

Package ‘gemma2’

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Title GEMMA Multivariate Linear Mixed Model

Version 0.1.3

Description Fits a multivariate linear mixed effects model that uses a polygenic term, after Zhou & Stephens (2014) (<<https://www.nature.com/articles/nmeth.2848>>). Of particular interest is the estimation of variance components with restricted maximum likelihood (REML) methods. Genome-wide efficient mixed-model association (GEMMA), as implemented in the package 'gemma2', uses an expectation-maximization algorithm for variance components inference for use in quantitative trait locus studies.

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Encoding UTF-8

LazyData true

URL <https://github.com/fboehm/gemma2>

BugReports <https://github.com/fboehm/gemma2/issues>

Suggests covr, testthat, knitr, rmarkdown, readr

RoxygenNote 7.1.1

VignetteBuilder knitr

Imports methods, Matrix

Language en-US

NeedsCompilation no

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calc_omega	<i>Calculate Omega matrices</i>
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Description

Calculate Omega matrices

Usage

calc_omega(eval, D_l)

Arguments

- eval vector of eigenvalues from decomposition of relatedness matrix
- D_l vector of length d_size

Value

list of length 2. First entry in the list is the symmetric matrix OmegaU. Second entry in the list is the symmetric matrix OmegaE.

Examples

calc_omega(eval = 50:1, D_l = runif(2))

calc_qi	<i>Calculate Qi (inverse of Q) and log determinant of Q</i>
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Description

Calculate Qi (inverse of Q) and log determinant of Q

Usage

```
calc_qi(eval, D_l, X)
```

Arguments

eval	vector of eigenvalues from decomposition of relatedness matrix
D_l	vector of length d_size
X	design matrix

Value

a list of length two. First entry in the list is a symmetric numeric matrix, Qi, the inverse of the Q matrix. The second entry in the outputted list is the log determinant of the matrix Q for use in likelihood calculations.

Examples

```
as.matrix(readr::read_tsv(system.file("extdata",
"mouse100.cXX.txt",
package = "gemma2")),
col_names = FALSE)[, 1:100]) -> kinship
eigen2(kinship) -> e2_out
e2_out$values -> eval
e2_out$vectors -> U
eigen_proc(V_g = diag(c(1.91352, 0.530827)),
V_e = diag(c(0.320028, 0.561589))) -> ep_out

calc_qi(eval = eval,
D_l = ep_out[[4]],
X = t(rep(1, 100)) %*% U)
```

calc_sigma	<i>Calculate Sigma_ee and Sigma_uu matrices</i>
------------	---

Description

Calculate Sigma_ee and Sigma_uu matrices

Usage

calc_sigma(eval, D_l, X, OmegaU, OmegaE, UltVeh, Qi)

Arguments

eval	eigenvalues vector from decomposition of relatedness matrix
D_l	vector
X	design matrix
OmegaU	matrix
OmegaE	matrix
UltVeh	matrix
Qi	inverse of Q matrix

calc_XHiY	<i>Calculate XHiY</i>
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Description

Calculate XHiY

Usage

calc_XHiY(eval, D_l, X, UltVehiY)

Arguments

eval	vector of eigenvalues from the decomposition of the relatedness matrix
D_l	vector of length d_size
X	design matrix
UltVehiY	a matrix

Value

numeric vector

Examples

```

readr::read_tsv(system.file("extdata",
"mouse100.pheno.txt",
package = "gemma2"),
col_names = FALSE) -> pheno
phe16 <- as.matrix(pheno[, c(1, 6)])
as.matrix(readr::read_tsv(system.file("extdata",
"mouse100.cXX.txt",
package = "gemma2"),
col_names = FALSE)[, 1:100]) -> kinship
eigen2(kinship) -> eout
eout$values -> eval
eout$vectors -> U
UltVehi <- matrix(c(0, -1.76769, -1.334414, 0),
nrow = 2,
byrow = FALSE) # from output of eigen_proc()
calc_XHiY(eval = eval,
UltVehiY = UltVehi %*% t(phe16) %*% U
)

```

center_kinship	<i>Center a relatedness matrix, after Zhou's GEMMA function CenterMatrix</i>
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Description

Center a relatedness matrix, after Zhou's GEMMA function CenterMatrix

Usage

```
center_kinship(mat)
```

Arguments

mat	a relatedness matrix
-----	----------------------

Value

a centered relatedness matrix

Examples

```

readr::read_tsv(system.file("extdata",
"mouse100.cXX.txt",
package = "gemma2"),
col_names = FALSE)[, 1:100] -> kinship
e_out <- eigen2(as.matrix(kinship))
center_kinship(as.matrix(kinship)) -> kinship_centered

```

eigen2	<i>Calculate eigendecomposition and return ordered eigenvalues and eigenvectors</i>
--------	---

Description

Calculate eigendecomposition and return ordered eigenvalues and eigenvectors

Usage

```
eigen2(spd, decreasing = FALSE)
```

Arguments

spd	a semi-positive definite matrix
decreasing	argument passed to order()

Value

a list with 2 components, the eigenvalues and the eigenvectors

Examples

```
readr::read_tsv(system.file("extdata",
"mouse100.cXX.txt",
package = "gemma2"),
col_names = FALSE)[, 1:100] -> kinship
e_out <- eigen2(as.matrix(kinship))
```

eigen_proc	<i>Eigendecomposition procedure for Vg and Ve</i>
------------	---

Description

Eigendecomposition procedure for Vg and Ve

Usage

```
eigen_proc(V_g, V_e, tol = 1/10000)
```

Arguments

V_g	a d_size by d_size covariance matrix
V_e	a d_size by d_size covariance matrix
tol	a positive number indicating the tolerance for isSymmetric

Value

a named list of length 4 containing the outputs of eigendecomposition procedure

Examples

```
eigen_proc(diag(2), diag(2))
```

<i>gemma2</i>	<i>gemma2</i>
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Description

We implement an expectation-maximization algorithm for multivariate variance components after the GEMMA software's algorithm.

<i>MphCalcLogL</i>	<i>Calculate log likelihood</i>
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Description

Calculate log likelihood

Usage

```
MphCalcLogL(eval, D_l, Qi, UltVehiY, xHiy)
```

Arguments

<i>eval</i>	eigenvalues vector from decomposition of relatedness matrix
<i>D_l</i>	vector of eigenvalues from decomposition of Ve matrix
<i>Qi</i>	inverse of Q matrix
<i>UltVehiY</i>	matrix of (transformed) Y values
<i>xHiy</i>	vector

MphEM	<i>Perform expectation-maximization algorithm to infer V_g and V_e values for a pair of traits.</i>
-------	---

Description

Perform expectation-maximization algorithm to infer V_g and V_e values for a pair of traits.

Usage

```
MphEM(
  max_iter = 10000,
  max_prec = 1/1e+06,
  eval,
  X,
  Y,
  V_g,
  V_e,
  verbose_output = FALSE
)
```

Arguments

<code>max_iter</code>	maximum number of iterations for EM algorithm
<code>max_prec</code>	maximum precision for EM algorithm
<code>eval</code>	vector of eigenvalues from relatedness matrix decomposition
<code>X</code>	design matrix. Typically contains founder allele dosages.
<code>Y</code>	matrix of phenotype values
<code>V_g</code>	genetic covariance matrix
<code>V_e</code>	error covariance matrix
<code>verbose_output</code>	logical indicating whether to output entire collection of intermediate values for all iterations. Default is FALSE.

Value

a list of lists. Length of list corresponds to number of EM iterations

stagger_mats	<i>Stagger matrices within a larger, block-diagonal matrix</i>
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Description

Stagger matrices within a larger, block-diagonal matrix

Usage

```
stagger_mats(...)
```

Arguments

... one or more matrices, separated by commas

Value

a block-diagonal matrix, with the inputted matrices as blocks on the diagonal.

Examples

```
foo <- matrix(rnorm(40000), ncol = 8)
block_diag <- stagger_mats(foo, foo)
dim(foo)
dim(block_diag)
```

UpdateRL_B	<i>Update B for restricted log likelihood</i>
------------	---

Description

Update B for restricted log likelihood

Usage

```
UpdateRL_B(xHiy, Qi, d_size)
```

Arguments

xHiy	vector
Qi	Q inverse matrix
d_size	number of traits

See Also

Other expectation-maximization functions: [update_e\(\)](#), [update_u\(\)](#), [update_v\(\)](#)

update_e	<i>Update E</i>
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Description

Update E

Usage

update_e(UltVehiY, UltVehiBX, UltVehiU)

Arguments

- UltVehiY matrix of transformed Y values
- UltVehiBX matrix of transformed BX values
- UltVehiU matrix of transformed U values

See Also

Other expectation-maximization functions: [UpdateRL_B\(\)](#), [update_u\(\)](#), [update_v\(\)](#)

update_u	<i>Update U matrix</i>
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Description

Update U matrix

Usage

update_u(OmegaE, UltVehiY, UltVehiBX)

Arguments

- OmegaE the OmegaE matrix, calculated in calc_omega
- UltVehiY matrix
- UltVehiBX matrix

See Also

Other expectation-maximization functions: [UpdateRL_B\(\)](#), [update_e\(\)](#), [update_v\(\)](#)

Examples

```
readr::read_tsv(system.file("extdata",
"mouse100.pheno.txt",
package = "gemma2"),
col_names = FALSE) -> pheno
phe16 <- as.matrix(pheno[, c(1, 6)])
as.matrix(readr::read_tsv(system.file("extdata",
"mouse100.cXX.txt",
package = "gemma2"),
col_names = FALSE)[, 1:100]) -> kinship
eigen2(kinship) -> e2_out
e2_out$values -> eval
e2_out$vectors -> U
eigen_proc(V_g = diag(c(1.91352, 0.530827)),
V_e = diag(c(0.320028, 0.561589))) -> ep_out
UltVehi <- ep_out[[3]]
calc_omega(eval, ep_out$D_1) -> co_out
update_u(OmegaE = co_out[[2]],
        UltVehiY = UltVehi %*% t(phe16),
        UltVehiBX = matrix(c(-0.71342, -0.824482),
ncol = 1) %*% t(rep(1, 100))
)
```

update_v	<i>Update V_e and V_g</i>
----------	---------------------------

Description

Update V_e and V_g

Usage

```
update_v(eval, U, E, Sigma_uu, Sigma_ee, tol = 1/10000)
```

Arguments

eval	vector of eigenvalues from eigendecomposition of relatedness matrix
U	matrix
E	matrix
Sigma_uu	matrix
Sigma_ee	matrix
tol	a positive number indicating tolerance to be passed to isSymmetric()

See Also

Other expectation-maximization functions: [UpdateRL_B\(\)](#), [update_e\(\)](#), [update_u\(\)](#)

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