MATH 308 Assignment 4

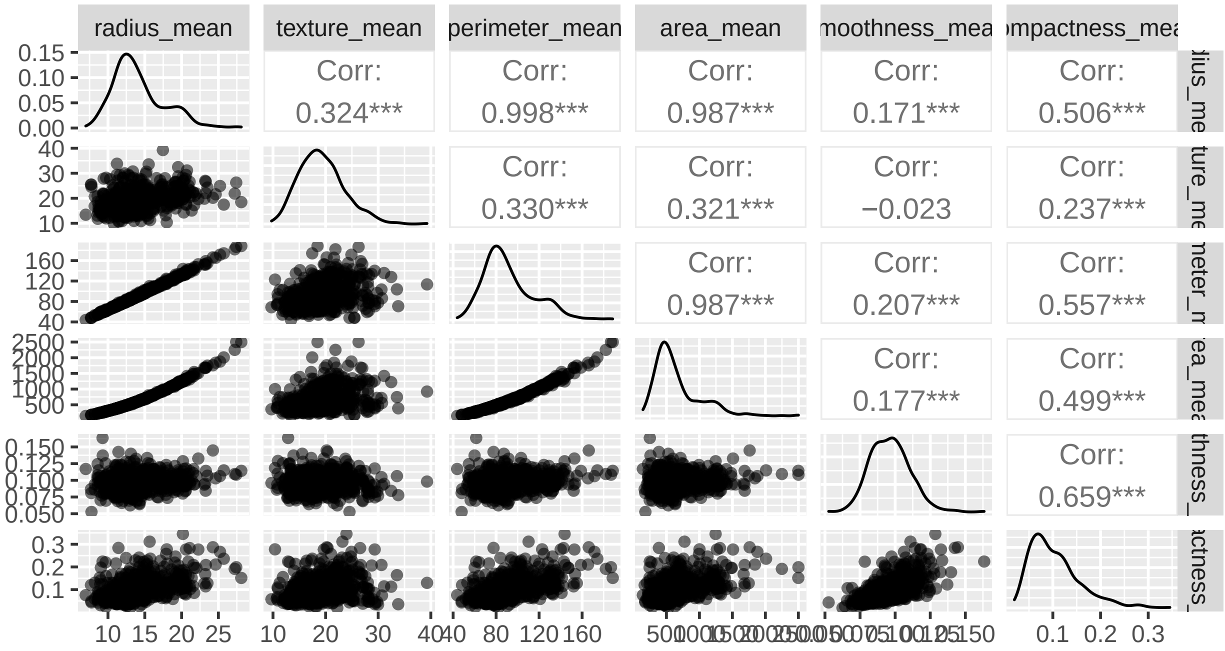
Breast cancer is the most common malignancy among women, accounting for nearly 1 in 3 cancers diagnosed among women in the United States, and it is the second leading cause of cancer death among women. Breast Cancer occurs as a result of abnormal growth of cells in the breast tissue, commonly referred to as a Tumor. The task given by the project is to perform principal component analysis (PCA) for the given continues data that stored in the dataset Breast-Cancer-Wisconsin created by Dr. William H. Wolberg. Thus, the first thing we did is to remove all the categorical data and useless data columns, such as column 'class'. Those column contains the categorical data as 1 or 2. In the first run, we chose to use the mean for our PCA on the data.

The real-valued features (continues data) are computed for each cell nucleus:

a) radius (mean of distances from center to points on the perimeter)
b) texture (standard deviation of gray-scale values)
c) perimeter
d) area
e) smoothness (local variation in radius lengths)
f) compactness (perimeter^2 / area - 1.0)
g) concavity (severity of concave portions of the contour)
h) concave points (number of concave portions of the contour)
i) symmetry
j) fractal dimension ("coastline approximation" - 1)

To better understand the correlation between variables, we present the pairwise plot. We only consider the first 6 variables here for the readibility of the figure.

```r
ggpairs(sub_df[3:8], aes(alpha = 0.1))
```



We have a look of mean

```r
## Mean
apply(sub_df[3:12] , 2, mean)
```

```
##             radius_mean            texture_mean          perimeter_mean 
##             14.12729174             19.28964851             91.96903339 
##               area_mean         smoothness_mean        compactness_mean 
##            654.88910369              0.09636028              0.10434098 
##          concavity_mean     concave.points_mean           symmetry_mean 
##              0.08879932              0.04891915              0.18116186 
## fractal_dimension_mean 
##              0.06279761
```

and variance as well.

```r
## Variance
apply(sub_df[3:12] , 2, var)
```

```
##             radius_mean            texture_mean          perimeter_mean 
##            1.241892e+01            1.849891e+01            5.904405e+02 
##               area_mean         smoothness_mean        compactness_mean 
##            1.238436e+05            1.977997e-04            2.789187e-03 
##          concavity_mean     concave.points_mean           symmetry_mean 
##            6.355248e-03            1.505661e-03            7.515428e-04 
## fractal_dimension_mean 
##            4.984872e-05
```

Since the variables all have different and incomparable scales, we need to scale them to unit variance when finding the principle components.

```r
br_cancer_mean.pca <- prcomp(sub_df[3:12], scale=TRUE)
summary(br_cancer_mean.pca)
```

```
## Importance of components:
##                           PC1    PC2     PC3    PC4     PC5     PC6     PC7
## Standard deviation     2.3406 1.5870 0.93841 0.7064 0.61036 0.35234 0.28299
## Proportion of Variance 0.5479 0.2519 0.08806 0.0499 0.03725 0.01241 0.00801
## Cumulative Proportion  0.5479 0.7997 0.88779 0.9377 0.97495 0.98736 0.99537
##                            PC8     PC9    PC10
## Standard deviation     0.18679 0.10552 0.01680
## Proportion of Variance 0.00349 0.00111 0.00003
## Cumulative Proportion  0.99886 0.99997 1.00000
```

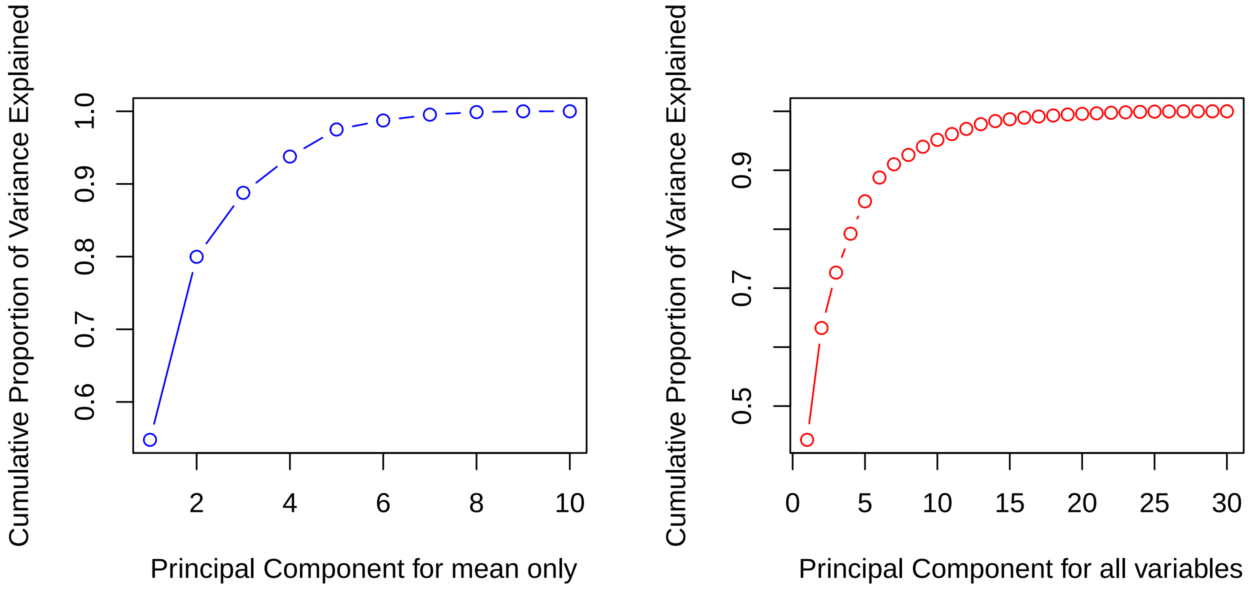
```r
br_cancer_all.pca <- prcomp(df[3:32], scale=TRUE)
summary(br_cancer_all.pca)
```

```
## 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
```

We have a look of cumulative proportion of variance explained. Notice that the first two components only explain 63% of the total vairance, which means more components are needed for data analysis. Applying ‘the 80% Rule’, we need to consider the first five components.

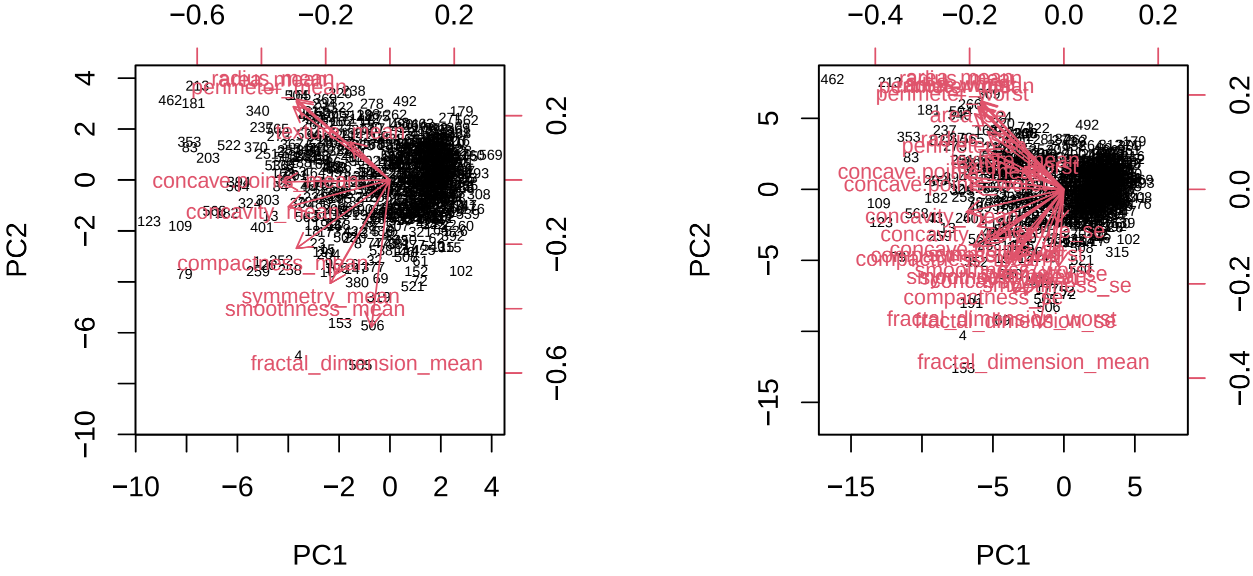
The plots below are the proportion of variance by every principal component only for mean and for all variables.

```
par(mfrow =c(1,2))
plot(cumsum(br_cancer_mean.pca$sdev^2/(sum(br_cancer_mean.pca$sdev^2))),
     xlab=" Principal Component for mean only",
     ylab ="Cumulative Proportion of Variance Explained",type='b',col =" blue")
plot(cumsum(br_cancer_all.pca$sdev^2/(sum(br_cancer_all.pca$sdev^2))),
     xlab=" Principal Component for all variables",
     ylab ="Cumulative Proportion of Variance Explained",type='b',col =" red")
```



Check the biplot

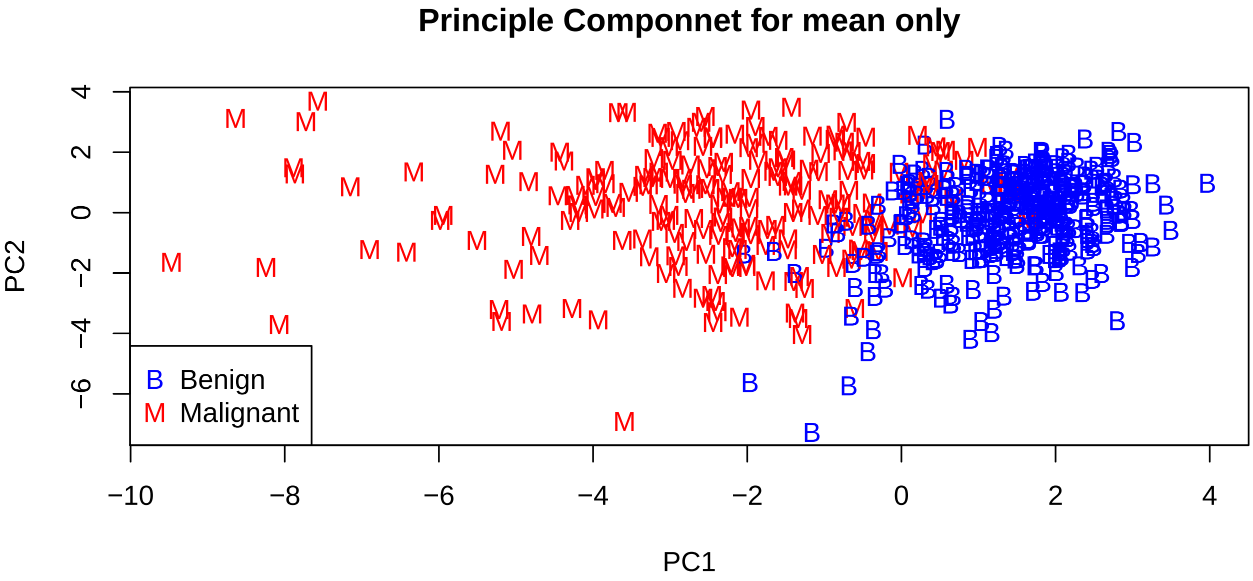
```
par(mfrow =c(1,2))
biplot(br_cancer_mean.pca,scale=0, cex = c(0.5, 0.75))
biplot(br_cancer_all.pca,scale=0, cex = c(0.5, 0.75))
```



We found a regular pattern that for the first main Principle Component, if we only take consideration in mean, PC is positive. In that way, considering all Principle Component of 30 variables, they maintain the corresponding positive or negative signs in most cases. In addition, standard deviations and worsts are strongly correlated with mean. That's the reason why we chose mean to summarize our dataset. By checking the biplots, for the first plot (using mean), PC1 is associated with concave point_mean, and PC2 is associated with radius_mean. The second plots show the same association with PC1 and PC2. This result also indicates that mean value is sufficient to represent the data.

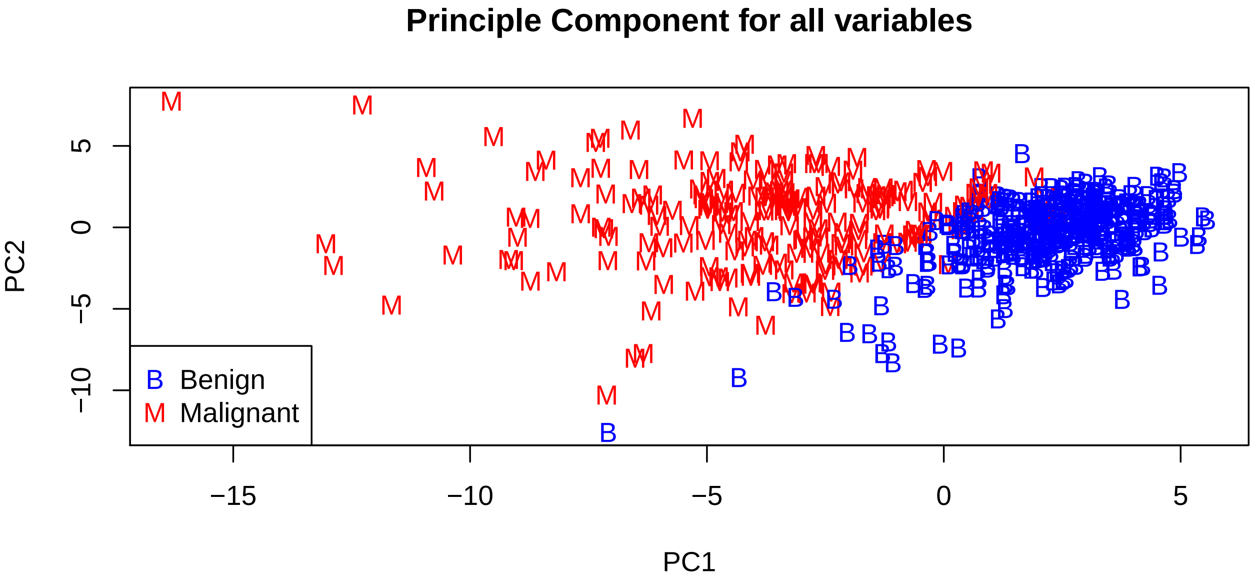
Next, we plot the first two projected X. In the first graph, the X is from PCA at which only mean is considered. In the second graph, mean, standard deviation and "worst" of all 10 features is considered. We find 10 mean variables are as good as 30 all mean, sd, worst variables in providing a seperation.

```r
plot(br_cancer_mean.pca$x[, 1:2], pch = ifelse(sub_df[, "diagnosis"] == "B", "B", "M"),
     col = ifelse(sub_df[, "diagnosis"] == "B", "blue", "red"),
     main="Principle Componnet for mean only")
legend("bottomleft", legend = c("Benign", "Malignant"),
       col = c("blue", "red"), pch = c("B", "M"))
```


Principle Componnet for mean only

In this plot, we have reduced the dimensions to 2, which keeps less information. Observing the plot above, we can see that these two variables can be separated by a line with Benign on the right side and Malignant on the other side. If we use the first five components, there will be much more variables and dimensions to analyze. However, using two dimensions can help us summarize the information better with lots of data existing.

```r
plot(br_cancer_all.pca$x[, 1:2], pch = ifelse(sub_df[, "diagnosis"] == "B", "B", "M"),
     col = ifelse(sub_df[, "diagnosis"] == "B", "blue", "red"),
     main="Principle Component for all variables")
legend("bottomleft", legend = c("Benign", "Malignant"),
       col = c("blue", "red"), pch = c("B", "M"))
```



Notice that in both cases, there exists a straight line that separates the benign and malignant observations. However, we see more overlapping in the case with only means. This may suggest the prediction based on means may not be as reliable as when all variables are considered.