

14.7: Rcmdr Multiway ANOVA

Introduction

We have been talking about the two-way randomized, balanced, replicated design. Here, we take you step by step through use of R to conduct the **multiway ANOVA**.

R code: [Multiway ANOVA](#)

Rcmdr: Statistics → **Means** → **Multiway ANOVA...** we will review this as Option 1

or

Rcmdr: Statistics → **Fit Models** → **Linear model...** we will review this as Option 2

In either case, as a reminder, your data set must be a stacked worksheet, like the data in this table.

Table 14.7.1. Data set, example.14.7[†]

Diet	Population	Response
A	1	4
A	1	6
A	1	5
A	2	5
A	2	8
A	2	9
B	1	12
B	1	15
B	1	11
B	2	5
B	2	7
B	2	8

Option 1

Your first option is to use the ANOVA menus via “Means.” This is a perfectly good way to handle a standard two-way, fully-crossed, **fixed effects** model. However, other designs will not run with this command and R will return a report of errors for ANOVA models that do not conform to the replicated, balanced, crossed design.

Rcmdr: Statistics → Means → Multiway Analysis of variance ...

Factors: highlight “Diet” AND “Population”

Response variable: pick one (in this window, all we see is “Response”)

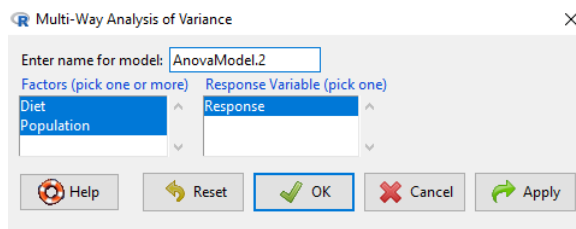


Figure 14.7.1: Multi-Way Analysis of Variance popup in R Commander.

 [†]Note:

Don't forget to convert numeric Population to factor

Interpret the output

```
AnovaModel.2 <- (lm(Response ~ Diet*Population, data=example.14.7))

Anova(AnovaModel.2)

Anova Table (Type II tests)
Response: Response
```

	Sum Sq	Df	F value	Pr(>F)
Diet	36.750	1	12.2500	0.008079 **
Population	10.083	1	3.3611	0.104104
Diet:Population	52.083	1	17.3611	0.003136 **
Residuals	24.000	8		

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

tapply(example.14.7 Response, list(Diet=example.14.7 Diet,
+ Population=example.14.7 Population), mean, na.rm=TRUE) # means
Population
Diet 1 2
A 5.00000 7.333333
B 12.66667 6.666667

tapply(example.14.7 Response, list(Diet=example.14.7 Diet,
+ Population=example.14.7 Population), sd, na.rm=TRUE) # std. deviations
Population
Diet 1 2
A 1.000000 2.081666
B 2.081666 1.527525

tapply(example.14.7 Response, list(Diet=example.14.71 Diet,
+ Population=example.14.7 Population), function(x) sum(!is.na(x))) # counts
Population
Diet 1 2
A 3 3
B 3 3
```

End R output

Summary of multi-way ANOVA command

The multi-way ANOVA command returns our ANOVA table plus the **adjusted means**, along with **standard deviations** and number of observations (counts). The adjusted means would then be good to put into a chart to present group comparisons following adjustments from the effects of levels within groups.

Rcmdr: Models → Graphs → Predictor effect plots ...

Here's the chart (hint: $\pm SEM = \frac{SD}{\sqrt{count}}$)

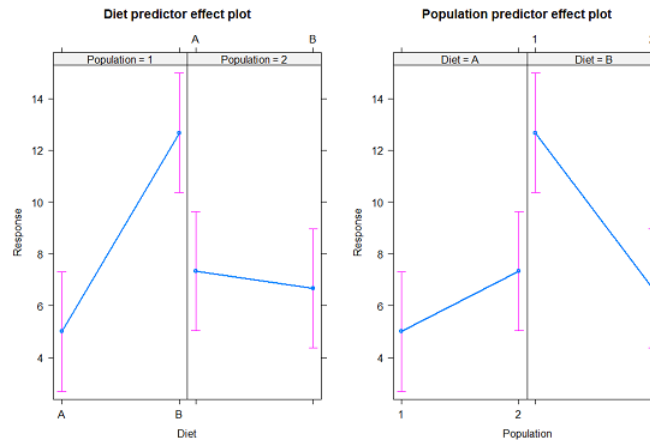


Figure 14.7.2: Plots of the predictor effects of each factor.

Option 2

A more general approach is to use the General linear model. This approach can handle the standard 2-way fixed effects ANOVA (above), but any other model as well. The model is `Response ~ Diet*Population` .

Rcmdr: Statistics → Fit Models → Linear model...

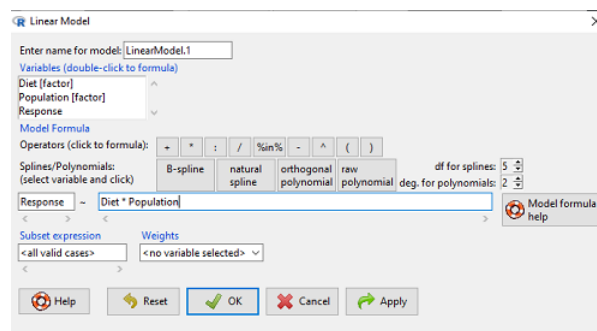


Figure 14.7.3: Linear Model screenshot in R Commander with model formula input.

Interpret the output

```
LinearModel.1 <- lm(Response ~ Diet * Population, data=example.14.7)

summary(LinearModel.1)

Call:
lm(formula = Response ~ Diet * Population, data = example.14.7)

Residuals:
Min 1Q Median 3Q Max
-2.3333 -1.1667 0.1667 1.0833 2.3333

Coefficients:
              Estimate Std. Error ..t value . Pr(>|t|)
(Intercept) .         5.000      1.000 .   5.000   .0.00105 **
Diet[T.B] .          7.667      1.414 .   5.421   .0.00063 ***
Population[T.2]       .2.333      1.414 .   1.650   .0.13757
```



```
Diet[T.B]:Population[T.2] -8.333      ..2.000      -4.167      .0.00314 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.732 on 8 degrees of freedom
Multiple R-squared:  0.8047, Adjusted R-squared:  0.7315
F-statistic: 10.99 on 3 and 8 DF, p-value: 0.003285
```

End R output

Lots to sort through, so let's begin with what is in common between the two approaches in `Rcmdr`, the Multi-way ANOVA command versus the linear model command.

Compare the two outputs

As a direct output, the linear model option does not provide an ANOVA summary table. Instead of our ANOVA table, the linear model returns estimates of coefficients along with *t*-test results for each coefficient of the model from the `lm()` command output

Recall that we can get ANOVA tables through the following R commands via `Rcmdr`.

Rcmdr: Models → Hypothesis tests → ANOVA Table.

Let's do so for this linear model (accept the default for type of tests = "Type II").

And the output is

```
Anova(LinearModel.1, type="II")
Anova Table (Type II tests)

Response: Response
      Sum Sq Df F value    Pr(>F)
Diet      36.750  1 12.2500 0.008079 **
Population 10.083  1  3.3611 0.104104
Diet:Population 52.083  1 17.3611 0.003136 **
Residuals    24.000  8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

End R output

Now we're in business, and, using the `lm()` function, we have the estimates for each model coefficient plus our ANOVA table.

Both methods give the same answer! Of course. Which to choose, Option 1 or Option 2? Use the `lm()` option: it is more flexible and covers more designs than the multiway ANOVA, which is strictly for the crossed fully replicated design.

Questions

1. Write out the two-way model described for the data in Table 14.7.1
2. Write the null hypotheses and provide a summary of the statistical significance of the model.

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