

class08: PCA Mini Project

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It is important to consider scaling your data before PCA.

For example:

```
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

```
colMeans(mtcars)
```

mpg	cyl	disp	hp	drat	wt	qsec
20.090625	6.187500	230.721875	146.687500	3.596563	3.217250	17.848750
vs	am	gear	carb			
0.437500	0.406250	3.687500	2.812500			

```
apply(mtcars,2,sd)
```

mpg	cyl	disp	hp	drat	wt
6.0269481	1.7859216	123.9386938	68.5628685	0.5346787	0.9784574
qsec	vs	am	gear	carb	
1.7869432	0.5040161	0.4989909	0.7378041	1.6152000	

```
x <- scale(mtcars)
head(x)
```

	mpg	cyl	disp	hp	drat
Mazda RX4	0.1508848	-0.1049878	-0.57061982	-0.5350928	0.5675137
Mazda RX4 Wag	0.1508848	-0.1049878	-0.57061982	-0.5350928	0.5675137
Datsun 710	0.4495434	-1.2248578	-0.99018209	-0.7830405	0.4739996
Hornet 4 Drive	0.2172534	-0.1049878	0.22009369	-0.5350928	-0.9661175
Hornet Sportabout	-0.2307345	1.0148821	1.04308123	0.4129422	-0.8351978
Valiant	-0.3302874	-0.1049878	-0.04616698	-0.6080186	-1.5646078

	wt	qsec	vs	am	gear
Mazda RX4	-0.610399567	-0.7771651	-0.8680278	1.1899014	0.4235542
Mazda RX4 Wag	-0.349785269	-0.4637808	-0.8680278	1.1899014	0.4235542
Datsun 710	-0.917004624	0.4260068	1.1160357	1.1899014	0.4235542
Hornet 4 Drive	-0.002299538	0.8904872	1.1160357	-0.8141431	-0.9318192
Hornet Sportabout	0.227654255	-0.4637808	-0.8680278	-0.8141431	-0.9318192
Valiant	0.248094592	1.3269868	1.1160357	-0.8141431	-0.9318192

	carb
Mazda RX4	0.7352031
Mazda RX4 Wag	0.7352031
Datsun 710	-1.1221521
Hornet 4 Drive	-1.1221521
Hornet Sportabout	-0.5030337
Valiant	-1.1221521

```
round(colMeans(x),2)
```

mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
0	0	0	0	0	0	0	0	0	0	0

```
round(apply(x,2,sd),2)
```

mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
1	1	1	1	1	1	1	1	1	1	1

The mean has been scaled to 0, and the SD to 1.

Unsupervised Learning Analysis of Human Breast Cancer Cells

1) Exploratory Data Analysis

```
# 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			

We don't want to pass the 'diagnosis' to the PCA, that is just the expert answer that we will later compare our analysis results to. So, we will remove it and also make a vector called 'diagnosis'.

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

```
# Create diagnosis vector for later
diagnosis <- wisc.df$diagnosis
```

- Q1. How many observations are in this dataset?

```
nrow(wisc.df)
```

```
[1] 569
```

There are 569 observations in the dataset.

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

```
# Use table to see how many observations have malignant diagnosis
table(diagnosis)['M']
```

```
M
212
```

There are 212 malignant diagnoses.

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

```
mean_names <- grep("_mean$", colnames(wisc.df))
length(mean_names)
```

```
[1] 10
```

10 columns have `_mean` in their name.

PCA

```
# Check column means and standard deviations
round(colMeans(wisc.data),2)
```

radius_mean	texture_mean	perimeter_mean
14.13	19.29	91.97
area_mean	smoothness_mean	compactness_mean
654.89	0.10	0.10
concavity_mean	concave.points_mean	symmetry_mean
0.09	0.05	0.18
fractal_dimension_mean	radius_se	texture_se
0.06	0.41	1.22
perimeter_se	area_se	smoothness_se
2.87	40.34	0.01
compactness_se	concavity_se	concave.points_se

	0.03	0.03	0.01
symmetry_se	fractal_dimension_se	radius_worst	
0.02	0.00	16.27	
texture_worst	perimeter_worst	area_worst	
25.68	107.26	880.58	
smoothness_worst	compactness_worst	concavity_worst	
0.13	0.25	0.27	
concave.points_worst	symmetry_worst	fractal_dimension_worst	
0.11	0.29	0.08	

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

radius_mean	texture_mean	perimeter_mean
3.52	4.30	24.30
area_mean	smoothness_mean	compactness_mean
351.91	0.01	0.05
concavity_mean	concave.points_mean	symmetry_mean
0.08	0.04	0.03
fractal_dimension_mean	radius_se	texture_se
0.01	0.28	0.55
perimeter_se	area_se	smoothness_se
2.02	45.49	0.00
compactness_se	concavity_se	concave.points_se
0.02	0.03	0.01
symmetry_se	fractal_dimension_se	radius_worst
0.01	0.00	4.83
texture_worst	perimeter_worst	area_worst
6.15	33.60	569.36
smoothness_worst	compactness_worst	concavity_worst
0.02	0.16	0.21
concave.points_worst	symmetry_worst	fractal_dimension_worst
0.07	0.06	0.02

```
# Perform PCA on wisc.data
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)?

0.4427 of the original variance is captured by PC1.

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

Looking at the cumulative proportion, we can see that 3 PCs are required to describe at least 70% of the original variance.

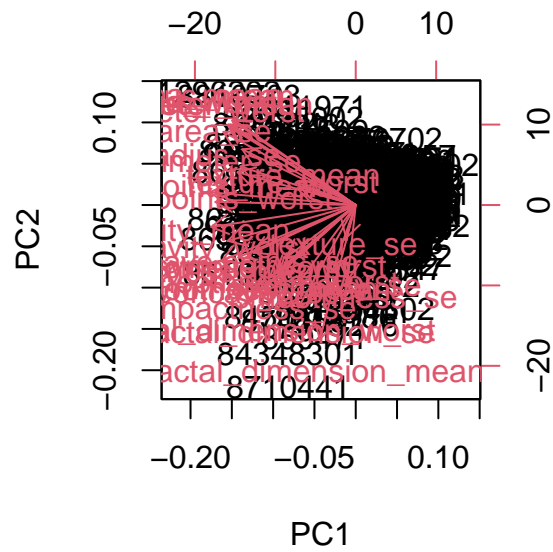
Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data?

Looking at the cumulative proportion, we can see that 7 PCs are required to describe at least 90% of the original variance.

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

It is very messy and difficult to understand.

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



Let's look at what is in this `wisc.pr`

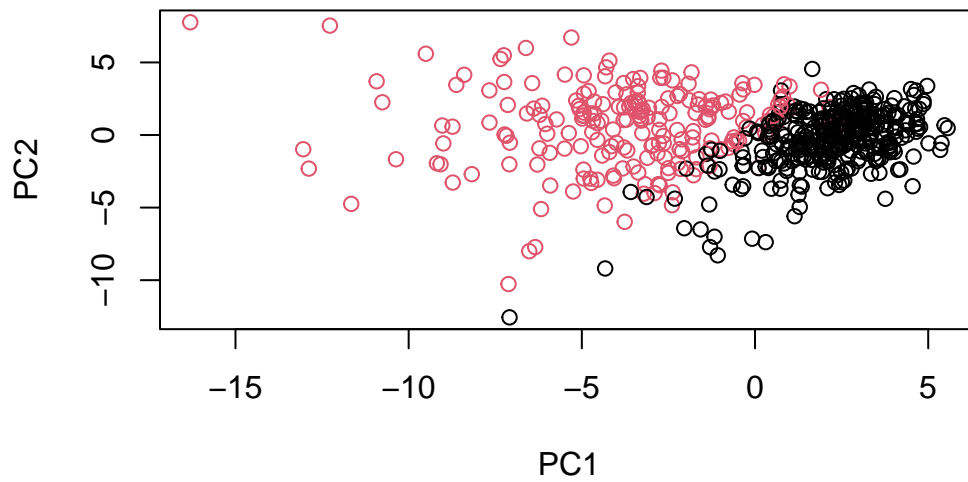
```
attributes(wisc.pr)
```

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

```
$class
[1] "prcomp"
```

Main ‘PC score plot’, ‘PC1 vs PC2 plot’

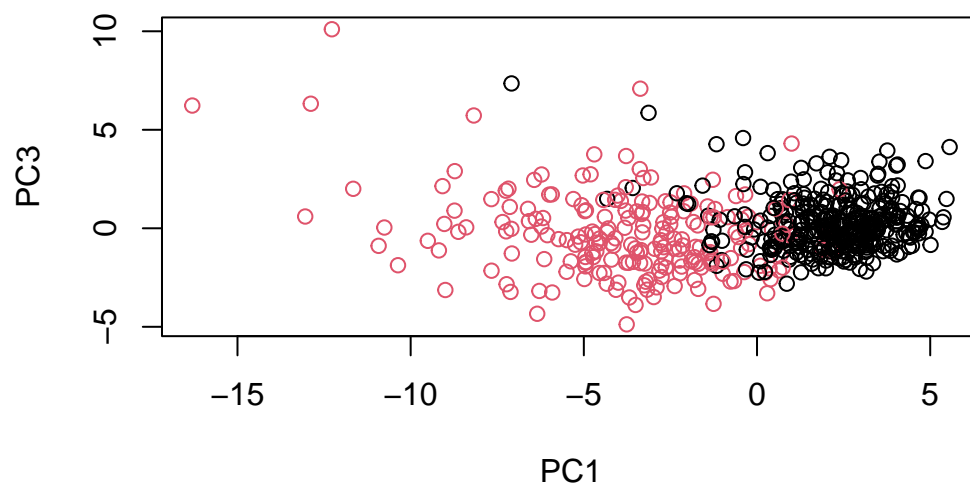
```
plot(wisc.pr$x[,1],wisc.pr$x[,2],col=as.factor(diagnosis),xlab = "PC1", ylab = "PC2")
```

```
# or plot(wisc.pr$x,col=as.factor(diagnosis))
```

Q8. Generate a similar plot for principal components 1 and 3. What do you notice about these plots? It is kind of similar to PC1 vs PC2 plot, but there is more overlap.

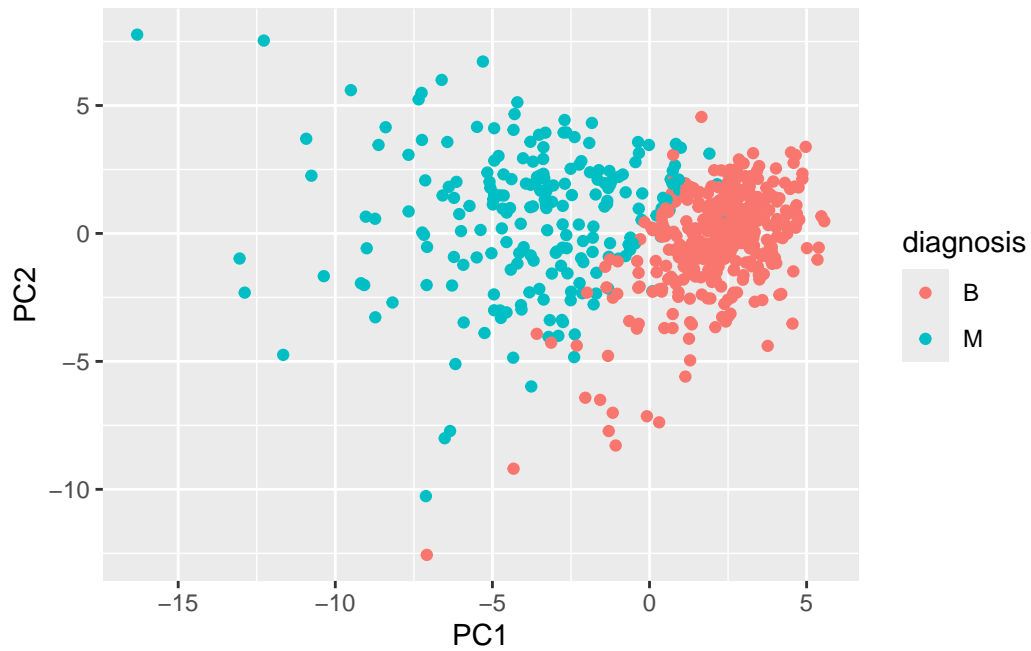
```
plot(wisc.pr$x[,1],wisc.pr$x[,3],col=as.factor(diagnosis),xlab = "PC1", ylab = "PC3")
```



```
# 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()
```

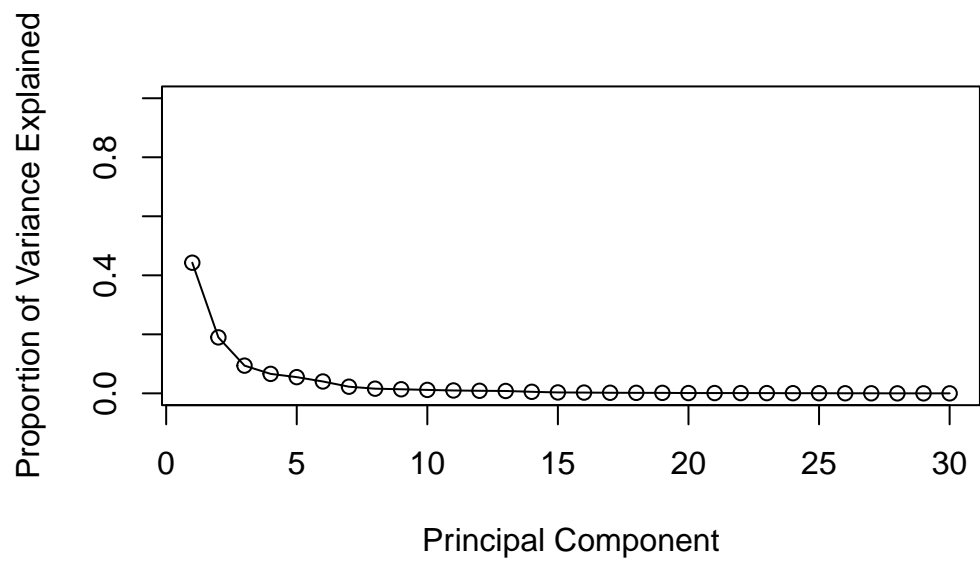


```
# Calculate variance of each component
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

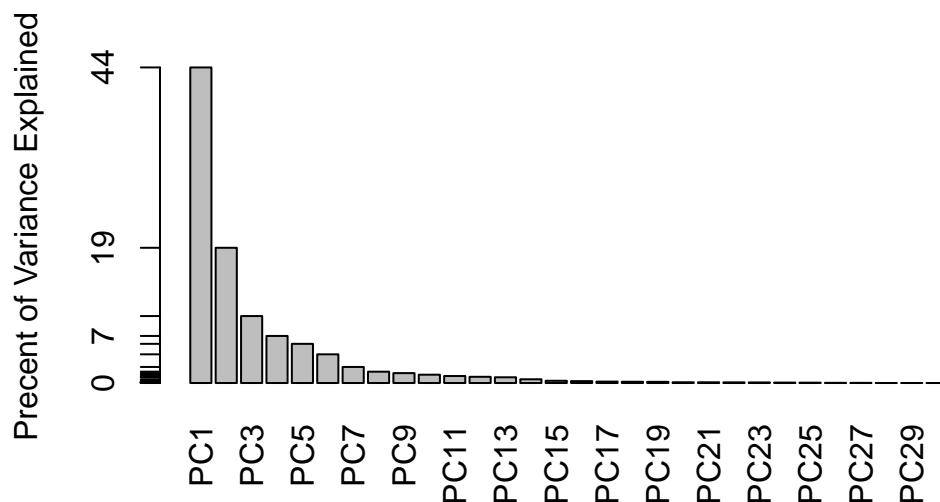
```
[1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

```
# 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 )
```



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`?

It is -0.2608538.

```
head(wisc.pr$rotation)
```

	PC1	PC2	PC3	PC4	PC5
radius_mean	-0.2189024	0.23385713	-0.008531243	0.04140896	-0.03778635
texture_mean	-0.1037246	0.05970609	0.064549903	-0.60305000	0.04946885
perimeter_mean	-0.2275373	0.21518136	-0.009314220	0.04198310	-0.03737466
area_mean	-0.2209950	0.23107671	0.028699526	0.05343380	-0.01033125
smoothness_mean	-0.1425897	-0.18611302	-0.104291904	0.15938277	0.36508853
compactness_mean	-0.2392854	-0.15189161	-0.074091571	0.03179458	-0.01170397
	PC6	PC7	PC8	PC9	PC10
radius_mean	0.018740790	-0.12408834	0.007452296	-0.223109764	0.09548644
texture_mean	-0.032178837	0.01139954	-0.130674825	0.112699390	0.24093407
perimeter_mean	0.017308445	-0.11447706	0.018687258	-0.223739213	0.08638562
area_mean	-0.001887748	-0.05165343	-0.034673604	-0.195586014	0.07495649
smoothness_mean	-0.286374497	-0.14066899	0.288974575	0.006424722	-0.06929268
compactness_mean	-0.014130949	0.03091850	0.151396350	-0.167841425	0.01293620
	PC11	PC12	PC13	PC14	PC15
radius_mean	-0.04147149	0.05106746	0.01196721	0.059506135	-0.05111877

texture_mean	0.30224340	0.25489642	0.20346133	-0.021560100	-0.10792242
perimeter_mean	-0.01678264	0.03892611	0.04410950	0.048513812	-0.03990294
area_mean	-0.11016964	0.06543751	0.06737574	0.010830829	0.01396691
smoothness_mean	0.13702184	0.31672721	0.04557360	0.445064860	-0.11814336
compactness_mean	0.30800963	-0.10401704	0.22928130	0.008101057	0.23089996
	PC16	PC17	PC18	PC19	PC20
radius_mean	-0.1505839	0.20292425	0.146712338	0.22538466	-0.04969866
texture_mean	-0.1578420	-0.03870612	-0.041102985	0.02978864	-0.24413499
perimeter_mean	-0.1144540	0.19482131	0.158317455	0.23959528	-0.01766501
area_mean	-0.1324480	0.25570576	0.266168105	-0.02732219	-0.09014376
smoothness_mean	-0.2046132	0.16792991	-0.352226802	-0.16456584	0.01710096
compactness_mean	0.1701784	-0.02030771	0.007794138	0.28422236	0.48868633
	PC21	PC22	PC23	PC24	PC25
radius_mean	-0.06857001	-0.07292890	-0.0985526942	-0.18257944	-0.01922650
texture_mean	0.44836947	-0.09480063	-0.0005549975	0.09878679	0.08474593
perimeter_mean	-0.06976904	-0.07516048	-0.0402447050	-0.11664888	0.02701541
area_mean	-0.01844328	-0.09756578	0.0077772734	0.06984834	-0.21004078
smoothness_mean	-0.11949175	-0.06382295	-0.0206657211	0.06869742	0.02895489
compactness_mean	0.19262140	0.09807756	0.0523603957	-0.10413552	0.39662323
	PC26	PC27	PC28	PC29	
radius_mean	-0.12947640	-0.13152667	2.111940e-01	0.211460455	
texture_mean	-0.02455666	-0.01735731	-6.581146e-05	-0.010533934	
perimeter_mean	-0.12525595	-0.11541542	8.433827e-02	0.383826098	
area_mean	0.36272740	0.46661248	-2.725083e-01	-0.422794920	
smoothness_mean	-0.03700369	0.06968992	1.479269e-03	-0.003434667	
compactness_mean	0.26280847	0.09774871	-5.462767e-03	-0.041016774	
	PC30				
radius_mean	0.702414091				
texture_mean	0.000273661				
perimeter_mean	-0.689896968				
area_mean	-0.032947348				
smoothness_mean	-0.004847458				
compactness_mean	0.044674186				

```
wisc.pr$rotation["concave.points_mean", 1]
```

```
[1] -0.2608538
```

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

We need 5 PCs to explain 80% of the data.

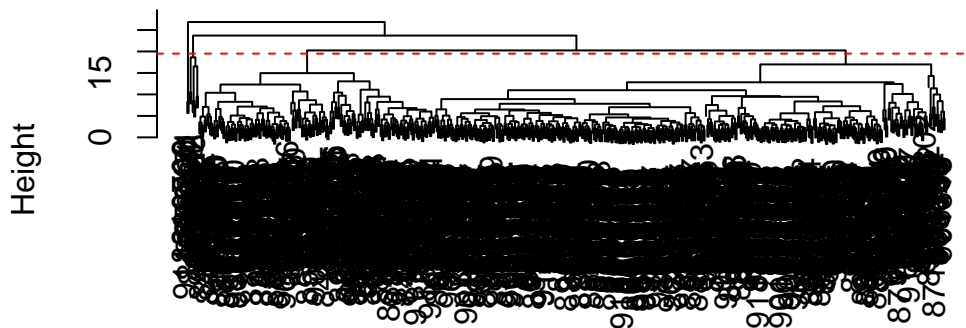
```
# Scale the wisc.data data using the "scale()" function
data.scaled <- scale(wisc.data)
```

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

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

```
plot(wisc.hclust)
abline(h = 19.5, col = "red", lty = 2)
```

Cluster Dendrogram



```
data.dist
hclust (*, "complete")
```

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

It is around 19-20.

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

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

```
diagnosis
wisc.hclust.clusters  B    M
```

1	12	165
2	2	5
3	343	40
4	0	2

Q11. Can you find a better cluster vs diagnoses match by cutting into a different number of clusters between 2 and 10?

```
wisc.hclust.clusters2 <- cutree(wisc.hclust, k =2)
table(wisc.hclust.clusters, diagnosis)
```

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

Two clusters would not work.

```
wisc.hclust.clusters3 <- cutree(wisc.hclust, k =3)
table(wisc.hclust.clusters, diagnosis)
```

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

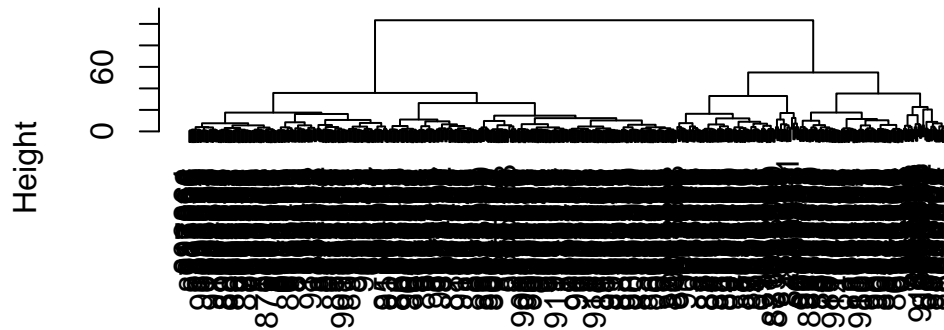
Three clusters is also not going to work. It seems 4 is the smallest number of clusters we can get here that would actually represent the separation.

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

Looking at single, complete, average and ward.D2 methods, my favorite is ward.D2. It is the cleanest-looking tree with good separation and long branch heights. Ward.D2 method minimizes variance within clusters.

```
d <- dist(wisc.pr$x[,1:3])
hc <- hclust(d, method='ward.D2')
plot(hc)
```

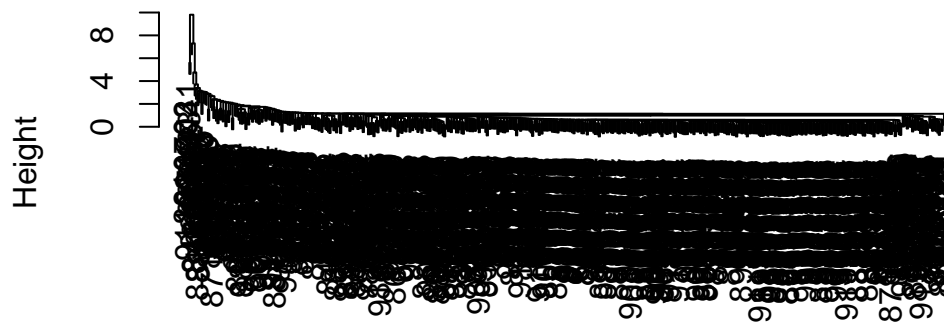

Cluster Dendrogram



```
d
hclust (*, "ward.D2")
```

```
hc2 <- hclust(d, method='single')
plot(hc2)
```

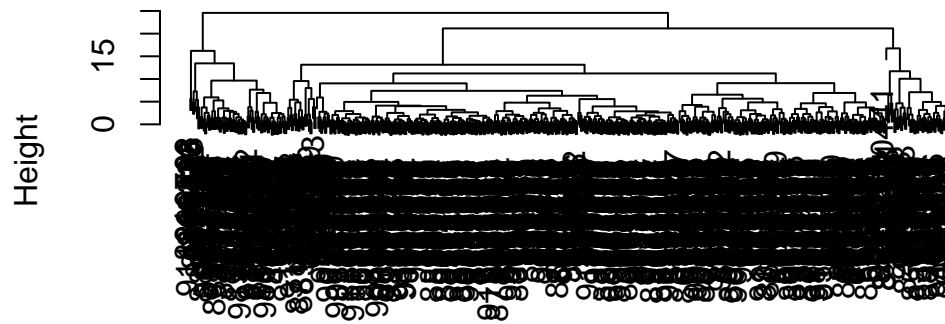
Cluster Dendrogram



```
d
hclust (*, "single")
```

```
hc3 <- hclust(d, method='complete')  
plot(hc3)
```

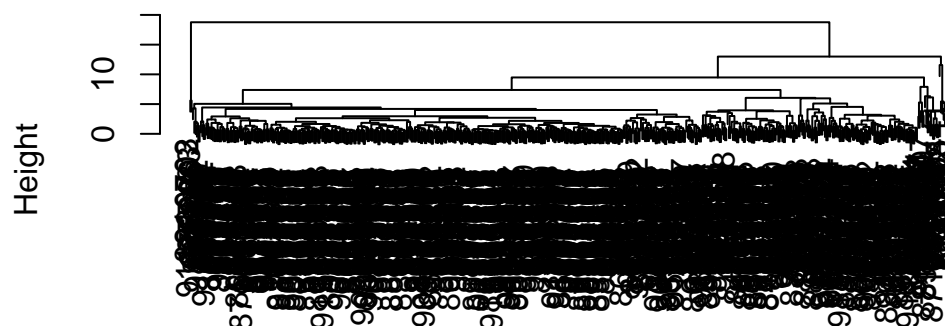
Cluster Dendrogram



d
hclust (*, "complete")

```
hc4 <- hclust(d, method='average')  
plot(hc4)
```

Cluster Dendrogram

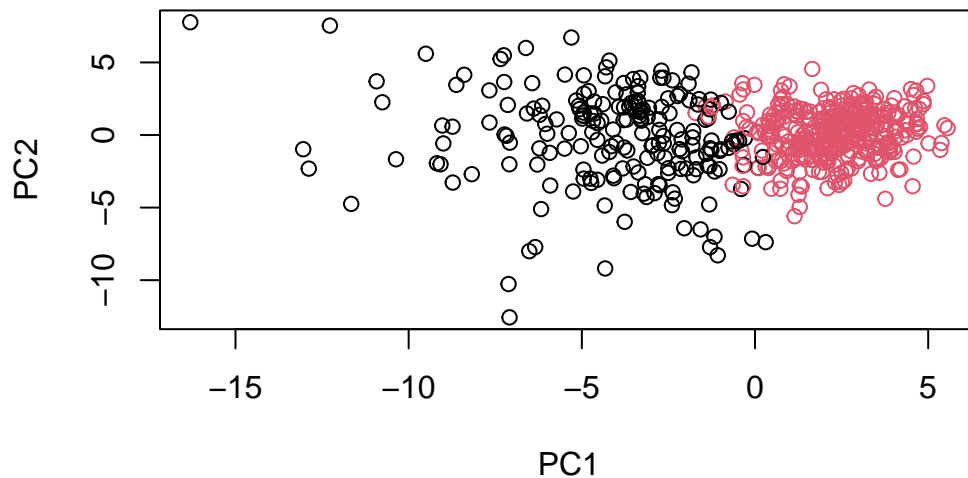


d
hclust (*, "average")

```
grps <- cutree(hc,k=2)  
table(grps, diagnosis)
```

	diagnosis	
grps	B	M
1	24	179
2	333	33

```
plot(wisc.pr$x, col=grps)
```



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

```
      grps
diagnosis 1  2
B      24 333
M     179  33
```

Q13. How well does the newly created model separate out the two diagnoses?

The model using PCA with two clusters looks pretty good and as we can see from the table results it has done quite a good job in correctly clustering the datapoints.

Q14. How well do the k-means and 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

As we can see, the model without PCA does a poor job at separating the diagnoses and requires 4 cluster minimum to yield any meaningful results like below. The output after PCA however looks much better and can separate samples well with two clusters.

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

```

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

```

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

```

      grps
diagnosis  1  2
      B  24 333
      M 179  33

```