

Package ‘bgchm’

November 2, 2023

Title Bayesian Analyses of Hybrid Zones with Hamiltonian Monte Carlo

Version 0.0.0.9000

Description What the package does (one paragraph).

License GPL (>= 3)

Encoding UTF-8

Roxygen list(markdown = TRUE)

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Biarch true

Depends R (>= 3.4.0)

Imports methods,
Rcpp (>= 0.12.0),
RcppParallel (>= 5.0.1),
rstan (>= 2.18.1),
rstantools (>= 2.3.1.1)

LinkingTo BH (>= 1.66.0),
Rcpp (>= 0.12.0),
RcppEigen (>= 0.3.3.3.0),
RcppParallel (>= 5.0.1),
rstan (>= 2.18.1),
StanHeaders (>= 2.18.0)

SystemRequirements GNU make

R topics documented:

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bgchm-package	<i>The 'bgchm' package.</i>
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Description

A DESCRIPTION OF THE PACKAGE

References

Stan Development Team (2022). RStan: the R interface to Stan. R package version 2.21.7.
<https://mc-stan.org>

est_genocl	<i>Estimate genomic clines using a hierarchical model with unknown cline variances</i>
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Description

Uses Hamiltonian Monte Carlo (HMC) for Bayesian inference of genomic clines from genetic data. This fits a hierarchical log-logistic model for genomic clines with two key parameters, cline center and cline gradient (i.e., slope, inversely proportional to cline width). The model also estimates the cline SDs across loci, SDc (variation in logit centers) and SDv (variation in log10 gradients).

Usage

```
est_genocl(
  Gx = NULL,
  G0 = NULL,
  G1 = NULL,
  p0 = NULL,
  p1 = NULL,
  H = NULL,
  model = "genotype",
  ploidy = "diploid",
  pldat = NULL,
  hier = TRUE,
  SDc = NULL,
  SDv = NULL,
  n_chains = 4
)
```

Arguments

Gx	genetic data for putative hybrids, matrix for known genotypes, list of matrixes for genotype likelihoods, matrix of ancestry for the ancestry model
G0	genetic data for parental reference set 0
G1	genetic data for parental reference set 1
p0	allele frequencies for parental reference set 0
p1	allele frequencies for parental reference set 1
H	hybrid indexes for the putative hybrids
model	genotype, glik, or ancestry
ploidy	diploid or mixed
pldat	ploidy data for mixed ploidy
hier	boolean, fit hierarchical model (TRUE) or assume cline SDs known (FALSE)
SDc	known cline center SD on logit scale
SDv	known cline gradient SD on log10 scale
n_chains	number of HMC chains for posterior inference

Value

list of parameter estimates and full HMC results from stan, this includes cline parameters (center and gradient) and standard deviations describing variability in clines across loci (SDc and SDv)

est_hi	<i>Function to estimate hybrid index</i>
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Description

Uses Hamiltonian Monte Carlo (HMC) for Bayesian inference of hybrid index from genetic data.

Usage

```
est_hi(
  Gx = NULL,
  G0 = NULL,
  G1 = NULL,
  p0 = NULL,
  p1 = NULL,
  model = "genotype",
  ploidy = "diploid",
  pldat = NULL
)
```

Arguments

Gx	genetic data for putative hybrids
G0	genetic data for parental reference set 0
G1	genetic data for parental reference set 1
p0	allele frequencies for parental reference set 0
p1	allele frequencies for parental reference set 1
model	genotype, glik, or ancestry
ploidy	diploid or mixed
pldat	ploidy data for mixed ploidy

Value

list of parameter estimates and full HMC results from stan

est_Q	<i>Function to estimate ancestry class proportions (Q)</i>
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Description

Uses Hamiltonian Monte Carlo (HMC) for Bayesian inference of ancestry classes from genetic data. Ancestry classes denote the proportion of an individual's genome where both gene copies come from source 1 (Q11), both gene copies come from source 0 (Q00), or where one gene copy comes from source 1 and one from source 0.

Usage

```
est_Q(
  Gx = NULL,
  G0 = NULL,
  G1 = NULL,
  p0 = NULL,
  p1 = NULL,
  model = "genotype",
  ploidy = "diploid",
  pldat = NULL
)
```

Arguments

Gx	genetic data for putative hybrids
G0	genetic data for parental reference set 0
G1	genetic data for parental reference set 1
p0	allele frequencies for parental reference set 0

p1	allele frequencies for parental reference set 1
model	genotype, glik, or ancestry
ploidy	diploid or mixed
pldat	ploidy data for mixed ploidy

Value

list of parameter estimates and full HMC results from stan, this includes Q (ancestry class proportions) and hybrid index, which is derived from Q

gencline_plot	<i>Plots genomic clines for a set of loci</i>
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Description

Plots a set of genomic clines.

Usage

```
gencline_plot(center = NULL, v = NULL, pdf = TRUE, outf = "tri_plot.pdf", ...)
```

Arguments

center	vector of cline centers (from est_gencline.R)
v	vector of cline gradients (from est_gencline.R)
pdf	a logical specifying whether results should be output to a pdf file
outf	a character string specifying the name of the output file if 'pdf=TRUE'
...	additional arguments for plotting

Value

A plot is produced, but there is no return value

`tri_plot`*Plots interpopulation ancestry (Q10) as a function of hybrid index*

Description

Creates a triangle plot of hybrid index versus interpopulation ancestry.

Usage

```
tri_plot(hi = NULL, Q10 = NULL, pdf = TRUE, outf = "tri_plot.pdf", ...)
```

Arguments

<code>hi</code>	a vector of hybrid index estimates (from <code>est_h</code> or <code>est_Q</code>)
<code>Q10</code>	a vector of interpopulation ancestry estimates (from <code>est_Q</code>)
<code>pdf</code>	a logical specifying whether results should be output to a pdf file
<code>outf</code>	a character string specifying the name of the output file if 'pdf=TRUE'
<code>...</code>	additional arguments for plotting

Value

A plot is produced, but there is no return value

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