

Package ‘NGBVS’

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Type Package

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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>.

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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: 0.2.0
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License: GPL-2

Maintainers

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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 phenotype, 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 thinning 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 Gammpp 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 thinning 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 .
gammasq	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	<i>Modified NG prior via FS scores.</i>
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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 Distribution

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 distribution.

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*. Commun. Statist. -Simula., **18**, 703–710.

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

See Also

[integrate](#), [uniroot](#), [spline](#)

Examples

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

s_ng

Standard NG prior.

Description

Standard Normal Gammpp 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 .
gammassq	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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