Package ‘rvTDT’

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Type Package
Title population control weighted rare-variants TDT
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Description

Used to compute population controls weighted rare variants transmission distortion test

Usage

rvTDT(ped, evs, maf.threshold=1, qc.proportion=0.8)
Arguments

ped contain the genotype information for all samples, assume m families and n snps, 3m * n matrix, each column represents a variant, coded by 0/1/2 (number of alternative alleles); each row represents a sample, the first m rows are for child, the second m rows are for mother, the last m rows are for father

evs contain the control information from evs, 4 columns: rowname: variant’s ID; chr_pos_ref_alt; col1: number of samples have genotype 2; col2: number of samples have genotype 1; col3: number of samples have genotype 0; col4: mean coverage at this locus

maf.threshold The allowed maximum of MAF that variants will be used in computation, for unweighted and weighted by MAF, the MAF is computed through parents genotype while weighted by population controls, the maf is computed through population controls

qc.proportion variants that have more than qc.proportion families with enough coverage will be used in computation

Details

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Value

An object of class rvTDT, basically a list including elements:

nfamily number of total families in computation
nsnptot the total number of snps that in the input files
nsnpcompute the number of snps that pass the QC
p_lc_1 p value of unweighted linear combinated TDT
p_lc_maf p value of linear combinated TDT weighted by MAF (dbeta(1,25,maf))
p_lc_pc p value of linear combinated TDT weighted by population controls
p_k_1 p value of unweighted kernel TDT
p_k_maf p value of kernel TDT weighted by MAF (dbeta(1,25,maf))
p_k_pc p value of kernel TDT weighted by population controls

Author(s)
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References

Yu Jiang, Glen A. Satten, Yujun Han, Michael P. Epstein, Erin L. Heinzen, David B. Goldstein, Andrew S. Allen; Utilizing Population Controls in Rare-Variant Case-Parent Association Tests

Examples

data(rvTDT.example)
attach(rvTDT.example)
rvTDT(ped,evs,maf.threshold=1)

rvTDT.example

Example data for rvTDT

Description

Example data for rvTDT.

Format

rvTDT.example contains the following objects:

ped  a numeric genotype matrix of 447 individuals and 19 SNPs. Each row represents a different individual, and each column represents a different SNP marker. The first 149 row are genotype of children and 150-298 rows are genotype of corresponding mather and the last 149 rows are corresponding father

evs a numeric matrix of evs information for 19 variants: rowname: varaint ID; chr_pos_ref_alt; col1: number of samples have genotype 2;col2: number of samples have genotype 1;col3: number of samples have genotype 0;col4: mean coverage at this locus

rvTDTs

compute weights from population controls

Description

compute the p value for TDTs

Usage

kernel_TDT(parent.geno,child.geno,snp.weight)
lc_TDT(parent.geno,child.geno,snp.weight)
TDT_permutation(parent.geno,child.geno,snp.weight1,snp.weight2,snp.weight3,nperm)
TrendWeights

Arguments

parent.geno  parents genotype
child.geno   child genotype
snp.weight   weights for each SNP
nperm        number of permutations
snp.weight1  weights =1 for all SNP
snp.weight2  weighted by MAF
snp.weight3  weighted by population controls

Details

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Value

pvalue   pvalues from the test

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References

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TrendWeights  compute weights from population controls

Description

Used to compute population controls weights using parents and controls genotype

Usage

TrendWeights(evs.sum,parent.sum)
TrendWeights

Arguments

- evs.sum: contain evs information
- parent.sum: contain summarized parents genotype information

Details

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Value

- weights: return the weights computed through Armitage-trend test

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References

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