

Package ‘TestDimorph’

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Type Package

Title Analysis Of The Interpopulation Difference In Degree of Sexual Dimorphism Using Summary Statistics

Version 0.2.0

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Description Provides two approaches of comparison; the univariate and the multivariate analysis in two or more populations. Since the main obstacle of performing systematic comparisons in anthropological studies is the absence of raw data, the current package offer a solution for this problem by allowing the use of published summary statistics of metric data (mean, standard deviation and sex specific sample size) as illustrated by the works of Greene, D. L. (1989) <doi:10.1002/ajpa.1330790113> and Konigsberg, L. W. (1991) <doi:10.1002/ajpa.1330840110>.

Imports

Rfast,plyr,rowr,stats,utils,reshape2,purrr,dplyr,caret,rlang,MASS,klaR,mda,corrplot,truncnorm,stringr

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AccuModel

Evaluation Of Sex-prediction Accuracy

Description

Testing the accuracy of different sex prediction models using the confusionMatrix function

Usage

```
AccuModel(f, x, y, byPop = TRUE, method = "lda", cutoff = 0.5,
  ref. = "F", post. = "M", ...)
```

Arguments

f	Formula in the form <code>groups ~ x1 + x2 + ...</code> . The grouping factor is placed to the left hand side while the numerical measurements are placed to the right hand side
x	Data frame to be fitted to the model
y	New data frame to be tested
byPop	Logical;if TRUE returns the accuracy in different populations, Default: TRUE.
method	Different methods of modeling see <code>details</code> , Default:'lda'
cutoff	cutoff value when using logistic regression, Default: 0.5
ref.	reference category in the grouping factor, Default: 'F'
post.	positive category in the grouping factor, Default: 'M'
...	additional arguments that can passed to modeling and confusionMatrix function.

Details

Data frames to be entered as input need to be arranged in a similar manner to `Howells` dataset. Methods used for modeling are:

`lda` linear discriminant analysis
`qda` quadratic discriminant analysis
`mda` mixture discriminant analysis
`fda` flexible discriminant analysis
`rda` regularized discriminant analysis
`glm` binomial logistic regression

Value

Accuracy parameters for the tested model

Examples

```
library(TestDimorph)
AccuModel(Sex~GOL+NOL+BNL, x = Howells, y = Howells, byPop = FALSE, method = "lda")
```

aovSS

Sex-Specific One-way ANOVA From Summary statistics

Description

Calculates sex specific one-way ANOVA followed by Tukey HSD from summary statistics.

Usage

```
aovSS(x, Pop = 1, pairwise = TRUE)
```

Arguments

<code>x</code>	Data frame containing summary statistics of both sexes for two or more populations.
<code>Pop</code>	Number of the column containing populations' names, Default: 1
<code>pairwise</code>	Logical; if <code>TRUE</code> runs multiple pairwise comparisons on different populations using Tukey HSD, Default: <code>TRUE</code>

Details

Data is entered in a wide format with each row representing a given population. `Pop` (first column by default) contains population names, `.mu` and `.sdev` contain means and standard deviations with `M` and `F` denoting males and females respectively. While `m` & `f` are the male and female sample sizes. By setting the option `pairwise` to `TRUE`, different pairwise combinations of populations can be compared with Tukey HSD post hoc test.

Value

Sex specific ANOVA tables and pairwise comparisons.

References

Timonov P, Fasova A, Radoinova D, Alexandrov A, Delev D (2014). “A study of sexual dimorphism in the femur among contemporary Bulgarian population.” *Eurasian Journal of Anthropology*, **5**(2), 46–53.

Curate F, Umbelino C, Perinha A, Nogueira C, Silva AM, Cunha E (2017). “Sex determination from the femur in Portuguese populations with classical and machine-learning classifiers.” *Journal of forensic and legal medicine*, **52**, 75–81.

Kranioti EF, Vorniotakis N, Galiatsou C, Iscan MY, Michalodimitrakis M (2009). “Sex identification and software development using digital femoral head radiographs.” *Forensic science international*, **189**(1-3), 113–e1.

Gulhan O, Harrison K, Kiris A (2015). “A new computer-tomography-based method of sex estimation: Development of Turkish population-specific standards.” *Forensic science international*, **255**, 2–8.

Examples

```
# Comparisons of femur head diameter in four populations
library(TestDimorph)
m <- c(150.00, 82.00, 36.00, 34.00)
f <- c(150.00, 58.00, 34.00, 24.00)
M.mu <- c(49.39, 48.33, 46.99, 45.20)
F.mu <- c(42.91, 42.89, 42.44, 40.90)
M.sdev <- c(3.01, 2.53, 2.47, 2.00)
F.sdev <- c(2.90, 2.84, 2.26, 2.90)
df <- cbind.data.frame(
  Pop = c('Turkish', 'Bulgarian', 'Greek', 'Portuguese '),
  m,
  f,
  M.mu,
  F.mu,
  M.sdev,
  F.sdev,
  stringsAsFactors = TRUE
)
aovSS(x = df)
```

Description

A dataset containing summary statistics for low density lipoprotein (LDL) and apolipoprotein-B (apo-B) levels in 604 baboons measured on two different diets: a basal diet 'chow' and a high cholesterol, saturated fat diet 'pink' (HCSF). The baboons were classified into one of three sub-species (*Papio hamadryas anubis*, *P.h. cynocephalus*, or *anubiscynocephalus hybrid*). Each animal was measured on each of the two diets.

Usage

```
baboon.parms_df
```

Format

A data frame with 12 rows and 8 variables

Trait Type of apolipoprotein

Sub Type of species

M.mu Means of lipoproteins in different species for males

F.mu Means of lipoproteins in different species for females

m Male sample sizes

f Female sample sizes

M.sdev Standard deviations for males

F.sdev Standard deviations for females

Note

The baboon data collection were supported by NIH grant HL28972 and NIH contract HV53030 to the Southwest Foundation for Biomedical Research (Now: Texas Biomedical Research Institute), and funds from the Southwest Foundation for Biomedical Research

References

Konigsberg LW (1991). "An historical note on the t-test for differences in sexual dimorphism between populations." *American journal of physical anthropology*, **84**(1), 93–96.

`baboon.parms_list` *Summary statistics of baboon data collection-data frame*

Description

A dataset containing summary statistics for low density lipoprotein (LDL) and apolipoprotein-B (apo-B) levels in 604 baboons measured on two different diets: a basal diet 'chow' and a high cholesterol, saturated fat diet 'pink' (HCSF). The baboons were classified into one of three sub-species (*Papio hamadryas anubis*, *P.h. cynocephalus*, or *anubiscynocephalus hybrid*). Each animal was measured on each of the two diets.

Usage

```
baboon.parms_list
```

Format

A list of 7 matrices.

R.res pooled within group correlation matrix

M.mu Means of lipoproteins in different species for males

F.mu Means of lipoproteins in different species for females

m Male sample sizes

f Female sample sizes

M.sdev Standard deviations for males

F.sdev Standard deviations for females

Note

The baboon data collection were supported by NIH grant HL28972 and NIH contract HV53030 to the Southwest Foundation for Biomedical Research (Now: Texas Biomedical Research Institute), and funds from the Southwest Foundation for Biomedical Research

References

Konigsberg LW (1991). "An historical note on the t-test for differences in sexual dimorphism between populations." *American journal of physical anthropology*, **84**(1), 93–96.

extract_sum

Summary Statistics Extraction

Description

Extract summary data needed for other functions from raw data.

Usage

```
extract_sum(x, Sex = 1, Pop = 2, firstX = 3, test = 1,  
  run = TRUE, pairwise = FALSE, padjust = "none",  
  lower_tail = FALSE, pairwise_tail = "two")
```

Arguments

<code>x</code>	Data frame containing raw data.
<code>Sex</code>	Number of the column containing gender (M for male and F for female), Default: 1.
<code>Pop</code>	Number of the column containing populations' names, Default: 2.
<code>firstX</code>	Number of the first column containing measured parameters, Default: 3.
<code>test</code>	1 for Greene t-test <code>Tg</code> , 2 for univariate, 3 for sex specific ANOVA <code>aoVSS</code> , 4 for multivariate and 5 for <code>pMatrix</code> , Default: 1.
<code>run</code>	Logical; if TRUE runs the corresponding test after data extraction, Default: TRUE.
<code>pairwise</code>	Logical; if TRUE runs multiple comparisons after multi or univariate analysis, Default: FALSE.
<code>padjust</code>	Method of p value adjustment for multiple comparisons following <code>p.adjust.methods</code> , Default: 'none'.
<code>lower_tail</code>	Logical; if TRUE probabilities are $P[X \leq x]$, otherwise, $P[X > x]$, Default: FALSE.
<code>pairwise_tail</code>	Number of t-test tails, Default: 'two'.

Details

Raw data is entered in a data frame similar in format to `Howells` data set. The first two columns contain gender `Sex` (M for male and F for female) (Default: 1) and populations' names `Pop` (Default: 2). Starting from `firstX` column (Default: 3), measured parameters are entered each in a separate column.

Value

Input for other functions using raw data.

Examples

```
# for multivariate test
library(TestDimorph)
extract_sum(Howells)
# for univariate test on a specific parameter
library(TestDimorph)
extract_sum(Howells, test = 2)
```

Howells

The Howells' craniometric data

Description

A subset of a dataset that consists of 82 craniometric measurements taken from approximately two thousands and half human crania from 28 geographically diverse populations.

Usage

Howells

Format

A data frame with 441 rows and 10 variables:

Sex 'M' for male and 'F' for female

Pop Populations' names

GOL Glabello occipital length

NOL Nasio occipital length

BNL Bastion nasion length

BBH Basion bregma height

XCB Maximum cranial breadth

XFB Max frontal breadth

ZYB Bizygomatic breadth

AUB Biauricular breadth

References

Howells WW (1995). "Who's who in skulls: ethnic identification of crania from measurements." *Papers of the Peabody Museum of Archaeology and Ethnology*, **82**.

Howells WW (1989). "Skull shapes and the map: craniometric analyses in the dispersion of modern Homo." *Papers of the Peabody Museum of Archaeology and Ethnology*, **79**.

Howells WW (1996). "Howells' craniometric data on the internet." *American Journal of Physical Anthropology: The Official Publication of the American Association of Physical Anthropologists*, **101**(3), 441–442.

Howells WW (1973). "Cranial variation in man: a study by multivariate analysis of patterns of difference among recent human populations." *Peabody Museum of Archaeology and Ethnology, Harvard Univ.*.

multivariate *Multivariate Analysis Of Sexual Dimorphism*

Description

Multivariate extension of Greene t-test Tg.

Usage

```
multivariate(x, R.res = NULL, Trait = 1, Pop = 2,
            univariate = FALSE, padjust = "none", lower_tail = FALSE)
```

Arguments

<code>x</code>	Data frame or list containing summary statistics of for multiple parameters measured in both sexes in two or more populations.
<code>R.res</code>	Pooled within correlational matrix, Default: NULL.
<code>Trait</code>	Number of the column containing names of measured traits, Default: 1.
<code>Pop</code>	Number of the column containing populations' names, Default: 2.
<code>univariate</code>	Logical; if TRUE conducts multiple univariate analyses on different parameters separately, Default: FALSE.
<code>padjust</code>	Method of p value adjustment following <code>p.adjust.methods</code> , Default: 'none'
<code>lower_tail</code>	Logical; if TRUE, probabilities are $P[X \leq x]$, otherwise, $P[X > x]$ for multivariate analysis, Default: FALSE

Details

Data can be entered either as a data frame where the first 2 columns contain traits to be measured `Trait` and the populations' names `Pop` and other columns containing different summary statistics as in `baboon.parms_df`. In that case the pooled within correlational matrix `R.res` should be entered as an argument. Another acceptable format is a list of matrices containing different summary statistics as well as the correlational matrix `R` as in `baboon.parms_list`. By setting the option `univariate` to TRUE, multiple ANOVAs can be run on each parameter independently with the required p value correction `padjust`.

Value

MANOVA or ANOVA table(s).

References

Konigsberg LW (1991). "An historical note on the t-test for differences in sexual dimorphism between populations." *American journal of physical anthropology*, **84**(1), 93–96.

Examples

```
# x is a data frame with separate correlational matrix
library(TestDimorph)
multivariate(x = baboon.parms_df, R.res = R)
# x is a list with the correlational matrix included
library(TestDimorph)
multivariate(baboon.parms_list, univariate = TRUE, padjust = 'bonferroni')
```

pMatrix

Visualization Of t-Greene Pairwise Comparisons

Description

Returns a graphical or numerical correlational matrix of p-values for the interpopulation degree of sexual dimorphism as measured by Greene t-test

Usage

```
pMatrix(x = NULL, Pop = 1, lower_tail = FALSE, tail = "two",
        padjust = "none", plot = FALSE, ...)
```

Arguments

x	Data frame containing summary statistics of both sexes for two or more populations, Default: NULL
Pop	Number of the column containing populations' names, Default: 1
lower_tail	Logical; if TRUE probabilities are $P[X \leq x]$, otherwise, $P[X > x]$, Default: FALSE
tail	Number of t test tails, Default: 'two'
padjust	padjust Method of p value adjustment for multiple comparisons following <code>p.adjust.methods</code> , Default: 'none'
plot	Logical; if TRUE graphical matrix of p-values, Default: TRUE
...	additional arguments that can be passed to <code>corrplot</code> function.

Details

Data is entered in a wide format with each row representing a given population. `Pop` (first column by default) contains population names, `.mu` and `.sdev` contain means and standard deviations with `M` and `F` denoting males and females respectively. While `m&f` are the male and female sample sizes. When more than two populations are tested, `p.adjust.methods: c('holm', 'hochberg', 'hommel', 'bonferroni')` can be used for p value adjustment.

Value

Graphical or numerical matrix of p-values from Greene t-test pairwise comparisons.

References

- Timonov P, Fasova A, Radoinova D, Alexandrov A, Delev D (2014). “A study of sexual dimorphism in the femur among contemporary Bulgarian population.” *Eurasian Journal of Anthropology*, **5**(2), 46–53.
- Curate F, Umbelino C, Perinha A, Nogueira C, Silva AM, Cunha E (2017). “Sex determination from the femur in Portuguese populations with classical and machine-learning classifiers.” *Journal of forensic and legal medicine*, **52**, 75–81.
- Kranioti EF, Vorniotakis N, Galiatsou C, Iscan MY, Michalodimitrakis M (2009). “Sex identification and software development using digital femoral head radiographs.” *Forensic science international*, **189**(1-3), 113–e1.
- Gulhan O, Harrison K, Kiris A (2015). “A new computer-tomography-based method of sex estimation: Development of Turkish population-specific standards.” *Forensic science international*, **255**, 2–8.

Examples

```
# Comparisons of femur head diameter in four populations
library(TestDimorph)
m <- c(150.00, 82.00, 36.00, 34.00)
f <- c(150.00, 58.00, 34.00, 24.00)
M.mu <- c(49.39, 48.33, 46.99, 45.20)
F.mu <- c(42.91, 42.89, 42.44, 40.90)
M.sdev <- c(3.01, 2.53, 2.47, 2.00)
F.sdev <- c(2.90, 2.84, 2.26, 2.90)
df <- cbind.data.frame(
  Pop = c('Turkish', 'Bulgarian', 'Greek', 'Portuguese '),
  m,
  f,
  M.mu,
  F.mu,
  M.sdev,
  F.sdev,
  stringsAsFactors = TRUE
)
pMatrix(x = df, plot=TRUE, method = 'ellipse', type = 'lower', col = c('#AEB6E5',
'#B1A0DB', '#B788CD', '#BC6EB9', '#BC569E', '#B6407D', '#A93154'), is.corr =
FALSE, tl.cex = 0.8, tl.col = 'black', sig.level = 0.05, insig =
'label_sig', pch.cex = 2.5, tl.pos = 'ld', win.asp = 1, tl.srt =
0.1, number.cex = 0.5, na.label = 'NA')
```

Description

Pooled within group correlation matrix for baboon data

Usage

R

Format

A 4*4 numerical matrix

RawGen

*Raw Data Generation By Truncated Distribution***Description**

Generates raw data from summary statistics using left truncated normal distribution

Usage

```
RawGen(v, format = "wide", complete_cases = FALSE)
```

Arguments

`v` a data frame or a named list containing summary statistics for different parameters

`format` The form of the resultant data frame either : 'long' or 'wide', Default: 'wide'

`complete_cases` Logical; if TRUE rows with missing values will be removed, Default: FALSE

Details

Data can be entered as a data frame, with `Pop` (first column by default) containing population names, `Parms` containing names of tested parameter(s), `.mu` and `.sdev` containing means and standard deviations with M and F denoting males and females respectively. While `m&f` are the male and female sample sizes. Data also can be entered as a list of multiple data frames with similar structure but different parameters are entered as names of the list.

References

Hussein MHA, Abulnoor BAE (2019). "Sex estimation of femur using simulated metapopulation Database: a preliminary investigation." *Forensic Science International: Reports*. ISSN 2665-9107, doi: 10.1016/j.fsir.2019.100009¹.

¹<https://doi.org/10.1016/j.fsir.2019.100009>

Examples

```
# Comparison of two femur parameters in two populations
library(TestDimorph)
Pop <- as.factor(rep(c("Bulgarian", "Greek"), 2))
Parms <- as.factor(c(rep("MXFL", 2), rep("MLD", 2)))
m <- c(82.0, 36.0, 82.00, 36.00)
M.mu <- c(461.80, 440.40, 27.67, 27.74)
M.sdev <- c(19.9, 19.6, 2.21, 1.79)
f <- c(58.00, 34.0, 58.00, 34.00)
F.mu <- c(411.70, 409.80, 24.89, 26.69)
F.sdev <- c(23.2, 21.4, 1.78, 2.42)
df <- cbind.data.frame(Pop, Parms, m, M.mu, M.sdev, f, F.mu, F.sdev)
RawGen(df)
```

Tg

*Greene t-test of Sexual Dimorphism***Description**

Calculates the significance of the differences in degree sexual dimorphism between two populations using a modified Greene t-test which uses summary statistics as input.

Usage

```
Tg(x = NULL, Pop = 1, m = NULL, m2 = NULL, f = NULL, f2 = NULL,
   M.mu = NULL, M.mu2 = NULL, F.mu = NULL, F.mu2 = NULL,
   M.sdev = NULL, M.sdev2 = NULL, F.sdev = NULL, F.sdev2 = NULL,
   lower_tail = FALSE, tail = "two", padjust = "none")
```

Arguments

x	Data frame containing summary statistics of both sexes for two or more populations, Default: NULL
Pop	Number of the column containing populations' names, Default: 1
m	Number of male sample size in the first population, Default: NULL
m2	Number of male sample size in the second population, Default: NULL
f	Number of female sample size in the first population, Default: NULL
f2	Number of female sample size in the second population, Default: NULL
M.mu	Means for males in the first population, Default: NULL
M.mu2	Means for males in the second population, Default: NULL
F.mu	Means for females in the first population, Default: NULL
F.mu2	Means for females in the second population, Default: NULL
M.sdev	Standard deviation for males in the first population, Default: NULL
M.sdev2	Standard deviation for males in the second population, Default: NULL

<code>F.sdev</code>	Standard deviation for females in the first population, Default: NULL
<code>F.sdev2</code>	Standard deviation for females in the second population, Default: NULL
<code>lower_tail</code>	Logical; if TRUE probabilities are $P[X \leq x]$, otherwise, $P[X > x]$., Default: FALSE
<code>tail</code>	Number of t test tails, Default: 'two'
<code>padjust</code>	Method of p value adjustment for multiple comparisons following <code>p.adjust.methods</code> , Default: 'none'

Details

Summary statistics can be entered directly as arguments in case of comparing two populations. Alternatively, data can be entered in a wide format with each row representing a given population. `Pop` (first column by default) contains population names, `.mu` and `.sdev` contain means and standard deviations with M and F donating males and females. While `m&f` are the male and female sample sizes respectively. When more than two populations are entered as input, `p.adjust.methods`: `c('holm', 'hochberg', 'hommel', 'bonferroni', 'BH', 'BY', 'fdr', 'none')` can be used for p value adjustment.

Value

Degree of freedom, t and p values for Tg test.

References

- Greene DL (1989). "Comparison of t-tests for differences in sexual dimorphism between populations." *American Journal of Physical Anthropology*, **79**(1), 121–125.
- Timonov P, Fasova A, Radoinova D, Alexandrov A, Delev D (2014). "A study of sexual dimorphism in the femur among contemporary Bulgarian population." *Eurasian Journal of Anthropology*, **5**(2), 46–53.
- Gulhan O, Harrison K, Kiris A (2015). "A new computer-tomography-based method of sex estimation: Development of Turkish population-specific standards." *Forensic science international*, **255**, 2–8.

Examples

```
# Summary data in a data frame
library(TestDimorph)
Pop <- c('Turkish', 'Bulgarian')
m <- c(150.00, 82.00)
f <- c(150.00, 58.00)
M.mu <- c(49.39, 48.33)
F.mu <- c(42.91, 42.89)
M.sdev <- c(3.01, 2.53)
F.sdev <- c(2.90, 2.84)
df <- cbind.data.frame(
  Pop,
  m,
  f,
  M.mu,
```

```

    F.mu,
    M.sdev,
    F.sdev,
    stringsAsFactors = TRUE
  )
  Tg(x = df)

```

univariate

Univariate Analysis Of Sexual Dimorphism

Description

Calculation of the significance of the differences in interpopulation degree of sexual dimorphism using a modified one-way ANOVA which utilizes summary statistics as input.

Usage

```

univariate(x, Pop = 1, lower_tail = FALSE, padjust = "none",
  pairwise = FALSE, pairwise_tail = "two")

```

Arguments

<code>x</code>	Data frame containing summary statistics of both sexes for two or more populations.
<code>Pop</code>	Number of the column containing populations' names, Default: 1
<code>lower_tail</code>	Logical; if TRUE probabilities are $P[X \leq x]$, otherwise, $P[X > x]$., Default: FALSE
<code>padjust</code>	Method of p value adjustment for multiple comparisons following <code>p.adjust.methods</code> , Default: 'none'
<code>pairwise</code>	Logical; if TRUE runs multiple pairwise comparisons on different populations using Tg test, Default: FALSE
<code>pairwise_tail</code>	Number of t test tails, Default: 'two'

Details

Data is entered in a wide format with each row representing a given population. `Pop` (first column by default) contains population names, `.mu` and `.sdev` contain means and standard deviations with `M` and `F` donating males and females respectively. While `m` & `f` are the male and female sample sizes.

When more than two populations are tested, `p.adjust.methods: c('holm', 'hochberg', 'hommel', 'bonfer` can be used for p value adjustment.

Value

ANOVA table

References

- Konigsberg LW (1991). “An historical note on the t-test for differences in sexual dimorphism between populations.” *American journal of physical anthropology*, **84**(1), 93–96.
- Timonov P, Fasova A, Radoinova D, Alexandrov A, Delev D (2014). “A study of sexual dimorphism in the femur among contemporary Bulgarian population.” *Eurasian Journal of Anthropology*, **5**(2), 46–53.
- Curate F, Umbelino C, Perinha A, Nogueira C, Silva AM, Cunha E (2017). “Sex determination from the femur in Portuguese populations with classical and machine-learning classifiers.” *Journal of forensic and legal medicine*, **52**, 75–81.
- Kranioti EF, Vorniotakis N, Galiatsou C, Iscan MY, Michalodimitrakis M (2009). “Sex identification and software development using digital femoral head radiographs.” *Forensic science international*, **189**(1-3), 113–e1.
- Gulhan O, Harrison K, Kiris A (2015). “A new computer-tomography-based method of sex estimation: Development of Turkish population-specific standards.” *Forensic science international*, **255**, 2–8.

Examples

```
# Comparisons of femur head diameter in four populations
library(TestDimorph)
m <- c(150.00, 82.00, 36.00, 34.00)
f <- c(150.00, 58.00, 34.00, 24.00)
M.mu <- c(49.39, 48.33, 46.99, 45.20)
F.mu <- c(42.91, 42.89, 42.44, 40.90)
M.sdev <- c(3.01, 2.53, 2.47, 2.00)
F.sdev <- c(2.90, 2.84, 2.26, 2.90)
df <- cbind.data.frame(
  Pop = c('Turkish', 'Bulgarian', 'Greek', 'Portuguese '),
  m,
  f,
  M.mu,
  F.mu,
  M.sdev,
  F.sdev,
  stringsAsFactors = TRUE
)
univariate(x = df, pairwise = TRUE, padjust = 'bonferroni')
```