

# 10 - Multivariate Analysis of Variance

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## Comparing Several Mult Pop'n Means (Multivariate ANOVA)

Random samples, collected from each of  $g$  populations,

Population 1:	$\mathbf{X}_{11}, \mathbf{X}_{12}, \dots, \mathbf{X}_{1n_1}$
Population 2:	$\mathbf{X}_{21}, \mathbf{X}_{22}, \dots, \mathbf{X}_{2n_2}$
$\vdots$	$\vdots$
Population $g$ :	$\mathbf{X}_{g1}, \mathbf{X}_{g2}, \dots, \mathbf{X}_{gn_g}$

- MANOVA is used first to investigate whether the population mean vectors are the same and, if not, which mean components differ significantly.

## Review of Univariate ANOVA

- $X_{\ell 1}, X_{\ell 2}, \dots, X_{\ell n_\ell}$  is a random sample from an  $N(\mu_\ell, \sigma^2)$  population,  $\ell = 1, 2, \dots, g$
- random samples are independent
- $H_0 : \mu_1 = \mu_2 = \dots = \mu_g$
- $\mu_\ell = \mu + (\mu_\ell - \mu) = \mu + \tau_\ell$ , where  $\tau_\ell = \mu_\ell - \mu$ .
- The null hypothesis becomes  $H_0 : \tau_1 = \tau_2 = \dots = \tau_g = 0$
- The response  $X_{\ell j} \sim N(\mu + \tau_\ell, \sigma^2)$ , can be written as

$$X_{\ell j} = \mu + \tau_\ell + e_{\ell j}$$

where the  $e_{\ell j}$  are independent  $N(0, \sigma^2)$  random variables.

- To define uniquely the model parameters and their least squares estimates, we impose the constraint

$$\sum_{\ell=1}^g n_\ell \tau_\ell = 0.$$

The analysis of variance is based upon an analogous decomposition of the observations

$$\begin{aligned}x_{\ell j} &= \bar{x} + (\bar{x}_{\ell} - \bar{x}) + (x_{\ell j} - \bar{x}_{\ell}) \\ &= \bar{x} + \hat{\tau}_{\ell} + \hat{e}_{\ell j}\end{aligned}$$

(obs) = (overall sample mean) +  
(estimated treatment effect) + (residual)

Note that, for all  $\ell = 1, 2, \dots, g$ ,

$$\sum_{\ell=1}^{n_{\ell}} (x_{\ell j} - \bar{x})^2 = n_{\ell} (\bar{x}_{\ell} - \bar{x})^2 + \sum_{j=1}^{n_{\ell}} (x_{\ell j} - \bar{x}_{\ell})^2,$$

since  $\sum_{j=1}^{n_{\ell}} (x_{\ell j} - \bar{x}_{\ell}) = 0$ .

Summing both sides over  $\ell$  we get

$$\sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (x_{\ell j} - \bar{x})^2 = \sum_{\ell=1}^g n_{\ell} (\bar{x}_{\ell} - \bar{x})^2 + \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (x_{\ell j} - \bar{x}_{\ell})^2$$

$$\left( \begin{array}{c} SS_{cor} \\ \text{total} \\ (\text{corrected}) \text{ SS} \end{array} \right) = \left( \begin{array}{c} SS_{tr} \\ \text{between} \\ (\text{samples}) \text{ SS} \end{array} \right) + \left( \begin{array}{c} SS_{res} \\ \text{within} \\ (\text{samples}) \text{ SS} \end{array} \right)$$

OR

$$\sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} x_{\ell j}^2 = (n_1 + n_2 + \cdots + n_g) \bar{x}^2 + \sum_{\ell=1}^g n_{\ell} (\bar{x}_{\ell} - \bar{x})^2$$

$$+ \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (x_{\ell j} - \bar{x}_{\ell})^2$$

$$(SS_{obs}) = (SS_{mean}) + (SS_{tr}) + (SS_{res})$$

## ANOVA Table

Source of variation	Sum of Squares( $SS$ )	Degrees of freedom( $d.f.$ )
Treatments	$SS_{tr} = \sum_{\ell=1}^g n_{\ell}(\bar{x}_{\ell} - \bar{x})^2$	$g - 1$
Residual (error)	$SS_{res} = \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (x_{\ell j} - \bar{x}_{\ell})^2$	$\sum_{\ell=1}^g n_{\ell} - g$
Total (corrected for the mean)	$SS_{cor} = \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (x_{\ell j} - \bar{x})^2$	$\sum_{\ell=1}^g n_{\ell} - 1$

## ANOVA Test for Comparing Univariate Means

- The usual  $F$ -test rejects  $H_0 : \tau_1 = \tau_2 = \cdots = \tau_g = 0$  at level  $\alpha$  if

$$F = \frac{SS_{tr}/(g-1)}{SS_{res}/(\sum_{\ell=1}^g n_{\ell} - g)} > F_{g-1, \sum n_{\ell} - g}(\alpha)$$

where  $F_{g-1, \sum n_{\ell} - g}(\alpha)$  is the upper  $(100\alpha)$ th percentile of the  $F$ -distribution with  $g-1$  and  $\sum n_{\ell} - g$  degrees of freedom.

- This is equivalent to rejecting  $H_0$  for large values of  $SS_{tr}/SS_{res}$  or for large values of  $1 + SS_{tr}/SS_{res}$ .
- The multivariate generalization rejects  $H_0$  for small values of the reciprocal

$$\frac{1}{1 + SS_{tr}/SS_{res}} = \frac{SS_{res}}{SS_{res} + SS_{tr}}$$

# Multivariate Analysis of Variance (MANOVA)

- MANOVA Model for Comparing  $g$  Population Mean Vectors

$$\mathbf{X}_{\ell j} = \mu + \tau_{\ell} + \mathbf{e}_{\ell j}, \quad j = 1, 2, \dots, n_{\ell} \text{ and } \ell = 1, 2, \dots, g$$

where the  $\mathbf{e}_{\ell j}$  are independent  $N_p(0, \Sigma)$  variables.

- The parameter vector  $\mu$  is an overall mean (level), and  $\tau_{\ell}$  represents the  $\ell$ th treatment effect with  $\sum_{\ell=1}^g n_{\ell} \tau_{\ell} = 0$ .



A vector of observations may be decomposed

$$\mathbf{x}_{\ell j} = \bar{\mathbf{x}} + (\bar{\mathbf{x}}_{\ell} - \bar{\mathbf{x}}) + (\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})$$

$$\text{(observation)} = \begin{pmatrix} \text{overall sample} \\ \text{mean } \hat{\mu} \end{pmatrix} + \begin{pmatrix} \text{estimated} \\ \text{treatment} \\ \text{effect } \hat{\tau}_{\ell} \end{pmatrix} + \begin{pmatrix} \text{residual} \\ \hat{\mathbf{e}}_{\ell j} \end{pmatrix}$$

Similarly, we have

$$\begin{aligned}
 \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (\mathbf{x}_{\ell j} - \bar{\mathbf{x}})(\mathbf{x}_{\ell j} - \bar{\mathbf{x}})' &= \sum_{\ell=1}^g n_{\ell} (\bar{\mathbf{x}}_{\ell} - \bar{\mathbf{x}})(\bar{\mathbf{x}}_{\ell} - \bar{\mathbf{x}})' + \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})(\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})' \\
 \begin{pmatrix} SS_{cor} \\ \text{total} \\ \text{(corrected) SS} \end{pmatrix} &= \begin{pmatrix} SS_{tr} \\ \text{between} \\ \text{(samples) SS} \end{pmatrix} + \begin{pmatrix} SS_{res} \\ \text{within} \\ \text{(samples) SS} \end{pmatrix} \\
 &= \mathbf{B} + \mathbf{W}
 \end{aligned}$$

The within sum of squares and cross products matrix can be expressed as

$$\begin{aligned}\mathbf{W} &= \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})(\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})' \\ &= (n_1 - 1)\mathbf{S}_1 + (n_2 - 1)\mathbf{S}_2 + \cdots + (n_g - 1)\mathbf{S}_g\end{aligned}$$

where  $\mathbf{S}_{\ell}$  is the sample covariance matrix for the  $\ell$ th sample.

## MANOVA Table

The hypothesis of no treatment effects

$$H_0 : \tau_1 = \tau_2 = \cdots = \tau_g = 0$$

is tested by considering the relative sizes of the treatment and residual sums of squares and cross products.

Matrix of sum of squares and cross products( <i>SSP</i> )		Degrees of freedom( <i>d.f.</i> )
Treatments:	$\mathbf{B} = \sum_{\ell=1}^g n_{\ell}(\bar{\mathbf{x}}_{\ell} - \bar{\mathbf{x}})(\bar{\mathbf{x}}_{\ell} - \bar{\mathbf{x}})'$	$g - 1$
Residual:	$\mathbf{W} = \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})(\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})'$	$\sum_{\ell=1}^g n_{\ell} - g$
Total:	$\mathbf{B} + \mathbf{W} = \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (\mathbf{x}_{\ell j} - \bar{\mathbf{x}})(\mathbf{x}_{\ell j} - \bar{\mathbf{x}})'$	$\sum_{\ell=1}^g n_{\ell} - 1$

## Wilks' Lambda $\Lambda^*$

- One test of

$$H_0 : \tau_1 = \tau_2 = \cdots = \tau_g = 0$$

involves generalized variances. We reject  $H_0$  if the ratio of generalized variances

$$\Lambda^* = \frac{|\mathbf{W}|}{|\mathbf{B} + \mathbf{W}|} = \frac{\left| \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})(\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})' \right|}{\left| \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (\mathbf{x}_{\ell j} - \bar{\mathbf{x}})(\mathbf{x}_{\ell j} - \bar{\mathbf{x}})' \right|} \text{ is too small.}$$

- The quantity  $\Lambda^*$  originally by Wilks corresponds to the equivalent form of the F-test of  $H_0$ : no treatment effects in the univariate case.

## Wilks' Lambda $\Lambda^*$ (cont)

- Wilks  $\Lambda^*$  can also be expressed as a function of the eigenvalues  $\hat{\lambda}_1, \hat{\lambda}_2, \dots, \hat{\lambda}_s$  of  $\mathbf{W}^{-1}\mathbf{B}$  as

$$\Lambda^* = \prod_{i=1}^s \left( \frac{1}{1 + \hat{\lambda}_i} \right), \text{ where } s = \min(p, g - 1) = \text{rank}(B)$$

## Distribution of Wilks' Lambda, $\Lambda^*$

No. of variables	No. of groups	Sampling distribution for multivariate normal data
$p = 1$	$g \geq 2$	$\left( \frac{\sum n_{\ell} - g}{g-1} \right) \left( \frac{1 - \Lambda^*}{\Lambda^*} \right) \sim F_{g-1, \sum n_{\ell} - g}$
$p = 2$	$g \geq 2$	$\left( \frac{\sum n_{\ell} - g - 1}{g-1} \right) \left( \frac{1 - \sqrt{\Lambda^*}}{\sqrt{\Lambda^*}} \right) \sim F_{2(g-1), 2(\sum n_{\ell} - g - 1)}$
$p \geq 1$	$g = 2$	$\left( \frac{\sum n_{\ell} - p - 1}{p} \right) \left( \frac{1 - \Lambda^*}{\Lambda^*} \right) \sim F_{p, \sum n_{\ell} - g - 1}$
$p \geq 1$	$g = 3$	$\left( \frac{\sum n_{\ell} - p - 2}{p} \right) \left( \frac{1 - \sqrt{\Lambda^*}}{\sqrt{\Lambda^*}} \right) \sim F_{2p, 2(\sum n_{\ell} - p - 2)}$

## Distribution of Wilks' Lambda, $\Lambda^*$ (cont)

For other cases and large sample sizes,  $\sum_{\ell} n_{\ell} = n$  large, we reject  $H_0$  at significance level  $\alpha$  if

$$-\left(-n-1-\frac{(p+g)}{2}\right) \ln \Lambda^* > \chi^2_{p(g-1)}(\alpha) \text{ or}$$
$$\Lambda^* < \exp \left[ -\left(-n-1-\frac{(p+g)}{2}\right)^{-1} \chi^2_{p(g-1)}(\alpha) \right]$$



## Rootstock Data

The data contains four dependent variables as follows:

- six different rootstocks (Tree Number)
- trunk girth at four years ( $\text{mm} \times 100$ )
- extension growth at four years (m)
- trunk girth at 15 years ( $\text{mm} \times 100$ )
- weight of tree above ground at 15 years ( $\text{lb} \times 1000$ )

```
library(ACSWR) # data is in package ACSWR  
data("rootstock")  
colnames(rootstock) <- c("Tree.Num", "Girth.4y",  
  "Growth.4y", "Girth.15y", "WgtAbvGrnd.15y")
```

```
head(rootstock)
```

#	Tree.Num	Girth.4y	Growth.4y	Girth.15y	WgtAbvGrnd.15y
# 1	1	1.1	2.6	3.6	0.76
# 2	1	1.2	2.9	3.8	0.82
# 3	1	1.1	2.9	3.9	0.93
# 4	1	1.2	3.8	3.9	1.01
# 5	1	1.1	3.0	3.6	0.77
# 6	1	1.1	2.3	3.5	0.73

## Setting up the data

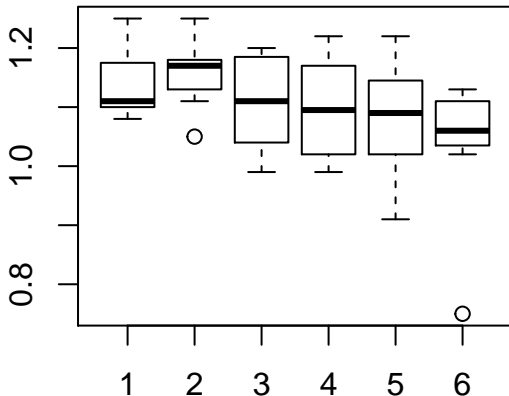
The `manova()` function in R accepts formula interface  $y \sim x$ , where  $y$  is the matrix of dependent variables (measurement value) and  $x$  as the independent factor variable (population tree number).

```
dep.variable <- as.matrix(rootstock[, 2:5]) # dependent variables  
tree.number <- as.factor(rootstock[, 1]) # independent variable
```

## Side-by-Side Boxplots for Girth at 4 yrs

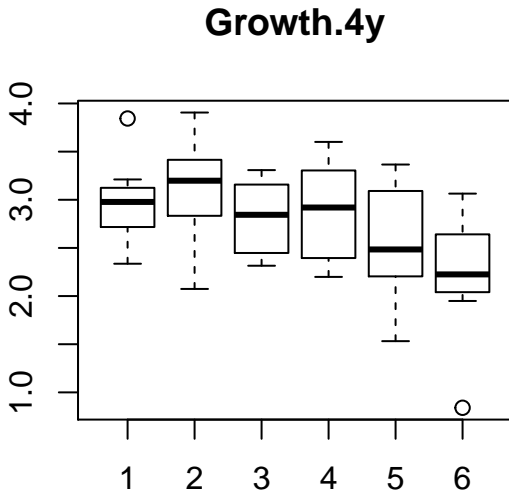
```
boxplot(Girth.4y ~ Tree.Num, data = rootstock,  
        main = "Girth.4y", xlab = "Tree Number")
```

### Girth.4y



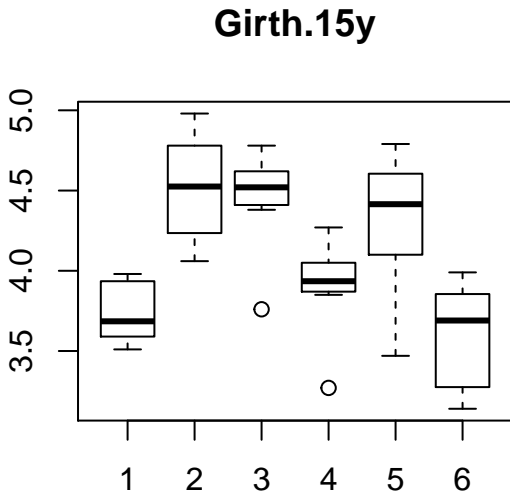
## Side-by-Side Boxplots for Growth at 4 yrs

```
boxplot(Growth.4y ~ Tree.Num, data = rootstock,  
        main = "Growth.4y", xlab = "Tree Number")
```



## Side-by-Side Boxplots for Girth at 15 yrs

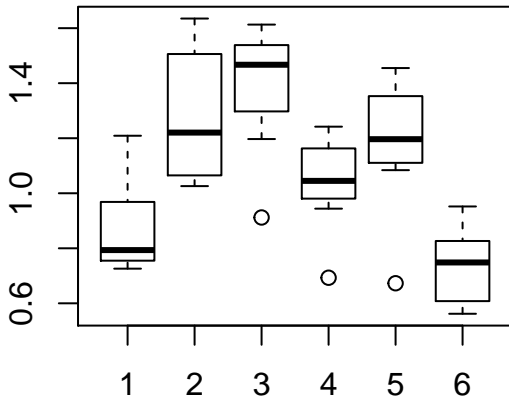
```
boxplot(Girth.15y ~ Tree.Num, data = rootstock,  
        main = "Girth.15y", xlab = "Tree Number")
```



## Side-by-Side Boxplots for Weight Above Ground at 15 yrs

```
boxplot(WgtAbvGrnd.15y ~ Tree.Num, data = rootstock,  
        main = "WgtAbvGrnd.15y", xlab = "Tree Number")
```

### WgtAbvGrnd.15y



## Summary Statistics

```
library(mosaic) # need mosaic package  
mean(Girth.4y ~ Tree.Num, data = rootstock)
```

```
#   1   2   3   4   5   6  
# 1.1 1.2 1.1 1.1 1.1 1.0
```

```
mean(Growth.4y ~ Tree.Num, data = rootstock)
```

```
#   1   2   3   4   5   6  
# 3.0 3.1 2.8 2.9 2.6 2.2
```



## Summary Statistics

```
mean(Girth.15y ~ Tree.Num, data = rootstock)
```

```
#    1    2    3    4    5    6  
# 3.7 4.5 4.5 3.9 4.3 3.6
```

```
mean(WgtAbvGrnd.15y ~ Tree.Num, data = rootstock)
```

```
#    1    2    3    4    5    6  
# 0.87 1.28 1.39 1.04 1.18 0.74
```

## MANOVA Test in R

$y$  is the matrix of dependent variables (measurement value);  $x$  as the independent factor variable (population tree number).

```
rootstock.model <- manova( dep.variable ~ tree.number )  
summary(rootstock.model, test = "W") # argument test = W
```

```
#           Df Wilks approx F num Df den Df  Pr(>F)  
# tree.number  5 0.154      4.94    20   130 7.7e-09 ***  
# Residuals   42  
# ---  
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

The MANOVA procedure gives a Wilks' test statistic of 0.154 and a p-value below 0.05, thus  $H_0$  is rejected and it is concluded there are significant differences in the means measurements of the six different rootstocks.

## Equivalent Test Statistics

In the context of random samples from several populations, the multivariate tests are based on the matrices

$$\mathbf{B} = \sum_{\ell=1}^g n_{\ell}(\bar{\mathbf{x}}_{\ell} - \bar{\mathbf{x}})(\bar{\mathbf{x}}_{\ell} - \bar{\mathbf{x}})' \quad \text{and} \quad \mathbf{W} = \sum_{\ell=1}^g \sum_{j=1}^{n_{\ell}} (\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})(\mathbf{x}_{\ell j} - \bar{\mathbf{x}}_{\ell})'$$

We have used

$$\text{Wilks lambda statistic } \Lambda^* = \frac{|\mathbf{W}|}{|\mathbf{B} + \mathbf{W}|}$$

which is equivalent to the likelihood ratio test.

## Other Multivariate Statistics

Three other multivariate test statistics are regularly included in the output of statistical packages

$$\text{Lawley-Hotelling Trace} = \text{tr}[\mathbf{B}\mathbf{W}^{-1}]$$

$$\text{Pillai trace} = \text{tr}[\mathbf{B}(\mathbf{B} + \mathbf{W})^{-1}]$$

$$\text{Roy's largest root} = \text{maximum eigenvalue of } \mathbf{W}(\mathbf{B} + \mathbf{W})^{-1}$$

## Equivalent Test Statistics

- All four of these tests appear to be nearly equivalent for extremely large samples.
- For moderate sample sizes, all comparisons are based on what is necessarily a limited number of cases studied by simulation.
- From the simulations reported, the first three tests have similar power, while the last, Roy's test, behaves differently.
- Its power is best only when there is a single nonzero eigenvalue and, at the same time, the power is large.

- There is also some suggestion that Pillai's trace is slightly more robust against nonnormality.
- All four statistics apply in the two-way setting and in even more complicated MANOVA.
- When, and only, when the multivariate tests signals a difference, or departure from the null hypothesis, do we probe deeper.

## Pillai's Statistic

```
summary(rootstock.model)  # default output
```

```
#           Df Pillai approx F num Df den Df Pr(>F)
# tree.number  5      1.3      4.07    20    168  2e-07 ***
# Residuals    42
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

## Hotelling-Lawley's Statistic

```
summary(rootstock.model, test = "H")
```

```
#               Df Hotelling-Lawley approx F num Df den Df  L
# tree.number   5               2.92      5.48    20   150 2
# Residuals    42
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```



## Roy's Statistics

```
summary(rootstock.model, test = "R")
```

```
#           Df  Roy approx F num Df den Df Pr(>F)
# tree.number  5 1.88      15.8      5      42 1e-08 ***
# Residuals    42
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

## Individual ANOVA's on the four tree measurements I

```
summary(aov(dep.variable ~ tree.number))
```

```
# Response Girth.4y :
```

```
#           Df Sum Sq Mean Sq F value Pr(>F)
# tree.number  5  0.074  0.01471    1.93   0.11
# Residuals  42  0.320  0.00762
```

```
#
```

```
# Response Growth.4y :
```

```
#           Df Sum Sq Mean Sq F value Pr(>F)
# tree.number  5     4.2    0.840    2.91 0.024 *
# Residuals  42    12.1    0.289
```

```
# ---
```

```
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

```
#
```

```
# Response Girth.15y :
```

## Individual ANOVA's on the four tree measurements II

```
#               Df Sum Sq Mean Sq F value    Pr(>F)
# tree.number   5     6.11    1.223      12 3.1e-07 ***
# Residuals    42     4.29    0.102
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
#
# Response WgtAbvGrnd.15y :
#               Df Sum Sq Mean Sq F value    Pr(>F)
# tree.number   5     2.49    0.499     12.2 2.6e-07 ***
# Residuals    42     1.72    0.041
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

Accounting for multiple comparisons with Bonferonni corrected alpha level ( $0.04/4 = 0.0125$ ), there are significant differences only in the average of Girth after 15 yrs and Weight Above Ground after 15 yrs amongst the six groups.

## Post-Hoc Comparisons on Girth after 15 yrs I

```
Girth.15yr.fit <- aov(dep.variable[,3] ~ tree.number)
TukeyHSD(Girth.15yr.fit)
```

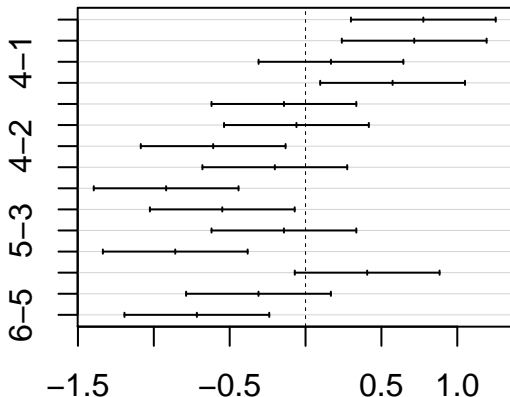
```
#   Tukey multiple comparisons of means
#     95% family-wise confidence level
#
# Fit: aov(formula = dep.variable[, 3] ~ tree.number)
#
# $tree.number
#      diff      lwr      upr p adj
# 2-1  0.78  0.299  1.253  0.00
# 3-1  0.72  0.239  1.193  0.00
# 4-1  0.17 -0.310  0.645  0.90
# 5-1  0.57  0.097  1.051  0.01
# 6-1 -0.14 -0.620  0.335  0.95
```

## Post-Hoc Comparisons on Girth after 15 yrs II

#	3-2	-0.06	-0.537	0.417	1.00
#	4-2	-0.61	-1.086	-0.132	0.01
#	5-2	-0.20	-0.680	0.275	0.80
#	6-2	-0.92	-1.396	-0.442	0.00
#	4-3	-0.55	-1.026	-0.072	0.02
#	5-3	-0.14	-0.620	0.335	0.95
#	6-3	-0.86	-1.336	-0.382	0.00
#	5-4	0.41	-0.071	0.883	0.14
#	6-4	-0.31	-0.787	0.167	0.39
#	6-5	-0.72	-1.193	-0.239	0.00

```
plot(TukeyHSD(Girth.15yr.fit))
```

## 95% family-wise confidence level



Differences in mean levels of tree.number

## Post-Hoc on Weight Above Grnd after 15 yrs I

```
WgtAbvGrnd.15y.fit <- aov(dep.variable[,4] ~ tree.number)
print(TukeyHSD(WgtAbvGrnd.15y.fit))
```

```
#   Tukey multiple comparisons of means
#     95% family-wise confidence level
#
# Fit: aov(formula = dep.variable[, 4] ~ tree.number)
#
# $tree.number
#           diff      lwr      upr p adj
# 2-1    0.409   0.1071   0.7117 0.00
# 3-1    0.520   0.2180   0.8225 0.00
# 4-1    0.168  -0.1344   0.4702 0.57
# 5-1    0.310   0.0076   0.6122 0.04
# 6-1   -0.136  -0.4384   0.1662 0.76
```

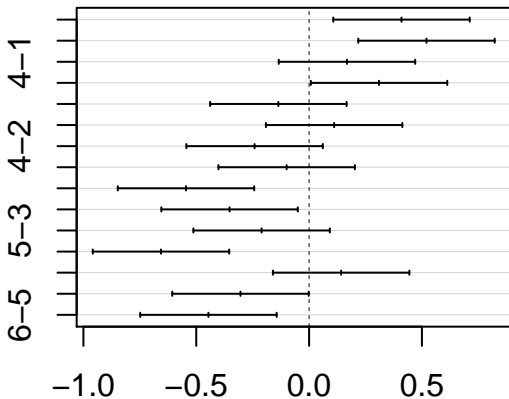
## Post-Hoc on Weight Above Grnd after 15 yrs II

# 3-2	0.111	-0.1914	0.4132	0.88
# 4-2	-0.241	-0.5438	0.0608	0.18
# 5-2	-0.099	-0.4018	0.2028	0.92
# 6-2	-0.545	-0.8478	-0.2432	0.00
# 4-3	-0.352	-0.6547	-0.0501	0.01
# 5-3	-0.210	-0.5127	0.0919	0.32
# 6-3	-0.656	-0.9587	-0.3541	0.00
# 5-4	0.142	-0.1603	0.4443	0.73
# 6-4	-0.304	-0.6063	-0.0017	0.05
# 6-5	-0.446	-0.7483	-0.1437	0.00



```
plot(TukeyHSD(WgtAbvGrnd.15y.fit))
```

## 95% family-wise confidence level



Differences in mean levels of tree.number