Package ‘RHSDB’

October 25, 2022

Type Package

Title Ryan-Holm Step-Down Bonferroni or Sidak Procedure

Version 0.2.0

Description The Ryan-Holm step-down Bonferroni or Sidak procedure is to control the family-wise (experiment-wise) type I error rate in the multiple comparisons. This procedure provides the adjusting p-values and adjusting CIs. The methods used in this package are referenced from John Ludbrook (2000) <doi:10.1046/j.1440-1681.2000.03223.x>.

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NeedsCompilation no

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Description

This procedure provides the adjusting p-values and adjusting CIs.
rh.sd.bonferroni

Usage

rh.sd.bonferroni(p, effect, effect.se, df, type, sig, side, digits)

Arguments

- `p`: the raw p values
- `effect`: the effect size from the multiple comparisons, e.g. the mean difference from t test or paried t test
- `effect.se`: the standard error of effect size from the multiple comparisons, e.g. the standard error of mean difference from t test or paried t test
- `df`: the degree of freedom of hypothesis test, e.g. n1+n2-2 for t test, n-1 for paried t test
- `type`: the type of the effect size, default is "mean"
- `sig`: the significance level, default is 0.05
- `side`: "one" or "two" sided hypothesis test
- `digits`: the number of decimal digits

Value

- `p.adj`: the adjusted p value
- `ci.adj.l`: the lower limit of adjusted confidence interval
- `ci.adj.u`: the upper limit of adjusted confidence interval

Note

Please feel free to contact us, if you have any advice and find any bug!

Reference:

Update:
Version 0.1.0: The first version.
Version 0.2.0: Fix the bug for maintaining monotonicity of the ranking p-values.

See Also

- `rh.sd.sidak`

Examples

```r
p <- c(0.217, 0.00028, 0.001, 0.024, 0.719, 0.00033)
effect <- c(16, 74, -85, -38, 29, 5, 91)
effect.se <- c(12, 16, 14, 9, 12, 16, 20)
df <- 16
rh.sd.bonferroni(p, effect, effect.se, df)
```
**Description**

This procedure provides the adjusting p-values and adjusting CIs.

**Usage**

```
rh.sd.sidak(p, effect, effect.se, df, type, sig, side, digits)
```

**Arguments**

- `p`: the raw p values
- `effect`: the effect size from the multiple comparisons, e.g. the mean difference from t test or paried t test
- `effect.se`: the standard error of effect size from the multiple comparisons, e.g. the standard error of mean difference from t test or paried t test
- `df`: the degree of freedom of hypothesis test, e.g. n1+n2-2 for t test, n-1 for paried t test
- `type`: the type of the effect size, default is "mean"
- `sig`: the significance level, default is 0.05
- `side`: "one" or "two" sided hypothesis test
- `digits`: the number of decimal digits

**Value**

- `p.adj`: the adjusted p value
- `ci_adj.l`: the lower limit of adjusted confidence interval
- `ci_adj.u`: the upper limit of adjusted confidence interval

**Note**

Please feel free to contact us, if you have any advice and find any bug!

Reference:


Update:

- Version 0.1.0: The first version.
- Version 0.2.0: Fix the bug for maintaining monotonicity of the ranking p-values.

**See Also**

`rh.sd.bonferroni`
Examples

```r
p <- c(0.217, 0.00028, 0, 0.001, 0.024, 0.719, 0.00033)
effect <- c(16, 74, -85, -38, 29, 5, 91)
effect.se <- c(12, 16, 14, 9, 12, 16, 20)
df <- 16
rh.sd.sidak(p, effect, effect.se, df)
```
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