

# Package ‘mbRes’

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**Type** Package

**Title** Exploration of Multiple Biomarker Responses using Effect Size

**Version** 0.1.7

**Description** Summarize multiple biomarker responses of aquatic organisms to contaminants using Cliff’s delta, as described in Pham & Sokolova (2023) <[doi:10.1002/ieam.4676](https://doi.org/10.1002/ieam.4676)>.

**Depends** R (>= 4.2.0)

**Imports** stats, ggplot2 (>= 3.4.1), cowplot (>= 1.1.1), magrittr (>= 2.0.3), tibble (>= 3.2.1), dplyr (>= 1.1.1), forcats (>= 1.0.0), tidyr (>= 1.3.0), purrr (>= 1.0.1), data.table (>= 1.14.8), scales (>= 1.2.1)

**Suggests** RProbSup (>= 3.0)

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

**License** GPL-3

**Encoding** UTF-8

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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 (2023) [doi:10.1002/ieam.4676](https://doi.org/10.1002/ieam.4676).

## Guidelines

`mbr` and `visual` are the main functions to compute and visualize Cliff's delta and S-value which are results of `cliff` and `resampling`. `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, see [blaise2002](#) and [beliaeff2002](#)). The others (`ggheat` and `ggdot`) are helper functions and are not meant to be called directly by users.

## Updates

`mbr.cliff` and `mbr.glass` simply compute and visualize Cliff's delta and Glass's delta.

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**Author(s)**

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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](https://doi.org/10.1002/etc.5620210629).

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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.

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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
```



---

mbr.cliff                      *Compute Cliff's delta simplified*

---

**Description**

mbr.cliff summarizes Cliff's delta for multiple groups and multiple biomarkers.

**Usage**

```
mbr.cliff(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.

**Examples**

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

---

mbr.glass                      *Compute Glass's delta simplified*

---

**Description**

mbr.glass summarizes Glass's delta for multiple groups and multiple biomarkers.

**Usage**

```
mbr.glass(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.

## Examples

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

---

plotsam

*Visualize Hypothetical Samples*

---

## 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`*Measure Statistical Uncertainty*

---

**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 <a href="#">set.seed</a> 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

*Generate Hypothetical Samples*


---

**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>
--------	--

---

**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 <a href="#">mbr</a> .
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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