Package: lit (via r-universe)

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Type Package

Title Latent Interaction Testing for Genome-Wide Studies

Version 1.0.1

Maintainer Andrew Bass <ajbass@emory.edu>

Description Identifying latent genetic interactions in genome-wide association studies using the Latent Interaction Testing (LIT) framework. LIT is a flexible kernel-based approach that leverages information across multiple traits to detect latent genetic interactions without specifying or observing the interacting variable (e.g., environment). LIT accepts standard PLINK files as inputs to analyze large genome-wide association studies.

URL https://github.com/ajbass/lit

License LGPL

Encoding UTF-8

VignetteBuilder knitr

RoxygenNote 7.2.3

LinkingTo Rcpp, RcppArmadillo, RcppEigen

Imports Rcpp (>= 1.0.11), genio, CompQuadForm

Suggests testthat (>= 3.0.0), knitr, rmarkdown

NeedsCompilation yes

Author Andrew Bass [aut, cre], Michael Epstein [aut]

Repository https://cran.r-universe.dev

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`gamut_plink` *GAMuT*

Description

The `GAMuT` function is a kernel-based multivariate association test. Note that our code to process plink files builds from the `genio` R package.

Usage

```
gamut_plink(y, file, adjustment = NULL, pop_struct = NULL, verbose = TRUE)
```

Arguments

`y`	matrix of traits (n observations by k traits)
`file`	path to plink files
`adjustment`	matrix of covariates to adjust traits
`pop_struct`	matrix of PCs that captures population structure
`verbose`	If TRUE (default) print progress.

Value

A data frame of p-values where the columns are the cross products/squared residuals and the rows are SNPs.

See Also

`lit_plink`, `marginal_plink`

Examples

```
# set seed
set.seed(123)

# path to plink files
file <- system.file("extdata", 'sample.bed', package = "genio", mustWork = TRUE)

# Generate trait expression
Y <- matrix(rnorm(10*4), ncol = 4)

out <- gamut_plink(Y, file = file)
```

`lit` *Latent Interaction Testing*

Description

`lit` performs a kernel-based testing procedure, Latent Interaction Testing (LIT), using a set of traits and SNPs. LIT tests whether the squared residuals (SQ) and cross products (CP) are statistically independent of the genotypes. In particular, we construct a kernel matrix for the SQ/CP terms to measure the pairwise similarity between individuals, and also construct an analogous one for the genotypes. We then test whether these two matrices are independent. Currently, we implement the linear and projection kernel functions to measure pairwise similarity between individuals. We then combine the p-values of these implementations using a Cauchy combination test to maximize the number of discoveries.

Usage

```
lit(y, x, adjustment = NULL, pop_struct = NULL)
```

Arguments

`y`	matrix of traits (n observations by k traits)
`x`	matrix of SNPs (n observations by m SNPs)
`adjustment`	matrix of covariates to adjust traits
`pop_struct`	matrix of PCs that captures population structure

Value

A data frame of p-values where the columns are

- `wlit`: LIT using a linear kernel
- `ulit`: LIT using a projection kernel
- `alit`: Cauchy combination test of the above two LIT implementations

See Also

lit_plink

Examples

```
# set seed
set.seed(123)

# Generate SNPs and traits
X <- matrix(rbinom(10*2, size = 2, prob = 0.25), ncol = 2)
Y <- matrix(rnorm(10*4), ncol = 4)

out <- lit(Y, X)
```

---

lit_h *LIT correcting for dominance effects*

Description

Internal use for now

Usage

```
lit_h(y, x, adjustment = NULL, pop_struct = NULL)
```

Arguments

y	matrix of traits (n observations by k traits)
x	matrix of SNPs (n observations by m SNPs)
adjustment	matrix of covariates to adjust traits
pop_struct	matrix of PCs that captures population structure

---

lit_plink *Latent Interaction Testing*

Description

lit_plink performs a kernel-based testing procedure, Latent Interaction Testing (LIT), using a set of traits and SNPs. LIT tests whether the squared residuals (SQ) and cross products (CP) are statistically independent of the genotypes. In particular, we construct a kernel matrix for the SQ/CP terms to measure the pairwise similarity between individuals, and also construct an analogous one for the genotypes. We then test whether these two matrices are independent. Currently, we implement the linear and projection kernel functions to measure pairwise similarity between individuals. We then combine the p-values of these implementations using a Cauchy combination test to maximize the number of discoveries. This function is suitable for large datasets (e.g., UK Biobank) in plink format. Note that our code to process plink files builds from the genio R package

Usage

```
lit_plink(y, file, adjustment = NULL, pop_struct = NULL, verbose = TRUE)
```

Arguments

y	matrix of traits (n observations by k traits)
file	path to plink files
adjustment	matrix of covariates to adjust traits
pop_struct	matrix of PCs that captures population structure
verbose	If TRUE (default) print progress.

Value

A data frame of p-values where the columns are

- wlit: LIT using a linear kernel
- ulit: LIT using a projection kernel
- alit: Cauchy combination test of the above two LIT implementations

See Also

lit

Examples

```
# set seed
set.seed(123)

# path to plink files
file <- system.file("extdata", 'sample.bed', package = "genio", mustWork = TRUE)

# Generate trait expression
Y <- matrix(rnorm(10*4), ncol = 4)

out <- lit_plink(Y, file = file)
```

---

marginal *Marginal (SQ/CP) approach*

Description

The marginal function performs a trait-by-trait univariate test for latent interactions using the squared residuals and cross products.

Usage

```
marginal(y, x, adjustment = NULL, pop_struct = NULL)
```

Arguments

y	matrix of traits (n observations by k traits)
x	matrix of SNPs (n observations by m SNPs)
adjustment	matrix of covariates to adjust traits
pop_struct	matrix of PCs that captures population structure

Value

A data frame of p-values where the columns are the cross products/squared residuals and the rows are SNPs.

See Also

marginal_plink

Examples

```
# set seed
set.seed(123)

# Generate SNPs and traits
X <- matrix(rbinom(10*2, size = 2, prob = 0.25), ncol = 2)
Y <- matrix(rnorm(10*4), ncol = 4)

out <- marginal(Y, X)
```

---

marginal_plink *Marginal (SQ/CP) approach*

Description

The marginal_plink function performs a trait-by-trait univariate test for latent interactions using the squared residuals and cross products. This function is suitable for large datasets (e.g., UK Biobank) in plink format. Note that our code to process plink files builds from the genio R package.

Usage

```
marginal_plink(y, file, adjustment = NULL, pop_struct = NULL, verbose = TRUE)
```

Arguments

y	matrix of traits (n observations by k traits)
file	path to plink files
adjustment	matrix of covariates to adjust traits
pop_struct	matrix of PCs that captures population structure
verbose	If TRUE (default) print progress.

Value

A data frame of p-values where the columns are the cross products/squared residuals and the rows are SNPs.

See Also

marginal_plink

Examples

```
# set seed
set.seed(123)

# Path to plink files
file <- system.file("extdata", 'sample.bed', package = "genio", mustWork = TRUE)

# Generate trait expression
Y <- matrix(rnorm(10*4), ncol = 4)

out <- marginal_plink(Y, file = file)
```

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