

Package ‘IMAGE’

July 28, 2019

Title Integrated Methylation QTL Mapping and Allele-Specific Analysis

Version 1.0

Date 2019-06-30

Description Performs mQTL (methylation quantitative-trait locus) mapping in bisulfite sequencing studies by fitting a binomial mixed model and then incorporating the allelic-specific methylation pattern. Based on Fan, Yue; Vilgalys, Tauras P.; Sun, Shiquan; Peng, Qinke; Tung, Jenny; Zhou, Xiang (2019) <doi:10.1101/615039>.

License GPL-2

Imports Rcpp (>= 0.12.19), foreach, doParallel, parallel, Matrix

LinkingTo Rcpp, RcppArmadillo

Encoding UTF-8

LazyData true

BugReports <https://github.com/umich-biostatistics/IMAGE/issues>

RoxygenNote 6.1.1

NeedsCompilation yes

Author Xiang Zhou [aut],
Shiquan Sun [aut],
Yue Fan [aut],
Michael Kleinsasser [cre]

Maintainer Michael Kleinsasser <mkleinsa@umich.edu>

Depends R (>= 3.5.0)

Repository CRAN

Date/Publication 2019-07-28 11:10:08 UTC

R topics documented:

ExampleData	2
example_results	2
image	3

ExampleData	<i>Example data set to test the IMAGE method</i>
-------------	--

Description

A list containing the data needed to use the `image` function.

Usage

```
ExampleData
```

Format

A list three elements:

data A `data.frame` with columns `r`, `y`, `r1`, `r2`, `y1`, `y2`

geno A `data.frame` with columns `hap1` and `hap2`

K A 100X100 matrix

example_results	<i>Example results using the example data set</i>
-----------------	---

Description

A data set containing the output of `image` function call on the included data set `ExampleData`.

Usage

```
example_results
```

Format

A `data.frame` with 1000 rows and 9 variables (columns):

Loc ordinal number of SNP-CpG pair being analyzed

numIDV number of observations of SNP-CpG pair being analyzed

beta the fixed effect parameter estimate for the predictor of interest

se_beta the standard deviation of fixed effect

pvalue P-value for the fixed effect, based on the wald test

h2 heritability of the transformed rate

sigma total variance component

converged a logical indicator for convergence

time time to converge

 image

High-powered detection of genetic effects on DNA methylation

Description

Perform high-powered detection of genetic effects on DNA methylation using integrated methylation QTL (methylation quantitative-trait locus) mapping and allele-specific analysis.

Usage

```
image(geno, data, K, Covariates = NULL, numCore = 1,
      fit.maxiter = 500, fit.tol = 1e-05, verbose = TRUE)
```

Arguments

geno	a data list containing the genotype data
data	a data list containing the methylation data
K	a known kinship matrix. This matrix should be a positive semi-definite matrix with dimensions equal to the sample size
Covariates	a matrix containing the covariates subject to adjustment (Default = NULL)
numCore	a positive integer specifying the number of cores for parallel computing (default = 1)
fit.maxiter	a positive integer specifying the maximum number of iterations when fitting the generalized linear mixed model (default = 500)
fit.tol	a positive number specifying tolerance, the difference threshold for parameter estimates below which iterations should be stopped (default = 1e-5)
verbose	include verbose output

Value

A `data.frame` containing the following named elements:

- `loc`: ordinal number of SNP-CpG pair being analyzed
- `numIDV`: number of observations of SNP-CpG pair being analyzed
- `beta`: the fixed effect parameter estimate for the predictor of interest
- `se_beta`: the standard deviation of fixed effect
- `pvalue`: P value for the fixed effect, based on the Wald test
- `h2`: heritability of the transformed rate
- `sigma2`: total variance component
- `converged`: a logical indicator for convergence
- `time`: time to converge

References

Fan, Y., Vilgalys, T.P., Sun, S., Peng, Q., Tung, J. and Zhou, X., 2019. High-powered detection of genetic effects on DNA methylation using integrated methylation QTL mapping and allele-specific analysis. *bioRxiv*, p.615039.

Examples

```
# This example demonstrates IMAGE:

data(ExampleData)
geno <- ExampleData$geno
K <- ExampleData$K
data <- ExampleData$data
res=image(geno,data,K)

# We've saved the results of the example above to show an example of
# the outputs IMAGE produces:
data(example_results)

# Toy example for testing purposes only:

geno <- list()
geno$hap1 = matrix(sample(c(0,1),25, replace = TRUE, prob = c(0.6,0.4)),
                   nrow = 5, ncol = 5)
geno$hap2 = matrix(sample(c(0,1),25, replace = TRUE, prob = c(0.6,0.4)),
                   nrow = 5, ncol = 5)

data <- list()
data$r = matrix(sample(0:50,25, replace = TRUE), nrow = 5, ncol = 5)
data$y = matrix(sample(0:50,25, replace = TRUE), nrow = 5, ncol = 5)
data$r1 = matrix(sample(0:50,25, replace = TRUE), nrow = 5, ncol = 5)
data$r2 = matrix(sample(0:50,25, replace = TRUE), nrow = 5, ncol = 5)
data$y1 = matrix(sample(0:50,25, replace = TRUE), nrow = 5, ncol = 5)
data$y2 = matrix(sample(0:50,25, replace = TRUE), nrow = 5, ncol = 5)

K = matrix(runif(25,-0.1,0.1), nrow = 5, ncol = 5)

res=image(geno,data,K)
```