Package 'segregatr'

October 14, 2022

Title Segregation Analysis for Variant Interpretation

Version 0.2.0

Description An implementation of the full-likelihood Bayes factor (FLB) for evaluating segregation evidence in clinical medical genetics. The method was introduced by Thompson et al. (2003) <doi:10.1086/378100>, and further popularised by Bayrak-Toydemir et al. (2008) <doi:10.1016/j.yexmp.2008.03.006>. This implementation allows custom penetrance values and liability classes, and includes specialised pedigree visualisations.

License GPL-3

URL https://github.com/magnusdv/segregatr

BugReports https://github.com/magnusdv/segregatr/issues

Encoding UTF-8

Language en-GB

Depends pedtools

Imports pedprobr

Suggests testthat (>= 2.1.0)

RoxygenNote 7.1.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2021-04-15 07:40:03 UTC

R topics documented:

FLB *Full-likelihood Bayes factor*

Description

Computes the Bayes factor for co-segregation, as described by Thompson et al. (2003).

Usage

```
FLB(
  x,
  carriers,
  noncarriers = NULL,
  freq,
  affected,
  unknown = NULL,
  proband,
  penetrances,
  liability = NULL,
  details = FALSE,
  plot = FALSE,
  ...
)
```

Arguments

x	A pedtools::ped() object.
carriers	A character vector (or coercible to such), containing the ID labels of pedigree members known to carry the variant in question.
noncarriers	A character vector (or coercible to such), containing the ID labels of pedigree members known *not* to carry the variant in question.
freq	A single number strictly between 0 and 1: the population frequency of the observed allele.
affected	The affected pedigree members.
unknown	Pedigree members with unknown affection status.
proband	The ID label of the proband. This person must also be in both carriers and affected.
penetrances	Either a numeric vector of length 3, corresponding to (f0, f1, f2) or a matrix or data frame with 3 columns. Each row contains the penetrance values of a liability class.
liability	A vector of length pedsize(x), containing for each pedigree member the row number of penetrances which should be used for that individual. (If penetrances is just a vector, it will be used for all classes.) If liability is NULL (the default), it is set to 1 for all individuals.

details	A logical, indicating if detailed output should be returned (for debugging purposes).
plot	A logical.
...	Optional plot parameters passed on to pedtools::plot.ped().

Value

A positive number. If details = TRUE, a list of intermediate results is returned.

References

Thompson D, Easton DF, Goldgar DE. *A full-likelihood method for the evaluation of causality of sequence variants from family data.* Am J Hum Genet, 2003. doi: 10.1086/378100.

Examples

```
x = nuclearPed(2)

FLB(x, carriers = 3:4, aff = 3:4, unknown = 1:2,
    freq = 0.0001, penetrances = c(0, 1, 1), proband = 3)
```

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plotSegregation *Pedigree plot for segregation analysis*

Description

Plots a pedigree showing the segregation of a variant.

Usage

```
plotSegregation(
  x,
  affected = NULL,
  unknown = NULL,
  proband = NULL,
  carriers = NULL,
  noncarriers = NULL,
  cex = 1,
  margins = rep(1, 4),
  ...
)
```

Arguments

x	A pedtools::ped() object.
affected	The affected pedigree members.
unknown	Pedigree members with unknown affection status.
proband	The ID label of the proband. This person must also be in both carriers and affected.
carriers	A character vector (or coercible to such), containing the ID labels of pedigree members known to carry the variant in question.
noncarriers	A character vector (or coercible to such), containing the ID labels of pedigree members known *not* to carry the variant in question.
cex, margins	Arguments passed on to pedtools::plot.ped().
...	Optional plot parameters passed on to pedtools::plot.ped().

Examples

```
x = nuclearPed(2)
plotSegregation(x, affected = 3:4, unknown = 1:2, proband = 3,
                carriers = 3:4, margins = c(1,3,1,1))
```

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segregatr *segregatr: Segregation Analysis for Identifying Pathogenic Variants*

Description

An implementation of the full-likelihood Bayes factor (FLB) for evaluating segregation evidence in clinical medical genetics. The method was introduced by Thompson et al. (2003), and further popularised by Bayrak-Toydemir et al. (2008). This implementation allows custom penetrance values and liability classes, and includes specialised pedigree visualisations.

References

Thompson D, Easton DF, Goldgar DE. *A full-likelihood method for the evaluation of causality of sequence variants from family data.* Am J Hum Genet, 2003. doi: 10.1086/378100.

Bayrak-Toydemir et al. *Likelihood ratios to assess genetic evidence for clinical significance of uncertain variants: Hereditary hemorrhagic telangiectasia as a model.* Exp Mol Pathol, 2008. doi: 10.1016/j.yexmp.2008.03.006.

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