Package ‘aspi’

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Title Analysis of Symmetry of Parasitic Infections

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Description Tools for the analysis and visualization of bilateral asymmetry in parasitic infections.

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`aspi` *ASPI: Analysis of Symmetry in Parasitic Infections*

Description

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Author(s)

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`diplostomum_eyes_excl_lenses` *Numbers of Diplostomum metacercariae recorded from the eyes (excluding lenses) of each of 50 ruffe.*

Description

A dataset containing the numbers of Diplostomum metacercariae recovered from the eyes (excluding lenses) of each of 50 ruffe, Gymnocephalus cernuus from Llyn Tegid, a mesotrophic lake in north Wales.

Usage

```
diplostomum_eyes_excl_lenses
```

Format

A data frame with 50 rows and 2 variables (row names are host IDs):

left number of metacercariae in left eye

right number of metacercariae in the right eye

`diplostomum_lenses` *Numbers of Diplostomum metacercariae recorded from the lenses of the eyes of each of 50 ruffe.*

Description

A dataset containing the numbers of Diplostomum metacercariae recovered from the lenses of the eyes of each of 50 ruffe, Gymnocephalus cernuus from Llyn Tegid, a mesotrophic lake in north Wales.

Usage

```
diplostomum_lenses
```

Format

A data frame with 50 rows and 2 variables (row names are host IDs):

left number of metacercariae in lens of left eye

right number of metacercariae in lens of right eye

`eb.test` *Exact binomial tests*

Description

Assess symmetry of parasitic infections by performing exact binomial tests on pooled data and individual hosts.

Usage

```
eb.test(x)
```

Arguments

`x`	a matrix or data frame with two numeric columns; first column is for left-side and 2nd column for right-side. Identifiers for hosts can be provided as row names.

Details

This function performs a binomial exact tests with the null hypothesis of a 1:1 ratio. It takes as its argument a matrix or data frame with two numeric columns; first column is for left-side and 2nd column for right-side. Identifiers for hosts can be provided as row names. Uninfected hosts (zero count for both left and right sides) are ignored.

Value

It returns a list containing two elements:

`pooled`	p-value for pooled binomial exact test (null hypothesis: the ratio of the total number of parasites from each side doesn't differ from 1:1).
`hosts`	data.frame of results of binomial exact tests performed on the distribution of parasites in each host.

Examples

```
eb.test(diplostomum_lenses)
```

`g.test` *Replicated G-tests of goodness-of-fit*

Description

Perform replicated G-tests of goodness-of-fit to assess symmetry of parasitic infections.

Usage

```
g.test(x)
```

Arguments

`x`	a matrix or data frame with two numeric columns; first column is for left-side and 2nd column for right-side. Identifiers for hosts can be provided as row names.

Details

This function implements Sokal & Rohlf's (1995) G-test for the specific case of an expected 1:1 ratio The function takes as its argument a matrix or data frame with two numeric columns; first column is for left-side and 2nd column for right-side. Identifiers for hosts can be provided as row names. Uninfected hosts (zero count for both left and right sides) are ignored. Cannot be applied to data containing zero counts; use eb.test instead.

Value

A list containing two data.frames:

`summary`	results of total, heterogeneity and pooled G-tests. Data frame has four columns: test, degrees of freedom, G-statistic and p-value.
`hosts`	results of individual G-tests on distribution of parasites in each host. Data frame has seven columns: Host (ID), Left (count of parasites on left side), Right (count of parasites on right side), G (G-statistic), p (p-value), BH (p-value adjusted using Benjamini and Hochberg's procedure for controlling the false discovery rate) and Holm (p-value adjusted using Holm's method).

References

R.R. Sokal & F.J. Rohlf (1995) Biometry. 3rd Edition. New York: W.H. Freeman and Company. 887 pp.

Examples

```
g.test(diplostomum_eyes_excl_lenses)
```

`plotHistogram` *Plot histogram*

Description

Creates a histogram showing distribution of fold differences in abundance of parasites between left and right sides of host.

Usage

```
plotHistogram(x, nBreaks = 10, ...)
```

Arguments

`x`	a matrix or data frame with two numeric columns; first column is for left-side and 2nd column for right-side. Identifiers for hosts can be provided as row names.
`nBreaks`	number of cells for the histogram. A suggestion only; breakpoints will be set to pretty values.
`...`	optional further arguments and graphical parameters passed to plot.

Details

plot.Histogram creates a histogram showing distribution of fold differences in abundance of parasites between left and right sides. For each infected host the number of parasites on the right side is divided by the number of parasites on the left side, and the result binary log transformed. The log2 ratio will be negative if there are more parasites on the left than right and positive if there are more parasites on the right than left. A log2 ratio of one corresponds to a one-fold difference, i.e. double the number of parasites. Perfect symmetry is a log2 ratio of zero.

Examples

```
plotHistogram(diplostomum_eyes_excl_lenses)
plotHistogram(diplostomum_eyes_excl_lenses,nBreaks=20,
main="Diplostomum metacercariae in eyes of ruffe")
```

`plotVolcano` *Volcano plot*

Description

Produces scatterplot of statistical significance vs fold difference in parasite abundance between left and right.

Usage

```
plotVolcano(x, test = "G", pAdj = "BH", sigThresh = 0.05, ...)
```

Arguments

`x`	a matrix or data frame with two numeric columns; first column is for left-side and 2nd column for right-side. Identifiers for hosts can be provided as row names.
`test`	if set to "G" (default) a G-test is performed; otherwise an exact binomial test is performed.
`pAdj`	method for correcting p-values for multiple comparisons. If set to "BH" (default), Benjamini & Hochberg’s procedure is used to control the false discovery rate (FDR); otherwise Holm’s methos is used to control the familywise error rate (FWER).
`sigThresh`	significance threshold (defaults to 0.05); p-values below this value will be called significant.
`...`	optional further arguments and graphical parameters passed to plot.

Details

plot.Volcano creates a volcano plot, i.e. a scatterplot of statistical significance (-log10(p-value)) vs fold difference (log2 ratio - as calculated for the histogram above) in parasite abundance between left and right. Each point in the scatterplot represents the parasite distribution in an individual host. A dashed horizontal line represents the user-defined p-value threshold for significance. If a parasite distribution deviates significantly from symmetry it is shown as a red square, otherwise as a blue circle.

Examples

```
plotVolcano(diplostomum_eyes_excl_lenses)
plotVolcano(diplostomum_eyes_excl_lenses, test="G", pAdj="BH", sigThresh=0.1,
main="Diplostomum metacercariae in eyes of ruffe")
```

`simulated_asymmetry_inconsistent_bias` *Simulated data showing bilateral asymmetry with insconsistent bias*

Description

Simulated data for 10 hosts, providing an example of bilateral asymmetry with inconsistent bias.

Usage

```
simulated_asymmetry_inconsistent_bias
```

Format

A data frame with 10 rows and 2 variables:

left number of parasites on the left side

right number of parasites on the right side

`simulated_left_bias_heterogeneous_proportions` *Simulated data showing left bias with heterogeneous proportions*

Description

Simulated data for 10 hosts, providing an example of bilateral asymmetry with left bias and the left:right ratio varying between hosts.

Usage

```
simulated_left_bias_heterogeneous_proportions
```

Format

A data frame with 10 rows and 2 variables:

left number of parasites on the left side

right number of parasites on the right side

`simulated_left_bias_homogeneous_proportions`

Simulated data for showing left bias with homogeneous proportions

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Description

Simulated data for 10 hosts, providing an example of bilateral asymmetry with left bias and a similar left:right ratio in all hosts.

Usage

```
simulated_left_bias_homogeneous_proportions
```

Format

A data frame with 10 rows and 2 variables:

left	number of parasites on the left side
right	number of parasites on the right side

`simulated_symmetrical_infection`

Simulated data showing bilateral symmetry

Description

Simulated data for 10 hosts, providing an example of bilateral symmetry.

Usage

```
simulated_symmetrical_infection
```

Format

A data frame with 10 rows and 2 variables:

left	number of parasites on the left side
right	number of parasites on the right side

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