Package 'ammiBayes'

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Type Package

Title Bayesian Ammi Model for Continuous Data with or without Additive
and Dominance Effect

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Depends R (>= 4.0.0)

VignetteBuilder R.rsp

Imports lattice, latticeExtra, distfree.cr, coda, spam, movMF, msm,
bayesplot, Hmisc

Suggests ggpubr, R.rsp

Description Flexible multi-environment trials analysis via MCMC method for Additive Main Effects and Multiplicative Interaction Model (AMMI) for continuous data.
Biplot with the averages and regions of confidence can be generated. The chains run in parallel on Linux systems and run serially on Windows.

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

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AMMI algorithm

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[ammiBayes](#)

ammiBayes	*Bayesian Ammi Model for Continuous Data with or without additive and dominance effect*

Description

Bayesian Ammi Model for Continuous Data with or without additive and dominance effect.

Usage

```
ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep, M=NULL, algorithm="AMMI",
          iterations=3000, jump=2, burn=500,
          Var.error=0.5, Var.env=0.5, Var.gen=0.5, Var.a=0.5, Var.d=0.5,
          chains=2)
```

Arguments

Y	Response variable vector
Gen	Genotype effects vector. Must be defined as factor
Env	Environmental effects vector. Must be defined as factor
Rep	Repetition vector. Must be defined as factor
M	The matrix of SNP markers of order nxp (n is the number of genotypes and p is the number of markers) that is composed of the values 0, 1 and 2, which correspond to the alleles a, aA(Aa) or AA of the respective marker
algorithm	AMMI, AMMIGBlup or AMMIGBlupD. By default is AMMI
iterations	Total of iterations after burnin and jump
jump	Jump of iterations
burn	Initial burn
Var.error	Priori for the variance of error. Default is 0.5
Var.env	Priori for the variance of environment. Default is 0.5
Var.gen	Priori for the variance of genotype. Default is 0.5
Var.a	Additive variance. Default is 0.5
Var.d	Dominant variance. Default is 0.5
chains	Number of chains. See details.

Details

The code is run in parallel for linux SO. If you are using Windows, the execution of the code will be serially.

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Examples

```
library(ammiBayes)
data(ammiData)

Env  <- factor(ammiData$amb)
Rep <- factor(ammiData$rep)
Gen  <- factor(ammiData$gen)
Y   <- ammiData$prod

model <- ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep, iter=10,
 burn=1, jump=2, chains=2)

summary(model)
```

---

ammiBayes.conf.plot   *Plot ammiBayes object with confidence region*

Description

Plot the confidence regions for genotype and environment effects

Usage

```
ammiBayes.conf.plot(model, conf=0.95, pars.gen=NULL, pars.env=NULL,
                gen.labels=NULL, env.labels=NULL,
                col.env="red", col.gen="green",
                alpha.env=80, alpha.gen=80,
                col.text.env="black", col.text.gen="black",
                border.gen="transparent", border.env="transparent",
                cex.env=1, cex.gen=1, lty.gen=1, lty.env=1,
                lwd.gen=1, lwd.env=1, xlab, ylab, col.grid="grey",
                lty.grid=2, lwd.grid=1, change.signal=FALSE, change.scale=0.1,
                plot.gen=TRUE, plot.env=TRUE)
```

Arguments

model	An object of the ammiBayes class
conf	Significant level for the confidence region. By default is 0.95.
pars.gen	An optional character vector of genotype names. If pars is omitted all genotypes are included.
pars.env	An optional character vector of environment names. If pars is omitted all environments are included.
gen.labels	Optional vector for the name of the genotypes.
env.labels	Optional vector for the name of the environments.
col.env	Color for the confidence region of the environment. Default is "red".

`col.gen`	Color for the confidence region of the genotype. Default is "green".
`alpha.env`	Specifies the opacity of the confidence region for the environment. Default is 80.
`alpha.gen`	Specifies the opacity of the confidence region for the genotype. Default is 80.
`col.text.env`	Define the color of environment names.
`col.text.gen`	Define the color of genotype names.
`border.gen`	Define the color for the border of the confidence region of genotype. Default is "transparent".
`border.env`	Define the color for the border of the confidence region of environment. Default is "transparent".
`cex.env`	Scale for the font size of the environment names. Default is 1
`cex.gen`	Scale for the font size of the genotype names. Default is 1
`lty.gen`	Line type for the border of confidence region of genotype. Default is 1
`lty.env`	Line type for the border of confidence region of environment. Default is 1
`lwd.gen`	Line width for the border of confidence region of genotype. Default is 1
`lwd.env`	Line width for the border of confidence region of environment. Default is 1
`xlab`	Label for the x-axis
`ylab`	Label for the y-axis
`col.grid`	Define the color for the grid. Default is "grey"
`lty.grid`	Line type of grid. Default is 2
`lwd.grid`	Line width of grid. Default is 1
`change.signal`	Changes the signal of the chain for better visualization. By default is FALSE
`change.scale`	When change.signal=TRUE the scale can be changed. By default it is 0.05
`plot.gen`	Plot effects of genotypes. By default is TRUE
`plot.env`	Plot effects of environment. By default is TRUE

Details

The confidence regions are defined using the package distfree.cr.

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Examples

```
library(ammiBayes)
data(ammiData)

Env  <- factor(ammiData$amb)
Rep <- factor(ammiData$rep)
Gen  <- factor(ammiData$gen)
Y   <- ammiData$prod

model <- ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep, iter=10, burn=1, jump=2, chains=2)

ammiBayes.conf.plot(model)
```

---

ammiBayes.gen.plot   *Plot genotype effects from ammiBayes object*

Description

Plot the posterior mean for an ammiBayes object

Usage

```
ammiBayes.gen.plot(x, lwd=1, lty=1, pch=18, method="bars",
     col=NULL, ylim=NULL, draw.mean=TRUE, col.mean="red",
   lty.mean=2, xlab="Genotype", ylab=NULL, gen.names=NULL)
```

Arguments

x	An object from gen.effects function.
lwd	A line width, a positive number, default is 1.
lty	The line type. Default is 1.
pch	Either an integer specifying a symbol or a single character to be used as the default in plotting points.
method	Defaults to "bars" to draw error-bar type plots. See panel.xYplot.
col	Define the color of genotype bands. See xYplot.
ylim	A numeric vector of length 2 giving minimum and maximum for the y-axis.

draw.mean	If TRUE, a line representing the average of all genotypes is plotted on the graph.
col.mean	Define the color for the average of all genotypes.
lty.mean	Line type for the average of all genotypes.
xlab	Label for the x-axis.
ylab	Label for the y-axis.
gen.names	Define the names of genotypes on the x-axis. By default are the levels of the Genotypes.

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See Also

xYplot

Examples

```
library(ammiBayes)
data(ammiData)


Env  <- factor(ammiData$amb)
Rep <- factor(ammiData$rep)
Gen  <- factor(ammiData$gen)
Y  <- ammiData$prod

model <- ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep, iter=10, burn=1, jump=2, chains=2)

genot.effects <- gen.effects(model)


ammiBayes.gen.plot(genot.effects)
```

---

ammiBayes.mean.plot   *Plot ammiBayes object*

Description

Plot the means for the ammiBayes object

Usage

```
ammiBayes.mean.plot(model, pars.gen=NULL, pars.env=NULL,
                gen.labels=NULL, env.labels=NULL,
                col.text.gen="darkgreen", col.text.env="red",
                ylim=NULL, xlim=NULL, cex.env=1, cex.gen=1,
                xlab,ylab, col.grid="grey", lty.grid=2, lwd.grid=1)
```

Arguments

model	An object of the ammiBayes class
pars.gen	An optional character vector of genotype names. If pars is omitted all genotypes are included.
pars.env	An optional character vector of environment names. If pars is omitted all environments are included.
gen.labels	Optional vector for the name of the genotypes
env.labels	Optional vector for the name of the environments
col.text.gen	Define the color of genotype names
col.text.env	Define the color of environment names
ylim	Define the limites applied to the y-axis
xlim	Define the limites applied to the x-axis
cex.env	Scale for the font size of the environment names. Default is 1
cex.gen	Scale for the font size of the genotype names. Default is 1
xlab	Label for the x-axis
ylab	Label for the y-axis
col.grid	Define the color for the grid. Default is "grey"
lty.grid	Line type of grid
lwd.grid	Line width of grid

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Examples

```
library(ammiBayes)
data(ammiData)


Env  <- factor(ammiData$amb)
Rep <- factor(ammiData$rep)
Gen  <- factor(ammiData$gen)
Y  <- ammiData$prod

model <- ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep, iter=10, burn=1, jump=2, chains=2)


ammiBayes.mean.plot(model)
```

---

ammiData   *Dataset for example*

Description

Simulated dataset in completely randomized design to illustrate the resources of the `ammiBayes` package.

Usage

```
data(ammiData)
```

Details

amb = Environment (4 environments)

rep = Repetition (9 repetitions)

gen = Genotype (6 genotypes)

prod = Variabel response

---

ammiDominance   *Example dataset for running the AMMI, AMMIGBlup, and AM-*
                             MIGBlupD models.

Description

Simulated dataset for the AMMI, AMMIGBlup, and AMMIGBlupD models. The object am-
miDominance is a list where the first element contains the experiment information and the second
object in the list contains the molecular marker information.

Usage

```
data(ammiDominance)
```

Details

dat.gen is a data frame containing information on 16 genotypes, 6 environments, 30 replicates, and
the observed variable Y.

data.marks is a 16 x 1791 matrix, where the rows represent genotypes and the columns represent
the molecular markers associated with the genotypes.

AMMIGBlup   *AMMIGBlup algorithm*

Description

AMMIGBlup algorithm

Details

Internal use

See Also

ammiBayes

AMMIGBlupD   *AMMIGBlupD algorithm*

Description

AMMIGBlupD algorithm

Details

Internal use

See Also

[ammiBayes](#)

---

detect.interaction   *Detect GxE interaction*

Description

Run the AMMI Bayesian model for continuous data.

Usage

```
detect.interaction(model, type="gen", conf=0.95)
```

Arguments

model	An object ammiBayes
type	Defines the genotypes ("gen") or environments ("env") to be detected with interaction. By default is genotype.
conf	Define the probability of the area of confidence. By default is 0.95.

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Examples

```
library(ammiBayes)
data(ammiData)

Env  <- factor(ammiData$amb)
Rep <- factor(ammiData$rep)
Gen  <- factor(ammiData$gen)
Y  <- ammiData$prod

model <- ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep, iter=10,
 burn=1, jump=2, chains=2)

# detect.interaction(model)
```

---

diagnosis.ammiBayes   *Bayesian AMMI for ordinal data*

Description

Extract the MCMC chain for diagnosis

Usage

```
diagnosis.ammiBayes(x, pars=NULL)
```

Arguments

x	An object of class ammiBayes
pars	It should be set, such as "Genotype", "Rep", "L", "Gen.PC1", "Gen.PC2", "Env.PC1", "Env.PC2", "Comp.var". See details

Details

The output is compatible for diagnosis with the coda and bayesplot packages. Examples can be seen on the website: bayesplot

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Examples

```
# Not run
library(ammiBayes)
library(bayesplot)
library(ggpubr)

data(ammiData)

Env  <- factor(ammiData$amb)
Rep <- factor(ammiData$rep)
Gen  <- factor(ammiData$gen)
Y   <- ammiData$prod

model <- ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep, iter=1000, burn=10, jump=2, chains=2)

gen.diagnosis <- diagnosis.ammiBayes(model, pars="Genotype")


mcmc_trace(gen.diagnosis)
mcmc_dens_overlay(gen.diagnosis)
mcmc_areas(gen.diagnosis)

dens <- bayesplot::mcmc_dens_overlay(gen.diagnosis)
trac <- bayesplot::mcmc_trace(gen.diagnosis, facet_args=list(ncol=1))

ggpubr::ggarrange(trac,dens, common.legend=TRUE)
```

---

gen.effects *Bayesian AMMI for continous data*

Description

Extract the effects of genotypes and HPD interval

Usage

```
gen.effects(x, prob=0.95)
```

Arguments

x	An object of class ammiBayes
prob	Probability for HPD interval. Default is 0.95

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Examples

```
library(ammiBayes)
data(ammiData)

Env  <- factor(ammiData$amb)
Rep <- factor(ammiData$rep)
Gen  <- factor(ammiData$gen)
Y  <- ammiData$prod

model <- ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep, iter=10, burn=1, jump=2, chains=2)

gen.effects(model)
```

---

predict.ammiBayes   *Bayesian AMMI for continuous data*

Description

Extract predict values and HPD interval

Usage

```
## S3 method for class 'ammiBayes'
predict(object, prob=0.95, ...)
```

Arguments

object	An object of class ammiBayes
prob	Probability for HPD interval. Default is 0.95
...	Potential further arguments (required by generic).

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Examples

```
library(ammiBayes)
data(ammiData)

Env  <- factor(ammiData$amb)
Rep <- factor(ammiData$rep)
Gen  <- factor(ammiData$gen)
Y  <- ammiData$prod

model <- ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep, iter=10, burn=1, jump=2, chains=2)

predict(model)
```

---

summary.ammiBayes   *Summary Method for ammiBayes object*

Description

Returns (and prints) a summary list for `ammiBayes` object.

Usage

```
    ## S3 method for class 'ammiBayes'
summary(object, ...)
```

Arguments

object	A given object of the class `ammiBayes`.
...	Potential further arguments (required by generic).

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See Also

ammiBayes

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