Class 8: Mini-project

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Background

This mini-project explores unsupervised learning techniques applied to the Wisconsin Breast Cancer Diagnostic Data Set, which contains measurements of human breast mass cell nuclei.

The project guides the user through exploratory data analysis, performing and interpreting Principal Component Analysis (PCA) to reduce the dimensionality of the data while retaining variance, and applying hierarchical clustering with different linkage methods. It also includes an optional section on K-means clustering for comparison. The ultimate goal is to combine PCA and clustering to better separate benign and malignant cell samples, evaluating the results using metrics like sensitivity and specificity, and finally demonstrating how to predict the classification of new samples using the developed PCA model.

Data import

Our data come from the University of Wisconsin Medical Center.

```
wisc.df <- read.csv("WisconsinCancer.csv", row.names = 1)
head(wisc.df)</pre>
```

	diagnogie	radius me	an t	evture mean	perimeter_mean	area mean	
842302	M			10.38	122.80	1001.0	
842517	M			17.77	132.90		
84300903	M			21.25	130.00		
84348301	M			20.38	77.58		
84358402	M			14.34	135.10		
843786	M			15.70	82.57		
0.4.0.0.0			pact		ncavity_mean co	oncave.poi	
842302		.11840		0.27760	0.3001		0.14710
842517		.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 fract	al_d	limension_mea	n radius_se te	kture_se p	erimeter_se
842302	0.	2419		0.0787	1 1.0950	0.9053	8.589
842517	0.	1812		0.0566	7 0.5435	0.7339	3.398
84300903	0.	2069		0.0599	9 0.7456	0.7869	4.585
84348301	0.	2597		0.0974	4 0.4956	1.1560	3.445
84358402	0.	1809		0.0588	3 0.7572	0.7813	5.438
843786	0.	2087		0.0761	3 0.3345	0.8902	2.217
	area_se s	moothness_	se c	compactness_s	e concavity_se	concave.po	oints_se
842302	153.40	0.0063	99	0.0490	4 0.05373	_	0.01587
842517	74.08	0.0052	25	0.0130	0.01860		0.01340
84300903	94.03	0.0061	50	0.0400	6 0.03832		0.02058
84348301	27.23	0.0091	10	0.0745	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
             0.01389
842517
                                 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
                             1956.0
                                               0.1238
                  158.80
                                                                 0.1866
84300903
                  152.50
                             1709.0
                                               0.1444
                                                                 0.4245
                                               0.2098
84348301
                   98.87
                              567.7
                                                                 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
                  0.6869
84348301
                                        0.2575
                                                       0.6638
84358402
                                                       0.2364
                  0.4000
                                        0.1625
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
```

#Separate diagnosis column from rest of data
wisc.data <- wisc.df[, -1]
head(wisc.data)</pre>

	radius_mean	texture_mean	perimeter_mean	${\tt area_mean}$	smoothness_mean
842302	17.99	10.38	122.80	1001.0	0.11840
842517	20.57	17.77	132.90	1326.0	0.08474
84300903	19.69	21.25	130.00	1203.0	0.10960
84348301	11.42	20.38	77.58	386.1	0.14250
84358402	20.29	14.34	135.10	1297.0	0.10030
843786	12.45	15.70	82.57	477.1	0.12780

	compactness mean	concavity mean	concave noint	s_mean symmetry_mean
842302	0.27760	0.3001	-	0.14710 0.2419
842517	0.07864	0.0869		0.1812
84300903	0.15990	0.1974		.12790 0.2069
84348301	0.28390	0.2414		.10520 0.2597
84358402	0.13280	0.1980		.10430 0.1809
843786	0.17000	0.1578		.08089 0.2087
010700				erimeter_se area_se
842302	-	.07871 1.0950	_ •	8.589 153.40
842517		.05667 0.5435		3.398 74.08
84300903		.05999 0.7456		4.585 94.03
84348301		.09744 0.4956		3.445 27.23
84358402		.05883 0.7572		5.438 94.44
843786		.07613 0.3345		2.217 27.19
010100	smoothness_se com			
842302	0.006399	0.04904	0.05373	0.01587
842517	0.005225	0.01308	0.01860	0.01340
84300903		0.04006	0.03832	0.02058
84348301	0.009110	0.07458	0.05661	0.01867
84358402		0.02461	0.05688	0.01885
843786	0.007510	0.03345	0.03672	0.01137
	symmetry_se fract			
842302	0.03003	0.006193		
842517	0.01389	0.003532		
84300903		0.004571		25.53
84348301	0.05963	0.009208	3 14.91	
84358402	0.01756	0.005115		
843786	0.02165	0.005082		
	perimeter_worst a	area_worst smoot	hness_worst c	ompactness_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_w	vorst 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	n_worst		

842302	0.11890
842517	0.08902
84300903	0.08758
84348301	0.17300
84358402	0.07678
843786	0.12440

```
diagnosis <- factor(wisc.df$diagnosis)</pre>
```

How many observations are in this dataset?

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

[1] 569

There are 569 observations.

Question 2

How many of the observations have a malignant diagnosis?

```
table(diagnosis)
```

diagnosis

 $\mathsf{B} \mathsf{M}$

357 212

212 of the observations have a malignant diagnosis.

Question 3

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

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

[1] 1 2 3 4 5 6 7 8 9 10

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

[1] 10

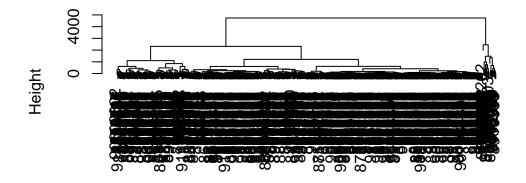
10 variables are suffixed with _mean.

Clustering

Let's try hclust()

```
hc <- hclust(dist(wisc.data))
plot(hc)</pre>
```

Cluster Dendrogram



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

We can extract clusters from this dendrogram with the function cutree().

```
groups <- cutree(hc, k = 2)</pre>
```

How many individuals are in each cluster?

table(groups)

```
groups
1 2
549 20
```

We can generate a cross-table that compares our cluster groups vector with our diagnosis vector.

table(diagnosis, groups)

```
groups
diagnosis 1 2
B 357 0
M 192 20
```

PCA

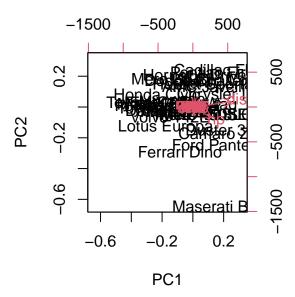
Scaling

head(mtcars)

```
mpg cyl disp hp drat
                                         wt qsec vs am gear carb
Mazda RX4
                21.0
                          160 110 3.90 2.620 16.46 0
                                                    1
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
                          360 175 3.15 3.440 17.02 0 0
                                                          3
                                                              2
                       8
Valiant
                18.1
                          225 105 2.76 3.460 20.22 1 0
                                                          3
                                                              1
```

We could do a PCA of this data as is, but it could be misleading.

```
pc <- prcomp(mtcars)
biplot(pc)</pre>
```



Let's look at the mean and standard deviation of each column.

colMeans(mtcars)

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

apply(mtcars, 2, sd)

```
disp
                                                         drat
      mpg
                   cyl
                                              hp
                                                                        wt
6.0269481
            1.7859216 123.9386938
                                     68.5628685
                                                   0.5346787
                                                                0.9784574
     qsec
                                            gear
                                                         carb
                    ٧s
1.7869432
            0.5040161
                         0.4989909
                                      0.7378041
                                                   1.6152000
```

We can scale this data before PCA to get a better representation and analysis of all the columns.

```
mtscale <- scale(mtcars)
round(colMeans(mtscale))</pre>
```

```
cyl disp
                 hp drat
mpg
                           wt qsec
                                      ٧s
                                            am gear carb
  0
       0
                  0
                       0
                             0
                                  0
                                       0
                                             0
                                                  0
             0
```

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

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

```
pc.scale <- prcomp(mtcars, scale = T)</pre>
```

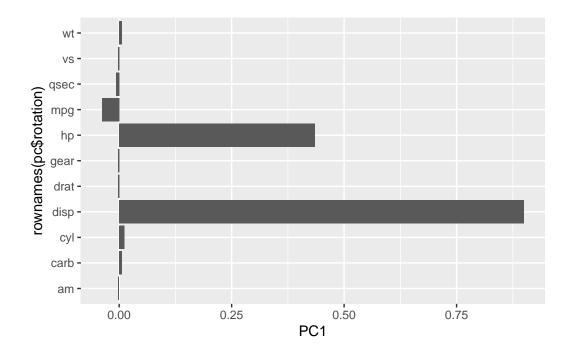
We can look at the two main results figures from PCA - the PC plot (aka score plot, ordination plot, PC1 vs PC2 plot) and the loadings plot.

A loadings plot of the unscaled PCA results

```
library(ggplot2)
```

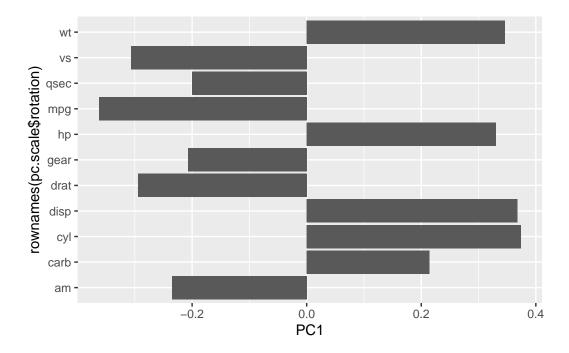
Warning: package 'ggplot2' was built under R version 4.4.3

```
ggplot(pc$rotation) +
  aes(PC1, rownames(pc$rotation)) +
  geom_col()
```



Loadings plot for scaled data

```
ggplot(pc.scale$rotation) +
aes(PC1, rownames(pc.scale$rotation)) +
geom_col()
```



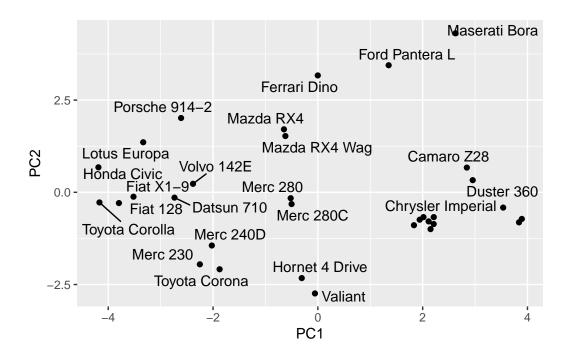
PC plot

```
library(ggrepel)
```

Warning: package 'ggrepel' was built under R version 4.4.3

```
ggplot(pc.scale$x) +
  aes(PC1, PC2, label = rownames(pc.scale$x)) +
  geom_point() +
  geom_text_repel()
```

Warning: ggrepel: 9 unlabeled data points (too many overlaps). Consider increasing max.overlaps



Key point: In general we will set scale = TRUE when we do PCA. This is not the default but probably should be.

Back to cancer data

```
# Do the data need to be scaled?
colMeans(wisc.data)
```

perimeter_mean	texture_mean	radius_mean
9.196903e+01	1.928965e+01	1.412729e+01
compactness_mean	smoothness_mean	area_mean
1.043410e-01	9.636028e-02	6.548891e+02
symmetry_mean	concave.points_mean	concavity_mean
1.811619e-01	4.891915e-02	8.879932e-02
texture_se	radius_se	fractal_dimension_mean
1.216853e+00	4.051721e-01	6.279761e-02
smoothness_se	area_se	perimeter_se
7.040979e-03	4.033708e+01	2.866059e+00
concave.points_se	concavity_se	compactness_se
1.179614e-02	3.189372e-02	2.547814e-02
radius_worst	fractal_dimension_se	symmetry_se

```
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
                                2.900756e-01
        1.146062e-01
                                                         8.394582e-02
```

apply(wisc.data, 2, sd)

perimeter_mean	texture_mean	radius_mean
2.429898e+01	4.301036e+00	3.524049e+00
compactness_mean	${\tt smoothness_mean}$	area_mean
5.281276e-02	1.406413e-02	3.519141e+02
symmetry_mean	concave.points_mean	concavity_mean
2.741428e-02	3.880284e-02	7.971981e-02
texture_se	radius_se	<pre>fractal_dimension_mean</pre>
5.516484e-01	2.773127e-01	7.060363e-03
smoothness_se	area_se	perimeter_se
3.002518e-03	4.549101e+01	2.021855e+00
concave.points_se	concavity_se	compactness_se
6.170285e-03	3.018606e-02	1.790818e-02
radius_worst	${\tt fractal_dimension_se}$	symmetry_se
4.833242e+00	2.646071e-03	8.266372e-03
area_worst	perimeter_worst	texture_worst
5.693570e+02	3.360254e+01	6.146258e+00
${\tt concavity_worst}$	${\tt compactness_worst}$	${\tt smoothness_worst}$
2.086243e-01	1.573365e-01	2.283243e-02
${\tt fractal_dimension_worst}$	symmetry_worst	concave.points_worst
1.806127e-02	6.186747e-02	6.573234e-02

The data have different units and different variances, so they should be scaled.

```
wisc.pr <- prcomp(wisc.data, scale = T)
summary(wisc.pr)</pre>
```

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
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
```

From your results, what proportion of the original variance is captured by the first principal components (PC1)?

PC1 captures 44.27% of the original variance.

Question 5

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

3 PCs are required to capture 70% of the original variance in the data.

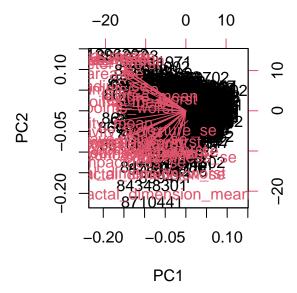
Question 6

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

7 PCs are required to describe 90% of the original variance in the data.

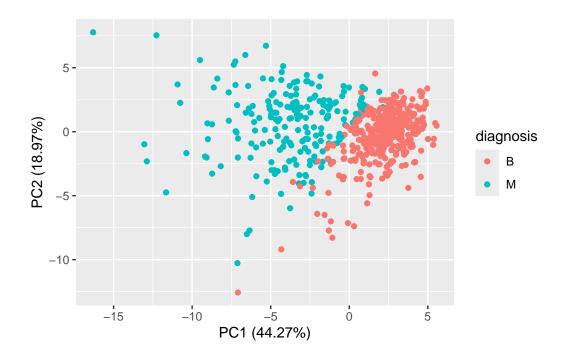
What stands out to you about this plot? Is it easy or difficult to understand? Why?

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



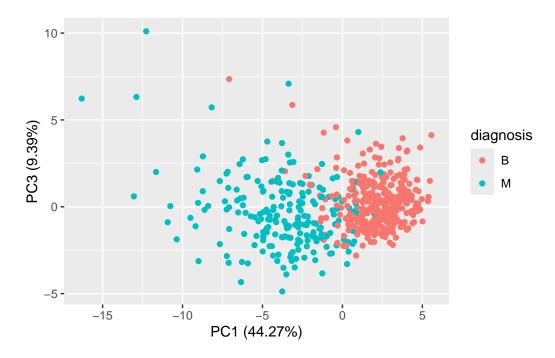
There is a lot going on in this plot. It is difficult to tell what is going on with the data because there are many observations and the labels obscure trends.

```
ggplot(wisc.pr$x) +
aes(x = PC1, y = PC2, col = diagnosis) +
geom_point() +
labs(x = "PC1 (44.27%)", y = "PC2 (18.97%)")
```



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

```
ggplot(wisc.pr$x) +
aes(x = PC1, y = PC3, col = diagnosis) +
geom_point() +
labs(x = "PC1 (44.27%)", y = "PC3 (9.39%)")
```



The PC1 axis is the same, so the horizontal placement of the points has not changed. PC3 captures less variance than does PC2, so there is not as much separation in the vertical axis as there is in the plot with PC2. As a result, there is more overlap between the benign and malignant groups in the PC1 vs PC3 plot.

Variance

Variance of each PC

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

[1] 13.281608 5.691355 2.817949 1.980640 1.648731 1.207357

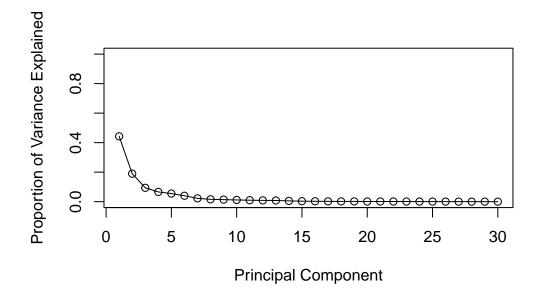
Variance of original data explained by each PC

```
pve <- pr.var / sum(pr.var)
head(pve)</pre>
```

[1] 0.44272026 0.18971182 0.09393163 0.06602135 0.05495768 0.04024522

Scree plot

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



Communicating PCA results

Question 9

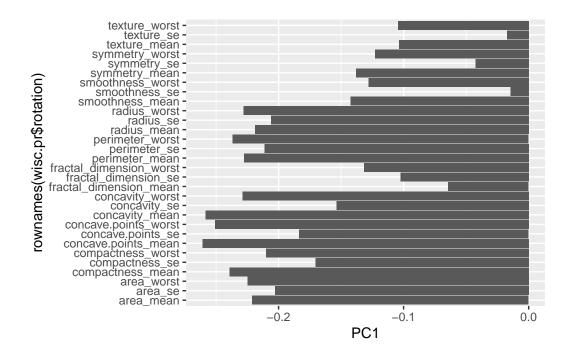
For the first principal component, what is the component of the loading vector (i.e. wisc.pr\$rotation[,1]) for the feature concave.points_mean?

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

[1] -0.2608538

PC1 loadings plot

```
ggplot(wisc.pr$rotation) +
aes(PC1, rownames(wisc.pr$rotation)) +
geom_col()
```



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

```
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
                       0.69037 0.6457 0.59219 0.5421 0.51104 0.49128 0.39624
Standard deviation
Proportion of Variance 0.01589 0.0139 0.01169 0.0098 0.00871 0.00805 0.00523
                       0.92598 0.9399 0.95157 0.9614 0.97007 0.97812 0.98335
Cumulative Proportion
                          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
                       0.16565 0.15602 0.1344 0.12442 0.09043 0.08307 0.03987
Standard deviation
Proportion of Variance 0.00091 0.00081 0.0006 0.00052 0.00027 0.00023 0.00005
                       0.99749 0.99830 0.9989 0.99942 0.99969 0.99992 0.99997
Cumulative Proportion
                          PC29
                                  PC30
Standard deviation
                       0.02736 0.01153
Proportion of Variance 0.00002 0.00000
Cumulative Proportion
                       1.00000 1.00000
```

5 PCs are required to explain 80% of the variance of the data.

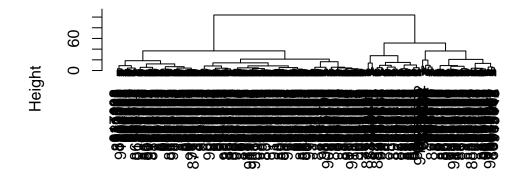
Questions 11 - 14 use hclust() and kmeans(), done earlier/omitted

Combining methods

We can take our PCA results and use them as a basis set for other analyses, such as clustering.

```
wisc.pr.hclust <- hclust(dist(wisc.pr$x[, 1:2]), method = "ward.D2")
plot(wisc.pr.hclust)</pre>
```

Cluster Dendrogram



dist(wisc.pr\$x[, 1:2]) hclust (*, "ward.D2") We can "cut" this tree to yield our clusters.

```
pc.groups <- cutree(wisc.pr.hclust, k = 2)
table(pc.groups)</pre>
```

```
pc.groups
    1    2
195 374
```

How do these cluster groups compare to the diagnoses?

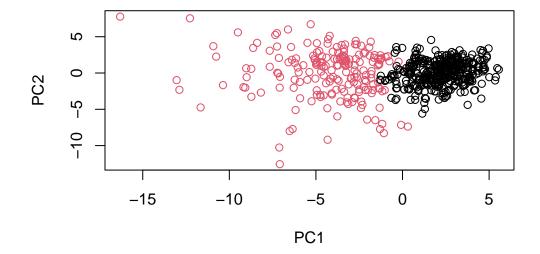
```
table(diagnosis, pc.groups)
```

```
pc.groups
diagnosis 1 2
B 18 339
M 177 35
```

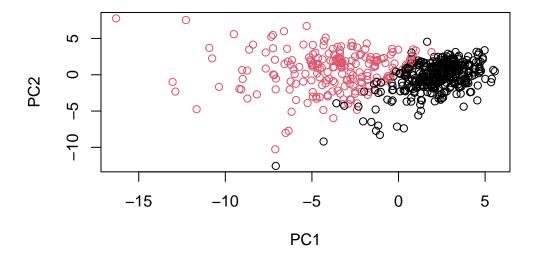
```
pc.groups <- as.factor(pc.groups)
levels(pc.groups)</pre>
```

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

```
pc.groups <- relevel(pc.groups, 2)
plot(wisc.pr$x[,1:2], col=pc.groups)</pre>
```



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



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

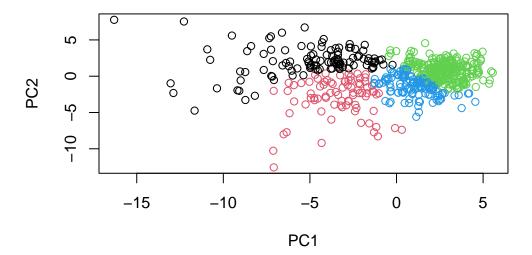
```
pc.groups_4 <- cutree(wisc.pr.hclust, k = 4)
table(pc.groups_4)</pre>
```

```
pc.groups_4
1 2 3 4
112 83 250 124
```

```
table(diagnosis, pc.groups_4)
```

```
pc.groups_4
diagnosis 1 2 3 4
B 0 18 232 107
M 112 65 18 17
```

```
plot(wisc.pr$x[,1:2], col=pc.groups_4)
```



Group 1 is composed entirely of malignant observations, but groups 2-4 are mixed. Group 2 is mostly malignant, and groups 3 and 4 are mostly benign. There is better separation compared

to regular hclust(), but the additional groups make it unclear whether the separation is better than that with only two groups.

Question 16

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.

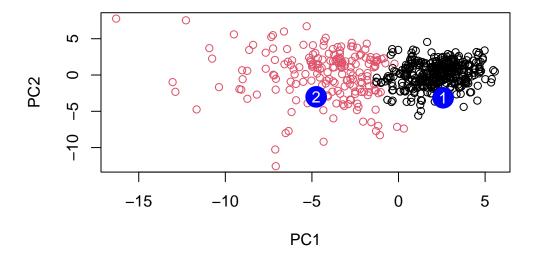
They did pretty badly. The hierarchical clustering only separated out 20 observations out of the 212 that were diagnosed as malignant. We can do much better after PCA.

Prediction

```
new <- read.csv(url("https://tinyurl.com/new-samples-CSV"))
npc <- predict(wisc.pr, newdata = new)
npc</pre>
```

```
PC1
                     PC2
                                PC3
                                           PC4
                                                     PC5
                                                                 PC6
                                                                            PC7
[1,] 2.576616 -3.135913 1.3990492 -0.7631950 2.781648 -0.8150185 -0.3959098
[2,] -4.754928 -3.009033 -0.1660946 -0.6052952 -1.140698 -1.2189945
                                                                     0.8193031
           PC8
                      PC9
                                PC10
                                          PC11
                                                    PC12
                                                               PC13
                                                                        PC14
[1,] -0.2307350 0.1029569 -0.9272861 0.3411457 0.375921 0.1610764 1.187882
[2,] -0.3307423 0.5281896 -0.4855301 0.7173233 -1.185917 0.5893856 0.303029
          PC15
                     PC16
                                 PC17
                                                         PC19
                                             PC18
                                                                     PC20
[1,] 0.3216974 -0.1743616 -0.07875393 -0.11207028 -0.08802955 -0.2495216
[2,] 0.1299153 0.1448061 -0.40509706 0.06565549
                                                   0.25591230 -0.4289500
           PC21
                      PC22
                                            PC24
                                                        PC25
                                 PC23
                                                                      PC26
[1,]
     0.1228233 0.09358453 0.08347651 0.1223396
                                                  0.02124121
                                                              0.078884581
[2,] -0.1224776 0.01732146 0.06316631 -0.2338618 -0.20755948 -0.009833238
             PC27
                         PC28
                                      PC29
                                                   PC30
     0.220199544 -0.02946023 -0.015620933 0.005269029
[2,] -0.001134152  0.09638361  0.002795349 -0.019015820
```

```
plot(wisc.pr$x[,1:2], col=pc.groups)
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
```



Which of these new patients should we prioritize for follow up based on your results?

We should prioritize patient 2 for follow-up. Patient 2 clusters with the malignant cluster, while Patient 1 is in the benign cluster, so we should collect more data from Patient 2.