

Package ‘GEVACO’

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Type Package

Title Joint Test of Gene and GxE Interactions via Varying Coefficients

Version 1.0.0

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Depends R (>= 3.6)

Description A novel statistical model to detect the joint genetic and dynamic gene-environment (GxE) interaction with continuous traits in genetic association studies. It uses varying-coefficient models to account for different GxE trajectories, regardless whether the relationship is linear or not. The package includes one function, `GxEtest()`, to test a single genetic variant (e.g., a single nucleotide polymorphism or SNP), and another function, `GxEscreen()`, to test for a set of genetic variants. The method involves a likelihood ratio test described in Crainiceanu, C. M., and Ruppert, D. (2004) <doi:10.1111/j.1467-9868.2004.00438.x>.

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Encoding UTF-8

LazyData true

Imports nlme, RLRsim, stats

Suggests rmarkdown, knitr

RoxygenNote 7.1.0

VignetteBuilder knitr

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NeedsCompilation no

Repository CRAN

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cov_example	<i>Covariate Information</i>
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Description

Dataset containing example covariate information for analysis

Usage

```
cov_example
```

Format

A dataframe with 500 rows and 4 variables:

y phenotypic factor of interest

BMI BMI in kg/m²

age age in years

sex sex coded as 1 & 2

geno_example	<i>Genotypic Information</i>
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Description

Dataset containing example genotypic information for analysis, coded as 0 1 2. Has 500 observations and assumes a minor allele frequency threshold of 0.05. We included the first 20 SNPs to meet this threshold in this example. Each column holds the information for an individual SNP, and each row contains the genotypic information for that observation.

Usage

```
geno_example
```

Format

An object of class `matrix` with 500 rows and 20 columns.

GxEscreen	<i>Gene-Environment Interaction: Genome-wide Screen</i>
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Description

Function to test for the joint genetic and gene-environment interaction effects for a set of variant using a LRT model

Usage

```
GxEscreen(dat, geno, nsim = 1e+05, K = 7)
```

Arguments

dat	a data frame with covariate information. Col 1 should be phenotype, col 2 should be environmental factor, col 3 and later should be additional covariates
geno	a genotype matrix with 0-1-2 coding
nsim	the number of replicates in obtaining the p-value (standard 1e5)
K	the number of knots used to control the flexibility in modeling GxE interaction

Value

a vector containing the p-value from the LRT associated with each SNP

Examples

```
GxEscreen(cov_example, geno_example, nsim=1e5, K=7)
```

GxEtest	<i>Joint test for genetic and gene-environment interaction effects for a single SNP</i>
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Description

Function to test for the joint genetic and gene-environment interaction effects for a single variant using a LRT model

Usage

```
GxEtest(dat, snp_genotype, nsim = 1e+05, K)
```

Arguments

dat	a data frame with covariate information. Column 1 should be phenotype, column 2 should be the environmental factor of interest, columns 3 and later should be additional covariates
snp_geno	a vector containing genotypic information of SNP of interest to be tested
nsim	the number of replicates in obtaining the p-value (standard 1e5)
K	the number of knots used to control the flexibility in modeling GxE interaction

Value

empirical p-value obtained as the proportion of T0 that are greater than the observed test statistic T

References

Crainiceanu, C. M., & Ruppert, D. (2004). Likelihood ratio tests in linear mixed models with one variance component. *Journal of the Royal Statistical Society Series B-Statistical Methodology*, 66, 165-185. doi: 10.1111/j.1467-9868.2004.00438.x

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