

Package ‘HiLMM’

April 13, 2015

Type Package

Title Estimation of Heritability in Linear Mixed Models

Version 1.1

Date 2015-04-13

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Description Estimation of heritability with confidence intervals in linear mixed models.

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NeedsCompilation no

Repository CRAN

Date/Publication 2015-04-13 22:50:52

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HiLMM-package	<i>Estimation of heritability in linear mixed models</i>
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Description

The package contains two functions: `estim_herit` computes heritability when the random effects follow either a Gaussian distribution or a mixture of a Dirac and a Gaussian distribution. It also provides a confidence interval of heritability when the random effects are Gaussian. The function `data_simu` allows the user to generate dataset which are compatible with the arguments of HiLMM.

Details

Package: HiLMM
Type: Package
Version: 1.0
Date: 2014-04-10
License: GPL-2

Author(s)

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References

The method is developed in the paper "Heritability estimation in sparse high dimensional linear mixed models" (A.Bonnet,E.Gassiat,C.Levy-Leduc,2014)

Examples

```
library(HiLMM)
data_HiLMM=data_simu(100,1000,0.7,1)
Y=data_HiLMM$Y
W=data_HiLMM$W
estim_herit(Y,W)$heritability
estim_herit(Y,W)$CI_low
estim_herit(Y,W)$CI_up
estim_herit(Y,W)$standard_deviation
```

data_simu	<i>function to generate a dataset which is compatible with the arguments of the function HiLMM</i>
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Description

This function generates a dataset which contains a matrix corresponding to the genetic information and a vector of observations. This dataset corresponds to the type of arguments which is expected in the function HiLMM.

Usage

```
data_simu(n, N, eta_star, q)
```

Arguments

n	size of the vector of observations that the user wants to generate.
N	number of columns of the genetic information matrix that the user wants to generate.
eta_star	value of the heritability.
q	proportion of non zero components in the random effects associated to the genetic information matrix.

Value

Y	vector of observations of size n
W	Matrix of size n x N which contains entries with 0,1 and 2

Examples

```

library(HiLMM)
data_sim=data_simu(100,1000,0.5,0.5)
Y=data_sim$Y
W=data_sim$W
## The function is currently defined as
function (n, N, eta_star, q)
{
  sigma_u = 1
  P = runif(N, 0.1, 0.5)
  W = matrix(0, n, N)
  for (j in 1:N) {
    W[, j] = rbinom(n, 2, P[j])
  }
  nb_comp_non_zero = q * N
  sigma_e = sqrt(q * N * sigma_u^2 * (1 - eta_star)/eta_star)
  b = sample(1:N, nb_comp_non_zero)
  a1 = sort(b)
  u = rnorm(nb_comp_non_zero, 0, sigma_u)
  e = rnorm(n, 0, sigma_e)
  U = matrix(0, N)
  U[a1] = u
  Z = scale(W, center = TRUE, scale = TRUE)
  Y = Z %*% U + e
  list(Z = Z, Y = Y)
}

```

Description

The function computes heritability when the random effects follow either a Gaussian distribution or a mixture of a Dirac and a Gaussian distribution. It also provides a confidence interval of heritability when the random effects are Gaussian.

Usage

```
estim_herit(Y,W)
```

Arguments

Y	vector of observations of size n
W	matrix with n rows and N columns

Value

heritability	Heritability
CI_low	Lower bound of the confidence interval
CI_up	Upper bound of the confidence interval
standard_deviation	Standard deviation

Author(s)

Anna Bonnet

References

The method is developed in the paper "Heritability estimation in high dimensional linear mixed models" (A.Bonnet,E.Gassiat,C.L??vy-Leduc,2014)

Examples

```
library(HiLMM)
data(Y)
data(W)
estim_herit(Y,W)$heritability
estim_herit(Y,W)$CI_low
estim_herit(Y,W)$CI_up
estim_herit(Y,W)$standard_deviation
```

W

genetic information matrix

Description

matrix of size 100x100 which contains entries with 0,1,2.

Y	<i>observations</i>
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Description

vector of observations of size 100

Usage

```
data("Y")
```

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