Non-parametric Comparisons with **agricolae**

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Contents

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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 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)
```

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)
```

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)
```

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)
```

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

```
function (y, trt, alpha = 0.05, correct = TRUE, simulate.p.value = FALSE,
    group = TRUE, main = NULL, console = TRUE)
```

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
```

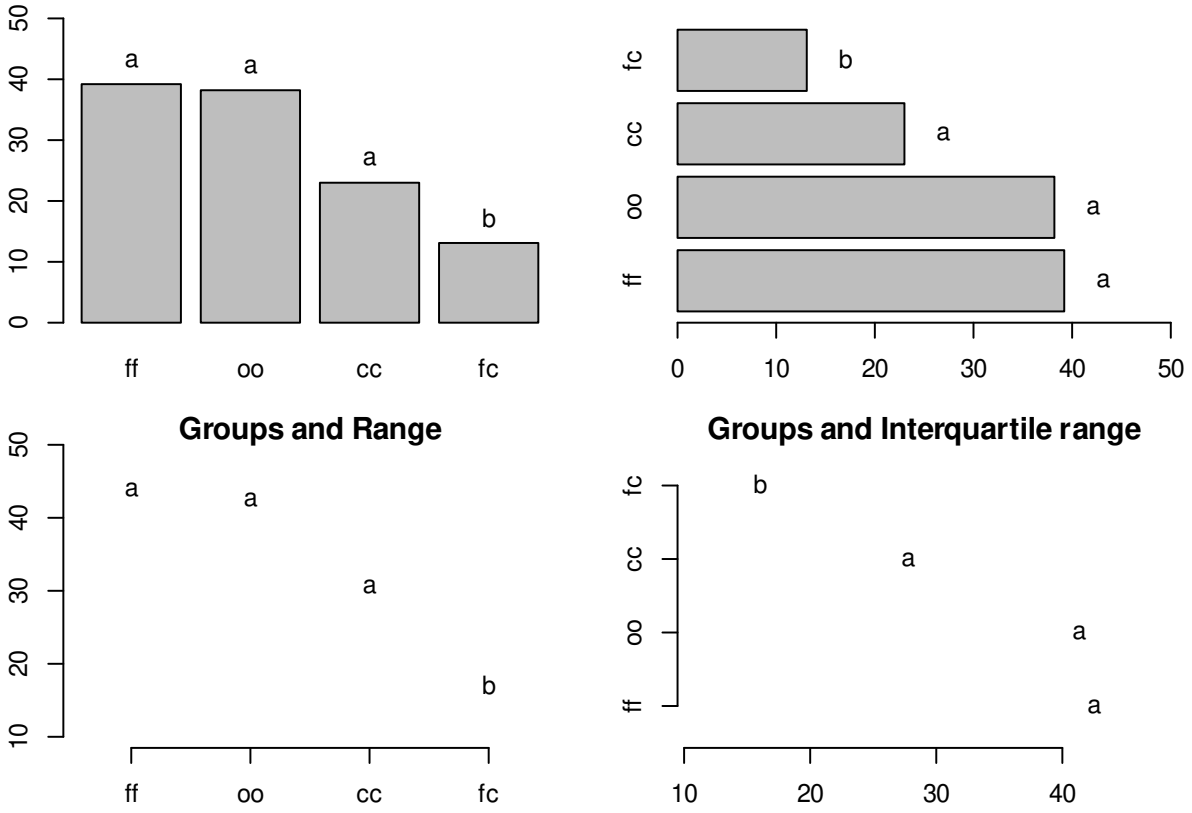

Figure 1: Grouping of treatments and its variation, Median method

```
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)
```

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,
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.