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R topics documented:

NGBVS-package ................................................. 2
asym_m_ng .................................................. 2
asym_s_ng .................................................. 4
m_ng ....................................................... 5
Random value generation from the Generalized Inverse Gaussian Distribution .................................................. 6
s_ng ....................................................... 7

Index 9
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
Date: 2020-01-16
License: GPL-2

Maintainers

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Author(s)

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Usage

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

Arguments

y A vector of the phenotype, 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 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 \( \psi \).
lambda A vector of the posterior distribution of \( \lambda \).
gammasq A vector of the posterior distribution of \( \gamma^2 \).
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)
asy_m_ng(y = rbinom(500, 1, 0.5), data = data, FS = FS)
asym_s_ng  

Description

Standard 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_s_ng(y, data, medstar = 1, numb = 100, burnin = 1, every = 1)

Arguments

y  A vector of the phenotype, 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 $\psi$.
lambda  A vector of the posterior distribution of $\lambda$.
gammasq  A vector of the posterior distribution of $\gamma^2$.

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

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

**Arguments**
- `y`: A vector of the phenotype.
- `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.
- `sigma2`: A vector of the posterior distribution of $\sigma^2$.
- `psi`: A matrix of the posterior distribution of $\psi$.
- `lambda`: A vector of the posterior distribution of $\lambda$.
- `gamma2`: A vector of the posterior distribution of $\gamma^2$.
- `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

```r
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

Description

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

Usage

```r
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.


**s_ng**

**See Also**

*integrate*, *unirroot*, *spline*

**Examples**

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

**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**

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

**Arguments**

- `y`: A vector of the phenotype.
- `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 $\sigma^2$.
- `psi`: A matrix of the posterior distribution of $\psi$.
- `lambda`: A vector of the posterior distribution of $\lambda$.
- `gammasq`: A vector of the posterior distribution of $\gamma^2$.

**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

asym_m_ng, 2
asym_s_ng, 4
integrate, 7
m_ng, 5
NGBVS-package, 2

Random value generation from the Generalized Inverse Gaussian Distribution, 6
rgig(Random value generation from the Generalized Inverse Gaussian Distribution), 6

s_ng, 7
spline, 7

uniroot, 7