Package ‘ammiBayes’

May 7, 2026

Type Package

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

Version 2.1-1

Date 2026-02-26

Maintainer Fabio M. Correa <`fmcron@protonmail.com`>

Author Fabio M. Correa [aut, cre] (ORCID:
<`https://orcid.org/0000-0002-6708-9316`>),
Luciano A. Oliveira [aut],
Carlos P. Silva [aut],
Cristian T. E. Mendes [aut],
Alessandra Q. Silva [aut],
Joel J. Nuvunga [aut],
Larissa C. V. Boas [aut],
Marcio Balestre [ths],
Julio S. S. Bueno-Filho [ths]

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

Date/Publication 2026-03-02 10:00:02 UTC

Contents

`AMMI` *AMMI algorithm*

Description

AMMI algorithm

Details

Internal use

See Also

`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.

Author(s)

Luciano A. Oliveira
Carlos P. Silva
Cristian T. E. Mendes
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Joel J. Nuvunga
Larissa C. V. Boas
Marcio Balestre
Julio S. S. Bueno-Filho
Fabio M. Correa

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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`.

Author(s)

Luciano A. Oliveira
Carlos P. Silva
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Julio S. S. Bueno-Filho
Fabio M. Correa

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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.

Author(s)

Luciano A. Oliveira
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Fabio M. Correa

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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

Author(s)

Luciano A. Oliveira
Carlos P. Silva
Cristian T. E. Mendes
Alessandra Q. Silva

Joel J. Nuvunga
Marcio Balestre
Julio S. S. Bueno-Filho
Fabio M. Correa

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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 AMMIGBlupD models.*

Description

Simulated dataset for the AMMI, AMMIGBlup, and AMMIGBlupD models. The object ammiDominance 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.

Author(s)

Luciano A. Oliveira
Carlos P. Silva
Cristian T. E. Mendes
Alessandra Q. Silva
Joel J. Nuvunga
Marcio Balestre
Larissa C. V. Boas
Julio S. S. Bueno-Filho
Fabio M. Correa

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`

Author(s)

Luciano A. Oliveira
Carlos P. Silva
Cristian T. E. Mendes
Alessandra Q. Silva
Joel J. Nuvunga
Marcio Balestre
Julio S. S. Bueno-Filho
Fabio M. Correa

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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

Author(s)

Luciano A. Oliveira
Carlos P. Silva
Cristian T. E. Mendes
Alessandra Q. Silva
Joel J. Nuvunga
Marcio Balestre
Julio S. S. Bueno-Filho
Fabio M. Correa

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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).

Author(s)

Luciano A. Oliveira
Carlos P. Silva
Cristian T. E. Mendes
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Joel J. Nuvunga
Marcio Balestre
Julio S. S. Bueno-Filho
Fabio M. Correa

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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).

Author(s)

Luciano A. Oliveira
Carlos P. Silva
Cristian T. E. Mendes
Alessandra Q. Silva
Joel J. Nuvunga
Marcio Balestre
Julio S. S. Bueno-Filho
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See Also

`ammiBayes`

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