Homework 5

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This homework requires `wine.csv`, and the `tidyverse` and `Rtsne` packages. Install them if you haven't already!
See the following link for how to add new packages to Binder: https://github.com/rjenki/BIOS512?tab=readme-ov-file#adding-packages-to-installr-later.
For readability and easier processing, please make each question part a different code chunk.

```
#exporting to rmd
#library(rmarkdown)
#convert_ipynb("./BIOS512_hw5_Brookes.ipynb", output = xfun::with_ext("./BIOS512_HW5_Brookes.ipynb", "R
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.2     v tibble    3.3.0
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.1.0
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

```
library(Rtsne)
```

Question 1

```
wine <- read.csv("./hw5_data/wine.csv")
```

a) Import your data.

```
str(wine)
```

b) Check out the columns present using one of R's data frame summary.

```
## 'data.frame':    178 obs. of  14 variables:
##  $ Alcohol                     : num  14.2 13.2 13.2 14.4 13.2 ...
##  $ Malicacid                   : num  1.71 1.78 2.36 1.95 2.59 1.76 1.87 2.15 1.64 1.35 ...
##  $ Ash                         : num  2.43 2.14 2.67 2.5 2.87 2.45 2.45 2.61 2.17 2.27 ...
##  $ Alcalinity_of_ash           : num  15.6 11.2 18.6 16.8 21 15.2 14.6 17.6 14 16 ...
##  $ Magnesium                   : int  127 100 101 113 118 112 96 121 97 98 ...
##  $ Total_phenols               : num  2.8 2.65 2.8 3.85 2.8 3.27 2.5 2.6 2.8 2.98 ...
##  $ Flavanoids                  : num  3.06 2.76 3.24 3.49 2.69 3.39 2.52 2.51 2.98 3.15 ...
##  $ Nonflavanoid_phenols        : num  0.28 0.26 0.3 0.24 0.39 0.34 0.3 0.31 0.29 0.22 ...
##  $ Proanthocyanins             : num  2.29 1.28 2.81 2.18 1.82 1.97 1.98 1.25 1.98 1.85 ...
##  $ Color_intensity             : num  5.64 4.38 5.68 7.8 4.32 6.75 5.25 5.05 5.2 7.22 ...
##  $ Hue                         : num  1.04 1.05 1.03 0.86 1.04 1.05 1.02 1.06 1.08 1.01 ...
##  $ X0D280_0D315_of_diluted_wines: num  3.92 3.4 3.17 3.45 2.93 2.85 3.58 3.58 2.85 3.55 ...
##  $ Proline                     : int  1065 1050 1185 1480 735 1450 1290 1295 1045 1045 ...
##  $ class                       : int  1 1 1 1 1 1 1 1 1 1 ...
```

```r
#changing class to character

wine$class <- as.character(wine$class)

str(wine)
```

```
## 'data.frame':    178 obs. of  14 variables:
##  $ Alcohol                     : num  14.2 13.2 13.2 14.4 13.2 ...
##  $ Malicacid                   : num  1.71 1.78 2.36 1.95 2.59 1.76 1.87 2.15 1.64 1.35 ...
##  $ Ash                         : num  2.43 2.14 2.67 2.5 2.87 2.45 2.45 2.61 2.17 2.27 ...
##  $ Alcalinity_of_ash           : num  15.6 11.2 18.6 16.8 21 15.2 14.6 17.6 14 16 ...
##  $ Magnesium                   : int  127 100 101 113 118 112 96 121 97 98 ...
##  $ Total_phenols               : num  2.8 2.65 2.8 3.85 2.8 3.27 2.5 2.6 2.8 2.98 ...
##  $ Flavanoids                  : num  3.06 2.76 3.24 3.49 2.69 3.39 2.52 2.51 2.98 3.15 ...
##  $ Nonflavanoid_phenols        : num  0.28 0.26 0.3 0.24 0.39 0.34 0.3 0.31 0.29 0.22 ...
##  $ Proanthocyanins             : num  2.29 1.28 2.81 2.18 1.82 1.97 1.98 1.25 1.98 1.85 ...
##  $ Color_intensity             : num  5.64 4.38 5.68 7.8 4.32 6.75 5.25 5.05 5.2 7.22 ...
##  $ Hue                         : num  1.04 1.05 1.03 0.86 1.04 1.05 1.02 1.06 1.08 1.01 ...
##  $ X0D280_0D315_of_diluted_wines: num  3.92 3.4 3.17 3.45 2.93 2.85 3.58 3.58 2.85 3.55 ...
##  $ Proline                     : int  1065 1050 1185 1480 735 1450 1290 1295 1045 1045 ...
##  $ class                       : chr  "1" "1" "1" "1" ...
```

```r
wine %>% select(where(is.numeric)) %>%
  summary()
```

c) Get summary statistics on the numeric variables.

```
##     Alcohol        Malicacid          Ash        Alcalinity_of_ash
##  Min.   :11.03   Min.   :0.740   Min.   :1.360   Min.   :10.60    
##  1st Qu.:12.36   1st Qu.:1.603   1st Qu.:2.210   1st Qu.:17.20    
##  Median :13.05   Median :1.865   Median :2.360   Median :19.50    
##  Mean   :13.00   Mean   :2.336   Mean   :2.367   Mean   :19.49    
##  3rd Qu.:13.68   3rd Qu.:3.083   3rd Qu.:2.558   3rd Qu.:21.50    
##  Max.   :14.83   Max.   :5.800   Max.   :3.230   Max.   :30.00    
```

```
##    Magnesium      Total_phenols     Flavanoids    Nonflavanoid_phenols
##  Min.   : 70.00   Min.   :0.980   Min.   :0.340   Min.   :0.1300      
##  1st Qu.: 88.00   1st Qu.:1.742   1st Qu.:1.205   1st Qu.:0.2700      
##  Median : 98.00   Median :2.355   Median :2.135   Median :0.3400      
##  Mean   : 99.74   Mean   :2.295   Mean   :2.029   Mean   :0.3619      
##  3rd Qu.:107.00   3rd Qu.:2.800   3rd Qu.:2.875   3rd Qu.:0.4375      
##  Max.   :162.00   Max.   :3.880   Max.   :5.080   Max.   :0.6600      
##  Proanthocyanins Color_intensity       Hue        
##  Min.   :0.410   Min.   : 1.280   Min.   :0.4800  
##  1st Qu.:1.250   1st Qu.: 3.220   1st Qu.:0.7825  
##  Median :1.555   Median : 4.690   Median :0.9650  
##  Mean   :1.591   Mean   : 5.058   Mean   :0.9574  
##  3rd Qu.:1.950   3rd Qu.: 6.200   3rd Qu.:1.1200  
##  Max.   :3.580   Max.   :13.000   Max.   :1.7100  
##  X0D280_0D315_of_diluted_wines    Proline      
##  Min.   :1.270                 Min.   : 278.0  
##  1st Qu.:1.938                 1st Qu.: 500.5  
##  Median :2.780                 Median : 673.5  
##  Mean   :2.612                 Mean   : 746.9  
##  3rd Qu.:3.170                 3rd Qu.: 985.0  
##  Max.   :4.000                 Max.   :1680.0  
```

Question 2

a) Scale and center your data *Hint:* Use a `mutate()` statement across all columns **except class** with `function(x) as.numeric(scale(x))`.

```
wine_scaled <- wine %>%
  mutate(across(where(is.numeric), ~as.numeric(scale(.))))

summary(wine_scaled)
```

```
##     Alcohol           Malicacid            Ash           Alcalinity_of_ash 
##  Min.   :-2.42739   Min.   :-1.4290   Min.   :-3.66881   Min.   :-2.663505  
##  1st Qu.:-0.78603   1st Qu.:-0.6569   1st Qu.:-0.57051   1st Qu.:-0.687199  
##  Median : 0.06083   Median :-0.4219   Median :-0.02375   Median : 0.001514  
##  Mean   : 0.00000   Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.000000  
##  3rd Qu.: 0.83378   3rd Qu.: 0.6679   3rd Qu.: 0.69614   3rd Qu.: 0.600395  
##  Max.   : 2.25341   Max.   : 3.1004   Max.   : 3.14745   Max.   : 3.145637  
##    Magnesium        Total_phenols        Flavanoids      Nonflavanoid_phenols
##  Min.   :-2.0824   Min.   :-2.10132   Min.   :-1.6912   Min.   :-1.8630     
##  1st Qu.:-0.8221   1st Qu.:-0.88298   1st Qu.:-0.8252   1st Qu.:-0.7381     
##  Median :-0.1219   Median : 0.09569   Median : 0.1059   Median :-0.1756     
##  Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.0000   Mean   : 0.0000     
##  3rd Qu.: 0.5082   3rd Qu.: 0.80672   3rd Qu.: 0.8467   3rd Qu.: 0.6078     
##  Max.   : 4.3591   Max.   : 2.53237   Max.   : 3.0542   Max.   : 2.3956     
##  Proanthocyanins    Color_intensity        Hue          
##  Min.   :-2.06321   Min.   :-1.6297   Min.   :-2.08884  
##  1st Qu.:-0.59560   1st Qu.:-0.7929   1st Qu.:-0.76540  
##  Median :-0.06272   Median :-0.1588   Median : 0.03303  
##  Mean   : 0.00000   Mean   : 0.0000   Mean   : 0.00000  
##  3rd Qu.: 0.62741   3rd Qu.: 0.4926   3rd Qu.: 0.71116  
##  Max.   : 3.47527   Max.   : 3.4258   Max.   : 3.29241  
```

```
##  X0D280_0D315_of_diluted_wines    Proline           class
##  Min.   :-1.8897              Min.   :-1.4890   Length:178
##  1st Qu.:-0.9496              1st Qu.:-0.7824   Class :character
##  Median : 0.2371              Median :-0.2331   Mode  :character
##  Mean   : 0.0000              Mean   : 0.0000
##  3rd Qu.: 0.7864              3rd Qu.: 0.7561
##  Max.   : 1.9554              Max.   : 2.9631
```

b) Based on what you saw in the summary statistic table from the imported data, why would scaling and centering this data be helpful before we perform PCA? It is helpful because the raw data is not centered around a common point. All the summary values range to varying degrees above zero, and it is difficult to work with the data without a standardized or centered scale. We have to scale and center so PCA can rotate around a common center.

Question 3

```
PCA_wine <- wine_scaled %>% select(where(is.numeric)) %>%
                                 prcomp(); # runs PCA on d
PCA_wine
```

a) Perform PCA

```
## Standard deviations (1, .., p=13):
##  [1] 2.1692972 1.5801816 1.2025273 0.9586313 0.9237035 0.8010350 0.7423128
##  [8] 0.5903367 0.5374755 0.5009017 0.4751722 0.4108165 0.3215244
##
## Rotation (n x k) = (13 x 13):
##                                   PC1          PC2         PC3         PC4
## Alcohol                      -0.144329395 -0.483651548 -0.20738262 -0.01785630
## Malicacid                     0.245187580 -0.224930935  0.08901289  0.53689028
## Ash                           0.002051061 -0.316068814  0.62622390 -0.21417556
## Alcalinity_of_ash             0.239320405  0.010590502  0.61208035  0.06085941
## Magnesium                    -0.141992042 -0.299634003  0.13075693 -0.35179658
## Total_phenols                -0.394660845 -0.065039512  0.14617896  0.19806835
## Flavanoids                   -0.422934297  0.003359812  0.15068190  0.15229479
## Nonflavanoid_phenols          0.298533103 -0.028779488  0.17036816 -0.20330102
## Proanthocyanins              -0.313429488 -0.039301722  0.14945431  0.39905653
## Color_intensity               0.088616705 -0.529995672 -0.13730621  0.06592568
## Hue                          -0.296714564  0.279235148  0.08522192 -0.42777141
## X0D280_0D315_of_diluted_wines -0.376167411  0.164496193  0.16600459  0.18412074
## Proline                      -0.286752227 -0.364902832 -0.12674592 -0.23207086
##                                    PC5         PC6         PC7         PC8
## Alcohol                       0.26566365 -0.21353865 -0.05639636 -0.39613926
## Malicacid                    -0.03521363 -0.53681385  0.42052391 -0.06582674
## Ash                           0.14302547 -0.15447466 -0.14917061  0.17026002
## Alcalinity_of_ash            -0.06610294  0.10082451 -0.28696914 -0.42797018
## Magnesium                    -0.72704851 -0.03814394  0.32288330  0.15636143
## Total_phenols                 0.14931841  0.08412230 -0.02792498  0.40593409
## Flavanoids                    0.10902584  0.01892002 -0.06068521  0.18724536
## Nonflavanoid_phenols          0.50070298  0.25859401  0.59544729  0.23328465
```

```
## Proanthocyanins              -0.13685982  0.53379539  0.37213935 -0.36822675
## Color_intensity               0.07643678  0.41864414 -0.22771214  0.03379692
## Hue                           0.17361452 -0.10598274  0.23207564 -0.43662362
## X0D280_0D315_of_diluted_wines  0.10116099 -0.26585107 -0.04476370  0.07810789
## Proline                       0.15786880 -0.11972557  0.07680450 -0.12002267
##                                      PC9        PC10        PC11         PC12
## Alcohol                      -0.50861912 -0.21160473  0.22591696  0.26628645
## Malicacid                     0.07528304  0.30907994 -0.07648554 -0.12169604
## Ash                           0.30769445  0.02712539  0.49869142  0.04962237
## Alcalinity_of_ash            -0.20044931 -0.05279942 -0.47931378  0.05574287
## Magnesium                    -0.27140257 -0.06787022 -0.07128891 -0.06222011
## Total_phenols                -0.28603452  0.32013135 -0.30434119  0.30388245
## Flavanoids                   -0.04957849  0.16315051  0.02569409  0.04289883
## Nonflavanoid_phenols         -0.19550132 -0.21553507 -0.11689586 -0.04235219
## Proanthocyanins               0.20914487 -0.13418390  0.23736257  0.09555303
## Color_intensity              -0.05621752  0.29077518 -0.03183880 -0.60422163
## Hue                          -0.08582839  0.52239889  0.04821201 -0.25921400
## X0D280_0D315_of_diluted_wines -0.13722690 -0.52370587 -0.04642330 -0.60095872
## Proline                       0.57578611 -0.16211600 -0.53926983  0.07940162
##                                     PC13
## Alcohol                      -0.01496997
## Malicacid                    -0.02596375
## Ash                           0.14121803
## Alcalinity_of_ash            -0.09168285
## Magnesium                    -0.05677422
## Total_phenols                 0.46390791
## Flavanoids                   -0.83225706
## Nonflavanoid_phenols         -0.11403985
## Proanthocyanins               0.11691707
## Color_intensity               0.01199280
## Hue                           0.08988884
## X0D280_0D315_of_diluted_wines  0.15671813
## Proline                      -0.01444734
```

```r
summary(PCA_wine)
```

```
## Importance of components:
##                          PC1    PC2    PC3     PC4     PC5     PC6     PC7
## Standard deviation     2.169 1.5802 1.2025 0.95863 0.92370 0.80103 0.74231
## Proportion of Variance 0.362 0.1921 0.1112 0.07069 0.06563 0.04936 0.04239
## Cumulative Proportion  0.362 0.5541 0.6653 0.73599 0.80162 0.85098 0.89337
##                            PC8     PC9   PC10    PC11    PC12    PC13
## Standard deviation     0.59034 0.53748 0.5009 0.47517 0.41082 0.32152
## Proportion of Variance 0.02681 0.02222 0.0193 0.01737 0.01298 0.00795
## Cumulative Proportion  0.92018 0.94240 0.9617 0.97907 0.99205 1.00000
```

```r
#PC1 Proportion of variance + PC2 proportion of variance
0.361+0.1921
```

b) How much of the total variance is explained by PC1? PC2? What function do we use to see that information?

```
## [1] 0.5531
```

Total Proportion of Variance explained by PC1 and PC2 is 0.5531.

c) Why are we doing PCA first? Reduces noise and dimensionality in the data. It also helps to capture the most variation in the data to create new axes.

d) What is the rotation matrix? Print it explicitly. *Hint:* Check the notes for a simple way to do this!

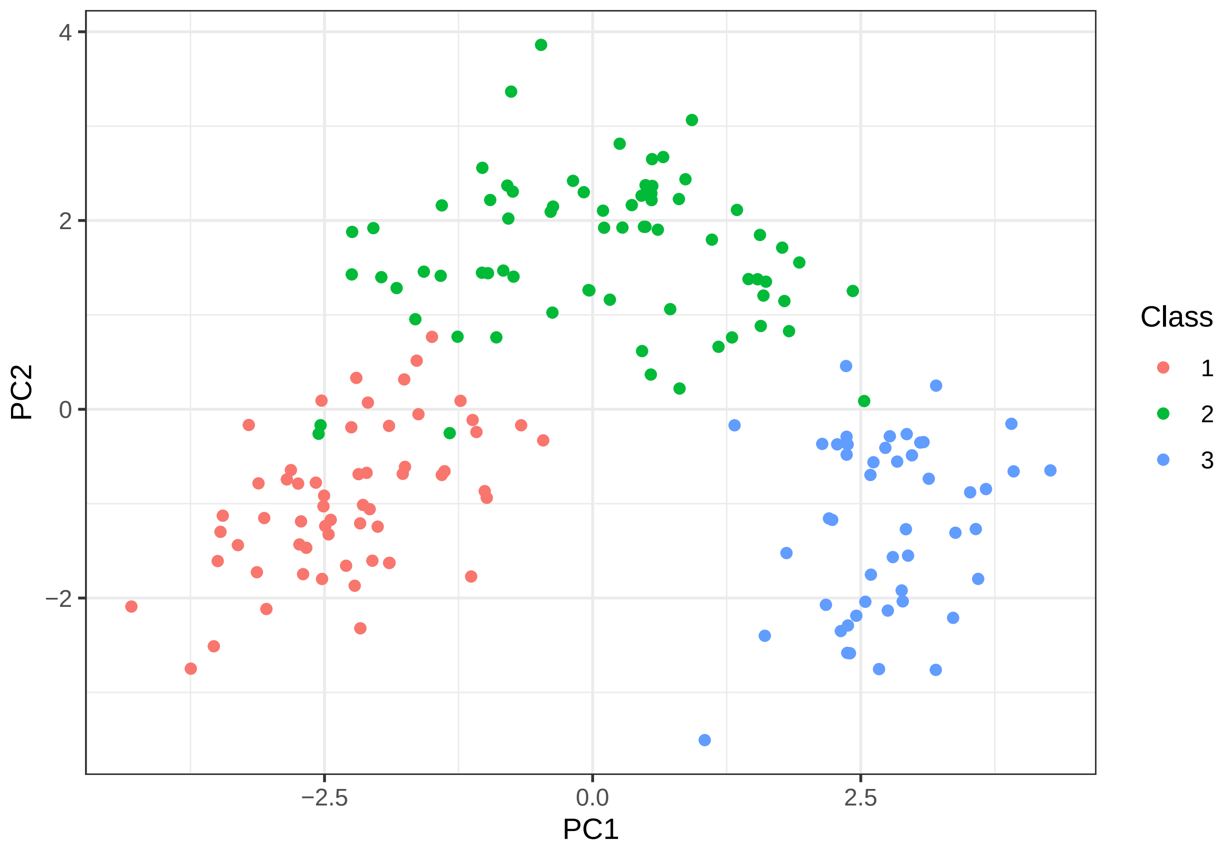
```
print(PCA_wine$rotation) # PCA_wine$rotation is the rotation matrix
```

```
##                                     PC1          PC2         PC3         PC4
## Alcohol                    -0.144329395 -0.483651548 -0.20738262 -0.01785630
## Malicacid                   0.245187580 -0.224930935  0.08901289  0.53689028
## Ash                         0.002051061 -0.316068814  0.62622390 -0.21417556
## Alcalinity_of_ash           0.239320405  0.010590502  0.61208035  0.06085941
## Magnesium                  -0.141992042 -0.299634003  0.13075693 -0.35179658
## Total_phenols              -0.394660845 -0.065039512  0.14617896  0.19806835
## Flavanoids                 -0.422934297  0.003359812  0.15068190  0.15229479
## Nonflavanoid_phenols        0.298533103 -0.028779488  0.17036816 -0.20330102
## Proanthocyanins            -0.313429488 -0.039301722  0.14945431  0.39905653
## Color_intensity             0.088616705 -0.529995672 -0.13730621  0.06592568
## Hue                        -0.296714564  0.279235148  0.08522192 -0.42777141
## X0D280_0D315_of_diluted_wines -0.376167411  0.164496193  0.16600459  0.18412074
## Proline                    -0.286752227 -0.364902832 -0.12674592 -0.23207086
##                                   PC5         PC6         PC7         PC8
## Alcohol                     0.26566365 -0.21353865 -0.05639636 -0.39613926
## Malicacid                  -0.03521363 -0.53681385  0.42052391 -0.06582674
## Ash                         0.14302547 -0.15447466 -0.14917061  0.17026002
## Alcalinity_of_ash          -0.06610294  0.10082451 -0.28696914 -0.42797018
## Magnesium                  -0.72704851 -0.03814394  0.32288330  0.15636143
## Total_phenols               0.14931841  0.08412230 -0.02792498  0.40593409
## Flavanoids                  0.10902584  0.01892002 -0.06068521  0.18724536
## Nonflavanoid_phenols        0.50070298  0.25859401  0.59544729  0.23328465
## Proanthocyanins            -0.13685982  0.53379539  0.37213935 -0.36822675
## Color_intensity             0.07643678  0.41864414 -0.22771214  0.03379692
## Hue                         0.17361452 -0.10598274  0.23207564 -0.43662362
## X0D280_0D315_of_diluted_wines  0.10116099 -0.26585107 -0.04476370  0.07810789
## Proline                     0.15786880 -0.11972557  0.07680450 -0.12002267
##                                   PC9        PC10        PC11        PC12
## Alcohol                    -0.50861912 -0.21160473  0.22591696  0.26628645
## Malicacid                   0.07528304  0.30907994 -0.07648554 -0.12169604
## Ash                         0.30769445  0.02712539  0.49869142  0.04962237
## Alcalinity_of_ash          -0.20044931 -0.05279942 -0.47931378  0.05574287
## Magnesium                  -0.27140257 -0.06787022 -0.07128891 -0.06222011
## Total_phenols              -0.28603452  0.32013135 -0.30434119  0.30388245
## Flavanoids                 -0.04957849  0.16315051  0.02569409  0.04289883
## Nonflavanoid_phenols       -0.19550132 -0.21553507 -0.11689586 -0.04235219
## Proanthocyanins             0.20914487 -0.13418390  0.23736257  0.09555303
## Color_intensity            -0.05621752  0.29077518 -0.03183880 -0.60422163
## Hue                        -0.08582839  0.52239889  0.04821201 -0.25921400
```

```
## X0D280_0D315_of_diluted_wines -0.13722690 -0.52370587 -0.04642330 -0.60095872
## Proline                        0.57578611 -0.16211600 -0.53926983  0.07940162
##                                      PC13
## Alcohol                       -0.01496997
## Malicacid                     -0.02596375
## Ash                            0.14121803
## Alcalinity_of_ash             -0.09168285
## Magnesium                     -0.05677422
## Total_phenols                  0.46390791
## Flavanoids                    -0.83225706
## Nonflavanoid_phenols          -0.11403985
## Proanthocyanins                0.11691707
## Color_intensity                0.01199280
## Hue                            0.08988884
## X0D280_0D315_of_diluted_wines  0.15671813
## Proline                       -0.01444734
```

e) Plot PC1 vs. PC2, using the wine class as labels for coloring. *Hint:* You'll first need a data set with only PC1 and PC2, then add back the class variable from your scaled data set with a `mutate()` statement. Then, you can use `color = factor(class)` in your `ggplot` statement.

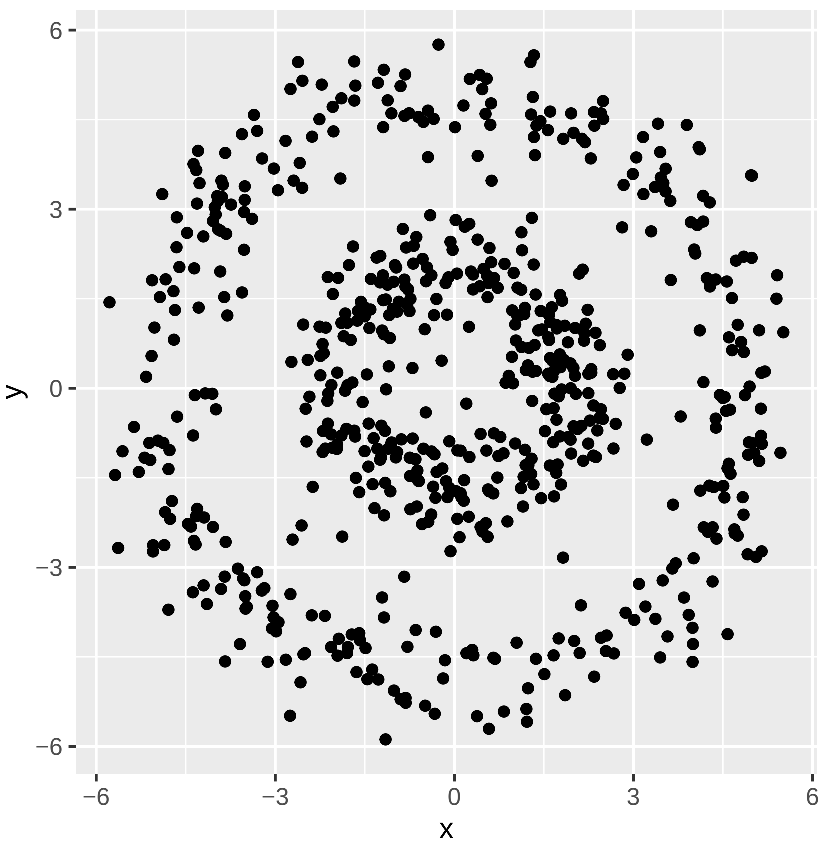
```
PC1_PC2_only <- PCA_wine$x %>% as.data.frame() %>%  select(c("PC1", "PC2"))

PC1_PC2_only$class <-wine_scaled$class

#plotting PC1 vs PC2

library(ggplot2)
ggplot(PC1_PC2_only, aes(x = PC1, y = PC2, color = factor(class))) +
  geom_point() +
  labs(color = "Class") +
  theme_bw()
```



f) What do you see after plotting PC1 vs. PC2? What does this mean in context of wine classes? The wine classes are clustered on the graph, but overlap some on the PC1 and PC2 axis. Class 2 shares some similarities with Class 1 and 2. However, there seems to be distinct clustering on chemical profiles that define the different wine classes.

g) Give an example of data where PCA would fail. You can describe the data or do a simulation. *Hint:* Our notes have a few examples! PCA would fail on a dataset with a non-linear space. A real life example of this would be calculating differences in a dataset of facial expressions. This dataset would not be linear because facial expression patterns could not be maniuplated on a linear space. Example simulation:

```
circular_data <- tibble(r = sample(c(2,5),size=650,replace=TRUE) + rnorm(650,0,0.5),
            theta = runif(650,0,2*pi)) %>%
    transmute(x=r*cos(theta),
              y=r*sin(theta));
ggplot(circular_data, aes(x,y)) + geom_point() + coord_fixed()
```



h) Explain the difference between vector space and manifold, and how these terms apply to what we did/will do with T-SNE. A vector space is a set of variables along a field that follow a mathematical structure that assumes linearity, which means they can be added and scale them.

The manifold is the local vector space of a set. While a vector space assumes linearity, a manifold can be non-linear but resembles the local vector space.

In PAC, we scaled the data and placed it on a vector space by rotating individual points. In T-SNE, it assumes the data lies on a manifold and preserves local neighborhood relationships to calculate the probability that two points are neighbors.

Question 4

a) Perform T-SNE Set `seed = 123`.
Hint: Subset your PCA results to PC1–PC10, add the class variable back in, remove duplicates, then perform T-SNE.

```
library(Rtsne)

wine_PCA_DF <- PCA_wine$x %>% as.data.frame() %>% select(PC1:PC10)

#adding wine class back
wine_PCA_DF$class <- wine$class

#removing duplicates
```

```r
wine_PCA_no_duplicates <- wine_PCA_DF %>% filter(!duplicated(.))

str(wine_PCA_no_duplicates)
```

```
## 'data.frame':    178 obs. of  11 variables:
##  $ PC1  : num  -3.31 -2.2 -2.51 -3.75 -1.01 ...
##  $ PC2  : num  -1.439 0.332 -1.028 -2.749 -0.867 ...
##  $ PC3  : num  -0.165 -2.021 0.98 -0.176 2.021 ...
##  $ PC4  : num  -0.215 -0.291 0.723 0.566 -0.409 ...
##  $ PC5  : num  -0.691 0.257 0.25 0.311 -0.298 ...
##  $ PC6  : num  -0.223 -0.925 0.548 0.114 -0.405 ...
##  $ PC7  : num  0.5947 0.0536 0.423 -0.3823 0.4428 ...
##  $ PC8  : num  0.065 1.022 -0.343 0.642 0.416 ...
##  $ PC9  : num  -0.6396 0.308 1.1745 -0.0524 -0.3259 ...
##  $ PC10 : num  -1.0181 -0.1593 -0.113 -0.2387 0.0781 ...
##  $ class: chr  "1" "1" "1" "1" ...
```

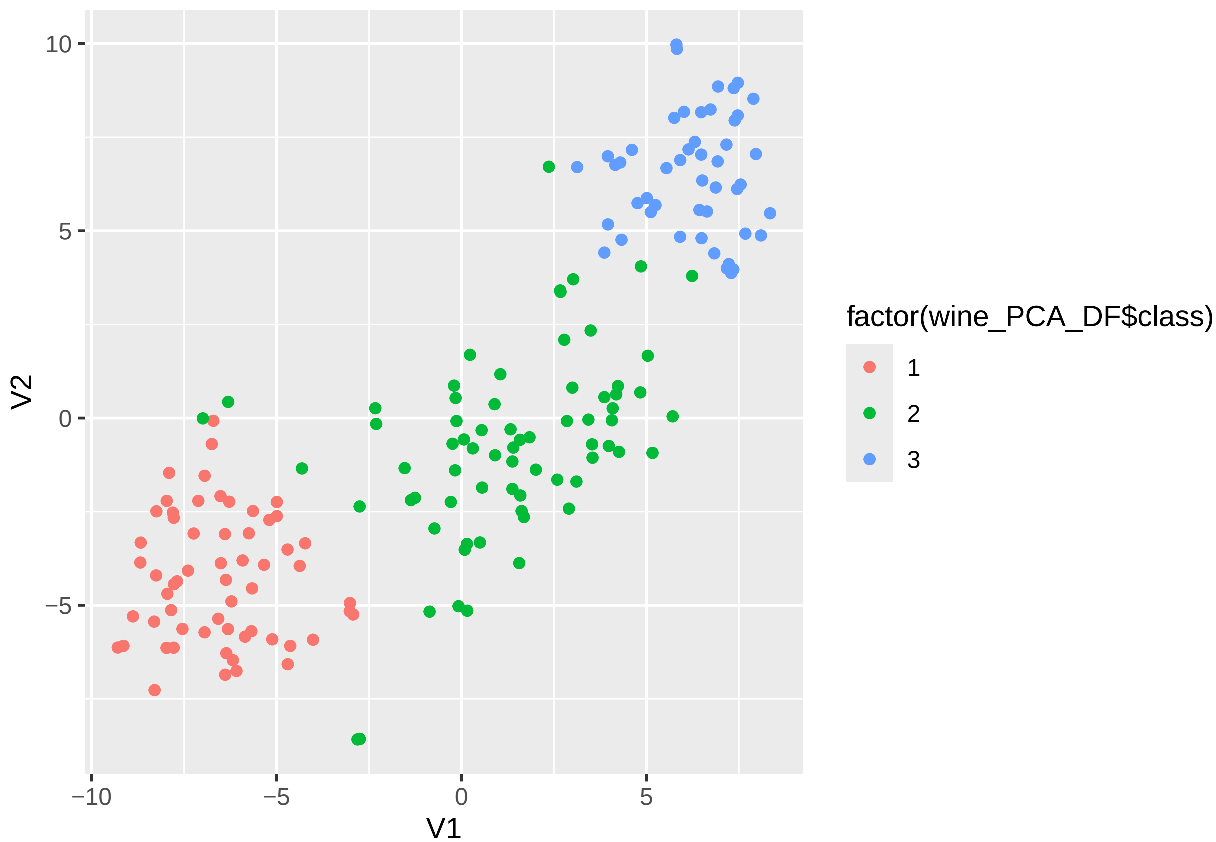
```r
set.seed(123)

tsne_wine <- wine_PCA_no_duplicates %>% select(-class) %>%
                  Rtsne(.,
                  dims = 2,
                  perplexity = 30,
                  verbose = FALSE,
                  check_duplicates = FALSE
                )
```

b) Plot the results in 2D *Hint:* Convert your T-SNE results to a tibble and add back the class variable from your scaled data set using a `mutate()` statement. Then, you can use `color = factor(class)` in your `ggplot` statement.

```r
results <- as_tibble(tsne_wine$Y)
```

```
## Warning: The `x` argument of `as_tibble.matrix()` must have unique column names if
## `.name_repair` is omitted as of tibble 2.0.0.
## i Using compatibility `.name_repair`.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```r
ggplot(results, aes(V1, V2)) + geom_point(aes(color = factor(wine_PCA_DF$class)))
```



c) Why didn't we stop at PCA? We didn't stop at PCA because while PCA is great at reducing redundancy and dimensionality in the data, T-SNE is better are visualizing the complex spacial relationship of this data by predicting the probability of two points being neighbors. This helps visualize the similarities and differences of the wine classes in the original data.

d) What other types of data does this workflow make sense for? Genomics and gene expression data would make sense because of the complex biological relationships/clusters that exist. Another type of data would be neural activity data because it has high dimensionality and noisiness but could be reduced to determine clustering.