# Package 'ScottKnottESD'

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Type Package

Version 2.0.3

Title The Scott-Knott Effect Size Difference (ESD) Test

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| Description  The Scott-Knott Effect Size Difference (ESD) test is a mean comparison approach that leverages a hierarchical clustering to partition the set of treatment means (e.g., means of variable importance scores, means of model performance) into statistically distinct groups with non-negligible difference [Tantithamthavorn et al., (2018) <doi:10.1109 tse.2018.2794977="">].</doi:10.1109> |
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| ScottKnottESD-package "check.ANOVA.assumptions" "long2wide" "normalize" example maven print.sk_esd sk_esd  |

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ScottKnottESD-package The Scott-Knott Effect Size Difference (ESD) Test

#### **Description**

The Scott-Knott Effect Size Difference (ESD) test is a mean comparison approach that leverages a hierarchical clustering to partition the set of treatment means (e.g., means of variable importance scores, means of model performance) into statistically distinct groups with non-negligible difference [Tantithamthavorn et al., (2018) <doi:10.1109/TSE.2018.2794977>]. It is an alternative approach of the Scott-Knott test that considers the magnitude of the difference (i.e., effect size) of treatment means with-in a group and between groups. Therefore, the Scott-Knott ESD test (v2.x) produces the ranking of treatment means while ensuring that (1) the magnitude of the difference for all of the treatments in each group is negligible; and (2) the magnitude of the difference of treatments between groups is non-negligible.

The mechanism of the Scott-Knott ESD test (v2.x) is made up of 2 steps:

(Step 1) Find a partition that maximizes treatment means between groups. We begin by sorting the treatment means. Then, following the original Scott-Knott test, we compute the sum of squares between groups (i.e., a dispersion measure of data points) to identify a partition that maximizes treatment means between groups.

(Step 2) Splitting into two groups or merging into one group. Instead of using a likelihood ratio test and a Chi-square distribution as a splitting and merging criterion (i.e., a hypothesis testing of the equality of all treatment means), we analyze the magnitude of the difference for each pair for all of the treatment means of the two groups. If there is any one pair of treatment means of two groups are non-negligible, we split into two groups. Otherwise, we merge into one group. We use the Cohen effect size — an effect size estimate based on the difference between the two means divided by the standard deviation of the two treatment means  $(d = (mean(x_1) - mean(x_2))/s.d.)$ .

Unlike the earlier version of the Scott-Knott ESD test (v1.x) that post-processes the groups that are produced by the Scott-Knott test, the Scott-Knott ESD test (v2.x) pre-processes the groups by merging pairs of statistically distinct groups that have a negligible difference.

#### **Details**

Package: ScottKnottESD

Type: Package
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## Author(s)

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Maintainer: Chakkrit (Kla) Tantithamthavorn <kla@chakkrit.com>

#### References

Chakkrit Tantithamthavorn, Shane McIntosh, Ahmed E. Hassan, Kenichi Matsumoto, An Empirical Comparison of Model Validation Techniques for Defect Prediction Models. IEEE Transactions on Software Engineering. 43(1): 1-18 (2017). <doi:10.1109/TSE.2016.2584050>

Chakkrit Tantithamthavorn, Shane McIntosh, Ahmed E. Hassan, Kenichi Matsumoto, The Impact of Automated Parameter Optimization for Defect Prediction Models. IEEE Transactions on Software Engineering. Early Access. (2018). <doi:10.1109/TSE.2018.2794977>

#### See Also

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#### **Examples**

```
library(ScottKnottESD)
sk <- sk_esd(example)
plot(sk)
sk <- sk_esd(maven)
plot(sk)</pre>
```

"check.ANOVA.assumptions"

Check basic ANOVA assumptions

### **Description**

Check the normality assumption of the input dataset using the Kolmogorov-Smirnov Test and the homogeneity of variances assumption of the input dataset using the Levene's test.

## Usage

```
check.ANOVA.assumptions(x, alpha = 0.05, ...)
```

## Arguments

```
x A wide-format data frame.alpha The significance level.... Optional parameters.
```

#### Value

A wide-format data frame.

"long2wide"

### Author(s)

Chakkrit Tantithamthavorn (kla@chakkrit.com)

## **Examples**

```
check.ANOVA.assumptions(example)
```

"long2wide"

Convert data from long format to wide format

## Description

Convert data from long format to wide format

## Usage

```
long2wide(x, ...)
```

## Arguments

x A long-format data frame.

... Optional parameters.

#### Value

A wide-format data frame.

## Author(s)

Chakkrit Tantithamthavorn (kla@chakkrit.com)

## **Examples**

```
long2wide(melt(example, id.vars=0))
```

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"normalize"

Normalize non-normal distributions using the Box-Cox Power Transformation

## Description

Normalize non-normal distributions using the Box-Cox Power Transformation

## Usage

```
normalize(x, ...)
```

## Arguments

x A wide-format data frame.

... Optional parameters.

## Value

A wide-format data frame.

#### Author(s)

Chakkrit Tantithamthavorn (kla@chakkrit.com)

## **Examples**

```
normalized.data <- normalize(example)</pre>
```

example

An example dataset of Breiman's variable importance scores

## Description

A dataset containing software metrics of 1,000 calculation of Breiman's variable importance scores

## Usage

example

6 maven

#### **Format**

A data frame with 1,000 rows and 9 variables:

LOC lines of code

Components the numbers of components

Subsystem the numbers of subsystems

**Files** the numbers of files

**Commit** the numbers of commits

Churn the numbers of churns

Ownership ownership

Authorship authorship

Experience developer's experience ...

#### Source

https://github.com/klainfo/ScottKnottESD/

maven

An example dataset of Breiman's variable importance scores

#### **Description**

A dataset containing software metrics of 1,000 calculation of Breiman's variable importance scores

## Usage

maven

#### **Format**

A data frame with 1,000 rows and 27 variables:

Avg\_CloneLineCount An average physical lines of clone siblings of a clone.

**Avg\_CountLineComment** An average comment lines in the methods that contain clone siblings of a clone.

**Avg\_Cyclomatic** McCabe Cyclomatic complexity of the method that contains the clone.

**Avg\_ImproveCommitCount** Number of commits that impact the method containing the clone.

Avg\_LineAdded Number of lines added into the method that contains the clone.

Avg\_LineCodeCount Number of source code lines in the method that contains the clone.

**Avg\_MaxNesting** Maximum nesting level of control constructs in the method that contains the clone.

**Avg\_NewFeatureCommitCount** Number of commits that introduce new feature and that impact the method containing the clone.

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Avg\_RatioCommentToCode Ratio of CommentLineCount to LineCodeCount.

Avg\_RatioLineCodeCount Ratio of LineCount to CloneLineCount.

Avg\_TokenCount Number of tokens in the clone.

**CloneType** Type of clone class to which the clone belongs.

**Diff\_CloneLineCount** Number of physical lines in the clone.

**Diff\_CountLineComment** Number of comment lines in the method that contains the clone.

**Diff\_Cyclomatic** McCabe Cyclomatic complexity of the method that contains the clone.

**Diff\_DeveloperCount** Number of distinct developers who modified the method that contains the clone.

**Diff\_Essential** Numberical measure of structuredness of the method that contains the clone.

Diff\_FanIn Number of unique methods that call the method containg the clone.

**Diff\_FanOut** Number of unique methods that are called by the method containing the clone.

**Diff\_FixCommitCount** Number of commits with a description of fixing bugs and that impact the method containing the clone.

**Diff\_LineCodeDeclCount** Number of declarative source code lines in the method that contains the clone.

**Diff\_LineCount** Number of lines in the method that contains the clone.

**Diff\_LineDeleted** Number of lines deleted from the method that contains the clone.

**Diff\_NewFeatureCommitCount** Number of commits that introduce new feature and that impact the method containing the clone.

**Diff\_TokenCount** Number of tokens in the clone.

**Max\_DirectoryDistance** Number of directories that are traversed from the method containing one sibling to the method containing another sibling of the clone.

**SiblingCount** Number of clone siblings in the clone.

#### **Source**

https://github.com/klainfo/ScottKnottESD/

print.sk\_esd

Print sk\_esd objects

#### **Description**

S3 method to print sk\_esd objects.

#### Usage

```
## S3 method for class 'sk_esd'
print(x, ...)
```

 $8 sk_esd$ 

#### **Arguments**

x A sk\_esd object

... Optional parameters.

#### Value

The sk.esd ranks

sk\_esd A function to check the magnitude of the difference for all pairs of treatments

### **Description**

A function to check the magnitude of the difference for all pairs of treatments

An enhancement of the Scott-Knott test (which cluster distributions into statistically distinct ranks) that takes effect size into consideration.

### Usage

```
checkDifference(ranking, data)
sk_esd(x, alpha = 0.05, ...)
```

### **Arguments**

ranking A ranking that is produced by the Scott-Knott ESD test
data a data frame of treatment means

x A wide-format data frame.

alpha The significance level.

... Optional parameters.

## Value

A result of the magnitude of the difference for all pairs of treatments.

A sk\_esd object.

## Author(s)

Chakkrit Tantithamthavorn (kla@chakkrit.com)

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# Examples

```
sk <- sk_esd(example)
checkDifference(sk$groups, example)
sk <- sk_esd(example)
plot(sk)
sk <- sk_esd(maven)
plot(sk)</pre>
```

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