

Package ‘ammiBayes’

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Type Package

Title Bayesian Ammi Model for Continuous Data

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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

LazyData true

Description Flexible multi-environment trials analysis via MCMC method for Additive Main Effects and Multiplicative 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

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ammiBayes	<i>Bayesian AMMI for continuous data</i>
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Description

Run the AMMI Bayesian model for continuous data.

Usage

```
ammiBayes(Y=Y, Gen=Gen, Env=Env, Rep=Rep,
           iterations=3000, jump=2, burn=500,
           Var.error=0.5, Var.env=0.5, Var.gen=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
iterations	Total of iterations after burnin and jumo
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
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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References

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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,
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 of the sample. By default is FALSE
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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See Also

[lattice](#)

Examples

```
library(ammiBayes)
data(amiData)

Env <- factor(amiData$amb)
Rep <- factor(amiData$rep)
Gen <- factor(amiData$gen)
Y <- amiData$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.bands=NULL, ylim=NULL,  
                  xlab=NULL, ylab=NULL, gen.names=NULL)
```

Arguments

x	An object from <code>gen.effects</code> 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.bands	Define the color of genotype bands. See xYplot .
ylim	A numeric vector of length 2 giving minimum and maximum for the y-axis.
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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See Also

[lattice](#)

Examples

```
library(ammiBayes)
data(amiData)

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

`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(ammBayes)
library(bayesplot)
library(ggpubr)

data(ammData)

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

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

gen.diagnosis <- diagnosis.ammBayes(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

<code>x</code>	An object of class ammiBayes
<code>prob</code>	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(ammBayes)
data(ammData)

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

model <- ammBayes(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 'ammBayes'
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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