Class08

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Save Input Data File

```
fna.data <- "WisconsinCancer.csv"
```

Storing

```
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

Remove 1st Column

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

Diagnosis Vector

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

```
[1] "M" "M" "M" "M" "M" "M"
```

Benign v Malignant Count

```
table(diagnosis)
```

```
diagnosis
  B   M
357 212
```

Q1. How Many Observations in this Dataset?

569 Observations

Q2. How many Malignant?

212 Cases

Q3. How many Variables in Data are Suffixed with '_mean'?

```
mean_check <- length(grep("_mean", colnames(wisc.data)))
mean_check
```

```
[1] 10
```

Checking Column Means and SD

```r
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
```

PCA

```r
wisc.pr <- prcomp(wisc.data, scale=T)
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. What proportion of the original variance is captured by the first principal components (PC1)?

.4427

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

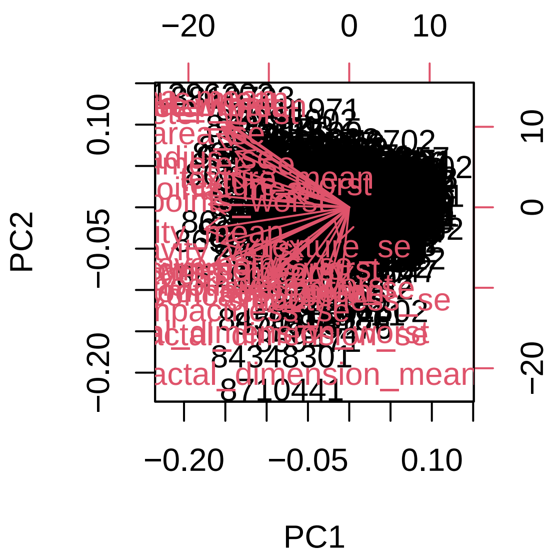
Cumulative proportion exceeds 70% at PC3 (0.72636). Therefore, three principal components (PC1, PC2, and PC3) are required to explain at least 70% of the original variance in the data.

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

Cumulative proportion exceeds 90% at PC7 (0.91010). Therefore, seven principal components (PC1-PC7) are required to explain at least 90% of the original variance in the data

Biplot

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

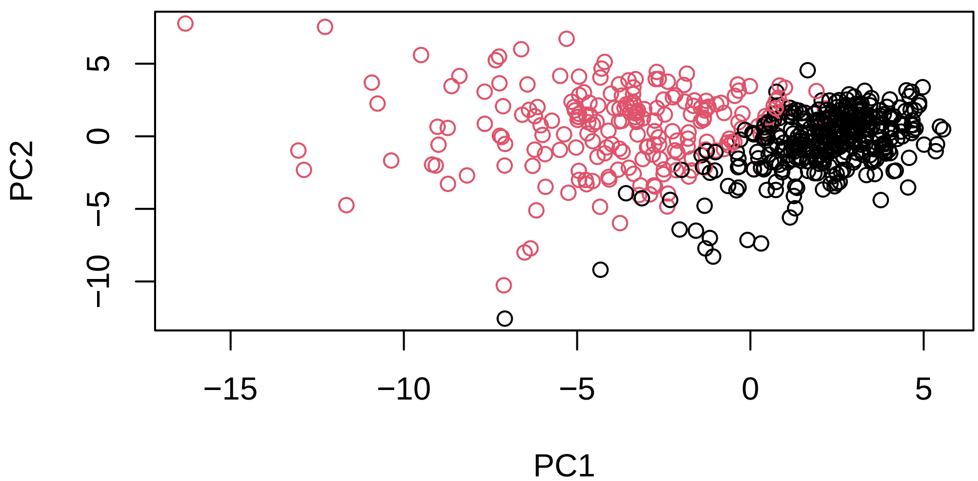


Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why?

This plot is a hot mess, need to generate our own plots for better understanding.

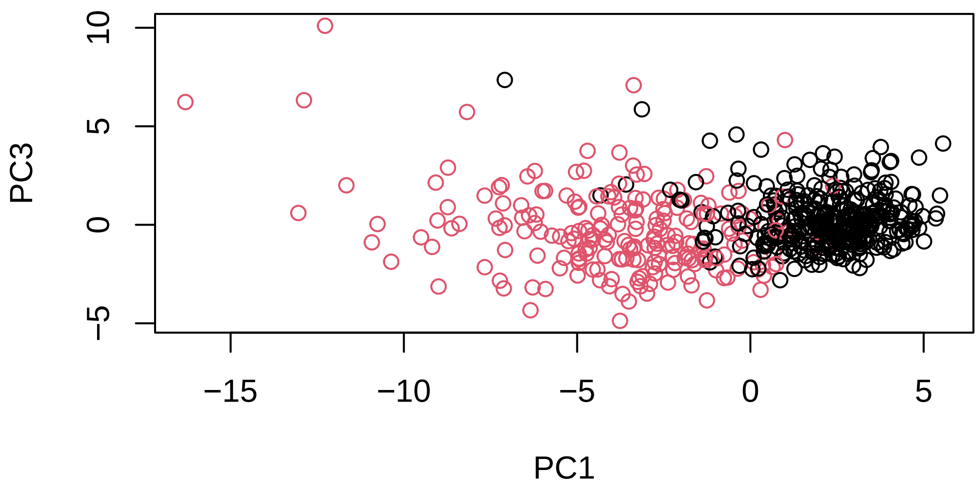
Main "PC Score Plot", "PC1vPC2 Plot"

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



Q8. Generating PC1 and PC3 Plot

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



This plot is not as clearly separated as PC1 vs PC2

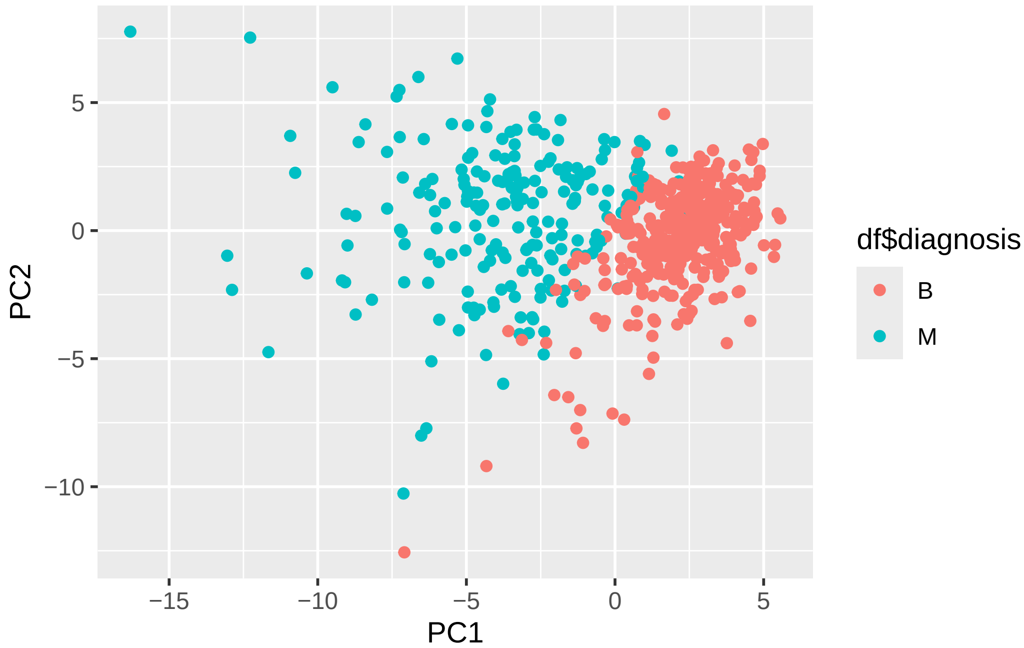
Creating Data.Frame for ggplot

```
df <- as.data.frame(wisc.pr$x)
df$diagnosis <- diagnosis
```

Making Scatterplot using ggplot2

```
library(ggplot2)
ggplot(df) +
  aes(PC1,PC2, col=df$diagnosis) +
  geom_point()
```

```
Warning: Use of `df$diagnosis` is discouraged.
i Use `diagnosis` instead.
```



Calculating Variance of Each Component

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

```
[1] 3.644394 2.385656 1.678675 1.407352 1.284029 1.098798
```

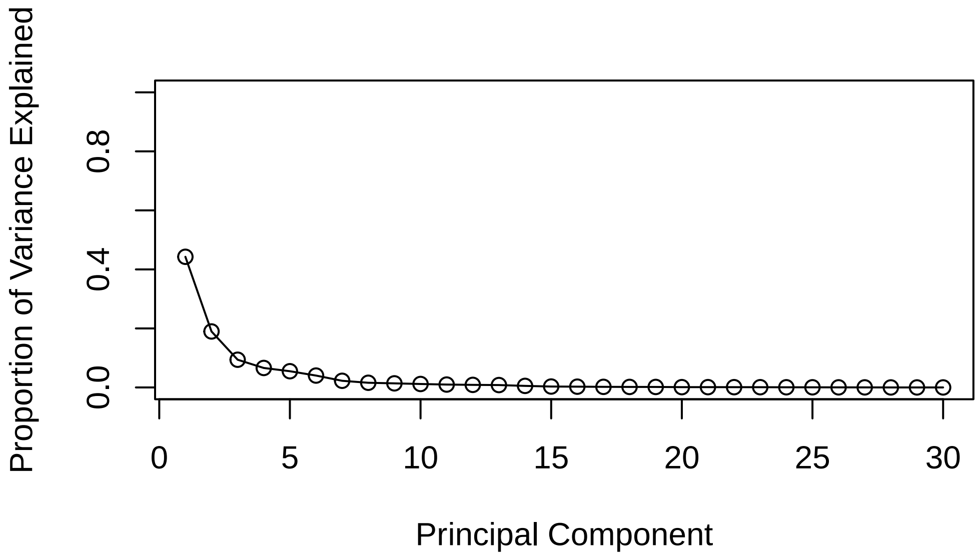
Variance Explained by Each Principal Component: pve

```
pr.var <- wisc.pr$sdev^2
pve <- pr.var/sum(pr.var)
pve
```

```
 [1] 4.427203e-01 1.897118e-01 9.393163e-02 6.602135e-02 5.495768e-02
 [6] 4.024522e-02 2.250734e-02 1.588724e-02 1.389649e-02 1.168978e-02
[11] 9.797190e-03 8.705379e-03 8.045250e-03 5.233657e-03 3.137832e-03
[16] 2.662093e-03 1.979968e-03 1.753959e-03 1.649253e-03 1.038647e-03
```

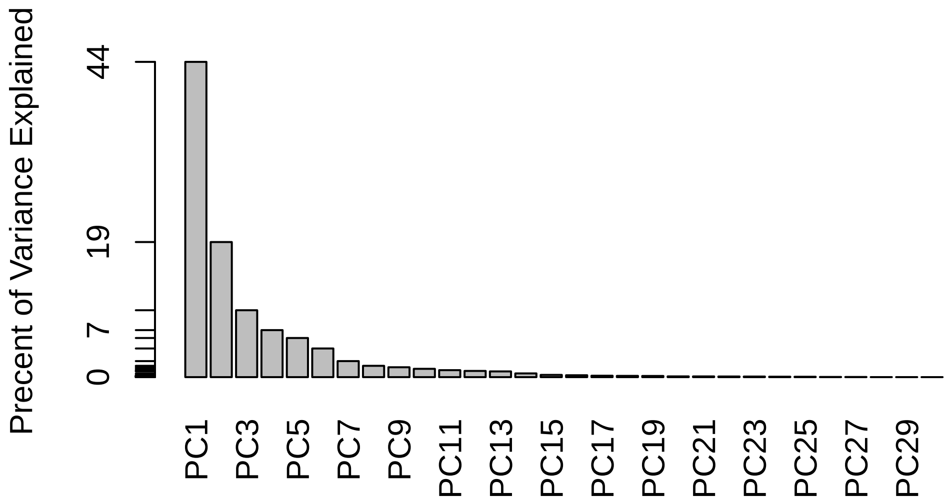
```
[21] 9.990965e-04 9.146468e-04 8.113613e-04 6.018336e-04 5.160424e-04
[26] 2.725880e-04 2.300155e-04 5.297793e-05 2.496010e-05 4.434827e-06
```

```r
plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



Alternative Scree Plot of Same Data

```r
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?

```r
loadings <- wisc.pr$rotation[, 1]
concave_points_loading <- loadings[names(wisc.data) == "concave.points_mean"]
head(concave_points_loading)
```

```
concave.points_mean
         -0.2608538
```

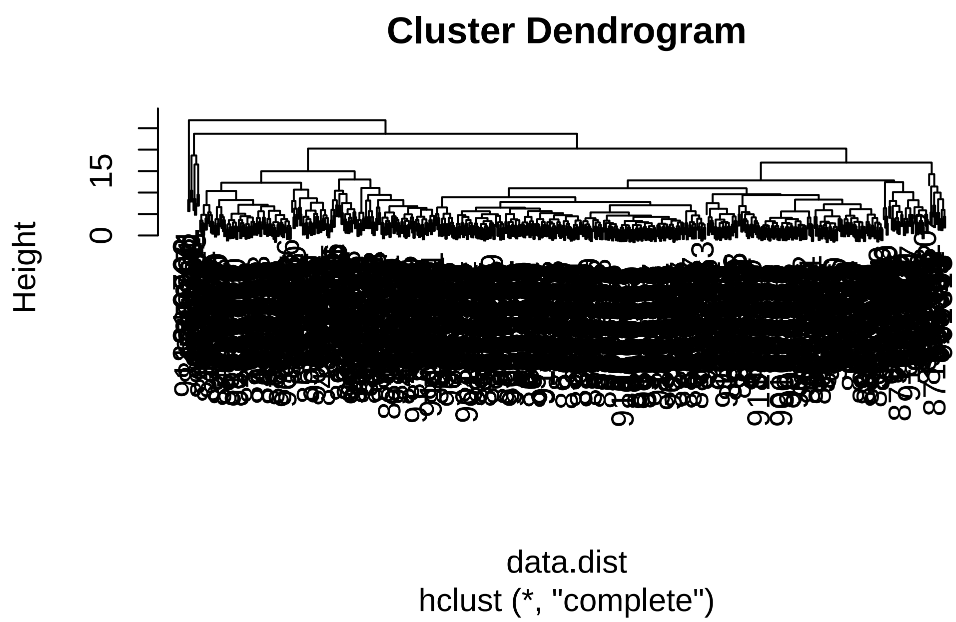
Q10. What is the minimum number of principal components required to explain 80% of the variance of the data?

Cumulative proportion exceeds 80% at PC5 (0.84734). Therefore, seven principal components (PC1-PC5) are required to explain at least 80% of the original variance in the data.

Hierarchical Clustering

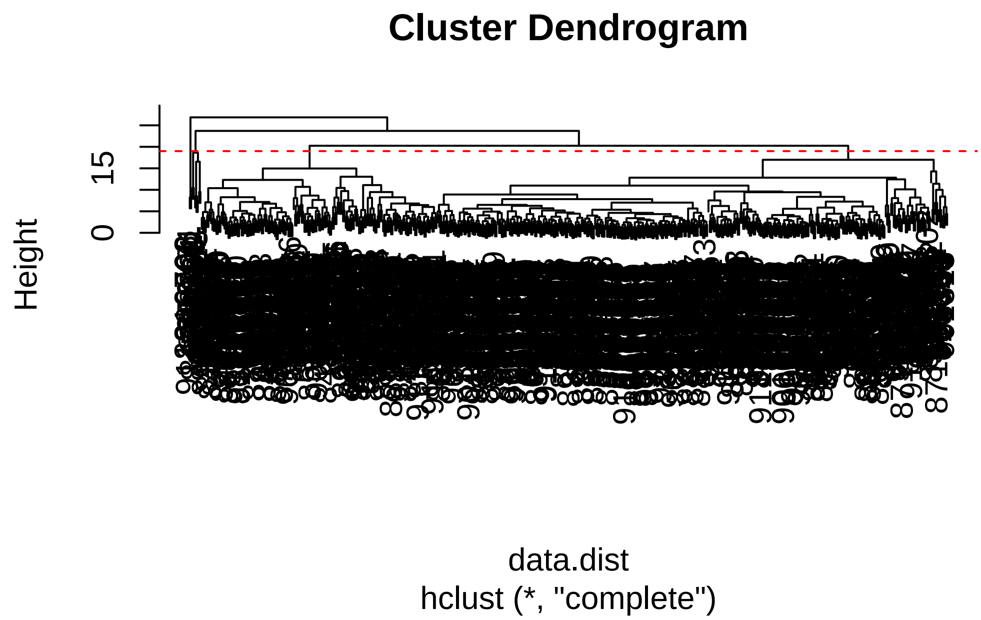
Scale Function

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



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

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



h = 19

Selecting Number of Clusters

```
wisc.hclust.clusters <- cutree(wisc.hclust, h = 19)
table(wisc.hclust.clusters, diagnosis)
```

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

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

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

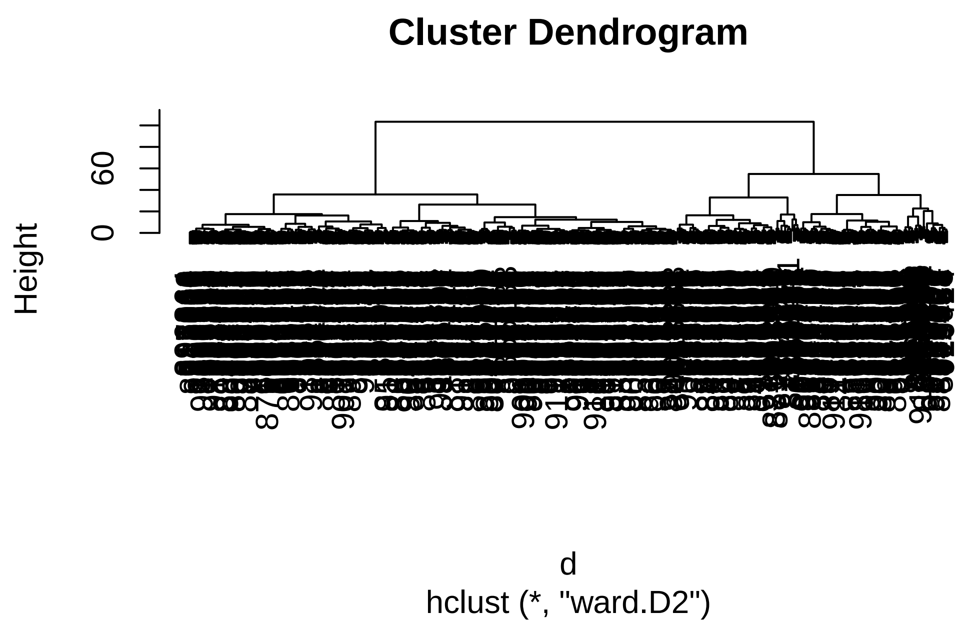
```
                     diagnosis
wisc.hclust.clusters2   B   M
                    1 357 210
                    2   0   2
```

```r
wisc.hclust.clusters10 <- cutree(wisc.hclust, k=10)
table(wisc.hclust.clusters10, diagnosis)
```

```
                      diagnosis
wisc.hclust.clusters10   B   M
                    1   12  86
                    2    0  59
                    3    0   3
                    4  331  39
                    5    0  20
                    6    2   0
                    7   12   0
                    8    0   2
                    9    0   2
                    10   0   1
```

Combining PCA and Clustering

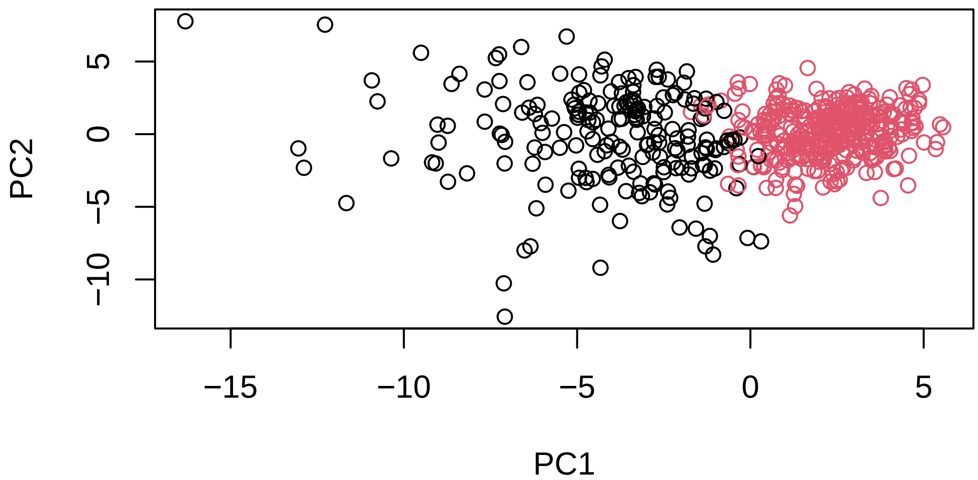
```r
d <- dist(wisc.pr$x[,1:3])
hc <-hclust(d, method="ward.D2")
plot(hc)
```



Cutree into 2 groups/branches

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

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

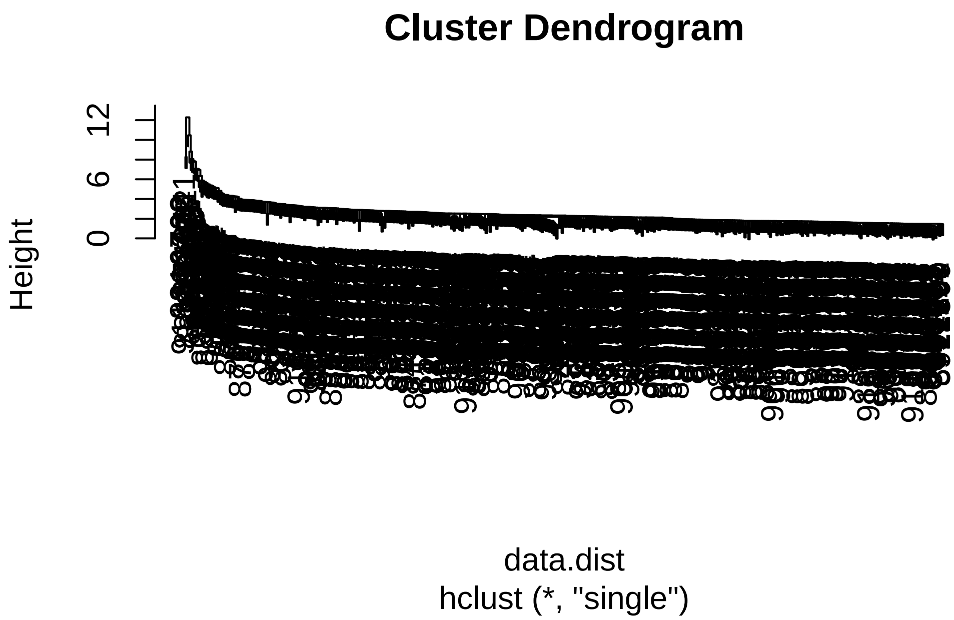


Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

My favorite is ward.d2 it produces the cleanest and most balanced clustering.

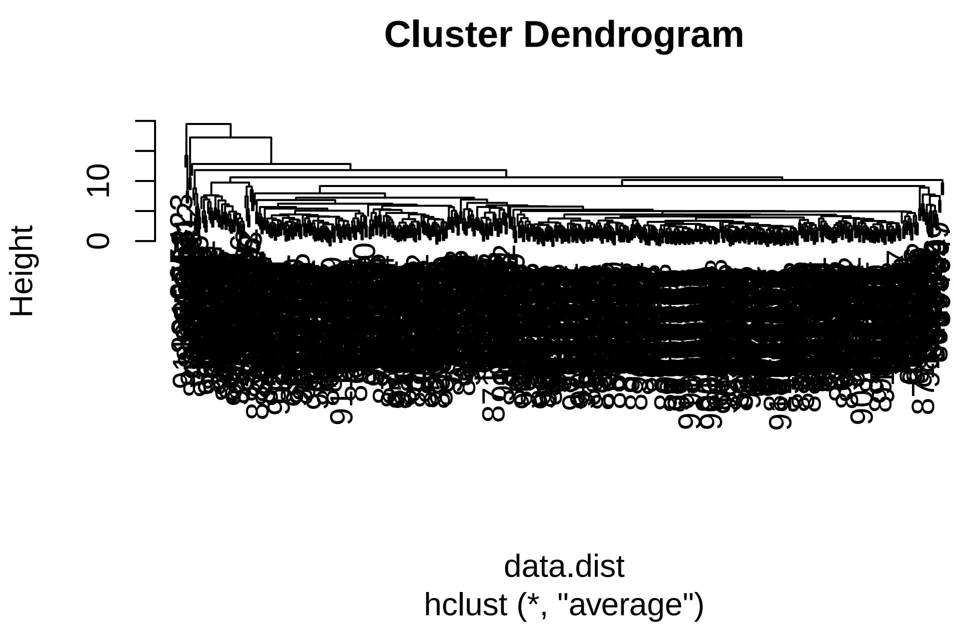
Single

```
wist.single.clust <- hclust(data.dist, method="single")
plot(wist.single.clust)
```



Average

```r
wist.average.clust <- hclust(data.dist, method="average")
plot(wist.average.clust)
```



Ward.D2

```r
wist.D2.clust <- hclust(data.dist, method="ward.D2")
plot(wist.D2.clust)
```