Package 'LIS'

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Type Package

Title Information and Sample Size Calculation Based on LIME method

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Description Calculate information per individual and needed sample size based on LIME method to identify association, imprinting and maternal effects.

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Depends numDeriv

NeedsCompilation no

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`LIS-package` *Information and Sample Size Calculation Based on LIME method*

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Details

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References

Zhang, F., Khalili, A. and Lin, S. (2015). Optimum Study Design for Detecting Imprinting and Maternal Effects Based on Partial Likelihood. Biometrics.

Han, M., Hu, Y. Q. and Lin, S. (2013). Joint detection of association, imprinting and maternal effects using all children and their parents. European Journal of Human Genetics 27, 1449-1456.

Yang, J. and Lin, S. (2013). Robust partial likelihood approach for detecting imprinting and maternal effects using cae-control families. Annals of Applied Statistics 7, 249-268.

Examples

```
#when pilot data is not provided
info_sample(prev=0.05,maf=0.1,R1=2,R2=3,S1=2,S2=3,Rim=1/3,prop=0.5,pfmisscase=0,pfmisscon

#when pilot data is provided
pilot_data<-matrix(c(75,45,150,90,75,105,150,210),nrow=2,ncol=4,byrow=TRUE)

info_sample(prev=0.05,maf=0.1,R1=2,R2=3,S1=2,S2=3,Rim=1/3,cri=0.1,pilot_data=pilot_data)
```

`info_sample` *Information and Sample Size Based on LIME method*

Description

Calculate information per individual and needed sample size based on LIME method to identify association, imprinting and maternal effects.

Usage

```
info_sample(prev = 0.05, maf = 0.1, R1 = 2, R2 = 3, S1 = 2, S2 = 3, Rim = 1/3, p
```

Arguments

`prev`	disease prevalence. Default value is 0.05.
`maf`	minor allele frequency,defaulty value is 0.1.
`R1`	value for parameter R_1, the effect of one copy of an individual's own minor allele. Default value is 1.
`R2`	value for parameter R_2, the effect of two copies of an individual's own minor allele. Default value is 1.
`S1`	value for parameter S_1, the effect of one copy of the mother's minor allele. Default value is 1.
`S2`	value for parameter S_2, the effect of two copies of the mother's minor allele. Default value is 1.
`Rim`	value for parameter R_im, imprinting effect. Default value is 1.

`prop`	proportion of case families. Default value is 0.5.
`pfmisscase`	missing rate for fathers in case families. Default value is 0.5.
`pfmisscontrol`	missing rate for fathers in control families. Default value is 0.7.
`cri`	the criteria to calculate sample size to guarantee the standard deviation of the parameter is smaller than the parameter multiplied by the criteria. Default value is 0.1.
`pilot_data`	Optional argument. If pilot data are provided, then they are used to calculate needed sample size to get the standard deviation smaller than the criteria multiplied by the parameter. Pilot data should be a 2*4 demensional matrix. The first row includes count of complete case families, complete control families, additional siblings in complete case families and in complete control families, respectively. The second row includes count of incomplete case families, incomplete control families, additional siblings in incomplete case families and in incomplete control families, respectively.

Details

'info_sample' calculates information per individual and sample size needed to make sure the standard deviation is smaller than the parameter multiplied by the criteria.

prev, *maf*,*R1*,*R2*,*S1*,*S2*,*Rim*, and *cri* are required. If *pilot_data* is not provided, *prop*, *pfmisscase* and *pfmisscontrol* are required.

Value

`info`	Information per individual. When pilot data is not provided, information per individual will be given for five situations when each family has 0, 1, 2, 3, and 4 additional siblings, respectively.
`needed_multiples_of_pilot_data_sample_size`	When *pilot_data* is provided, the sample size is a vector of length 5, which represents the times of sample size of pilot_data to make sure estimated standard deviation smaller than the parameter multiplied by the criteria.
`sample size`	When *pilot_data* is not provided, sample sizes will be given for five situations when each family has 0, 1, 2, 3, and 4 additional siblings, respectively, to make sure estimated standard deviation smaller than the parameter multiplied by the criteria.

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