The Hypothesis

\( H_0 : \mu_1 = \mu_2 = \ldots = \mu_k = \mu \)

\( H_a : \text{Not } H_0 \)

1 The Model

Let \( \tau_j = \mu_j - \mu \)

\[ y_{ij} = \mu + \tau_j + \epsilon_{ij} \]

where, \( y_{ij} \) is the \( i \)-th observation in the \( j \)-th level of the treatment, \( \mu \) is the overall or grand mean, \( \tau_j \) represents the effect of the \( j \)-th level, and \( \epsilon_{ij} \) is the error associated with the \( i \)-th observation in the \( j \)-th level.

Hypothesis

We are interested in testing:

\[ H_0 : \tau_1 = \tau_2 = \ldots = \tau_j = \ldots = \tau_k = 0 \text{ versus } H_1 : \text{Not } H_0 \]

The alternative hypothesis here suggests that even if one of the mean levels of the population is not equivalent with the others, we are going to reject the null hypothesis.

The fundamental assumption here is that the treatment levels are fixed. Namely, those levels are predetermined by the experimenter prior to performance of the experiment. This is called a "fixed effect" model. Alternatively, we may assume that the levels of the treatment are samples drawn from a distribution, typically a Normal distribution. That is, we assume that for all \( j = 1, \ldots, k \), \( \tau_j \sim N(0, \sigma_j) \).
ANOVA TABLE

We don’t know what $\mu, \tau_j$ are, so we tend to estimate those by sampling from the population. The right substitutes for these parameters in the sample world are: $\bar{y}_i$ and $\bar{y}_{ij}$ respectively.

Consider the following steps:

$$y_{ij} = y_{ij} + \bar{y}_{..} - \bar{y}_{..} - \bar{y}_{..}$$

$$y_{ij} - \bar{y}_{..} = y_{ij} - \bar{y}_{..} + \bar{y}_{..} - \bar{y}_{..}$$

$$(y_{ij} - \bar{y}_{..})^2 = (y_{ij} - \bar{y}_{..})^2 + (\bar{y}_{..} - \bar{y}_{..})^2 + 2(y_{ij} - \bar{y}_{..})(\bar{y}_{..} - \bar{y}_{..})$$

$$\sum_{j=1}^{k} \sum_{i=1}^{n_j} (y_{ij} - \bar{y}_{..})^2 = \sum_{j=1}^{k} \sum_{i=1}^{n_j} (y_{ij} - \bar{y}_{..})^2 + \sum_{j=1}^{k} \sum_{i=1}^{n_j} (\bar{y}_{..} - \bar{y}_{..})^2 + \sum_{j=1}^{k} \sum_{i=1}^{n_j} 2(y_{ij} - \bar{y}_{..})(\bar{y}_{..} - \bar{y}_{..})$$

But

$$\sum_{j=1}^{k} \sum_{i=1}^{n_j} 2(y_{ij} - \bar{y}_{..})(\bar{y}_{..} - \bar{y}_{..}) = 2 \sum_{j=1}^{k} (\bar{y}_{..} - \bar{y}_{..}) \sum_{i=1}^{n_j} (y_{ij} - \bar{y}_{..}) = 0 \times \sum_{i=1}^{n_j} (y_{ij} - \bar{y}_{..}) = 0$$

Therefore:

$$\sum_{j=1}^{k} \sum_{i=1}^{n_j} (y_{ij} - \bar{y}_{..})^2 = \sum_{j=1}^{k} \sum_{i=1}^{n_j} (y_{ij} - \bar{y}_{..})^2 + \sum_{j=1}^{k} \sum_{i=1}^{n_j} (\bar{y}_{..} - \bar{y}_{..})^2$$

In other words:

Total Sum of Squares = Within-level Sum of Squares + Between-levels Sum of Squares

or:

$$SS_{total} = SS_{between} + SS_{within}$$
### ANOVA TABLE

<table>
<thead>
<tr>
<th>Source</th>
<th>Sum of Squares</th>
<th>Degrees of Freedom</th>
<th>Mean Squares</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between (Model)</td>
<td>$\sum_{j=1}^{k} \sum_{i=1}^{n_j} (\bar{y}<em>{ij} - \bar{y}</em>{.})^2$</td>
<td>$k - 1$</td>
<td>$SS_{between}/k - 1$</td>
</tr>
<tr>
<td>Within (Error)</td>
<td>$\sum_{j=1}^{k} \sum_{i=1}^{n_j} (y_{ij} - \bar{y}_{.j})^2$</td>
<td>$N - k$</td>
<td>$SS_{error}/N - k$</td>
</tr>
<tr>
<td>Total</td>
<td>$\sum_{j=1}^{k} \sum_{i=1}^{n_j} (y_{ij} - \bar{y}_{.})^2$</td>
<td>$N - 1$</td>
<td>$SS_{total}/N - 1$</td>
</tr>
</tbody>
</table>

Next, we calculate:

$$F = \frac{MS_{model}}{MS_{error}} \sim F(k - 1, N - k)$$

Subsequently, we look at the magnitude of the $F$-ratio. If it was larger than the theoretical cumulative $f$-value with the same degrees of freedoms, we will reject the null hypothesis.
Example 1: Cathode Problem

(Hicks and Turner, 1999) ”The Cathode warm-up time in seconds was determined for three different tube types using eight observations on each type of tube. The order of experimentation was completely randomized. The results were as tabulated.”

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>19</td>
<td>20</td>
<td>16</td>
</tr>
<tr>
<td>23</td>
<td>20</td>
<td>15</td>
</tr>
<tr>
<td>26</td>
<td>32</td>
<td>18</td>
</tr>
<tr>
<td>18</td>
<td>27</td>
<td>26</td>
</tr>
<tr>
<td>20</td>
<td>40</td>
<td>19</td>
</tr>
<tr>
<td>20</td>
<td>24</td>
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<td>18</td>
<td>22</td>
<td>19</td>
</tr>
<tr>
<td>35</td>
<td>18</td>
<td>18</td>
</tr>
</tbody>
</table>

Rows are warm-up times. Columns are tube-type.

The Cathode warm-up time in seconds was determined for three different tube types using eight observations on each type of tube. The order of experimentation was completely randomized. The results were as tabulated.

First the data:

A  B  C
19  20  16
23  20  15
26  32  18
18  27  26
20  40  19
20  24  17
18  22  19
35  18  18
We run: one-way ANOVA in R using the following simple codes. Notice that I have converted the cathode.code variable to a factor variable in order to distinguish three factors associated with three tube-types.

```r
> data.cathode<-c(19,23,26,18,20,18,35,20,20,20,32,27,40,24,22,18,16,15,18,26,19,17,19,18)
> code.cathode<-c(1,1,1,1,1,1,1,2,2,2,2,2,2,2,2,2,3,3,3,3,3,3,3,3)
> code.cathode<-as.factor(code.cathode)
> code.cathode
[1] 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3
Levels: 1 2 3
> anova(lm(data.cathode~code.cathode))
Analysis of Variance Table

Response: data.cathode

                  Df  Sum Sq Mean Sq  F value  Pr(>F)
code.cathode      2 190.08  95.04 2.86040 0.07968 .
Residuals        21 697.75  33.23
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Always plot the data! In the case of ANOVA it is extremely beneficial to start with side-by-side-box plots (figure 1, left):

```r
> boxplot(data.cathode~code.cathode)
```
Figure 1. Side-by-side boxplots (left) and stripchart (right) for the cathode data.

We can also use stripcharts to see the position of the means and errors (figure 1, right. See Dalgaeard, page 118):

```r
> xbar <- tapply(data.cathode, code.cathode, mean)
> s <- tapply(data.cathode, code.cathode, sd)
> n <- tapply(data.cathode, code.cathode, length)
> sem <- s/sqrt(n)
> stripchart(data.cathode ~ code.cathode, "jitter", jit=0.05, pch=16, vert=T)
> arrows(1:3, xbar + sem, 1:3, xbar - sem, angle=90, code=3, length=0.1)
> lines(1:3, xbar, pch=4, type="b", cex=2)
```
Example 2: Tensile Strength Problem

(Montgomery, 1997) The tensile strength of a new synthetic fiber that will be used to make cloth for men’s shirt is to be tested. In particular, the engineer is interested in the percent of cotton used in the blend of the materials for the fiber. "He suspects increasing cotton will increase the strength”. For various levels of cotton use, he measures the strength of "five" shirts. The results are included in the following table:

<table>
<thead>
<tr>
<th></th>
<th>15%</th>
<th>20%</th>
<th>25%</th>
<th>30%</th>
<th>35%</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>7</td>
<td>12</td>
<td>14</td>
<td>19</td>
<td>7</td>
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</tr>
<tr>
<td>4</td>
<td>11</td>
<td>18</td>
<td>19</td>
<td>19</td>
<td>15</td>
</tr>
<tr>
<td>5</td>
<td>9</td>
<td>18</td>
<td>19</td>
<td>23</td>
<td>11</td>
</tr>
</tbody>
</table>

Rows are observations. Columns are cotton percentages.

> fabric.data<-c(7,7,15,11,9,12,17,12,18,18,14,18,18,19,19,19,25,22,19,23,7,10,11,15,11)
> fabric.groups<-c(1,1,1,1,2,2,2,2,3,3,3,3,3,4,4,4,4,4,4,5,5,5,5,5)
> fabric.groups<-factor(fabric.groups)
> length(fabric.data)
[1] 25
> length(fabric.groups)
[1] 25

> fabric.groups
[1] 1 1 1 1 2 2 2 2 3 3 3 3 4 4 4 4 4 5 5 5 5
Levels: 1 2 3 4 5

> anova(lm(fabric.data~fabric.groups))
Analysis of Variance Table
Figure 2. Side-by-side boxplots in the tensile strength problem.

Response: fabric.data

```
Df  Sum Sq  Mean Sq F value Pr(>F)
fabric.groups   4   475.76   118.94  14.757 9.128e-06 ***
Residuals      20   161.20    8.06
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> boxplot(fabric.data~fabric.groups)
```
Pairwise Comparisons

1. Bonferonni Corrections

```r
> pairwise.t.test(fabric.data,fabric.groups,p.adj="bonferroni")
```

Pairwise comparisons using t tests with pooled SD

data:  fabric.data and fabric.groups

```
  1  2  3  4
 2 0.0541 - - -
 3 0.0031 1.0000 - -
 4 2.1e-05 0.0251 0.3754 -
 5 1.0000 0.1859 0.0116 7.0e-05
```

P value adjustment method: bonferroni

2. Holm Corrections - Less Conservative

```r
> pairwise.t.test(fabric.data,fabric.groups)
```

Pairwise comparisons using t tests with pooled SD

data:  fabric.data and fabric.groups

```
  1  2  3  4
 2 0.0270 - - -
 3 0.0025 0.4694 - -
 4 2.1e-05 0.0151 0.1126 -
 5 0.5838 0.0744 0.0081 6.3e-05
```

P value adjustment method: holm