Package 'GxEScanR'

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Type Package

Title Run GWAS/GWEIS Scans Using Binary Dosage Files

Version 2.0.2

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Description Tools to run genome-wide association study (GWAS) and
genome-wide by environment interaction study (GWEIS) scans using the genetic
data stored in a binary dosage file. The user provides a data frame with
the subject's covariate data and the information about the binary dosage
file returned by the BinaryDosage::getbdinfo() routine.

License GPL-3

Encoding UTF-8

Language en-US

Imports Rcpp (>= 1.0.4), prodlim

LinkingTo Rcpp, RcppArmadillo

RoxygenNote 7.1.1

Suggests BinaryDosage, testthat (>= 2.1.0), covr, knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation yes

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R topics documented:

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gwas   *gwas*

Description

Run a gwas using genetic data from a binary dosage file

Usage

```
gwas(data, bdinfo, snps, outfile, skipfile, minmaf, blksize, binary)
```

Arguments

data	Data frame containing the subject ID, phenotype and covariates
bdinfo	Information about the binary dosage file returned from the BinaryDosage::getbdinfo routine
snps	The SNPs to be used in the scan. This may be an integer vector indicate which SNPs to use in the binary dosage file or a character vector of the SNP IDs to use. The value may also be "all", indicating to use all SNPs. The default value is "all".
outfile	The file name for the results Can be blank. If the value is "", the results are returned as a data frame. Default value is ""
skipfile	The name of the file to write the SNPs that were not used and the reason they weren't used. If the value is blank, there is no output of the unused SNPs. Default value is "".
minmaf	Minimum minor allele frequency of SNPs to include in analysis. SNPS that have less than 20 minor alleles observed will be excluded from the analysis regardless of the value of minmaf. A value of 0 indicates to use all the SNPs that have 20 minor alleles observed. Default value is 0.
blksize	Size of blocks of SNPs to read in at one time. Larger blocks can improve overall speed but require larger amounts of computer memory. A value of 0 indicates to use the recommended block size. Default value is 0.
binary	Logical value indicating if the phenotype is a binary value. Default value is false.

Value

0

Examples

```
bdinfo <- readRDS(system.file("extdata/pdata_4_1.bdinfo", package = "GxEScanR"))
covdata <- readRDS(system.file("extdata/covdata.rds", package = "GxEScanR"))

results <- gwas(data = covdata, bdinfo = bdinfo, binary = FALSE)
```

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gweis   *gweis*

Description

Run a gweis using genetic data from a binary dosage file

Usage

```
gweis(data, bdinfo, snps, outfile, skipfile, minmaf, blksize, binary)
```

Arguments

data	Data frame containing the subject ID, phenotype and covariates
bdinfo	Information about the binary dosage file returned from the BinaryDosage::getbdinfo routine
snps	The SNPs to be used in the scan. This may be an integer vector indicate which SNPs to use in the binary dosage file or a character vector of the SNP IDs to use. The value may also be "all", indicating to use all SNPs. The default value is "all".
outfile	The file name for the results Can be blank. If the value is "", the results are returned as a data frame. Default value is ""
skipfile	The name of the file to write the SNPs that were not used and the reason they weren't used. If the value is blank, there is no output of the unused SNPs. Default value is "".
minmaf	Minimum minor allele frequency of SNPs to include in analysis. SNPS that have less than 20 minor alleles observed will be excluded from the analysis regardless of the value of minmaf. A value of 0 indicates to use all the SNPs that have 20 minor alleles observed. Default value is 0.
blksize	Size of blocks of SNPs to read in at one time. Larger blocks can improve overall speed but require larger amounts of computer memory. A value of 0 indicates to use the recommended block size. Default value is 0.
binary	Logical value indicating if the phenotype is a binary value. Default value is false.

Value

0

Examples

```
bdinfo <- readRDS(system.file("extdata/pdata_4_1.bdinfo", package = "GxEScanR"))
covdata <- readRDS(system.file("extdata/covdata.rds", package = "GxEScanR"))

results <- gweis(data = covdata, bdinfo = bdinfo)
```

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