

Package ‘bayesammi’

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Type Package

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

Version 0.3.0

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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](https://doi.org/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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NeedsCompilation no

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bayes_amm	<i>Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model</i>
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Description

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

Usage

```
## Default S3 method:
bayes_amm(.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>)
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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](https://doi.org/10.2135/cropsci2010.06.0343))

Examples

```
data(Maiz)

fm1 <-
  bayes_amm(
    .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_ammii()'`. 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@uf1.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](https://doi.org/10.2135/cropsci2010.06.0343))

Examples

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

fm1 <-
  bayes_amm(
    .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

Calculates 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](https://doi.org/10.2135/cropsci2010.06.0343))

Examples

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

ge_amm

AMMI of Genotype by Environment Interaction Model

Description

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

Usage

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

```
## Default S3 method:
ge_amm(.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](https://doi.org/10.2135/cropsci2010.06.0343))

Examples

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

ge_eff

Genotype by Environment Interaction Effects

Description

Calculates 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](https://doi.org/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

Calculates 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](https://doi.org/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

Calculates 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](https://doi.org/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

Calculates 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](https://doi.org/10.2135/cropsci2010.06.0343))

Examples

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

g_eff

Genotype Effects

Description

Calculates 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](https://doi.org/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>)
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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](https://doi.org/10.2135/cropsci2010.06.0343))

Examples

```
data(Maiz)
```

matrix_k	<i>k</i> 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](https://doi.org/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](https://doi.org/10.2135/cropsci2010.06.0343))

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