Package 'BATools'

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Type Package

Title Bayesian Antedependent Model for Whole Genome Prediction

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Description Bayesian Antedependence Model

License GPL-3

R topics documented:

BATools-package   *BATools–a Bayesian Antedependence Model*

Description

BATools package is an implementation of Bayesian Antedependence

Model Details

Package:	BATools
Type:	Package
Version:	1.0
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The package include two major functions: anteBayesA and anteBayesB. AnteBayesA is the antedependence extension of BayesA type of Model and AnteBayesB is the antedependence extension of BayesB type of Model.

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References

W. Yang, R. J. Tempelman. 2012. A Bayesian Antedependence Model for Whole Genome Prediction. *Genetics*, vol. 190 (4) pp. 1491-1501.

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anteBayesA   *Bayesian Antedependence Model*

Description

The function applies Antedependence BayesA Model

Usage

```
anteBayesA(y,Z,startpi, startdf, startscale, truepi, truedef, truescale, truet,
 numiter, skip, burnIn,Seed,Save.at)
```

Arguments

y	The phenotype
Z	The genotype matrix coded in "0/1/2"
startpi	The starting value of π, which is the ratio of SNP effect variance that is non-zero. When $\pi = 1$, it is BayesA. Otherwise, it is BayesB.
startdf	The starting value of the degree of freedom parameter of SNP effect variance
startscale	The starting value of the scale parameter of SNP effect variance
truepi	A boolean value. If truepi = TRUE, means we fix pi to the starting value; If truepi=FALSE, we sample pi.
truedef	A boolean value. If truedef = TRUE, means we fix the degree of freedom to the starting value; If truedef=FALSE, we sample the degree of freedom of SNP effect variances.
truescale	A boolean value. If truescale = TRUE, means we fix the scale to the starting value; If truescale=FALSE, we sample the scale of SNP effect variances.
truet	A boolean value. If truet = TRUE, means we do not sample the antedependence association parameter t; If truet=FALSE, we sample t.
numiter	The number of iterations for MCMC sampling
skip	The number of iterations for skip
burnIn	The number of iterations for burnIn in MCMC sampling
Seed	The seed for the random generator
Save.at	The folder or the prefix for saving the MCMC sampling results

Examples

```
data(LD)
startpi = 1
startdf = 10
startscale = 0.001
truepi = TRUE
truedef = FALSE
truescale = FALSE
truet=FALSE
numiter=10500
skip = 2
burnIn = 5000
Seed=2
MCMCrun = anteBayesA(y,Z1.marker,startpi=startpi,startdf=startdf,startscale=startscale,
                truepi = truepi, truedef = truedef, truescale = truescale,truet=truet,
                numiter=numiter,skip=skip,burnIn=burnIn,Seed=2,Save.at="")
```

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anteBayesB   *Bayesian Antedependence Model*

Description

The function applies Antedependence BayesB Model

Usage

```
anteBayesB(Seed, startpi, startdf, startscale, alphapi, betapi, truepi, truedef, truescale, true
 numiter, skip, burnIn)
```

Arguments

y	The phenotype
Z	The genotype matrix coded in "0/1/2"
startpi	The starting value of π, which is the ratio of SNP effect variance that is non-zero. When $\pi = 1$, it is BayesA. Otherwise, it is BayesB.
startdf	The starting value of the degree of freedom parameter of SNP effect variance
startscale	The starting value of the scale parameter of SNP effect variance
alphapi	The value of α for sampling π
betapi	The value of β for sampling π
truepi	A boolean value. If truepi = TRUE, means we fix pi to the starting value; If truepi=FALSE, we sample pi.
truedef	A boolean value. If truedef = TRUE, means we fix the degree of freedom to the starting value; If truedef=FALSE, we sample the degree of freedom of SNP effect variances.
truescale	A boolean value. If truescale = TRUE, means we fix the scale to the starting value; If truescale=FALSE, we sample the scale of SNP effect variances.
truet	A boolean value. If truet = TRUE, means we do not sample the antedependence association parameter t; If truet=FALSE, we sample t.

numiter	The number of iterations for MCMC sampling
skip	The number of iterations for skip
burnIn	The number of iterations for burnIn in MCMC sampling
Seed	The seed for the random generator
Save.at	The folder or the prefix for saving the MCMC sampling results

Examples

```
data(LD)
startpi = 0.5
startdf = 10
startscale = 0.01
alphapi = 1
betapi = 10
truepi = FALSE
truedef = FALSE
truescale = FALSE
truet=FALSE
numiter=10500
skip = 2
burnIn = 5000
MCMCrun = anteBayesB(y,Z1.marker,startpi=startpi,startdf=startdf,startscale=startscale,alphapi=alphapi,
betapi=betapi,truepi = truepi, truedef = truedef, truescale = truescale,truet=truet,numiter=numiter,
skip=skip,burnIn=burnIn,Seed=4,Save.at="")
```

BayesA   *Bayesian WGP Model*

Description

The function applies BayesA Model

Usage

```
BayesA(y,Z, startpi, startdf, startscale, truepi, truedef, truescale, numiter,
 skip, burnIn,Seed, Save.at)
```

Arguments

y	The phenotype
Z	The genotype matrix coded in "0/1/2"
startpi	The starting value of π, which is the ratio of SNP effect variance that is non-zero. When $\pi = 1$, it is BayesA. Otherwise, it is BayesB.
startdf	The starting value of the degree of freedom parameter of SNP effect variance
startscale	The starting value of the scale parameter of SNP effect variance
truepi	A boolean value. If truepi = TRUE, means we fix pi to the starting value; If truepi=FALSE, we sample pi.
truedef	A boolean value. If truedef = TRUE, means we fix the degree of freedom to the starting value; If truedef=FALSE, we sample the degree of freedom of SNP effect variances.

truescale	A boolean value. If truescale = TRUE, means we fix the scale to the starting value; If truescale=FALSE, we sample the scale of SNP effect variances.
numiter	The number of iterations for MCMC sampling
skip	The number of iterations for skip
burnIn	The number of iterations for burnIn in MCMC sampling
Seed	The seed for the random generator
Save.at	The folder or the prefix for saving the MCMC sampling results

Examples

```
data(LD)
startpi = 1
startdf = 10
startscale = 0.001
truepi = TRUE
truedef = FALSE
truescale = FALSE
numiter=10500
skip = 2
burnIn =5000
MCMCrun = BayesA(y,Z1.marker,startpi=startpi,startdf=startdf,startscale=startscale,
                 truepi = truepi, truedef = truedef, truescale = truescale,
                 numiter=numiter,skip=skip,burnIn=burnIn,Seed=1,Save.at="")
```

BayesB	*Bayesian WGP Model*

Description

The function applies BayesA Model

Usage

```
BayesB(y,Z, startpi, startdf, startscale, alphapi, betapi, truepi, truedef, truescale, numiter,
skip, burnIn,Seed,Save.at)
```

Arguments

y	The phenotype
Z	The genotype matrix coded in "0/1/2"
startpi	The starting value of π, which is the ratio of SNP effect variance that is non-zero. When $\pi = 1$, it is BayesA. Otherwise, it is BayesB.
startdf	The starting value of the degree of freedom parameter of SNP effect variance
startscale	The starting value of the scale parameter of SNP effect variance
alphapi	The value of α for sampling π
betapi	The value of β for sampling π
truepi	A boolean value. If truepi = TRUE, means we fix pi to the starting value; If truepi=FALSE, we sample pi.

truedef   A boolean value. If truedef = TRUE, means we fix the degree of freedom to the starting value; If truedef=FALSE, we sample the degree of freedom of SNP effect variances.

truescale   A boolean value. If truescale = TRUE, means we fix the scale to the starting value; If truescale=FALSE, we sample the scale of SNP effect variances.

numiter   The number of iterations for MCMC sampling

skip   The number of iterations for skip

burnIn   The number of iterations for burnIn in MCMC sampling

Seed   The seed for the random generator

Save.at   The folder or the prefix for saving the MCMC sampling results

Examples

```
data(LD)
startpi = 0.5
startdf = 10
startscale = 0.01
alphapi = 1
betapi = 10
truepi = FALSE
truedef = FALSE
truescale = FALSE
numiter=10500
skip = 2
burnIn = 5000
MCMCrun = BayesB(y,Z1.marker,startpi=startpi,startdf=startdf,startscale=startscale,
alphapi=alphapi,betapi=betapi,truepi = truepi, truedef = truedef,
truescale = truescale, numiter=numiter,skip=skip,burnIn=burnIn,Seed=1,Save.at="")
```

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