Package ‘Pstat’

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Description Calculating Pst values to assess differentiation among populations from a set of quantitative traits is the primary purpose of such a package. Pst value is an index that measures the level of phenotypic differentiation among populations (Leinonen et al., 2006). The bootstrap method provides confidence intervals and distribution histograms of Pst. Variations of Pst in function of the parameter c/h^2 are studied as well. Finally, the package proposes different transformations especially to eliminate any variation resulting from allometric growth (calculation of residuals from linear regressions, Reist standardizations or Aitchison transformation).
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Description

This package aims at calculating Pst values to assess differentiation among populations from a set of quantitative traits (with the function ‘Pst’). The bootstrap method provides confidence intervals and distribution histograms of Pst (with the function ‘BootPstk’). Variations of Pst in function of the parameter c/h^2 are studied (with the function ‘TracePst’) as well. Moreover the package allows users to transform theirs datas in three different ways in particular to eliminate any variation resulting from allometric growth (calculation of residuals from linear regressions -with the function ‘Res’, Reist standardizations -with the function ‘ReistTrans’- or Aitchison transformation -with the function ‘AitTrans’-).

Author(s)

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References


Examples

data(test)
# test1=AitTrans(test)
# Pst(test1,csh=0.2,a=2)
test2=ReistTrans(test,r=9)
# BootPstk(test2,k=4,b=3,Ri=c(3,7:17),Pw=c("C","D"),bars=50)
# TracePst(test2,col=c(7,9:12),Fst=0.3,Ri=c(22,27,195),Rp=c("A","C","E"),ci=0)
Description

'AitTrans' calculates log-ratio transformed measurements to account for individual size-effects.

Usage

AitTrans(M)

Arguments

M  a dataframe with as many rows as individuals. The first column contains the name of the population to which the individual belongs, the others contain quantitative variables.

Value

the data frame with transformed variables.

Author(s)

Blondeau Da Silva Stephane - Da Silva Anne.

References


Examples

data(test)
AitTrans(test)
BootPstk

Description

'BootPstk' performs a bootstrap resampling procedure with all individuals of the selected populations and calculates Pst values of quantitative measures considered. This function provides a confidence interval or the distribution of Pst.

Usage

BootPstk(M, b = 1, csh = 1, boot = 1000, k, Ri = 0, Rp = 0, Pw = 0, pe = 0.95, bars = 20)

Arguments

M         a dataframe with as many rows as individuals. The first column contains the name of the population to which the individual belongs, the others contain quantitative variables.

b         if b=1 all the boot values of Pst are returned, if b=2 these values (ordered) and the confidence interval are returned, if b=3 these values (ordered) and Pst distribution histogram are returned.

csh       the value of c/h^2, where c is the assumed additive genetic proportion of differences between populations and where h^2 is (narrow-sense heritability) the assumed additive genetic proportion of differences between individuals within populations.

boot      the number of data frames generated to determine the confidence interval or to construct the distribution (with the bootstrap method).

k         the number of the column containing the quantitative measure considered.

Ri        a vector containing each number of individual to be deleted. The vector Ri must contain existent individuals, each of them once.

Rp        a vector containing the names of the populations to be deleted.

Pw        a vector containing the names of the two populations considered to obtain pairwise Pst.

pe        the confidence level of the calculated interval.

bars      the maximum number of bars the histogram may have. Note that unfilled bars are taken into account.

Value

In any case, the sizes of each population considered. If a=1 a vector containing the boot values of Pst. If a=2 an ordered vector containing values of Pst and the confidence interval (also a vector). If a=3 an ordered vector containing values of Pst and the Pst distribution histogram.
**Pst**

**Author(s)**

Blondeau Da Silva Stephane - Da Silva Anne.

**Examples**

```r
data(test)
# BootPstk(test,k=2)
# BootPstk(test,k=7,b=2,csh=0.8,boot=2000,Ri=18)
# BootPstk(test,k=12,b=2,Ri=c(22,27,195),Rp=c("A","B","E"),pe=0.9)
# BootPstk(test,k=4,b=3,Ri=c(1:160),bars=50)
# BootPstk(test,k=4,b=3,Ri=c(3,7:17),Pw=c("C","D"),bars=50)
```

---

**Pst**

*Pst values and Pst confidence intervals*

**Description**

'Pst' calculates Pst values of the quantitative measures considered and also their confidence intervals, Pst value being an index that measures the level of phenotypic differentiation among populations (Leinonen et al., 2006).

**Usage**

```r
Pst(Mat, csh = 1, col = 1, a = 1, boot = 1000, Pw = 0, Rp = 0, Ri = 0, pe = 0.95)
```

**Arguments**

- **Mat**: a dataframe with as many rows as individuals. The first column contains the name of the population to which the individual belongs, the others contain quantitative variables.
- **csh**: the value of c/h^2, where c is the assumed additive genetic proportion of differences between populations and where h^2 is (narrow-sense heritability) the assumed additive genetic proportion of differences between individuals within populations.
- **col**: a vector with the number of the selected columns (i.e. the quantitative measures considered).
- **a**: if a=1 the values of Pst are returned, if a=2 their confidence intervals are added.
- **boot**: the number of data frames generated to determine the confidence interval with the bootstrap method.
- **Pw**: a vector containing the names of the two populations considered to obtain pairwise Pst.
- **Rp**: a vector containing the names of the populations to be deleted.
- **Ri**: a vector containing each number of individual to be deleted. The vector Ri must contain existent individuals, each of them once.
- **pe**: the confidence level of the calculated interval.
Value

The sizes of each population considered. Pst values of the selected populations (for quantitative traits considered) and if a=2 their confidence intervals.

Author(s)

Blondeau Da Silva Stephane - Da Silva Anne.

References


Examples

data(test)
Pst(test)
# Pst(test,csh=0.2,a=2)
# Pst(test,col=c(2,12),a=2,Rp=c("C","D"))
# Pst(test,col=c(5,8:11),a=2,boot=2000,Ri=56,Rp="A",pe=0.9)
# Pst(test,a=2,Ri=c(7,55:59),Pw=c("A","D"))

ReistTrans

Reist standardization

Description

'ReistTrans' calculates residuals (size adjusted measurements) from Reist tranformations to eliminate any variation resulting from allometric growth. There is a single regressor (one of the quantitative traits).

Usage

ReistTrans(M, r)

Arguments

M a dataframe with as many rows as individuals. The first column contains the name of the population to which the individual belongs, the others contain quantitative variables.

r the number of the column containing the quantitative trait used as a regressor.
Value

the data frame of adjusted variables, the column containing the quantitative trait used as a regressor being deleted.

Note

dispensable quantitative measures can easily be deleted in the main functions of R.

Author(s)

Blondeau Da Silva Stephane - Da Silva Anne.

References


Examples

```r
data(test)
names(test)[9]
ResistTrans(test,r=9)
```

Res

Residuals from a linear regression

Description

'Res' calculates residuals from simple linear regressions (in particular to eliminate any variation resulting from allometric growth). These regression adjustments assume the existence of linear relationships between the dependent variables and the regressor (one of the column of the data frame).

Usage

`Res(M, r)`
Arguments

M  a dataframe with as many rows as individuals. The first column contains the name of the population to which the individual belongs, the others contain quantitative variables.

r  the number of the column containing the quantitative trait used as a regressor.

Value

the data frame of adjusted variables, the column containing the quantitative trait used as a regressor being deleted.

Note

dispensable quantitative measures can easily be deleted in the main functions of R.

Author(s)

Blondeau Da Silva Stephane - Da Silva Anne.

Examples

```r
data(test)
names(test)[9]
Res(test,r=9)
```

test  Example of a data frame

Description

a dataframe containing 200 rows (i.e. 200 individuals). The first column contains the name of the population ("A", "B", "C", "D" and "E") to which the individual belongs, the 11 others contain quantitative measures.

Usage

```r
data("test")
```

References

Examples

data(test)

Description

'TracePst' plots the curves of the functions that map c/h^2 onto Pst (for chosen quantitative measures). Indeed, Pst depends on the value of c/h^2, where c is the assumed additive genetic proportion of differences between populations and where h^2 is (narrow-sense heritability) the assumed additive genetic proportion of differences between individuals within populations.

Usage

TracePst(Mat, col = 1, ci = 1, boot = 1000, pe = 0.95, Fst = -1, Pw = 0, Rp = 0, Ri = 0, xm = 2, pts = 30)

Arguments

Mat: a dataframe with as many rows as individuals. The first column contains the name of the population to which the individual belongs, the others contain quantitative variables.

col: a vector with the number of the selected columns (i.e. the quantitative measures considered).

ct: if ci=1 the confidence interval of Pst is plotted.

boot: the number of data frames generated to determine the confidence interval or to construct the dotted lines representing this confidence interval (using the bootstrap method).

pe: the confidence level of the calculated interval.

Fst: the value of Wright's Fst, if available.

Pw: a vector containing the names of the two populations considered to obtain pairwise Pst.

Rp: a vector containing the names of the populations to be deleted.

Ri: a vector containing each number of individual to be deleted. The vector Ri must contain existent individuals, each of them once.

xm: the maximum on x-axis (values of c/h^2).

pts: number of points used to plot the curves.

Value

In any case, the sizes of each population considered. The expected curves.
Note
The time required to construct the dotted lines associated with the confidence intervals might be fairly long depending on the user choices.

Author(s)
Blondeau Da Silva Stephane - Da Silva Anne.

References

Examples

```
data(test)
# TracePst(test)
# TracePst(test,boot=2000,col=7,Ri=18,pe=0.9,pts=40,xm=4)
TracePst(test,col=c(7,9:11),Fst=0.3,Ri=c(22,27,195),Rp=c("A","C","E"),ci=0)
# TracePst(test,Ri=c(3,7:17),Pw=c("C","D"))
```
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