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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R topics documented:

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rh.sd.bonferroni   *Ryan-Holm Step-Down Bonferroni Procedure*

Description

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

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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:

1. John Ludbrook (2000). MULTIPLE INFERENCES USING CONFIDENCE INTERVALS. Clinical and Experimental Pharmacology and Physiology. 27: 212-215.

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

```
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.bonferroni(p,effect,effect.se,df)
```

rh.sd.sidak	*Ryan-Holm Step-Down Sidak Procedure*

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:

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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

```
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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