

# Package ‘replicatedpp2w’

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**Type** Package

**Title** Two-Way ANOVA-Like Method to Analyze Replicated Point Patterns

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**Depends** spatstat.utils

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**Description** Test for effects of both individual factors and their interaction on replicated spatial patterns in a two factorial design, as explained in Ramon et al. (2016) <doi:10.1111/ecog.01848>.

**Imports** spatstat

**License** GPL (>= 2)

**NeedsCompilation** no

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croton	<i>Replicated Point Pattern of Croton</i>
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### Description

A list with a) a list of 16 point patterns (with the `ppp` format of `spatstat`) of *Croton wagneri* in Southern Ecuador; b) a factor with different elevations ("high", "slow") and c) a factor with different topographical conditions ("steep" or "flat" slope) for each point pattern. Each point pattern is actually the result of a random thinning (50 percent) of the original pattern analyzed by Ramon et al. (in revision).

**Usage**

```
data("croton")
```

**References**

Ramon, P., De la Cruz, M., Chacon-Labela, J. & Escudero, A. (in revision). A new two-way ANOVA-like method for analyzing replicated point patterns in ecology.

**Examples**

```
data(croton)
```

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K2w

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*Two-Way ANOVA-Like Method to Analyze Replicated Point Patterns*


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**Description**

Test for effects of both individual factors and their interaction on replicated spatial patterns in a two factorial design.

**Usage**

```
K2w(pplist = NULL, dataKijk = NULL, nijk = NULL, r, r0 = NULL, rmax = NULL,
    trata, tratB = NULL, wt = NULL, nsim = 999, correction = "trans", ...)
## S3 method for class 'k2w'
print(x,...)
## S3 method for class 'k2w'
plot(x, trata=NULL, ..., lty = NULL, col = NULL,
     lwd = NULL, xlim = NULL, ylim = NULL, xlab = NULL, ylab = NULL,
     legend = TRUE, legendpos = "topleft", fun="L", main=NULL)
```

**Arguments**

pplist	A list of point patterns with the <a href="#">ppp</a> format of <b>spatstat</b> . This argument is alternative to dataKijk.
dataKijk	A data.frame with the K-functions (in columns) of each of the replicated point patterns. This argument is alternative to pplist.
nijk	A vector with the number of points in each of the replicated point patterns.
r	Vector of values for the argument r at which the K functions have been or should be evaluated. If the K functions are to be computed (i.e., if dataKijk is NULL), first element of r should be 0.
r0	Minimum r value for which K(r) estimates will be employed to compute BTSS.
rmax	Maximum r value for which K(r) estimates will be employed to compute BTSS.
trata	A factor assigning the levels of the first factor to each point pattern replicate.
tratB	A factor assigning the levels of the second factor to each point pattern replicate.

wt	A weighting function employed to compute the BTSS. It can be either an R expression, a vector (with <code>length(wt) == length(r)</code> ) or a single value (i.e., same weight for all distances). By default, K2w will use $wt=r^{-2}$ .
nsim	Number of resamples to estimate the sampling distribution of the BTSS statistic.
correction	Any selection of the options "border", "bord.modif", "isotropic", "Ripley", "translate", "translation", "none" or "best". It specifies the edge correction to be applied if K functions should be computed.
...	Additional arguments for <code>Kest</code> function of <b>spatstat</b> (only applies if K functions should be computed) or additional graphical arguments for the <code>matplot</code> function.
x	an object of class <code>k2w</code> .
trat	(optional) Factor employed to compute the averaged K functions that will be plotted. By default, <code>plot.k2w</code> plots averaged functions for the interaction (i.e., for combination of levels of factors) if two factors have been employed in the analysis or for the levels of the unique factor employed (in the case of one-way analysis). To select some specific display, use one of these: "tratA" (for the levels of the first factor), "tratB" (for the levels of the second factor) or "tratAB" (for the combinations of levels of both factors).
lty	(optional) numeric vector of values of the graphical parameter <code>lty</code> controlling the line type of each plot.
col	(optional) numeric vector of values of the graphical parameter <code>col</code> controlling the colour of each K function.
lwd	(optional) numeric vector of values of the graphical parameter <code>lwd</code> controlling the line width of each plot.
xlim	(optional) range of x axis.
ylim	(optional) range of y axis.
xlab	(optional) label for x axis.
ylab	(optional) label for y axis.
legend	Logical flag or NULL. If <code>legend=TRUE</code> , the algorithm plots a legend in the top left corner of the plot, explaining the meaning of the different line types and colours.
legendpos	The position of the legend. Either a character string keyword (see <code>legend</code> for keyword options) or a pair of coordinates in the format <code>list(x,y)</code> .
fun	One of "K" or "L" to select the function to be displayed. By default, $L(r) = \sqrt{K(r)/\pi} - r$ would be plotted.
main	text to display as the title of the plot. By default, the name of the <code>k2w</code> object would be shown.

## Details

This function implements an extension of the non-parametric one-way ANOVA-like method of Diggle et al. (1991) to the two-way case, and particularly to test the effects of the interaction of two factors on the spatial structure of replicated point patterns. From a set of K functions, it generates weighted averaged K functions for each level and combinations of levels of the factors and computes a statistic analogous to a *between-treatment sum of squares* (BTSS) in classical ANOVA. More details are available in Ramon et al. (in revision).

**Value**

K2w returns an object of class k2w. Basically, a list with components:

btss.i	Between treatment sum of squares (BTSS) for factor A.
btss.j	BTSS for factor B.
btss.ij	BTSS for the interaction of factors A and B.
btss.i.res	Resampled distribution of the BTSS statistic for factor A.
btss.j.res	Resampled distribution of BTSS for factor B.
btss.ij.res	Resampled distribution of BTSS for the interaction of factors A and B.
KrepA	Weighted average of the replicated K functions for each level of factor A.
KrepB	Weighted average of the replicated K functions for each level of factor B.
KrepAB	Weighted average of the replicated K functions for each combination of levels of factors A and B.
K0i	Global weighted average (i.e., all K functions averaged together).
K0j	Global weighted average (i.e., all K functions averaged together).
K0ij	Global weighted average (i.e., all K functions averaged together).
Rik	Data.frame with the residual functions for factor A.
Rjk	Data.frame with the residual functions for factor B.
Rijk	Data.frame with the residual functions for the interaction of factors A and B.
nsumA	Total number of points among the replicates in each level of factor A.
nsumB	Total number of points among the replicates in each level of factor B.
nsumAB	Total number of points among the replicates in each combination of levels of factors A and B.
wt	Weighting function employed to compute the BTSS.
trata	Factor A.
tratB	Factor B.
tratAB	Factor with the combination of levels of A and B.
dataKijk	Data.frame with the empirical, replicated, K-functions.
nijk	Vector with the number of points in each replicate.
r	Vector of r distances at which K functions are estimated.
r0	Minimum r value for which K values have been employed to compute BTSS.
KA.res	Data.frame with the weighted average of replicated K functions for each level of factor A, for each of the nsim resamples.
KB.res	Data.frame with the weighted average of replicated K functions for each level of factor B, for each of the nsim resamples.
KAB.res	Data.frame with the weighted average of replicated K functions for each combination of levels of factors A and B, for each of the nsim resamples.
nameA	name of the R object with factor A.
nameB	name of the R object with factor B.

**Author(s)**

Marcelino de la Cruz

**References**

Diggle, P.J., Nicholas, L. & Benes, F.M. (1991) Analysis of Variance for Replicated Spatial Point Patterns in Clinical Neuroanatomy. *Journal of the American Statistical Association*, 86: 618-625.

Ramon, P., De la Cruz, M., Chacon-Labela, J. & Escudero, A. (2016). A new two-way ANOVA-like method for analyzing replicated point patterns in ecology. *Ecography*, 39:1109-1117.

**Examples**

```
# Get the data
data(croton)

croton.2w <- K2w(pplist=croton$list.ppp, r=seq(0,8, by=0.1),
               tratA=croton$elevation, tratB=croton$slope, nsim=99)

croton.2w

plot(croton.2w)

plot(croton.2w, "tratB")
```

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