Class08 Mini Project

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Preparing the data

Answer Q1-Q15, Q14 is optional

```
# Save your input data file into your Project directory

fna.data<- "WisconsinCancer.csv"


# Complete the following code to input the data and store as wisc.df
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
```

```r
# We can use -1 here to remove the first column
wisc.data <- wisc.df[,-1]
```

Finally, 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.

```
# Create diagnosis vector for later
diagnosis <- as.numeric(wisc.df$diagnosis == "M")
diagnosis
```

```
  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [38] 0 1 1 1 1 1 1 1 1 0 1 0 0 0 0 0 1 1 0 1 1 0 0 0 0 1 0 1 1 0 0 0 0 1 0 1 1
 [75] 0 1 0 1 1 0 0 0 1 1 0 1 1 1 0 0 0 1 0 0 1 1 0 0 0 1 1 0 0 0 0 1 0 0 1 0 0
[112] 0 0 0 0 0 0 1 1 1 0 1 1 0 0 0 1 1 0 1 0 1 1 0 1 1 0 0 1 0 0 1 0 0 0 0 1 0
[149] 0 0 0 0 0 0 0 0 1 0 0 0 0 1 1 0 1 0 0 1 1 0 0 1 1 0 0 0 0 1 0 0 1 1 1 0 1
[186] 0 1 0 0 0 1 0 0 1 1 0 1 1 1 1 0 1 1 1 0 1 0 1 0 0 1 0 1 1 1 1 0 0 1 1 0 0
[223] 0 1 0 0 0 0 0 1 1 0 0 1 0 0 1 1 0 1 0 0 0 0 1 0 0 0 0 0 1 0 1 1 1 1 1 1 1
[260] 1 1 1 1 1 1 1 0 0 0 0 0 0 1 0 1 0 0 1 0 0 1 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0
[297] 0 1 0 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 1 0 0 0 0 1 1 1 0 0
[334] 0 0 1 0 1 0 1 0 0 0 1 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 1 1 0 1 1
[371] 1 0 1 1 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 1 0 0 1 1 0 0 0 0 0 0 1 0 0 0 0 0 0
[408] 0 1 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 1 1 0 1 0 0 0 0 0 1 0 0
[445] 1 0 1 0 0 1 0 1 0 0 0 0 0 0 0 0 1 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 1 0
[482] 0 0 0 0 0 0 1 0 1 0 0 1 0 0 0 0 0 1 1 0 1 0 1 0 0 0 0 0 1 0 0 1 0 1 0 1 1
[519] 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 1 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[556] 0 0 0 0 0 0 0 1 1 1 1 1 1 0
```

Exploratory data analysis

> Q1. How many observations are in this dataset?

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

```
[1] 569
```

> Answer: There are 569 observations in this dataset from the number of rows counted.

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

```
table(diagnosis) # 0s = benigne, 1s = malignant
```

```
diagnosis
  0   1
357 212
```

> Answer: There are 212 observations that have the malignant diagnosis, and 357 observations with benigne diagnosis.

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

```r
length(grep("_mean", colnames(wisc.data)))
```

```
[1] 10
```

> Answer: There are 10 features in the data that are suffixed with _mean.

The functions dim(), nrow(), table(), length() and grep() may be useful for answering the first 3 questions above.

2.Principal Component Analysis

Performing PCA

```r
# Check column means and standard deviations

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
#Execute PCA with the prcomp() function on the wisc.data, scaling if appropriate, and assi
```

```r
# Perform PCA on wisc.data by completing the following code
#Inspect a summary of the results with the summary() function.

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

# Look at summary of results
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)?

Answer: 0.4427 proportion or 44.27% of the original variance is captured by the first principal components (PC1).

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

Answer: From the row cumulative proportion, three principal components (PC3) are required to describe at least 70% of the original variance in the data, yielding a proportion of 0.72636.

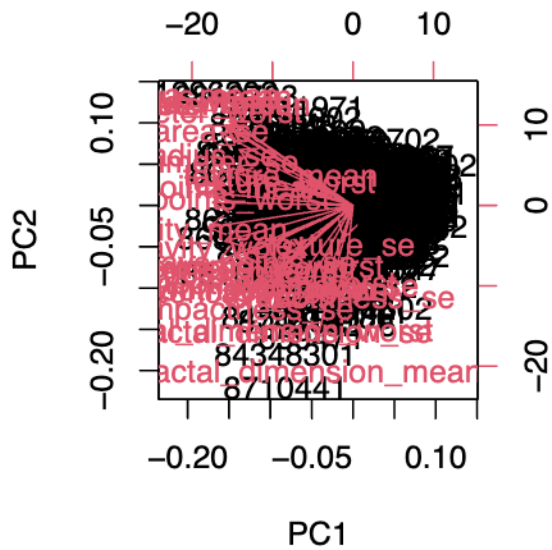
Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data?

Answer: From the row cumulative proportion, seven principal components (PC7) are required to describe at least 90% of the original variance in the data, yielding a proportion of 0.91010.

Interpreting PCA results

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

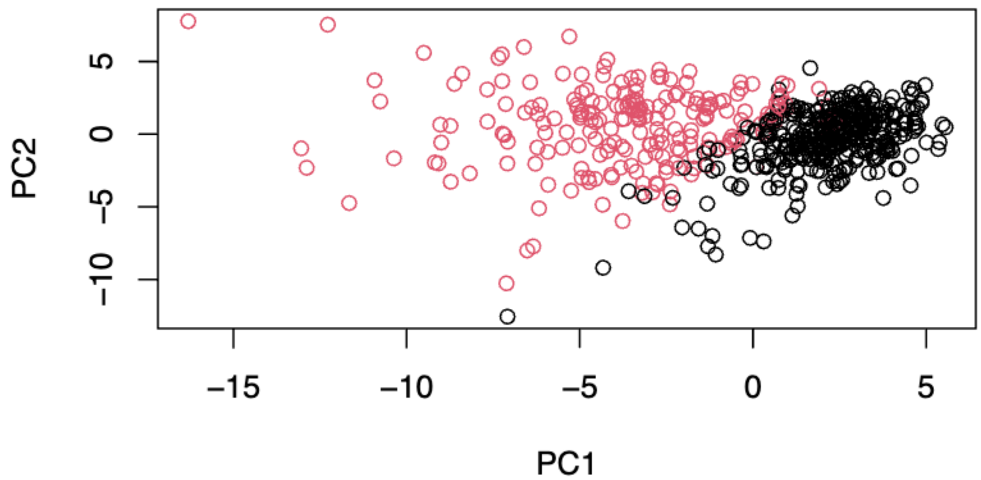
```r
biplot(wisc.pr)
```



> Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why? HINT: This is a hot mess of a plot and we will need to generate our own plots to make sense of this PCA result.
>
> Answer: The part of the plot that stands out is that it is a biplot that is plotted in two colors, with the column as red and rows as black. The trend of the plot is really difficult to understand and is very confusing, because we cannot clearly observe how the row and column datas compare, and could not identify the particular trend it is trying to demonstrate.

Lets generate a more standard scatter plot of each observation along principal components 1 and 2 and color the points by the diagnosis.

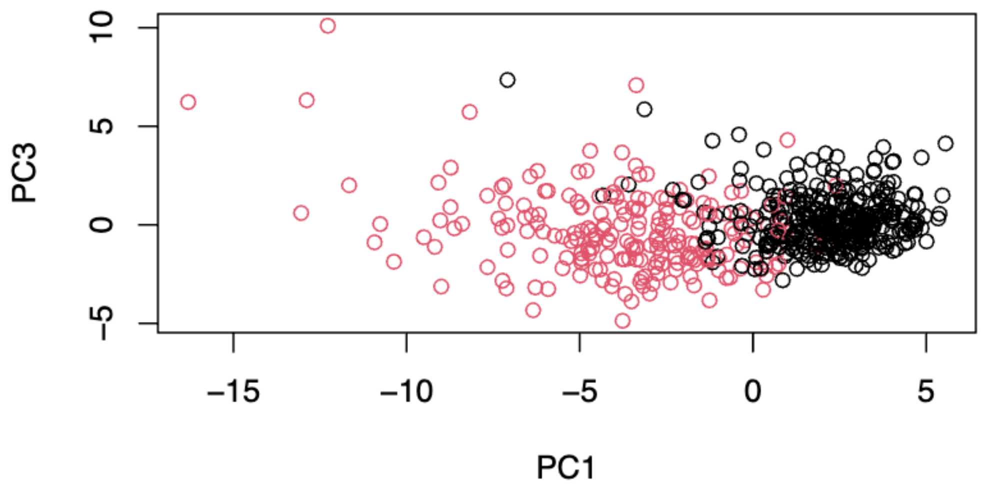
```r
# Scatter plot observations by components 1 and 2

plot(wisc.pr$x[,c(1,2)], col = (diagnosis+1),
     xlab = "PC1", ylab = "PC2")
```



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

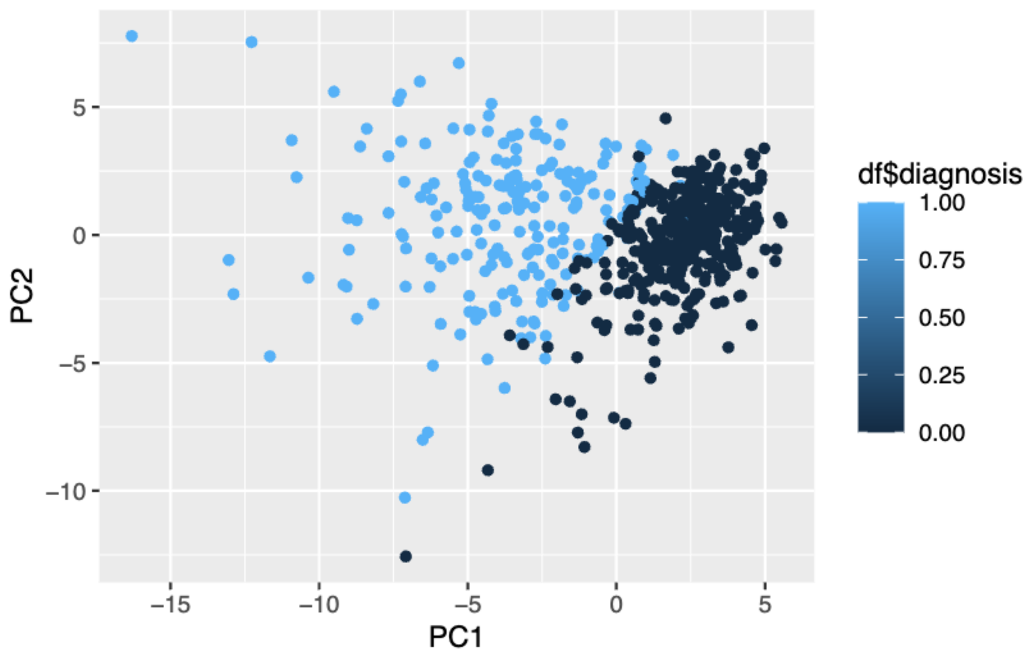
Answer: I noticed that the PC2 vs PC1 plot point scatters are more spread out compared to the PC3 vs PC1 plot. The PC3 vs PC1 plot data points are more concentrated on the bottom right corner of the graph axis and are more closely packed together.

```
# Repeat for components 1 and 3

plot(wisc.pr$x[, c(1,3)], col = (diagnosis+1),
     xlab = "PC1", ylab = "PC3")
```



Use ggplot2 package to make a fancy figure of the 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= df$diagnosis) + geom_point()
```

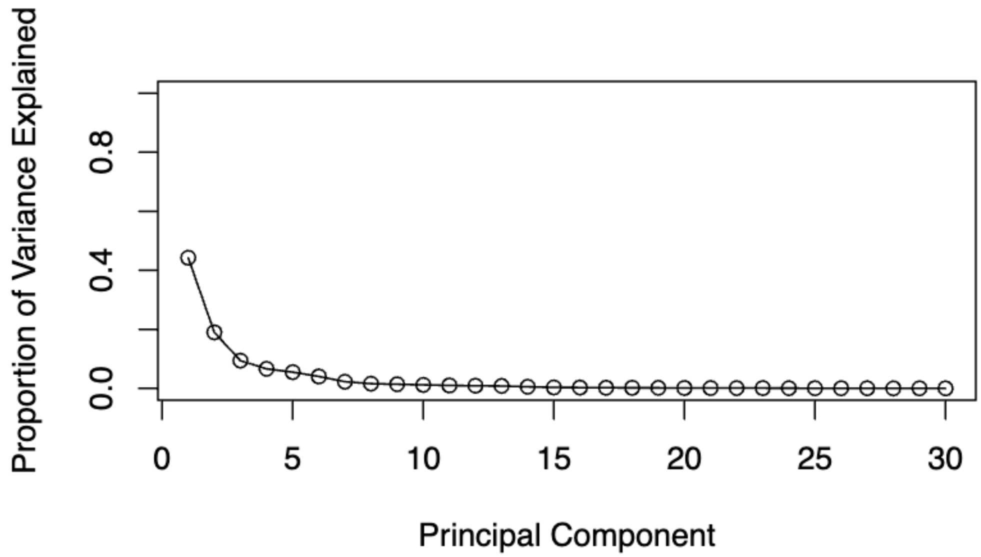


Variance explained

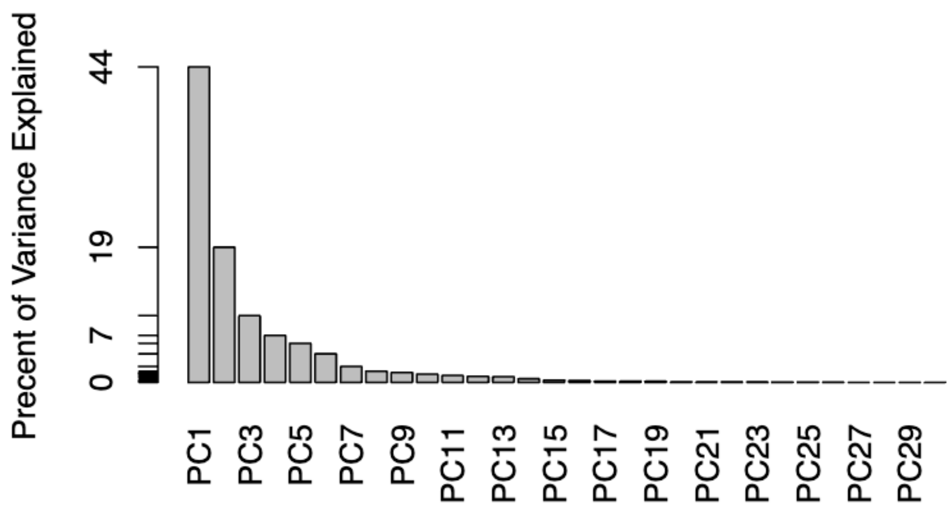
```
# Calculate variance of each component
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

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

```
# Variance explained by each principal component: pve
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?

```
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
```

Answer: The component of the loading vector for the feature concave.points_mean of the first principal component is -0.26085376.

Q10. What is the minimum number of principal components required to explain 80% of the variance of the data?

```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
```

Answer: By looking at the cumulative proportion, a minimum of five principal components (PC5) required to explain 80% of the variance of the data, which yields a proportion of 0.84734 of the variance.

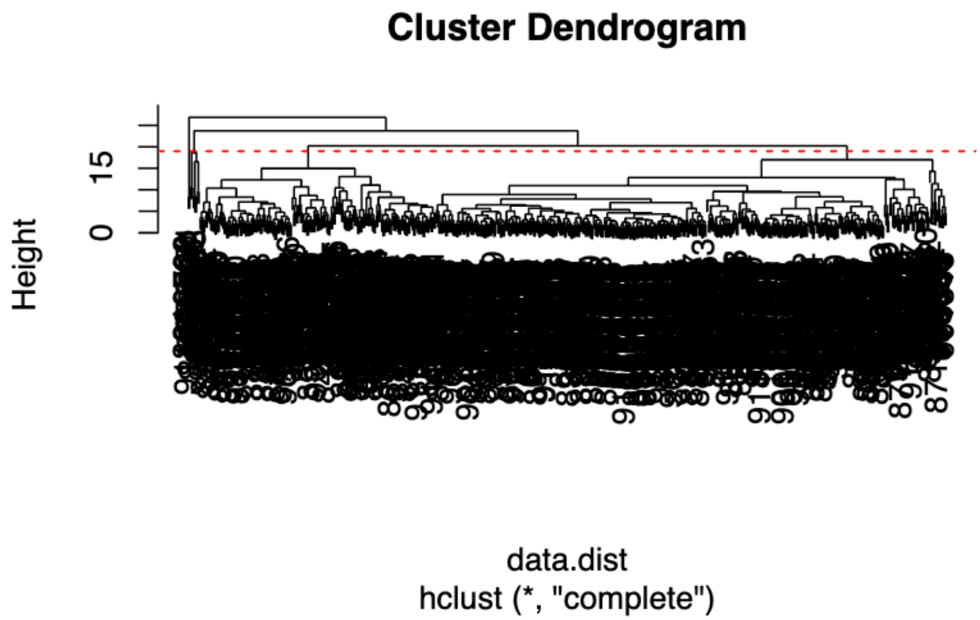
3. Hierarchical clustering

```
# 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

data.dist <- dist(data.scaled)


#Create a hierarchical clustering model using complete linkage. Manually specify the metho

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

Results of hierarchical clustering

> Q11. Using the plot() and abline() functions, what is the height at which the clustering model has 4 clusters?
>
> Answer: The height that the clustering model have four clusters is estimated to be around a height of 19 or close to 20.

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



Selecting number of clusters

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

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

```
  842302   842517 84300903 84348301 84358402   843786   844359 84458202 
       1        1        1        2        1        1        1        1 
  844981 84501001   845636 84610002   846226   846381 84667401 84799002 
       1        2        3        1        1        3        1        1 
  848406 84862001   849014  8510426  8510653  8510824  8511133   851509 
       3        1        1        3        3        3        1        1 
  852552   852631   852763   852781   852973   853201   853401   853612 
       1        1        1        1        1        3        1        1 
85382601   854002   854039   854253   854268   854941   855133   855138 
       1        1        1        1        1        3        3        1 
  855167   855563   855625   856106 85638502   857010 85713702    85715 
       3        1        1        1        1        1        3        1 
  857155   857156   857343   857373   857374   857392   857438 85759902 
       3        3        3        3        3        1        3        3 
```

857637	857793	857810	858477	858970	858981	858986	859196
1	1	3	3	3	3	1	3
85922302	859283	859464	859465	859471	859487	859575	859711
1	1	3	3	2	3	1	3
859717	859983	8610175	8610404	8610629	8610637	8610862	8610908
1	1	3	3	3	1	2	3
861103	8611161	8611555	8611792	8612080	8612399	86135501	86135502
3	1	1	1	3	1	3	1
861597	861598	861648	861799	861853	862009	862028	86208
3	1	3	3	3	3	1	1
86211	862261	862485	862548	862717	862722	862965	862980
3	3	3	3	3	3	3	3
862989	863030	863031	863270	86355	864018	864033	86408
3	1	1	3	1	3	3	3
86409	864292	864496	864685	864726	864729	864877	865128
3	3	3	3	3	1	1	3
865137	86517	865423	865432	865468	86561	866083	866203
3	1	2	3	3	3	1	3
866458	866674	866714	8670	86730502	867387	867739	868202
1	1	3	1	1	3	1	3
868223	868682	868826	868871	868999	869104	869218	869224
3	3	1	3	3	3	3	3
869254	869476	869691	86973701	86973702	869931	871001501	871001502
3	3	1	3	3	3	3	3
8710441	87106	8711002	8711003	8711202	8711216	871122	871149
2	3	3	3	1	3	3	3
8711561	8711803	871201	8712064	8712289	8712291	87127	8712729
3	1	1	3	1	3	3	3
8712766	8712853	87139402	87163	87164	871641	871642	872113
1	3	3	3	1	3	3	3
872608	87281702	873357	873586	873592	873593	873701	873843
3	1	3	3	1	1	1	3
873885	874158	874217	874373	874662	874839	874858	875093
1	3	3	3	3	3	2	3
875099	875263	87556202	875878	875938	877159	877486	877500
3	1	1	3	1	3	1	1
877501	877989	878796	87880	87930	879523	879804	879830
3	3	1	1	3	3	3	3
8810158	8810436	881046502	8810528	8810703	881094802	8810955	8810987
1	3	1	3	4	3	1	1
8811523	8811779	8811842	88119002	8812816	8812818	8812844	8812877
3	3	1	1	3	3	3	1
8813129	88143502	88147101	88147102	88147202	881861	881972	88199202

3	3	3	3	3	1	1	3
88203002	88206102	882488	88249602	88299702	883263	883270	88330202
3	1	3	3	1	1	3	1
88350402	883539	883852	88411702	884180	884437	884448	884626
3	3	3	3	1	3	3	3
88466802	884689	884948	88518501	885429	8860702	886226	886452
3	3	1	3	1	3	1	3
88649001	886776	887181	88725602	887549	888264	888570	889403
1	1	1	1	1	3	1	3
889719	88995002	8910251	8910499	8910506	8910720	8910721	8910748
1	1	3	3	3	3	3	3
8910988	8910996	8911163	8911164	8911230	8911670	8911800	8911834
1	3	3	3	3	3	3	3
8912049	8912055	89122	8912280	8912284	8912521	8912909	8913
1	3	1	1	3	3	3	3
8913049	89143601	89143602	8915	891670	891703	891716	891923
3	3	3	3	3	3	3	3
891936	892189	892214	892399	892438	892604	89263202	892657
3	3	3	3	1	3	1	3
89296	893061	89344	89346	893526	893548	893783	89382601
3	3	3	3	3	3	3	3
89382602	893988	894047	894089	894090	894326	894329	894335
3	3	3	3	3	1	3	3
894604	894618	894855	895100	89511501	89511502	89524	895299
3	3	3	1	3	3	3	3
8953902	895633	896839	896864	897132	897137	897374	89742801
1	1	1	1	3	3	3	1
897604	897630	897880	89812	89813	898143	89827	898431
3	1	3	1	3	3	3	1
89864002	898677	898678	89869	898690	899147	899187	899667
3	3	3	3	3	3	3	1
899987	9010018	901011	9010258	9010259	901028	9010333	901034301
1	1	3	3	3	3	3	3
901034302	901041	9010598	9010872	9010877	901088	9011494	9011495
3	3	3	3	3	1	1	3
9011971	9012000	9012315	9012568	9012795	901288	9013005	901303
1	1	1	3	1	1	3	3
901315	9013579	9013594	9013838	901549	901836	90250	90251
3	3	3	1	3	3	3	3
902727	90291	902975	902976	903011	90312	90317302	903483
3	3	3	3	3	1	3	3
903507	903516	903554	903811	90401601	90401602	904302	904357
1	1	3	3	3	3	3	3

90439701	904647	904689	9047	904969	904971	905189	905190
1	3	3	3	3	3	3	3
90524101	905501	905502	905520	905539	905557	905680	905686
1	3	3	3	3	3	3	3
905978	90602302	906024	906290	906539	906564	906616	906878
3	1	3	3	3	1	3	3
907145	907367	907409	90745	90769601	90769602	907914	907915
3	3	3	3	3	3	1	3
908194	908445	908469	908489	908916	909220	909231	909410
1	1	3	1	3	3	3	3
909411	909445	90944601	909777	9110127	9110720	9110732	9110944
3	3	3	3	3	3	1	3
911150	911157302	9111596	9111805	9111843	911201	911202	9112085
3	1	3	1	3	3	3	3
9112366	9112367	9112594	9112712	911296201	911296202	9113156	911320501
3	3	3	3	1	4	3	3
911320502	9113239	9113455	9113514	9113538	911366	9113778	9113816
3	3	3	3	1	1	3	3
911384	9113846	911391	911408	911654	911673	911685	911916
3	3	3	3	3	3	3	1
912193	91227	912519	912558	912600	913063	913102	913505
3	3	3	3	3	3	3	1
913512	913535	91376701	91376702	914062	914101	914102	914333
3	3	3	3	1	3	3	3
914366	914580	914769	91485	914862	91504	91505	915143
1	3	1	1	3	1	3	1
915186	915276	91544001	91544002	915452	915460	91550	915664
3	3	3	3	3	1	3	3
915691	915940	91594602	916221	916799	916838	917062	917080
1	3	3	3	1	1	3	3
917092	91762702	91789	917896	917897	91805	91813701	91813702
3	1	3	3	3	3	1	3
918192	918465	91858	91903901	91903902	91930402	919537	919555
3	3	3	3	3	1	3	1
91979701	919812	921092	921362	921385	921386	921644	922296
3	1	3	3	3	1	3	3
922297	922576	922577	922840	923169	923465	923748	923780
3	3	3	3	3	3	3	3
924084	924342	924632	924934	924964	925236	925277	925291
3	3	3	3	3	3	3	3
925292	925311	925622	926125	926424	926682	926954	927241
3	3	1	1	1	1	3	1
92751							

```
3
```

```
# Use the table() function to compare the cluster membership to the actual diagnoses

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

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

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

```
wisc.hclust.clusters <- cutree(wisc.hclust, k=6)
table(wisc.hclust.clusters,diagnosis)
```

```
                    diagnosis
wisc.hclust.clusters   0   1
                   1  12 165
                   2   0   5
                   3 331  39
                   4   2   0
                   5  12   1
                   6   0   2
```

> Answer: A better number for cluster vs diagnoses match could be six clusters, where clusters 3, 4, and 5 demonstrates benign diagnosis, while clusters 1, 2, and 6 demonstrate malignant diagnosis.

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".

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

```r
wisc.hclust1 <- hclust(data.dist, method="ward.D2")
wisc.hclust1.clusters <- cutree(wisc.hclust1, k=2)
table(wisc.hclust1.clusters, diagnosis)
```

```
                     diagnosis
wisc.hclust1.clusters   0   1
                    1  20 164
                    2 337  48
```

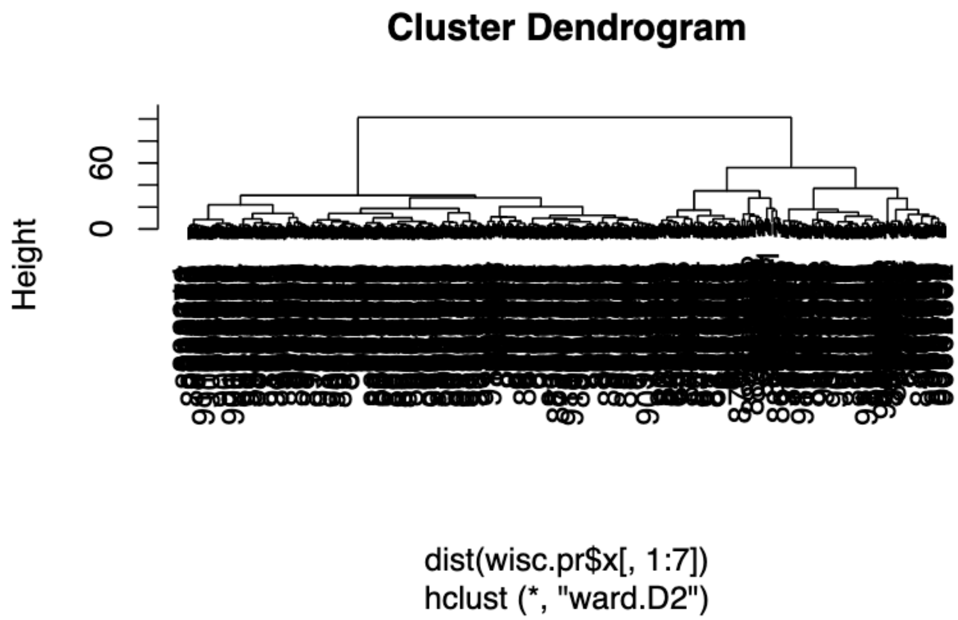
Answer: My favorate method to use is the ward.D2 method, because this method produces two clear clusters of the diagnosis types, by cutting them into two groups. This allows for easier identification of which clusters is the benign and which is malignant diagnosis.

Q14. Optional K-means clustering (Skipped)

5. Combining methods

Clustering on PCA results

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



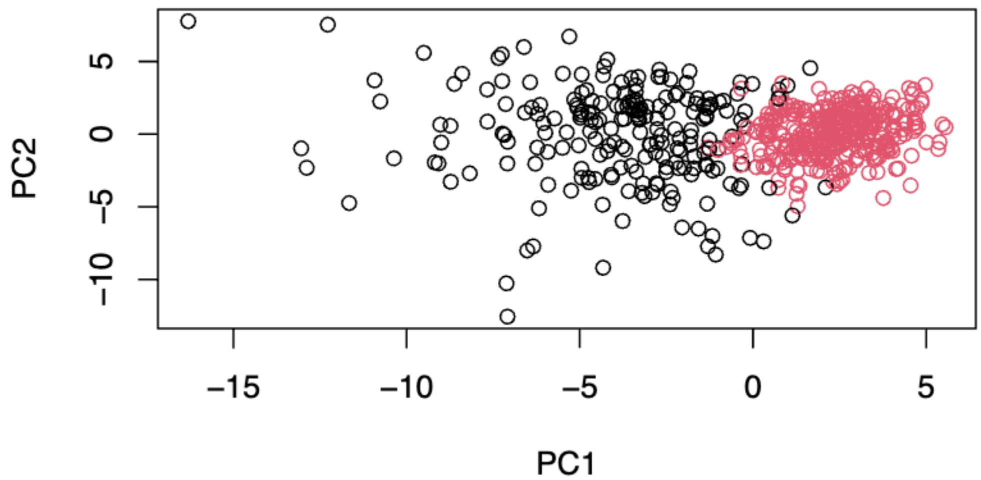

```r
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

```
grps
  1   2 
216 353 
```

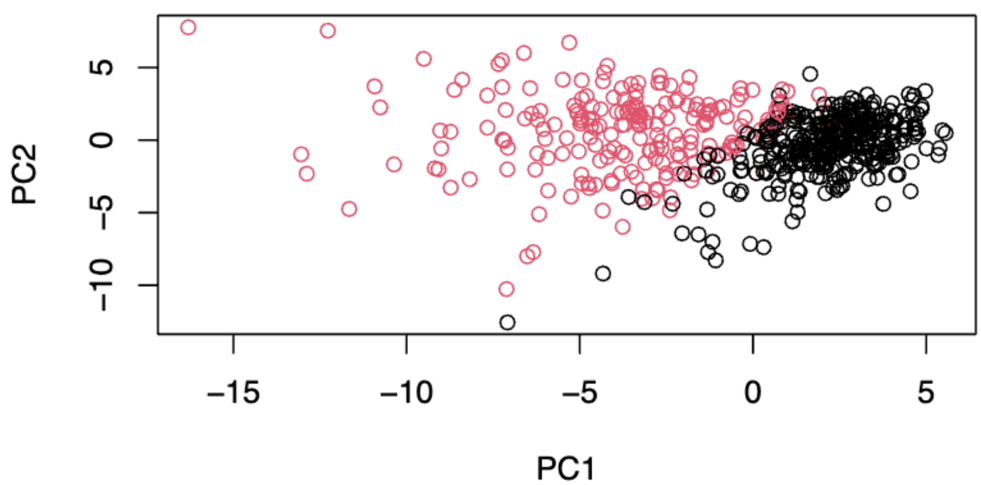
```r
table(grps, diagnosis)
```

```
    diagnosis
grps   0   1
   1  28 188
   2 329  24
```

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




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



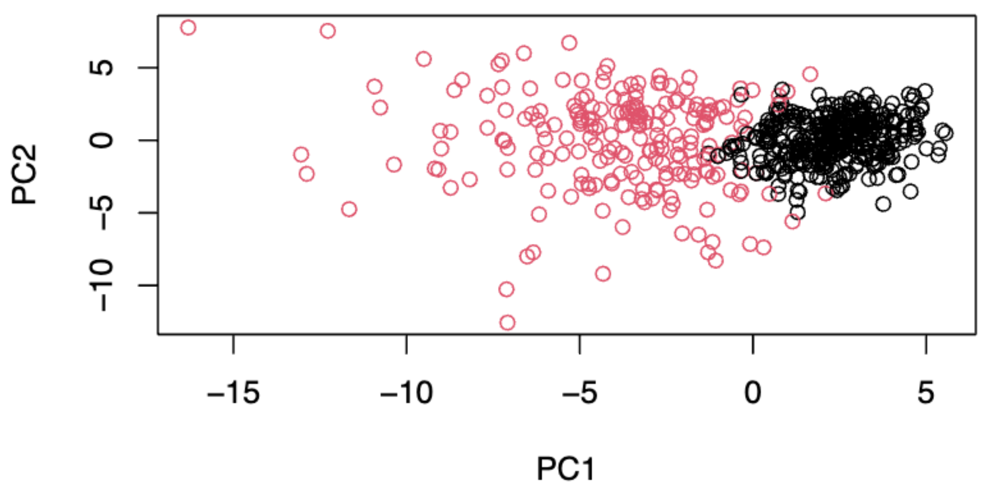
```r
g <- as.factor(grps)
levels(g)
```

```
[1] "1" "2"
```

```r
#To match things up we can turn our groups into a factor and reorder the levels so cluster

g <- relevel(g,2)
levels(g)
```

```
[1] "2" "1"
```

```r
# Plot using our re-ordered factor
plot(wisc.pr$x[,1:2], col=g)
```




```r
## Use the distance along the first 7 PCs for clustering i.e. wisc.pr$x[, 1:7]

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

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

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

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

```
                        diagnosis
wisc.pr.hclust.clusters   0   1
                      1  28 188
                      2 329  24
```

Q15. How well does the newly created model with four clusters separate out the two diagnoses?

Answer: According to the table comparing actual diagnosis, the new model work very well in separating out the two diagnoses.