# HW 3

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**Problem 1**

**(a)**

```r
data1 <- read.csv(file="wastewater.csv", header=TRUE)
AF <- data1$AF
FS <- data1$FS
FCC <- data1$FCC
treatment <- c(AF, FS, FCC)
method <- c(rep("AF",10), rep("FS",10), rep("FCC",10))
model <- aov(treatment ~ method, data=data1)
summary(model)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## method       2 1251.5   625.8   60.63 1.03e-10 ***
## Residuals   27  278.7    10.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Since p-value $= 1.03 \times 10^{-10} < 0.05$, we could conclude that there is significant difference among three treatment methods.

**(b)**

```r
boxplot(treatment ~ method, data=data1)
```
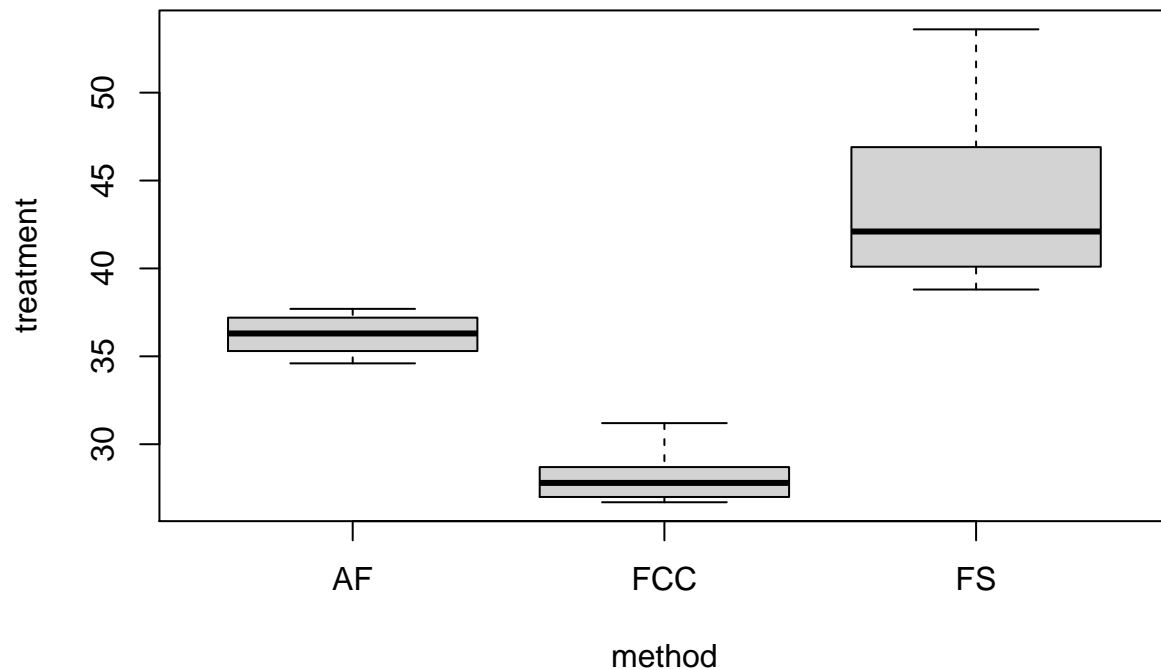
Since the overall value of foam separation is larger than other groups, its removal ability should be the best.

**Problem 2**

```r
data2 <- read.csv(file="Fern.csv", header=TRUE)
growth <- data2$Response_area
block <- data2$Block_age
treatment <- data2$wave_light
model <- aov(growth ~ block+treatment, data=data2)
summary(model)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## block         1  76793   76793  22.697 0.0176 *
## treatment     3  21954    7318   2.163 0.2713
## Residuals     3  10150    3383
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**(a)**
Age is the blocking variable.
Since p-value = 0.0176 < 0.05, we could conclude that the blocking effect (age) exists at 5% level of significance.

```
boxplot(growth ~ block, data=data2, main="Boxplot of growths and blocks")
```
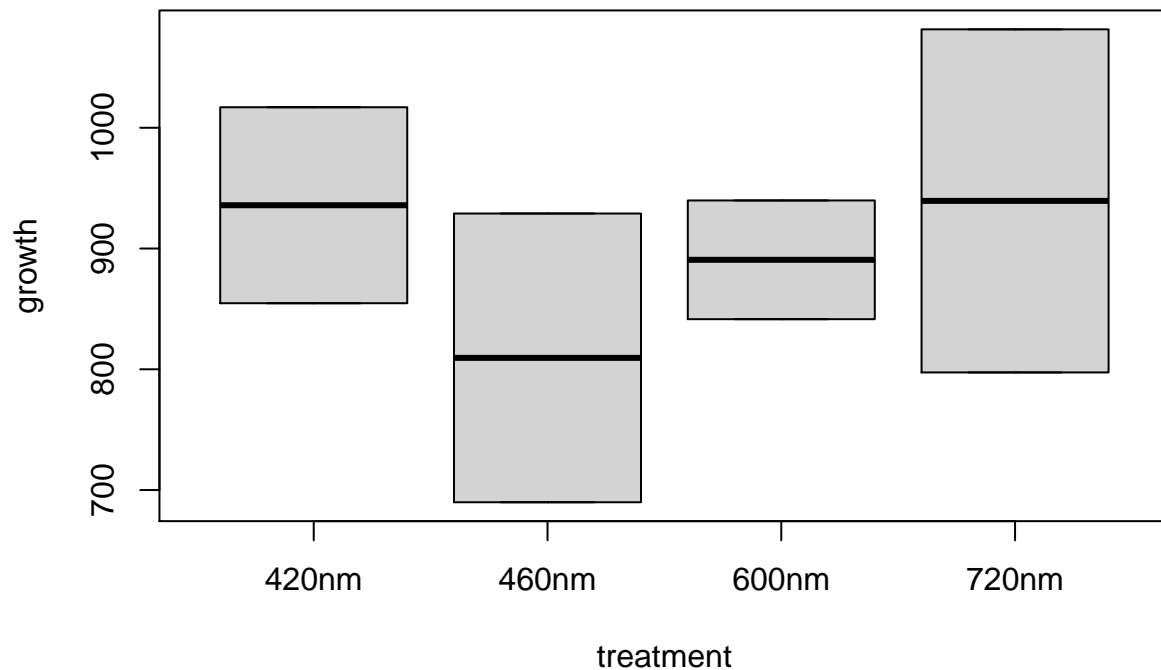
**Boxplot of growths and blocks**
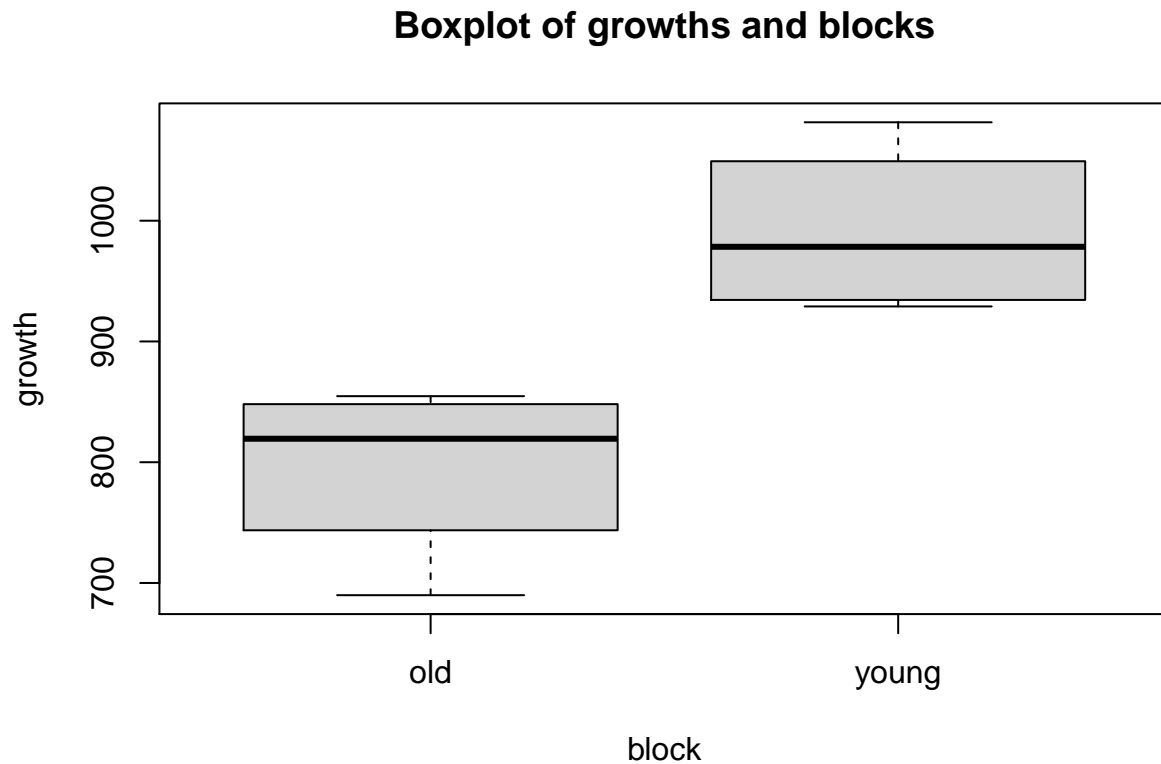


We could get the same conclusion from the boxplot.

**(b)**
Since p-value $= 0.2713 > 0.05$, we could conclude that the treatment effect (wavelength of light) does not exist at 5% level of significance.

```
boxplot(growth ~ treatment, data=data2, main="Boxplot of growths and treatments")
```

# Boxplot of growths and treatments



We could get the same conclusion from the boxplot.

**Problem 3**

**(a)**

```r
data3 <- read.csv(file="Cotinine.csv", header=TRUE)
cotinine <- data3$cotinine
gender <- as.factor(data3$Gender)
racial <- as.factor(data3$Race)

interaction.plot(x.factor = racial,      # variable to plot on x-axis
                 trace.factor = gender, # variable to specify "traces"; here, lines
                 response = cotinine,   # variable to plot on y-axis
                 fun = mean,            # summary statistic to be plotted for response variable
                 type = "b",            # type of plot, here "l" for lines
                 xlab = "Racial",
                 ylab = "Cotinine")
```
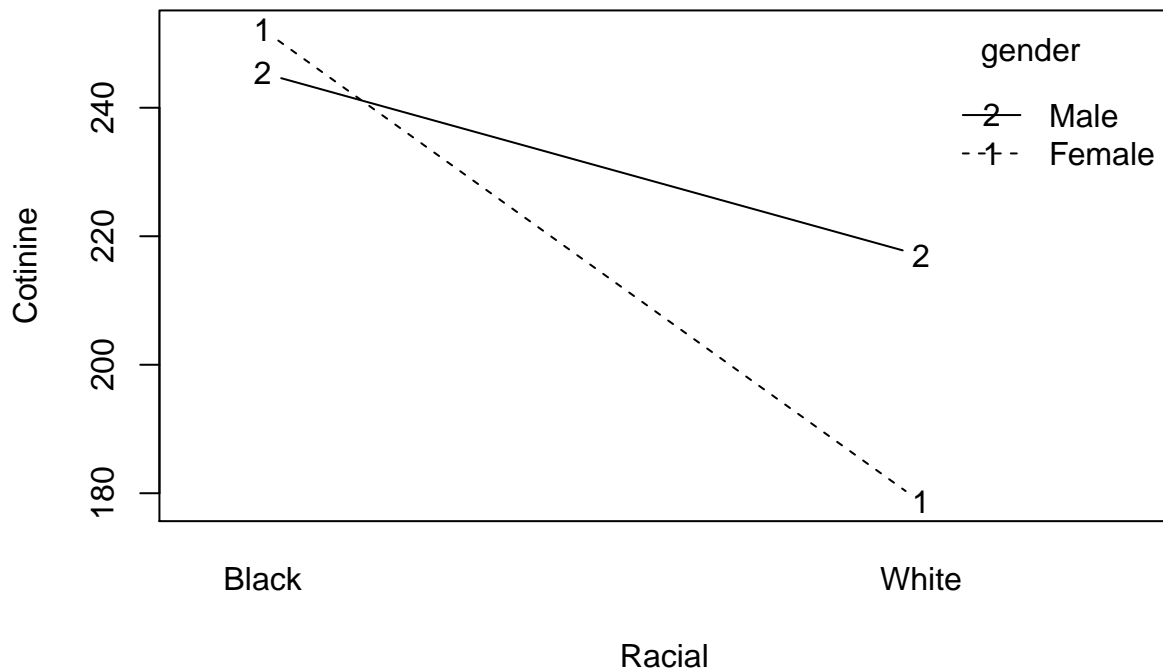
Since the two lines aren't parallel, we could infer that there exists interaction effect.

**(b)**

```r
data3 <- data.frame(cotinine, gender, racial)
model <- aov(cotinine ~ gender+racial+gender*racial, data=data3)
summary(model)
```

```
##               Df Sum Sq Mean Sq F value Pr(>F)
## gender         1   1248    1248   0.204  0.657
## racial         1  13005   13005   2.129  0.164
## gender:racial  1   2554    2554   0.418  0.527
## Residuals     16  97731    6108
```

Since p-value $= 0.527 > 0.05$, we could conclude that the interaction effect does not exist at 5% level of significance.

**(c)**

```r
model <- aov(cotinine ~ gender+racial, data=data3)
summary(model)
```

```
##               Df Sum Sq Mean Sq F value Pr(>F)
```

```
## gender      1    1248    1248   0.212  0.651
## racial      1   13005   13005   2.205  0.156
## Residuals  17  100285    5899
```

For gender factor, since p-value $= 0.651 > 0.05$, we could conclude that the gender factor has no effect on the cotinine level.
For racial factor, since p-value $= 0.156 > 0.05$, we could conclude that the racial factor has no effect on the cotinine level as well.

```
model <- aov(cotinine ~ gender, data=data3[which(racial=="White"),])
summary(model)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## gender       1   3686    3686   0.509  0.496
## Residuals    8  57955    7244
```

Since p-value $= 0.496 > 0.05$, we could conclude that the white racial has no effect on the cotinine level.

```
model <- aov(cotinine ~ gender, data=data3[which(racial=="Black"),])
summary(model)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## gender       1    116     116   0.023  0.883
## Residuals    8  39776    4972
```

Since p-value $= 0.883 > 0.05$, we could conclude that the black racial has no effect on the cotinine level.