Package ‘HardyWeinberg’

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Description Contains tools for exploring Hardy-Weinberg equilibrium (Hardy, 1908; Weinberg, 1908) <doi:10.1126/science.28.706.49> for bi and multi-allelic genetic marker data. All classical tests (chi-square, exact, likelihood-ratio and permutation tests) with bi-allelic variants are included in the package, as well as functions for power computation and for the simulation of marker data under equilibrium and disequilibrium. Routines for dealing with markers on the X-chromosome are included (Graffelman & Weir, 2016) <doi: 10.1038/hdy.2016.20>, including Bayesian procedures. Some exact and permutation procedures also work with multi-allelic variants. Special test procedures that jointly address Hardy-Weinberg equilibrium and equality of allele frequencies in both sexes are supplied, for the bi and multi-allelic case. Functions for testing equilibrium in the presence of missing data by using multiple imputation are also provided. Implements several graphics for exploring the equilibrium status of a large set of bi-allelic markers: ternary plots with acceptance regions, log-ratio plots and Q-Q plots.
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**HardyWeinberg-package**

**Statistical Tests and Graphics for Hardy-Weinberg Equilibrium**

**Description**

Contains tools for exploring Hardy-Weinberg equilibrium (Hardy, 1908; Weinberg, 1908) \(<\text{doi:10.1126/science.28.706.49}>\) for bi and multi-allelic genetic marker data. All classical tests (chi-square, exact, likelihood-ratio and permutation tests) with bi-allelic variants are included in the package, as well as functions for power computation and for the simulation of marker data under equilibrium and disequilibrium. Routines for dealing with markers on the X-chromosome are included (Graffelman & Weir, 2016) \(<\text{doi:10.1038/hdy.2016.20}>\), including Bayesian procedures. Some exact and permutation procedures also work with multi-allelic variants. Special test procedures that jointly address Hardy-Weinberg equilibrium and equality of allele frequencies in both sexes are supplied, for the bi and multi-allelic case. Functions for testing equilibrium in the presence of missing data by using multiple imputation are also provided. Implements several graphics for exploring the equilibrium status of a large set of bi-allelic markers: ternary plots with acceptance regions, log-ratio plots and Q-Q plots.

**Details**

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The most important function of the package is `HWternaryPlot` that can be used to create ternary plots with acceptance regions for HWE. Other routines implement statistical tests for HWE such as `HWChisq` and `HWRatio`.

Author(s)

Jan Graffelman
Maintainer: Jan Graffelman <jan.graffelman@upc.edu>

References


Examples

```r
library(HardyWeinberg)

# draw random SNPs from a population that is in HWE

set.seed(123)

m <- 100 # number of markers
n <- 100 # sample size

X <- HWData(n,m)
out <- HWternaryPlot(X,100,region=1,vertex.cex=2,signifcolour=TRUE)
```

### af

*Function to compute allele frequencies*

**Description**

Function `af` computes the allele frequencies for a matrix or a vector containing genotypic compositions.

**Usage**

`af(x)`

**Arguments**

`x` a vector or matrix with compositions
Value

a vector with allele frequencies

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

See Also

maf

Examples

```r
x <- as.vector(rmultinom(1,100,c(0.5,0.4,0.1)))
x <- x/sum(x)
print(x)
print(af(x))
```

### Description

Function `aftest` tests equality of allele frequencies for males and females for bi-allelic marker data by means of a Fisher exact test.

### Usage

```r
Aftest(x, verbose = TRUE, ...)
```

### Arguments

- `x`: a vector containing the genotypic counts c(A,B,AA,AB,BB) for a bi-allelic X-chromosomal markers.
- `verbose`: `verbose = TRUE` prints results, `verbose = FALSE` is silent.
- `...`: additional arguments for function `fisher.test`.

### Details

Function `Aftest` constructs the contingency table of sex by allele, and call `fisher.test` to test for equality of allele frequencies. The test assumes Hardy-Weinberg equilibrium.

### Value

- `AC`: Two-way table of sex by allele
- `pval`: p-value of the test
Author(s)
Jan Graffelman <jan.graffelman@upc.edu>

See Also
hwChisq, hwExact

Examples
rs5968922 <- c(A=392, B=212, AA=275, AB=296, BB=80)
AFtest(rs5968922)

agcounts          Calculate allele and genotype counts for X-chromosomal markers

Description
Function agcounts determines sample size, minor are major allele counts, allele counts in females, numbers of males and females and allele frequencies for a vector of genotypes counts of an X-chromosomal markers.

Usage
agcounts(x, verbose = FALSE)

Arguments
  x          a vector of X-chromosomal genotype counts (A,B,AA,AB,BB)
  verbose    print the counts if (verbose = TRUE)

Value
  n          sample size
  nA         number of A alleles
  nB         number of B alleles
  nf         number of females
  nm         number of males
  nAf        number of A alleles in females
  nBf        number of B alleles in females
  nt         total number of alleles
  fAA        number of AA females
  fAB        number of AB females
  fBB        number of BB females
  pA          overall A allele frequency
  pB          overall B allele frequency
**Description**

Function `alleles` extracts the names of the alleles from a named genotype vector.

**Usage**

```r
alleles(x, fromlabels = TRUE)
```

**Arguments**

- `x` A named or unnamed genotype vector (e.g. `c(AA=10, AB=20, BB=5)`)
- `fromlabels` extract genotypes from the labels of the vector elements, or from the vector elements themselves.

**Value**

A character vector with the alleles

**Author(s)**

Jan Graffelman (jan.graffelman@upc.edu)

**See Also**

`n.alleles`

**Examples**

```r
x <- c(AA=10, AG=10, GG=10, AT=5)
als.x <- alleles(x)
```
### Alzheimer

**Genotype frequencies for 70 SNPs related to Alzheimer’s disease**

**Description**

The dataframe contains the genotype frequencies MM, Mm and mm for the 70 SNPs for both cases and controls. The data are taken from table 7.11 in Laird & Lange.

**Usage**

`data(Alzheimer)`

**Format**

A data frame containing 70 observations.

**Source**

Laird, N. M. and Lange, C. Table 7.11, p. 124

**References**


---

### dgraffelmanweir.bi

**Calculate Graffelman-Weir exact density for bi-allelic X-chromosomal variant**

**Description**

Function `dgraffelmanweir` calculate the probability $P(N_{AB}=nab \text{ and } M_{A}=ma|N_{A}=na)$ for a bi-allelic X-chromosomal variant.

**Usage**

`dgraffelmanweir.bi(x, y)`

**Arguments**

- **x** vector with male genotype counts (A,B)
- **y** vector with female genotype counts (AA,AB,BB)

**Value**

a single real number
Calculate Levene's exact density for k alleles

dlevene

Author(s)
Jan Graffelman <jan.graffelman@upc.edu>

References

See Also
HWExact, HWExactStats

Examples
males <- c(A=392, B=212)
females <- c(AA=275, AB=296, BB=80)
prob <- dgraffelmanweir.bi(males,females)
print(prob)

Description
Function dlevene calculates Levene’s exact density for a diploid system with k alleles.

Usage
dlevene(N)

Arguments
N A lower triangular matrix with genotype counts

Details
The supplied matrix of genotype counts should be triangular, with the homozygote counts on the diagonal, and all heterozygote counts below the diagonal.

Value
a single real number

Author(s)
Jan Graffelman (jan.graffelman@upc.edu)
References

See Also
HWExact

Examples
```r
x <- c(AA=12, AB=19, AC=13, BB=7, BC=5, CC=0)
x <- toTriangular(x)
prob <- dlevene(x)
print(prob)
```

---

dlevene.bi  
**Calculate Levene’s density for a bi-allelic variant**

Description
Program dlevene.bi calculates Levene’s density (P(AB|A)) for a bi-allelic variant.

Usage
dlevene.bi(x)

Arguments
x  
a vector of genotype counts (AA, AB, BB)

Value
a single real number

Author(s)
Jan Graffelman (jan.graffelman@upc.edu)

References

See Also
dlevene, HWExact
EAFExact

Examples

```r
x <- c(AA=298, AB=489, BB=213)
prob <- dlevene.bi(x)
print(prob)
```

---

EAFExact: *Exact test for equality of allele frequencies in males and females*

Description

EAFExact uses a Fisher Exact test to compare allele frequencies in males and females for variants with k alleles (k \(\geq 2\)).

Usage

```
EAFExact(m, f, verbose = TRUE)
```

Arguments

- `m`: vector or triangular matrix with male genotype counts
- `f`: vector or triangular matrix with female genotype counts
- `verbose`: print output (TRUE) or not (FALSE)

Details

For bi-allelic autosomal variants the genotype counts can be supplied as vectors ((AA, AB, BB) for males, and (AA, AB, BB) for females). For X-chromosomal bi-allelic variants the genotype counts can also be supplied as vectors ((A, B) for males, and (AA, AB, BB) for females). For multi-allelic autosomal variants male and genotype counts can be supplied as vectors (AA, AB, AC, BB, BC, CC, ...) or as a triangular matrix, where matrix rows and columns are labelled with the allele name (A, B, C, ...). For multi-allelic X-chromosomal variants, male genotype counts must be supplied as a vector (A, B, C, ...) and female genotype counts must be supplied as a triangular matrix. See the examples below.

Value

- `pval`: p-value
- `tab`: table with allele counts

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

See Also

- `fisher.test`
Examples

#
# bi-allelic autosomal
#

m <- c(AA=60, AB=96, BB=44)
f <- c(AA=44, AB=97, BB=59)
EAFtest <- EAFExact(m, f)

#
# bi-allelic X-chromosomal
#

males <- c(A=392, B=212)
females <- c(AA=275, AB=296, BB=80)
EAFtest <- EAFExact(males, females, verbose=TRUE)

#
# tri-allelic autosomal
#

males <- c(AA=20, AB=52, AC=34, BB=17, BC=51, CC=26)
females <- c(AA=28, AB=55, AC=33, BB=18, BC=50, CC=16)
EAFtest <- EAFExact(males, females, verbose=TRUE)

#
# tri-allelic X-chromosomal
#

males <- c(A=15, B=17, C=24)
females <- toTriangular(c(AA=4, AB=2, AC=13, BB=6, BC=19, CC=4))
EAFtest <- EAFExact(males, females, verbose=TRUE)

---

fisherz

*Fisher’s z transformation*

Description

Calculates Fisher’s z transformation for a correlation coefficient

Usage

`fisherz(r)`

Arguments

- `r`  
a correlation coefficient
**Description**

`GenerateSamples` generates all possible genotypic compositions (AA, AB, BB) for a given sample size `n`.

**Usage**

`GenerateSamples(n = 5)`

**Arguments**

- `n` the desired sample size

**Value**

returns a matrix with in each row a possible genotypic composition for the given sample size.

**Author(s)**

Jan Graffelman <jan.graffelman@upc.edu>

**Examples**

GenerateSamples(5)
Description

Function genlabels sets the names of a vector or matrix of genotype counts.

Usage

genlabels(X)

Arguments

X a 3 (or 5) element vector with genotype counts, a matrix of genotype counts (3 or 5 columns)

Value

A vector or a matrix

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

See Also

hwchisq

Examples

x <- c(25,50,25)
x <- genlabels(x)

Description

The dataframe contains the genotype frequencies in generic notation, AA, AB and BB the first 225 polymorphic SNPs without missing data on chromosome 1 of the Han Chinese in Beijing. The data are compiled from the HapMap project, phase 3.2, containing genotype information of 84 individuals.

Usage

data(HapMapCHBChr1)
**Format**

A matrix containing 225 rows and 3 columns (AA, AB, BB).

**Source**


**References**


---

**HWABO**

Estimate allele frequencies and test for Hardy-Weinberg equilibrium with a tri-allelic ABO system.

---

**Description**

Function `af.em` takes four genotype counts ("A","B","AB","OO") and estimates the three allele frequencies using the EM algorithm.

**Usage**

```
HWABO(x, p = c(1/3, 1/3, 1/3), maxiter = 50, tol = 1e-10, verbose = TRUE)
```

**Arguments**

- `x`: a vector with genotype counts ("A","B","AB","OO").
- `p`: a vector with initial allele frequencies (by default (1/3,1/3,1/3)).
- `maxiter`: maximum number of iterations.
- `tol`: tolerance for convergence, 1e-10 by default.
- `verbose`: print iteration history or not.

**Value**

- `pn`: vector with estimated allele frequencies.
- `It.hist`: iteration history with log-likelihood.
- `expected`: expected genotype counts under HWE.

**Author(s)**

Jan Graffelman <jan.graffelman@upc.edu>

**See Also**

`af`
Examples

```r
> x <- c(fA=182,fB=60,nAB=17,n00=176)
> a1.fre <- HWAIC(x)
> a12 <- HWAIC0(x, p=c(0.99,0.01,0.01), maxiter=25)
> a13 <- HWAIC0(x, p=c(0.01,0.99,0.01), maxiter=25)
> a14 <- HWAIC0(x, p=c(0.01,0.01,0.99), maxiter=25)
```

HWAIC  

`Compute Akaike's Information Criterion (AIC) for HWP and EAF models`

Description

Function `HWAIC` calculates Akaike's Information Criterion for six different models that describe a bi-allelic genetic variant: A: Hardy-Weinberg proportions and equality of allele frequencies in the sexes (HWP & EAF); B: EAF and equality of inbreeding coefficients in the sexes (EIC); C: EAF; D: HWP; E: EIC; F: None of the previous.

Usage

`HWAIC(x, y, tracing = 0)`

Arguments

- `x` Male genotype counts (AA,AB,BB)
- `y` Female genotype counts (AA,AB,BB)
- `tracing` Activate tracing in the maximization of some likelihoods (0=no tracing; 1:tracing)

Details

The log-likelihood for the six models is calculated. For two models (C and E) this is done numerically using package `RSolnp`.

Value

A named vector containing 6 values for AIC

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

References

Perform all tests for Hardy-Weinberg equilibrium

**Description**

`HWAlltests` performs all classical frequentists tests for Hardy-Weinberg equilibrium and lists their p-values.

**Usage**

```r
HWAlltests(x, verbose = TRUE, include.permutation.test = FALSE, x.linked = FALSE)
```

**Arguments**

- `x`: a vector with a set of genotype counts (AA, AB, BB)
- `verbose`: print output if set to TRUE
- `include.permutation.test`: turns on the permutation test if set to TRUE
- `x.linked`: `x.linked` = FALSE indicates the marker is autosomal (default), and `x.linked` = TRUE indicates it resides on the X-chromosome.

**Details**

By default the permutation test is not performed in order to reduce computing time.

**Value**

A dataframe with test statistics and p-values.

**Author(s)**

Jan Graffelman <jan.graffelman@upc.edu>

**See Also**

`HWLratio`, `HWChisq`, `HWExact`
**Examples**

```r
x <- c(298, 489, 213)
names(x) <- c("MM", "MN", "NN")
HWAlltests(x, verbose=TRUE)
```

---

**HWAllr**

*Compute additive log-ratio transformation*

---

**Description**

HWAllr computes the additive log-ratio transformation for genotype counts of bi-allelic genetic markers.

**Usage**

```r
HWAllr(X, zeroadj = 0.5, denominator = 2)
```

**Arguments**

- **X**: A matrix of genotype counts (columns AA, AB and BB)
- **zeroadj**: A zero adjustment parameter (0.5 by default)
- **denominator**: The genotype count put in the denominator of the log-ratio (1=AA, 2=AB, 3=BB)

**Value**

A matrix or vector of log-ratio coordinates

**Author(s)**

Jan Graffelman (jan.graffelman@upc.edu)

**References**


**See Also**

HWClr, HWIlr

**Examples**

```r
X <- HWData(100, 100)
Y <- HWAllr(X)
```
**HWAlrPlot**  
*Plot genetic markers in additive log-ratio coordinates*

**Description**

HWAlrPlot creates a scatter plot of the log-ratio coordinates of bi-allelic genetic markers. Hardy-Weinberg equilibrium is indicated by a straight line in the plot.

**Usage**

```r
HWAlrPlot(X, zeroadj = 0.5)
```

**Arguments**

- `X`: A matrix of genotype counts (columns AA, AB, BB)
- `zeroadj`: Zero-adjustment parameter. Zero counts in the count matrix are substituted by zeroadj which is 0.5 by default.

**Value**

NULL

**Author(s)**

Jan Graffelman (jan.graffelman@upc.edu)

**References**


**See Also**

HWClrPlot, HWIlrPlot

**Examples**

```r
X <- HWClo(HWData(100, 100))
HWAlrPlot(X)
```
HWChisq

Chi square tests for Hardy Weinberg equilibrium

Description

HWChisq performs the chi-square test for Hardy-Weinberg equilibrium both for autosomal and X-chromosomal markers.

Usage

HWChisq(X, cc = 0.5, verbose = TRUE, x.linked = FALSE, phifixed = NULL)

Arguments

X a vector containing the genotypic counts (AA, AB, BB for autosomal markers and c(A, B, AA, AB, BB) for X-chromosomal markers).
cc the continuity correction parameter (default cc = 0.5).
verbose = TRUE prints results, verbose = FALSE is silent.
x.linked FALSE indicates the marker is autosomal (default), and TRUE indicates it resides on the X-chromosome.
phifixed (For X-chromosomal markers only) phifixed=NULL indicates that the fraction of males (females) should be estimated from the data (default). If set to any other value (e.g. phifixed=0.5) then the sample is assumed to come from a population with the specified fraction of males.

Details

HWChisq does a chi-square test for Hardy-Weinberg equilibrium, and by default applies a continuity correction. For extreme allele frequencies, the continuity correction can lead to excessive type 1 error rates, and is better turned off in that case. The continuity correction can be turned off by specifying cc=0.

HWChisq can do the chi-square test for both autosomal and X-chromosomal markers. By setting x.linked = TRUE the marker will be assumed to be on the X-chromosome, and the count vector supplied should have 5 elements instead of 3 elements for an autosomal marker. For X-chromosomal markers argument phifixed is in general best left to its default value (NULL). Only in specific situations where the theoretical population sex ratio is known (e.g. in simulation studies where a universe with known gender ratio is sampled) phifixed could be set to the theoretical ratio of interest.

When alternative is set to less, a one-sided test for against a negative inbreeding coefficient (heterozygote excess) is performed. When alternative is set to greater a one-sided test for against a positive inbreeding coefficient (lack of heterozygotes) is performed.
**Value**

`HWChisq` returns a list with the components:

- `chisq`  value of the chi-square statistic. NA is returned if the marker is monomorphic.
- `pval`  p-value of the chi-square test for Hardy-Weinberg equilibrium.
- `D`  Half the deviation from Hardy-Weinberg equilibrium for the AB genotype.
- `p`  the allele frequency of A.
- `f`  the inbreeding coefficient.
- `expected`  the expected counts under Hardy-Weinberg equilibrium

**Author(s)**

Jan Graffelman <jan.graffelman@upc.edu>

**References**


For the chi-square test for X-linked markers:


**See Also**

`HWLRatio`, `HWChisqStats`

**Examples**

```r
# Test for an autosomal blood group marker
#
x <- c(MM=298, MN=489, NN=213)
HW.test <- HWChisq(x, verbose=TRUE)
#
# Same test without continuity correction
#
HW.test <- HWChisq(x, cc=0, verbose=TRUE)
#
# Test for an X-chromosomal SNP.
#
rs5968922 <- c(A=392, B=212, AA=275, AB=296, BB=80)
HW.test <- HWChisq(rs5968922, cc=0, x.linked=TRUE, verbose=TRUE)
```
HWChisqMat

Matrix version of HWChisq

Description

HWChisqMat executes the Chisquare test for HWE for each row in a matrix.

Usage

\texttt{HWChisqMat(X, ...)}

Arguments

\texttt{X} \quad A \texttt{n times 3 matrix of genotypic counts (AA,AB,BB)}

\texttt{...} \quad \texttt{extra arguments that are passed on to HWChisq}

Value

\texttt{pvalvec} \quad \texttt{Vector with the p-values of each test}

\texttt{chisqvec} \quad \texttt{Vector with the chi-square statistics}

\texttt{Dvec} \quad \texttt{Vector with deviations from independence}

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

See Also

\texttt{HWChisq}

Examples

\begin{verbatim}
X <- HWData(100,10)
colnames(X) <- c("MM","MN","NN")
Results <- HWChisqMat(X)
Output <- cbind(X,Results$chisqvec,Results$pvalvec)
print(Output)
\end{verbatim}
HWChisqStats

| HWChisqStats | Fast computation of chi-square statistics for Hardy-Weinberg equilibrium |

Description

HWChisqStats is a function for the fast computation of chi-square statistics (or the corresponding p-values) for a large set of bi-allelic markers (typically SNPs).

Usage

HWChisqStats(X, x.linked = FALSE, pvalues = FALSE)

Arguments

- **X**: A matrix with genotype counts, one row per marker. X should have 5 columns for an X-chromosomal data set and 3 columns for an autosomal data set.
- **x.linked**: Logical indicating whether the markers are autosomal (x.linked = FALSE) or X-chromosomal (x.linked = TRUE).
- **pvalues**: Logical indicated whether chi-square statistics should be returned (pvalues = FALSE) or whether p-values should be returned (pvalues = TRUE).

Details

Matrix X should strictly comply with the following format. For an autosomal dataset it should contain the 3 genotype counts in order (AA, AB, BB). For an X-chromosomal dataset it should contain the 5 genotype counts in order (A, B, AA, AB, BB) where A and B are the male counts and AA, AB and BB the female counts.

This function was written for speed improvement, and should be much faster than looping over the rows of X with HWChisq. There is no error checking on the supplied data matrix.

Value

A vector of chi-square statistics

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

References


See Also

HWChisq
Examples

# # Autosomal example
#
set.seed(123)
X <- HWData(1000, 100)
monom <- (X[, 2] == 0 & X[, 1] == 0) | (X[, 2] == 0 & X[, 3] == 0)
X <- X[monom] # exclude monomorphics
Chisq.stats <- HWChisqStats(X, x.linked=FALSE, pvalues=FALSE)
Chisq.pvals <- HWChisqStats(X, x.linked=FALSE, pvalues=TRUE)

# # Chromosomal example
#
X <- HWData(1000, 100, n.males=50, nA=75, x.linked=TRUE)
Chisq.stats <- HWChisqStats(X, x.linked=TRUE, pvalues=FALSE)
Chisq.pvals <- HWChisqStats(X, x.linked=TRUE, pvalues=TRUE)

hwclo
Convert genotype counts to compositions

Description
Function hwclo divides each row of a matrix by its total, and so produces matrix of compositions.

Usage
hwclo(X)

Arguments
X A matrix of (genotype) counts

Value
A matrix

Author(s)
Jan Graffelman <jan.graffelman@upc.edu>

See Also
HWAlr, HWClr, HWIlr

Examples
X <- HWData(2, 100)
Y <- hwclo(X)
**Description**

`HWClr` computes the centred log-ratio transformation for genotype counts of bi-allelic genetic markers.

**Usage**

```r
HWClr(X, zeroadj = 0.5)
```

**Arguments**

- **X**: A matrix of genotype counts (columns AA, AB and BB)
- **zeroadj**: A zero adjustment parameter (0.5 by default)

**Value**

A matrix or vector of log-ratio coordinates

**Author(s)**

Jan Graffelman (jan.graffelman@upc.edu)

**References**


**See Also**

`HWAlr`, `HWIlr`

**Examples**

```r
X <- HWData(100,100)
Y <- HWClr(X)
```
**HWClnPlot**

*Plot genetic markers in centred log-ratio coordinates*

**Description**

HWClnPlot creates a scatter plot of the centred log-ratio coordinates of bi-allelic genetic markers. Hardy-Weinberg equilibrium is indicated by a straight line in the plot.

**Usage**

```r
HWClnPlot(x, zeroadj = 0.5)
```

**Arguments**

- **x**: A matrix of genotype counts (columns AA, AB, BB)
- **zeroadj**: Zero-adjustment parameter. Zero counts in the count matrix are substituted by `zeroadj` which is 0.5 by default.

**Value**

NULL

**Author(s)**

Jan Graffelman (jan.graffelman@upc.edu)

**References**


**See Also**

HWAlnPlot, HWIlnPlot

**Examples**

```r
X <- HWCln(HWData(100, 100))
HWClnPlot(X)
```
HWCondProbAB  Compute probability of a genotypic sample

Description

Computes the probability of a particular genotypic sample given the allele count, sample size and number of heterozygotes.

Usage

HWCondProbAB(n, nA, nAB)

Arguments

n  n is the total sample size (total number of individuals)
nA  nA is the number of A alleles in the sample
nAB  nAB is the number of heterozygotes in the sample

Value

p  probability of the particular sample

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

See Also

HWExact

Examples

x <- c(298,489,213)
names(x) <- c("MM","MN","NN")
n <- sum(x)
nMN <- x[2]
p <- HWCondProbAB(n,nM,nMN)
**HWD**

*Compute disequilibrium statistic D*

---

**Description**

Function `HWD` computes Weir’s disequilibrium coefficient D.

**Usage**

```r
HWD(x)
```

**Arguments**

- `x`: a vector of genotype counts (AA, AB, BB)

**Value**

Returns the disequilibrium coefficient

**Author(s)**

Jan Graffelman <jan.graffelman@upc.edu>

**References**


**See Also**

`HWf` `HWChisq`

**Examples**

```r
x <- c(MM=298, MN=489, NN=213)
D <- HWD(x)
cat("Diseasequilibrium coefficient: ", D, "\n")
```
HWData

Generate genetic marker data in or out of Hardy-Weinberg Equilibrium

Description

HWData generates samples of genotypic counts under various schemes. It mainly uses sampling from the multinomial distribution given Hardy-Weinberg allele frequencies.

Usage

```r
HWData(nm = 100, n = rep(100, nm), f = rep(0, nm), p = NULL, conditional = FALSE, exactequilibrium = FALSE, pdist = "runif", x.linked = FALSE, nA = NULL, n.males=rep(round(0.5*n),nm), ...)```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>nm</td>
<td>The number of bi-allelic markers.</td>
</tr>
<tr>
<td>n</td>
<td>The sample sizes.</td>
</tr>
<tr>
<td>f</td>
<td>The inbreeding coefficients (only for autosomal markers)</td>
</tr>
<tr>
<td>p</td>
<td>A vector of allele frequencies</td>
</tr>
<tr>
<td>conditional</td>
<td>If TRUE Haldane’s distribution is used for sampling, if FALSE a multinomial distribution is used. Replaces parameter pfixed from the previous version of the package</td>
</tr>
<tr>
<td>exactequilibrium</td>
<td>Generates data in exact HWE if set to TRUE</td>
</tr>
<tr>
<td>pdist</td>
<td>Take a random allele frequency from a uniform or beta distribution of pfixed = FALSE and p is not given.</td>
</tr>
<tr>
<td>x.linked</td>
<td>Simulated autosomal markers (x.linked=FALSE, the default) or X-chromosomal markers (x.linked=TRUE)</td>
</tr>
<tr>
<td>nA</td>
<td>A vector of minor allele counts, one for each marker. If not specified, it will be calculated from p</td>
</tr>
<tr>
<td>n.males</td>
<td>The number of males (only relevant if x.linked = TRUE)</td>
</tr>
<tr>
<td>...</td>
<td>Specific parameters for the uniform or beta</td>
</tr>
</tbody>
</table>

Details

The exactequilibrium option only takes effects for autosomal markers (x.linked=FALSE) and multinomial sampling (conditional=FALSE).

Option pfixed is deprecated and replaced by conditional

HWData returns a matrix of genotype counts, nm by 3 for autosomal markers or nm by 5 for X-chromosomal markers. Output is no longer supplied in the compositional form. Function HWClo can be used to convert the genotype counts to a composition.
If the inbreeding coefficient is specified \((f)\) it will only take effect for autosomal markers \((x\_linked=FALSE)\) and multinomial sampling \((conditional=FALSE)\).

**Value**

\[X\] A matrix containing the genotype counts.

**Author(s)**

Jan Graffelman (jan.graffelman@upc.edu)

**See Also**

`hwternaryplot`

**Examples**

```r
nm <- 100
n <- 100
out <- HWData(nm,n)
```

---

**Description**

`HWExact` performs an exact test for Hardy-Weinberg equilibrium

**Usage**

```r
HWExact(X, alternative = "two.sided", pvaluetype = "selome", x.linked = FALSE, verbose = TRUE)
```

**Arguments**

- **X**: vector with the genotype counts AA, AB, BB
- **alternative**: `two.sided` (default) will perform a two-sided test where both an excess and a dearth of heterozygotes count as evidence against HWE. `less` is a one-sided test where only dearth of heterozygotes counts a evidence against HWE, `greater` is a one-sided test where only excess of heterozygotes counts as evidence against HWE.
- **pvaluetype**: if `pvaluetype` is set to `dost` then the p-value of a two-sided test is computed as twice the tail area of a one-sided test. When set to `selome`, the p-value is computed as the sum of the probabilities of all samples less or equally likely as the current sample. When set to `midp`, the p-value is computed as half the probability of the current sample + the probabilities of all samples that are more extreme.
x.linked  x.linked=FALSE indicates the marker is autosomal (default), and x.linked=TRUE indicates it resides on the X-chromosome.

verbose  print results or not.

Details

HWExact uses the recursion equations described by Wigginton et. al.

For testing large sets of bi-allelic variants, use the faster code in HWExactStats.

For large samples, HWExact may give the error message: "evaluation nested too deeply: infinite recursion". This can usually be resolved by increasing R’s limit on nested expressions with options(expressions=10000) or a higher limit. With higher limits, the error message "protect(): protection stack overflow" can occur. This error can usually be resolved by increasing R’s protection stack with the command line option --max-ppsize 100000 or higher values. However, with such large samples the exact test will give virtually the same result as a chi-square test, and it may be easier to use HWChisq in these circumstances.

Value

pval  p-value of the exact test
prob  probabilities of all possible samples with the same sample size and minor allele count
pofthesample  probability of the observed sample

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References


See Also

HWLRatio, HWChisq, HWExactStats

Examples

# Example for an autosomal marker using the standard exact p-value
#
x <- c(298,489,213)
names(x) <- c("MM","MN","NN")
HW.test <- HWExact(x,verbose=TRUE)
#
HWExactMat

Matrix version of HWExact

Description

HWExactMat executes a fast Exact test for HWE for each row in a matrix.

Usage

HWExactMat(X, ...)

Arguments

X      A n times 3 matrix of genotypic counts (AA,AB,BB)
...
extra arguments that are passed on to HWExact

Value

pvalvec     Vector with the p-values of each test

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

See Also

HWExact

Examples

X <- HWData(100,10)
colnames(X) <- c("MM","MN","NN")
Results <- HWExactMat(X)
Output <- cbind(X,Results$pvalvec)
print(Output)
**Description**

HWExactPrevious performs an exact test for Hardy-Weinberg equilibrium

**Usage**

```r
HWExactPrevious(X, alternative = "two.sided", pvaluetype = "selome", x.linked = FALSE, verbose = FALSE)
```

**Arguments**

- **X**: vector with the genotype counts AA, AB, BB
- **alternative**: two.sided (default) will perform a two-sided test where both an excess and a dearth of heterozygotes count as evidence against HWE. less is a one-sided test where only dearth of heterozygotes counts a evidence against HWE, greater is a one-sided test where only excess of heterozygotes counts as evidence against HWE.
- **pvaluetype**: if pvaluetype is set to dost then the p-value of a two-sided test is computed as twice the tail area of a one-sided test. When set to selome, the p-value is computed as the sum of the probabilities of all samples less or equally likely as the current sample. When set to midp, the p-value is computed as half the probability of the current sample + the probabilities of all samples that are more extreme.
- **x.linked**: x.linked=FALSE indicates the marker is autosomal (default), and x.linked=TRUE indicates it resides on the X-chromosome.
- **verbose**: print results or not.

**Details**

HWExactPrevious uses the recursion equations described by Wigginton et. al.

For large samples, HWExactPrevious may give the error message: "evaluation nested too deeply: infinite recursion". This can usually be resolved by increasing R’s limit on nested expressions with `options(expressions=100000)` or a higher limit. With higher limits, the error message "protect(): protection stack overflow" can occur. This error can usually be resolved by increasing R’s protection stack with the command line option `--max-psize 100000` or higher values. However, with such large samples the exact test will give virtually the same result as a chi-square test, and it may be easier to use HWChisq in these circumstances.

**Value**

- **pval**: p-value of the exact test
- **prob**: probabilities of all possible samples with the same sample size and minor allele count
- **pofthesample**: probability of the observed sample
Author(s)
Jan Graffelman (jan.graffelman@upc.edu)

References

See Also
HWLRatio, HWHisq

Examples

# Example autosomal marker
x <- c(298, 489, 213)
names(x) <- c("MM","MN","NN")
## Not run: HW.test <- HWExactPrevious(x,verbose=TRUE)
# Example X-linked marker
rs5968922 <- c(A=392, B=212, AA=275, AB=296, BB=80)
## Not run: HWExactPrevious(rs5968922,x.linked=TRUE,verbose=TRUE)

---

**HWExactStats**

*Computation of Exact p-values for Hardy-Weinberg equilibrium for sets of SNPs*

**Description**

HWExactStats is a function for the computation of Exact p-values for a large set of bi-allelic markers (typically SNPs).

**Usage**

HWExactStats(X, x.linked = FALSE, plinkcode = TRUE, midp = FALSE, ...)

**Arguments**

- **X**
  A matrix with genotype counts, one row per marker. X should have 5 columns for an X-chromosomal data set and 3 columns for an autosomal data set.

- **x.linked**
  Logical indicating whether the markers are autosomal (x.linked=FALSE) or X-chromosomal (x.linked=TRUE).

- **plinkcode**
  Logical indicating whether to use faster C++ code from the PLINK software.

- **midp**
  Logical indicating whether to use the mid p-value for the C++ code or not

- **...**
  Extra arguments that are passed on to HWExact
Heatmap

Details

Matrix X should strictly comply with the following format. For an autosomal dataset it should contain the 3 genotype counts in order (AA,AB,BB). For an X-chromosomal dataset it should contain the 5 genotype counts in order (A,B,AA,AB,BB) where A and B are the male counts and AA, AB and BB the female counts.

Argument plinkcode=TRUE (the default) will use C++ code for faster calculation (functions snphwe2 and snphwex) with larger datasets. The C++ code was generously shared by Christopher Chang, and the same code is used in the program PLINK (2.0).

Value

A vector of p-values

Author(s)

Jan Graffelman <jan.graffelman@upc.edu> (R code) and Christopher Chang <chrchang523@gmail.com> (C++ code)

References


See Also

HWExact

Examples

#
# Autosomal example
#
set.seed(123)
X <- HWData(1000,100)
monom <- (X[,2]==0 & X[,1]==0) | (X[,2]==0 & X[,3]==0)
X <- X[!monom,] # exclude monomorphics
Exact.pvalues <- HWExactStats(X,x.linked=FALSE)
#
# X-chromosomal example
#
X <- HWData(1000,100,n.males=50,nA=75,x.linked=TRUE)
Exact.pvalues <- HWExactStats(X,x.linked=TRUE)
**HWf**

*Computation of inbreeding coefficient*

**Description**

`HWf` computes the inbreeding coefficient for a sample of genotypes.

**Usage**

`HWf(x)`

**Arguments**

- `x`: a vector of genotype counts (AA, AB, BB)

**Details**

For monomorphic markers a warning is issued, and the estimate for the inbreeding coefficient is set to zero.

**Value**

Returns the inbreeding coefficient (intra-class correlation coefficient)

**Author(s)**

Jan Graffelman <jan.graffelman@upc.edu>

**References**


**See Also**

`HWChisq`

**Examples**

```r
x <- c(MM=298, MN=489, NN=213)
f <- HWf(x)
cat("Inbreeding coefficient: ", f, "\n")
```
Description

HWGenotypePlot makes a scatterplots of the AB or BB frequency versus the AA frequency and represents a blue curve indicating the Hardy-Weinberg equilibrium condition.

Usage

HWGenotypePlot(x, plottype = 1, xlab = expression(f[AA]), ylab = ifelse(plottype == 1, expression(f[AB]), expression(f[BB])), asp = 1, pch = 19, xlim = c(0, 1), ylim = c(0, 1), cex = 1, cex.axis = 2, cex.lab = 2, ...)

Arguments

x A matrix of genotype counts or frequencies with three columns (AA, AB, BB)
plottype plottype=1 produces a plot of AB versus AA, plottype=2 produced a plot of BB versus AA.
xlab A label for the x axis
ylab A label for the y axis
asp Aspec ratio (1 by default)
pch Plotting charachter (19 by default)
xlim Limits for the x axis (0-1 by default)
ylim Limits for the y axis (0-1 by default)
cex Character expansion factor (1 by default)
cex.axis Character expansion factor for the axes (2 by default)
cex.lab Character expansion factor for labels of axis (2 by default)
... Additional arguments for the plot function

Value

NULL

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

See Also

HWternaryplot
Examples

```r
n <- 100 # sample size
m <- 100 # number of markers
Xc <- HWClo(HWData(n,m))
HWGenotypePlot(Xc, plottype=1, main="Heterozygote-homozygote scatterplot")
```

**HWI1r**  
*Compute isometric log ratio coordinates.*

**Description**

HWI1r computes isometric log ratio coordinates for genotypic compositions (AA, AB, BB)

**Usage**

```r
HWI1r(X, zeroadj = 0.5)
```

**Arguments**

- `X`: A matrix of genotype counts, markers in rows, counts for AA, AB and BB in three columns
- `zeroadj`: Adjustment for zeros (0.5 by defaults)

**Value**

A matrix of log ratio coordinates.

**Author(s)**

Jan Graffelman (jan.graffelman@upc.edu)

**References**


**See Also**

HWAlr, HWClr

**Examples**

```r
X <- HWData(100,100)
Y <- HWI1r(X)
```
\textbf{HWIlrPlot} \hspace{1cm} \textit{Plot bi-allelic genetic markers in isometric log ratio coordinates}

\section*{Description}

\texttt{HWIlrPlot} makes a scatter plot of the isometric log ratio coordinates for bi-allelic markers.

\section*{Usage}

\texttt{HWIlrPlot(X, zeroadj = 0.5, \ldots)}

\section*{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} Matrix of genotype counts, one marker per row, AA, AB and BB in three columns
  \item \texttt{zeroadj} \hspace{1cm} Adjustment for zero values (0.5 by default)
  \item \ldots \hspace{1cm} Additional arguments for function \texttt{plot}
\end{itemize}

\section*{Value}

A matrix of log ratio coordinates.

\section*{Author(s)}

Jan Graffelman (jan.graffelman@upc.edu)

\section*{References}


\section*{See Also}

\texttt{HWAlrPlot,HWClrPlot}

\section*{Examples}

\begin{verbatim}
X <- HWClo(HWData(100,100))
HWIlrPlot(X)
\end{verbatim}
HWLRAllTests

Perform most relevant likelihood ratio test for Hardy-Weinberg equilibrium and equality of allele frequencies

Description

Function HWLRAllTests performs a set of likelihood ratio tests in relation with Hardy-Weinberg proportions (HWP) and equality of allele frequencies (EAF) for autosomal bi-allelic genetic variants.

Usage

HWLRAllTests(x, y)

Arguments

x Male genotype counts (AA,AB,BB)
y Female genotype counts (AA,AB,BB)

Details

Function HWLRAllTests calls HWLRtest and calculates the p-value of six different tests: 1) joint HWP and EAF (A-F); 2) EAF irrespective of HWP (C-F); 3) HWP irrespective of EAF (D-F); 4) HWP versus EIC (given EAF) (A-B); 5) EIC irrespective of EAF (E-F) and 6) HWP versus EIC. Letters refer to scenarios described by Graffelman & Weir (2017).

Value

A named vector with six p-values

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

References


See Also

HWLRtest
Examples

```r
males <- c(AA=11, AB=32, BB=13)
females <- c(AA=14, AB=23, BB=11)
pvalues <- HWLRAllTests(males, females)
print(pvalues)
```

**Description**

`HWLRatio` performs the Likelihood ratio test for Hardy Weinberg equilibrium, both for autosomal and X-chromosomal markers.

**Usage**

```r
HWLRatio(x, verbose = TRUE, x.linked = FALSE)
```

**Arguments**

- `x` a vector containing the genotypic counts (AA, AB, BB).
- `verbose` `verbose = TRUE` prints results, `verbose = FALSE` is silent.
- `x.linked` `x.linked = FALSE` indicates the marker is autosomal (default), and `x.linked = TRUE` indicates it resides on the X-chromosome.

**Value**

`HWLRatio` returns a list with the components:

- `Lambda` the likelihood ratio
- `G2` `-2*log(Lambda)`
- `pval` the p-value

**Author(s)**

Jan Graffelman <jan.graffelman@upc.edu>

**References**


**See Also**

`HWChisq`
Examples

```r
x <- c(298, 489, 213)
names(x) <- c("MM", "MN", "NN")
HWL.test <- HWLratio(x, verbose=TRUE)
#
# Test for an X-chromosomal SNP.
#
rs5968922 <- c(A=392, B=212, AA=275, AB=296, BB=80)
HWL.test <- HWLratio(rs5968922, x.linked=TRUE, verbose=TRUE)
```

Description

Program `HWLtest` performs a likelihood ratio test comparing two scenarios for an autosomal bi-allelic genetic variant. The scenarios concern Hardy-Weinberg proportions (HWP) and equality of allele frequencies (EAF) in both sexes. The different scenarios are described by Graffelman & Weir (2017).

Usage

```r
HWLtest(x, y, scene.null = "S1", scene.alt = "S6", verbose = TRUE, tracing = 0)
```

Arguments

- **x**: Male genotype counts
- **y**: Female genotype counts
- **scene.null**: Scenario under the null hypothesis (E.g. "S1")
- **scene.alt**: Scenario under the alternative hypothesis (E.g. "S6")
- **verbose**: print output or not
- **tracing**: Show tracing of the numeric likelihood maximization (1) or not (0).

Details

The different scenarios are indicated with S1, S2, S3, S4, S6 and S6. S1 refers to Hardy-Weinberg proportions and equality of allele frequencies. S2 refers to equality of allele frequencies and equality of inbreeding coefficients for the two sexes. S3 refers to equality of allele frequencies irrespective of HWP. S4 refers to HWP irrespective of allele frequencies. S5 refers to equality of inbreeding coefficients irrespective of allele frequencies. S6 is unrestricted.

Value

- **G2**: Likelihood ratio statistic
- **df**: Degrees of freedom of the likelihood ratio statistic
- **pval**: p-value
**Author(s)**

Jan Graffelman <jan.graffelman@upc.edu>

**References**


**See Also**

hwaic

**Examples**

```r
males <- c(AA=11, AB=32, BB=13)
females <- c(AA=14, AB=23, BB=11)

# # test EAF
#
#
lr1.out <- HWLRtest(males,females,scene.null="S3",scene.alt="S6")

# # test EIC given EAF
#
#
lr2.out <- HWLRtest(males,females,scene.null="S2",scene.alt="S3")

# # test HWP versus EIC, given EAF.
#
#
lr3.out <- HWLRtest(males,females,scene.null="S1",scene.alt="S2")
```

---

**HWMissing**

Test a bi-allelic marker for Hardy-Weinberg equilibrium in the presence of missing genotype information.

**Description**

Function *HWMissing* imputes missing genotype data with a multinomial logit model that uses information from allele intensities and/or neighbouring markers. Multiple imputation algorithms implemented in the Mice package are used to obtain imputed data sets. Inference for HWE is carried out by estimating the inbreeding coefficient or exact p-values for each imputed data set, and by combining all estimates using Rubin’s pooling rules.
Usage

```r
HWMissing(X, imputecolumn = 1, m = 50, coding = c(0,1,2), verbose = FALSE, alpha = 0.05,
          varest = "oneovern", statistic = "chisquare", alternative = "two.sided", ...)
```

Arguments

- **X**
  - An input data frame. By default, the first column should contain the SNP with missing values.

- **imputecolumn**
  - Indicates which column of the supplied data frame is to be imputed (by default, the first column, `imputecolumn`=1)

- **m**
  - The number of imputations (50 by default)

- **coding**
  - Indicates how the genotype data is coded (e.g. 0 for AA, 1 for AB, and 2 for BB).

- **verbose**
  - `verbose` = TRUE prints results, `verbose` = FALSE is silent.

- **alpha**
  - Significance level (0.05 by default) used when computing confidence intervals

- **varest**
  - Estimator for the variance of the inbreeding coefficient. `varest="oneovern"` is the default and sets the variance under the null (1/n). `varest="bailey"` uses an approximation (see details).

- **statistic**
  - If `statistic = "chisquare"` then inbreeding coefficients (equivalent to chisquare statistics) will be computed for each imputed data set and then combined. If `statistic = "exact"` then one-sided exact tests will be computed for each imputed data set and the resulting p-values will be combined.

- **alternative**
  - `two.sided` (default) will perform a two-sided test where both an excess and a dearth of heterozygotes count as evidence against HWE. `less` is a one-sided test where only dearth of heterozygotes counts as evidence against HWE, `greater` is a one-sided test where only excess of heterozygotes counts as evidence against HWE.

- **...**
  - Additional options for function `mice` of the Mice package

Details

The function `HWMissing` tests one genetic marker (e.g. a SNP) with missings for HWE. By default, this marker is supposed to be the first column of data frame `X`. The other columns of `X` contain covariates to be used in the imputation model. Covariates will typically be other, correlated markers or allele intensities of the SNP to be imputed. Covariate markers should be coded as factor variables whereas allele intensities should be numerical variables. By default, a polytomous regression model will be used to impute the missings. If the covariates also contain missings, an imputation method for each column of `X` can be specified by using the method of `mice` (see example below).

If there are no covariates, missings can be imputed under the MCAR assumption. In that case, missings are imputed by taking a random sample from the observed data. This is what `HWMissing` will do if no covariates are supplied, `X` being a single factor variable.

Several estimators for the variance of the inbreeding coefficient have been described in the literature. The asymptotic variance of the inbreeding coefficient under the null hypothesis is 1/n, and is used if `varest = "oneovern"` is used. This is the recommended option. Alternatively, the approximation described in Weir (p. 66) can be used with `varest = "bailey"`.
**Value**

- **Res**: A vector with the inbreeding coefficient, a confidence interval for the inbreeding coefficient, a p-value for a HWE test and missing data statistics.
- **Xmat**: A matrix with the genotypic composition of each of the \( m \) imputed data sets.

**Author(s)**

Jan Graffelman <jan.graffelman@upc.edu>

**References**


http://dx.doi.org/10.1371/journal.pone.0083316

http://www.jstatsoft.org/v64/i03/.

**See Also**

HWChisq

**Examples**

```r
data(Markers)
## Not run:
set.seed(123)
Results <- HWMissing(Markers[,1],m=50,verbose=TRUE)$Res # no covariates, imputation assuming MCAR.
set.seed(123)
Results <- HWMissing(Markers[,1:3],m=50,verbose=TRUE)$Res # impute with two allele intensities.
set.seed(123)
Results <- HWMissing(Markers[,c(1,4,5)],m=50,verbose=TRUE)$Res # impute with two covariate SNPs
## End(Not run)
```

**HWPerm**  
*Permutation test for Hardy-Weinberg equilibrium*

**Description**

Function `HWPerm` does a permutation test for Hardy-Weinberg equilibrium using a user-supplied test statistic.

**Usage**

```
HWPerm(x, nperm = 17000, verbose = TRUE, x.linked = FALSE, 
FUN = ifelse(x.linked,Chisquare.x,Chisquare), ...)
```
Arguments

x A vector of genotype counts (AA, AB, BB)
np The number of permutations
verbose verbose = TRUE will print results, verbose = FALSE is silent.
x.linked x.linked = FALSE indicates the marker is autosomal (default), and x.linked = TRUE indicates it resides on the X-chromosome.
FUN An function call for calculating the test statistic for HWE (see examples below)
... Additional parameters for the function call argument FUN

Details

The set of alleles for the observed sample is permuted. Consequently, the test is conditional on allele frequency.

Value

HWPerm returns a list with the components:

stat value of the chosen test statistic for the observed sample.
pval p-value of the permutation test.

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

References


See Also

```
HWChisq, HWExact, HWLRatio
```

Examples

```r
x <- c(MM=298, MN=489, NN=213)
## Not run:
HW.test <- HWPerm(x, nperm=10000, verbose=TRUE) # uses default chi-square statistic
HW.test <- HWPerm(x, nperm=10000, verbose=TRUE, function(z)
HWChisq(z)$chisq, cc=0.5) # uses chi-square statistic with continuity correction.
HW.test <- HWPerm(x, nperm=10000, verbose=TRUE, function(y) HWLRatio(y)$G2)
# uses likelihood ratio statistic.
HWPerm(x, nperm=10000, verbose=TRUE, function(y) 1-HWExact(y)$pval)
# uses exact test p-value
# # Permutation test for a marker on the X chromosome
#
rs5968922 <- c(A=392, B=212, AA=275, AB=296, BB=80)
HW.test <- HWPerm(rs5968922, nperm=10000, x.linked=TRUE, verbose=TRUE)
```
**Description**

Function `HWPermmult` implements permutation tests for Hardy-Weinberg equilibrium for autosomal and X-chromosomal variants.

**Usage**

```r
HWPerm.mult(x, y = NULL, nperm = 17000, eps = 0, verbose = TRUE, ...)
```

**Arguments**

- `x`: vector or triangular matrix with male genotype counts
- `y`: vector or triangular matrix with female genotype counts
- `nperm`: number of permutations (17,000 by default)
- `eps`: a tolerance that can be set for comparing probabilities in order to include tied outcomes
- `verbose`: print output or not
- `...`: additional arguments

**Details**

This function approximates exact test probabilities for joint tests for HWE and equality of allele frequencies for variants with multiple alleles. For purely bi-allelic variant `HWPerm` can be used which allows for more statistics than just probabilities.

If argument `y` is not specified, gender is considered irrelevant, and `x` contains total genotype counts. If `x` and `y` are specified, `x` should contain male genotype counts and `y` female genotype counts. `x` and `y` can be vectors if the variant is bi-allelic, but are assumed lower triangular if there are more than two alleles. `x` is still a vector if there are multiple alleles but the variant is X-chromosomal. See the examples given below.

**Value**

- `pofthesample`: probability of the observed sample
- `pseudodist`: probabilities of simulated samples
- `pval`: p-value

**Author(s)**

Jan Graffelman `<jan.graffelman@upc.edu>`
References


See Also

HWPerm

Examples

```r
# bi-allelic autosomal
#
x1 <- c(AA=298, AB=489, BB=213)
## Not run:
out <- HWPerm.mult(x1)
## End(Not run)

# bi-allelic X-chromosomal
#
x2.m <- c(A=39, B=21)
x2.f <- toTriangular(c(AA=28, AB=30, BB=8))
## Not run:
out <- HWPerm.mult(x2.m, x2.f)
## End(Not run)

# autosomal k alleles not accounting for gender
#
x3 <- c(AA=12, AB=19, AC=13, BB=7, BC=5, CC=0)
x3 <- toTriangular(x3)
## Not run:
out <- HWPerm.mult(x3)
## End(Not run)

# X-chromosomal k alleles
#
x4.m <- c(A=15, B=17, C=24)
x4.f <- toTriangular(c(AA=4, AB=2, AC=13, BB=6, BC=19, CC=4))
## Not run:
out <- HWPerm.mult(x4.m, x4.f)
## End(Not run)
```
HWPosterior

Calculation of posterior probabilities and Bayes factors for Hardy-Weinberg tests at X-chromosomal variants.

Description

Function `HWPosterior` calculates posterior probabilities and Bayes factors for tests for Hardy-Weinberg equilibrium of X-chromosomal variants. Four possible models are considered, and the posterior probabilities and Bayes factors for each model are calculated.

Usage

```
HWPosterior(X, verbose = TRUE, prior.af = c(0.5,0.5), prior.gf = c(0.333,0.333,0.333))
```

Arguments

- `X` A vector of genotype counts. The order c(A,B,AA,AB,BB) is assumed. Differently ordered vectors can be supplied but then elements must be labeled by their genotype
- `verbose` prints results if `verbose = TRUE`
- `prior.af` Beta prior parameters for male and female allele frequencies
- `prior.gf` Dirichlet prior parameters for female genotype frequencies

Details

Default priors are used for genotype and allele frequencies.

Value

A matrix with posterior probabilities and Bayes factors.

Author(s)

Xavi Puig <xavier.puig@upc.edu> and Jan Graffelman <jan.graffelman@upc.edu>
References

See Also
HWChisq, HWEexact, HWEexactStats

Examples
x <- c(A=43, B=13, AA=26, AB=19, BB=3)
out <- HWPosterior(x, verbose=TRUE)

HWPower

**Compute the power of a test for Hardy-Weinberg equilibrium.**

Description
HWPower is a function that computes the power of a test for Hardy-Weinberg equilibrium.

Usage
HWPower(n = 100, nA = 100, pA = 0.5, y = c(AA=25, AB=50, BB=25), alpha = 0.05, theta = 4, f = NULL, test = "exact", alternative = "two.sided", pvaluetype = "selome", cc = 0.5)

Arguments
- **n**: The sample size
- **nA**: The minor allele count
- **pA**: The minor allele frequency
- **y**: A sample of genotype counts (AA, AB, BB)
- **alpha**: The significance level (0.05 by default)
- **theta**: The degree of disequilibrium (theta = 4 is equilibrium, theta > 4 is heterozygote excess, theta < 4 is heterozygote dearth)
- **f**: The inbreeding coefficient. Overrules theta if specified.
- **test**: The type of test for which power is to be computed. Can be "exact" (default) or "chisq" (chi-square)
- **alternative**: The nature of the alternative hypothesis ("two.sided" (default), "greater" or "less")
- **pvaluetype**: The type of p-value used in an exact test ("selome", "dost" or "midp")
- **cc**: Continuity correction parameter for the chi-square test (0.5 by default)
Details

`HWPower` uses the Levene-Haldane distribution (distribution of the number of heterzygotes given the minor allele count) for computing power.

`HWPower` can be used in three different ways. In principle, the power is calculated on the basis of the sample size (\(n\)) and the minor allele count (\(n_A\)). Alternatively, the user may specify sample size (\(n\)) and minor allele frequency (\(p_A\)). Finally, power can also be calculated directly from a sample of genotype counts. In that case the calculated power is the power for a sample of the given sample size and minor allele count. The three ways to use `HWPower` are illustrated in the example section.

Value

- if `test = "exact"` the power of the exact test is computed for the given significance level and minor allele count.
- if `test = "chisq"` the power of the chi-square test is computed for the given significance level and minor allele count.

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References


See Also

`HWExact`

Examples

```r
pw.chisq <- HWPower(n=100,nA=100,alpha=0.05,test="chisq",theta=16)
print(pw.chisq)
pw.exact <- HWPower(n=100,nA=100,alpha=0.05,test="exact",theta=16,pvaluetype="selome")
print(pw.exact)
pw.exact <- HWPower(n=100,nA=100)
print(pw.exact)
pw.exact <- HWPower(n=100,pA=0.5)
print(pw.exact)
pw.exact <- HWPower(y=c(AA=25,AB=50,BB=25))
print(pw.exact)
```
HWQqplot  

A Q-Q plot for Hardy-Weinberg equilibrium

Description

HWQqplot creates a Q-Q plot for the p-values obtained in an Exact test for Hardy-Weinberg equilibrium. Empirical p-values are plotted against multiple simulated quantiles of the theoretical p-value distribution.

Usage

```
HWQqplot(x, nsim = 100, fit = "curve", logplot = FALSE,
         main = "Q-Q plot for HWE", mm = NULL, pvaluetype = "selome", ...)
```

Arguments

- **x**  
  Data matrix with genotype counts, one row for each sample, 3 columns
- **nsim**  
  Number of samples drawn from the null distribution (100 by default)
- **fit**  
  If fit is set to "line" straight lines will be fitted to the simulated samples, if set to "curve", ascending curves will be shown.
- **logplot**  
  If logplot is set to true, then the log10 of the p-values will be used in the plot. If not, untransformed p-values will be used.
- **main**  
  Title for the plot
- **mm**  
  Maximal value for x and y axis in the plot
- **pvaluetype**  
  Type of p-value to be used in an exact test. Can be "selome" (default), "midp" or "dost".
- ...  
  Any additional arguments for the plot instruction

Details

HWQqplot constructs a Q-Q plot of the p-values of an exact test for Hardy-Weinberg equilibrium. Under the null, this p-value is not uniform. HWQqplot samples from the theoretical null distribution, taking into account that markers may vary in allele frequency and in sample size (due to missing values). For each simulated sample a grey curve or line is shown. A green reference line with intercept 0 and slope 1 is also shown in the plot.

Value

NULL

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>
References


See Also

HWternaryplot HWexact qqplot

Examples

```r
## Not run:
set.seed(1234)
n <- 200 # sample size
m <- 100 # number of markers
X <- HWData(n,m)$X
HWQqplot(X,logplot=TRUE,pvaluetype="selome",main="Q-Q Plot for HWE")
```

```
## End(Not run)
```

**Description**

**HWternaryplot** is a routine that draws a ternary plot for three-way genotypic compositions (AA, AB, BB), and represents the acceptance region for different tests for Hardy-Weinberg equilibrium (HWE) in the plot. This allows for graphical testing of a large set of markers (e.g. SNPs) for HWE. The (non) significance of the test for HWE can be inferred from the position of the marker in the ternary plot. Different statistical tests for HWE can be done graphically with this routine: the ordinary chisquare test, the chisquare test with continuity correction and the Haldane's exact test.

**Usage**

```r
HWternaryplot(X, n = NA, addmarkers = TRUE, newframe = TRUE, hwcurve = TRUE, vbounds = TRUE, mafbounds = FALSE, mafvalue = 0.05, axis = 0, region = 1, vertexlab = colnames(X), alpha = 0.05, vertex.cex = 1, pch = 19, cc = 0.5, markercol = "black", markerbgcol = "black", cex = 0.75, axislab = "", verbose = FALSE, markerlab = NULL, markerpos = NULL, mcex = 1, connect = FALSE, curvecols = rep("black",5), signifcolour = TRUE, curtyp = "solid", ssf = "max", pvaluetype = "selome", ...)
```

**Arguments**

- **X**: a matrix of \( n \) genotypic compositions or counts. If it is a matrix of compositions, \( X \) should have \( n \) rows that sum 1, and 3 columns, with the relative frequencies of AA, AB and BB respectively. Argument \( n \) should be supplied as well. If \( X \) is a matrix of raw genotypic counts, it should have 3 columns with the absolute counts of AA, AB and BB respectively. Argument \( n \) may be supplied and will
be used for painting acceptance regions. If not supplied \( n \) is computed from the data in \( X \).

- **addmarkers**: represent markers by dots in the triangle (addmarkers=TRUE) or not (addmarkers=FALSE).

- **newframe**: allows for plotting additional markers in an already existing ternary plot. Overplotting is achieved by setting newframe to FALSE. Setting newframe = TRUE (default) will create a new ternary plot.

- **hwcurve**: draw the HW parabola in the plot (hwcurve=TRUE) or not (hwcurve=FALSE).

- **vbounds**: indicate the area corresponding to expected counts > 5 (vbounds=TRUE) or not (vbounds=FALSE).

- **mafvalue**: a critical value for the minor allele frequency (MAF).

- **axis**: draw a vertex axis
  - 0 = no axis is drawn
  - 1 = draw the AA axis
  - 2 = draw the AB axis
  - 3 = draw the BB axis

- **region**: the type of acceptance region to be delimited in the triangle
  - 0 = no acceptance region is drawn
  - 1 = draw the acceptance region corresponding to a Chi-square test
  - 2 = draw the acceptance region corresponding to a Chi-square test with continuity correction
  - 3 = draw the acceptance region corresponding to a Chi-square test with continuity correction for \( D > 0 \)
  - 4 = draw the acceptance region corresponding to a Chi-square test with continuity correction for \( D < 0 \)
  - 5 = draw the acceptance regions for all preceding tests simultaneously
  - 6 = draw the acceptance region corresponding to a Chi-square test with continuity correction with the upper limit for \( D > 0 \) and the lower limit for \( D < 0 \)
  - 7 = draw the acceptance region corresponding to a two-sided exact test

- **vertexlab**: labels for the three vertices of the triangle

- **alpha**: significance level (0.05 by default)

- **vertex.cex**: character expansion factor for the labels of the vertices of the triangle.

- **pch**: the plotting character used to represent the markers.

- **cc**: value for the continuity correction parameter (0.5 by default).

- **markercol**: vector with colours for the marker points in the triangle.

- **markerbgcol**: vector with background colours for the marker points in the triangle.

- **cex**: expansion factor for the marker points in the triangle.

- **axislab**: a label to be put under the horizontal axis.
verbose print information on the numerically found cut-points between curves of the
acceptance region and the edges of the triangle.
markerlab labels for the markers in the triangle.
markerpos positions for the marker labels in the triangle (1,2,3 or 4).
mceX character expansion factor for the labels of the markers in the ternary plot.
connect connect the represented markers by a line in the ternary plot.
curvecols a vector with four colour specifications for the different curves that can be used
to delimit the HW acceptance region. E.g. curvecols=c("red", "green", "blue", "black", "purple") will paint the Hardy-Weinberg curve red, the limits of the acceptance region for an ordinary chi-square test for HWE green, the limits of the acceptance region for a chi-square test with continuity correction when D > 0 blue and the limits of the acceptance region for a chi-square test with continuity correction when D < 0 black, and the limits of the exact acceptance region purple.
signifcolour colour the marker points automatically according to the result of a significance test (green markers non-significant, red markers significant). signifcolour only takes effect if region is set to 1, 2 or 7.
curtyp style of the drawn curves ("dashed", "solid", "dotted", ...)
ssf sample size function ("max", "min", "mean", "median", ...). Indicates how the sample size for drawing acceptance regions is determined from the matrix of counts.
pvaluetype method to compute p-values in an exact test ("dost" or "selome")
... other arguments passed on to the plot function (e.g. main for a main title).

Details

HWternaryplot automatically colours significant markers in red, and non-significant markers in green if region is set to 1, 2 or 7.

Value

minp minimum allele frequency above which testing for HWE is appropriate (expected counts exceeding 5).
maxp maximum allele frequency below which testing for HWE is appropriate.
inrange number of markers in the appropriate range.
percinrange percentage of markers in the appropriate.
nsignif number of significant markers (only if region equals 1, 2 or 7.)

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

References

See Also

\texttt{HWChisq}

Examples

\begin{verbatim}
  n <- 100 # sample size
  m <- 100 # number of markers

  X <- HWDData(n,m)
  HWternaryPlot(X,100,region=1,hwcurve=TRUE,vbounds=FALSE,vertex.cex=2)
\end{verbatim}

\begin{verbatim}
  HWTriExact  Exact test for Hardy-Weinberg equilibrium and equality of allele frequencies for tri-allelic variants.
\end{verbatim}

Description

Function \texttt{HWTriExact} does a standard exact test for Hardy-Weinberg equilibrium of a tri-allelic variant, and also does joint exact tests for equilibrium and equality of allele frequencies if the genotype counts are given separately for both sexes.

Usage

\texttt{HWTriExact(x, y = NULL, eps = 0, nperm = 17000, verbose = TRUE)}

Arguments

- \texttt{x}: vector with 6 genotype counts (AA,AB,AC,BB,BC,CC)
- \texttt{y}: vector with 6 or 3 genotype counts (AA,AB,AC,BB,BC,CC) or (A,B,C)
- \texttt{eps}: a tolerance that can be set for comparing exact probabilities
- \texttt{nperm}: number of permutations (only relevant for autosomal stratified by gender)
- \texttt{verbose}: print output or not

Details

If only \texttt{x} is specified, an exact test for an autosomal variant with three alleles will be performed. If both \texttt{x} and \texttt{y} are supplied as vectors with 6 elements, a permutation test for HWE and equality of allele frequencies (EAF) for an autosomal variant is performed, using \texttt{nperm} permutations. The distribution of the probabilities is returned in \texttt{pseudodist}. The computational cost of a completed enumeration algorithm can be prohibitive in this case. If \texttt{x} is supplied as a length 6 vector, and \texttt{y} as a length 3 vector, the variant is assumed to be X-chromosomal, \texttt{x} containing female genotype counts and \texttt{y} containing male genotype counts. In this case a joint exact test for HWE and EAF for an X-chromosomal tri-allelic variant is executed. See the examples in the example section below.
Value

pval             The p-value of the sample
pseudodist       Distribution of probabilities obtained by simulation
pofthesample     The probability of the observed sample

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

References


See Also

HWPerm.mult

Examples

#
# Autosomal tri-allelic (not accounting for gender)
#

x <- c(AA=20,AB=31,AC=26,BB=15,BC=12,CC=0)
## Not run: out <- HWTriExact(x)

#
# Autosomal tri-allelic accounting for gender
#

males <- c(A=1,B=21,C=34)
females <- c(AA=0,AB=1,AC=0,BB=8,BC=24,CC=15)
## Not run: out <- HWTriExact(females,males)

#
# X-chromosomal tri-allelic accounting for gender
#

males <- c(A=1,B=21,C=34)
females <- c(AA=0,AB=1,AC=0,BB=8,BC=24,CC=15)
## Not run: out <- HWTriExact(females,males)
### ifisherz

*Inverse Fisher z transformation*

**Description**

Calculates the inverse of Fisher's z transformation

**Usage**

```r
ifisherz(y)
```

**Arguments**

- `y` a real number

**Value**

A correlation coefficient in the range (-1,1)

**Author(s)**

Jan Graffelman (jan.graffelman@upc.edu)

**See Also**

`cor`

**Examples**

```r
r <- 0.5
print(ifisherz(fisherz(r)))
```

### JPTmultiallelicsChr7

*Multi-allelic autosomal variants of the Japanese population of the 1000 genomes project*

**Description**

JPTmultiallelicsChr7 contains three selected multi-allelic variants on chromosome 7 from the Japanese sample of the 1000 genomes project.

**Usage**

```r
data("JPTmultiallelicsChr7")
```
**Format**

List object with fields m4,f4; m5,f5; m6,f6;

**Details**

The list object contains male and female genotype counts for 3 multi-allelic variants on chromosome 7 of the JPT sample of the 1000 genomes project.

**Source**

The [1000 genomes project](https://www.1000genomes.org).

**References**


**Examples**

```r
data(JPTmultiallelicsChr7)
str(JPTmultiallelicsChr7)
```

---

**JPTmultiallelicsChrX**  
*Multi-allelic X-chromosomal variants of the Japanese population of the 1000 genomes project*

**Description**

`JPTtriaallelicsChrX` contains four selected multi-allelic variants on the X chromosome from the Japanese sample of the 1000 genomes project.

**Usage**

```r
data("JPTmultiallelicsChrX")
```

**Format**

List object with fields m4,f4; m5,f5; m6,f6; m7,f7

**Details**

The list object contains male and female genotype counts for four multi-allelic variants of the JPT sample of the 1000 genomes project.

**Source**

The [1000 genomes project](https://www.1000genomes.org).
References


Examples

```r
data(JPTmultiallelicsChrX)
m4 <- JPTmultiallelicsChrX$m4
f4 <- JPTmultiallelicsChrX$f4
```

---

**JPTtriallelicsChr7**

*Tri-allelic variants on chromosome 7 of the Japanese (JPT) sample of the 1000 genomes project*

Description

**JPTtriallelics** contains six selected tri-allelic variants on chromosome 7 from the Japanese sample of the 1000 genomes project.

Usage

```r
data("JPTtriallelicsChr7")
```

Format

A data frame with 6 observations on the following 14 variables.

- **id**: RS identifier
- **pos**: position in base pairs
- **mAa**: number of AA males
- **mAb**: number of AB males
- **mAc**: number of AC males
- **mBb**: number of BB males
- **mBc**: number of BC males
- **mCc**: number of CC males
- **fAa**: number of AA females
- **fAb**: number of AB females
- **fAc**: number of AC females
- **fBb**: number of BB females
- **fBc**: number of BC females
- **fCc**: number of CC females
Source

The 1000 genomes project.

References


Examples

data(JPTtriallelicsChrX)
str(JPTtriallelicsChrX)

---

**JPTtriallelicsChrX**  
Tri-allelic variants on the X-chromosome of the Japanese (JPT) sample of the 1000 genomes project

Description

**JPTtriallelicsChrX** contains five selected tri-allelic variants on the X chromosome from the Japanese sample of the 1000 genomes project.

Usage

data("JPTtriallelicsChrX")

Format

A data frame with 5 observations on the following 12 variables:

- **id**: Identifier of the polymorphism
- **pos**: Position of the polymorphism in base pairs
- **chr**: Chromosome
- **A**: Number of males with A genotype
- **B**: Number of males with B genotype
- **C**: Number of males with C genotype
- **AA**: Number of AA females
- **AB**: Number of AB females
- **AC**: Number of AC females
- **BB**: Number of BB females
- **BC**: Number of BC females
- **CC**: Number of CC females
Source

The 1000 genomes project.

References


Examples

data(JPTriallelicsChrX)
str(JPTriallelicsChrX)

mac

Compute the minor allele count.

Description

mac computes the smallest allele count for a given vector of genotype counts.

Usage

mac(X)

Arguments

X  a vector or matrix with genotype counts (AA, AB, BB)

Value

a vector of the minor allele counts

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

See Also

maf

Examples

X <- as.vector(rmultinom(1,100,c(0.5,0.4,0.1)))
names(X) <- c("AA","AB","BB")
print(X)
print(mac(X))
**maf**

Function to compute minor allele frequencies

**Description**

Function `maf` computes the minor allele frequency for a matrix or vector of compositions.

**Usage**

`maf(x)`

**Arguments**

- `x`: a vector or matrix of genotypic compositions

**Value**

A vector of minor allele frequencies.

**Author(s)**

Jan Graffelman (jan.graffelman@upc.edu)

**Examples**

```r
X <- as.vector(rmultinom(1,100,c(0.5,0.4,0.1)))
X <- X/sum(X)
print(X)
print(maf(X))
```

---

**MakeCounts**

Create genotype counts from bi-allelic marker data

**Description**

`MakeCounts` creates a matrix of genotype counts, with one row for each bi-allelic marker, containing 4 columns with the counts AA, AB, BB and NA (missings) respectively.

**Usage**

`MakeCounts(X, alleles, pos1 = 1, pos2 = 3, coding = c(AA=0,AB=1,BB=2))`
Arguments

X  A matrix or dataframe with bi-allelic genotyping information, markers in columns, individuals in rows

alleles  a vector of alleles for each marker (e.g. c("A/T", "A/G", ...)). Only relevant if X is a matrix with text entries.

pos1  position of the first allele in the allele string (1 by default)

pos2  position of the second allele in the allele string (3 by default)

coding  indicates how homozygotes and heterozygote are coded as numbers. Only relevant if X is a matrix with numeric entries.

Details

MakeCounts is thought for bi-allelic marker data only. Missings should be coded by NA. It produces the right input for HWternaryPlot.

Heterozygotes may be coded in the data as "AB" or "BA". Both entries will be counted as a heterozygote.

Value

A matrix of 4 columns

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

See Also

HWternaryPlot

Examples

SNP1 <- c("GG", "GG", "GG", "GG", "GG", "GG", "GG", "GG")
SNP2 <- c("CG", "CG", "CC", "GG", "GG", "CG", "CG", "CG")
SNP3 <- c("AA", "AA", "AA", "AG", "AA", "AG", "AA", "AA")
SNP4 <- c("GG", "GG", "GG", "GG", "GG", "GG", "GG", "GG")
SNP5 <- c("CC", "CC", "CC", "CC", "CC", "CT", "CT", "CT")
X <- cbind(SNP1, SNP2, SNP3, SNP4, SNP5)
print(Y)
W <- matrix(sample(c(0,1,2,NA),100,replace=TRUE),nrow=10,ncol=5)
Z <- MakeCounts(W, coding=c(0,1,2))
Description

`MakeFactor` converts bi-allelic genetic marker data, whether coded numerically as (0,1,2) or as (GG,GT,TT), etc. into standard factors coded as AA, AB, BB.

Usage

```r
MakeFactor(x, coding = c(0, 1, 2))
```

Arguments

- `x`: A vector containing genotyping results
- `coding`: Describes the numerical coding of the genotype data in order AA, AB and BB. Only relevant if `x` is numerical

Details

If `x` is a factor, it will be coerced to a factor with levels AA, AB and BB. Important detail: the produced factors will have only those levels that are observed in the data. E.g., if genotyping results only consist of (0,1), then the resulting factor will not have level BB (which would be an empty category)

Value

A factor variable

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

See Also

`MakeCounts`

Examples

```r
y <- c(1,1,0,0,2,2)
data.frame(y, MakeFactor(y))

y <- c(2,2,3,3,1,1)
data.frame(y, MakeFactor(y, coding=c(1,2,3)))

data(Markers)
data.frame(Markers[,1], MakeFactor(Markers[,1], coding=c(1,2,3)))
```
### Markers

**Description**

The dataframe contains the genotypes of 3 SNPs and two allele intensities of 146 individuals. The first column is a GT polymorphism that has missing values for several individuals. The second and third column (iG and iG) are the allele intensities of this polymorphism. Column 4 and 5 are covariate SNPs (an AC and an AG polymorphism) that have no missing values.

**Usage**

```r
data(Markers)
```

**Format**

A data frame containing 146 rows and 5 columns

**References**


### Mourant

**Description**

The dataframe contains the genotype frequencies MM, MN and NN for the MN blood group locus for 216 populations. The data are taken from table 2.5 in Mourant et al., using only entries with a sample size of at least 500.

**Usage**

```r
data(Mourant)
```

**Format**

A data frame containing 216 observations.

**Source**

Mourant et al, Table 2.5

**References**

n.alleles  

Description

Function n.alleles determines the number of alleles in a named genotype vector.

Usage

n.alleles(x, ...)

Arguments

x  A named genotype vector (e.g. c(AA=10,AB=20,BB=5))
...
extra arguments that are passed on to alleles

Value

integer

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

See Also

alleles

Examples

x <- c(AA=25,AB=50,BB=25)
k <- n.alleles(x)
print(k)

recode  

Description

function recode recodes bi-allelic genetic marker information expressed as strings (e.g. "AA", "AB", "BB") into numerical form.

Usage

recode(X, alleles, values = c(0, 1, 2), pos1 = 1, pos2 = 3, minor = FALSE, verbose = FALSE)
Arguments

- **x**: A matrix or dataframe of bi-allelic markers, individuals in rows, markers in columns.
- **alleles**: A vector with the alleles for each marker (e.g. c("A/T", "A/G", etc)).
- **values**: A vector of numeric values for AA, AB and BB. ((0,1,2) by default).
- **pos1**: Position of the first allele in the allele string (1 by default).
- **pos2**: Position of the second allele in the allele string (3 by default).
- **minor**: Coding is according to the number of copies of the minor allele. If `minor = TRUE`, the value of 2 reflects two copies of the minor allele, and the value 0 reflects no copies of the minor allele.
- **verbose**: Print progress on the conversion or not.

Details

`recode` is written for bi-allelic marker data only. Heterozygotes may be coded both as AB or BA. By default, the second allele specified (e.g. "T" in "A/T") is counted in the recoding, and homozygotes AA are coded as 0 and homozygotes TT as 2.

Value

A numerical matrix, individuals in rows, markers in columns.

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

See Also

`makecounts`

Examples

```r
SNP1 <- c("GG", "GG", "GG", "GG", "GG", "GG", "GG")
SNP2 <- c("GG", "GG", "GG", "GG", "GG", "GG", "GG")
SNP3 <- c("AA", "AA", "AA", "AA", "AA", "AA", "AA")
SNP4 <- c("GG", "GG", "GG", "GG", "GG", "GG", "GG")
SNP5 <- c("CC", "CC", "CC", "CC", "CC", "CT", "CT")
X <- cbind(SNP1, SNP2, SNP3, SNP4, SNP5)
print(Y)
```
strsort

Sort tokens of a set of strings

Description

Function strsort collapses all tokens of a vector of strings in a single string with sorted tokens.

Usage

strsort(s)

Arguments

s a vector of character strings

Value

a string

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

See Also

alleles

Examples

x <- c("AA","AB","BB","AC","CC")
print(strsort(x))

thetatof

Convert theta to an inbreeding coefficient

Description

Function Thetatof converts disequilibrium measure theta to an inbreeding coefficient.

Usage

Thetatof(p, theta = 4)

Arguments

p the allele frequency
theta the disequilibrium parameter
Value

a real number

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References


See Also

HwF

Examples

f <- ThetatoF(0.5, 4)

```r
f <- ThetatoF(0.5, 4)
```

Function toTriangular converts a named vector of genotype counts into a triangular matrix format, with homozygotes on the diagonal and heterozygotes below the diagonal.

Usage

toTriangular(x)

Arguments

x

A vector of genotype counts

Value

a matrix

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

Examples

```r
x <- c(AA=20, AB=52, AC=34, BB=17, BC=51, CC=26)
print(x)
X <- toTriangular(x)
print(X)
```
Description

Function UniqueGenotypeCounts creates a matrix containing only the unique rows in the given matrix, together with their frequency of occurrence.

Usage

UniqueGenotypeCounts(X, verbose = TRUE)

Arguments

X A n by 3 matrix with genotypic counts (AA, AB, BB)
verbose If TRUE then print some statistics

Value

A matrix with 4 columns, AA, AB, BB, and frequency of occurrence

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

See Also

GenerateSamples

Examples

set.seed(123)
X <- HWData(n=100,nm=100)
print(nrow(X))
Y <- UniqueGenotypeCounts(X)
print(nrow(Y))
print(sum(Y$w))
vaf

Computes the sample variance of the allele frequency for a biallelic marker.

Description

Function vaf computes the sample variance of the allele frequencies of a single sample or a matrix of samples.

Usage

vaf(x, hw = FALSE)

Arguments

x vector or matrix with genotype counts (AA,AB,BB)
hw assume Hardy-Weinberg proportions (hw=TRUE) or not (hw=FALSE)

Details

For biallelic markers the variance of the minor allele frequency equals the variance of the major allele frequency.

Value

a numeric vector of variances.

Author(s)

Jan Graffelman <jan.graffelman@upc.edu>

References


See Also

af, maf

Examples

x <- c(MM=298, MN=489, NN=213)
pA <- af(x)
vA <- vaf(x)
cat("allele frequency:" ,pA,"\n")
cat("sample variance allele frequency:" ,vA,"\n")
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