Package ‘bayesammi’

May 7, 2026

Type Package

Title Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model

Version 0.3.0

Maintainer Muhammad Yaseen <`myaseen208@gmail.com`>

Description Performs Bayesian estimation of the additive main effects and multiplicative interaction (AMMI) model. The method is explained in Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G. and Cornelius, P.L. (2011) (<doi:10.2135/cropsci2010.06.0343>).

Depends R (>= 3.1)

Imports dplyr, ggplot2, ggrepel, ks, lme4, magrittr, MASS, mvtnorm, purrr, rlang, rstiefel, scales, stats, tibble, tidyr, tmvtnorm

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Note 1. School of Mathematical & Statistical Sciences, Clemson University, Clemson, South Carolina, USA 2. Department of Mathematics & Statistics, University of Agriculture Faisalabad, Faisalabad, Pakistan

NeedsCompilation no

Author Muhammad Yaseen [aut, cre],
Jose Crossa [aut, ctb],
Sergio Perez-Elizalde [aut, ctb],
Diego Jarquin [aut, ctb],
Jose Miguel Cotes [aut, ctb],
Kert Viele [aut, ctb],
Genzhou Liu [aut, ctb],
Paul L. Cornelius [aut, ctb],
Julian Garcia Abadillo Velasco [aut, ctb]

Repository CRAN

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Contents

`bayes_ammi` *Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model*

Description

Performs Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model

Usage

```
## Default S3 method:
bayes_ammi(.data, .y, .gen, .env, .rep, .nIter)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor
`.rep`	Replication Factor
`.nIter`	Number of Iterations

Value

Genotype by Environment Interaction Model

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Jose Crossa (<`j.crossa@cgiar.org`>)
3. Sergio Perez-Elizalde (<`sergiop@colpos.mx`>)
4. Diego Jarquin (<`diego.jarquin@gmail.com`>)
5. Jose Miguel Cotes
6. Kert Viele
7. Genzhou Liu
8. Paul L. Cornelius

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
data(Maiz)

fm1 <-
 bayes_ammi(
     .data  = Maiz
   , .y     = y
   , .gen   = entry
   , .env   = site
   , .rep   = rep
   , .nIter = 20
  )
names(fm1)
fm1$mu1
fm1$tau1
fm1$tao1
fm1$delta1
fm1$lambdas1
fm1$alphas1
fm1$gammas1

library(ggplot2)

Plot1Mu <-
  ggplot(data = fm1$mu1, mapping = aes(x = 1:nrow(fm1$mu1), y = mu)) +
  geom_line(color = "blue") +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = expression(mu), x = "Iterations") +
  theme_bw()
print(Plot1Mu)
```

```
Plot2Mu <-
  ggplot(data = fm1$mu1, mapping = aes(mu)) +
  geom_histogram() +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = "Frequency", x = expression(mu)) +
  theme_bw()
print(Plot2Mu)


Plot1Sigma2 <-
  ggplot(data = fm1$tau1, mapping = aes(x = 1:nrow(fm1$tau1), y = tau)) +
  geom_line(color = "blue") +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = expression(sigma^2), x = "Iterations") +
  theme_bw()
print(Plot1Sigma2)


Plot2Sigma2 <-
  ggplot(data = fm1$tau1, mapping = aes(tau)) +
  geom_histogram() +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = "Frequency", x = expression(sigma^2)) +
  theme_bw()
print(Plot2Sigma2)


# Plot of Alphas
Plot1Alpha1 <-
  ggplot(data = fm1$tao1, mapping = aes(x = 1:nrow(fm1$tao1), y = tao1)) +
  geom_line(color = "blue") +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = expression(alpha[1]), x = "Iterations") +
  theme_bw()
print(Plot1Alpha1)

Plot2Alpha1 <-
  ggplot(data = fm1$tao1, mapping = aes(tao1)) +
  geom_histogram() +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = "Frequency", x = expression(alpha[1])) +
  theme_bw()
print(Plot2Alpha1)

Plot1Alpha2 <-
  ggplot(data = fm1$tao1, mapping = aes(x = 1:nrow(fm1$tao1), y = tao2)) +
  geom_line(color = "blue") +
  scale_x_continuous(labels = scales::comma) +
```

```
  scale_y_continuous(labels = scales::comma) +
  labs(y = expression(alpha[2]), x = "Iterations") +
  theme_bw()
print(Plot1Alpha2)

Plot2Alpha2 <-
  ggplot(data = fm1$tao1, mapping = aes(tao2)) +
  geom_histogram() +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = "Frequency", x = expression(alpha[2])) +
  theme_bw()
print(Plot2Alpha2)

# Plot of Betas
Plot1Beta1 <-
  ggplot(data = fm1$delta1, mapping = aes(x = 1:nrow(fm1$delta1), y = delta1)) +
  geom_line(color = "blue") +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = expression(beta[1]), x = "Iterations") +
  theme_bw()
print(Plot1Beta1)

Plot2Beta1 <-
  ggplot(data = fm1$delta1, mapping = aes(delta1)) +
  geom_histogram() +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = "Frequency", x = expression(beta[1])) +
  theme_bw()
print(Plot2Beta1)


Plot1Beta2 <-
  ggplot(data = fm1$delta1, mapping = aes(x = 1:nrow(fm1$delta1), y = delta2)) +
  geom_line(color = "blue") +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = expression(beta[2]), x = "Iterations") +
  theme_bw()
print(Plot1Beta2)

Plot2Beta2 <-
  ggplot(data = fm1$delta1, mapping = aes(delta2)) +
  geom_histogram() +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = "Frequency", x = expression(beta[2])) +
  theme_bw()
print(Plot2Beta2)
```

```
Plot1Beta3 <-
  ggplot(data = fm1$delta1, mapping = aes(x = 1:nrow(fm1$delta1), y = delta3)) +
  geom_line(color = "blue") +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = expression(beta[3]), x = "Iterations") +
  theme_bw()
print(Plot1Beta3)

Plot2Beta3 <-
  ggplot(data = fm1$delta1, mapping = aes(delta3)) +
  geom_histogram() +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(y = "Frequency", x = expression(beta[3])) +
  theme_bw()
print(Plot2Beta3)


BiplotAMMI <-
  ggplot(data = fm1$alphas0, mapping = aes(x = alphas1, y = alphas2)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
  geom_text(aes(label = 1:nrow(fm1$alphas0)),
            vjust = "inward", hjust = "inward") +
  geom_point(data = fm1$gammas0, mapping = aes(x = gammas1, y = gammas2)) +
  geom_segment(data = fm1$gammas0,
               aes(x = 0, y = 0, xend = gammas1, yend = gammas2),
               arrow = arrow(length = unit(0.2, "cm"))
               , alpha = 0.75, color = "red") +
  geom_text(data = fm1$gammas0,
            aes(x = gammas1, y = gammas2,
                label = paste0("E", 1:nrow(fm1$gammas0))),
            vjust = "inward", hjust = "inward") +
  scale_x_continuous(
    limits = c(-max(abs(c(range(fm1$alphas0[, 1:2], fm1$gammas0[, 1:2]))))
               , max(abs(c(range(fm1$alphas0[, 1:2], fm1$gammas0[, 1:2])))))) +
  scale_y_continuous(
    limits = c(-max(abs(c(range(fm1$alphas0[, 1:2], fm1$gammas0[, 1:2]))))
               , max(abs(c(range(fm1$alphas0[, 1:2], fm1$gammas0[, 1:2])))))) +
  labs(title = "MCO Method", x = expression(PC[1]), y = expression(PC[2])) +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

print(BiplotAMMI)


BiplotBayesAMMI <-
  ggplot(data = fm1$alphas1, mapping = aes(x = alphas1, y = alphas2)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
```

```
  geom_text(aes(label = 1:nrow(fm1$alphas1)),
            vjust = "inward", hjust = "inward") +
  geom_point(data = fm1$gammas1, mapping = aes(x = gammas1, y = gammas2)) +
  geom_segment(data = fm1$gammas1,
               aes(x = 0, y = 0, xend = gammas1, yend = gammas2),
               arrow = arrow(length = unit(0.2, "cm"))
               , alpha = 0.75, color = "red") +
  geom_text(data = fm1$gammas1,
            aes(x = gammas1, y = gammas2,
                label = paste0("E", 1:nrow(fm1$gammas1))),
            vjust = "inward", hjust = "inward") +
  scale_x_continuous(
    limits = c(-max(abs(c(range(fm1$alphas1[, 1:2], fm1$gammas1[, 1:2]))))
               , max(abs(c(range(fm1$alphas1[, 1:2], fm1$gammas1[, 1:2])))))) +
  scale_y_continuous(
    limits = c(-max(abs(c(range(fm1$alphas1[, 1:2], fm1$gammas1[, 1:2]))))
               , max(abs(c(range(fm1$alphas1[, 1:2], fm1$gammas1[, 1:2])))))) +
  labs(title = "Bayesian Method", x = expression(PC[1]), y = expression(PC[2])) +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

print(BiplotBayesAMMI)
```

`biplots` *Biplots*

Description

biplots

Usage

```
## Default S3 method:
biplots(
  model,
  burnin = 0.3,
  thin = 0.2,
  pb = 0.05,
  plot_stable = TRUE,
  plot_unstable = TRUE,
  ncolors = 5
)
```

Arguments

`model`	Output from ‘bayes_ammi()‘. This should contain the results of the Bayesian AMMI model, including all sampled iterations.

`burnin`	Numeric. Percentage of iterations to discard as burn-in to avoid the effects of random initializations during sampling. For example, ‘burnin = 0.1‘ removes the first 10% of iterations.
`thin`	Numeric. Proportion of sampled iterations to retain for analysis. For example, ‘thin = 0.2‘ keeps 20% of the iterations, selecting 1 out of every 5 iterations.
`pb`	Numeric. Significance levels for the contours in the plot. Smaller values of ‘pb‘ result in wider contours, while higher values create smaller, more specific contours.
`plot_stable`	Logical. If ‘TRUE‘, stable instances are highlighted in the output plot.
`plot_unstable`	Logical. If ‘TRUE‘, unstable instances are highlighted in the output plot.
`ncolors`	Integer. Specifies the number of distinct colors to use in the plot. Adjust this to control the visual differentiation of elements in the plot.

Value

A list with the following components:

plot A plot displaying the contours and final biplot values.

contour_data A ‘data.frame‘ containing the data used to create the contours.

biplot_data A ‘data.frame‘ containing the data used to recreate the final biplot values.

Author(s)

1. Julian Garcia Abadillo Velasco (<`garciaabadillo.j@ufl.edu`>)
2. Diego Jarquin (<`diego.jarquin@gmail.com`>)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
## Not run:
data(Maiz)

fm1 <-
  bayes_ammi(
    .data = Maiz,
    .y = y,
    .gen = entry,
    .env = site,
    .rep = rep,
    .nIter = 200
  )

library(ggplot2)
```

```
output_05 <- biplots(model = fm1, plot_stable = TRUE, plot_unstable = TRUE, pb = 0.05)
output_05

output_95 <- biplots(model = fm1, plot_stable = TRUE, plot_unstable = TRUE, pb = 0.95)
output_95

## End(Not run)
```

`e_eff` *Environment Effects*

Description

Calcuates Environment Effects

Usage

```
## Default S3 method:
e_eff(.data, .y, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Environment Effects

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
data(Maiz)
e_eff(
    .data  = Maiz
   , .y    = y
   , .gen  = entry
   , .env  = site
   )
```

`ge_ammi` *AMMI of Genotype by Environment Interaction Model*

Description

Performs Additive Main Effects and Multiplication Interaction Analysis of Genotype by Environment Interaction Model

Usage

```
ge_ammi(.data, .y, .gen, .env, .rep)

## Default S3 method:
ge_ammi(.data, .y, .gen, .env, .rep)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor
`.rep`	Replication Factor

Value

Genotype by Environment Interaction Model

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
data(Maiz)
fm1 <-
   ge_ammi(
      .data  = Maiz
     , .y    = y
     , .gen  = entry
     , .env  = site
     , .rep  = rep
     )
```

`ge_eff` *Genotype by Environment Interaction Effects*

Description

Calcuates Genotype by Environment Interaction Effects

Usage

```
## Default S3 method:
ge_eff(.data, .y, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Genotype by Environment Interaction Effects

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
data(Maiz)
ge_eff(
    .data  = Maiz
   , .y    = y
   , .gen  = entry
   , .env  = site
   )
```

---

ge_mean *Genotype by Environment Interaction Means*

Description

Calcuates Genotype by Environment Interaction Means

Usage

```
## Default S3 method:
ge_mean(.data, .y, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Genotype by Environment Interaction Means

Author(s)

1. Muhammad Yaseen (`<myaseen208@gmail.com>`)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
data(Maiz)
ge_mean(
    .data  = Maiz
   , .y    = y
   , .gen  = entry
   , .env  = site
   )
```

`ge_model` *Genotype by Environment Interaction Model*

Description

Calcuates Genotype by Environment Interaction Model

Usage

```
ge_model(.data, .y, .gen, .env, .rep)

## Default S3 method:
ge_model(.data, .y, .gen, .env, .rep)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor
`.rep`	Replication Factor

Value

Genotype by Environment Interaction Model

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
data(Maiz)
fm1 <-
   ge_model(
      .data  = Maiz
     , .y    = y
     , .gen  = entry
     , .env  = site
     , .rep  = rep
     )
```

`ge_var` *Genotype by Environment Interaction Variances*

Description

Calcuates Genotype by Environment Interaction Variances

Usage

```
## Default S3 method:
ge_var(.data, .y, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Genotype by Environment Interaction Variances

Author(s)

1. Muhammad Yaseen (`<myaseen208@gmail.com>`)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
data(Maiz)
ge_var(
    .data  = Maiz
   , .y    = y
   , .gen  = entry
   , .env  = site
   )
```

`g_eff` *Genotype Effects*

Description

Calcuates Genotype Effects

Usage

```
## Default S3 method:
g_eff(.data, .y, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Genotype Effects

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
data(Maiz)
g_eff(
    .data  = Maiz
   , .y    = y
   , .gen  = entry
   , .env  = site
   )
```

`Maiz` *Data for Genotypes by Environment Interaction (GEI)*

Description

`Maiz` is used for performing Genotypes by Environment Interaction (GEI) Analysis.

Usage

```
data(Maiz)
```

Format

A `data.frame` 1320 obs. of 6 variables.

Details

- Gen Genotype
- Institute Institute
- Rep Replicate
- Block Block
- Env Environment
- Yield Yield Response

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Jose Crossa (<`j.crossa@cgiar.org`>)
3. Sergio Perez-Elizalde (<`sergiop@colpos.mx`>)
4. Diego Jarquin (<`diego.jarquin@gmail.com`>)
5. Jose Miguel Cotes
6. Kert Viele
7. Genzhou Liu
8. Paul L. Cornelius

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

Examples

```
data(Maiz)
```

`matrix_k` *k Matrix*

Description

Gives k matrix

Usage

```
matrix_k(n)

## Default S3 method:
matrix_k(n)
```

Arguments

`n`	Number of columns

Value

Matrix

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

`orthnorm` *Orthogonal Normalization*

Description

Perform Orthogonal Normalization of a matrix

Usage

```
orthnorm(u = NULL, basis = TRUE, norm = TRUE)

## Default S3 method:
orthnorm(u = NULL, basis = TRUE, norm = TRUE)
```

Arguments

`u`	Matrix
`basis`	Logical argument by default TRUE
`norm`	Logical argument by default TRUE

Value

Matrix

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J.M., Viele, K., Liu, G., and Cornelius, P.L. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model *Crop Science*, **51**, 1458–1469. (doi: 10.2135/cropsci2010.06.0343)

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