Package ‘NGBVS’

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Type Package

Title Bayesian Variable Selection for SNP Data using Normal-Gamma

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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>.

License GPL (>= 2)

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Contents

`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

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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

`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.
`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.
`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(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.
`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` *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 Distribution

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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.
`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( rnorm(500 * 30), ncol = 30)
s_ng(y = rnorm(500), data = data)
```

Index