

Package ‘NGBVS’

July 21, 2025

Type Package

Title Bayesian Variable Selection for SNP Data using Normal-Gamma

Version 0.3.0

Date 2022-09-12

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Depends R (>= 3.6.0)

Imports stats, Rfast

Description Posterior distribution of case-control fine-mapping. Specifically, Bayesian variable selection for single-nucleotide polymorphism (SNP) data using the normal-gamma prior. Alenazi A.A., Cox A., Juarez M., Lin W-Y. and Walters, K. (2019) Bayesian variable selection using partially observed categorical prior information in fine-mapping association studies, Genetic Epidemiology. <[doi:10.1002/gepi.22213](https://doi.org/10.1002/gepi.22213)>.

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

Date/Publication 2022-09-16 16:36:05 UTC

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NGBVS-package

Bayesian Variable Selection for SNP Data using Normal-Gamma

Description

The NGBVS package provides posterior distribution of case-control fine-mapping. Specifically Bayesian variable selection for Single-Nucleotide Polymorphism (SNP) data using the Normal-Gamma prior.

Details

Package: NG
 Type: Package
 Version: 0.3.0
 Date: 2022-09-112
 License: GPL-2

Maintainers

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Author(s)

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asym_m_ng

Modified NG prior via FS scores

Description

Modified Normal Gamma prior calculates the posterior distribution for the fine mapping cases-controls study. The number of case-controls must be greater than the number of SNPs.

Usage

```
asym_m_ng(y, data, FS, medstar = c(0.01, 0.0001), numb = 100, burnin = 1, every = 1)
```

Arguments

<code>y</code>	A vector of the pheontype, where takes 0s and 1s.
<code>data</code>	An $N \times p$ finemap data, where N and p denote the samples and number of SNPs respectively.
<code>FS</code>	FS scores for each SNP and it takes value from 0 and 1 or NA for missing FS.
<code>medstar</code>	The value of M where M takes two values.
<code>numb</code>	Number of samples for each SNP.
<code>burnin</code>	The amount of burn-in for the MCMC sample.
<code>every</code>	The amount of thining for the MCMC sample.

Value

A list including:

<code>alpha</code>	A vector of the posterior distribution of the intercept.
<code>beta</code>	A matrix of the posterior distribution of the effect sizes.
<code>psi</code>	A matrix of the posterior distribution of ψ .
<code>lambda</code>	A vector of the posterior distribution of λ .
<code>gammasq</code>	A vector of the posterior distribution of γ^2 .
<code>W</code>	A vector of the posterior distribution of W .
<code>H</code>	A vector of the posterior distribution of H .

Author(s)

Abulaziz Alenazi.

R implementation and documentation: Abulaziz Alenazi <a.alenazi@nbu.edu.sa>.

Examples

```
set.seed(1)
data <- matrix(sample( c( 0, 1, 2 ), 500 * 30, replace = TRUE,
prob <- c( 0.35, 0.35, 0.3)), ncol = 30 )
FS <- sample( c( 0.1, 0.5, 0.7, NA ), ncol( data ), replace = TRUE)
asym_m_ng(y = rbinom(500, 1, 0.5), data = data, FS = FS)
```

asym_s_ng

*Standard NG prior***Description**

Standard Normal Gammp prior calculates the posterior distribution for the fine mapping cases-controls study. The number of case-controls must be greater than the number of SNPs.

Usage

```
asym_s_ng(y, data, medstar = 1, numb = 100, burnin = 1, every = 1)
```

Arguments

y	A vector of the pheontype, where takes 0s and 1s.
data	An $N \times p$ finemap data, where N and p denote the samples and number of SNPs respectively.
medstar	The value of M.
numb	Number of samples for each SNP.
burnin	The amount of burn-in for the MCMC sample.
every	The amount of thining for the MCMC sample.

Value

A list including:

alpha	A vector of the posterior distribution of the intercept.
beta	A matrix of the posterior distribution of the effect sizes.
psi	A matrix of the posterior distribution of ψ .
lambda	A vector of the posterior distribution of λ .
gamma _{sq}	A vector of the posterior distribution of γ^2 .

Author(s)

Abulaziz Alenazi.

R implementation and documentation: Abulaziz Alenazi <a.alenazi@nbu.edu.sa>.

Examples

```
set.seed( 1 )
data <- matrix(sample( c( 0, 1, 2 ), 500 * 30, replace = TRUE,
prob = c( 0.35, 0.35, 0.3)), ncol = 30)
asym_s_ng(y = rbinom(500, 1, 0.5), data = data)
```

m_ng

*Modified NG prior via FS scores***Description**

Modified Normal Gammp prior calculates the posterior distribution for the fine mapping study. The number of individuals must be greater than the number of SNPs.

Usage

```
m_ng (y, data, FS, medstar = c(0.01, 0.0001), numb = 100, burnin = 1, every = 1)
```

Arguments

y	A vector of the pheontype.
data	An $N \times p$ finemap data, where N and p denote the samples and number of SNPs respectively.
FS	FS scores for each SNP and it takes value from 0 and 1 or NA for missing FS.
medstar	The value of M where M takes two values.
numb	Number of samples for each SNP.
burnin	The amount of burn-in for the MCMC sample.
every	The amount of thining for the MCMC sample.

Value

A list including:

alpha	A vector of the posterior distribution of the intercept.
beta	A matrix of the posterior distribution of the effect sizes.
sigmasq	A vector of the posterior distribution of σ^2 .
psi	A matrix of the posterior distribution of ψ .
lambda	A vector of the posterior distribution of λ .
gammasq	A vector of the posterior distribution of γ^2 .
W	A vector of the posterior distribution of W .
H	A vector of the posterior distribution of H .

Author(s)

Abulaziz Alenazi.

R implementation and documentation: Abulaziz Alenazi <a.alenazi@nbu.edu.sa>.

Examples

```
set.seed( 1 )
data <- matrix(rnorm(500 * 30), ncol = 30)
FS <- sample( c( 0.1, 0.5, 0.7, NA ), ncol( data ), replace = TRUE)
m_ng(y = rnorm( 500 ), data = data, FS = FS)
```

Random value generation from the Generalized Inverse Gaussian
Distribution

*Random value generation from the Generalized Inverse Gaussian Dis-
tribution*

Description

Random value generation from the Generalized Inverse Gaussian (GIG) Distribution.

Usage

```
rgig(n = 10, lambda = 1, chi = 1, psi = 1)
```

Arguments

n	Number of observations.
lambda	A shape and scale and parameter.
chi	Shape parameter. Must be positive.
psi	Scale parameter. Must be positive.

Details

rgig uses the code from the GIG-random number generator from the R package *fBasics*. I copied the code from the "ghyp" package because it had not longer a maintainer.

Value

A vector with random values from the GIG distrigution.

Author(s)

David Luethi. Minor changes made by Abdulaziz Alenazi <a.alenazi@nbu.edu.sa>.

References

The algorithm for simulating generalized inverse gaussian variates is copied from the R package *fBasics* from Diethelm Wuertz.

Dagpunar, J.S. (1989). *An easily implemented generalised inverse Gaussian generator*. Communications in Statistics-Computation and Simulation, **18**, 703–710.

Raible S. (2000). *Levy Processes in Finance: Theory, Numerics and Empirical Facts*, PhD Thesis, University of Freiburg, Germany, 161 pages.

Examples

```
x <- rgig(n = 10, lambda = 1, chi = 1, psi = 1)
```

s_ng

*Standard NG prior***Description**

Standard Normal Gammp prior calculates the posterior distribution for the fine mapping study. The number of individuals must be greater than the number of SNPs.

Usage

```
s_ng(y, data, medstar = 1, numb = 100, burnin = 1, every = 1)
```

Arguments

y	A vector of the pheontype.
data	An $N \times p$ finemap data, where N and p denote the samples and number of SNPs respectively.
medstar	The value of M.
numb	Number of samples for each SNP.
burnin	The amount of burn-in for the MCMC sample.
every	The amount of thining for the MCMC sample.

Value

A list including:

alpha	A vector of the posterior distribution of the intercept.
beta	A matrix of the posterior distribution of the effect sizes.
sigmasq	A vector of the posterior distribution of σ^2 .
psi	A matrix of the posterior distribution of ψ .
lambda	A vector of the posterior distribution of λ .
gamma	A vector of the posterior distribution of γ^2 .

Author(s)

Abulaziz Alenazi.

R implementation and documentation: Abulaziz Alenazi <a.alenazi@nbu.edu.sa>.

Examples

```
set.seed(1)
data <- matrix( rnorm(500 * 30), ncol = 30)
s_ng(y = rnorm(500), data = data)
```

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