

Non-parametric Comparisons with **agricolae**

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1 Non-parametric Comparisons

The functions for non-parametric multiple comparisons included in **agricolae** are: **kruskal**, **waerden.test**, **friedman** and **durbin.test** (Conover, 1999).

The post hoc nonparametrics tests (**kruskal**, **friedman**, **durbin** and **waerden**) are using the criterium Fisher's least significant difference (LSD).

The function **kruskal** is used for N samples ($N > 2$), populations or data coming from a completely random experiment (populations = treatments).

The function **waerden.test**, similar to **kruskal-wallis**, uses a normal score instead of ranges as **kruskal** does.

The function **friedman** is used for organoleptic evaluations of different products, made by judges (every judge evaluates all the products). It can also be used for the analysis of treatments of the randomized complete block design, where the response cannot be treated through the analysis of variance.

The function **durbin.test** for the analysis of balanced incomplete block designs is very used for sampling tests, where the judges only evaluate a part of the treatments.

The function **Median.test** for the analysis the distribution is approximate with chi-squared ditribution with degree free number of groups minus one. In each comparison a table of 2×2 (pair of groups) and the criterion of greater or lesser value than the median of both are formed, the chi-square test is applied for the calculation of the probability of error that both are independent. This value is compared to the alpha level for group formation.

Montgomery book data (Montgomery, 2002). Included in the **agricolae** package

```
data(corn)
str(corn)
```

```
'data.frame':  34 obs. of  3 variables:
 $ method      : int  1 1 1 1 1 1 1 1 1 2 ...
 $ observation: int  83 91 94 89 89 96 91 92 90 91 ...
 $ rx          : num  11 23 28.5 17 17 31.5 23 26 19.5 23 ...
```

For the examples, the `agricolae` package data will be used

1.1 Kruskal-Wallis

It makes the multiple comparison with Kruskal-Wallis. The parameters by default are $\alpha = 0.05$.

```
str(kruskal)
```

```
function (y, trt, alpha = 0.05, p.adj = c("none", "holm", "hommel",
      "hochberg", "bonferroni", "BH", "BY", "fdr"), group = TRUE,
      main = NULL, console = FALSE)
- attr(*, "srcref")= 'srcref' int [1:8] 42 3 202 3 3 3 42 202
..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0x55a22fab4dd0>
```

1.1.1 Analysis

```
outKruskal<-with(corn,kruskal(observation,method,group=TRUE, main="corn", console=TRUE))
```

```
Study: corn
Kruskal-Wallis test's
Ties or no Ties
```

```
Critical Value: 26
Degrees of freedom: 3
Pvalue Chisq  : 1.1e-05
```

```
method, means of the ranks
```

```
observation r
1          21.8 9
2          15.3 10
3          29.6 7
4           4.8 8
```

```
Post Hoc Analysis
```

```
t-Student: 2
Alpha      : 0.05
Groups according to probability of treatment differences and alpha level.
```

Treatments with the same letter are not significantly different.

```
observation groups
```

| | | |
|---|------|---|
| 3 | 29.6 | a |
| 1 | 21.8 | b |
| 2 | 15.3 | c |
| 4 | 4.8 | d |

The object output has the same structure of the comparisons see the functions `plot.group(agricolae)`, `bar.err(agricolae)` and `bar.group(agricolae)`.

1.1.2 Kruskal-Wallis: adjust P-values

To see `p.adjust.methods()`

```
out<-with(corn,kruskal(observation,method,group=TRUE, main="corn", p.adj="holm"))
print(out$group)
```

| | observation | groups |
|---|-------------|--------|
| 3 | 29.6 | a |
| 1 | 21.8 | b |
| 2 | 15.3 | c |
| 4 | 4.8 | d |

```
out<-with(corn,kruskal(observation,method,group=FALSE, main="corn", p.adj="holm"))
print(out$comparison)
```

| | Difference | pvalue | Signif. |
|-------|------------|--------|---------|
| 1 - 2 | 6.5 | 0.0079 | ** |
| 1 - 3 | -7.7 | 0.0079 | ** |
| 1 - 4 | 17.0 | 0.0000 | *** |
| 2 - 3 | -14.3 | 0.0000 | *** |
| 2 - 4 | 10.5 | 0.0003 | *** |
| 3 - 4 | 24.8 | 0.0000 | *** |

1.2 Friedman

The data consist of b mutually independent k -variate random variables called b blocks. The random variable is in a block and is associated with treatment. It makes the multiple comparison of the Friedman test with or without ties. A first result is obtained by `friedman.test` of R.

```
str(friedman)
```

```
function (judge, trt, evaluation, alpha = 0.05, group = TRUE, main = NULL,
  console = FALSE)
- attr(*, "srcref")= 'srcref' int [1:8] 46 3 192 3 3 3 46 192
..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0x55a22c7a8ba8>
```

1.2.1 Analysis

```
data(grass)
out<-with(grass,friedman(judge,trt, evaluation,alpha=0.05, group=FALSE,
main="Data of the book of Conover",console=TRUE))
```

Study: Data of the book of Conover

trt, Sum of the ranks

```

      evaluation  r
t1          38 12
t2          24 12
t3          24 12
t4          34 12

```

Friedman's Test

=====

Adjusted for ties

Critical Value: 8.1

P.Value Chisq: 0.044

F Value: 3.2

P.Value F: 0.036

Post Hoc Analysis

Comparison between treatments

Sum of the ranks

| | difference | pvalue | signif. | LCL | UCL |
|---------|------------|--------|---------|-------|-------|
| t1 - t2 | 14.5 | 0.015 | * | 3.0 | 25.98 |
| t1 - t3 | 13.5 | 0.023 | * | 2.0 | 24.98 |
| t1 - t4 | 4.0 | 0.483 | | -7.5 | 15.48 |
| t2 - t3 | -1.0 | 0.860 | | -12.5 | 10.48 |
| t2 - t4 | -10.5 | 0.072 | . | -22.0 | 0.98 |
| t3 - t4 | -9.5 | 0.102 | | -21.0 | 1.98 |

1.3 Waerden

A nonparametric test for several independent samples. Example applied with the sweet potato data in the **agricolae** basis.

```
str(waerden.test)
```

```

function (y, trt, alpha = 0.05, group = TRUE, main = NULL, console = FALSE)
- attr(*, "srcref")= 'srcref' int [1:8] 46 3 166 3 3 3 46 166
..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0x55a2307f2338>

```

1.3.1 Analysis

```

data(sweetpotato)
outWaerden<-with(sweetpotato,waerden.test(yield,virus,alpha=0.01,group=TRUE,console=TRUE))

```

Study: yield ~ virus

Van der Waerden (Normal Scores) test's

Value : 8.4

Pvalue: 0.038

Degrees of Freedom: 3

virus, means of the normal score

```

      yield  std r
cc -0.23 0.30 3
fc -1.06 0.35 3
ff  0.69 0.76 3
oo  0.60 0.37 3

```

Post Hoc Analysis

Alpha: 0.01 ; DF Error: 8

Minimum Significant Difference: 1.3

Treatments with the same letter are not significantly different.

Means of the normal score

```

      score groups
ff  0.69      a
oo  0.60      a
cc -0.23     ab
fc -1.06     b

```

The comparison probabilities are obtained with the parameter group = **FALSE**.

```
names(outWaerden)
```

```
[1] "statistics" "parameters" "means"      "comparison" "groups"
```

To see outWaerden\$comparison

```
out<-with(sweetpotato,waerden.test(yield,virus,group=FALSE,console=TRUE))
```

Study: yield ~ virus

Van der Waerden (Normal Scores) test's

Value : 8.4

Pvalue: 0.038

Degrees of Freedom: 3

virus, means of the normal score

```

      yield  std r
cc -0.23 0.30 3
fc -1.06 0.35 3
ff  0.69 0.76 3
oo  0.60 0.37 3

```

Post Hoc Analysis

Comparison between treatments

mean of the normal score

| | difference | pvalue | signif. | LCL | UCL |
|---------|------------|--------|---------|--------|--------|
| cc - fc | 0.827 | 0.0690 | . | -0.082 | 1.736 |
| cc - ff | -0.921 | 0.0476 | * | -1.830 | -0.013 |
| cc - oo | -0.837 | 0.0664 | . | -1.746 | 0.072 |
| fc - ff | -1.749 | 0.0022 | ** | -2.658 | -0.840 |
| fc - oo | -1.665 | 0.0029 | ** | -2.574 | -0.756 |
| ff - oo | 0.084 | 0.8363 | | -0.825 | 0.993 |

1.4 Median test

A nonparametric test for several independent samples. The median test is designed to examine whether several samples came from populations having the same median (Conover, 1999). See also Figure 1.

In each comparison a table of 2x2 (pair of groups) and the criterion of greater or lesser value than the median of both are formed, the chi-square test is applied for the calculation of the probability of error that both are independent. This value is compared to the alpha level for group formation.

```
str(Median.test)
```

```
function (y, trt, alpha = 0.05, correct = TRUE, simulate.p.value = FALSE,
  group = TRUE, main = NULL, console = TRUE)
- attr(*, "srcref")= 'srcref' int [1:8] 53 3 154 3 3 3 53 154
..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0x55a2283e10d8>
```

```
str(Median.test)
```

```
function (y, trt, alpha = 0.05, correct = TRUE, simulate.p.value = FALSE,
  group = TRUE, main = NULL, console = TRUE)
- attr(*, "srcref")= 'srcref' int [1:8] 53 3 154 3 3 3 53 154
..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0x55a2283e10d8>
```

1.4.1 Analysis

```
data(sweetpotato)
outMedian<-with(sweetpotato,Median.test(yield,virus,console=TRUE))
```

The Median Test for yield ~ virus

Chi Square = 6.7 DF = 3 P.Value 0.083

Median = 28

| | Median | r | Min | Max | Q25 | Q75 |
|----|--------|---|-----|-----|-----|-----|
| cc | 23 | 3 | 22 | 28 | 22 | 26 |
| fc | 13 | 3 | 11 | 15 | 12 | 14 |
| ff | 39 | 3 | 28 | 42 | 34 | 40 |
| oo | 38 | 3 | 32 | 40 | 35 | 39 |

Post Hoc Analysis

Groups according to probability of treatment differences and alpha level.

Treatments with the same letter are not significantly different.

```
      yield groups
```

```
ff      39      a
oo      38      a
cc      23      a
fc      13      b
```

```
names(outMedian)
```

```
[1] "statistics" "parameters" "medians"      "comparison" "groups"
```

```
outMedian$statistics
```

```
Chisq Df p.chisq Median
6.7 3 0.083 28
```

```
outMedian$medians
```

```
Median r Min Max Q25 Q75
cc      23 3 22 28 22 26
fc      13 3 11 15 12 14
ff      39 3 28 42 34 40
oo      38 3 32 40 35 39
```

```
oldpar<-par(mfrow=c(2,2),mar=c(3,3,1,1),cex=0.8)
```

```
# Graphics
```

```
bar.group(outMedian$groups,ylim=c(0,50))
```

```
bar.group(outMedian$groups,xlim=c(0,50),horiz = TRUE)
```

```
plot(outMedian)
```

```
Warning in plot.group(outMedian): NAs introduced by coercion
```

```
plot(outMedian,variation="IQR",horiz = TRUE)
```

```
Warning in plot.group(outMedian, variation = "IQR", horiz = TRUE): NAs
introduced by coercion
```

```
par(oldpar)
```

1.5 Durbin

durbin.test; example: Myles Hollander (p. 311) Source: W. Moore and C.I. Bliss. (1942) A multiple comparison of the Durbin test for the balanced incomplete blocks for sensorial or categorical evaluation. It forms groups according to the demanded ones for level of significance (alpha); by default, 0.05.

```
str(durbin.test)
```

```
function (judge, trt, evaluation, alpha = 0.05, group = TRUE, main = NULL,
```

```
  console = FALSE)
```

```
- attr(*, "srcref")= 'srcref' int [1:8] 58 3 197 3 3 3 58 197
```

```
..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0x55a22bdd8b90>
```

1.5.1 Analysis

```
days <-gl(7,3)
```

```
chemical<-c("A","B","D","A","C","E","C","D","G","A","F","G", "B","C","F",
" B","E","G","D","E","F")
```

```
toxic<-c(0.465,0.343,0.396,0.602,0.873,0.634,0.875,0.325,0.330, 0.423,0.987,0.426,
```

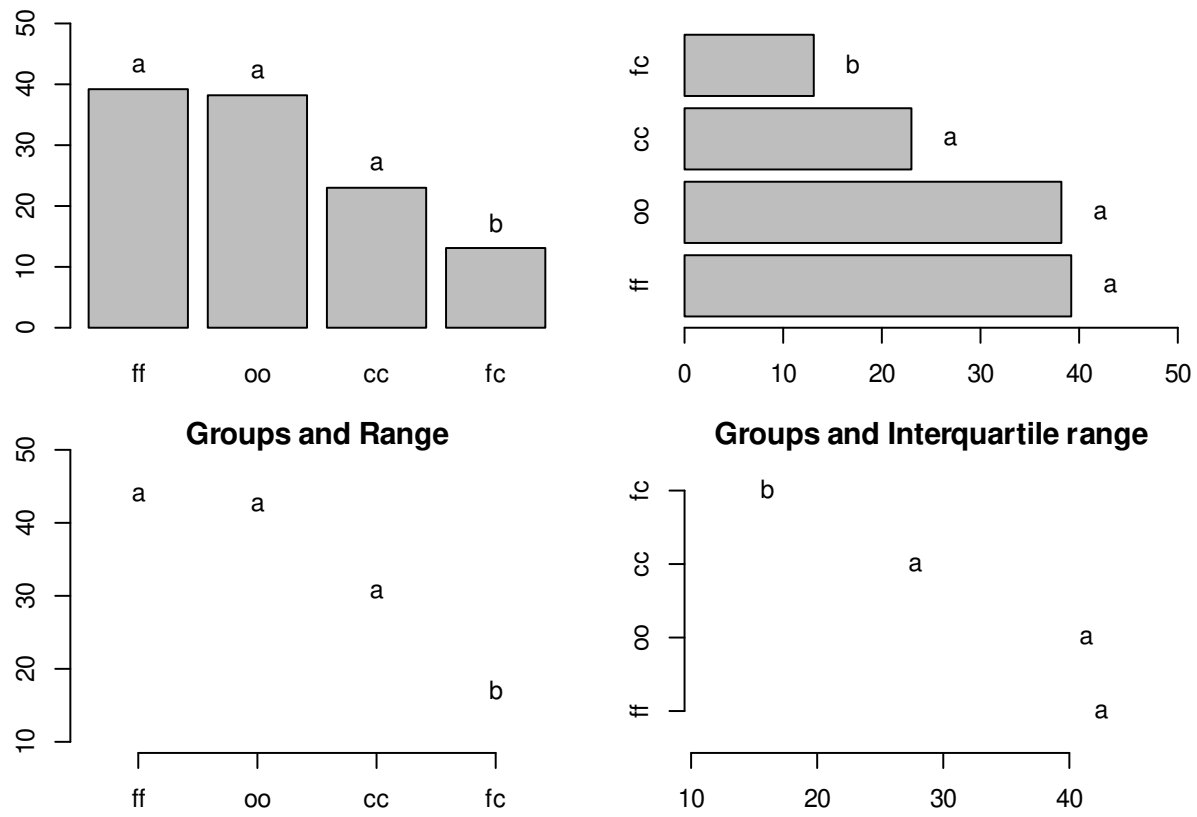


Figure 1: Grouping of treatments and its variation, Median method


```
0.652,1.142,0.989,0.536,0.409,0.309, 0.609,0.417,0.931)
head(data.frame(days,chemical,toxic))
```

```
  days chemical toxic
1     1         A  0.47
2     1         B  0.34
3     1         D  0.40
4     2         A  0.60
5     2         C  0.87
6     2         E  0.63
```

```
out<-durbin.test(days,chemical,toxic,group=FALSE,console=TRUE,
main="Logarithm of the toxic dose")
```

Study: Logarithm of the toxic dose
chemical, Sum of ranks

```
      sum
A      5
B      5
C      9
D      5
E      5
F      8
G      5
```

Durbin Test

=====

```
Value      : 7.7
DF 1       : 6
P-value    : 0.26
Alpha      : 0.05
DF 2       : 8
t-Student  : 2.3
```

Least Significant Difference
between the sum of ranks: 5

Parameters BIB

```
Lambda      : 1
Treatmeans  : 7
Block size  : 3
Blocks      : 7
Replication : 3
```

Comparison between treatments
Sum of the ranks

```
      difference pvalue signif.
A - B           0    1.00
A - C          -4    0.10
```

| | | |
|-------|----|------|
| A - D | 0 | 1.00 |
| A - E | 0 | 1.00 |
| A - F | -3 | 0.20 |
| A - G | 0 | 1.00 |
| B - C | -4 | 0.10 |
| B - D | 0 | 1.00 |
| B - E | 0 | 1.00 |
| B - F | -3 | 0.20 |
| B - G | 0 | 1.00 |
| C - D | 4 | 0.10 |
| C - E | 4 | 0.10 |
| C - F | 1 | 0.66 |
| C - G | 4 | 0.10 |
| D - E | 0 | 1.00 |
| D - F | -3 | 0.20 |
| D - G | 0 | 1.00 |
| E - F | -3 | 0.20 |
| E - G | 0 | 1.00 |
| F - G | 3 | 0.20 |

```
names(out)
```

```
[1] "statistics" "parameters" "means"      "rank"      "comparison"
[6] "groups"
```

```
out$statistics
```

| chisq.value | p.value | t.value | LSD |
|-------------|---------|---------|-----|
| 7.7 | 0.26 | 2.3 | 5 |

References

Conover, W. J. (1999). Practical Nonparametric Statistics.

Montgomery, D. C. (2002). *Design and Analysis of Experiments*. John Wiley & Sons, New York.