# class 08

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4/28/23

Input the data

```
fna.data <- "WisconsinCancer.csv"
wisc.df <- read.csv(fna.data, row.names=1)
head(wisc.df)
```

```
         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
```

WE can use `-1` to remove the 1st column.

```r
wisc.data <- wisc.df[,-1]
head(wisc.data)
```

```
         radius_mean texture_mean perimeter_mean area_mean smoothness_mean
842302         17.99        10.38         122.80    1001.0         0.11840
842517         20.57        17.77         132.90    1326.0         0.08474
84300903       19.69        21.25         130.00    1203.0         0.10960
```

| | | | | | |
|---|---|---|---|---|---|
| 84348301 | 11.42 | 20.38 | 77.58 | 386.1 | 0.14250 |
| 84358402 | 20.29 | 14.34 | 135.10 | 1297.0 | 0.10030 |
| 843786 | 12.45 | 15.70 | 82.57 | 477.1 | 0.12780 |

| | compactness_mean | concavity_mean | concave.points_mean | symmetry_mean |
|---|---|---|---|---|
| 842302 | 0.27760 | 0.3001 | 0.14710 | 0.2419 |
| 842517 | 0.07864 | 0.0869 | 0.07017 | 0.1812 |
| 84300903 | 0.15990 | 0.1974 | 0.12790 | 0.2069 |
| 84348301 | 0.28390 | 0.2414 | 0.10520 | 0.2597 |
| 84358402 | 0.13280 | 0.1980 | 0.10430 | 0.1809 |
| 843786 | 0.17000 | 0.1578 | 0.08089 | 0.2087 |

| | fractal_dimension_mean | radius_se | texture_se | perimeter_se | area_se |
|---|---|---|---|---|---|
| 842302 | 0.07871 | 1.0950 | 0.9053 | 8.589 | 153.40 |
| 842517 | 0.05667 | 0.5435 | 0.7339 | 3.398 | 74.08 |
| 84300903 | 0.05999 | 0.7456 | 0.7869 | 4.585 | 94.03 |
| 84348301 | 0.09744 | 0.4956 | 1.1560 | 3.445 | 27.23 |
| 84358402 | 0.05883 | 0.7572 | 0.7813 | 5.438 | 94.44 |
| 843786 | 0.07613 | 0.3345 | 0.8902 | 2.217 | 27.19 |

| | smoothness_se | compactness_se | concavity_se | concave.points_se |
|---|---|---|---|---|
| 842302 | 0.006399 | 0.04904 | 0.05373 | 0.01587 |
| 842517 | 0.005225 | 0.01308 | 0.01860 | 0.01340 |
| 84300903 | 0.006150 | 0.04006 | 0.03832 | 0.02058 |
| 84348301 | 0.009110 | 0.07458 | 0.05661 | 0.01867 |
| 84358402 | 0.011490 | 0.02461 | 0.05688 | 0.01885 |
| 843786 | 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
```

Setup a separate new vector called `diagnosis` that contains the data from the diagnosis column of the original dataset. We will store this as a factor (useful for plotting) and use this later to check our results.

```r
diagnosis <- factor(wisc.df$diagnosis)
diagnosis
```

```
  [1] M M M M M M M M M M M M M M M M M M M B B B M M M M M M M M M M M M M M M
 [38] B M M M M M M M M B M B B B B B M M B M M B B B B M B M M B B B B M B M M
 [75] B M B M M B B B M M B M M M B B B M B B M M B B B M M B B B B M B B M B B
[112] B B B B B B M M M B M M B B B M M B M B M M B M M B B M B B M B B B B M B
[149] B B B B B B B B M B B B B M M B M B B M M B B M M B B B B M B B M M M B M
[186] B M B B B M B B M M B M M M M B M M M B M B M B B M B M M M M B B M M B B
[223] B M B B B B B M M B B M B B M M B M B B B B M B B B B B M B M M M M M M M
[260] M M M M M M M B B B B B B M B M B B M B B M B M M B B B B B B B B B B B B
[297] B M B B M B M B B B B B B B B B B B B B B M B B B M B M B B B B M M M B B
[334] B B M B M B M B B B M B B B B B B B M M M B B B B B B B B B B B M M B M M
[371] M B M M B B B B B M B B B B B M B B B M B B M M B B B B B B M B B B B B B
[408] B M B B B B B M B B M B B B B B B B B B B B B M B M M B M B B B B B M B B
[445] M B M B B M B M B B B B B B B B M M B B B B B B M B B B B B B B B B B M B
[482] B B B B B B M B M B B M B B B B B M M B M B M B B B B B M B B M B M B M M
[519] B B B M B B B B B B B B B B B M B M M B B B B B B B B B B B B B B B B B B
[556] B B B B B B B M M M M M M B
Levels: B M
```

### Exploratory data analysis

**Q1**. How many observations are in this dataset?

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

```
[1] 569
```

There are 569 observations.

**Q2**. How many of the observations have a malignant diagnosis?

```r
summary(diagnosis)
```

```
  B   M 
357 212 
```

> 212 observations have a malignant diagnosis.

**Q3**. How many variables/features in the data are suffixed with `_mean`?

```r
A=colnames(wisc.data)
A
```

```
 [1] "radius_mean"             "texture_mean"           
 [3] "perimeter_mean"          "area_mean"              
 [5] "smoothness_mean"         "compactness_mean"       
 [7] "concavity_mean"          "concave.points_mean"    
 [9] "symmetry_mean"           "fractal_dimension_mean" 
[11] "radius_se"               "texture_se"             
[13] "perimeter_se"            "area_se"                
[15] "smoothness_se"           "compactness_se"         
[17] "concavity_se"            "concave.points_se"      
[19] "symmetry_se"             "fractal_dimension_se"   
[21] "radius_worst"            "texture_worst"          
[23] "perimeter_worst"         "area_worst"             
[25] "smoothness_worst"        "compactness_worst"      
[27] "concavity_worst"         "concave.points_worst"   
[29] "symmetry_worst"          "fractal_dimension_worst"
```

```r
grep("_mean",A)
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

```r
length(grep("_mean",A))
```

```
[1] 10
```

10 variables are suffixed with `_mean`.

## Principal Component Analysis

### Performing PCA

It is important to check if the data need to be scaled before performing PCA. Recall two common reasons for scaling data include:

- The input variables use different units of measurement.
- The input variables have significantly different variances.

Check the mean and standard deviation of the features (i.e. columns) of the `wisc.data` to determine if the data should be scaled. Use the `colMeans()` and `apply()` functions like you've done before.

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

```
            radius_mean            texture_mean          perimeter_mean 
           1.412729e+01            1.928965e+01            9.196903e+01 
              area_mean         smoothness_mean        compactness_mean 
           6.548891e+02            9.636028e-02            1.043410e-01 
         concavity_mean     concave.points_mean           symmetry_mean 
           8.879932e-02            4.891915e-02            1.811619e-01 
 fractal_dimension_mean               radius_se              texture_se 
           6.279761e-02            4.051721e-01            1.216853e+00 
           perimeter_se                 area_se           smoothness_se 
           2.866059e+00            4.033708e+01            7.040979e-03 
         compactness_se            concavity_se       concave.points_se 
           2.547814e-02            3.189372e-02            1.179614e-02 
            symmetry_se    fractal_dimension_se            radius_worst 
           2.054230e-02            3.794904e-03            1.626919e+01 
          texture_worst         perimeter_worst              area_worst 
           2.567722e+01            1.072612e+02            8.805831e+02 
       smoothness_worst       compactness_worst         concavity_worst 
           1.323686e-01            2.542650e-01            2.721885e-01 
   concave.points_worst          symmetry_worst fractal_dimension_worst 
           1.146062e-01            2.900756e-01            8.394582e-02 
```

```r
apply(wisc.data,2,sd)
```

```
            radius_mean            texture_mean          perimeter_mean 
           3.524049e+00            4.301036e+00            2.429898e+01 
              area_mean         smoothness_mean        compactness_mean 
           3.519141e+02            1.406413e-02            5.281276e-02 
         concavity_mean     concave.points_mean           symmetry_mean 
           7.971981e-02            3.880284e-02            2.741428e-02 
 fractal_dimension_mean               radius_se              texture_se 
           7.060363e-03            2.773127e-01            5.516484e-01 
           perimeter_se                 area_se           smoothness_se 
           2.021855e+00            4.549101e+01            3.002518e-03 
         compactness_se            concavity_se       concave.points_se 
           1.790818e-02            3.018606e-02            6.170285e-03 
            symmetry_se    fractal_dimension_se            radius_worst 
           8.266372e-03            2.646071e-03            4.833242e+00 
          texture_worst         perimeter_worst              area_worst 
           6.146258e+00            3.360254e+01            5.693570e+02 
       smoothness_worst       compactness_worst         concavity_worst 
           2.283243e-02            1.573365e-01            2.086243e-01 
   concave.points_worst          symmetry_worst fractal_dimension_worst 
           6.573234e-02            6.186747e-02            1.806127e-02 
```

```r
wisc.pr <- prcomp(wisc.data,scale=TRUE )
```

```r
summary(wisc.pr)
```

```
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)?

```
attributes(wisc.pr)
```

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

$class
[1] "prcomp"
```

```
wisc.pr.var <- wisc.pr$sdev^2
wisc.pr.var.per<- round(wisc.pr.var/sum(wisc.pr.var)*100,1)
wisc.pr.var.per
```

```
 [1] 44.3 19.0  9.4  6.6  5.5  4.0  2.3  1.6  1.4  1.2  1.0  0.9  0.8  0.5  0.3
[16]  0.3  0.2  0.2  0.2  0.1  0.1  0.1  0.1  0.1  0.1  0.0  0.0  0.0  0.0  0.0
```

44.3% of the original variance is captured by the first principal components

```
PC1 <- wisc.pr$x[,1]
PC2 <- wisc.pr$x[,2]
```

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

```
wisc.pr.var.per[1]
```

```
[1] 44.3
```

```r
wisc.pr.var.per[1]+wisc.pr.var.per[2]
```

```
[1] 63.3
```

```r
wisc.pr.var.per[1]+wisc.pr.var.per[2]+wisc.pr.var.per[3]
```

```
[1] 72.7
```

3 principal components (PCs) are required to describe at least 70% of the original variance in the data.

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

```r
wisc.pr.var.per[1]+wisc.pr.var.per[2]+wisc.pr.var.per[3]+wisc.pr.var.per[4]
```

```
[1] 79.3
```

```r
wisc.pr.var.per[1]+wisc.pr.var.per[2]+wisc.pr.var.per[3]+wisc.pr.var.per[4]+wisc.pr.var.pe
```

```
[1] 84.8
```

```r
wisc.pr.var.per[1]+wisc.pr.var.per[2]+wisc.pr.var.per[3]+wisc.pr.var.per[4]+wisc.pr.var.pe
```

```
[1] 88.8
```

```r
wisc.pr.var.per[1]+wisc.pr.var.per[2]+wisc.pr.var.per[3]+wisc.pr.var.per[4]+wisc.pr.var.pe
```

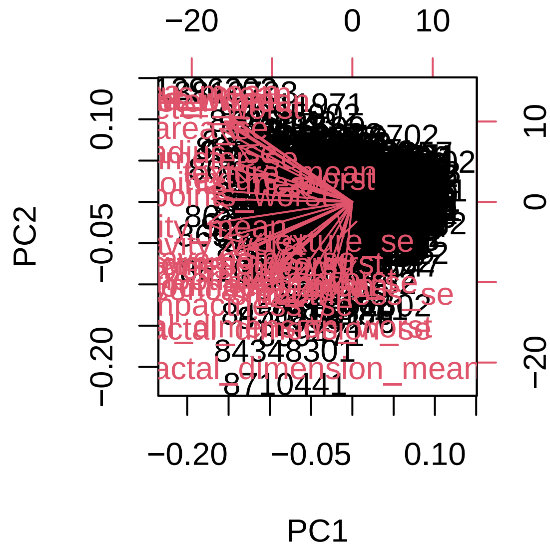
```
[1] 91.1
```

7 principal components (PCs) are required to describe at least 90% of the original variance in the data.

## Interpreting PCA results

Create a biplot of the `wisc.pr` using the `biplot()` function.

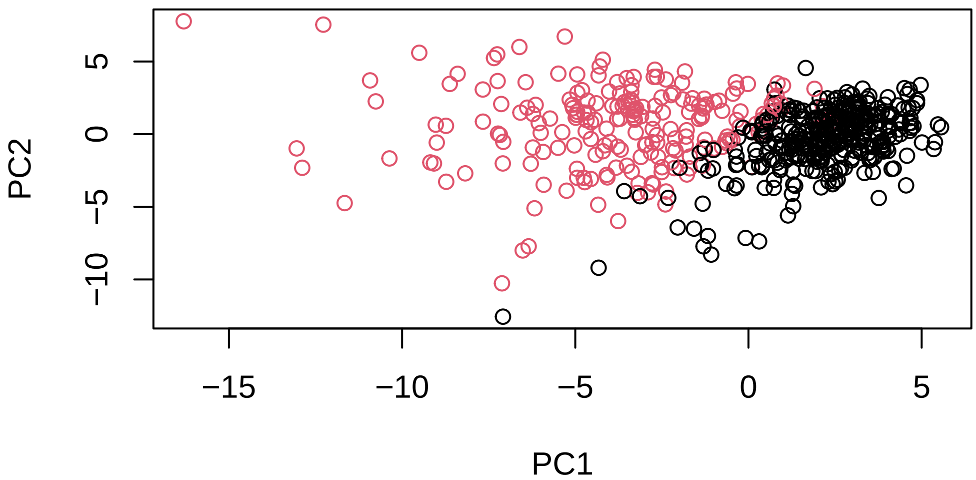
```r
biplot(wisc.pr)
```




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

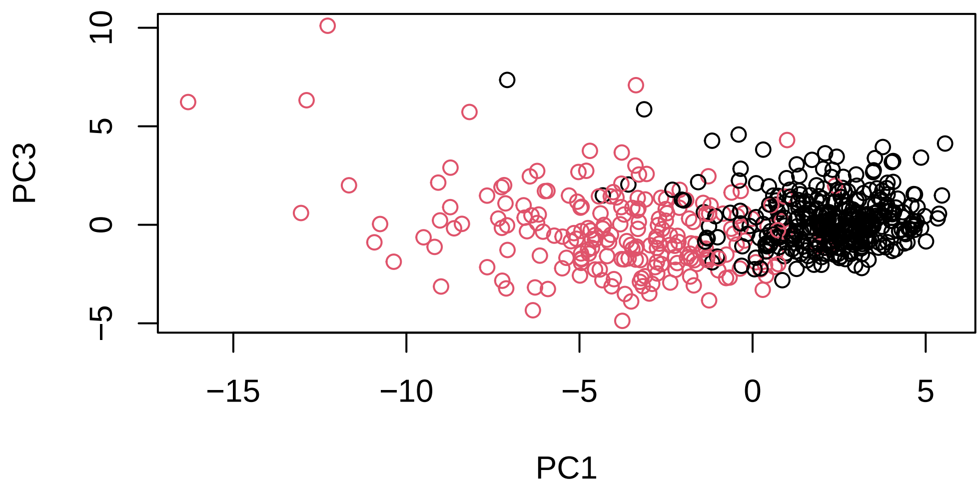
Too much captions. The data has not been filtered and processed.

```r
plot(PC1,PC2, col =
       diagnosis ,
     xlab = "PC1", ylab = "PC2")
```




Q8 Generate a similar plot for principal components 1 and 3. What do you notice about these plots?

```
# Repeat for components 1 and 3
plot(wisc.pr$x[,1], wisc.pr$x[,3], col =diagnosis,
     xlab = "PC1", ylab = "PC3")
```



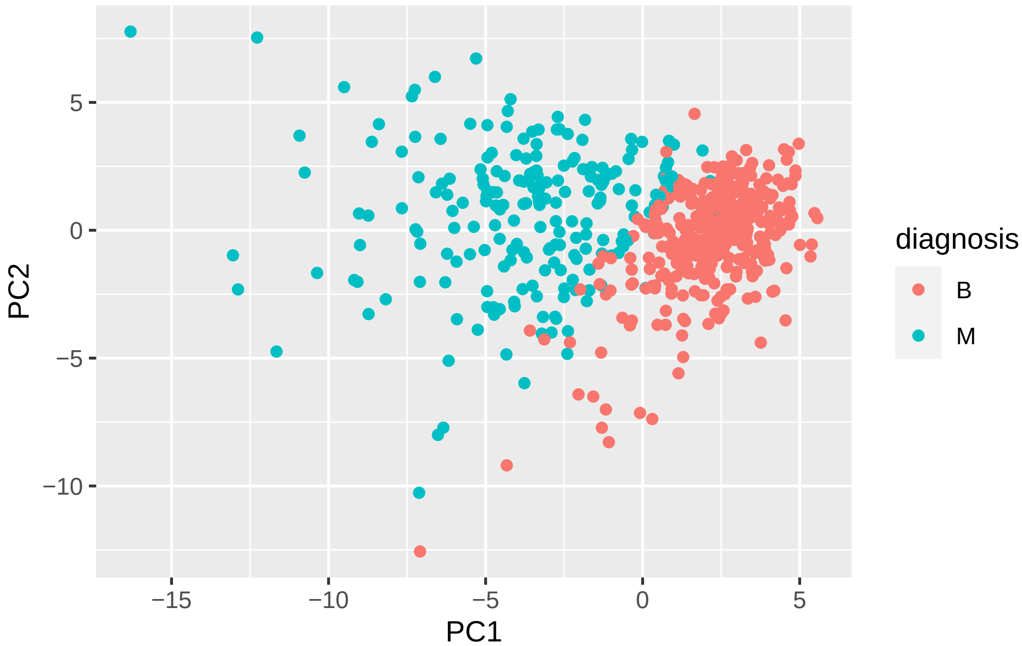

The malignment ones have similar distribution in values of PC 1.

As this is such a striking result let's see if we can use the **ggplot2** package to make a more fancy figure of these results

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

# Load the ggplot2 package
library(ggplot2)

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




### Variance explained

Calculate the variance of each principal component by squaring the sdev component of `wisc.pr` (i.e. `wisc.pr$sdev^2`). Save the result as an object called `pr.var`.

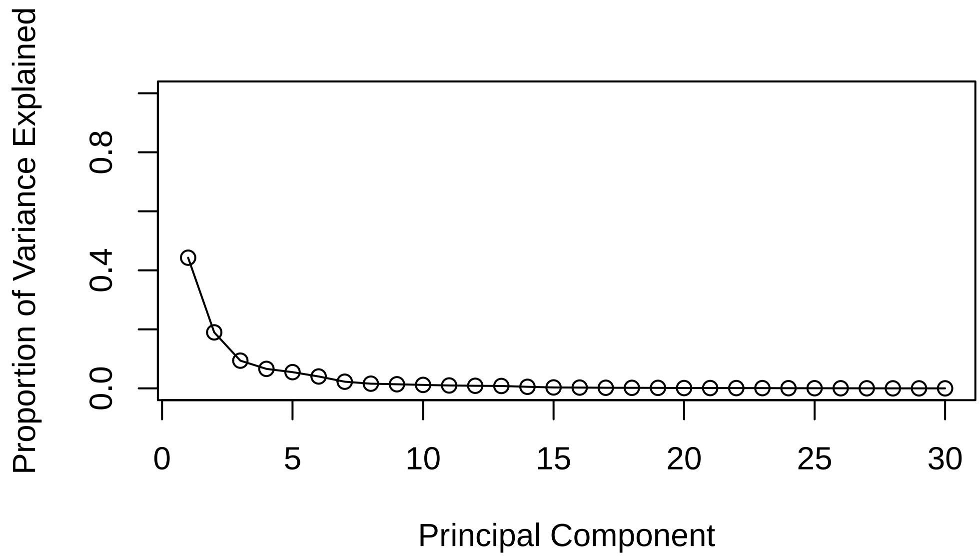
```
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

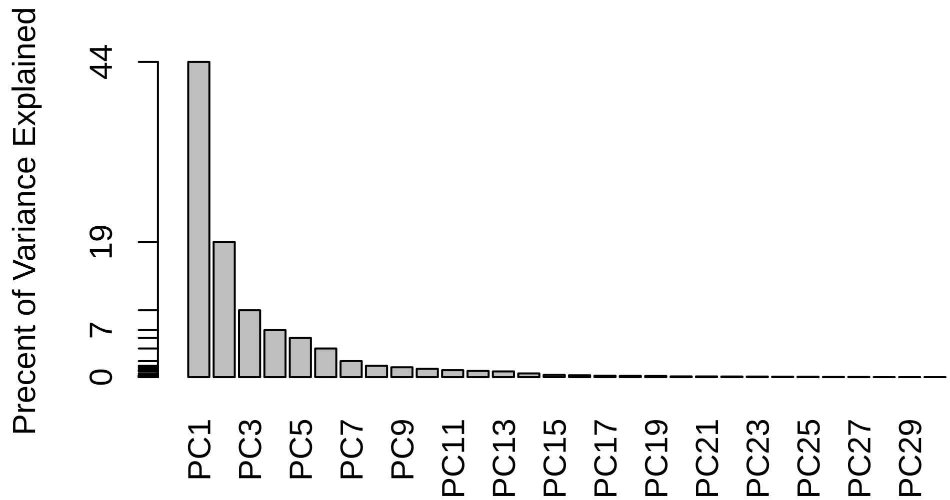
Calculate the variance explained by each principal component by dividing by the total variance explained of all principal components. Assign this to a variable called `pve` and create a plot of variance explained for each principal component./

```
pve <- pr.var /sum(pr.var)

# Plot variance explained for each principal component
plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```




```
# Alternative scree plot of the same data, note data driven y-axis
barplot(pve, ylab = "Precent of Variance Explained",
     names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```




## Communicating PCA results

**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.

```
wisc.pr$rotation[,1]
```

```
            radius_mean            texture_mean          perimeter_mean
            -0.21890244             -0.10372458             -0.22753729
              area_mean         smoothness_mean        compactness_mean
            -0.22099499             -0.14258969             -0.23928535
         concavity_mean     concave.points_mean           symmetry_mean
            -0.25840048             -0.26085376             -0.13816696
 fractal_dimension_mean               radius_se              texture_se
            -0.06436335             -0.20597878             -0.01742803
           perimeter_se                 area_se           smoothness_se
            -0.21132592             -0.20286964             -0.01453145
         compactness_se            concavity_se       concave.points_se
            -0.17039345             -0.15358979             -0.18341740
            symmetry_se    fractal_dimension_se            radius_worst
```

```
         -0.04249842          -0.10256832          -0.22799663
       texture_worst      perimeter_worst           area_worst
         -0.10446933          -0.23663968          -0.22487053
    smoothness_worst    compactness_worst      concavity_worst
         -0.12795256          -0.21009588          -0.22876753
concave.points_worst       symmetry_worst fractal_dimension_worst
         -0.25088597          -0.12290456          -0.13178394
```

The loading vector (i.e. `wisc.pr$rotation[,1]`) for the feature `concave.points_mean` is -0.26085376.

## 3. Hierarchical clustering

First scale the `wisc.data` data and assign the result to `data.scaled`.

```
# Scale the wisc.data data using the "scale()" function
data.scaled <- scale(wisc.data)
```

Calculate the (Euclidean) distances between all pairs of observations in the new scaled dataset and assign the result to `data.dist`.

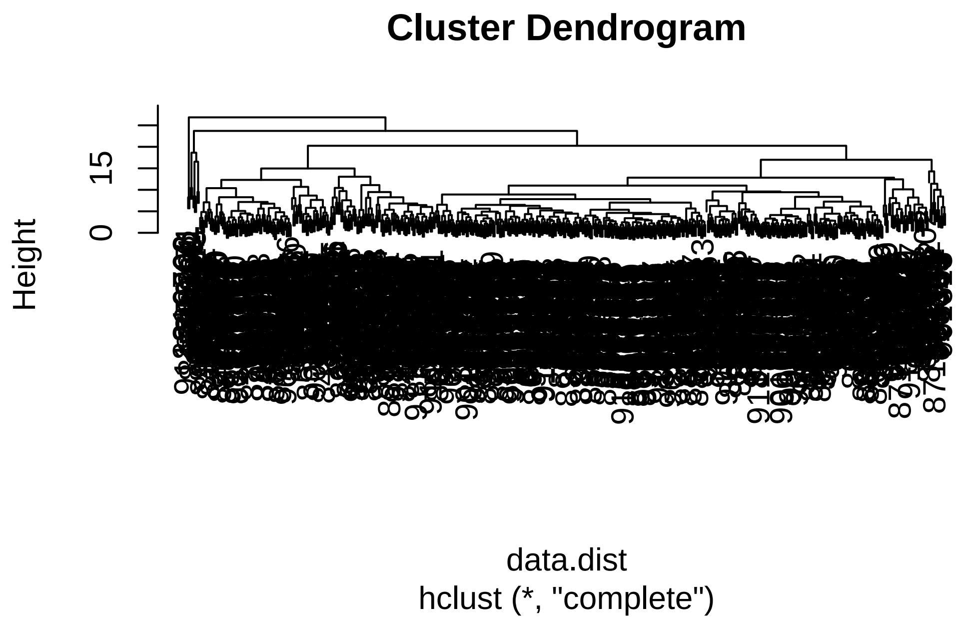
```
data.dist <-dist(data.scaled)
```

Create a hierarchical clustering model using complete linkage. Manually specify the method argument to hclust() and assign the results to `wisc.hclust`.

```
wisc.hclust <- hclust(data.dist, method="complete")
```

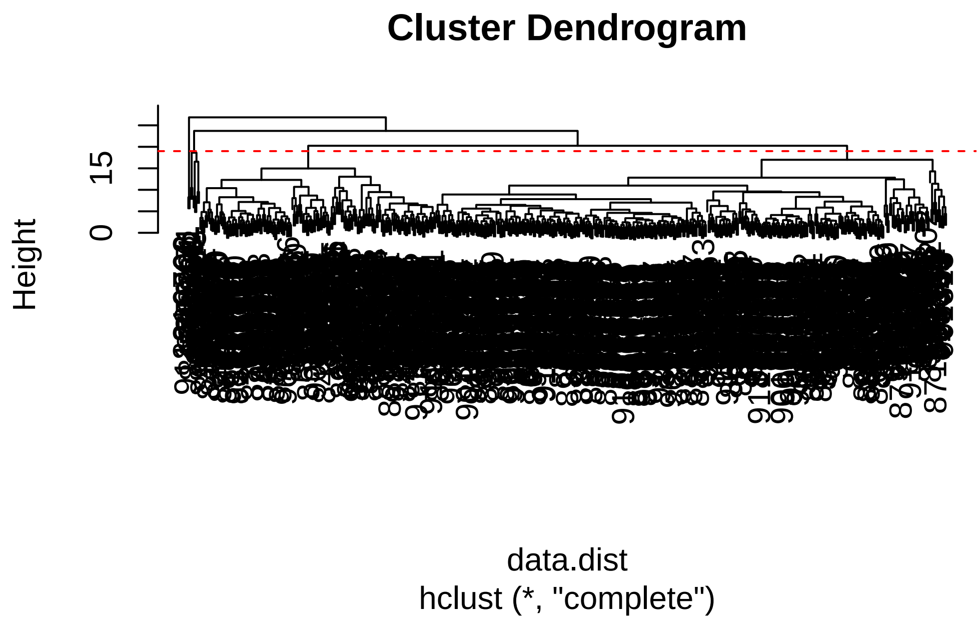
Q10 Using the `plot()` and `abline()` functions, what is the height at which the clustering model has 4 clusters?

```
plot(wisc.hclust)
```




I choose height =19

```
plot(wisc.hclust)
abline(h=19,col="red",lty=2)
```




### Selecting number of clusters

Use `cutree()` to cut the tree so that it has 4 clusters. Assign the output to the variable `wisc.hclust.clusters`.

```
wisc.hclust.clusters <- cutree(wisc.hclust,k=4)
```

We can use the `table()` function to compare the cluster membership to the actual diagnoses.

```
table(wisc.hclust.clusters, diagnosis)
```

```
                    diagnosis
wisc.hclust.clusters   B   M
                   1  12 165
                   2   2   5
                   3 343  40
                   4   0   2
```

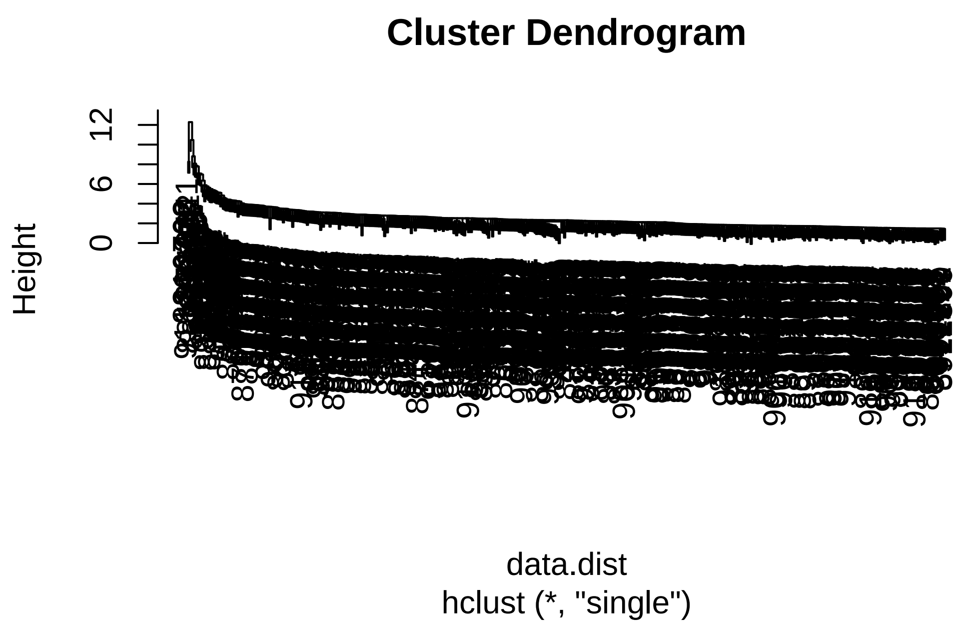
Here we picked four clusters and see that cluster 1 largely corresponds to malignant cells (with `diagnosis` values of 1) whilst cluster 3 largely corresponds to benign cells (with `diagnosis` values of 0).

### Using different methods

There are number of different *"methods"* we can use to combine points during the hierarchical clustering procedure. These include `"single"`, `"complete"`, `"average"` and (my favorite) `"ward.D2"`

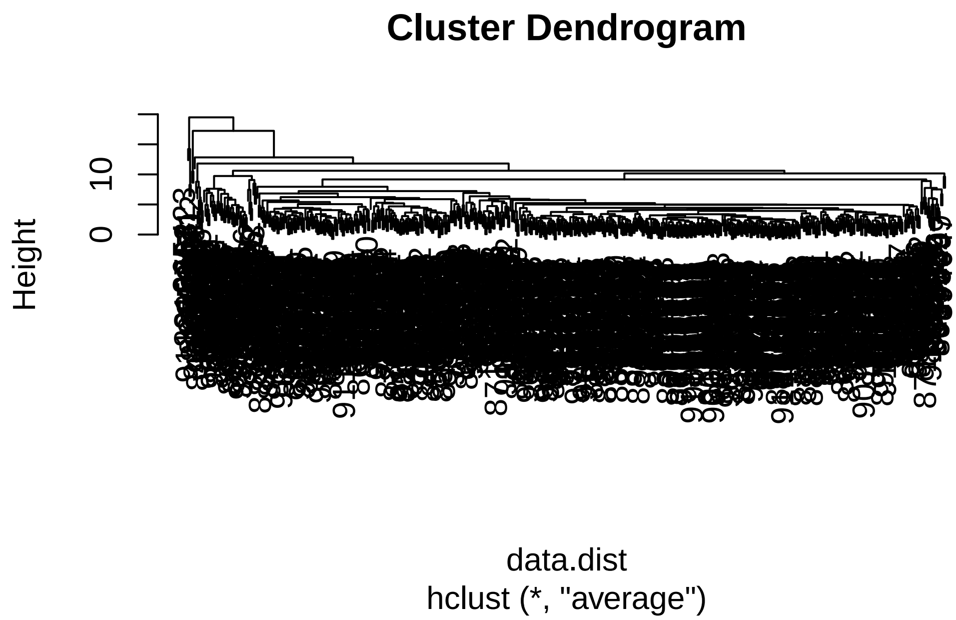
`"single"`

```
plot(hclust(data.dist, method="single"))
```



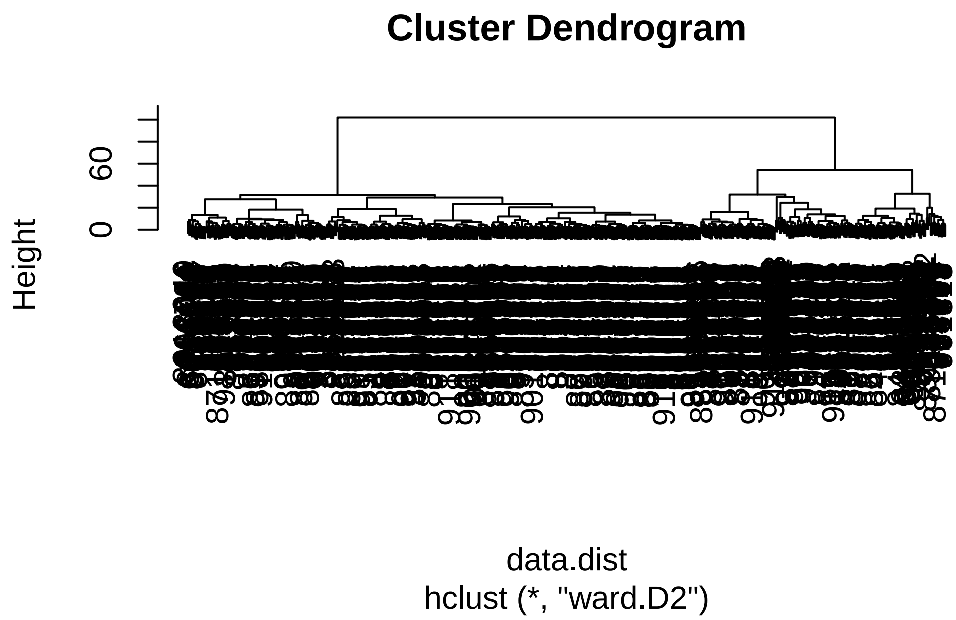

`"average"`

```
plot(hclust(data.dist, method="average"))
```




"ward.D2"

```
plot(hclust(data.dist, method="ward.D2"))
```




Q12 Which method gives your favorite results for the same `data.dist` dataset? Explain your reasoning.

I like ward.D2 the best. It looks more clear and more equally-distributed.

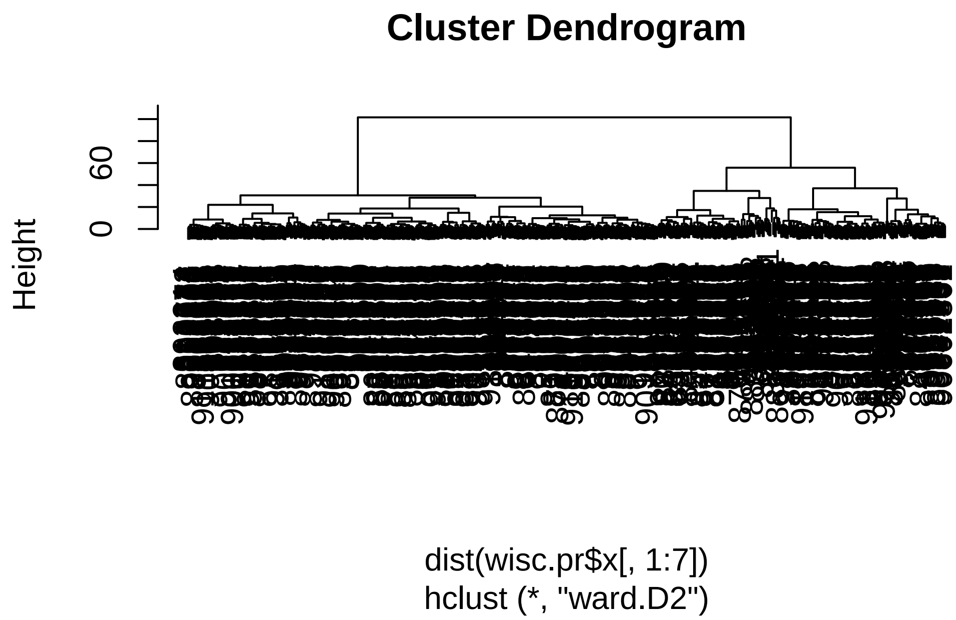
## 4. Combining methods

### Clustering on PCA results

Using the minimum number of principal components required to describe at least 90% of the variability in the data, create a hierarchical clustering model with the linkage `method="ward.D2"`. We use Ward's criterion here because it is based on multidimensional variance like principal components analysis. Assign the results to `wisc.pr.hclust`.

```
wisc.pr.hclust=hclust(dist(wisc.pr$x[,1:7]), method="ward.D2")
```

```
plot(wisc.pr.hclust)
```




```r
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

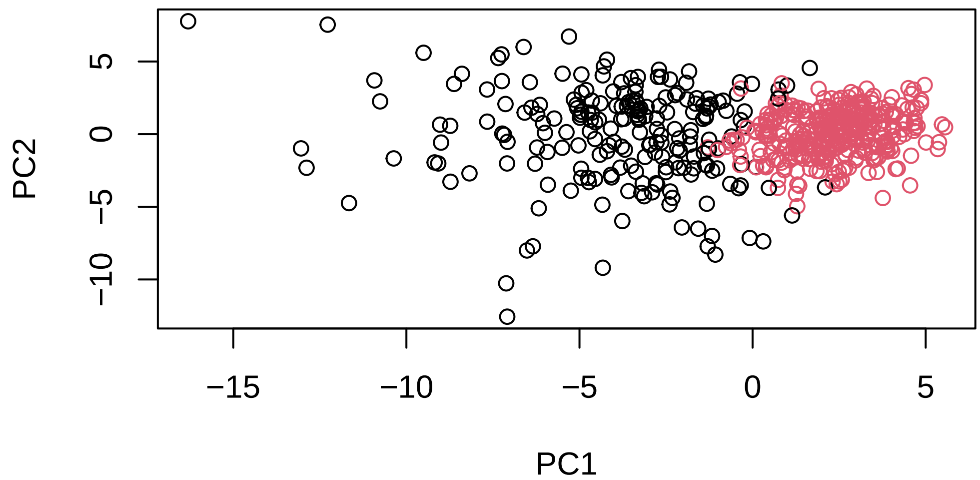
```
grps
  1   2 
216 353 
```

This looks much more promising than our previous clustering results on the original scaled data. Note the two main branches of or dendrogram indicating two main clusters - maybe these are malignant and benign.

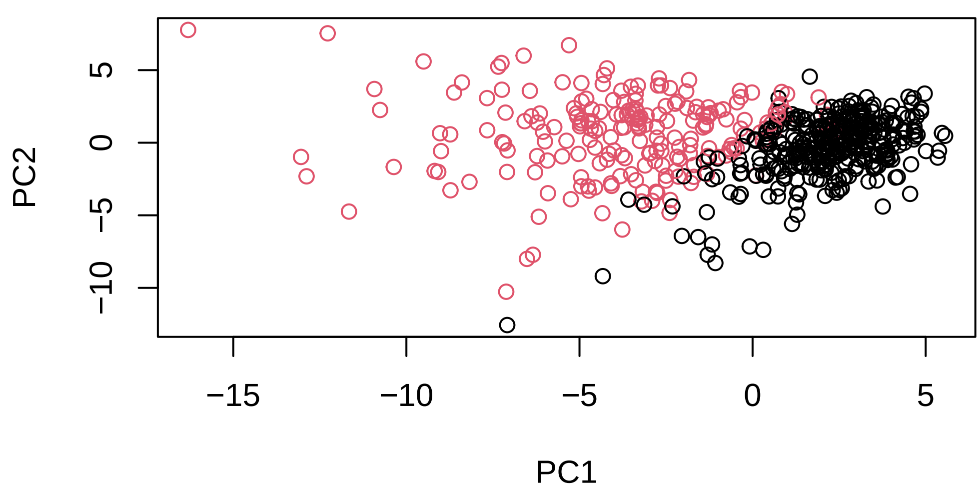
```r
table(grps, diagnosis)
```

```
    diagnosis
grps   B   M
   1  28 188
   2 329  24
```

```r
plot(wisc.pr$x[,1:2], col=grps)
```




```
plot(wisc.pr$x[,1:2], col=diagnosis)
```



Cut this hierarchical clustering model into 2 clusters and assign the results to `wisc.pr.hclust.clusters`.

```
wisc.pr.hclust.clusters <- cutree(wisc.pr.hclust, k=2)
```

Q13 How well does the newly created model with four clusters separate out the two diagnoses?

```
# Compare to actual diagnoses
table(wisc.pr.hclust.clusters, diagnosis)
```

```
                       diagnosis
wisc.pr.hclust.clusters   B   M
                      1  28 188
                      2 329  24
```

Q14 How well do the hierarchical clustering models you created in previous sections (i.e. before PCA) do in terms of separating the diagnoses? Again, use the `table()` function to compare the output of each model (`wisc.km$cluster` and `wisc.hclust.clusters`) with the vector containing the actual diagnoses.

```
table(wisc.hclust.clusters, diagnosis)
```

```
                    diagnosis
wisc.hclust.clusters   B   M
                   1  12 165
                   2   2   5
                   3 343  40
                   4   0   2
```

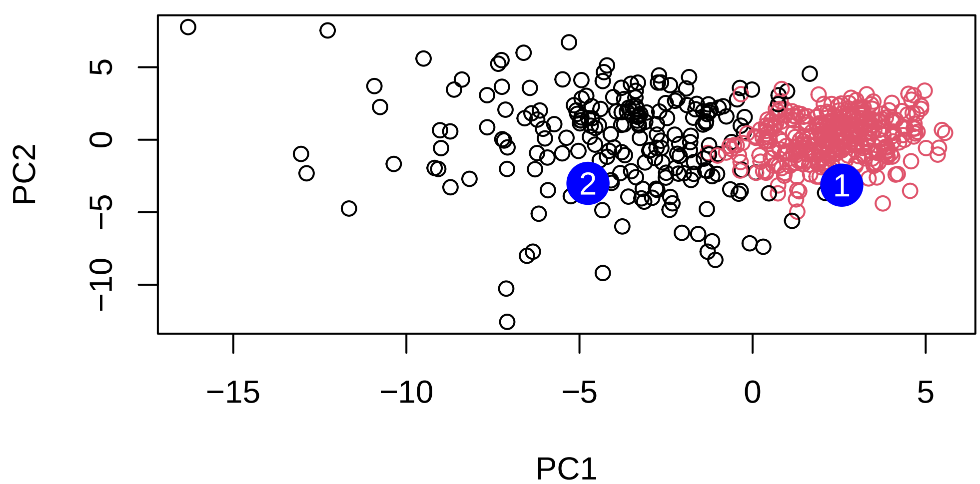
## 6. Prediction

We will use the `predict()` function that will take our PCA model from before and new cancer cell data and project that data onto our PCA space.

```
#url <- "new_samples.csv"
url <- "https://tinyurl.com/new-samples-CSV"
new <- read.csv(url)
npc <- predict(wisc.pr, newdata=new)
npc
```

```
           PC1       PC2        PC3        PC4       PC5        PC6        PC7
[1,]  2.576616 -3.135913  1.3990492 -0.7631950  2.781648 -0.8150185 -0.3959098
[2,] -4.754928 -3.009033 -0.1660946 -0.6052952 -1.140698 -1.2189945  0.8193031
            PC8       PC9       PC10      PC11      PC12      PC13     PC14
[1,] -0.2307350 0.1029569 -0.9272861 0.3411457  0.375921 0.1610764 1.187882
[2,] -0.3307423 0.5281896 -0.4855301 0.7173233 -1.185917 0.5893856 0.303029
          PC15       PC16        PC17        PC18        PC19       PC20
[1,] 0.3216974 -0.1743616 -0.07875393 -0.11207028 -0.08802955 -0.2495216
[2,] 0.1299153  0.1448061 -0.40509706  0.06565549  0.25591230 -0.4289500
           PC21       PC22       PC23       PC24        PC25         PC26
[1,]  0.1228233 0.09358453 0.08347651  0.1223396  0.02124121  0.078884581
[2,] -0.1224776 0.01732146 0.06316631 -0.2338618 -0.20755948 -0.009833238
             PC27        PC28         PC29         PC30
[1,]  0.220199544 -0.02946023 -0.015620933  0.005269029
[2,] -0.001134152  0.09638361  0.002795349 -0.019015820
```

```
plot(wisc.pr$x[,1:2], col=grps)
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
```




Black is group 1(M dominant), Red is group 2(B dominant)

Patient 1 should be prioritized.