

Package: McCOILR (via r-universe)

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Type Package

Title Rcpp implementation of THE REAL McCOIL

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Description Wrapper for THE REAL McCOIL in Rcpp. Becuase R is easieR.

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LazyData true

Depends R (>= 3.5)

Imports Rcpp, magrittr

Suggests knitr, devtools, rmarkdown, qpdf

LinkingTo Rcpp

RoxygenNote 7.1.2

VignetteBuilder knitr

SystemRequirements C++11

Encoding UTF-8

Repository <https://plasmogenepi.r-universe.dev>

RemoteUrl <https://github.com/OJWatson/McCOILR>

RemoteRef HEAD

RemoteSha a077dd09d0831283c49c410bc75cd16537cadb1f

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McCOILR

Wrapper for THE REAL McCOIL in Rcpp

Description

Wrapper for THE REAL McCOIL in Rcpp, so that package can be more easily run on distributed computing services and cluster infrastructure.

Details

Rcpp implementation of THE REAL McCOIL

References

1 Chang H-H, Worby CJ, Yeka A, Nankabirwa J, Kanya MR, Staedke SG, Dorsey G, Murphy M, Neafsey DE, Jeffreys AE, Hubbart C, Rockett KA, Amato R, Kwiatkowski DP, Buckee C, Greenhouse B. 2017. THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. PLOS Comput Biol 13: e1005348. doi:10.1371/journal.pcbi.1005348

McCOIL_categorical

The Real McCOIL categorical method function

Description

This function triggers the c code for the categorical method

Usage

```
McCOIL_categorical(  
  data,  
  maxCOI = 25,  
  threshold_ind = 20,  
  threshold_site = 20,  
  totalrun = 10000,  
  burnin = 1000,  
  M0 = 15,  
  e1 = 0.05,  
  e2 = 0.05,  
  err_method = 1,  
  path = getwd(),  
  output = "output.txt",  
  thin = 1  
)
```

Arguments

data	An R data frame of SNP calling information. Row names are names of samples and column names are names of assays.
maxCOI	Upper bound for COI. The default is 25.
threshold_ind	The minimum number of sites for a sample to be considered. The default is 20.
threshold_site	The minimum number of samples for a locus to be considered. The default is 20.
totalrun	The total number of MCMC iterations. The default is 10000.
burnin	The total number of burnin iterations. The default is 1000.
M0	Initial COI. The default is 15.
e1	The probability of calling heterozygous loci homozygous. The default is 0.05.
e2	The probability of calling homozygous loci heterozygous. The default is 0.05.
err_method	The default is 1. 1: use pre-specified e1 and e2 and treat them as constants. 2: use likelihood-free sampling for e1 and e2; 3: e1 and e2 are estimated with COI and allele frequencies
path	The default is the current directory.
output	The name of output file. The default is output.txt.
thin	Numeric for how much the chain is thinned. Default = 1, means every iteration is written to file. If it was 0.1 then every 10th iteration is written to file

Value

return summary of output as data.frame

McCOIL_categorical_cpp

McCOIL_categorical_cpp

Description

Categorical cpp code

Usage

McCOIL_categorical_cpp(paramList)

Arguments

paramList A list of parameters created with equivalent R function

Details

McCOIL_categorical_cpp implements THE REAL McCOIL categorical method

McCOIL_proportional *The Real McCOIL proportional method function*

Description

This function triggers the c code for the proportional method

Usage

```
McCOIL_proportional(
  dataA1,
  dataA2,
  maxCOI = 25,
  totalrun = 10000,
  burnin = 1000,
  M0 = 15,
  epsilon = 0.02,
  err_method = 1,
  path = getwd(),
  output = "output.txt",
  thin = 1
)
```

Arguments

dataA1	The intensity of signals of allele 1 from the SNP assay. Row names are names of samples and column names are names of assays.
dataA2	The intensity of signals of allele 2 from the SNP assay. Row names are names of samples and column names are names of assays.
maxCOI	Upper bound for COI. The default is 25.
totalrun	The total number of MCMC iterations. The default is 10000.
burnin	The total number of burnin iterations. The default is 1000.
M0	Initial COI. The default is 15.
epsilon	The level of measurement error (eest). The default is 0.2.
err_method	The default is 1. 1: use pre-specified epsilon; 2: use likelihood-free sampling for epsilon; 3: update epsilon according to likelihood (for 2 and 3, pre-specified epsilon was used as initial value)
path	The default is the current directory.
output	The name of output file. The default is output.txt.
thin	Numeric for how much the chain is thinned. Default = 1, means every iteration is written to file. If it was 0.1 then every 10th iteration is written to file

Value

summary of output as data.frame

McCOIL_proportional_cpp
McCOIL_proportional_cpp

Description

Proportional cpp code

Usage

McCOIL_proportional_cpp(paramList)

Arguments

paramList A list of parameters created with equivalent R function

Details

McCOIL_proportional_cpp implements THE REAL McCOIL proportional method

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