

Package: genepi (via r-universe)

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Type Package

Title Genetic Epidemiology Design and Inference

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Depends R (>= 2.0.0), stats

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Description Package for Genetic Epidemiologic Methods Developed at MSKCC. It contains functions to calculate haplotype specific odds ratio and the power of two stage design for GWAS studies.

License GPL (>= 2)

LazyLoad yes

NeedsCompilation yes

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Repository <https://veseshan.r-universe.dev>

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genepi-package

Functions for some genetic epidemiology methods.

Description

These functions provide code for genetic epidemiology methods developed at MSKCC. They currently include estimating haplotype disease risk and two stage designs for GWAS.

Details

Package: genepi
Type: Package
Version: 1.0.3
Date: 2023-08-31
License: GPL version 2 or later
LazyLoad: yes

There are two functions haplotypeOddsRatio and twoStagePower in this package.

Package will be archived and functions added to clinfun package

Author(s)

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References

Satagopan JM, Venkatraman ES, Begg CB. (2004) Two-stage designs for gene-disease association studies with sample size constraints. *Biometrics*

Venkatraman ES, Mitra N, Begg CB. (2004) A method for evaluating the impact of individual haplotypes on disease incidence in molecular epidemiology studies. *Stat Appl Genet Mol Biol*. v3:Article27.

haplotypeOddsRatio

Calculate haplotype disease risk.

Description

Haplotype disease risk is calculated resolving haplotype ambiguity and adjusting for covariates and population stratification.

Usage

```
haplotypeOddsRatio(formula, gtypevar, data, stratvar=NULL, nsim=100, tol=1e-8)
## S3 method for class 'haploOR'
print(x, ...)
```

Arguments

formula	The formula for logistic regression without the haplotype variable.
gtypevar	The variable names in the data frame corresponding to the loci of interest. Each variable counts the number of mutant genotypes a subject has at that locus. Legal values are 0, 1, 2 & NA.
data	The name of the dataframe being analyzed. It should have all the variables in the formula as well as those in genotype and stratvar.
stratvar	Name of the stratification variable. This is used to account for population stratification. The haplotype frequencies are estimated within each stratum.
nsim	Variance should be inflated to account for inferred ambiguous haplotypes. The estimates are recalculated by simulating the disease haplotype copy number and variance added to average.
tol	Tolerance limit for the EM algorithm convergence.
x	Object of class haploOR.
...	Other print options.

Details

This implements the method in the reference below.

Value

It is a list of class haploOR

call	The function call that produced this output.
coef	Table with estimated coefficients, standard error, Z-statistic and p-value.
var	Covariance matrix of the estimated log odds-ratios.
deviance	Average of the simulated deviances. Its theoretical properties are unknown.
aic	Average of the simulated aic.
null.deviance	Deviance of null model.
df.null	Degrees of freedom of null model.
df.residual	Degrees of freedom of full model.

The "print" method formats the results into a user-friendly table.

Author(s)

Venkatraman E. Seshan

References

Venkatraman ES, Mitra N, Begg CB. (2004) A method for evaluating the impact of individual haplotypes on disease incidence in molecular epidemiology studies. *Stat Appl Genet Mol Biol*. v3:Article27.

Examples

```
# simulated data with 2 loci haplotypes 1=00, 2=01, 3=10, 4=11
# control haplotype probabilities p[i] i=1,2,3,4
# haplotype pairs (i<=j) i=j: probs = p[i]^2 ; i<j: p[i]*p[j]
p <- c(0.25, 0.2, 0.2, 0.35)
p0 <- rep(0, 10)
l <- 0
for(i in 1:4) {for(j in i:4) {l <- l+1; p0[l] <- 2*p[i]*p[j]/(1+1*(i==j))}}
controls <- as.numeric(cut(runif(1000), cumsum(c(0,p0)), labels=1:10))
# case probabilities disease haplotype is 11
or <- c(2, 5)
p1 <- p0*c(1,1,1,2,1,1,2,1,2,8); p1 <- p1/sum(p1)
cases <- as.numeric(cut(runif(1000), cumsum(c(0,p1)), labels=1:10))
# now pool them together and set up the data frame
dat <- data.frame(status=rep(0:1, c(1000, 1000)))
# number of copies of mutant variant for locus 1
dat$gtype1 <- c(0,0,1,1,0,1,1,2,2,2)[c(controls, cases)]
# number of copies of mutant variant for locus 2
dat$gtype2 <- c(0,1,0,1,2,1,2,0,1,2)[c(controls, cases)]
# true number of copies of disease haplotype
dat$hcn <- c(0,0,0,1,0,0,1,0,1,2)[c(controls, cases)]
# model with genotypes only
haplotypeOddsRatio(status ~ 1, c("gtype1","gtype2"), dat)
# model from the logistic fit using the number of copies of disease haplotype
glm(status ~ factor(hcn), dat, family=binomial)
```

twoStagePower

Calculate the power of a two stage design for GWAS

Description

Calculate the power of a two stage design for GWAS under sample size or cost constraints. Implements methods in the references below.

Usage

```
twoStagePower(n=NULL, Cost=NULL, m=5000, mu=0.045, mu.loc=0.5, p=0.10,
              f=NULL, relcost=1, true.needed=1, rho=0, rho0=0, nsim=2000)
```

Arguments

n	The maximum sample size for the study.
Cost	Maximum available resource. One of Cost or n must be specified.
m	The number of markers in the study. Default is 5000. It will take a a long time to compute power for very large numbers e.g. 100000
mu	The mean vector for the markers that are associated with endpoint.
mu.loc	The locations of the true markers. Since the chromosome is mapped to the unit interval (0,1) the numbers should be between 0 and 1.
p	The proportion of markers taken to the second stage. The default is 0.1 which is found to be optimal.
f	The fraction of Cost or sample size allocated to the first stage. If not specified it uses 0.75 for the Cost constraint scenario and 0.5 for the sample size constraint scenario.
relcost	Specifies how expensive it is to genotype in the second stage compared to the first stage.
true.needed	The number of markers selected in the end. Can be a maximum of length of mu.loc (or mu).
rho, rho0	correlation between markers
nsim	Number of Monte Carlo replications to compute power.

Details

This implements the method in the reference below.

Value

It returns the power as a single numeric value

Author(s)

Jaya M. Satagopan & Venkatraman E. Seshan

References

Satagopan JM, Venkatraman ES, Begg CB. (2004) Two-stage designs for gene-disease association studies with sample size constraints. *Biometrics*

Examples

```
twoStagePower(n=1000)
twoStagePower(Cost=1000)
```

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