

Math 362: Mathematical Statistics II

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Last updated on April 12, 2021

2021 Spring

Chapter 13. Randomized Block Designs

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§ 13.1 Introduction

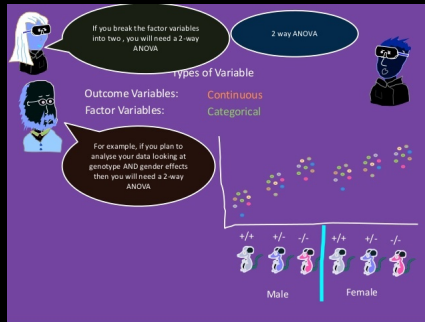
§ 13.2 The F Test for a Randomized Block Design

§ 13.A Appendix: Some Discussions and Extensions

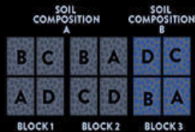
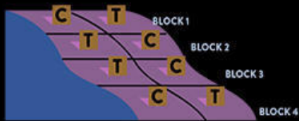
Rationale:

Reducing variability by blocking[†]

[†] *Blocking* is the arranging of experimental units in groups (blocks) that are similar to one another.



<https://www.slideshare.net/KevinHamill2/experimental-design-cartoon-part-5-sample-size>



Goal Reducing variability caused by

a *elevation.*

b *soil types.*

v.s.

c *complete randomized design*

} One-way ANOVA

Two-way ANOVA

<https://www.sare.org/Learning-Center/Bulletins/>

How-to-Conduct-Research-on-Your-Farm-or-Ranch/Text-Version/

Basics-of-Experimental-Design

Chapter 13. Randomized Block Designs

§ 13.1 Introduction

§ 13.2 The F Test for a Randomized Block Design

§ 13.A Appendix: Some Discussions and Extensions

Setup Y_{ij} indep. $\sim N(\mu_j + \beta_i, \sigma^2)$, i.e., $Y_{ij} = \mu_j + \beta_i + \epsilon_{ij}$, ϵ_{ij} i.i.d. $\sim N(0, \sigma^2)$

Table 13.2.1								
	Treatment Level					<i>Block Totals</i>	<i>Block Means</i>	<i>True Block Effects</i>
		<i>1</i>	<i>2</i>	...	<i>k</i>			
<i>Blocks</i>	1	Y_{11}	Y_{12}	...	Y_{1k}	$T_{1.}$	$\bar{Y}_{1.}$	β_1
	2	Y_{21}	Y_{22}		Y_{2k}	$T_{2.}$	$\bar{Y}_{2.}$	β_2
	\vdots	\vdots			\vdots	\vdots	\vdots	\vdots
	<i>b</i>	Y_{b1}	Y_{b2}		Y_{bk}	$T_{b.}$	$\bar{Y}_{b.}$	β_b
Sample totals		$T_{.1}$	$T_{.2}$		$T_{.k}$	$T_{..}$		
Sample means		$\bar{Y}_{.1}$	$\bar{Y}_{.2}$...	$\bar{Y}_{.k}$		$\bar{Y}_{..}$	
True means		μ_1	μ_2		μ_k			

Recall For one-way ANOVA,

$$Y_{ij} = \mu_j + \epsilon_{ij}$$

\Downarrow

$$\begin{aligned} SSTOT &= \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{..} \right)^2 \\ &= \sum_{i=1}^b \sum_{j=1}^k \left[\left(Y_{ij} - \bar{Y}_{.j} \right) + \left(\bar{Y}_{.j} - \bar{Y}_{..} \right) \right]^2 \\ &= \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{.j} \right)^2 + \text{zero cross term} + \sum_{i=1}^b \sum_{j=1}^k \left(\bar{Y}_{.j} - \bar{Y}_{..} \right)^2 \\ &= \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{.j} \right)^2 + b \sum_{j=1}^k \left(\bar{Y}_{.j} - \bar{Y}_{..} \right)^2 \\ &= SSE + SSTR \end{aligned}$$

$$SSTOT = SSE + SSTR$$

$$\Downarrow$$

$$\frac{SSTOT}{\sigma^2} = \frac{SSE}{\sigma^2} + \frac{SSTR}{\sigma^2}$$

$$\wr$$

$$\wr$$

$$\wr$$

$$\chi^2(bk - 1) \quad \chi^2(bk - k) \quad \perp \quad \chi^2(k - 1)$$

Under H_0

✓

Under H_0

$$H_0 : \mu_1 = \cdots = \mu_k$$

Symmetry If

$$Y_{ij} = \beta_i + \epsilon_{ij}$$

\Downarrow

$$\begin{aligned} SSTOT &= \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{..} \right)^2 \\ &= \sum_{i=1}^b \sum_{j=1}^k \left[\left(Y_{ij} - \bar{Y}_{i.} \right) + \left(\bar{Y}_{i.} - \bar{Y}_{..} \right) \right]^2 \\ &= \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{i.} \right)^2 + \text{zero cross term} + \sum_{i=1}^b \sum_{j=1}^k \left(\bar{Y}_{i.} - \bar{Y}_{..} \right)^2 \\ &= \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{i.} \right)^2 + k \sum_{i=1}^b \left(\bar{Y}_{i.} - \bar{Y}_{..} \right)^2 \\ &= SSE + SSB \end{aligned}$$

$$SSTOT = SSE + SSB$$

$$\Downarrow$$

$$\frac{SSTOT}{\sigma^2} = \frac{SSE}{\sigma^2} + \frac{SSB}{\sigma^2}$$

$$\wr$$

$$\wr$$

$$\wr$$

$$\chi^2(bk - 1) \quad \chi^2(bk - b) \quad \perp \quad \chi^2(b - 1)$$

Under \tilde{H}_0

✓

Under \tilde{H}_0

$$\tilde{H}_0 : \beta_1 = \cdots = \beta_b$$

Similarly If

$$Y_{ij} = \mu_j + \beta_i + \epsilon_{ij}$$

\Downarrow

$$\begin{aligned} SSTOT &= \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{..} \right)^2 \\ &= \sum_{i=1}^b \sum_{j=1}^k \left[\left(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..} \right) + \left(\bar{Y}_{i.} - \bar{Y}_{..} \right) + \left(\bar{Y}_{.j} - \bar{Y}_{..} \right) \right]^2 \\ &= \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..} \right)^2 + \sum_{i=1}^b \sum_{j=1}^k \left(\bar{Y}_{i.} - \bar{Y}_{..} \right)^2 \\ &\quad + \sum_{i=1}^b \sum_{j=1}^k \left(\bar{Y}_{.j} - \bar{Y}_{..} \right)^2 + \text{zero cross terms} \\ &= \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..} \right)^2 + k \sum_{i=1}^b \left(\bar{Y}_{i.} - \bar{Y}_{..} \right)^2 + b \sum_{j=1}^k \left(\bar{Y}_{.j} - \bar{Y}_{..} \right)^2 \\ &= SSE + SSB + SSTR \end{aligned}$$

$$SSTOT = SSE + SSB + SSTR$$

$$\Downarrow$$

$$\frac{SSTOT}{\sigma^2} = \frac{SSE}{\sigma^2} + \frac{SSB}{\sigma^2} + \frac{SSTR}{\sigma^2}$$

$$\{$$

$$\{$$

$$\{$$

$$\{$$

$$\chi^2(bk - 1) \quad \chi^2((k - 1)(b - 1)) \quad \perp \quad \chi^2(b - 1) \quad \perp \quad \chi^2(k - 1)$$

Under H_0 or \tilde{H}_0

✓

under \tilde{H}_0

under H_0

$$\tilde{H}_0 : \beta_1 = \cdots = \beta_b \quad \text{and} \quad H_0 : \mu_1 = \cdots = \mu_k$$

$$H_0 : \mu_1 \cdots = \mu_k$$

↓

Table 13.2.2					
Source	df	<i>SS</i>	<i>MS</i>	<i>F</i>	<i>P</i>
Treatments	$k - 1$	<i>SSTR</i>	$SSTR/(k - 1)$	$\frac{SSTR/(k - 1)}{SSE/(b - 1)(k - 1)}$	$P[F_{k-1, (b-1)(k-1)} \geq \text{obs. } F]$
Blocks	$b - 1$	<i>SSB</i>	$SSB/(b - 1)$	$\frac{SSB/(b - 1)}{SSE/(b - 1)(k - 1)}$	$P[F_{b-1, (b-1)(k-1)} \geq \text{obs. } F]$
Error	$(b - 1)(k - 1)$	<i>SSE</i>	$SSE/(b - 1)(k - 1)$		
Total	$n - 1$	<i>SSTOT</i>			

↑

$$\tilde{H}_0 : \beta_1 = \cdots = \beta_b$$

Computing formulas

$$C = \frac{T_{..}^2}{bk}$$

$$\textcolor{red}{SSTR} = b \sum_{j=1}^k \left(\bar{Y}_{.j} - \bar{Y}_{..} \right)^2 = b \sum_{j=1}^k \bar{Y}_{.j}^2 - bk \bar{Y}_{..}^2 = \frac{1}{b} \sum_{j=1}^k \bar{T}_{.j}^2 - C.$$

$$\textcolor{blue}{SSB} = k \sum_{i=1}^b \left(\bar{Y}_{i.} - \bar{Y}_{..} \right)^2 = k \sum_{i=1}^b \bar{Y}_{i.}^2 - bk \bar{Y}_{..}^2 = \frac{1}{k} \sum_{i=1}^b \bar{T}_{i.}^2 - C.$$

$$SSTOT = \sum_{i=1}^b \sum_{j=1}^k \left(Y_{ij} - \bar{Y}_{..} \right)^2 = \sum_{i=1}^b \sum_{j=1}^k Y_{ij}^2 - bk \bar{Y}_{..}^2 = \sum_{i=1}^b \sum_{j=1}^k Y_{ij}^2 - C.$$

$$SSE = SSTOT - \textcolor{blue}{SSB} - \textcolor{red}{SSTR}$$

E.g. Two methods to test wines: whether these two procedures produce the same measurements?

	DRS-FTIR	Standard
White wine 1	112.9	115.1
White wine 2	123.1	125.6
Red wine 1	135.2	132.4
Red wine 2	140.2	143.7

Test at $\alpha = 0.05$

$$H_0 : \mu_{DRS} = \mu_{STD} \quad \text{v.s.} \quad H_1 : \mu_{DRS} \neq \mu_{STD}$$

and

$$\tilde{H}_0 : \mu_{W1} = \mu_{W2} = \mu_{R1} = \mu_{R2} \quad \text{v.s.} \quad \tilde{H}_1 : \text{not equal}$$


```

1 > # Case Study 13.2.1
2 > # install.packages("ggpubr")
3 > DIRS <- c(112.9, 123.1, 135.2, 140.2)
4 > STD <- c(115.1, 125.6, 132.4, 143.7)
5 > Wines <- c("W1", "W2", "R1", "R2")
6 > # Create a data frame
7 > my_data <- data.frame(
8 +   method = rep(c("DIRS", "STD"),
9 +                 each = 4),
10 +   types = c(Wines, Wines),
11 +   concentration = c(DIRS, STD)
12 > # Show data
13 > print(my_data)
14   method types concentration
15 1 DIRS W1      112.9
16 2 DIRS W2      123.1
17 3 DIRS R1      135.2
18 4 DIRS R2      140.2
19 5 STD W1      115.1
20 6 STD W2      125.6
21 7 STD R1      132.4
22 8 STD R2      143.7

```

```

1 > # Compute t-test with equal
  variances
2 > res <- t.test(concentration ~ method,
3 +               data = my_data,
4 +               var.equal = TRUE)
5 > res
6
7 Two Sample t-test
8
9 data: concentration by method
10 t = -0.15721, df = 6, p-value = 0.8802
11 alternative hypothesis: true difference in
  means is not equal to 0
12 95 percent confidence interval:
13 -22.362 19.662
14 sample estimates:
15 mean in group DIRS mean in group STD
16 127.85 129.20

```

```

1 > # The following one-way ANOVA is
  equivalent
2 > # to the two-sample t test
3 > library(car)
4 > model3 = lm(concentration ~ method,
5 +             data=my_data)
6 > Anova(model3)
7 Anova Table (Type II tests)
8
9 Response: concentration
10      Sum Sq Df F value Pr(>F)
11 method  3.64  1  0.0247 0.8802
12 Residuals 884 87 6

```

```

1 > # Compute t-test with unequal
  variances
2 > res <- t.test(concentration ~ method,
3 +               data = my_data,
4 +               var.equal = FALSE)
5 > res
6
7 Welch Two Sample t-test
8
9 data: concentration by method
10 t = -0.15721, df = 5.9968, p-value =
  0.8802
11 alternative hypothesis: true difference in
  means is not equal to 0
12 95 percent confidence interval:
13 -22.3647 19.6647
14 sample estimates:
15 mean in group DIRS mean in group STD
16 127.85 129.20

```

1. Classical method
2. Welch approximation
3. one-way ANOVA



The same answer
(p-value)

Concl. Fail to reject H_0

```

1 > # Now let's carry out two-way
  ANOVA
2 > library(car)
3 > model = lm(concentration ~ method
  + types,
4 + data=my_data)
5 > Anova(model)
6 Anova Table (Type II tests)
7
8 Response: concentration
9      Sum Sq Df F value Pr(>F)
10 method   3.65  1  0.9154 0.409258
11 types   872.92  3 73.0787 0.002652 **
12 Residuals 11.94  3

```

```

1 > # Now let's try one-way ANOVA
2 > model2 = lm(concentration ~ types,
3 + data=my_data)
4 > Anova(model2)
5 Anova Table (Type II tests)
6
7 Response: concentration
8      Sum Sq Df F value Pr(>F)
9 types   872.92  3 74.657 0.0005739 ***
10 Residuals 15.59  4
11 ---
12 Signif. codes:  0 '***' 0.001 '**' 0.01 '*'
                  0.05 '.' 0.1 ' ' 1

```

1. Fail to reject H_0
2. Reject \tilde{H}_0

E.g. 2 https://rcompanion.org/rcompanion/d_08.html

Genotype	Female	Male
FF	2.838	1.884
	4.216	2.283
	2.889	4.939
	4.198	3.486
FS	3.550	2.396
	4.556	2.956
	3.087	3.105
	1.943	2.649
SS	3.620	2.801
	3.079	3.421
	3.586	4.275
	2.669	3.110

Test at $\alpha = 0.05$

$$H_0 : \mu_F = \mu_M \quad v.s. \quad H_1 : \mu_F \neq \mu_M$$

and

$$\tilde{H}_0 : \mu_{FF} = \mu_S = \mu_{SS} \quad v.s. \quad \tilde{H}_1 : \text{not all equal}$$

```

1 > Data
2   id   Sex Genotype Activity
3 1 1 male      ff    1.884
4 2 2 male      ff    2.283
5 3 3 male      fs    2.396
6 4 4 female    ff    2.838
7 5 5 male      fs    2.956
8 6 6 female    ff    4.216
9 7 7 female    ss    3.620
10 8 8 female    ff    2.889
11 9 9 female    fs    3.550
12 10 10 male    fs    3.105
13 11 11 female  fs    4.556
14 12 12 female  fs    3.087
15 13 13 male    ff    4.939
16 14 14 male    ff    3.486
17 15 15 female  ss    3.079
18 16 16 male    fs    2.649

```

```

1 17 17 female    fs    1.943
2 18 19 female    ff    4.198
3 19 20 female    ff    2.473
4 20 22 female    ff    2.033
5 21 24 female    fs    2.200
6 22 25 female    fs    2.157
7 23 26 male      ss    2.801
8 24 28 male      ss    3.421
9 25 29 female    ff    1.811
10 26 30 female    fs    4.281
11 27 32 female    fs    4.772
12 28 34 female    ss    3.586
13 29 36 female    ff    3.944
14 30 38 female    ss    2.669
15 31 39 female    ss    3.050
16 32 41 male      ss    4.275
17 33 43 female    ss    2.963
18 34 46 female    ss    3.236
19 35 48 female    ss    3.673
20 36 49 male      ss    3.110

```

```

1 > # Two-way ANOVA
2 > model = lm(Activity ~ Sex +
  Genotype,
3 + data=Data)
4 > Anova(model, type="II")
5 Anova Table (Type II tests)
6
7 Response: Activity
8           Sum Sq Df F value Pr(>F)
9 Sex           0.0681 1  0.0888 0.7676
10 Genotype 0.2772 2  0.1808 0.8354
11 Residuals 24.5285 32
12 > # One-way ANOVA
13 > model_Sex = lm(Activity ~ Sex,
14 + data=Data)
15 > Anova(model_Sex, type="II")
16 Anova Table (Type II tests)
17
18 Response: Activity
19           Sum Sq Df F value Pr(>F)
20 Sex           0.0681 1  0.0933 0.7619
21 Residuals 24.8057 34
22 > # One-way ANOVA
23 > model_Genotype = lm(Activity ~
  Genotype,
24 + data=Data)
25 > Anova(model_Genotype, type="II")
26 Anova Table (Type II tests)
27
28 Response: Activity
29           Sum Sq Df F value Pr(>F)
30 Genotype 0.2772 2  0.186 0.8312
31 Residuals 24.5965 33

```

Tukey's pairwise comparison

Replace $Q_{\alpha,k,b(k-k)}$ by $Q_{\alpha,k,(b-1)(k-1)}$

```

1 > # Tukey's pairwise comparison (One-
  way)
2 > model1 = aov(Activity ~ Genotype,
3 +             data=Data)
4 > TukeyHSD(model1, "Genotype",
  ordered = TRUE)
5     Tukey multiple comparisons of means
6     95% family-wise confidence level
7     factor levels have been ordered
8
9 Fit: aov(formula = Activity ~ Genotype,
  data = Data)
10
11 $Genotype
12      diff      lwr      upr      p
      adj
13 fs-ff 0.05483333 -0.8100204 0.919687
  0.9867505
14 ss-ff 0.20741667 -0.6574370 1.072270
  0.8272105
15 ss-fs 0.15258333 -0.7122704 1.017437
  0.9021607
  
```

```

1 > # Tukey's pairwise comparison (Two
  -way)
2 > model2 = aov(Activity ~ Sex +
  Genotype,
3 +             data=Data)
4 > TukeyHSD(model2, "Genotype",
  ordered = TRUE)
5     Tukey multiple comparisons of means
6     95% family-wise confidence level
7     factor levels have been ordered
8
9 Fit: aov(formula = Activity ~ Sex +
  Genotype, data = Data)
10
11 $Genotype
12      diff      lwr      upr      p
      adj
13 fs-ff 0.05483333 -0.8234920 0.9331586
  0.987114
14 ss-ff 0.20741667 -0.6709086 1.0857420
  0.831554
15 ss-fs 0.15258333 -0.7257420 1.0309086
  0.904729
  
```

Remark By two-way ANOVA, or through blocking one factor, we obtain

1. larger p -values:
more conservative to reject H_0 .
2. wider C.I.'s:
more conservative on our estimates.

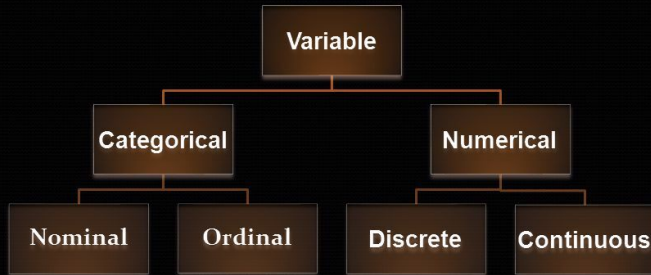
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Types of Variable with respect to data



Gender

1. Male
2. Female

Motivation

1. Highly Motivated
2. Moderately Motivated
3. Less Motivated

1. No of students
2. No of chairs
3. Collar size

1. Height
2. Weight
3. speed

	Numerical Values	Categorical Values
n Samples {	Sample 1 $y_{11} \dots y_{1m}$	$c_{11} \dots c_{1p}$
	Sample 2 $y_{21} \dots y_{2m}$	$c_{21} \dots c_{2p}$
	\vdots	\vdots
	Sample n $y_{n1} \dots y_{nm}$	$c_{n1} \dots c_{np}$
	m	p

		Dependent variable	
Independent variable		Continuous	Categorical
	Categorical	Linear Regression	Logistic Regression
	Continuous	t-test/ANOVA	Chi-square test

Indep. v.s. Dependent

1. Categorical v.s. Continuous

1.1 $p = 1, m = 1,$	One-way ANOVA
1.2 $p = 2, m = 1,$	Two-way ANOVA
1.3 $p \geq 3, m = 1,$	p -way ANOVA
1.4 $p = 1, m \geq 2,$	One-way MANOVA ^a
1.5 $p = 2, m \geq 2,$	Two-way MANOVA
1.6 $p \geq 3, m \geq 2,$	p -way ANOVA

^aMANOVA refers to the multivariate analysis of variance
ANOVA refers to the univariate analysis of variance.

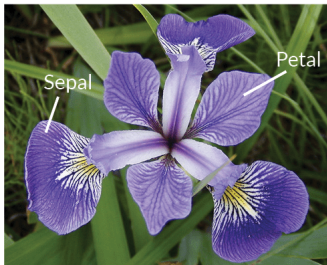
2. Continuous v.s. Continuous

2.1 $m_{ind} = 1, m_{dep} = 1,$	Simple linear regression
2.2 $m_{ind} \geq 2$	Multiple linear regression
2.3 $m_{dep} \geq 2$	Multivariate linear regression

E.g. One example for MANOVA¹.



¹<http://www.sthda.com/english/wiki/manova-test-in-r-multivariate-analysis-of-variance>



Iris Versicolor



Iris Setosa



Iris Virginica

```

1 > library(datasets)
2 > data(iris)
3 > summary(iris)
4   Sepal.Length Sepal.Width Petal.Length Petal.Width
   Species
5   Min. :4.300   Min. :2.000   Min. :1.000   Min. :0.100   setosa
   :50
6   1st Qu.:5.100 1st Qu.:2.800 1st Qu.:1.600 1st Qu.:0.300 versicolor
   :50
7   Median :5.800 Median :3.000 Median :4.350 Median :1.300 virginica
   :50
8   Mean :5.843   Mean :3.057   Mean :3.758   Mean :1.199
9   3rd Qu.:6.400 3rd Qu.:3.300 3rd Qu.:5.100 3rd Qu.:1.800
10  Max. :7.900   Max. :4.400   Max. :6.900   Max. :2.500
11 > my_data <- iris
12 > my_data
13   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
14 1         5.1         3.5         1.4         0.2   setosa
15 2         4.9         3.0         1.4         0.2   setosa
16 3         4.7         3.2         1.3         0.2   setosa
17 4         4.6         3.1         1.5         0.2   setosa
18 5         5.0         3.6         1.4         0.2   setosa
19 6         5.4         3.9         1.7         0.4   setosa
20 7         4.6         3.4         1.4         0.3   setosa
21 8         5.0         3.4         1.5         0.2   setosa
22 9         4.4         2.9         1.4         0.2   setosa
23 10        4.9         3.1         1.5         0.1   setosa

```



```

1 > # Compute MAOVA test now
2 > res.man <- manova(cbind(Sepal.Length, Petal.Length) ~ Species, data =
  iris)
3 > summary(res.man)
4           Df Pillai approx F num Df den Df Pr(>F)
5 Species      2 0.9885  71.829      4   294 < 2.2e-16 ***
6 Residuals 147
7 ---
8 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
9 > # Look to see which differ
10 > summary.aov(res.man)
11   Response Sepal.Length :
12           Df Sum Sq Mean Sq F value Pr(>F)
13 Species      2 63.212 31.606 119.26 < 2.2e-16 ***
14 Residuals 147 38.956  0.265
15 ---
16 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
17
18   Response Petal.Length :
19           Df Sum Sq Mean Sq F value Pr(>F)
20 Species      2 437.10 218.551 1180.2 < 2.2e-16 ***
21 Residuals 147 27.22  0.185
22 ---
23 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1:w

```

Concl.: Two variables are highly significantly different among species.