twoStageGwasPower

Description

Computes the critical values for a two-stage gwas association study and compute power for replication and joint analyses.

Details

Package: twoStageGwasPower
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Author(s)

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References

http://www.sph.umich.edu/csg/abecasis/CaTS/

| twoStageGwasPower | thresholds and power for two-stage gwas |

Description

Computes the critical values for a two-stage gwas association study and compute power for replication and joint analyses.

Usage

twoStageGwasPower(pD, pG, grr, inheritance = "multiplicative", pi.samples, pi.markers, alpha.marker,}

Arguments

| pD            | Probability of disease in the population (prevalence) |
| pG            | Frequency of disease allele in the population         |
| grr           | Genotypic relative risk                               |
| inheritance  | Inheritance type ("dominant", "recessive", "multiplicative", or "additive") |
| pi.samples    | Proportion of samples genotyped in Stage 1            |
| pi.markers    | Proportion of markers genotyped in Stage 2            |
alpha.marker  Significance level used for each marker, accounting for multiple comparisons among a large number of markers
n.cases  Number of cases
n.controls  Number of controls

Details
This function computes the critical values and powers of the replication and joint methods of analyzing a two-stage GWAS design. Details may be found in Skol AD, Scott, LJ, Abecasis GR, Boehnke M (2006)

Value
A list containing:

- power.SingleStage  Power of a one stage design
- power.joint  Power of a joint analysis
- power.rep  Power of a replication analysis (based only on the second stage markers)
- c1  Stage one threshold
- c2  Replication (stage two) threshold
- c.joint  Joint analysis threshold
- c.singleStage  Single stage design threshold
- penetrance.GG  Penetrance of the GG genotype (homozygous for disease allele)
- penetrance.Gg  Penetrance of the Gg genotype
- penetrance.gg  Penetrance of the gg genotype
- p0  disease allele frequency in controls
- p1  disease allele frequency in cases
- p.stageOne  probability that associated markers will be followed up in Stage 2
- savings  reduction in genotyping using two-stage design as compared to the single-stage design

Author(s)
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References
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Examples

# prevalence of disease is 0.10, the allele frequency is 0.40,
# a multiplicative model with 0.40 samples in the first stage and
# 10% of the markers selected for Stage 2. There are 1000 cases
# and 1000 controls, 300,000 markers, with a genome-wide alpha of 0.05

power.gwas.out <- twoStageGwasPower(pD=0.10, pG=0.40, grr=1.40,
                      inheritance="multiplicative", pi.samples=0.40, pi.markers=0.10,
                      alpha.marker=0.05/300000, n.cases=1000, n.controls=1000
)

power.gwas.out

# Same, but with 1% of markers selected for Stage 2
power.gwas.out2 <- twoStageGwasPower(pD=0.10, pG=0.40, grr=1.40,
                      inheritance="multiplicative", pi.samples=0.40, pi.markers=0.010,
                      alpha.marker=0.05/300000, n.cases=1000, n.controls=1000)

power.gwas.out2

# Same, but a dominant model with 4000 controls and 2000 cases
power.gwas.out3 <- twoStageGwasPower(pD=0.10, pG=0.40, grr=1.40,
                      inheritance="dominant", pi.samples=0.40, pi.markers=0.10,
                      alpha.marker=0.05/300000, n.cases=2000, n.controls=4000)

power.gwas.out3

twoStageNull

thresholds for two-stage gwas

Description

Computes thresholds for two-stage genome-wide association study for replication and joint analyses, and for a single-stage design

Usage

twoStageNull(pi.samples, pi.markers, alpha.marker)

Arguments

pi.samples Proportion of samples genotyped in Stage 1
pi.markers Proportion of markers genotyped in Stage 2
alpha.marker Significance level used for each marker, accounting for multiple comparisons among a large number of markers

Value

A list containing:

c1 Stage one threshold
c2 Replication (stage two) threshold
twoStageNull

c. joint Joint analysis threshold
c. singleStage Single stage design threshold

Author(s)
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References
http://www.sph.umich.edu/csg/abecasis/CaTS/

Examples
# compute thresholds for two-stage design with 40% of subjects selected for stage one
# and 10% of markers selected for follow-up in the second stage,
# with an alpha level of 0.05/300000
power.thresh.out <- twoStageNull(pi.samples=0.40, pi.markers=0.10,
                                 alpha.marker=0.05/300000)
power.thresh.out
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