

# Package ‘sobir’

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**Type** Package

**Title** Significance of Boundaries

**Version** 0.1.2

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**Description** Separates significant boundary constraints in a dataset from illusions. A modified permutation test is applied using the no-data zone areas above the top-left, top-right, bottom-right and bottom-left boundary lines as test statistics. The observed no-data zone areas are compared to the distribution of the random permutations to calculate a p-value for each boundary line. An article detailing the methodologies and rationale is currently in preparation.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.2

**Depends** R (>= 3.5.0)

**Suggests** testthat, knitr, rmarkdown

**Imports** ggplot2, raster, rlang, scales, sp, statmod, tidyr, dplyr,  
stringr, DescTools, devtools, usethis

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

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bpts_plot	<i>Boundary Points Plot</i>
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### Description

bpts\_plot creates a ggplot2 scatterplot of your bpts object with the boundary lines and no-data zones identified.

### Usage

```
bpts_plot(
  bpts,
  xlab = "x",
  ylab = "y",
  export_name = "bpts plot.png",
  save_plot = FALSE,
  colour = TRUE,
  legend.position = "right"
)
```

### Arguments

bpts	your bpts object created by the extract_bpts() function.
xlab	the x-axis label. Defaults to "".
ylab	the y-axis label. Defaults to "".
export_name	the filename of your plot if you choose to export it. Include .png suffix. Defaults to "bpts plot.png" if save_plot = TRUE.
save_plot	TRUE or FALSE to save the plot. Defaults to FALSE.
colour	TRUE or FALSE to plot using colour or in black and white. Defaults to TRUE.
legend.position	Define the position of the ggplot legend, as per ggplot capability. Default to "right".

### Value

a ggplot2 scatterplot

### Examples

```
a = rnorm(100,0,1)
b = rnorm(100,0,1)
bptsExample = extract_bpts(a,b)
bpts_plot(bptsExample, "a", "b")
```

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calc_area	<i>Calculate the no-data zone areas</i>
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**Description**

This function supports the other sobir functions by calculating the no-data zone areas

**Usage**

```
calc_area(xdat, ydat)
```

**Arguments**

xdat	a vector of the independent data
ydat	a vector of the dependent data

**Value**

a list of the no-data zone areas

**Examples**

```
a = rnorm(100,0,1)
b = rnorm(100,0,1)
calc_area(a,b)
```

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extract_bpts	<i>Extract boundary points</i>
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**Description**

extract\_bpts identifies the boundary points to a scatterplot and labels the relevant data for further analysis in the sobir package.

**Usage**

```
extract_bpts(xdat, ydat)
```

**Arguments**

xdat	a vector of the independent data
ydat	a vector of the dependent data

**Value**

a data frame of the two vectors with the boundary points and other relevant data labelled.

**Examples**

```
a = rnorm(100,0,1)
b = rnorm(100,0,1)
extract_bpts(a,b)
```

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perm\_area

*Calculate the permuted area*


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**Description**

perm\_area calculates the no-data zone areas for each permutation of the data simulated nsim times.

**Usage**

```
perm_area(xdat, ydat, nsim, boundary = "topl", method = "auto")
```

**Arguments**

xdat	a vector of the independent data
ydat	a vector of the dependent data
nsim	the number of simulations to run
boundary	character string indicating the boundary to test (default is "topl"). Possible values are "topl" (top-left), "topr" (top-right), "botl" (bottom-left), "botr" (bottom-right) or "all".
method	character string indicating computation method (default is "auto"). Possible values are "exact", "approximate" or "auto".

**Value**

a perm table that can be plotted directly using perm\_plot()

**Examples**

```
a = rnorm(100,0,1)
b = rnorm(100,0,1)
perm_area(a,b,10)
```

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perm_plot	<i>Perm Plot</i>
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**Description**

perm\_plot calculates the significance of the observed no-data zones and plots them relative to the simulations.

**Usage**

```
perm_plot(perm, histogram = TRUE)
```

**Arguments**

perm            a perm object generated by the perm\_area() function.  
 histogram      TRUE or FALSE. TRUE plots histograms while FALSE plots density plots.

**Value**

a ggplot2 histogram and p-value for each no-data zone

**Examples**

```
a = rnorm(100,0,1)
b = rnorm(100,0,1)
permExample = perm_area(a,b,10)
perm_plot(permExample, 100)
```

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WoodyAfrica	<i>Woody cover in Africa</i>
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**Description**

Woody cover percentage in Africa relative to mean annual precipitation (mm), as published by Sankaran et al. 2005 in Nature.

**Usage**

```
WoodyAfrica
```

**Format**

A data frame with 854 rows and 2 variables

**Details**

MAP = Mean annual precipitation, in mm Cover = Woody cover, in

**Source**

<https://doi.org/10.1038/nature04070>

**References**

Sankaran et al. (2005) Determinants of woody cover in African savannas. *Nature* 438, p846–849.

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WoodyTowoomba

*Woody cover in Towoomba*

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**Description**

Tree abundance in Towoomba Agricultural Development Center, South Africa relative to four soil fertilisation treatments and 16 soil nutrient and element concentrations, as published by Mills et al. 2017 in PLoS ONE.

**Usage**

WoodyTowoomba

**Format**

A data frame with 60 rows and 18 variables

**Details**

Treatment = 12 treatments of a combination of superphosphate (SP0-SP2; 0, 233, 466 kg/ha/yr) and ammonium sulphate (AS0-AS3; 0, 146, 291, 583, 1166 kg/ha/yr) fertilisation applications. TreeNum = Number of trees present following three decades of fertilisation and three subsequent decades of passive protection. EC, pH, B, C, Na, Mg, P, S, N, K, Ca, Mn, Cu, Zn, N\_NO3, N\_NH4 = Soil nutrient and element concentration of the pedoderm (0-2 cm) in mg/kg, except for pH (unitless), EC (uS/cm) and C (

**Source**

<https://doi.org/10.1371/journal.pone.0179848>

**References**

Mills et al. (2017) Effects of anabolic and catabolic nutrients on woody plant encroachment after long-term experimental fertilization in a South African savanna. *PLoS ONE* 12(6), p1-24.

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