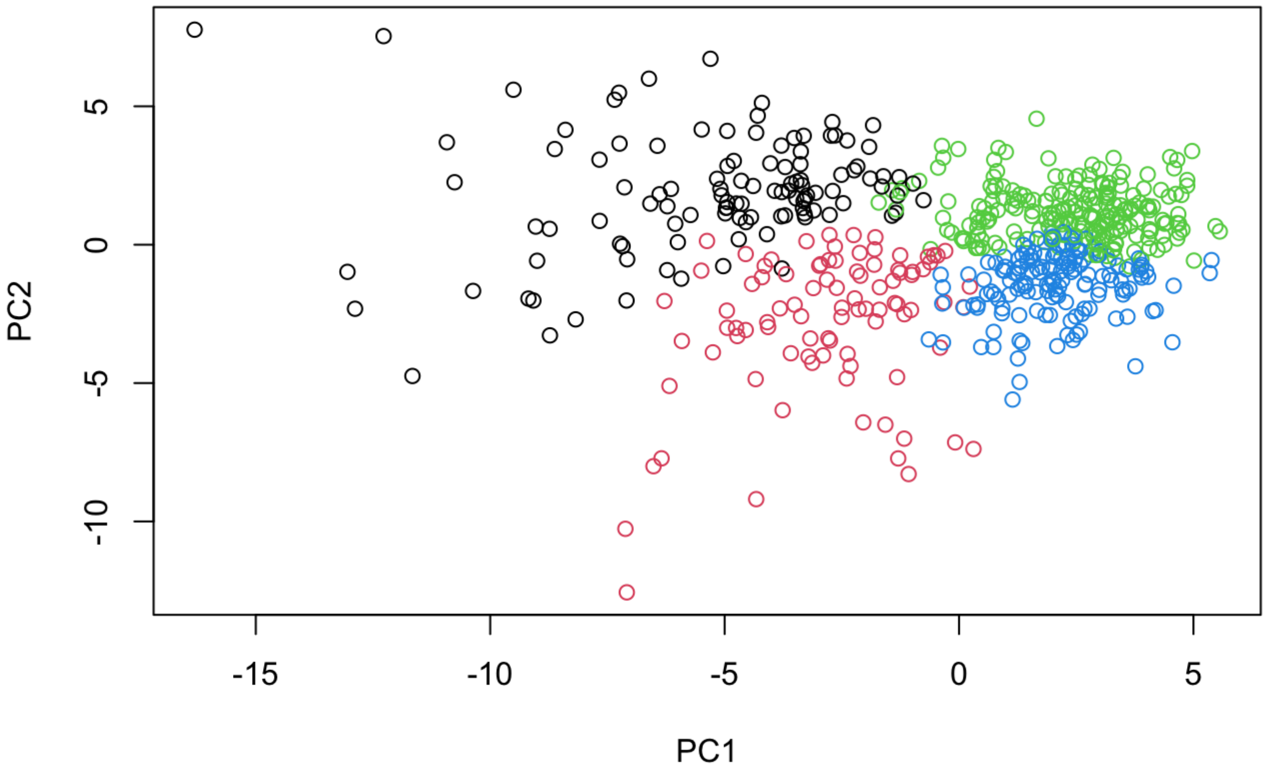
```
table(diagnosis, grps)
```

```
         grps
diagnosis   1   2   3   4
        B   0  24 184 149
        M 111  68  32   1
```

> Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

We can also plot our results using our clustering vector `grps`

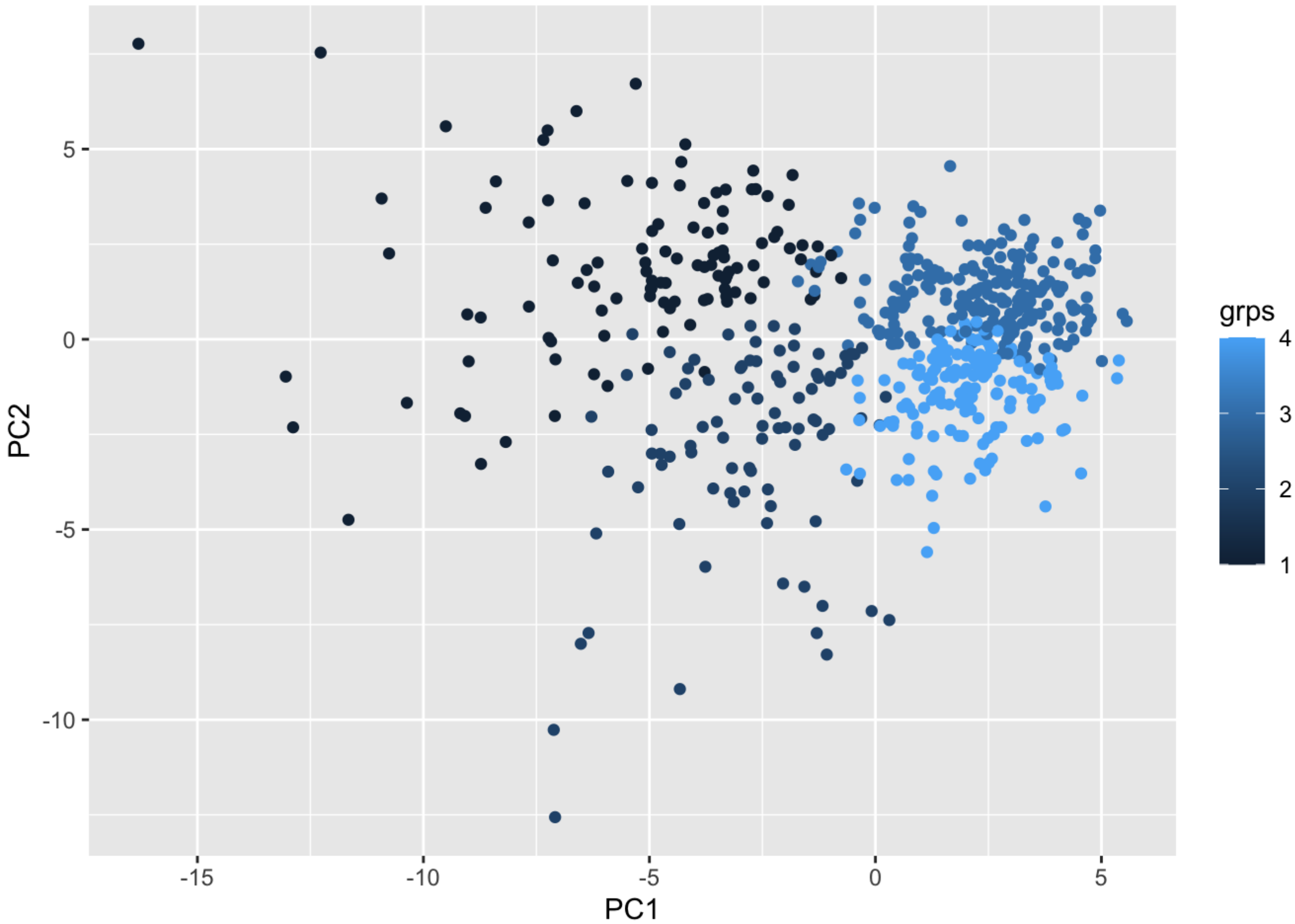
```
plot(pca$x[,1:2], col=grps)
```




```r
# Create a data.frame for ggplot
df <- as.data.frame(pca$x)
df$diagnosis <- diagnosis

# Load the ggplot2 package
library(ggplot2)

# Make a scatter plot colored by diagnosis
ggplot(df) +
  aes(PC1, PC2, col= grps) +
  geom_point()
```



> Q. Q15. What is the specificity (TN/(TN+FN)) and sensitivity(TP/(TP+FN)) of our current results?

Specificity= (333/(333+33)) = .91 Sensitivity = (179/(179+33)) = .84

Predicition

> Q16. Which of these new patients should we prioritize for follow up based on your results?

Patient 2 should follow up.