

Package ‘bayesammi’

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Type Package

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

Version 0.1.0

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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, lme4, magrittr, MASS, mvtnorm, rlang, rstiefel, scales, stats, tibble, tidyr, tmvtnorm

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R topics documented:

bayes_amm	2
e_eff	7
ge_amm	8
ge_eff	9
ge_mean	10
ge_model	11
ge_var	12
g_eff	13
Maiz	14
matrix_k	15
orthnorm	16

Index	17
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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

```
bayes_amm(.data, .y, .gen, .env, .rep, .nIter)
```

```
## 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)

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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)

```

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_amm1(
    .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)

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

Examples

```
data(Maiz)
```

matrix_k	<i>k Matrix</i>
----------	-----------------

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))

Index

*** datasets**

Maiz, [14](#)

bayes_amm, [2](#)

e_eff, [7](#)

g_eff, [13](#)

ge_amm, [8](#)

ge_eff, [9](#)

ge_mean, [10](#)

ge_model, [11](#)

ge_var, [12](#)

Maiz, [14](#)

matrix_k, [15](#)

orthnorm, [16](#)