

Mini Project

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Mini Project

Unsupervised learning analysis of breast cancer cells

The data itself comes from the Wisconsin Breast Cancer Diagnostic Data Set first reported by K. P. Benne and O. L. Mangasarian: “Robust Linear Programming Discrimination of Two Linearly Inseparable Sets”.

```
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	X			

```

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

```

```

wisc.data <- wisc.df[,-1]
#no more diagnosis column
wisc.data <- wisc.data[,-31]
#got rid of white space
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			

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

```
[1] 569
```

```
ncol(wisc.data)
```

```
[1] 30
```

We can use diagnosis as a factor to sum over specific factors

```
diagnosis <- as.factor(wisc.df$diagnosis)
```

How many individuals have a diagnosed cancer?

```
table(wisc.df$diagnosis)
```

```
  B    M  
357 212
```

How many variables have a suffix of “mean”

The `grep()` function will be used here

```
#obtain column names:  
col.names.vector <- colnames(wisc.data)  
#this is a vector  
length(grep("_mean",col.names.vector))
```

```
[1] 10
```

Starting the principal component analysis

Lets try PCA on this data to see what major features might be hidden in this large dimensional dataset.

Functions we want to use: `prcomp()`

`hclust(dist(x))`

`cutree(x,k=?)`

Initial data analysis **scaling**

```
round(colMeans(wisc.data), 2)
```

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

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

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

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

```
scale_false <- prcomp(wisc.data, scale = FALSE)
scale_true <- prcomp(wisc.data, scale = TRUE)
summary(scale_false)
```

Importance of components:

PC1	PC2	PC3	PC4	PC5	PC6	PC7
-----	-----	-----	-----	-----	-----	-----

Standard deviation	666.170	85.49912	26.52987	7.39248	6.31585	1.73337	1.347
Proportion of Variance	0.982	0.01618	0.00156	0.00012	0.00009	0.00001	0.000
Cumulative Proportion	0.982	0.99822	0.99978	0.99990	0.99999	0.99999	1.000
	PC8	PC9	PC10	PC11	PC12	PC13	PC14
Standard deviation	0.6095	0.3944	0.2899	0.1778	0.08659	0.05623	0.04649
Proportion of Variance	0.0000	0.0000	0.0000	0.0000	0.00000	0.00000	0.00000
Cumulative Proportion	1.0000	1.0000	1.0000	1.0000	1.00000	1.00000	1.00000
	PC15	PC16	PC17	PC18	PC19	PC20	PC21
Standard deviation	0.03642	0.0253	0.01936	0.01534	0.01359	0.01281	0.008838
Proportion of Variance	0.00000	0.0000	0.00000	0.00000	0.00000	0.00000	0.000000
Cumulative Proportion	1.00000	1.0000	1.00000	1.00000	1.00000	1.00000	1.000000
	PC22	PC23	PC24	PC25	PC26	PC27	
Standard deviation	0.00759	0.005909	0.005329	0.004018	0.003534	0.001918	
Proportion of Variance	0.00000	0.000000	0.000000	0.000000	0.000000	0.000000	
Cumulative Proportion	1.00000	1.000000	1.000000	1.000000	1.000000	1.000000	
	PC28	PC29	PC30				
Standard deviation	0.001688	0.001416	0.0008379				
Proportion of Variance	0.000000	0.000000	0.0000000				
Cumulative Proportion	1.000000	1.000000	1.0000000				

```
summary(scale_true)
```

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
```

```
#We will continue with scale = true

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

An example of when you don't want to re-scale is when you have all of the same units data (example a .pdb structure file, all the data is the same between proteins, and if you re-scale then you are altering the data!)

We see here that if we are un-scaled then PC1 covers 98 percent of the variance, but when we scale its only 44%

```
#we can perform a score plot
#aka a P.C. plot or
#ordination plots

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	

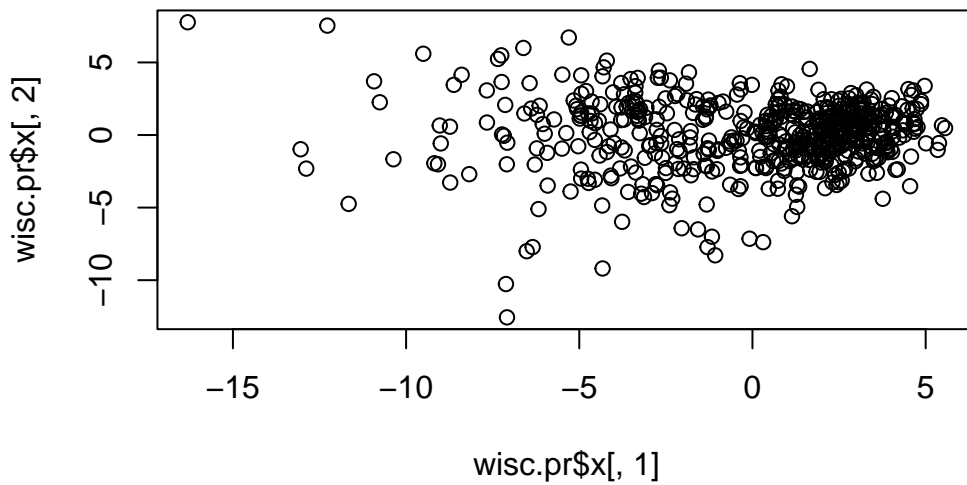
842302	-0.54907956	0.1336499	0.34526111	0.096430045	-0.06878939
842517	0.31801756	-0.2473470	-0.11403274	-0.077259494	0.09449530
84300903	-0.08789759	-0.3922812	-0.20435242	0.310793246	0.06025601
84348301	-0.03584323	-0.0267241	-0.46432511	0.433811661	0.20308706
84358402	-0.01869779	0.4610302	0.06543782	-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		

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

	PC1	PC2	PC3	PC4	PC5
radius_mean	-0.2189024	0.23385713	-0.008531243	0.04140896	-0.03778635
texture_mean	-0.1037246	0.05970609	0.064549903	-0.60305000	0.04946885
perimeter_mean	-0.2275373	0.21518136	-0.009314220	0.04198310	-0.03737466
area_mean	-0.2209950	0.23107671	0.028699526	0.05343380	-0.01033125
smoothness_mean	-0.1425897	-0.18611302	-0.104291904	0.15938277	0.36508853
compactness_mean	-0.2392854	-0.15189161	-0.074091571	0.03179458	-0.01170397
	PC6	PC7	PC8	PC9	PC10
radius_mean	0.018740790	-0.12408834	0.007452296	-0.223109764	0.09548644
texture_mean	-0.032178837	0.01139954	-0.130674825	0.112699390	0.24093407
perimeter_mean	0.017308445	-0.11447706	0.018687258	-0.223739213	0.08638562
area_mean	-0.001887748	-0.05165343	-0.034673604	-0.195586014	0.07495649
smoothness_mean	-0.286374497	-0.14066899	0.288974575	0.006424722	-0.06929268
compactness_mean	-0.014130949	0.03091850	0.151396350	-0.167841425	0.01293620
	PC11	PC12	PC13	PC14	PC15
radius_mean	-0.04147149	0.05106746	0.01196721	0.059506135	-0.05111877
texture_mean	0.30224340	0.25489642	0.20346133	-0.021560100	-0.10792242
perimeter_mean	-0.01678264	0.03892611	0.04410950	0.048513812	-0.03990294

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

```
plot(wisc.pr$x[,1],wisc.pr$x[,2])
```



**** each dot here is a patient! ****

We can now color based on diagnosis

```
plot(wisc.pr$x[,1],wisc.pr$x[,2],col=diagnosis,title="Malginant (red) vs Non Malignant (Bl
```

Warning in plot.window(...): "title" is not a graphical parameter

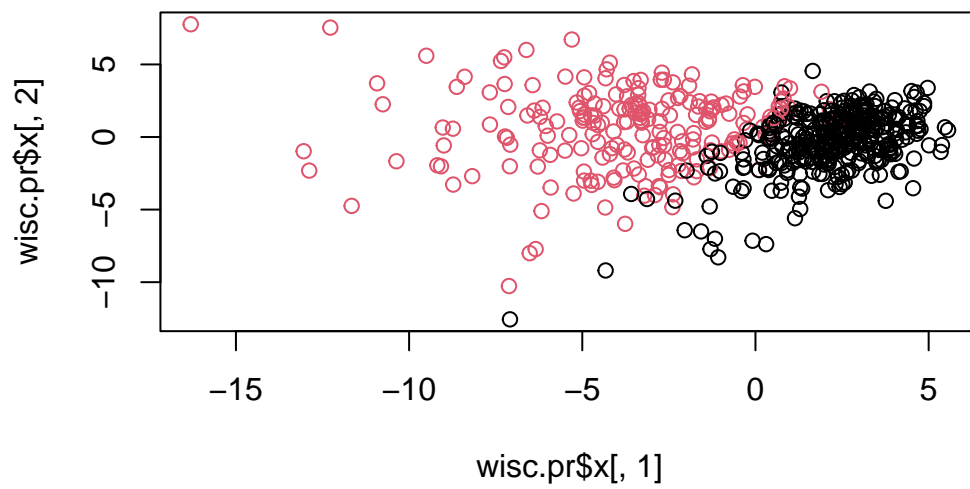
Warning in plot.xy(xy, type, ...): "title" is not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "title" is not a graphical parameter

Warning in axis(side = side, at = at, labels = labels, ...): "title" is not a graphical parameter

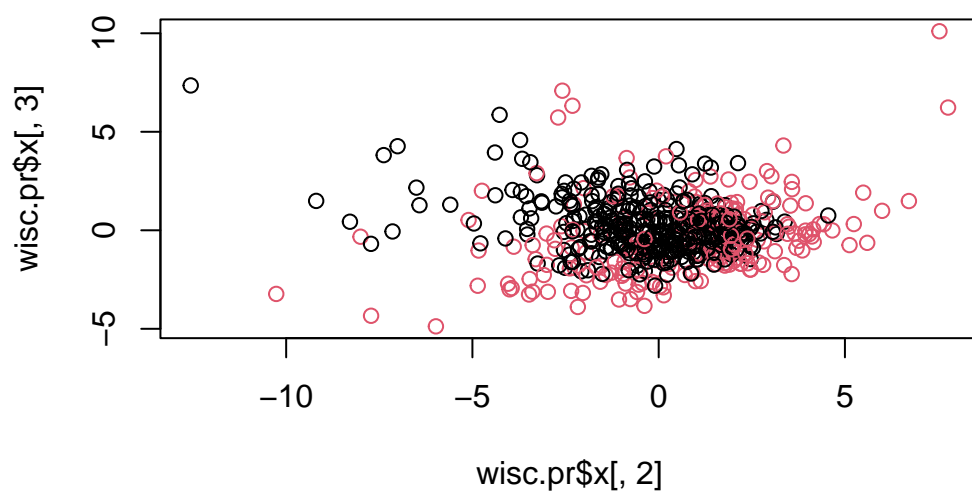
Warning in box(...): "title" is not a graphical parameter

Warning in title(...): "title" is not a graphical parameter

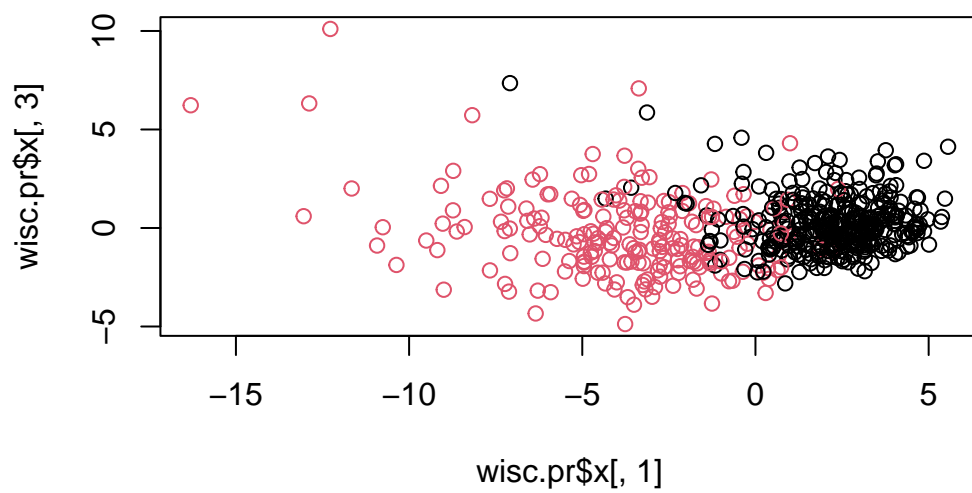


Can we plot other PCAs to see if we see such a stark contrast?

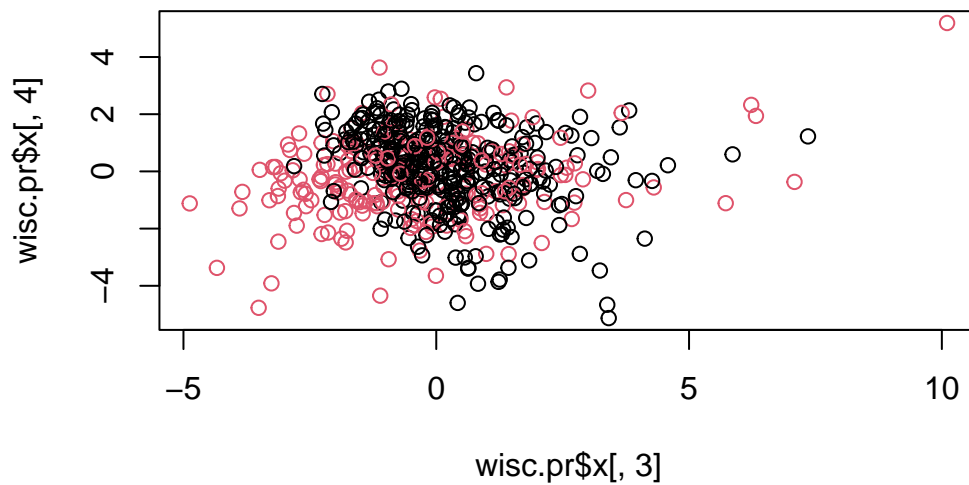
```
plot(wisc.pr$x[,2],wisc.pr$x[,3],col=diagnosis)
```



```
plot(wisc.pr$x[,1],wisc.pr$x[,3],col=diagnosis)
```



```
plot(wisc.pr$x[,3],wisc.pr$x[,4],col=diagnosis)
```



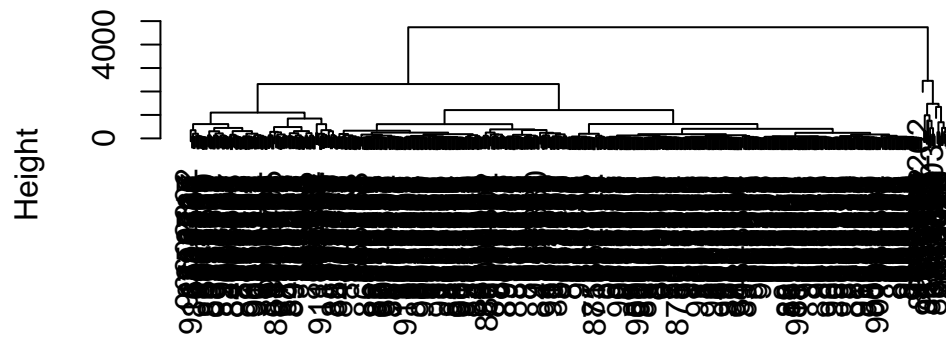
Comparing PCA1 and PCA2 are the best. 1 and 3 also work.

So now we want to eventually use these graphs and auto generate this so that we can find out which gives us the greatest distance between the two groups

we can use the distance function to do so?

```
wisc.pr.pca.1.2 <- cbind(x=wisc.pr$x[,1],y=wisc.pr$x[,2])  
  
wisc.pr.tree <- hclust(dist(wisc.pr.pca.1.2))  
  
wisc.pr.tree.original <- hclust(dist(wisc.data))  
  
plot(wisc.pr.tree.original)
```

Cluster Dendrogram

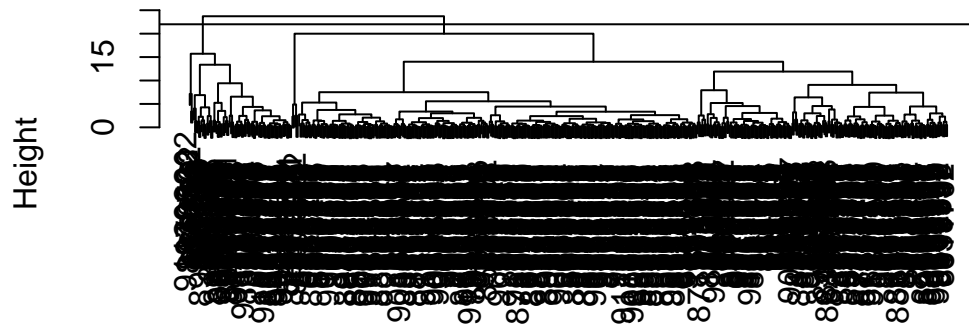


```
dist(wisc.data)
hclust (*, "complete")
```

```
plot(wisc.pr.tree)
```

```
#it looks like height of 22 looks like a good point to cut
abline(h=22)
```

Cluster Dendrogram



```
dist(wisc.pr.pca.1.2)
hclust (*, "complete")
```

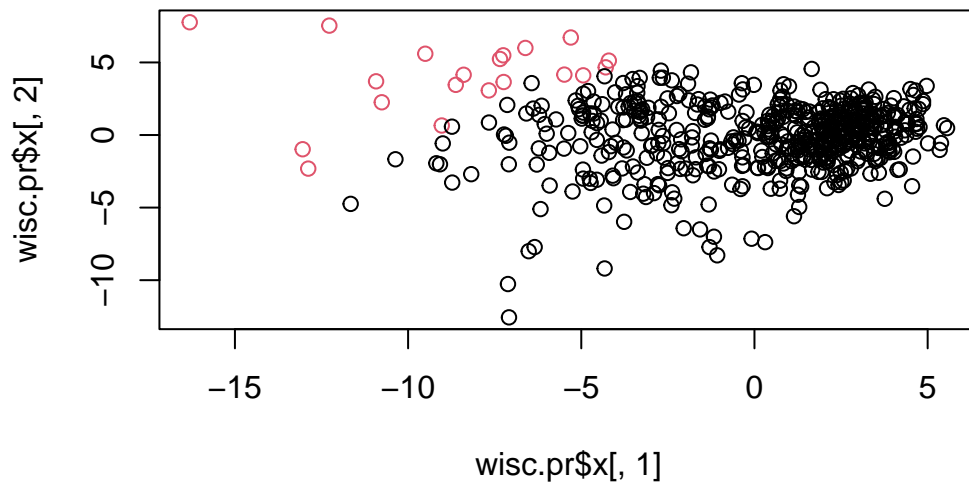
```
tree_groups <- cutree(wisc.pr.tree.original,k=2)
```

```
#Here we see that of the two groups,
#the group separation was very poor.
```

```
table(diagnosis, tree_groups)
```

	tree_groups	
diagnosis	1	2
B	357	0
M	192	20

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

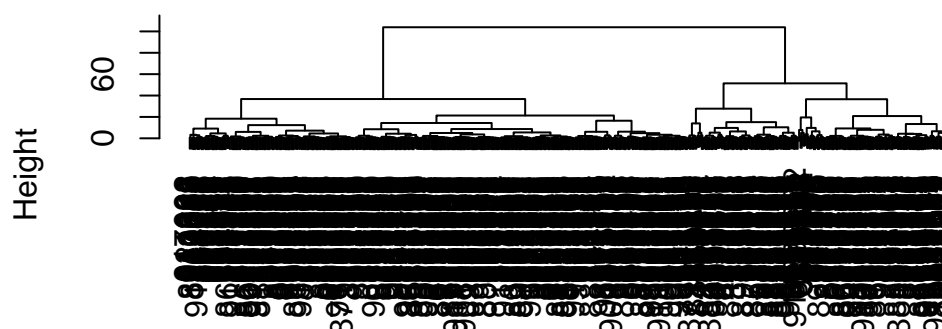



```
#k=2 here because we want two groups
#km.pr <- kmeans(wisc.pr.pca.1.2, centers = 2, nstart = 20)

#plot(wisc.pr.pca.1.2, col=km.pr$cluster)

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

Cluster Dendrogram



```
dist(wisc.pr$x[, 1:2])
hclust (*, "ward.D2")
```

```
table(diagnosis, cutree(newtree.pca,k=2))
```

```
diagnosis  1  2
B   18 339
M  177  35
```

Here we see that the three PCAs allow us to develop a table much better!

Infact the sensitivtiy of this algorithm might be good, lets find out!

```
summary(diagnosis)
```

```
B   M
357 212
```

```
tn <- 339
tp <- 177
fn <- 18
fp <- 35
sensitivity <- tp/(tp+fn)
```

```
specificity <- tn/(fp+tn)
#now we want to find out the values:

sensitivity
```

```
[1] 0.9076923
```

```
specificity
```

```
[1] 0.9064171
```

You can explore through utilizing more of the PCAs, however the sensitivity and specificity get worse! For example:

sensitivity and specificity for using [,1:3]:

sens: 0.88

spec: 0.91

sensitivity and specificity for using [,1:2]:

sens: 0.91

spec: 0.91

So actually, using just the first two PCAs provides a better model!

We can now use this as a predictive method!

`predict()` will take our PCA model from before and you can add new data to project onto our PCA space

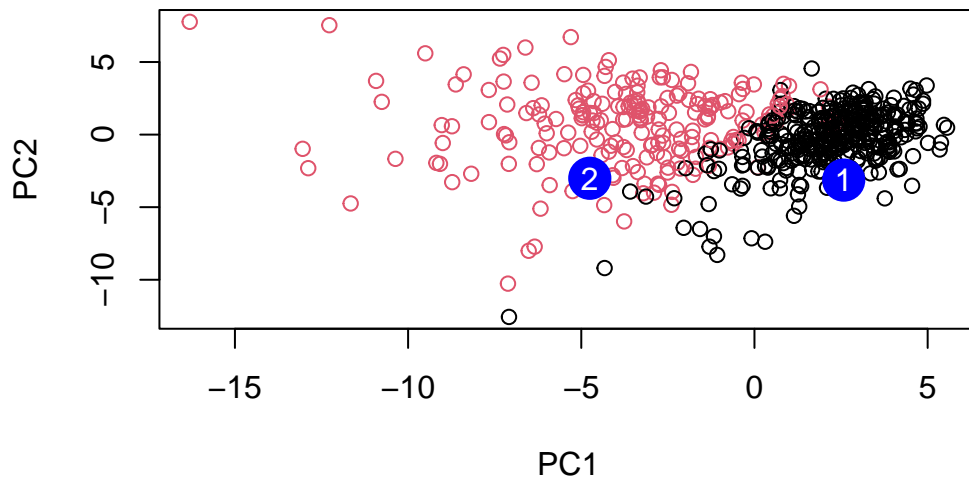
```
url <- "https://tinyurl.com/new-samples-CSV"
new <- read.csv(url)
npc <- predict(wisc.pr, newdata = new)
npc
```

	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	PC18	PC19	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	PC23	PC24	PC25	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			
[1,]	0.220199544	-0.02946023	-0.015620933	0.005269029			
[2,]	-0.001134152	0.09638361	0.002795349	-0.019015820			

```

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

```



I would follow up with patient 2, since the red group is the malignant group and patient 1 is closer to the non malignant group.

```
sessionInfo()
```

```
R version 4.2.1 (2022-06-23)
```

```
Platform: aarch64-apple-darwin20 (64-bit)
```

```
Running under: macOS Monterey 12.5.1
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRlapack.dylib
```

```
locale:
```

```
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
attached base packages:
```

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

```
loaded via a namespace (and not attached):
```

```
[1] compiler_4.2.1  magrittr_2.0.3  fastmap_1.1.0   cli_3.4.1  
[5] tools_4.2.1     htmltools_0.5.3 yaml_2.3.5      stringi_1.7.8  
[9] rmarkdown_2.16  knitr_1.40      stringr_1.4.1   xfun_0.33  
[13] digest_0.6.29   jsonlite_1.8.2  rlang_1.0.6     evaluate_0.17
```

Remember our goal is to: 1.) Reduce dimensionality 2.) Visualize multidimensional data
3.) Choose the most useful variables (features or PCA0s 4.) Identify groupings of objects 5.)
Identify outliers and remove if necessary