

Help

`isometry.test``package:unknown`

R Documentation

ISOMETRY TEST AND SIZE CORRECTION

Description:

Function to perform an isometry test, and therefore determine if the relationship between a reference and one or more response morphometric measurements scale by isometry or by allometry. It also performs the size corrections to eliminate the size variant in morphological comparisons. The output of the function is an array with the isometry test result and a matrix of size corrected variables.

Usage:

```
isometry.test (response, reference, specimen.id, expected.slope, alpha = 0.05)
```

Arguments:

`response`: vector, matrix or data frame with one or more response variables to be analyzed per specimen.

`reference`: vector, matrix or data frame with the reference variable to be analyzed per specimen.

`specimen.id`: character vector indicating the names of the specimens to be analyzed.

`expected.slope`: numeric vector indicating the expected slope for isometry (power of response/power of reference variable).

`alpha`: a numeric value >0 and <1 indicating the significance threshold for statistical analysis.

Details:

If "response", "reference" or "specimen.id" are inserted incorrectly, the function is not executed. If "expected.slope" and/or "alpha" are missing, or incorrect, default values of 1 to all response variables, and 0.05, are respectively determined.

To make it easier for the function, specimens should be in rows. Nevertheless, the function will most likely correct if the specimens are placed in columns instead.

Value:

An array including a data frame with the result "Isometry" or "Allometry" per response variable and a matrix with the size-corrected reference and response variables.

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References:

COLTON, T.F. (1999) Size and Shape in Biology. Pages 1-44, in Tested studies for laboratory teaching, Volume 20 (S. J. Karcher, Editor). Proceedings of the 20th Workshop/Conference of the Association for Biology Laboratory Education (ABLE), 399 pages.

LLEONART, J., SALAT, J., TORRES, G.J. (2000) Removing allometric effects of body size in morphological analysis. Journal of Theoretical Biology, 205, 85-93.

Examples:

```
# Example 1
height=c(153,174,183,171,48) #cm, exponential 1
arm.span=c(157.5,165.1,191.8,166.4,51) #cm, exponential 1
hand.size=c(17,17.8,17.5,17.5,6) #cm, exponential 1
table=data.frame(height,arm.span,hand.size)
rownames(table)=c("Ross","Rachel","Phoebe","Joey","Chandler&Monica")
table$id=c("Ross","Rachel","Phoebe","Joey","Chandler&Monica")

id=c("Ross","Rachel","Phoebe","Joey","Chandler&Monica")
t.table=matrix(c(height,arm.span,hand.size),nrow=3, ncol=5, byrow=T) #
example test with above table transposed.
colnames(t.table)=c("Ross","Rachel","Phoebe","Joey","Chandler&Monica")
t.table=as.data.frame(t.table)
t.table[1,]=as.numeric(t.table[1,])
t.table[4,]=id
rownames(t.table)=c("height","arm.span","hand.size","id")

isometry.test(table[,2:3], table[,1], table$id)
isometry.test(t.table[2:3,],t.table[1,],colnames(t.table))

# Example 2
library(MASS)
data(Animals)
animals=data.frame(Animals)

isometry.test(animals$brain, animals$body, rownames(animals))
```

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Last update: **2020/08/12 06:04**