

Class 8 mini-project

Matthew White

```
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

Let's look at the mean value of every column:

```
apply(mtcars, 2, mean)
```

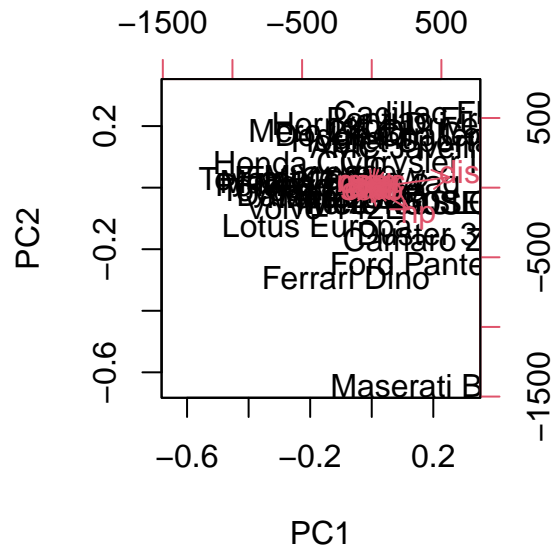
mpg	cyl	disp	hp	drat	wt	qsec
20.090625	6.187500	230.721875	146.687500	3.596563	3.217250	17.848750
vs	am	gear	carb			
0.437500	0.406250	3.687500	2.812500			

Let's look at "spread" via standard deviation sd()

```
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	

```
pca <- prcomp(mtcars)
biplot(pca)
```



Let's try scaling this data

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

	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

```
mean(mtscale)
```

```
[1] -1.573867e-16
```

```
sd(mtscale)
```

```
[1] 0.9856521
```

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

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

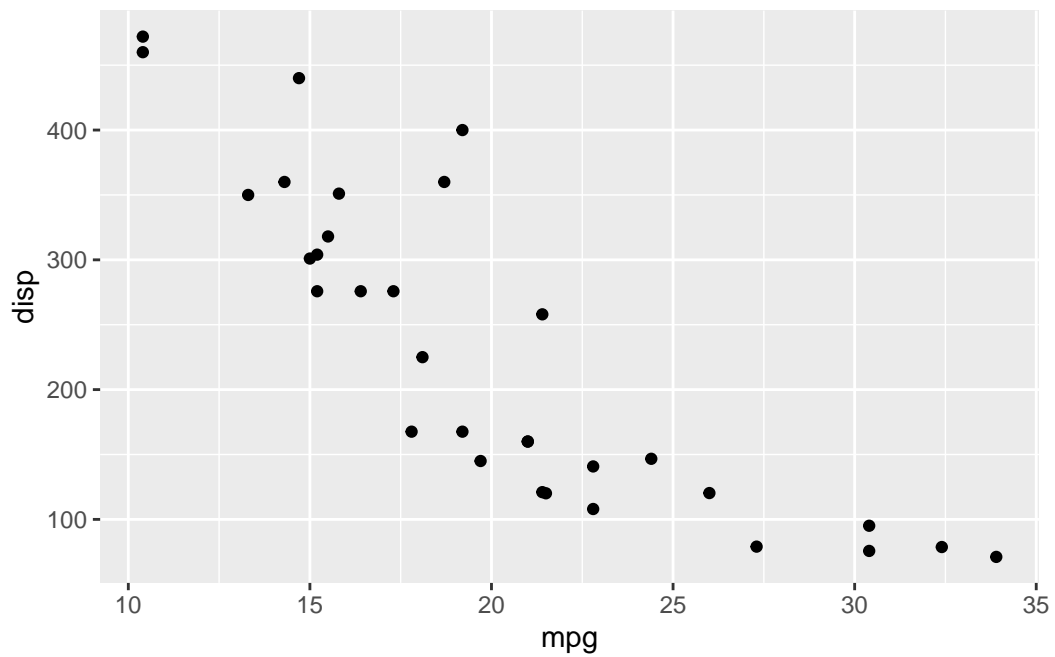
```
round(apply(mtscale, 2, sd))
```

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

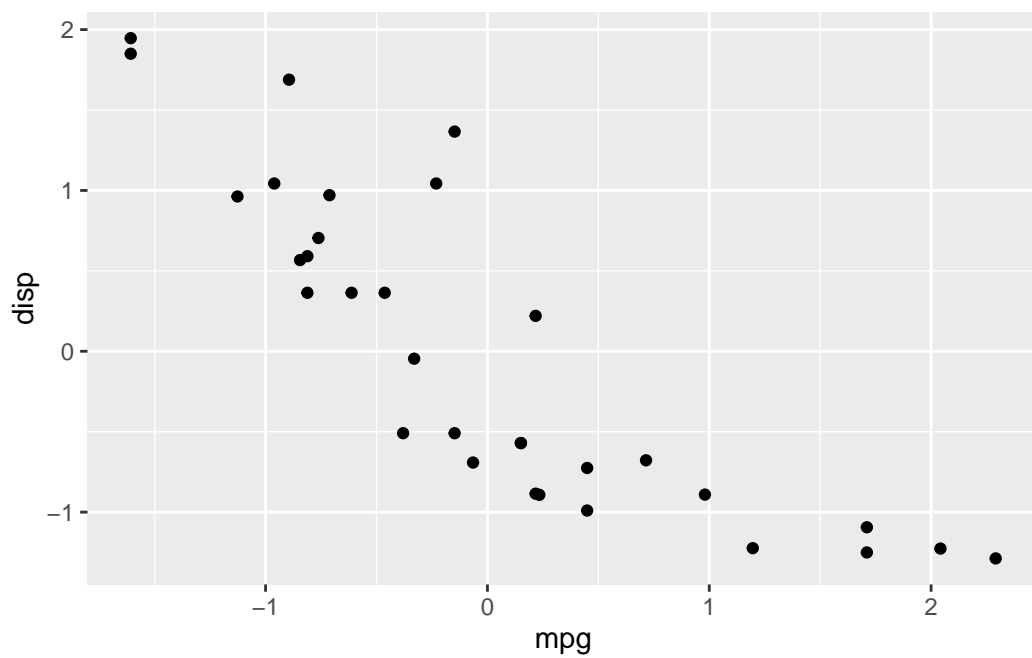
Let's plot

```
library(ggplot2)
```

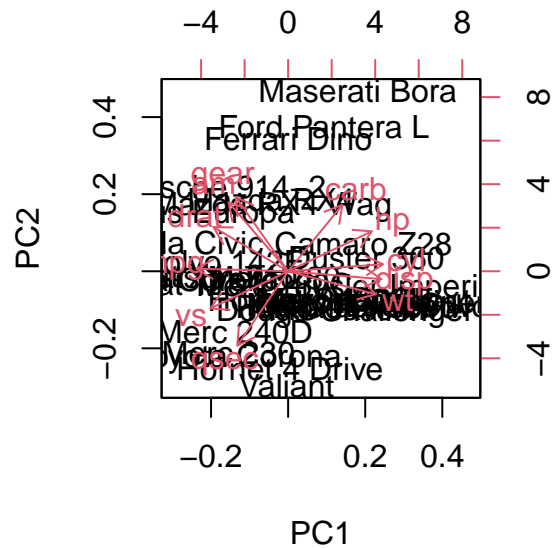
```
# disp v mpg for og and for scale dataset
ggplot(mtcars) + aes(mpg, disp) + geom_point()
```



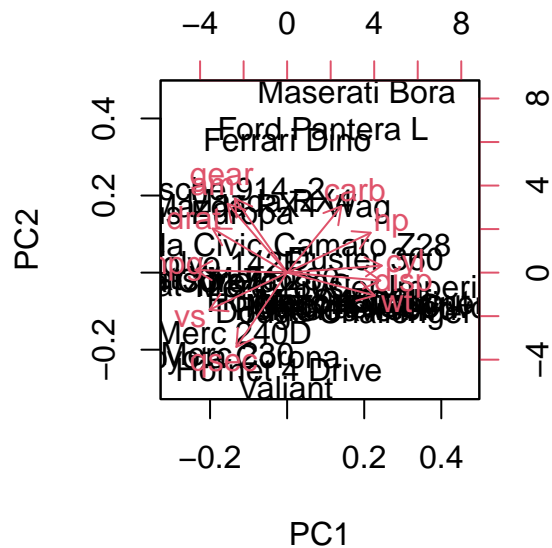
```
ggplot(mtcars, aes(mpg, disp)) + geom_point()
```



```
pca2 <- prcomp(mtscale)
biplot(pca2)
```



```
#can achieve same thing by setting scale argument to TRUE in prcomp() function
pca3 <- prcomp(mtcars, scale = T)
biplot(pca3)
```



##Mini Project Start

```
#row.names=1 tells to use the 1st column as the row names
wisc.df <- read.csv("WisconsinCancer.csv", 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				

```
dim(wisc.df)
```

```
[1] 569 31
```

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

	radius_mean	texture_mean	perimeter_mean	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.points_mean	symmetry_mean	
842302	0.27760	0.3001		0.14710	0.2419
842517	0.07864	0.0869		0.07017	0.1812
84300903	0.15990	0.1974		0.12790	0.2069
84348301	0.28390	0.2414		0.10520	0.2597
84358402	0.13280	0.1980		0.10430	0.1809
843786	0.17000	0.1578		0.08089	0.2087
	fractal_dimension_mean	radius_se	texture_se	perimeter_se	area_se
842302		0.07871	1.0950	0.9053	8.589 153.40
842517		0.05667	0.5435	0.7339	3.398 74.08
84300903		0.05999	0.7456	0.7869	4.585 94.03
84348301		0.09744	0.4956	1.1560	3.445 27.23
84358402		0.05883	0.7572	0.7813	5.438 94.44
843786		0.07613	0.3345	0.8902	2.217 27.19
	smoothness_se	compactness_se	concavity_se	concave.points_se	
842302	0.006399	0.04904	0.05373	0.01587	
842517	0.005225	0.01308	0.01860	0.01340	
84300903	0.006150	0.04006	0.03832	0.02058	
84348301	0.009110	0.07458	0.05661	0.01867	
84358402	0.011490	0.02461	0.05688	0.01885	
843786	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			

```
diagnosis <- wisc.df$diagnosis
head(diagnosis)
```

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

```
#make diagnosis data a factor so that it is understood as a categorical and not a continuous
diagnosis_f <- as.factor(diagnosis)
diagnosis_f
```

```
[1] M 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 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 B M M B B B M 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 M B M M M M M M M
[260] 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 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 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 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
[408] B M B B B B B M B B M B B B B B B B B B B 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 M M B B B B B B M 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
[556] B B B B B B B M M M M M M M B
Levels: B M
```

##Questions 1-3

```
#Q1 and Q2
dim(wisc.data)
```

```
[1] 569 30
```

```
table(diagnosis_f)
```

```
diagnosis_f
  B   M
357 212
```

```
#Q3, how many variables in the data are suffixed with _mean?
grep("_mean", colnames(wisc.data))
```

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

```
grep("_mean", colnames(diagnosis_f))
```

```
integer(0)
```

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

```
[1] 10
```

##PCA portion, Q4-6

Should scale our data in the PCA function!

```
#colMeans(wisc.data)
#apply(wisc.data,2,sd)

wisc.pr <- prcomp(wisc.data, scale = T)
x <- summary(wisc.pr)
x
```

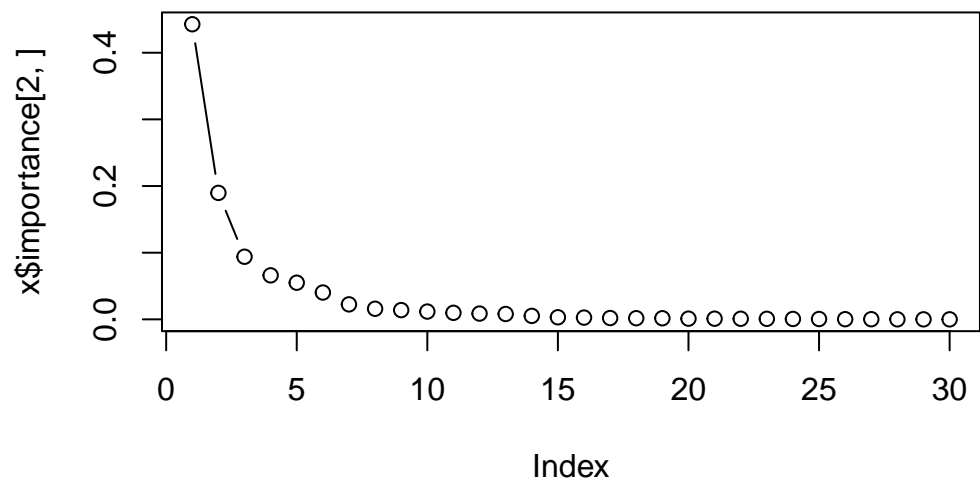
Importance of components:

	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					

##PCs are doing alright, but we still don't capture all variance in first couple PCs.

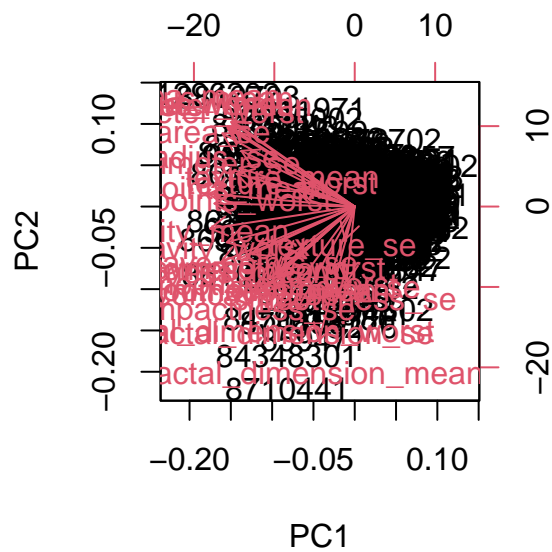
```
#Q4: Captured 44% of variance in PC1
#Q5: Require 3 PCs to capture at least 70% of og data variance
#Q6: Require 7 PCs to capture 90% variance
```

```
#can also plot this summary
plot(x$importance[2,], typ="b")
```



##Interpreting PCA results

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



```
#Q7: plot looks pretty shite. overcrowded, can't visualize any labels or results.
```

```
#x is the coordinates of the patient on new PC plot. The value in each PC for each individual.  
head(wisc.pr$x)
```

	PC1	PC2	PC3	PC4	PC5	PC6
842302	-9.184755	-1.946870	-1.1221788	3.6305364	1.1940595	1.41018364
842517	-2.385703	3.764859	-0.5288274	1.1172808	-0.6212284	0.02863116
84300903	-5.728855	1.074229	-0.5512625	0.9112808	0.1769302	0.54097615
84348301	-7.116691	-10.266556	-3.2299475	0.1524129	2.9582754	3.05073750
84358402	-3.931842	1.946359	1.3885450	2.9380542	-0.5462667	-1.22541641
843786	-2.378155	-3.946456	-2.9322967	0.9402096	1.0551135	-0.45064213

	PC7	PC8	PC9	PC10	PC11	PC12
842302	2.15747152	0.39805698	-0.15698023	-0.8766305	-0.2627243	-0.8582593
842517	0.01334635	-0.24077660	-0.71127897	1.1060218	-0.8124048	0.1577838
84300903	-0.66757908	-0.09728813	0.02404449	0.4538760	0.6050715	0.1242777
84348301	1.42865363	-1.05863376	-1.40420412	-1.1159933	1.1505012	1.0104267
84358402	-0.93538950	-0.63581661	-0.26357355	0.3773724	-0.6507870	-0.1104183
843786	0.49001396	0.16529843	-0.13335576	-0.5299649	-0.1096698	0.0813699

	PC13	PC14	PC15	PC16	PC17
842302	0.10329677	-0.690196797	0.601264078	0.74446075	-0.26523740
842517	-0.94269981	-0.652900844	-0.008966977	-0.64823831	-0.01719707
84300903	-0.41026561	0.016665095	-0.482994760	0.32482472	0.19075064
84348301	-0.93245070	-0.486988399	0.168699395	0.05132509	0.48220960
84358402	0.38760691	-0.538706543	-0.310046684	-0.15247165	0.13302526
843786	-0.02625135	0.003133944	-0.178447576	-0.01270566	0.19671335

	PC18	PC19	PC20	PC21	PC22
842302	-0.54907956	0.1336499	0.34526111	0.096430045	-0.06878939
842517	0.31801756	-0.2473470	-0.11403274	-0.077259494	0.09449530
84300903	-0.08789759	-0.3922812	-0.20435242	0.310793246	0.06025601
84348301	-0.03584323	-0.0267241	-0.46432511	0.433811661	0.20308706
84358402	-0.01869779	0.4610302	0.06543782	-0.116442469	0.01763433
843786	-0.29727706	-0.1297265	-0.07117453	-0.002400178	0.10108043

	PC23	PC24	PC25	PC26	PC27
842302	0.08444429	0.175102213	0.150887294	-0.201326305	-0.25236294
842517	-0.21752666	-0.011280193	0.170360355	-0.041092627	0.18111081
84300903	-0.07422581	-0.102671419	-0.171007656	0.004731249	0.04952586
84348301	-0.12399554	-0.153294780	-0.077427574	-0.274982822	0.18330078
84358402	0.13933105	0.005327110	-0.003059371	0.039219780	0.03213957
843786	0.03344819	-0.002837749	-0.122282765	-0.030272333	-0.08438081

	PC28	PC29	PC30
842302	-0.0338846387	0.045607590	0.0471277407

```

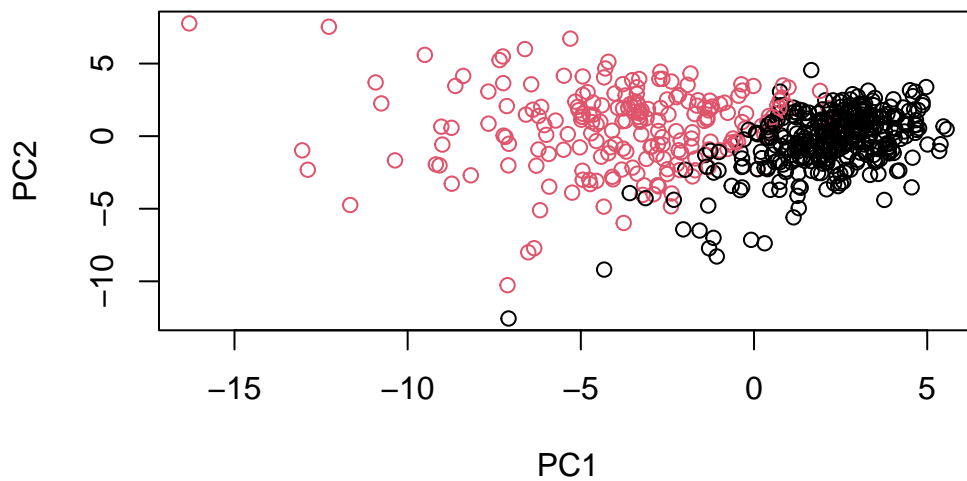
842517    0.0325955021 -0.005682424  0.0018662342
84300903  0.0469844833  0.003143131 -0.0007498749
84348301  0.0424469831 -0.069233868  0.0199198881
84358402 -0.0347556386  0.005033481 -0.0211951203
843786    0.0007296587 -0.019703996 -0.0034564331

```

```

#colored by diagnosis to assess if there is any difference in malignant and benign samples.
plot(wisc.pr$x, col = diagnosis_f, xlab = "PC1", ylab = "PC2")

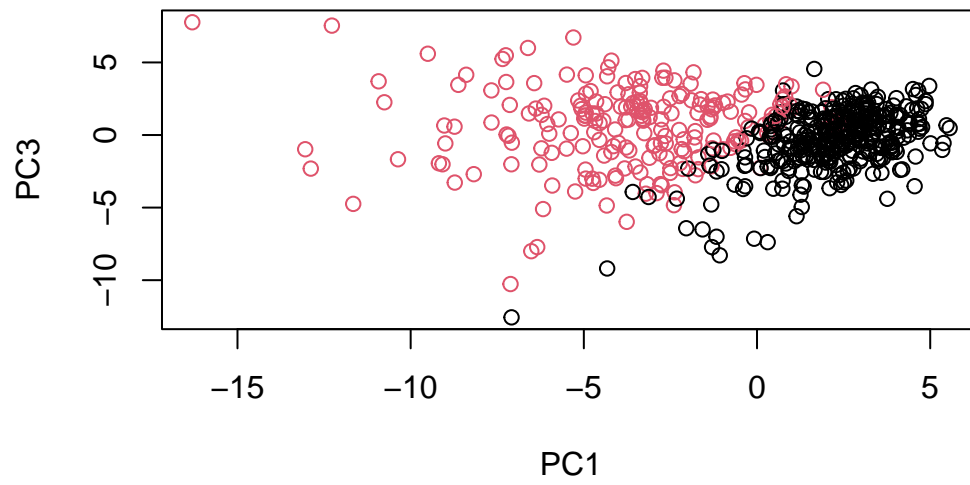
```



```

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

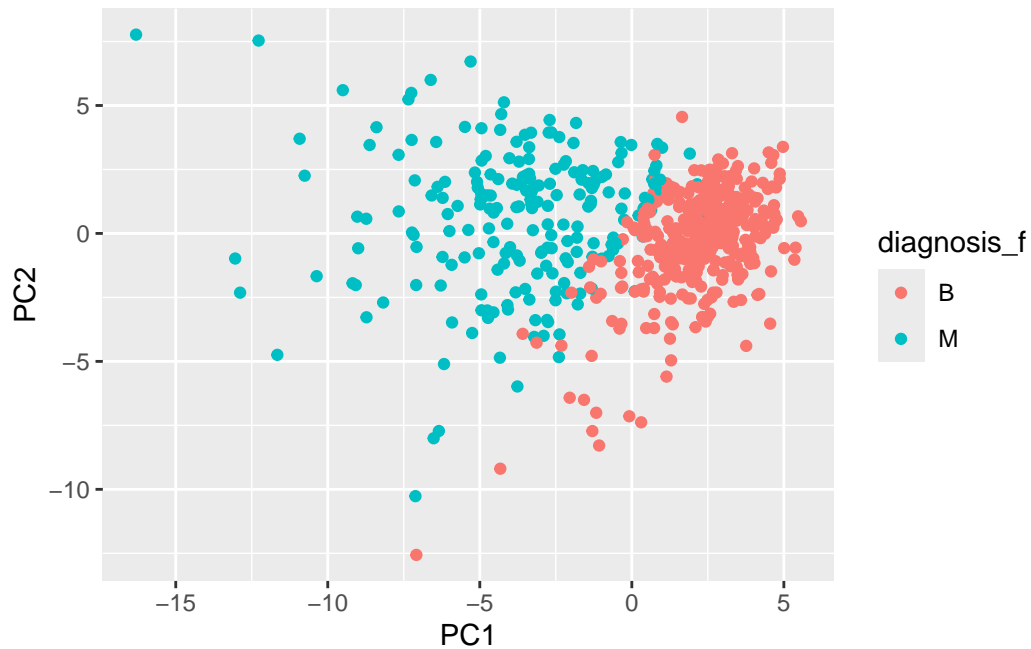
```



Now make a nicer ggplot version of the above

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

ggplot(df, aes(PC1, PC2, col = diagnosis_f)) + geom_point()
```



Now we can look at the proportion of variance explained by each principal component.

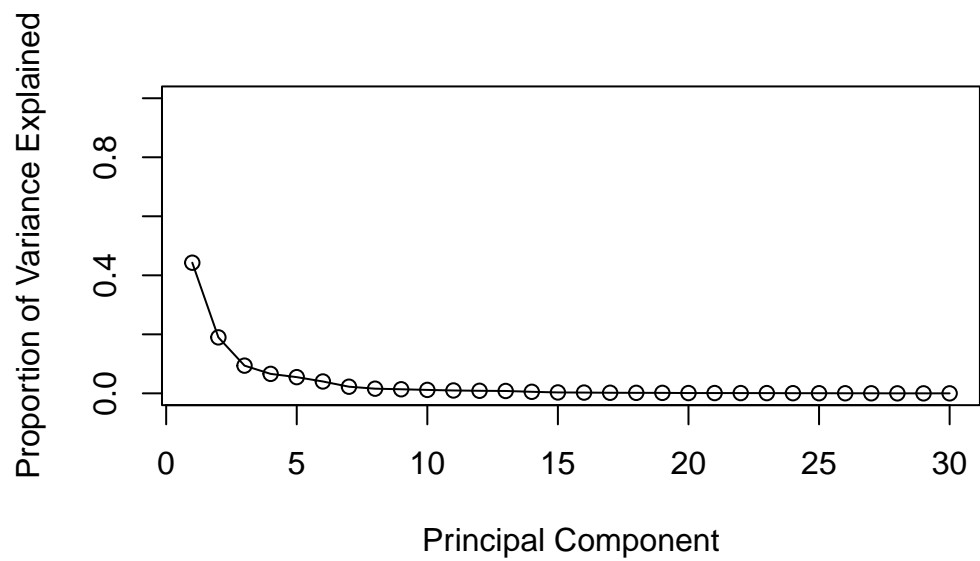
```
#Variance of each component
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

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

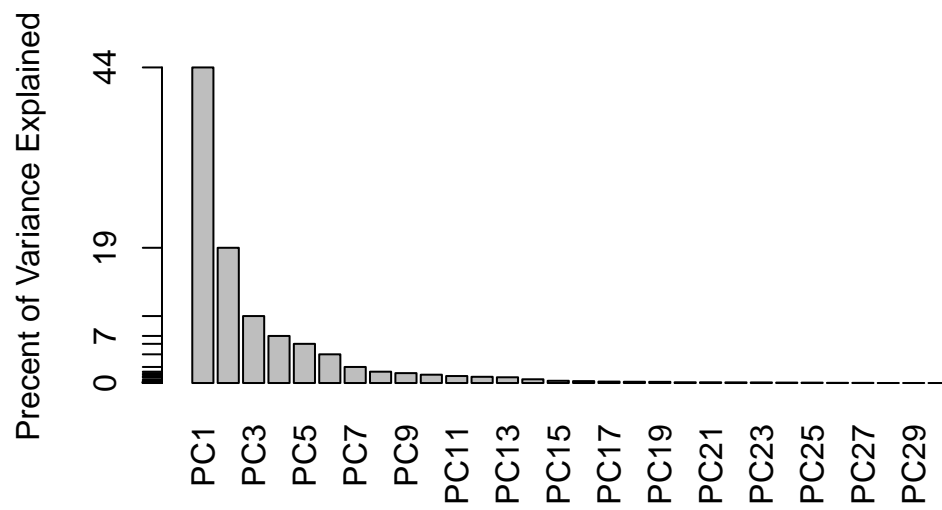
```
#variance explained by each principal component
pve <- pr.var/sum(pr.var)
head(pve)
```

```
[1] 0.44272026 0.18971182 0.09393163 0.06602135 0.05495768 0.04024522
```

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

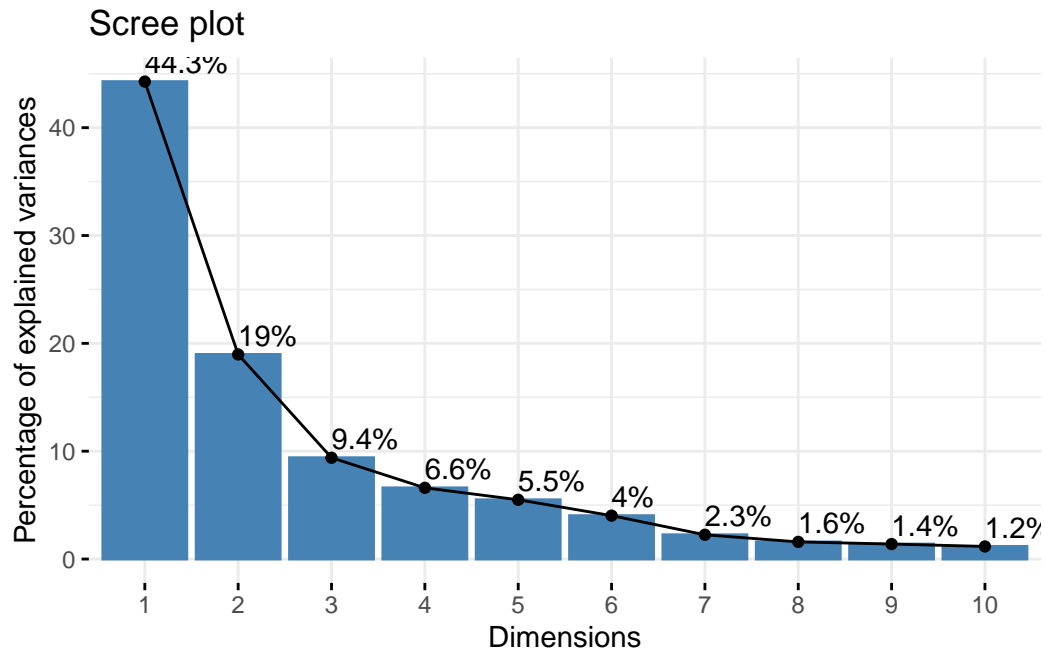
```
#scree plot of the same data
barplot(pve, ylab = "Precent of Variance Explained",
        names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100)
```



```
#factoextra makes prettier plot  
library(factoextra)
```

Welcome! Want to learn more? See two factoextra-related books at <https://goo.gl/ve3WBa>

```
fviz_eig(wisc.pr, addlabels = TRUE)
```

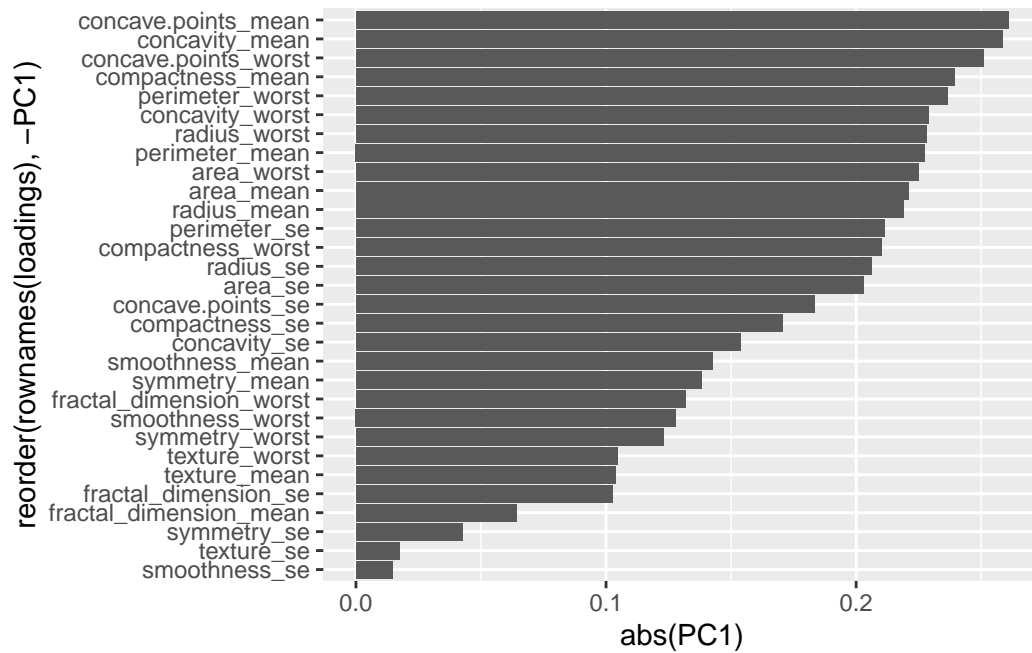


##Communicating PCA Results

#NOW, we are seeing how to look at variation (rotation of PC) explained by each variable (here)
`wisc.pr$rotation["concave.points_mean", 1]`

`[1] -0.2608538`

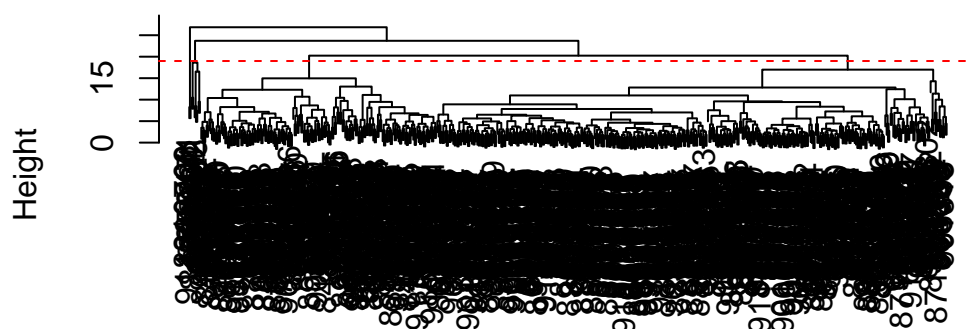
```
loadings <- wisc.pr$rotation
ggplot(loadings) + aes(abs(PC1), reorder(rownames(loadings), -PC1)) + geom_col()
```



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

#Q10
plot(wisc.hclust)
abline(h = 19, col = "red", lty = 2)
```

Cluster Dendrogram



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

```
#or
```

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

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

```
#Q11
```

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

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

```
5 0 2
```

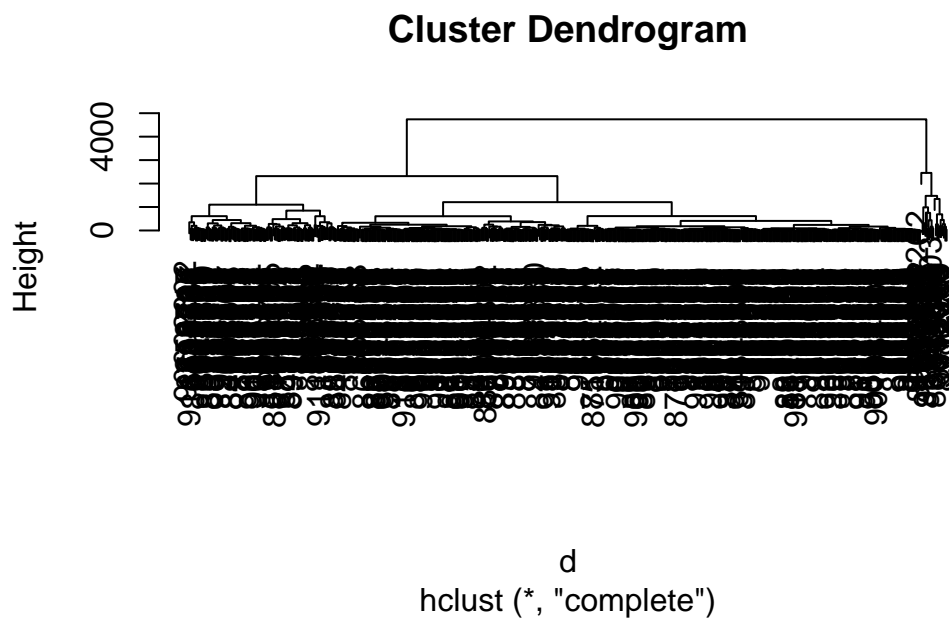
```
##K-means clustering
```

```
km <- kmeans(wisc.data, centers =2)  
table(km$cluster)
```

```
1 2  
438 131
```

```
##Hierarchical Clustering
```

```
d <- dist(wisc.data)  
hc <- hclust(d)  
plot(hc)
```



```
grps <- cutree(hc, k=3)  
table(grps)
```

```
grps
  1  2  3
549 19  1
```

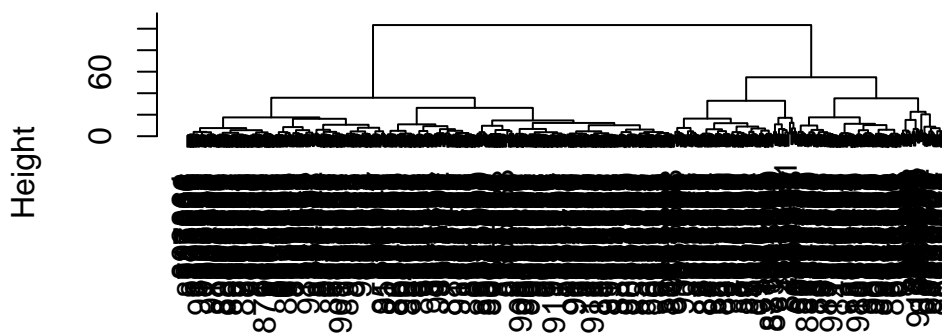
##Cluster in PC space

In other words, use my PCA results as the basis for clustering

```
#what is used to make older PCA plot
#wisc.pr$x

#make distance vector out of this in order to cluster hierarchically
d <- dist(wisc.pr$x[,1:3])
hc <- hclust(d, method = "ward.D2")
plot(hc)
```

Cluster Dendrogram



d
hclust (*, "ward.D2")

```
#Cut this tree to yield 2 groups/clusters (the benign and malignant groups)

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

```
grps
```

```
1 2
203 366
```

Compare to my expert M and B diagnosis_f

```
table(diagnosis_f)
```

```
diagnosis_f
  B  M
357 212
```

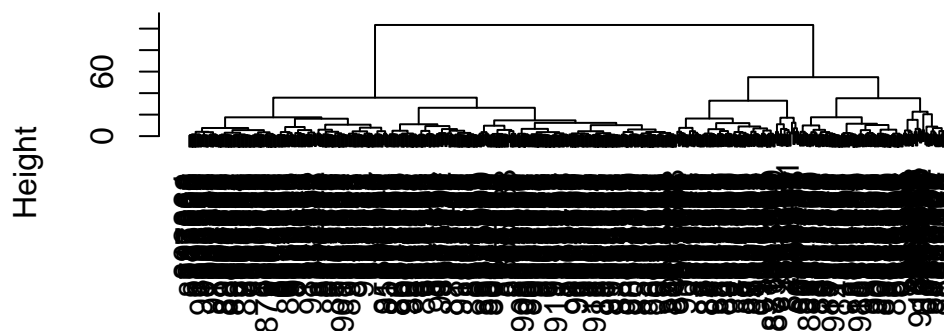
```
table(diagnosis_f, grps)
```

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

```
#Q12
```

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

Cluster Dendrogram

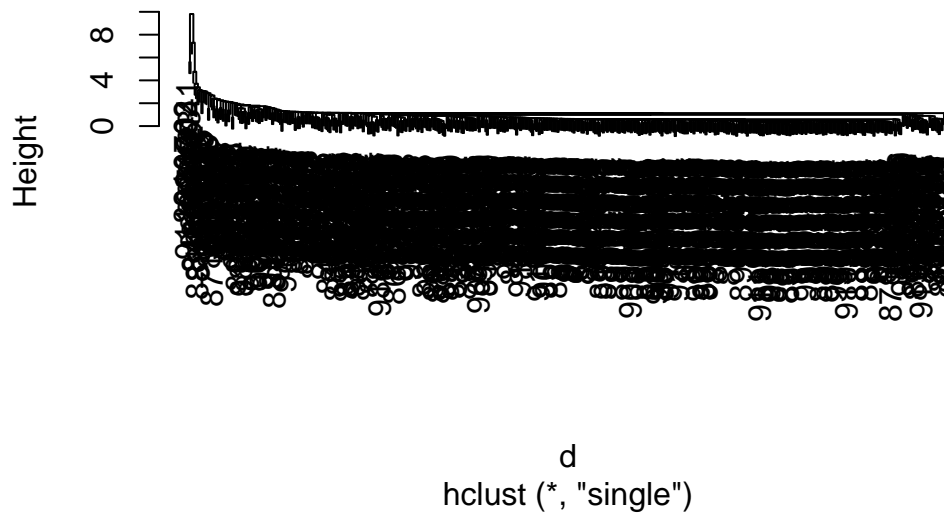


```
d
hclust (*, "ward.D2")
```



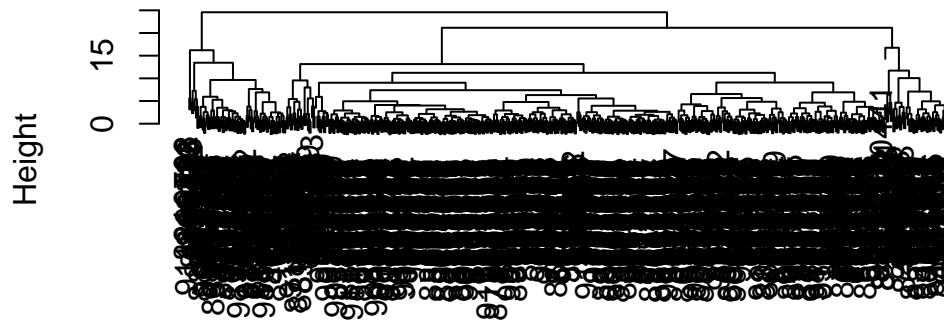
```
d <- dist(wisc.pr$x[,1:3])
hc <- hclust(d, method = "single")
plot(hc)
```

Cluster Dendrogram



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

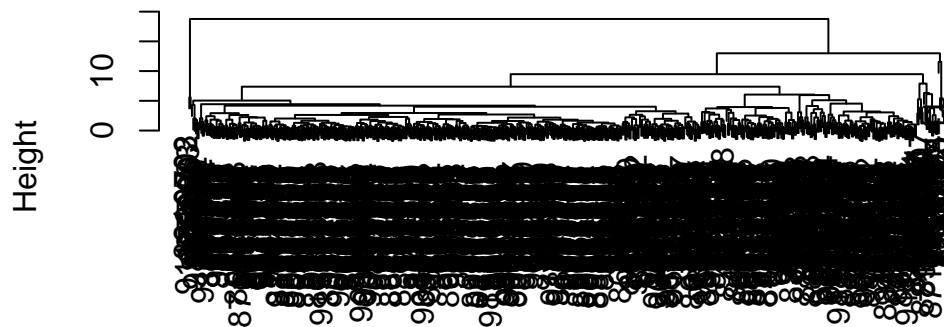
Cluster Dendrogram



d
hclust (*, "complete")

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

Cluster Dendrogram



d
hclust (*, "average")

```
#The ward.D2 method produces the dendrogram with highest crossbars and most easy to see two m  
#However, the complete method also lets us see that breaking into more clusters can provide a
```