Package ‘GeneticsDesign’

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Title Functions for designing genetics studies
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Imports gmodels, graphics, gtools (>= 2.4.0), mvtnorm, stats
Description This package contains functions useful for designing genetics
    studies, including power and sample-size calculations.
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NeedsCompilation no

R topics documented:

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Description

These functions are deprecated.

Usage

    power.casectrl(...)
Arguments

... All arguments are ignored

Details

The `power.casectl` function contained serious errors and has been replaced by `GPC.GeneticPower.Quantitative.Factor` or `GPC.GeneticPower.Quantitative.Numeric` as appropriate.

In specific, the `power.casectl` function used an expected contingency table to create the test statistic that was erroneously based on the underlying null, rather than on the marginal totals of the observed table. In addition, the modeling of dominant and recessive modes of inheritance had assumed a "perfect" genotype with no disease, whereas in reality a dominant or recessive mode of inheritance simply means that two of the genotypes will have an identical odds ratio compared to the 3rd genotype (the other homozygote).

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### GeneticPower.Quantitative.Numeric

*Power of Genetics Study*

#### Description

Compute power of quantitative genetics studies, when the genotype is handled as a numeric value (0,1,2) `GeneticPower.Quantitative.Numeric` or as a factor `GeneticPower.Quantitative.Factor`.

#### Usage

```r
GeneticPower.Quantitative.Numeric(
  N=1000,
  delta=1,
  freq=0.15,
  minh=c("additive", "dominant", "recessive"),
  sigma=1,
  OtherParms=0,
  alpha=0.05,
  numtests=1,
  moi=NULL,
  rsquared=NULL)
```

```r
GeneticPower.Quantitative.Factor(
  N=1000,
  delta=1,
  freq=0.15,
  minh=c("additive","dominant","recessive"),
  sigma=1,
  OtherParms=0,
  alpha=0.05,
  numtests=1,
  moi=NULL,
  rsquared=NULL)
```
GeneticPower.Quantitative.Numeric

Arguments

N  total samples in the analysis
delta  Treatment effect for an individual homozygote for the disease allele ('b') relative to an individual homozygote for the reference allele ('A')
freq  allele frequency of disease allele 'b'
minh  mode of inheritance: "additive", "dominant", "recessive". Default is "additive". This parameter is OVER-RIDDEN by moi.
sigma  standard deviation of the response phenotype

OtherParms  number of additional parameters (really, DOF) in the model that will reduce your overall DOF
alpha  desired significance level
numtests  number of tests to be corrected by Bonferroni adjustment before achieving 'alpha'
moi  continuous value between 0 and 1 (inclusive) specifying the mode of inheritance: 0 for recessive, 0.5 for additive, 1.0 for dominant. This parameter OVER-RIDES minh.
rsquared  fraction of total sum-of-squares explained by fit. This parameter OVER-RIDES delta AND sigma.

Details

The value of moi overrides any value specified for minh. Specifying a minh="recessive" is equivalent to specifying moi=0, minh="additive" is equivalent to moi=0.5, and minh="dominant" is equivalent to moi=1.0.

Author(s)

Craig L. Hyde <Craig.L.Hyde@pfizer.com> and Feng Gao <feng.gao1@pfizer.com>

Examples

GeneticPower.Quantitative.Numeric(
  N=50,
  freq=0.1,
  minh="recessive",
  alpha=0.05
)

GeneticPower.Quantitative.Factor(
  N=50,
  freq=0.1,
  minh="recessive",
  alpha=0.05
)

##
**Description**

Genetics power calculator for linear trend association studies.

**Usage**

```r
GPC(pA, pD, RRAa, RRAA, r2, pB,
   nCase=500, ratio=1, alpha=0.05, quiet=FALSE)
GPC.default(pA, pD, RRAa, RRAA, Dprime, pB,
   nCase=500, ratio=1, alpha=0.05, quiet=FALSE)
```

**Arguments**

- **pA**: High risk allele frequency (A).
- **pD**: Disease prevalence.
- **RRAa**: Genotype relative risk (Aa) = RR(Aa|aa)=Pr(D|Aa)/Pr(D|aa).
- **RRAA**: Genotype relative risk (AA) = RR(AA|aa)=Pr(D|AA)/Pr(D|aa).
- **r2**: LD measure. Assume that \(D > 0\).
- **Dprime**: LD measure.
- **pB**: Marker allele frequency (B).
- **nCase**: Number of cases.
- **ratio**: Control:case ratio = nControl/nCase.
- **alpha**: User-defined type I error rate.
- **quiet**: Print some intermediate results if quiet=FALSE.

**Details**

The power is for the test that disease is associated with a marker, given high risk allele frequency (A), disease prevalence, genotype relative risk (Aa), genotype relative risk (AA), LD measure (\(D'\) or \(r^2\)), marker allele frequency (B), number of cases, control:case ratio, and probability of the Type I error. The linear trend test (Cochran 1954; Armitage 1955) is used.

**Value**

- **power**: The estimated power for the association test.
- **ncp**: Non-centrality parameter.
- **mat.para**: A matrix of case-control parameters, including number of cases, number of controls, high risk allele frequency, prevalence, genotypic relative risk (Aa), genotypic relative risk (AA), genotypic risk for aa (baseline).
- **mat.B**: A matrix of marker locus B parameters, including marker allele frequency, linkage disequilibrium (\(D'\)), penetrance at marker genotype bb, penetrance at marker genotype Bb, penetrance at marker genotype BB, genotypic odds ratio Bb, genotypic odds ratio BB.
- **mat.aFreq**: A 2 by 2 matrix of expected allele frequencies \(Pr(B|D), Pr(b|D), Pr(B|non\ D), Pr(b|non\ D)\).
- **mat.gFreq**: A 3 by 2 matrix of expected genotype frequencies \(Pr(BB|D), Pr(Bb|D), Pr(bb|D), Pr(BB|non\ D), Pr(Bb|non\ D), Pr(bb|non\ D)\).
- **mat.stat**: Power estimates for a sequence of Type I errors.
Author(s)

Weiliang Qiu <stwxq@channing.harvard.edu>, Ross Lazarus <ross.lazarus@channing.harvard.edu>

References


Examples

```r
res1<-GPC(pA=0.05, pD=0.1, RRAa=1.414, RRAA=2, r2=0.9, pB=0.06, nCase=500, ratio=1, alpha=0.05, quiet=FALSE)
res2<-GPC.default(pA=0.05, pD=0.1, RRAa=1.414, RRAA=2, Dprime=0.9, pB=0.06, nCase=500, ratio=1, alpha=0.05, quiet=FALSE)
```

Description

Probability of observing all alleles with a given frequency in a sample of a specified size.

Usage

```r
gregorius(freq, N, missprob, tol = 1e-10, maxN = 10000, maxiter=100, showiter = FALSE)
```

Arguments

- `freq` (Minimum) Allele frequency (required)
- `N` Number of sampled genotypes
- `missprob` Desired maximum probability of failing to observe an allele.
- `tol` Omit computation for terms which contribute less than this value.
- `maxN` Largest value to consider when searching for N.
- `maxiter` Maximum number of iterations to use when searching for N.
- `showiter` Boolean flag indicating whether to show the iterations performed when searching for N.
Details

If \( f_{\text{req}} \) and \( N \) are provided, but \( \text{missprob} \) is omitted, this function computes the probability of failing to observe all alleles with true underlying frequency \( f_{\text{req}} \) when \( N \) diploid genotypes are sampled. This is accomplished using the sum provided in Corollary 2 of Gregorius (1980), omitting terms which contribute less than \( \text{tol} \) to the result.

When \( f_{\text{req}} \) and \( \text{missprob} \) are provide, but \( N \) is omitted. A binary search on the range of \([1, \text{maxN}]\) is performed to locate the smallest sample size, \( N \), for which the probability of failing to observe all alleles with true underlying frequency \( f_{\text{req}} \) is at most \( \text{missprob} \). In this case, \( \text{maxiter} \) specifies the largest number of iterations to use in the binary search, and \( \text{showiter} \) controls whether the iterations of the search are displayed.

Value

A list containing the following values:

- call: Function call used to generate this object.
- method: One of the strings, "Compute missprob given N and freq", or "Determine minimal N given missprob and freq", indicating which type of computation was performed.
- retval\$freq: Specified allele frequency.
- retval\$N: Specified or computed sample size.
- retval\$missprob: Computed probability of failing to observe all of the alleles with frequency \( f_{\text{req}} \).

Note

This code produces sample sizes that are slightly larger than those given in table 1 of Gregorius (1980). This appears to be due to rounding of the computed missprobs by the authors of that paper.

Author(s)

Code submitted by David Duffy <davidD@qumr.edu.au>, substantially enhanced by Gregory R. Warnes <warnes@bst.rochester.edu>.

References


Examples

```
# Compute the probability of missing an allele with frequency 0.15 when
# 20 genotypes are sampled:
gregorius(freq=0.15, N=20)

# Determine what sample size is required to observe all alleles with true
# frequency 0.15 with probability 0.95
gregorius(freq=0.15, missprob=1-0.95)
```
**Description**

Estimate power for genetic studies using baseline measurements via simulation.

**Usage**

```r
def power.genotype.conti(N, Rep = 2000, alpha = 0.05, ...)  
simu.genotype.conti(N, p=0.15, pi=0, me1=50, me2=me1, delta=-5,  
                     sd1=10, sd2=10, verbose=FALSE,  
                     minh=c('additive', 'dominant', 'recessive'),  
                     genotype.delta=TRUE, Factor=FALSE)
```

**Arguments**

- **N**  
  total number of subjects

- **p**  
  frequency of A (affected) allele

- **Rep**  
  number of simulation runs used to estimate power

- **alpha**  
  significance level

- **pi**  
  correlation coefficient

- **me1, me2**  
  mean of control and treatment groups

- **delta**  
  treatment/genotype effect

- **sd1,sd2**  
  standard deviation of the control and treatment groups

- **minh**  
  mode of inheritance, one of 'additive', 'dominant', or 'recessive'

- **genotype.delta**  
  logical indicating whether the treatment effect occurs only for an individual genotype (genotype.delta=TRUE) or for all genotypes (genotype.delta=FALSE)

- **Factor**  
  Should the simulated treatment variable 'Trt' be be treated as a factor variable (Factor=TRUE) or as a numeric variable (Factor=FALSE).

- **verbose**  
  Should information about each simulated data set and model fit be displayed.

- **...**  
  Arguments to be passed to simu.genotype.conti

**Value**

- Describe the value returned If it is a LIST, use

  ```r  
  comp1  
  Description of 'comp1'
  comp2  
  Description of 'comp2'
  ...
  ```

**Author(s)**

Michael Man, minor changes by Gregory R. Warnes <greg@random-technologies-llc.com>
References


See Also

power.casectrl

Examples

```r
## Not run:
# use defaults, 100 subjects
power.genotype.conti(N=100)

# same calculation, specifying all values
power.genotype.conti(N=100, Rep=2000, p=0.15, pi=0, me1=50, me2=50, delta=-5, 
                     sd1=10, sd2=10, verbose=FALSE, minh="additive", 
                     genotype.delta=TRUE, Factor=FALSE)

# Show details for small simulation study
power.genotype.conti(N=10, verbose=TRUE)

## End(Not run)
```
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