

Package ‘mbRes’

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Suggests RProbSup (>= 3.0)

BugReports <https://github.com/phamdn/mbRes/issues>

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mbRes-package	<i>mbRes: Exploration of Multiple Biomarker Responses using Effect Size</i>
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Description

Summarize multiple biomarker responses of aquatic organisms to contaminants using Cliff's delta, as described in Pham & Sokolova (in press).

Guidelines

`mbr` and `visual` are the main functions to compute and visualize Cliff's delta and S-value. `setpop`, `simul`, and `plotsam` simulate and visualize a hypothetical dataset. `compare` compares the results of Cliff's delta and two other integrated indices published earlier (i.e., RSI and IBR). The others are helper functions and are not meant to be called directly by users.

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Author(s)

Duy Nghia Pham & Inna M. Sokolova

`beliaeff2002`*Compute Integrated Biomarker Index*

Description

`beliaeff2002` calculates IBR in the hypothetical case study. This is not meant to be called directly.

Usage

```
beliaeff2002(sam_mean)
```

Arguments

`sam_mean` a data frame, the third output of [simul](#).

Value

`beliaeff2002` returns a data frame of IBR.

References

Beliaeff, B., & Burgeot, T. (2002). Integrated biomarker response: A useful tool for ecological risk assessment. *Environmental Toxicology and Chemistry*, 21(6), 1316–1322. doi:10.1002/etc.5620210629.

`blaise2002`*Compute Rank Sum Biomarker Index*

Description

`blaise2002` calculates RSI in the hypothetical case study. This is not meant to be called directly.

Usage

```
blaise2002(sam, sam_mean)
```

Arguments

`sam` a data frame, the first output of [simul](#).
`sam_mean` a data frame, the third output of [simul](#).

Value

`blaise2002` returns a data frame of RSI.

References

Blaise, C., Gagné, F., Pellerin, J., Hansen, P.-D., & Trottier, S. (2002). Molluscan shellfish biomarker study of the Quebec, Canada, Saguenay Fjord with the soft-shell clam, *Mya arenaria*. *Environmental Toxicology*, 17(3), 170–186. doi:10.1002/tox.10048.

cliff

Compute Effect Size

Description

cliff calculates Cliff's delta statistic using the rank sum method.

Usage

```
cliff(v1, v0)
```

Arguments

v1 a vector, biomarker values from the treatment group.
v0 a vector, biomarker values from the control group.

Value

cliff returns a numeric that is the Cliff's delta of the treatment group.

References

Cliff, N. (1993). Dominance statistics: Ordinal analyses to answer ordinal questions. *Psychological Bulletin*, 114(3), 494–509. doi:10.1037/00332909.114.3.494.

Vargha, A., & Delaney, H. D. (2000). A Critique and Improvement of the CL Common Language Effect Size Statistics of McGraw and Wong. *Journal of Educational and Behavioral Statistics*, 25(2), 101–132. doi:10.3102/10769986025002101.

Ruscio, J., & Mullen, T. (2012). Confidence Intervals for the Probability of Superiority Effect Size Measure and the Area Under a Receiver Operating Characteristic Curve. *Multivariate Behavioral Research*, 47(2), 201–223. doi:10.1080/00273171.2012.658329.

See Also

[CalcA1](#).

Examples

```
set.seed(1)
setting <- setpop()
temp <- simul(setting$pop_mean)
cliff(subset(temp$sam, Site == "S1", Bmk1, drop = TRUE),
subset(temp$sam, Site == "S0", Bmk1, drop = TRUE))
```

compare

*Compare RSI, IBR, and Cliff's delta***Description**

compare calculates RSI assigned values, IBR translated scores, and Cliff's delta in the hypothetical case study.

Usage

```
compare(sam, sam_mean)
```

Arguments

sam a data frame, the first output of [simul](#).
sam_mean a data frame, the third output of [simul](#).

Value

compare returns a list of length 5:

blaise RSI assigned values and final RSI.
beliaeff IBR translated scores and final IBR.
pham Cliff's delta and the average of absolute Cliff's delta.
fig1 ggplot object of comparisons among RSI assigned values, IBR translated scores, and Cliff's delta.
fig2 ggplot object of comparison among RSI, IBR, and the average of absolute Cliff's delta.

References

Blaise, C., Gagné, F., Pellerin, J., Hansen, P.-D., & Trottier, S. (2002). Molluscan shellfish biomarker study of the Quebec, Canada, Saguenay Fjord with the soft-shell clam, *Mya arenaria*. *Environmental Toxicology*, 17(3), 170–186. doi:10.1002/tox.10048.

Beliaeff, B., & Burgeot, T. (2002). Integrated biomarker response: A useful tool for ecological risk assessment. *Environmental Toxicology and Chemistry*, 21(6), 1316–1322. doi:10.1002/etc.5620210629.

Examples

```
set.seed(1)
setting <- setpop()
temp <- simul(setting$pop_mean)
compare(temp$sam, temp$sam_mean)
#might take more than 5s in some machines
```

ggdot

Make Dot Plot

Description

ggdot creates dot plot of the average of absolute Cliff's delta. This is not meant to be called directly.

Usage

```
ggdot(dat, hax, vax)
```

Arguments

dat	a data frame with at least two columns.
hax	a character, name of the column to be used as the horizontal axis.
vax	a character, name of the column to be used as the vertical axis.

Value

ggdot returns a ggplot object.

ggheat

Make Heatmap

Description

ggheat creates heatmaps of the Cliff's delta and S-value. This is not meant to be called directly.

Usage

```
ggheat(
  dat,
  hax,
  vax,
  cell,
  nm,
  lim,
  lo,
  hi,
  diverging = FALSE,
  env = parent.frame()
)
```

Arguments

dat	a data frame with at least three columns.
hax	a character, name of the column to be used as the horizontal axis.
vax	a character, name of the column to be used as the vertical axis.
cell	a character, name of the column to be used as the cells.
nm	a character, name of the heatmap.
lim	a numeric vector, limits of the color scale.
lo	a character, color of the color scale low end.
hi	a character, color of the color scale high end.
diverging	a logical, whether to use diverging color gradient.
env	an environment, to access outer scope variables.

Value

ggheat returns a ggplot object.

mbr

Compute Cliff's delta and S-value

Description

mbr summarizes Cliff's delta and S-value for multiple groups and multiple biomarkers.

Usage

```
mbr(df)
```

Arguments

`df` a data frame with the name of experimental groups or biomonitoring sites as the first column and the measurement of biomarkers as the remaining columns.

Details

The header of the first column can be any character, for example, 'group' or 'site'. The first name appearing in the first column will determine the control group or the reference site. The other names will be treatment groups or test sites. The header of the remaining columns will define the list of biomarkers.

Value

`mbr` returns a list of length 3:

`mess` a list of length 3 confirms the information about `df`.

`es` a data frame with 9 columns:

`test_site` treatment groups or test sites.

`ref_site` control group or reference site.

`t_size` the sample size of treatment group or test sites.

`r_size` the sample size of control group or reference site.

`biomarker` individual biomarker.

`delta` the Cliff's delta of treatment group or reference site.

`delta.abs` the absolute Cliff's delta.

`pval` the P-Value.

`sval` the surprisal or S-Value.

`idx` a data frame summarizes `delta.abs` and their average.

Examples

```
set.seed(1)
setting <- setpop()
temp <- simul(setting$pop_mean)
mbr(temp$sam)
#might take more than 5s in some machines
```

plotsam	<i>Visualize Hypothetical Samples</i>
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Description

plotsam plots the sample dataset of biomarker responses. This is used for the hypothetical case study.

Usage

```
plotsam(pop_mean_long, pop_profile, sam_long)
```

Arguments

pop_mean_long a data frame, the second output of [setpop](#).
pop_profile a data frame, the third output of [setpop](#).
sam_long a data frame, the second output of [simul](#).

Value

plotsam returns a ggplot object.

Examples

```
set.seed(1)  
setting <- setpop()  
temp <- simul(setting$pop_mean)  
plotsam(setting$pop_mean_long, setting$pop_profile, temp$sam_long)
```

resampling	<i>Measure Statistical Uncertainty</i>
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Description

resampling performs randomization test to calculate P-value and S-value.

Usage

```
resampling(v1, v0, nrand = 1999, seed = 1)
```

Arguments

<code>v1</code>	a vector, biomarker values from the treatment group.
<code>v0</code>	a vector, biomarker values from the control group.
<code>nrand</code>	an integer, the number of randomization samples. The default value is 1999.
<code>seed</code>	an integer, the seed for random number generation. Setting a seed ensures the reproducibility of the result. See set.seed for more details.

Value

`resampling` returns a one-row data frame with 3 numerics:

<code>delta</code>	the Cliff's delta of the treatment group.
<code>pval</code>	the observed P-value p under the null hypothesis.
<code>sval</code>	the S-value s calculated from P-value p .

References

Greenland, S. (2019). Valid P-Values Behave Exactly as They Should: Some Misleading Criticisms of P-Values and Their Resolution With S-Values. *The American Statistician*, 73(sup1), 106–114. doi:10.1080/00031305.2018.1529625.

Phipson, B., & Smyth, G. K. (2010). Permutation P-values Should Never Be Zero: Calculating Exact P-values When Permutations Are Randomly Drawn. *Statistical Applications in Genetics and Molecular Biology*, 9(1). doi:10.2202/15446115.1585.

See Also

[A1](#).

Examples

```
set.seed(1)
setting <- setpop()
temp <- simul(setting$pop_mean)
resampling(subset(temp$sam, Site == "S1", Bmk1, drop = TRUE),
subset(temp$sam, Site == "S0", Bmk1, drop = TRUE))
```

setpop

Define Hypothetical Populations

Description

`setpop` sets the true means of biomarker responses in populations. This is used for the hypothetical case study.

Usage

```
setpop()
```

Value

setpop returns a list of length 3:

pop_mean	true means of biomarker responses in populations.
pop_mean_long	true means of biomarker responses in long format.
pop_profile	profile of biomarkers.

simul	<i>Generate Hypothetical Samples</i>
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Description

simul yields a sample dataset of biomarker responses. This is used for the hypothetical case study.

Usage

```
simul(pop_mean, size = 75)
```

Arguments

pop_mean	a data frame, the first output of setpop.
size	an integer, the sample size.

Value

simul returns a list of length 3:

sam	sample dataset.
sam_long	sample dataset in long format.
sam_mean	sample means of biomarker responses.

visual	<i>Visualize Cliff's delta and S-value</i>
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Description

visual plots Cliff's delta and S-value for multiple groups and multiple biomarkers.

Usage

```
visual(rs, rotate = FALSE, display = TRUE)
```

Arguments

rs	a list, output of <code>mbr</code> .
rotate	a logical, whether to rotate the biomarker labels in figures.
display	a logical, whether to display cell values in heatmaps.

Value

visual returns a list of ggplot objects:

fig.delta	heatmap of Cliff's delta.
fig.sval	heatmap of S-value.
fig.avg	dot plot of the average of absolute Cliff's delta.
mbr_fig	combined heatmaps of Cliff's delta and S-value.

Examples

```
set.seed(1)
setting <- setpop()
temp <- simul(setting$pop_mean)
mbr_result <- mbr(temp$sam)
visual(mbr_result)
#might take more than 5s in some machines
```

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