

## MANOVA Test in R: Multivariate Analysis of Variance

≡ Tools

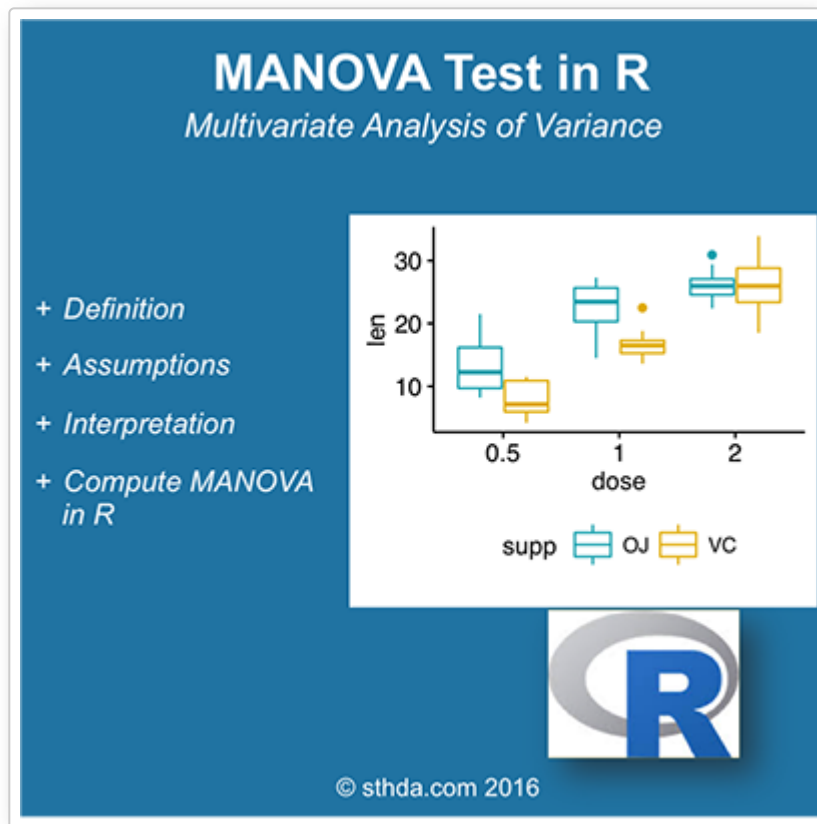
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### What is MANOVA test?

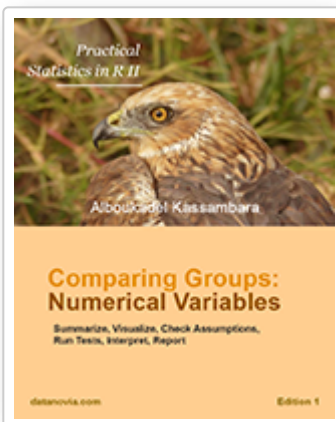
In the situation where there multiple response variables you can test them simultaneously using a **multivariate analysis of variance (MANOVA)**. This article describes how to compute **manova** in R.

For example, we may conduct an experiment where we give two treatments (A and B) to two groups of mice, and we are interested in the weight and height of mice. In that case, the weight and height of mice are two

dependent variables, and our hypothesis is that both together are affected by the difference in treatment. A multivariate analysis of variance could be used to test this hypothesis.



### Related Book:



Practical Statistics in R for  
Comparing Groups: Numerical  
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## Assumptions of MANOVA

MANOVA can be used in certain conditions:

- The dependent variables should be normally distributed within groups. The R function **mshapiro.test()** [in the **mvnormtest** package] can be used to perform the Shapiro-Wilk test for multivariate normality. This is useful in the case of MANOVA, which assumes **multivariate normality**.
- Homogeneity of variances across the range of predictors.
- Linearity between all pairs of dependent variables, all pairs of covariates, and all dependent variable-covariate pairs in each cell

## Interpretation of MANOVA

If the global multivariate test is significant, we conclude that the corresponding effect (treatment) is significant. In that case, the next question is to determine if the treatment affects only the weight, only the height or both. In other words, we want to identify the specific dependent variables that contributed to the significant global effect.

To answer this question, we can use one-way ANOVA (or univariate ANOVA) to examine separately each dependent variable.

## Compute MANOVA in R

### Import your data into R

1. **Prepare your data** as specified here: [url=/wiki/best-practices-for-preparing-your-data-set-for-r]Best practices for preparing your data set for R[url]
2. **Save your data** in an external .txt tab or .csv files
3. **Import your data into R** as follow:

```
# If .txt tab file, use this
my_data <- read.delim(file.choose())
# Or, if .csv file, use this
my_data <- read.csv(file.choose())
```

Here, we'll use iris data set:

```
# Store the data in the variable my_data
my_data <- iris
```

### Check your data

The R code below displays a random sample of our data using the function **sample\_n()** [in **dplyr** package]. First, install dplyr if you don't have it:

```
install.packages("dplyr")
```

```
# Show a random sample
set.seed(1234)
dplyr::sample_n(my_data, 10)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
94	5.0	2.3	3.3	1.0	versicolor
91	5.5	2.6	4.4	1.2	versicolor
93	5.8	2.6	4.0	1.2	versicolor
127	6.2	2.8	4.8	1.8	virginica
150	5.9	3.0	5.1	1.8	virginica
2	4.9	3.0	1.4	0.2	setosa
34	5.5	4.2	1.4	0.2	setosa
96	5.7	3.0	4.2	1.2	versicolor
74	6.1	2.8	4.7	1.2	versicolor
98	6.2	2.9	4.3	1.3	versicolor

? Question: We want to know if there is any significant difference, in *sepal* and *petal* length, between the different species.

## Compute MANOVA test

The function **manova()** can be used as follow:

```
sepl <- iris$Sepal.Length
petl <- iris$Petal.Length
# MANOVA test
res.man <- manova(cbind(Sepal.Length, Petal.Length) ~ Species, data = iris)
summary(res.man)
```

```
          Df Pillai approx F num Df den Df    Pr(>F)
Species    2 0.9885   71.829      4   294 < 2.2e-16 ***
Residuals 147
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Look to see which differ
summary.aov(res.man)
```

```

Response Sepal.Length :
      Df Sum Sq Mean Sq F value    Pr(>F)
Species      2  63.212   31.606   119.26 < 2.2e-16 ***
Residuals   147  38.956    0.265
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Response Petal.Length :
      Df Sum Sq Mean Sq F value    Pr(>F)
Species      2 437.10  218.551  1180.2 < 2.2e-16 ***
Residuals   147   27.22    0.185
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



From the output above, it can be seen that the two variables are highly significantly different among Species.

## See also

- Analysis of variance (ANOVA, parametric):
  - [\[url=/wiki/one-way-anova-test-in-r\]One-Way ANOVA Test in R\[/url\]](#)
  - [\[url=/wiki/two-way-anova-test-in-r\]Two-Way ANOVA Test in R\[/url\]](#)
- [\[url=/wiki/kruskal-wallis-test-in-r\]Kruskal-Wallis Test in R \(non parametric alternative to one-way ANOVA\) \[/url\]](#)

## Infos



This analysis has been performed using **R software** (ver. 3.2.4).



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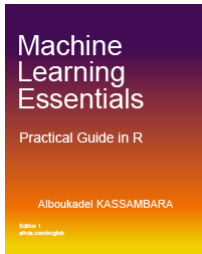
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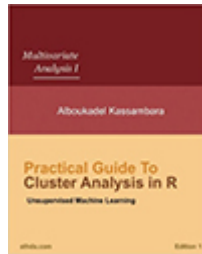
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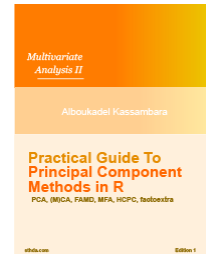
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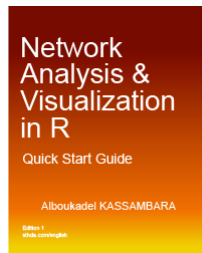
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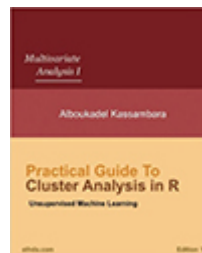
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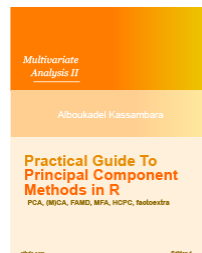


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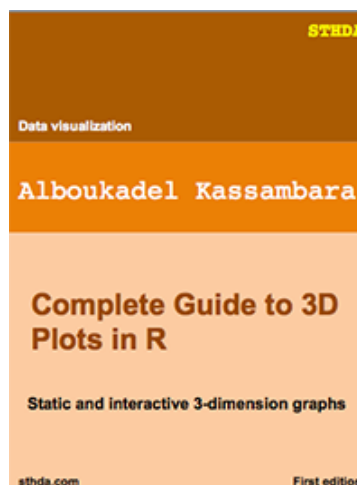
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