

Package ‘gwas’

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Type Package

Title The package contains some functions to calculate the maximum likelihood estimates of the parameters in a genetic LMM

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Description The package was written to perform classical GWAS for one-dimensional trait. It contains some functions written using ‘RcppArmadillo’ for faster implementation of multiple hypothesis testing in GWAS. The functions are used in calculating restricted maximum likelihood estimates of the variance parameters as well as MLE of SNP effect size under a typical genetic Linear Mixed Model.

License What license is it under?

Imports Rcpp (>= 1.0.7)

LinkingTo Rcpp, RcppArmadillo

RoxygenNote 7.2.0

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gwas-package	<i>The package contains some functions to calculate the maximum likelihood estimates of the parameters in a genetic LMM</i>
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Details

The DESCRIPTION file: This package was not yet installed at build time.

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~~ An overview of how to use the package, including the most ~~ ~~ important functions ~~

Author(s)

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References

~~ Literature or other references for background information ~~

See Also

~~ Optional links to other man pages, e.g. ~~ ~~ [<pkg>](#) ~~

Examples

~~ simple examples of the most important functions ~~

beta_hat_sigma_hat	<i>MLE and standard deviation of SNP effect size in genetic LMM</i>
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Description

'beta_hat_sigma_hat' returns the maximum likelihood estimate of SNP effect size and its standard deviation.

Usage

```
beta_hat_sigma_hat(K, X, y, log_lambda_tau_hat)
```

Arguments

K	The kinship matrix in genetic LMM
X	The augmented matrix of fixed effects which is obtained by augmenting the genotype vector of the SNP to the covariate matrix
y	The phenotype vector (should be a column matrix)
log_lambda_tau_hat	The 2-vector consisting of the log of RMLE estimates of λ and τ

Details

The MLE and standard deviation of SNP effect size is used in performing the hypothesis testing of no association. For more details, see our article.

Value

A vector of two elements where the first element is the MLE, and the second element is the standard deviation of the SNP effect size

gamma_tilda	<i>MLE of fixed effect sizes under known variance components</i>
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Description

'gamma_tilda' returns the MLE of covariate and SNP effect sizes in a genetic LMM when the variance components of polygenic effect and observational noise are known.

Usage

```
gamma_tilda(K, X, y, log_lambda_tau)
```

Arguments

K	The kinship matrix in genetic LMM
X	The augmented matrix of fixed effects which is obtained by augmenting the genotype vector of the SNP to the covariate matrix
y	The phenotype vector (should be a column matrix)
log_lambda_tau	The vector $(\log \lambda, \log \tau)$, where λ and τ are the two parameters used in the variance components of the genetic LMM.

Details

The MLE of covariate and SNP effect sizes for known values of λ and τ is used in finding the RMLE of (λ, τ) by maximizing the marginal likelihood. This in turn helps to find the unrestricted MLE of SNP effect size. For more details, see our article.

Value

MLE of γ , the vector of fixed effect sizes for known value of (λ, τ)

neglr_lambda_tau	<i>Marginal likelihood of variance parameters in genetic LMM</i>
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Description

'neglr_lambda_tau' returns the (negated) marginal likelihood of the parameters used in the variance component of the genetic LMM

Usage

```
neglr_lambda_tau(log_lambda_tau, K, X, y)
```

Arguments

log_lambda_tau	The vector $(\log\lambda, \log\tau)$, where λ and τ are the two parameters used in the variance components of the genetic LMM.
K	The kinship matrix in genetic LMM
X	The augmented matrix of fixed effects which is obtained by augmenting the genotype vector of the SNP to the covariate matrix
y	The phenotype vector (should be a column matrix)

Details

The marginal likelihood obtained is minimized (since it is negated) to find the RMLE of (λ, τ) . For more details, see our article.

Value

Marginal likelihood of (λ, τ)

V_lambda_tau	<i>Variance-covariance matrix of random components in LMM</i>
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Description

'V_lambda_tau' returns the variance-covariance matrix of the sum of polygenic effects and observational noise in a genetic LMM

Usage

```
V_lambda_tau(K, log_lambda_tau)
```

Arguments

K	The kinship matrix in genetic LMM
log_lambda_tau	The vector $(\log\lambda, \log\tau)$, where λ and τ are the two parameters used in the variance components of the genetic LMM.

Details

The variance covariance matrix is used in finding the RMLE of λ and τ . This eventually helps us to find the MLE of SNP effect size. For more details, see our article.

Value

$(1/\tau)(\lambda K + I)$

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