Package: hwde (via r-universe)

October 8, 2026

Version 0.67-3

Date 2023-08-21

Title Models and Tests for Departure from Hardy-Weinberg Equilibrium and Independence Between Loci

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Depends R (>= 2.0)

Description Fits models for genotypic disequilibria, as described in Huttley and Wilson (2000) <doi:10.1093/genetics/156.4.2127>, Weir (1996) and Weir and Wilson (1986). Contrast terms are available that account for first order interactions between loci. Also implements, for a single locus in a single population, a conditional exact test for Hardy-Weinberg equilibrium.

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URL https://github.com/jhmaindonald/hwde

LazyLoad yes

LazyData yes

Repository https://jhmaindonald.r-universe.dev

Date/Publication 2023-08-22 08:27:04 UTC

RemoteUrl https://github.com/jhmaindonald/hwde

RemoteRef HEAD

RemoteSha d655ddf5fe2db05c921a1f0c13594913e81553d7

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`decode.genotypes` *Creates contrasts that relate to a single locus*

Description

Vectors ma, maa and oset (offset) are returned.

Usage

```
decode.genotypes(genotype)
```

Arguments

`genotype`	The vector `genotype` holds two-letter codes for the three genotypes. For example, the values may be AA, Aa and aa.

Value

`oset`	The offset values that would be appropriate, in the multiplicative version of the model, if there was just this one locus.
`ma`	A contrast for the Hardy-Weinberg model, at this locus.
`maa`	A contrast that measures departure from the Hardy-Weinberg model, at this locus.
`types`	A vector of length three whose elements are the two-letter codes used for the three genotypes.

Note

Called by `make.contrasts`

Author(s)

J.H. Maindonald

See Also

`hwde`

Examples

```
decode.genotypes(rep(c("AA","Aa","aa"),2))
```

---

hwde *Fit relevant models, and test for various types of departure from Hardy-Weinberg equilibrium. Allows only 2 alleles per locus. The number of loci is arbitrary.*

Description

Fits models for genotypic disequilibria, as described in Huttley and Wilson (2000), Weir (1996) and Weir and Wilson (1986).

Usage

```
hwde(data = hwde::IndianIrish, gp = "Population", termlist = NULL, refmodel = NULL,
loci = paste("locus", 1:(dim(data)[2] - 1), sep = ""), observed = "Observed",
keep.models = FALSE, aovtable.print = TRUE, group.terms = TRUE, allele.chars = letters)
```

Arguments

`data`	Must have a column of frequencies, by default called `Observed`, and one or more columns giving genotype information, in the form AA, Aa, aa. or e.g., MM, MN, NN. (The choice of letters is arbitrary.) Additionally, there may be a column that gives information on groupings, by default called `Population`.
`gp`	Gives the name of the column, if any, that has information on groups within the data.
`termlist`	Use to specify a user-defined sequence of models. See the vignette **hwde.pdf** or **hwde.html**
`refmodel`	For each model in `termlist`, specifies a reference model, which will be updated to include the additional terms.
`loci`	Gives name(s) of columns that hold information on genotypes. By default, these are taken to be `locus1`, `locus2`, etc.
`observed`	Name (by default `Observed`) of the column that holds the frequenceies.
`keep.models`	Should a list be returned that holds the full sequence of models that were fitted?
`aovtable.print`	Should the anova table be printed?
`group.terms`	Should model terms be grouped according to hierarchy, for the anova table?
`allele.chars`	A sequence of letters used to code for the loci. By default *a*, *b*, *c*, ... are used

Details

See the document **hwde.pdf** or **hwde.html** for details. See the references (below) for information on the interpretation of model parameters.

Value

anovatab	anova (analysis of deviance) table
data.df	Data, and contrasts used in fitting the various models.
aovtab.terms	This string holds, for each model that is fitted. the terms that have appeared in the model formula. The text strings for the distinct models are concatenated.
models	Optionally, this holds the complete sequence of qmodel objects that were fitted

Author(s)

J.H. Maindonald

References

1. Huttley, G.A. and Wilson, S.R. 2000. Testing for concordant equilibria between population samples. *Genetics* **156**:2127-2135.
2. Weir, B.S. 1996. *Genetic Data Analysis II.* Sinauer.
3. Weir, B.S. and Wilson, S.R. 1986. Log-linear models for linked loci. *Biometrics* **42**:665-670.

See Also

make.contrasts, decode.genotypes

Examples

```
data(IndianIrish)
hwde(data=IndianIrish)
data(mendelABC)
hwde(data=mendelABC, loci=c("seedshape", "cotylcolor", "coatcolor"))
```

---

hwexact *Exact test of HWE*

Description

This function implements an exact SNP test of Hardy-Weinberg equilibrium. It is a wrapper for snphwe

Usage

```
hwexact(obs.hom1, obs.hets, obs.hom2, data, loci, observed)
```

Arguments

obs.hom1	Observed number of individuals homozygous for the common allele.
obs.hets	Observed number of heterozygous individuals.
obs.hom2	Observed number of individuals homozygous for the rare allele.
data	If not NULL, specifies a data frame holding the data.
loci	If data is not NULL, column that holds some combination of symbols of the form AA, Aa and aa.
observed	Column that holds the frequencies, if data is not NULL.

Value

The exact p-value testing departure from Hardy-Weinberg Equilibrium, conditional on the observed relative numbers of alleles of the two types

Author(s)

Randall Johnson – adapted from code by Wigginton et al

References

Wigginton, J.E.; Cutler, D.J. & Abecasis, G.R.; A Note on exact tests of Hardy-Weinberg equilibrium; American Journal of Human Genetics, 2005, 76, 887-93

Examples

```
hwexact(68, 28, 4)
```

IndianIrish *Observed genotype frequencies at MN and S loci, for 2 populations*

Description

The IndianIrish data frame has 18 rows and 4 columns. The data are genotype frequencies for two locations, for Xavante Indian and Irish populations respectively

Usage

```
data(IndianIrish)
```

Format

This data frame contains the following columns:

Population Factor with levels: Indian and Irish

locus1 Factor with levels: MM, MN and NN

locus2 Factor with levels: SS, Ss and ss

Observed a numeric vector giving the frequency for each category of the tale

Source

Mourant et al (1977) and Huttley and Wilson (2000).

References

1. Huttley, G.A. and Wilson, S.R. 2000. Testing for concordant equilibria between population samples. *Genetics* **156**, 2127-2135.
2. Mourant, A.E., Kopec, A.C. and Domaniewska-Sobczak, K. 1976. *The Distribution of the Human Blood Groups and Other Polymorphisms.* Oxford University Press.
3. Weir, B.S. 1996. *Genetic Data Analysis II.* Sinauer.

See Also

hwde

Examples

```
data(IndianIrish)
hwde(data=IndianIrish)
```

---

make.contrasts *Calculate contrasts required by the function*

Description

Calculates the contrasts that hwde uses in fitting models for genotypic disequilibrium. At present these are limited to first order interaction terms between the distinct loci, possibly with distinct values foe each different level of a grouping factor.

Usage

```
make.contrasts(data = data[, loci], allele.chars = letters)
```

Arguments

data	Data frame, with one column per locus, and as many rows as there are observations. Genotypes are represented using a two-letter code, e.g., AA, Aa, aa
allele.chars	By default the letters "a", "b", ..., one for each locus, are used.

Details

Any pair of letters can be used for the two alleles. The setting of allele.chars determines the coding used in the model formulae. This function is called by hwde

Value

`contrasts.df`	Data frame whose columns hold the contrasts that will be explanatory variables for the Poisson regression model.
`oset`	Offset vector for the GLM model.
`list.columns`	List in which each element is a text string that holds the codes for a sequence of model terms.

Author(s)

J.H. Maindonald

See Also

`identify.genotypes`, called by `make.contrasts`

Examples

```
make.contrasts(data=c("AA","Aa","aa"))
```

`mendelABC` *Mendel's F2 trifactorial data for seed shape (A: round or wrinkled), cotyledon color (B: albumen yellow or green), and seed coat color (C: grey-brown or white)*

Description

The `mendel3` data frame has 27 rows and 4 columns. Data are from Mendel (1886), and are reproduced in Fisher (1936) and Weir (1996).

Usage

```
data(mendelABC)
```

Format

This data frame contains the following columns:

seedshape Factor with levels: `AA`, `Aa` and `aa`

cotylcolor Factor with levels: `BB`, `Bb` and `bb`

coatcolor Factor with levels: `CC`, `Cc` and `cc`

Observed a numeric vector that holds the frequencies.

Details

The data are reviewed in detail in Fisher (1936). For a brief discussion, and references to work that revisits Fisher's conclusions, see Weir (1996).

Source

Data are from Mendel (1886), and are reproduced in Fisher (1936) and Weir (1996).

References

1. Fisher, R.A. 1936. Has Mendel's work been rediscovered? *Annals of Science* **1**:115-137.

2. Mendel, G. 1886. Versuche uber Pflanzen-Hybriden. Verhandlugen des Naturforschenden Vereines in Brunn **4**:3-47. (An English translation. with annotations, is available from http://www.esp.org/foundations/genetics/classical/gm-65.pdf NB also the English translation by Royal Horticultural Society of London, reprinted in Peters, J.A. 1959. *Classic Papers in Genetics.* Prentice-Hall.)

3. Weir, B.S. 1996. *Genetic Data Analysis II.* Sinauer.

Examples

```
## Lay table out as a 3D array, as in Fisher (1936)
abc <- aperm(array(mendelABC[,4], dim=c(3,3,3)), c(1,3,2))
dimnames(abc) <- list(B=c('BB','Bb','bb'),
                      A=c('AA','Aa','aa'),
                      C=c('CC','Cc','cc'))
abc
## Fit Hardy-Weinberg disequilibium model
hwde(mendelABC, loci=c("seedshape","cotylcolor","coatcolor"))
```

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