

Worksheet 11

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```
library(readxl)
wine <- read_excel("~/Desktop/STAT 301/Week 11/wine.xlsx")
wine
```

```
## # A tibble: 178 x 14
##   Type Alcohol Malic   Ash Alcalinity Magnesium Phenols Flavanoids
##   <dbl>   <dbl> <dbl> <dbl>      <dbl>      <dbl>   <dbl>      <dbl>
## 1     1    14.2  1.71  2.43      15.6        127     2.8        3.06
## 2     1    13.2  1.78  2.14      11.2        100     2.65        2.76
## 3     1    13.2  2.36  2.67      18.6        101     2.8        3.24
## 4     1    14.4  1.95  2.5       16.8        113     3.85        3.49
## 5     1    13.2  2.59  2.87       21         118     2.8        2.69
## 6     1    14.2  1.76  2.45      15.2        112     3.27        3.39
## 7     1    14.4  1.87  2.45      14.6         96     2.5        2.52
## 8     1    14.1  2.15  2.61      17.6        121     2.6        2.51
## 9     1    14.8  1.64  2.17       14         97     2.8        2.98
## 10    1    13.9  1.35  2.27       16         98     2.98        3.15
## # i 168 more rows
## # i 6 more variables: Nonflavanoids <dbl>, Proanthocyanins <dbl>, Color <dbl>,
## #   Hue <dbl>, Dilution <dbl>, Proline <dbl>
```

```
library(MASS)
```

```
wine$Type <- as.factor(wine$Type)
model3 <- lda(Type~.-Type, data = wine, prior = c(1/3, 1/3, 1/3))
model3$svd # singular value decomposition
```

```
## [1] 29.95777 18.22846
```

```
newtype <- data.frame(Alcohol=11, Malic=3, Ash=2.3, Alcalinity=21.5, Magnesium=99, Phenols=2.8, Flavanoids=3.15)
predict(object = model3, newdata = newtype)
```

```
## $class
## [1] 2
## Levels: 1 2 3
##
## $posterior
##           1           2           3
## 1 1.174894e-07 0.9999999 8.391195e-11
```

```
##  
## $x  
##      LD1      LD2  
## 1 -1.016777 -3.479244
```

```
library(ggplot2)  
result3 <- predict(model3)  
winedf <- data.frame(g3 = wine$Type, transcore3 = result3$x)  
ggplot(data = winedf, aes(x = transcore3.LD1, y = transcore3.LD2)) + geom_point(aes(color = g3))
```

