Class09_mini_project

Gabrielle Meza (A13747395)

10/27/2021

R Markdown

Inputing data, and setting up names. we dont want diagnosis becuase that is what we are trying to find, so we ar egetting rid of it in our dataset and then storing it as another piece for later refernece

```
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
```

```
wisc.data <- wisc.df[,-1]
diagnosis<- as.factor(wisc.df$diagnosis)
diagnosis
```

```
##   [1] 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
##  [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 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
## [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 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 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 B M M B B B B B B M 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
```

```
is.vector(diagnosis)
```

```
## [1] FALSE
```

Q1. How many observations are in this dataset?

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

```
## [1] 569
```

```
dim(wisc.data)
```

```
## [1] 569  30
```

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

= assigns a value, == pulls to find. also table(diagnosis)works

```
sum(diagnosis=="M")
```

```
## [1] 212
```

```
sum(diagnosis=="B")
```

```
## [1] 357
```

```
table(diagnosis)
```

```
## diagnosis
##   B   M
## 357 212
```

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

```
grep("_mean", colnames(wisc.data), value= TRUE )
```

```
##  [1] "radius_mean"            "texture_mean"           "perimeter_mean"
##  [4] "area_mean"              "smoothness_mean"        "compactness_mean"
##  [7] "concavity_mean"         "concave.points_mean"    "symmetry_mean"
## [10] "fractal_dimension_mean"
```

```
meanvar <- grep("_mean", colnames(wisc.data), value= TRUE )
length(meanvar)
```

```
## [1] 10
```

#Check your data scaling is correct

```
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
```

```
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
```

```
apply
```

```
## function (X, MARGIN, FUN, ..., simplify = TRUE)
## {
##     FUN <- match.fun(FUN)
##     simplify <- isTRUE(simplify)
##     dl <- length(dim(X))
##     if (!dl)
##         stop("dim(X) must have a positive length")
```

```
##     if (is.object(X))
##         X <- if (dl == 2L)
##             as.matrix(X)
##         else as.array(X)
##     d <- dim(X)
##     dn <- dimnames(X)
##     ds <- seq_len(dl)
##     if (is.character(MARGIN)) {
##         if (is.null(dnn <- names(dn)))
##             stop("'X' must have named dimnames")
##         MARGIN <- match(MARGIN, dnn)
##         if (anyNA(MARGIN))
##             stop("not all elements of 'MARGIN' are names of dimensions")
##     }
##     d.call <- d[-MARGIN]
##     d.ans <- d[MARGIN]
##     if (anyNA(d.call) || anyNA(d.ans))
##         stop("'MARGIN' does not match dim(X)")
##     s.call <- ds[-MARGIN]
##     s.ans <- ds[MARGIN]
##     dn.call <- dn[-MARGIN]
##     dn.ans <- dn[MARGIN]
##     d2 <- prod(d.ans)
##     if (d2 == 0L) {
##         newX <- array(vector(typeof(X), 1L), dim = c(prod(d.call),
##             1L))
##         ans <- forceAndCall(1, FUN, if (length(d.call) < 2L) newX[,
##             1] else array(newX[, 1L], d.call, dn.call), ...)
##         return(if (is.null(ans)) ans else if (length(d.ans) <
##             2L) ans[1L][-1L] else array(ans, d.ans, dn.ans))
##     }
##     newX <- aperm(X, c(s.call, s.ans))
##     dim(newX) <- c(prod(d.call), d2)
##     ans <- vector("list", d2)
##     if (length(d.call) < 2L) {
##         if (length(dn.call))
##             dimnames(newX) <- c(dn.call, list(NULL))
##         for (i in 1L:d2) {
##             tmp <- forceAndCall(1, FUN, newX[, i], ...)
##             if (!is.null(tmp))
##                 ans[[i]] <- tmp
##         }
##     }
##     else for (i in 1L:d2) {
##         tmp <- forceAndCall(1, FUN, array(newX[, i], d.call,
##             dn.call), ...)
##         if (!is.null(tmp))
##             ans[[i]] <- tmp
##     }
##     ans.list <- !simplify || is.recursive(ans[[1L]])
##     l.ans <- length(ans[[1L]])
##     ans.names <- names(ans[[1L]])
##     if (!ans.list)
##         ans.list <- any(lengths(ans) != l.ans)
```

```
##     if (!ans.list && length(ans.names)) {
##         all.same <- vapply(ans, function(x) identical(names(x),
##             ans.names), NA)
##         if (!all(all.same))
##             ans.names <- NULL
##     }
##     len.a <- if (ans.list)
##         d2
##     else length(ans <- unlist(ans, recursive = FALSE))
##     if (length(MARGIN) == 1L && len.a == d2) {
##         names(ans) <- if (length(dn.ans[[1L]]))
##             dn.ans[[1L]]
##         ans
##     }
##     else if (len.a == d2)
##         array(ans, d.ans, dn.ans)
##     else if (len.a && len.a%%d2 == 0L) {
##         if (is.null(dn.ans))
##             dn.ans <- vector(mode = "list", length(d.ans))
##         dn1 <- list(ans.names)
##         if (length(dn.call) && !is.null(n1 <- names(dn <- dn.call[1])) &&
##             nzchar(n1) && length(ans.names) == length(dn[[1]]))
##             names(dn1) <- n1
##         dn.ans <- c(dn1, dn.ans)
##         array(ans, c(len.a%/%d2, d.ans), if (!is.null(names(dn.ans)) ||
##             !all(vapply(dn.ans, is.null, NA)))
##             dn.ans)
##     }
##     else ans
## }
## <bytecode: 0x7ff833361d80>
## <environment: namespace:base>
```

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

44.27%

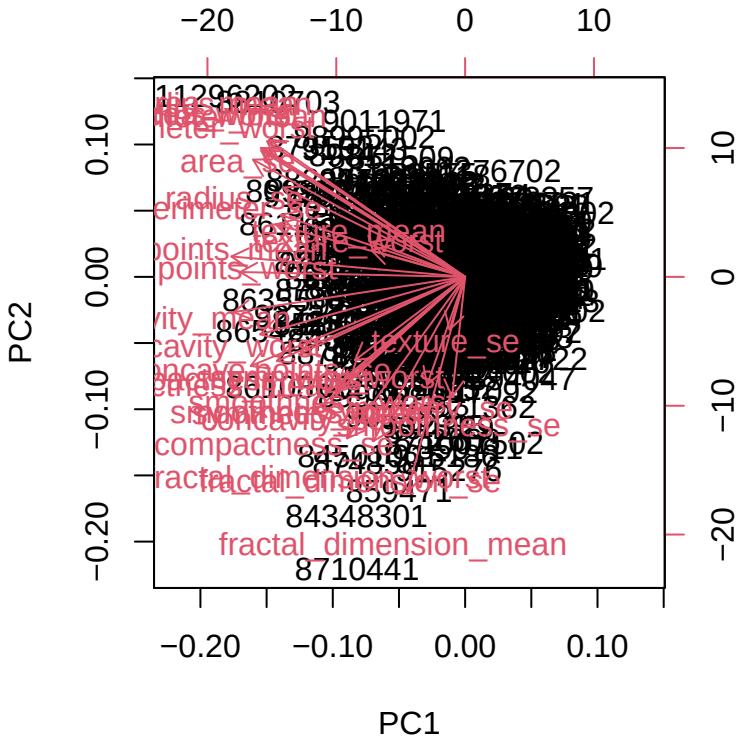
Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data?

Up to PC3

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

up to PC7

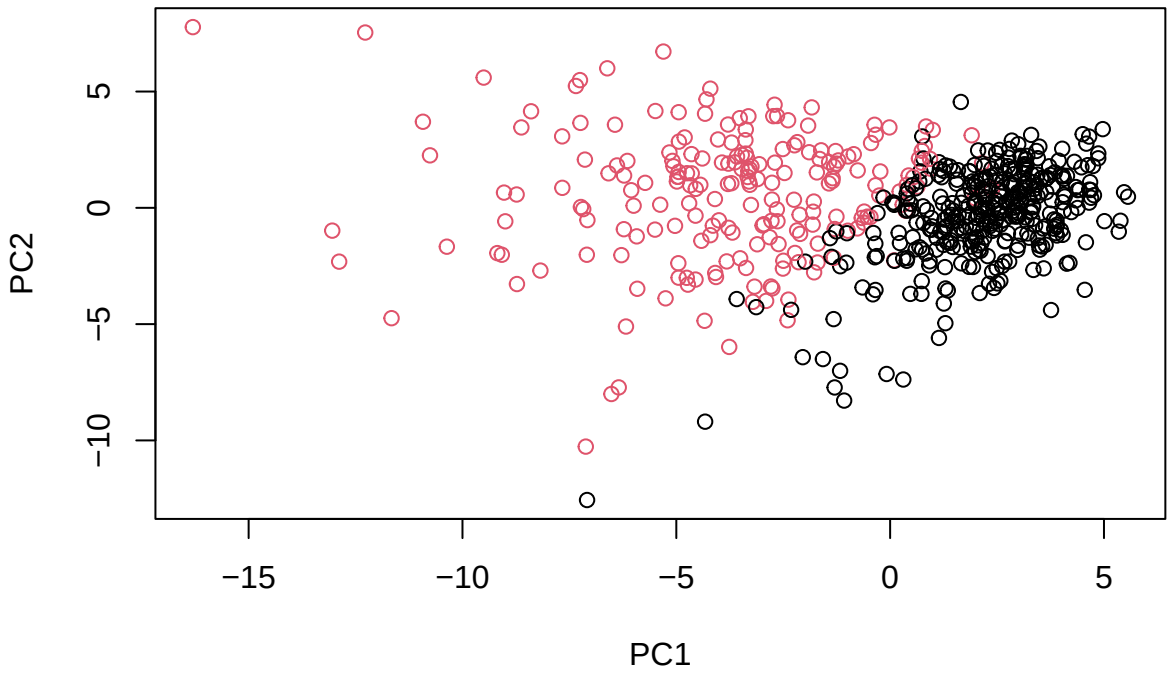
```
biplot(wisc.pr)
```



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

It is super jumbled. You can not really tel anything from this, it is so clumped together.

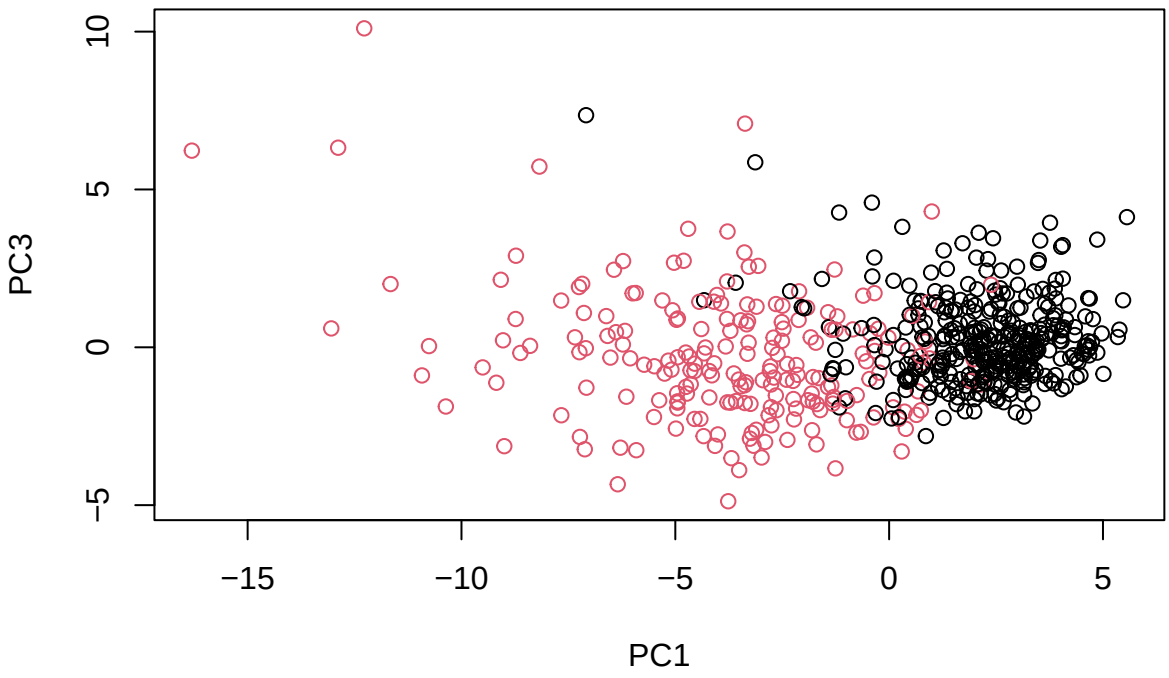
```
plot(wisc.pr$x[,1:2], col=diagnosis)
```



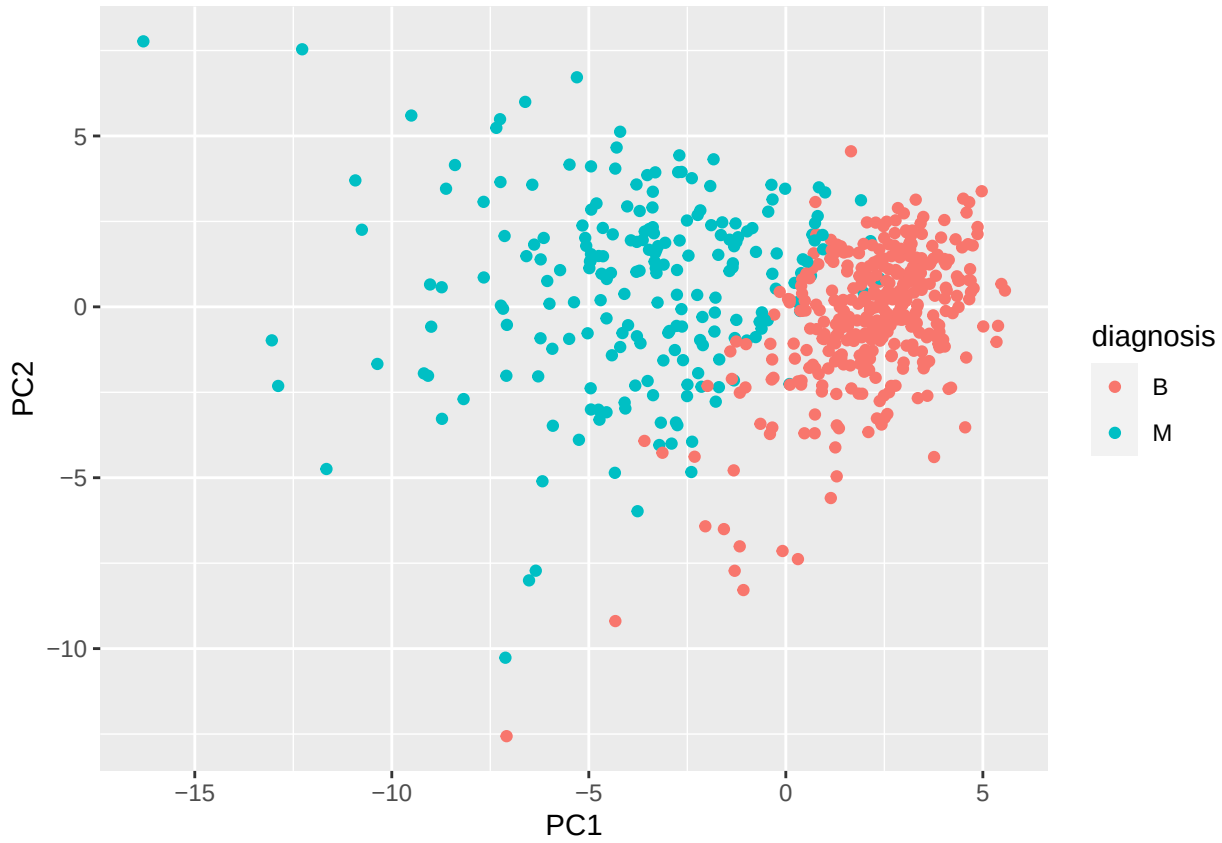
Q8. Generate a similar plot for principal components 1 and 3. What do you notice about these plots?

In the first plot, they are more differentiated, and spread out. Because principal component 2 explains more variance in the original data than principal component 3, you can see that the first plot has a cleaner cut separating the two subgroups

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




```
df <- as.data.frame(wisc.pr$x)
df$diagnosis <- diagnosis
library(ggplot2)
ggplot(df) +
  aes(PC1, PC2, col= diagnosis) +
  geom_point()
```

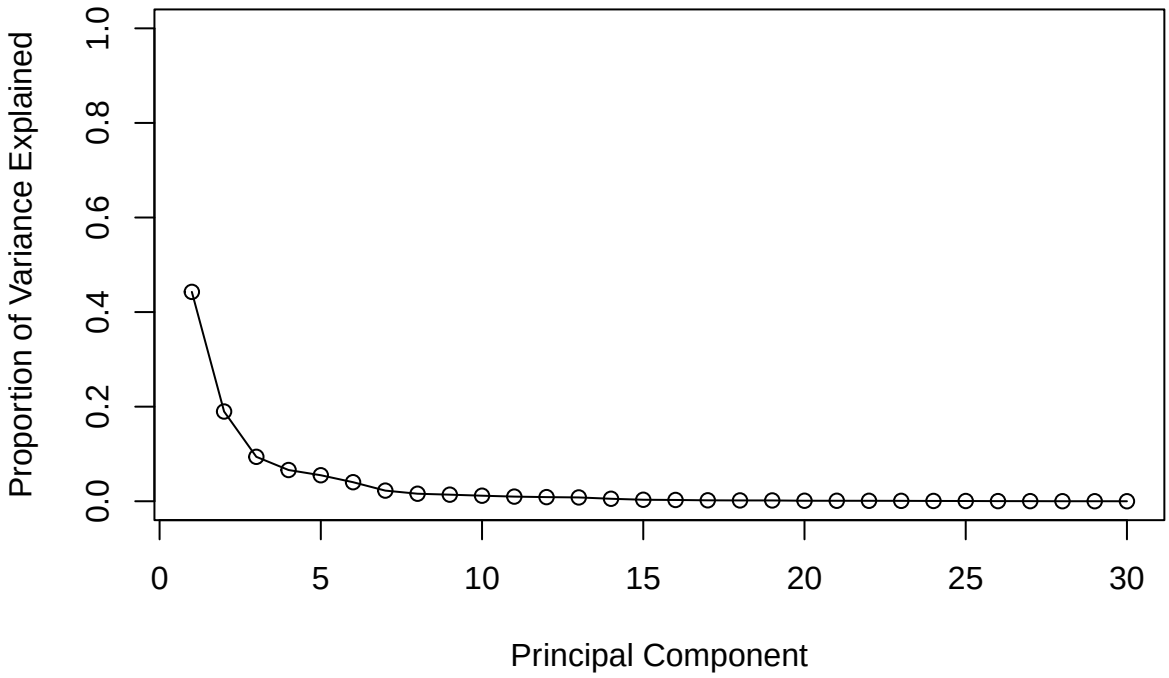



```
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

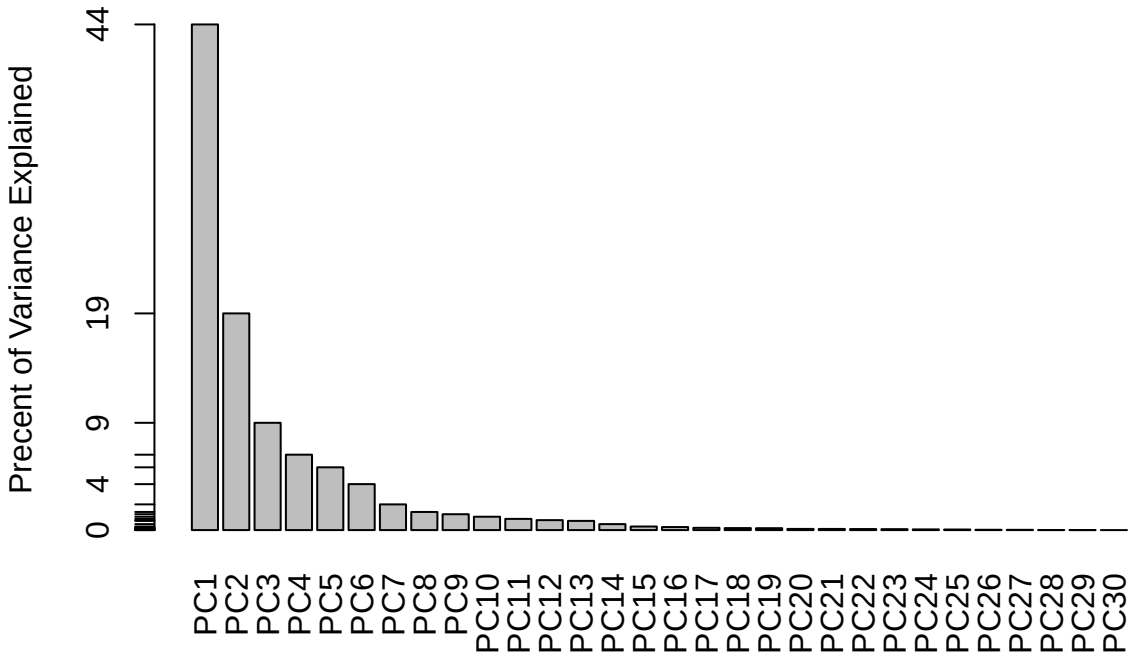
```
## [1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

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

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




```
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?

-0.26085376. this is the amount of shift in the axis rotation

```
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
```

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

You need 4 PCs to describe 80% of the varience. but that is with rounding up, so really 5

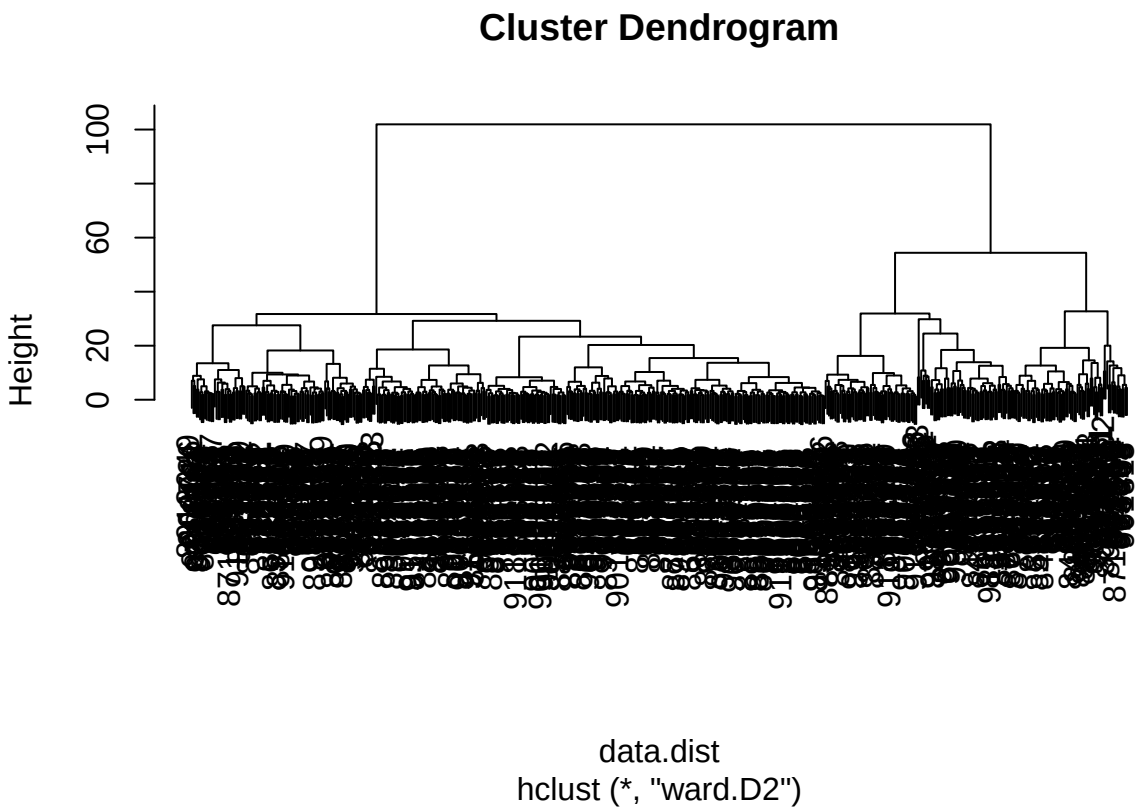
```
var <- summary(wisc.pr)
var
```

```
## 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
```

```
sum(var$importance[3,] < 0.8)
```

```
## [1] 4
```

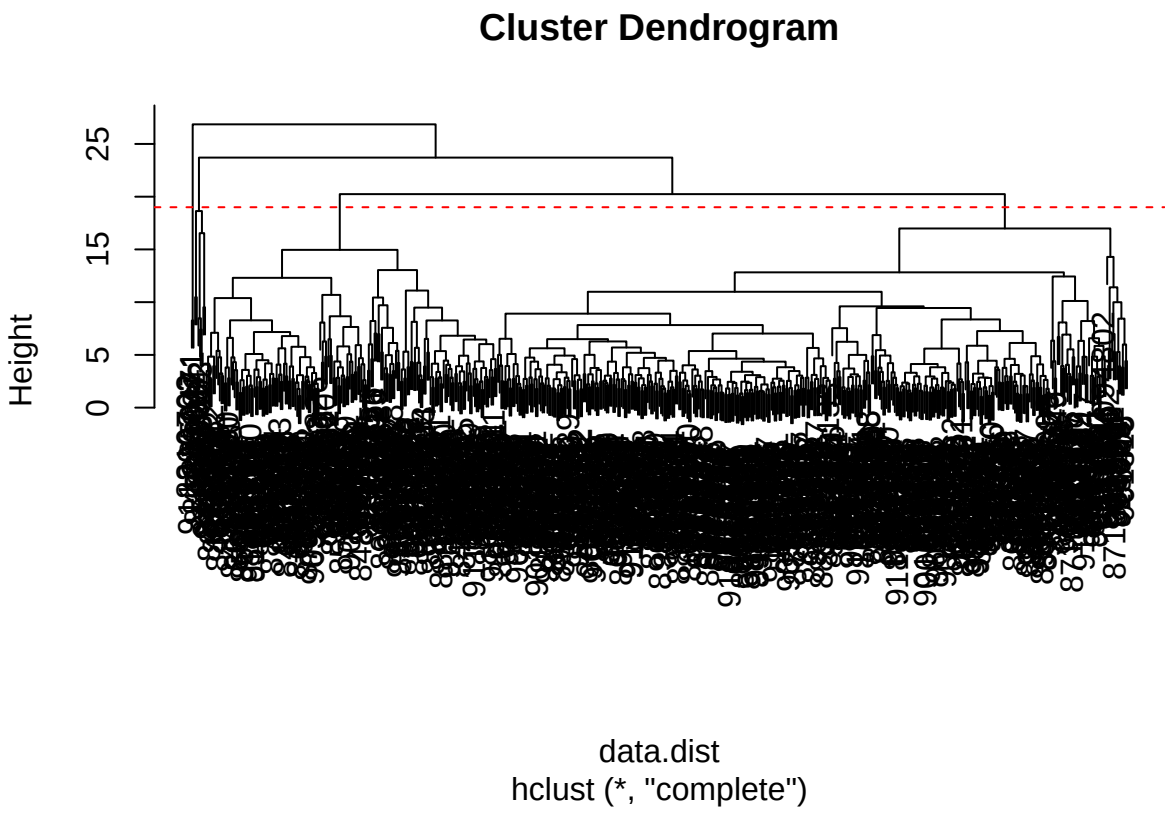
```
data.scaled <- scale(wisc.data)
data.dist <- dist(data.scaled)
wisc.hclust <- hclust(data.dist, "complete")
wisc.hclust.other <- hclust(data.dist, "ward.D2")
plot(wisc.hclust.other)
```



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

at height 19

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




```
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
```

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

4 and 5 seem to be good clusters becuase the seperate each diagnosis, and there are not a large amount of clusters with very few diagnosis clouding up the data.

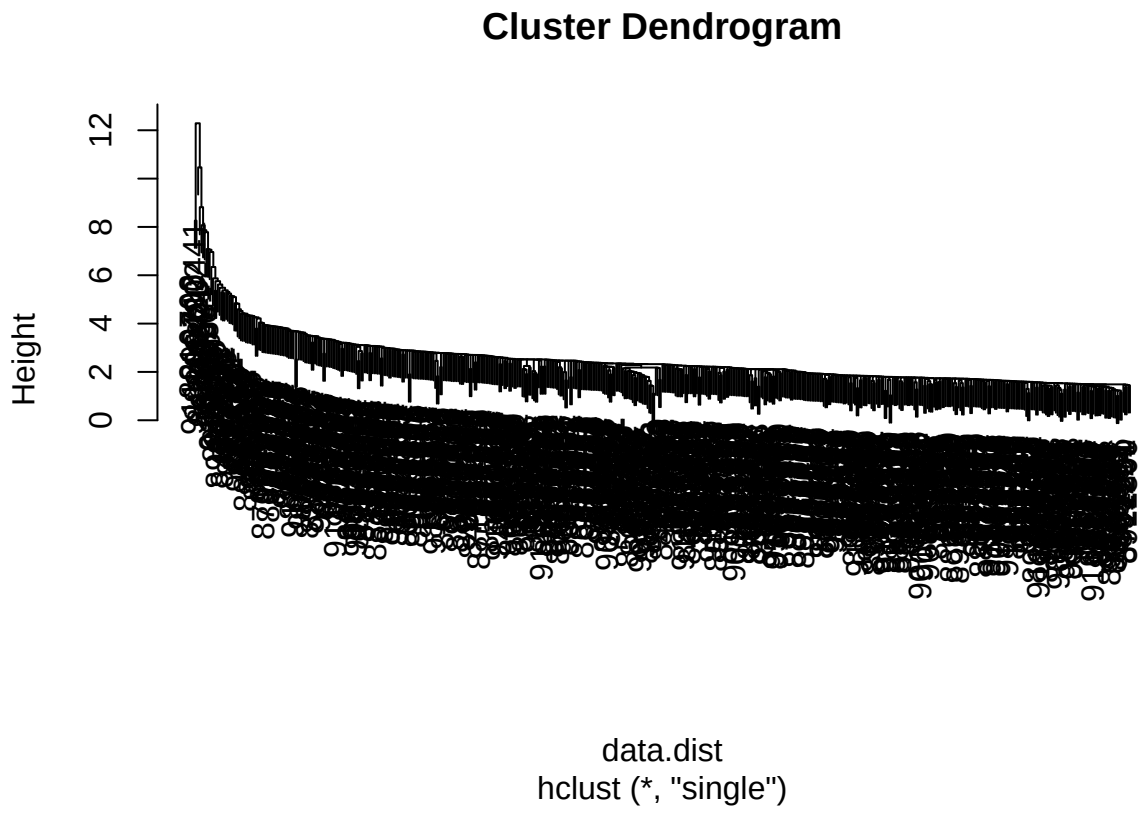
```
wisc.hclust.clusters.test <- cutree(wisc.hclust, k = 5)
table(wisc.hclust.clusters.test, diagnosis)
```

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

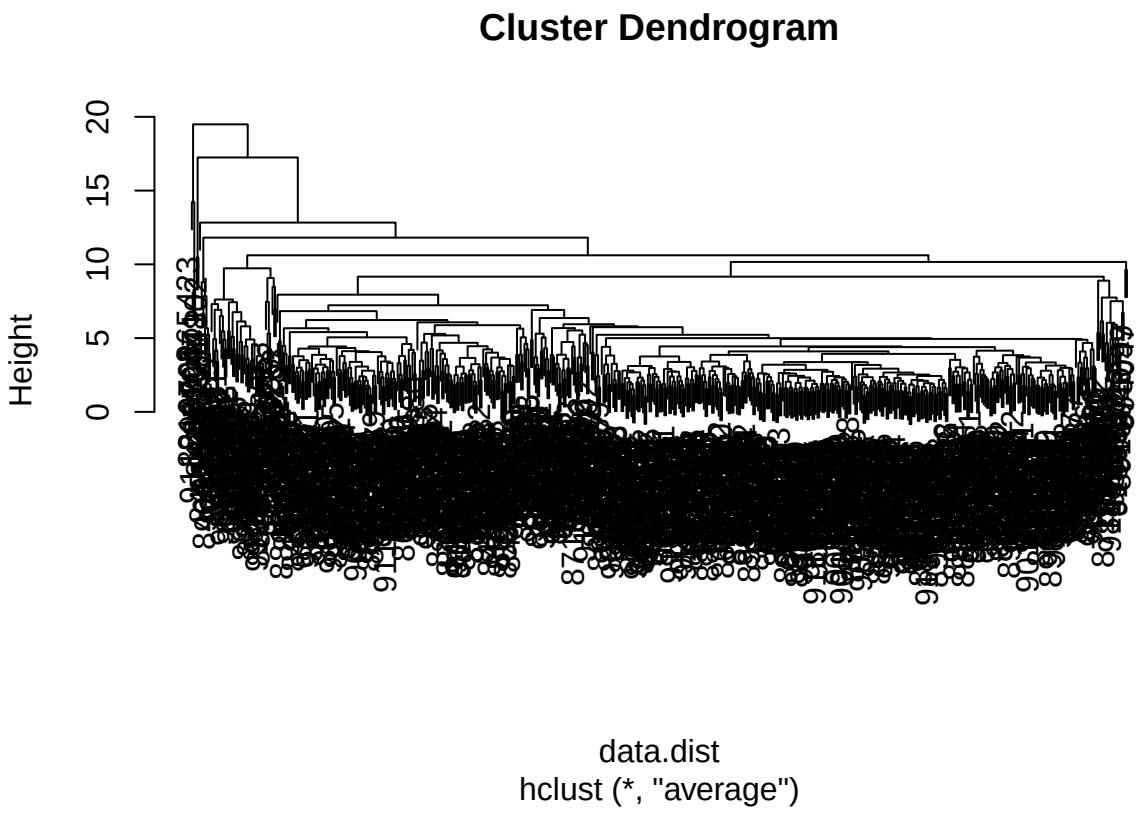
Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

i liked ward.D2 the most because it has a major set of clusters early on that define 2 groups, and then more branching occurs. this matches that in the cluster test there are 2 major groups that define B and M

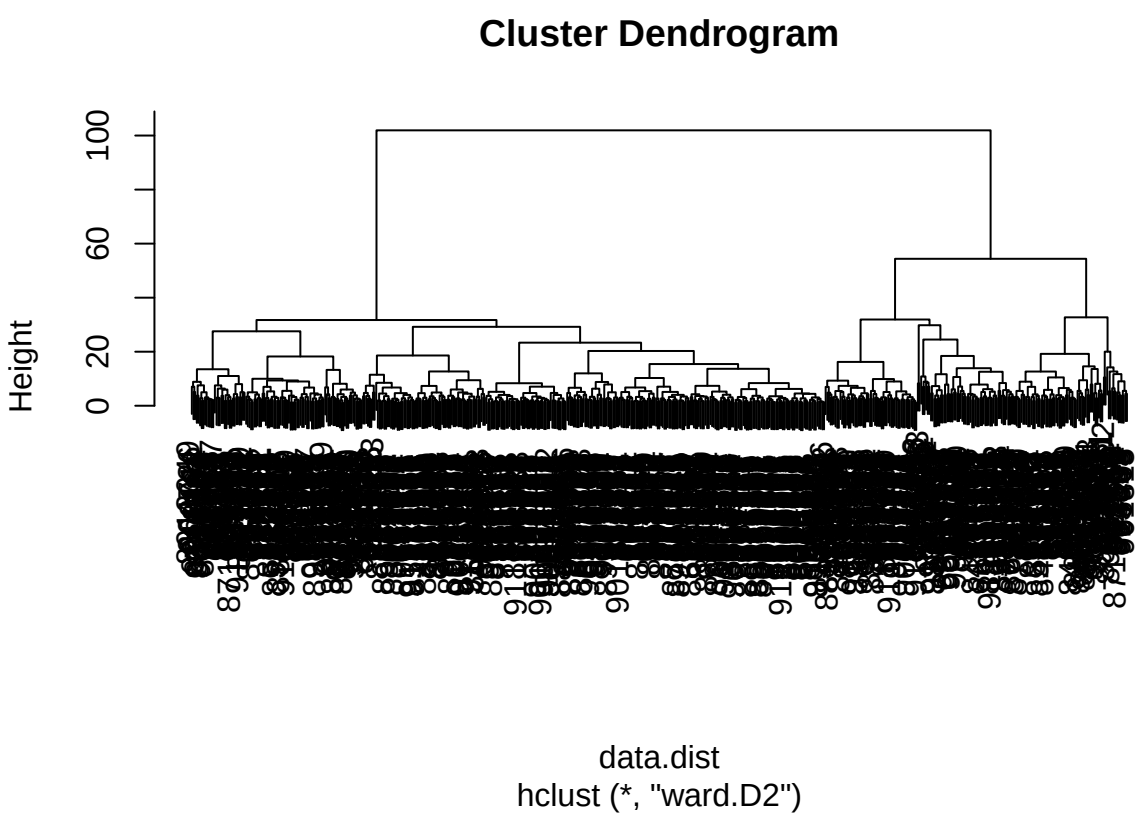
```
wisc.hclust.other <- hclust(data.dist, "single")
plot(wisc.hclust.other)
```




```
wisc.hclust.other1 <- hclust(data.dist, "average")
plot(wisc.hclust.other1)
```




```
wisc.hclust.other2 <- hclust(data.dist, "ward.D2")
plot(wisc.hclust.other2)
```


Cluster Dendrogram
Height
0
20
60
100
data.dist
hclust (*, "ward.D2")