Package 'peramo'

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Type Package

Title Permutation Tests for Randomization Model

Version 0.1.1

Description Perform permutation-based hypothesis testing for randomized experiments as described in Ernst (2004) <doi:10.1214/088342304000000396> and Manly (2007) <isbn:978-1-58488-541-2>.

Depends R (>= 4.2.0)

Imports magrittr (>= 2.0.3), dplyr (>= 1.0.10), stats, utils

Suggests multcompView(>= 0.1-8)

BugReports `https://github.com/phamdn/peramo/issues`

License GPL-3

Encoding UTF-8

RoxygenNote 7.2.3

LazyData true

NeedsCompilation no

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R topics documented:

`peramo-package` *peramo: Permutation Tests for Randomization Model*

Description

Perform permutation-based hypothesis testing for randomized experiments as described in Ernst (2004) doi:10.1214/088342304000000396 and Manly (2007) <isbn:978-1-58488-541-2>.

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Author(s)

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`AB` *Two-Group Permutation Test*

Description

`AB` performs A/B testing for two-group experiments.

Usage

```
AB(a, b, rand = 9999, seed = 1)
```

Arguments

`a`	the measurement of responses of the first group.
`b`	the measurement of responses of the second group.
`rand`	an integer, the number of randomization samples. The default value is 9999.
`seed`	an integer, the seed for random number generation. Setting a seed ensures the reproducibility of the result. See `set.seed` for more details.

Value

`AB` returns an one-row data frame with 6 columns:

`nA`	the sample size of the first group.
`mean.A`	the mean responses of the first group.
`nB`	the sample size of the second group.
`mean.B`	the mean responses of the second group.
`mean.dif`	the difference between two mean responses.
`pval`	the p-value.

References

Ernst, M. D. (2004). Permutation Methods: A Basis for Exact Inference. Statistical Science, 19(4), 676–685. doi:10.1214/088342304000000396.

Examples

```
AB(c(19, 22, 25, 26), c (23, 33, 40))
```

`copper` *Biomarker Responses of the Ragworms to Copper and Warming*

Description

Biomarker Responses of the Ragworms to Copper and Warming

Usage

```
Cu

bmk_worm
```

Format

An object of class `data.frame` with 60 rows and 6 columns.

An object of class `data.frame` with 210 rows and 22 columns.

`diffcalc` *Calculate the Differences between Means*

Description

Calculate the Differences between Means

Usage

```
diffcalc(vec, control)
```

Arguments

`vec`	a numeric vector, the mean responses.
`control`	a logical, whether the control group exists.

`ensulizole` *Biomarker Responses of the Blue Mussels to Organic UV Filters*

Description

Biomarker Responses of the Blue Mussels to Organic UV Filters

Usage

```
SoS

bmk_gill

bmk_digest
```

Format

An object of class `data.frame` with 15 rows and 7 columns.

An object of class `data.frame` with 120 rows and 24 columns.

An object of class `data.frame` with 120 rows and 24 columns.

Source

Pham, D. N., Sokolov, E. P., Falfushynska, H., & Sokolova, I. M. (2022). Gone with sunscreens: Responses of blue mussels (Mytilus edulis) to a wide concentration range of a UV filter ensulizole. Chemosphere, 309, 136736. doi:10.1016/j.chemosphere.2022.136736.

`nolesser` *Compare the Differences with Critical Values*

Description

Compare the Differences with Critical Values

Usage

```
nolesser(obs, cric)
```

Arguments

`obs`	a numeric, the observed difference.
`cric`	a numeric, the critical values of maximum absolute differences.

`owl` *One-Way Layout Permutation Test*

Description

`owl` performs the global test and multiple comparisons for single factor experiments.

Usage

```
owl(df, rand = 9999, alpha.post = 0.05, type.post = "control", seed = 1)
```

Arguments

`df`	a data frame with the name of experimental groups as the first column and the measurement of responses as the remaining columns.
`rand`	an integer, the number of randomization samples. The default value is 9999.
`alpha.post`	a numeric, the Type I error rate for multiple comparisons. The default value is 0.05.
`type.post`	the way of multiple comparisons, "all" for pairwise comparisons or "control" for only comparisons with the control group.
`seed`	an integer, the seed for random number generation. Setting a seed ensures the reproducibility of the result. See `set.seed` for more details.

Details

The first name appearing in the first column will determine the control group. The other names will be treatment groups.

Value

`owl` returns a list with 9 components:

`n.obs`	the sample sizes.
`avg.obs`	the mean responses.
`T.obs`	the T statistic for global test.
`pval`	the p-value for global test.
`pval.round`	the reported form of p-value.
`main.test`	the strength of evidence against the null hypothesis.
`d.multi.obs`	the differences in means for multiple comparisons.
`mad.cric`	the critical value of maximum absolute differences in means.
`post.test`	`TRUE` if the differences are significant.

References

Ernst, M. D. (2004). Permutation Methods: A Basis for Exact Inference. Statistical Science, 19(4), 676–685. doi:10.1214/088342304000000396.

Muff, S., Nilsen, E. B., O'Hara, R. B., & Nater, C. R. (2022). Rewriting results sections in the language of evidence. Trends in Ecology & Evolution, 37(3), 203–210. doi:10.1016/j.tree.2021.10.009.

Examples

```
ernst2004 <- data.frame(
group = factor(rep(c("style1", "style2", "style3"), each = 5 ),
levels = c("style1", "style2", "style3")),
speed = c( 135,91,111,87, 122, 175,130,514,283, NA,105,147,159,107,194))
owl(ernst2004, type.post = "all")
```

`owlStat` *Test Statistics for One-Way Layout Permutation Test*

Description

`owlStat` computes statistics for `owl`. This is not meant to be called directly.

Usage

```
owlStat(lov, env = parent.frame())
```

Arguments

`lov`	a list of vectors, responses by experimental groups.
`env`	an environment, to access outer scope variables.

Value

`owlStat` returns a list with 5 components:

`n`	the sample sizes.
`avg`	the mean responses.
`T`	the T statistic for global test.
`d.multi`	the differences in means for multiple comparisons.
`mad`	the maximum absolute differences in means.

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References

Ernst, M. D. (2004). Permutation Methods: A Basis for Exact Inference. Statistical Science, 19(4), 676–685. doi:10.1214/088342304000000396.

`twl` *Two-Way Layout Permutation Test*

Description

`twl` performs the global test and multiple comparisons for two-factor experiments.

Usage

```
twl(
  df,
  rand = 4999,
  seed = 1,
  mult = FALSE,
  simple = TRUE,
  control = TRUE,
  alpha = 0.05
)
```

Arguments

`df`	a data frame with the first and second columns containing the levels of the two main factors and the third column containing the measurement of responses.
`rand`	an integer, the number of randomization samples. The default value is 4999.
`seed`	an integer, the seed for random number generation. Setting a seed ensures the reproducibility of the result. See `set.seed` for more details.
`mult`	a logical, whether to perform multiple comparisons.
`simple`	a logical, whether to perform comparisons for simple effects.
`control`	a logical, whether to perform only comparisons with the control group.
`alpha`	a numeric, the Type I error rate for multiple comparisons. The default value is 0.05.

Details

The first levels appearing in the first and second columns will determine the control groups (if any). The other levels will be treatment groups.

Value

`twl` returns a list with possible components:

`n`, `n.main1`, and `n.main2`	the sample sizes.
`avg`, `avg.main1`, and `avg.main2`	the mean responses.
`Fs`	the F statistics, p-values, reported form of p-value, and strength of evidence against the null hypotheses.
`d.main1sub` and `d.main2sub` or `d.main1` and `d.main2`	the differences in means for multiple comparisons.
`mad.main1sub.cric` and `mad.main2sub.cric` or `mad.main1.cric` and `mad.main2.cric`	the critical value of maximum absolute differences in means.
`mult.test.main1sub` and `mult.test.main2sub` or `mult.test.main1` and `mult.test.main2`	`TRUE` if the differences are significant.

References

Manly, B. F. J. (2007). Randomization, bootstrap, and Monte Carlo methods in biology (3rd ed). Chapman & Hall/ CRC.

Ernst, M. D. (2004). Permutation Methods: A Basis for Exact Inference. Statistical Science, 19(4), 676–685. doi:10.1214/088342304000000396.

Muff, S., Nilsen, E. B., O'Hara, R. B., & Nater, C. R. (2022). Rewriting results sections in the language of evidence. Trends in Ecology & Evolution, 37(3), 203–210. doi:10.1016/j.tree.2021.10.009.

Motulsky, H. (2020). GraphPad Statistics Guide. GraphPad Software Inc. `https://www.graphpad.com/guides/prism/latest/statistics/index.htm`.

Examples

```
manly2007 <- data.frame(
month = factor(rep(c("jun", "jul", "aug", "sep"), each = 6 ),
levels = c("jun", "jul", "aug", "sep")),
size = factor(rep(c("small", "large"), each = 3, times = 4),
levels = c("small", "large")),
consume = c( 13,242,105,182,21,7,8,59,20,24,312,68,515,488,88,460,1223,990,18,44,21,140,40,27))
twl(manly2007)
twl(manly2007, mult = TRUE, simple = TRUE, control = FALSE)
 #might take more than 5s in some machines
```

`twlStat` *Test Statistics for Two-Way Layout Permutation Test*

Description

`twlStat` computes statistics for `twl`. This is not meant to be called directly.

Usage

```
twlStat(df, env = parent.frame())
```

Arguments

`df`	a data frame with the levels of the two main factors as the first and second columns and the measurement of responses as the third column.
`env`	an environment, to access outer scope variables.

Value

`twlStat` returns a list with at least 4 components:

`Fs`	the F statistics for global test.
`F.main1` and `F.main2`	the F statistics for the first main factor and the second main factor.
`F.int`	the F statistic for the interaction.

In case of multiple comparisons, additional components are:

`avg` or `avg.main1` and `avg.main2`	the mean responses for multiple comparisons.
`d.main1sub` and `d.main2sub` or `d.main1` and `d.main2`	the differences in means.
`mad.main1sub` and `mad.main2sub` or `mad.main1` and `mad.main2`	the maximum absolute differences in means.

References

Manly, B. F. J. (2007). Randomization, bootstrap, and Monte Carlo methods in biology (3rd ed). Chapman & Hall/ CRC.

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