Ch-03 R Codes

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Textbook: Montgomery, D. C. (2012). *Design and analysis of experiments*, 8th Edition. John Wiley & Sons.

Online handouts: https://github.com/PingYangChen/ANOVA_Course_R_Code

Chapter 3

One-way ANOVA

Read the csv file `3_PlasmaEtching.csv` in R. Make sure that in the `data.frame` the variable `Power` is a factor. If not sure, apply `as.factor()` function to set the property of the variable `Power` after reading the dataset.

```
df1 <- read.csv(file.path("data", "3_PlasmaEtching.csv"))
df1$Power <- as.factor(df1$Power)
```

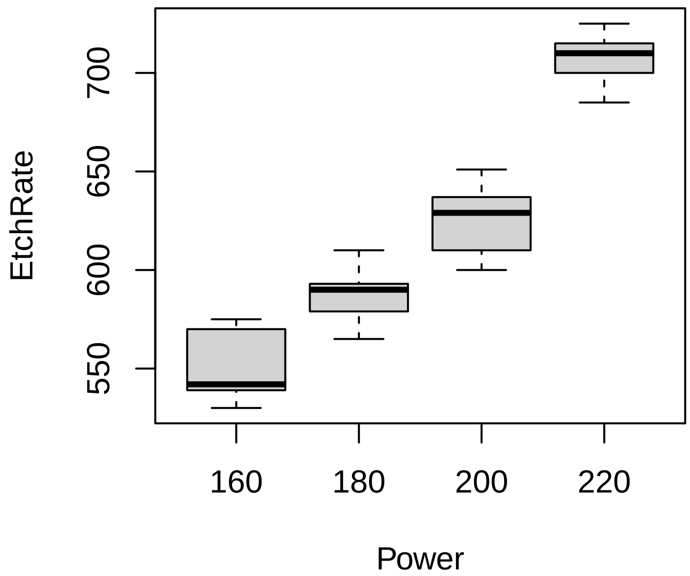
To compute descriptive statistics of the data in each subgroup of a dataset in R, we use `tapply()`.

```
tapply(df1$EtchRate, df1$Power, summary)
```

```
## $`160`
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   530.0   539.0   542.0   551.2   570.0   575.0
##
## $`180`
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   565.0   579.0   590.0   587.4   593.0   610.0
##
## $`200`
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   600.0   610.0   629.0   625.4   637.0   651.0
##
## $`220`
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##     685     700     710     707     715     725
```

Alternatively, boxplots provide a quick and direct means of observing the differences among the responses of the four treatments (groups or levels of a factor).

```
# Draw the grouped boxplot
boxplot(EtchRate ~ Power, data = df1)
```



The function `aov()` fits the ANOVA model. For one-way ANOVA, the command is as follows. Then, we call `summary()` to examine the ANOVA table.

```
fit <- aov(EtchRate ~ Power, data = df1)
summary(fit)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)    
## Power        3  66871   22290    66.8 2.88e-09 ***
## Residuals   16   5339     334                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model Adequacy Checking

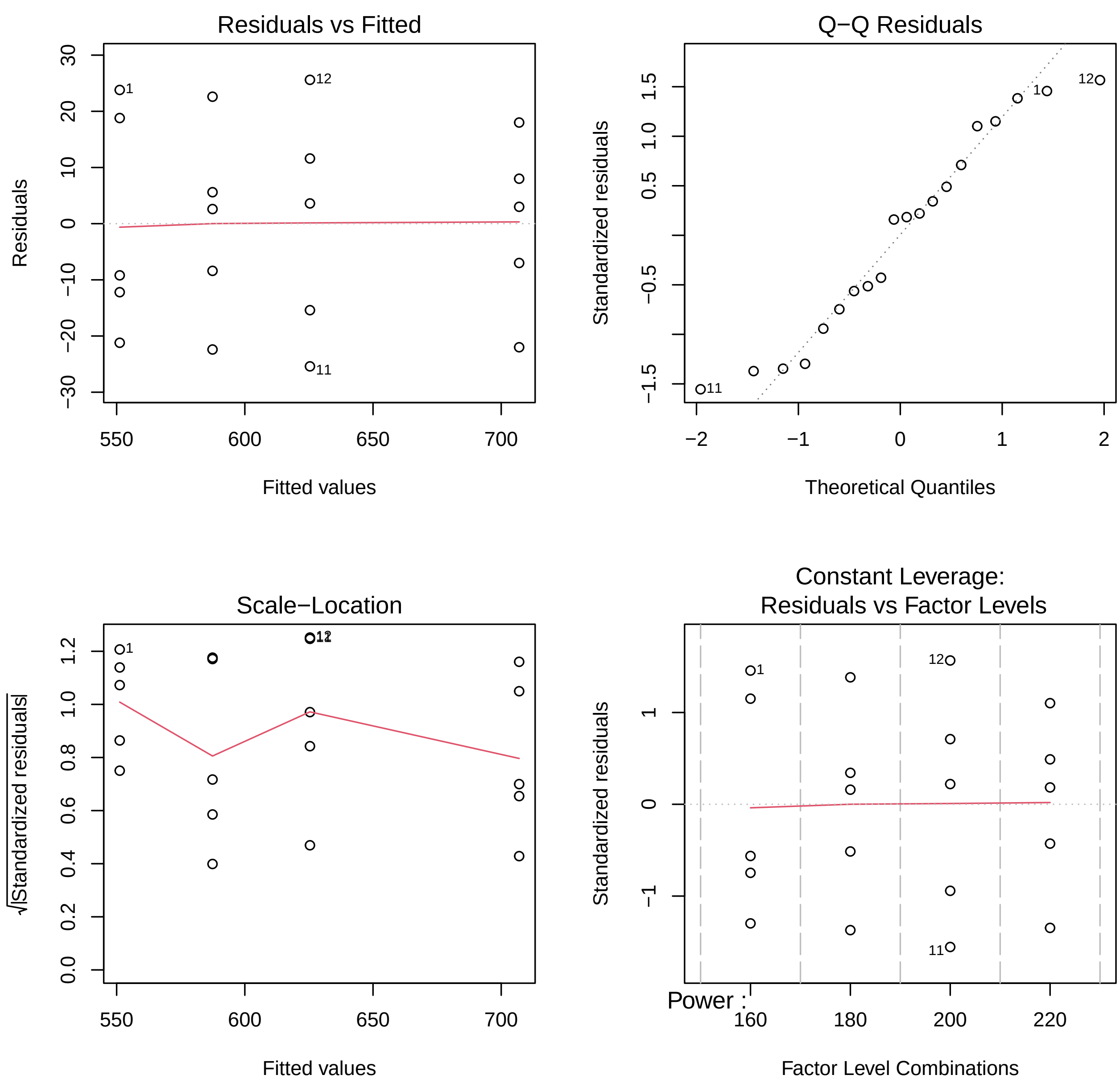
The adequacy of an ANOVA model can be studied from residual plots. The basic approach is to use the `plot()` function with the fitted ANOVA model object as its input argument. Since there are four residual plots, we can use `par(mfrow = c(2, 2))` before the `plot()` function to view all of them simultaneously.

The first (upper left) plot is the residual plot against the fitted values. This plot is used to check the consistency of the variance with changes in the fitted value. A lack of any visually obvious pattern in the dots on the plot is desired.

The second (upper right) plot is the residuals' Normal Quantile-Quantile (QQ) plot. Ideally, the dots form a straight line.

The remaining two plots at the bottom are standardized residuals against the fitted values and standardized residuals against the factor levels, respectively. They are also used to check the consistency of the variance.

```
par(mfrow = c(2, 2))
plot(fit)
```




```r
par(mfrow = c(1, 1))
```

Post-ANOVA Comparison of Means

The estimate of the overall mean μ and the Power's treatment effects τ_1 to τ_4 are

$$\hat{\mu} = \frac{1}{an}\sum_{i=1}^{a}\sum_{j=1}^{n} y_{ij} = \bar{y}_{..};$$

$$\hat{\tau}_1 = \frac{1}{n}\sum_{j=1}^{n} y_{1j} - \hat{\mu} = \bar{y}_{1.} - \bar{y}_{..}; \hat{\tau}_2 = \frac{1}{n}\sum_{j=1}^{n} y_{2j} - \hat{\mu} = \bar{y}_{2.} - \bar{y}_{..};$$

$$\hat{\tau}_3 = \frac{1}{n}\sum_{j=1}^{n} y_{3j} - \hat{\mu} = \bar{y}_{3.} - \bar{y}_{..}; \hat{\tau}_4 = \frac{1}{n}\sum_{j=1}^{n} y_{4j} - \hat{\mu} = \bar{y}_{4.} - \bar{y}_{..}.$$

The R codes are as follows.

```
mean(df1$EtchRate) # Overall
mean(df1$EtchRate[df1$Power == 160]) - mean(df1$EtchRate) # tau_1
mean(df1$EtchRate[df1$Power == 180]) - mean(df1$EtchRate) # tau_2
mean(df1$EtchRate[df1$Power == 200]) - mean(df1$EtchRate) # tau_3
mean(df1$EtchRate[df1$Power == 220]) - mean(df1$EtchRate) # tau_4
```

Following an ANOVA in which we have rejected the null hypothesis of equal treatment means, we wish to test all pairwise mean comparisons:

$$
\begin{aligned}
H_0 &: \ \mu_i = \mu_j \\
H_1 &: \ \mu_i \neq \mu_j
\end{aligned}
$$

for all $i \neq j$. Here, we introduce three approaches.

Pairwise t-tests

The straightforward approach to test for all pairs of the hypotheses is to conduct the Pairwise t-tests simultaneously. The following codes give the results under Bonferroni adjustment on the p-value.

```
pairwise.t.test(df1$EtchRate, df1$Power, p.adjust = "bonferroni")
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  df1$EtchRate and df1$Power
##
##     160     180     200
## 180 0.038   -       -
## 200 5.1e-05 0.028   -
## 220 2.2e-09 1.0e-07 1.6e-05
##
## P value adjustment method: bonferroni
```

Tukey's Test

Tukey's procedure makes use of the distribution of the studentized range statistic

$$q = \frac{\bar{y}_{max} - \bar{y}_{min}}{\sqrt{MS_E/n}}$$

where $\bar{y}_{max}$ and $\bar{y}_{min}$ are the largest and smallest sample means respectively, out of a group of p sample means. For equal sample sizes, Tukey's test declares two means significantly different if the absolute value of their sample differences exceeds

$$T_\alpha = q_\alpha(a, f)\sqrt{\frac{MS_E}{n}}$$

where $q_\alpha(a, f)$ is the upper α percentage points of q and f is the number of degrees of freedom associated with the MS_E. For more insights on the distribution of q, please refer to the textbook. Tukey's method is performed by the function `TukeyHSD()`.

```
TukeyHSD(fit)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = EtchRate ~ Power, data = df1)
```

```
##
## $Power
##          diff        lwr       upr     p adj
## 180-160  36.2   3.145624  69.25438 0.0294279
## 200-160  74.2  41.145624 107.25438 0.0000455
## 220-160 155.8 122.745624 188.85438 0.0000000
## 200-180  38.0   4.945624  71.05438 0.0215995
## 220-180 119.6  86.545624 152.65438 0.0000001
## 220-200  81.6  48.545624 114.65438 0.0000146
```

Fisher's LSD Method

The R package **agricolae** provides the function `LSD.test()` to perform Fisher's LSD test. Adjustment for the P-value is necessary. Typically, we set `p.adj = "bonferroni"` for the Bonferroni method.

```r
if (!("agricolae" %in% rownames(installed.packages()))) {
  install.packages("agricolae")
}
library(agricolae)
out <- LSD.test(fit, "Power", p.adj = "bonferroni")
print(out)
```

```
## $statistics
##   MSerror Df   Mean       CV  t.value      MSD
##     333.7 16 617.75 2.957095 3.008334 34.75635
##
## $parameters
##         test  p.ajusted name.t ntr alpha
##   Fisher-LSD bonferroni  Power   4  0.05
##
## $means
##     EtchRate      std r       se      LCL      UCL Min Max Q25 Q50 Q75
## 160    551.2 20.01749 5 8.169455 533.8815 568.5185 530 575 539 542 570
## 180    587.4 16.74216 5 8.169455 570.0815 604.7185 565 610 579 590 593
## 200    625.4 20.52559 5 8.169455 608.0815 642.7185 600 651 610 629 637
## 220    707.0 15.24795 5 8.169455 689.6815 724.3185 685 725 700 710 715
##
## $comparison
## NULL
##
## $groups
##     EtchRate groups
## 220    707.0      a
## 200    625.4      b
## 180    587.4      c
## 160    551.2      d
##
## attr(,"class")
## [1] "group"
```

The most important parts of the outputs are shown below:

- `$means` displays the estimated mean of the etching rate at each level of power.
- `$groups` indicates the significance of the difference in the etching rate at each level of power. The column groups in `$groups` encodes the treatment levels with no significant difference in the etching rate by the same alphabet letter.