Package ‘pedgene’

April 10, 2024

Type Package

Title Gene-Level Variant Association Tests for Pedigree Data

Version 3.9

Date 2024-05-09

Description Gene-level variant association tests with disease status for pedigree data: kernel and burden association statistics.

License GPL (>= 2)

LazyLoad yes

Depends R (>= 4.2.0), stats, Matrix, CompQuadForm, survey, kinship2

NeedsCompilation no

URL https://analytictools.mayo.edu/research/pedgene/

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Repository CRAN

Date/Publication 2024-04-10 09:40:02 UTC

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`example.geno` *Example datasets for pedgene*

Description

example.geno: a data frame with minor allele count for subjects (rows) at variant positions (columns); example.ped: pedigree and trait data for subjects in example.geno; example.map: gene and chromosome for variant positions in example.geno; example.relation: special (twin) relationships for individuals in example.ped

Usage

```
data(example.geno)
data(example.ped)
data(example.map)
data(example.relation)
```

Format

`example.geno` -data frame with minor allele count for 20 variant positions:

`ped` pedigree ID, character or numeric

`person` person ID, used with ped to match subjects to their row in example.ped

`AA.1-AA.10,AX.1-AX.10` genotype columns at 10 positions for each of 2 simulated genes

`example.ped` -data frame with pedigree structure and trait values in the following columns:

`ped` pedigree ID, character or numeric

`person` person ID, a unique ID within each pedigree

`father` father ID, 0 if no father

`mother` mother ID, 0 if no mother

`sex` coded as 1 for male, 2 for female

`trait` phenotype, either case-control status coded as 1 for affected and 0 for unaffected, or a continuous value. Subjects with missing (NA) will be removed from the analysis

`trait.adjusted` an optional variable for covariate-adjusted trait. If trait.adjusted is present in the data.frame, then gene-level tests are adjusted for covariates using residuals = (trait - trait.adjusted). Otherwise, gene-level tests are not adjusted for covariates, in which case residuals = trait - mean(trait)

`example.map` - data frame with columns for gene name and chromosome:

`chrom` chromosome code (1-23,X allowed) where the gene is located

`gene` gene identifier

`example.relation` - matrix specifying special relationships between pairs of individuals in the following columns:

`ped` pedigree ID, character or numeric

`id1` person1 ID, used with ped to match subjects to their row in example.ped

`id2` person2 ID, used with ped to match subjects to their row in example.ped

`code` any of the following: 1=Monozygotic twin, 2=Dizygotic twin, 3=Twin of unknown zygosity, and 4=Spouse

Source

Simulated data for testing purposes

Examples

```
data(example.geno)
data(example.ped)
data(example.map)
data(example.relation)
```

`format_relation` *Internal utility to format the matrix used to specify special relationships between pairs of individuals*

Description

Internal utility to format the matrix used to specify special relationships between pairs of individuals. See kinship2::pedigree for details.

Usage

```
format_relation(relation)
```

Arguments

`relation` A matrix for one or more special relationships

Value

A matrix for one or more special relationships as required by pedgene

Author(s)

Alessia Visconti, King's College London (alessia.visconti@kcl.ac.uk).

See Also

pedgene, kinship

pedgene *Compute Kernel and Burden Statistics for Pedigree Data (possibly with unrelated subjects)*

Description

Compute linear kernel and burden statistics for gene-level analysis of data that includes pedigree-related subjects, and possibly unrelated subjects.

Usage

```
pedgene(ped, geno, map=NULL, male.dose=2,
                    checkpeds=TRUE, verbose.return=FALSE,
                    weights=NULL, weights.beta=c(1,25),
                    weights.mb=FALSE, relation=NULL,
                    method="kounen", acc.davies=1e-5)
```

Arguments

`ped` A data.frame with variables that define the pedigree structure (typical format used by LINKAGE and PLINK), trait (phenotype), and optionally a covariate-adjusted trait (for covariate-adjusted gene level statistics). The columns in the data.frame must be named as follows:

- famid: pedigree ID, character or numeric allowed
- person: person ID, a unique ID within each pedigree, numeric or character allowed
- father: father ID, 0 if no father
- mother: mother ID, 0 if no mother
- sex: coded as 1 for male, 2 for female
- trait: phenotype, either case-control status coded as 1 for affected and 0 for unaffected, or a continuous value. Subjects with missing (NA) will be removed from the analysis
- trait.adjusted: an optional variable for covariate-adjusted trait. If trait.adjusted is present in the data.frame, then gene-level tests are adjusted for covariates using residuals = (trait - trait.adjusted). Otherwise, gene-level tests are not adjusted for covariates, in which case residuals = trait - mean(trait) where the mean is taken on all subjects passed into pedgene before removing subjects who do not have genotype data.

`geno` Data.frame or matrix with genotypes for subjects (rows) at each variant position (columns). The first two columns are required to be named `famid` and `person`, which are used to match subjects to their data in the `ped` data.frame. The genotypes are coded as 0, 1, 2 for autosomal markers (typically a count of the number of the less-frequent allele). For X-chromosome markers, females are coded 0, 1, 2, and males coded 0, 1. Missing genotypes (NA) are allowed.

`map` Optional data.frame with columns "chrom" and "gene", one row per variant column in geno. The gene name can be any identifier for the gene. The chromosome can be either numeric or character, where the calculations will differ between autosomes vs X chromosome (allow "X"/"x"/23, converted to "X" in results)

`male.dose` When analyzing the X-chromosome, male.dose defines how male genotypes should be analyzed. male.dose can be between 0 and 2, but is typically either 1 or 2. Ozbek and Clayton show that male.dose = 2 is powerful in the presence of X-chromosome dosage compensation in females.

`checkpeds` logical, if FALSE, the method will skip the pedigree checking step, which can be intensive for large studies

`verbose.return` logical, if TRUE, return the pedigree, geno, and map objects used in the tests after initial cleanup, e.g., the removal of monomorphic variants. They are returned in the pedgene object in a list called "save"

`weights.beta` Weights based on a function of the minor allele frequency (maf) and the Beta distribution

`weights` optional user-specified weights, a vector of weights for each variant column of geno. If none given, the Beta weights are applied

`weights.mb` logical, if TRUE and no user-given weights, apply the Madsen-Browning weights per variant: 1/sqrt(maf*(1-maf)). The hierarchy of weights used is 1) user-specified weights, 2) Madsen-Browning if weights.mb=TRUE and weights=NULL, 3) Beta density weights (default if no other weights are set)

`relation` Optional data.frame/matrix with 4 columns (id, person1, person2, code) specifying special relationships between pairs of individuals and used by the kinship function. Codes are : 1=Monozygotic twin, 2=Dizygotic twin, 3=Twin of unknown zygosity, and 4=Spouse. The last is necessary in order to place a marriage with no children into the plot. See kinship2::pedigree for details.

`method` method for calculating the kernel test p-value. Kounen's saddlepoint approximation (default) is based on the survey package, and has been found to have less faults (e.g., returned missing value) than Davies' method (see Chen et al., 2012). The Davies method, which computes an exact p-value for a mixture of chi-square distributions, is also provided. The accuracy of the Davies method depends on the numerical accuracy parameter (acc.davies), which can be difficult to specify ahead of time.

`acc.davies` Numerical accuracy parameter used in the Davies' method for calculating the kernel test p-value. In some instances, a p-value from the kernel test is out of range, in which case the p-value is set to 0 or 1, depending on which direction the p-value was out of range.

Details

The pedgene function is a wrapper function to call pedgene.stats on one gene at a time. The pedgene.stats function calculates gene-level tests for associations with a trait among subjects, accounting for relationships among subjects based on known pedigree relationships (see Schaid et al). This is achieved by the kinship function in the kinship2 package. The kernel association statistic uses a weighted linear kernel, with default weights based on the beta distribution and the sample minor

allele frequency. The burden statistic is based on a weighted sum of variants. If a gene only has one variant, the kernel test reduces to the burden statistic. Variant positions that have zero variance are removed from the analysis because they do not contribute information.

Note that if ped contains extra people that are not necessary to define relationships of people with genotype data, their trait value will still be used in mean(trait) in calculating trait.adjusted if trait.adjusted is not given as a column in ped.

Value

An object of the pedgene S3 class, with the following elements:

`call:` function call

`pgdf:` data.frame with gene name, chromosome, n-variants per gene(after removing uncessary variants), n-variants removed per gene, kernel and burden test statistics and p-values. Kernel p-values are based on either Kuonen (1999) or Davies (1980) method. The burden statistic has a standard normal distribution, so the sign of the burden statistic gives information on the direction of association (positive value implies large burden score are positively associated with larger trait values). When a gene has only 1 variant, the kernel test reduces to the burden test. In this instance, the kernel statistic (chi-square) is the square of the burden statistic (standard normal), with both having the same p-value. When a gene has no markers after removing zero-variance markers, the gene test stastistics and p-values are all NA.

`save:` If verbose.return was set to TRUE, a list containing the cleaned form of the data that was input to pedgene and is used in the tests: ped, geno, and map

Author(s)

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References

Schaid DJ, McDonnell SK, Sinnwell JP, Thibodeau SN (2013) Multiple Genetic Variant Association Testing by Collapsing and Kernel Methods With Pedigree or Population Structured Data. Genetic Epidemiology, 37(5):409-18.

Ozbek U (2012) Statistics for X-chromosome association. 62nd Annual Meeting of The American Society of Human Genetics; Program #22. San Francisco, California.

Clayton D (2008) Testing for association on the X chromosome. Biostatistics 9:593-600

Chen H, Meigs J, Dupuis J (2012) Sequence kernel association test for quantitative traits in family samples. Genetic Epidem 37:196-204

Kounen D (1999) Saddle point approximatinos for distributions of quadratic forms in normal variables. Biometrika 86:929 -935

Davies RB (1980) Algorithm AS 155: The Distribution of a Linear Combination of chi-2 Random Variables, Journal of the Royal Statistical Society. Series C (Applied Statistics), 29(3):323-33

See Also

pedigreeChecks, example.ped

Examples

```
# example data with the same 10 variants for an autosome and X chromosome
# pedigree data on 39 subjects including 3 families and unrelateds
data(example.ped)
data(example.geno)
data(example.map)

# gene tests (chroms 1 and X) with male.dose=2
pg.m2 <- pedgene(example.ped, example.geno, example.map, male.dose=2)
# same genes, with male.dose=1
pg.m1 <- pedgene(example.ped, example.geno, example.map, male.dose=1)

## print and summary methods
print(pg.m2, digits=3)
summary(pg.m1, digits=3)
```

---

pedigreeChecks *Validity checks on pedigree data*

Description

Checks for valid IDs, sex codes for data in a single pedigree

Usage

```
pedigreeChecks(pedigree, male.code = 1, female.code = 2)
```

Arguments

`pedigree`	data frame with variables named person, father, mother, sex.
`male.code`	sex code for males
`female.code`	sex code for females

Details

A series of basic pedigree checks

Value

valid = TRUE or FALSE for validity of pedigree data

Author(s)

Daniel J. Schaid (schaid@mayo.edu).

`quadfactor` *Internal utility to calculate a constant quadratic factor for gene-level statistics variances, over all pedigrees*

Description

Internal utility to calculate a constant quadratic factor for gene-level statistics variances over all pedigrees, for either autosomes or X chromosome

Usage

```
quadfactor(kinmat, chrom, resid, sex, male.dose)
```

Arguments

`kinmat`	A kinship matrix for one or more pedigrees
`chrom`	character string for chromosome number, if "X", the method accounts for sex code
`resid`	the residual based on the trait minus the group mean or adjusted trait value for each subject
`sex`	See pedgene
`male.dose`	See pedgene

Value

Constant quadratic factor for gene-level statistics variances, for autosomes and X chromosome

Author(s)

Daniel J. Schaid, Mayo Clinic (schaid@mayo.edu).

See Also

pedgene, kinship

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