

Package ‘baystability’

May 7, 2026

Type Package

Title Bayesian Stability Analysis of Genotype by Environment Interaction (GEI)

Version 0.2.0

Maintainer Muhammad Yaseen <myaseen208@gmail.com>

Description Performs general Bayesian estimation method of linear–bilinear models for genotype × environment interaction. The method is explained in Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) (<doi:10.1007/s13253-011-0063-9>).

Depends R (>= 3.1)

Imports dplyr, ggplot2, lme4, MASS, rstiefel, rlang, scales, stats, tibble, tidyr

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

NeedsCompilation no

Author Muhammad Yaseen [aut, cre],
Diego Jarquin [aut, ctb],
Sergio Perez-Elizalde [aut, ctb],
Juan Burgueño [aut, ctb],
Jose Crossa [aut, ctb]

Repository CRAN

Date/Publication 2024-10-15 04:40:03 UTC

Contents

bayes_amm	2
cultivo2008	9
cultivo2009	10
e_eff	11
ge_amm	12

ge_eff	13
ge_mean	14
ge_model	15
ge_var	16
g_eff	17
matrix_k	18
orthnorm	19

Index	20
--------------	-----------

bayes_amm	<i>Bayesian Estimation of Genotype by Environment Interaction Model</i>
-----------	---

Description

Bayesian estimation method of linear–bilinear models for Genotype by Environment 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. Diego Jarquin (<diego.jarquin@gmail.com>)
3. Sergio Perez-Elizalde (<sergiop@colpos.mx>)
4. Juan Burgueño (<j.burgueno@cgiar.org>)
5. Jose Crossa (<j.crossa@cgiar.org>)

References

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear-Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. ([doi:10.1007/s13253-011-0063-9](https://doi.org/10.1007/s13253-011-0063-9))

Examples

```
## Not run:
library(baystability)
library(dplyr)
data(cultivo2008)
fm1 <-
  ge_amm(
    .data = cultivo2008
    , .y = y
    , .gen = entry
    , .env = site
    , .rep = rep
  )

r0 <- fm1$g
c0 <- fm1$e
n0 <- fm1$Rep
k0 <- fm1$k

mu0 <- fm1$mu
sigma20 <- fm1$sigma2
tau0 <- fm1$tau
tao0 <- fm1$tao
delta0 <- fm1$delta
lambdas0 <- fm1$lambdas
alphas0 <- fm1$alphas
gammas0 <- fm1$gammas

ge_means0 <- fm1$ge_means$ge_means

data(cultivo2008)

fm2 <-
  ge_amm(
    .data = cultivo2009
    , .y = y
    , .gen = entry
    , .env = site
    , .rep = rep
  )

k <- fm2$k
alphasa <- fm2$alphas
gammasa <- fm2$gammas
```

```

alphas1 <-
  tibble::as_tibble(fm2$alphas, .name_repair = "unique") %>%
  setNames(paste0("V", 1:ncol(.)))
gammas1 <-
  tibble::as_tibble(fm2$gammas, .name_repair = "unique") %>%
  setNames(paste0("V", 1:ncol(.)))

# Biplots OLS
library(ggplot2)
BiplotOLS1 <-
  ggplot(data = alphas1, mapping = aes(x = V1, y = V2)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
  geom_text(aes(label = 1:nrow(alphas1)), vjust = "inward", hjust = "inward") +
  scale_x_continuous(
    limits = c(-max(abs(c(range(alphas1[, 1:2])))),
              , max(abs(c(range(alphas1[, 1:2])))))) +
  scale_y_continuous(
    limits = c(-max(abs(c(range(alphas1[, 1:2])))),
              , max(abs(c(range(alphas1[, 1:2])))))) +
  labs(title = "OLS", x = expression(u[1]), y = expression(u[2])) +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
print(BiplotOLS1)

BiplotOLS2 <-
  ggplot(data = gammas1, mapping = aes(x = V1, y = V2)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
  geom_text(aes(label = 1:nrow(gammas1)), vjust = "inward", hjust = "inward") +
  scale_x_continuous(
    limits = c(-max(abs(c(range(gammas1[, 1:2])))),
              , max(abs(c(range(gammas1[, 1:2])))))) +
  scale_y_continuous(
    limits = c(-max(abs(c(range(gammas1[, 1:2])))),
              , max(abs(c(range(gammas1[, 1:2])))))) +
  labs(title = "OLS", x = expression(v[1]), y = expression(v[2])) +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
print(BiplotOLS2)

BiplotOLS3 <-
  ggplot(data = alphas1, mapping = aes(x = V1, y = V2)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
  geom_text(aes(label = 1:nrow(alphas1)), vjust = "inward", hjust = "inward") +
  geom_point(data = gammas1, mapping = aes(x = V1, y = V2)) +

```

```

geom_segment(data = gammas1, aes(x = 0, y = 0, xend = V1, yend = V2),
             arrow = arrow(length = unit(0.2, "cm")), alpha = 0.75, color = "red") +
geom_text(data = gammas1,
          aes(x = V1, y = V2, label = paste0("E", 1:nrow(gammas1))),
          , vjust = "inward", hjust = "inward") +
scale_x_continuous(
  limits = c(-max(abs(c(range(alphas1[, 1:2], gammas1[, 1:2])))),
            , max(abs(c(range(alphas1[, 1:2], gammas1[, 1:2])))))) +
scale_y_continuous(
  limits = c(-max(abs(c(range(alphas1[, 1:2], gammas1[, 1:2])))),
            , max(abs(c(range(alphas1[, 1:2], gammas1[, 1:2])))))) +
labs(title = "OLS", x = expression(PC[1]), y = expression(PC[2])) +
theme_bw() +
theme(plot.title = element_text(hjust = 0.5))
print(BiplotOLS3)

data(cultivo2009)
fm3 <-
  bayes_amm(
    .data = cultivo2009
    , .y = y
    , .gen = entry
    , .env = site
    , .rep = rep
    , .nIter = 200
  )

Mean_Alphas <- fm3$Mean_Alphas %>% setNames(paste0("V", 1:ncol(.)))
Mean_Gammas <- fm3$Mean_Gammas %>% setNames(paste0("V", 1:ncol(.)))

# Biplots Bayesian
BiplotBayes1 <-
  ggplot(data = Mean_Alphas, mapping = aes(x = V1, y = V2)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
  geom_text(aes(label = 1:nrow(Mean_Alphas)),
            vjust = "inward"
            , hjust = "inward") +
  scale_x_continuous(
    limits = c(-max(abs(c(range(Mean_Alphas[, 1:2])))),
              , max(abs(c(range(Mean_Alphas[, 1:2])))))) +
  scale_y_continuous(
    limits = c(-max(abs(c(range(Mean_Alphas[, 1:2])))),
              , max(abs(c(range(Mean_Alphas[, 1:2])))))) +
  labs(title = "Bayes", x = expression(u[1]), y = expression(u[2])) +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

print(BiplotBayes1)

```

```

BiplotBayes2 <-
  ggplot(data = Mean_Gammas, mapping = aes(x = V1, y = V2)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
  geom_text(aes(label = 1:nrow(Mean_Gammas)), vjust = "inward", hjust = "inward") +
  scale_x_continuous(
    limits = c(-max(abs(c(range(Mean_Gammas[, 1:2])))),
               , max(abs(c(range(Mean_Gammas[, 1:2])))))) +
  scale_y_continuous(
    limits = c(-max(abs(c(range(Mean_Gammas[, 1:2])))),
               , max(abs(c(range(Mean_Gammas[, 1:2])))))) +
  labs(title = "Bayes", x = expression(v[1]), y = expression(v[2])) +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

print(BiplotBayes2)

BiplotBayes3 <-
  ggplot(data = Mean_Alphas, mapping = aes(x = V1, y = V2)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_vline(xintercept = 0) +
  geom_text(aes(label = 1:nrow(Mean_Alphas)),
            vjust = "inward", hjust = "inward") +
  geom_point(data = Mean_Gammas, mapping = aes(x = V1, y = V2)) +
  geom_segment(data = Mean_Gammas,
              aes(x = 0, y = 0, xend = V1, yend = V2),
              arrow = arrow(length = unit(0.2, "cm"))
              , alpha = 0.75, color = "red") +
  geom_text(data = Mean_Gammas,
            aes(x = V1, y = V2,
                label = paste0("E", 1:nrow(Mean_Gammas))),
            vjust = "inward", hjust = "inward") +
  scale_x_continuous(
    limits = c(-max(abs(c(range(Mean_Alphas[, 1:2], Mean_Gammas[, 1:2])))),
               , max(abs(c(range(Mean_Alphas[, 1:2], Mean_Gammas[, 1:2])))))) +
  scale_y_continuous(
    limits = c(-max(abs(c(range(Mean_Alphas[, 1:2], Mean_Gammas[, 1:2])))),
               , max(abs(c(range(Mean_Alphas[, 1:2], Mean_Gammas[, 1:2])))))) +
  labs(title = "Bayes", x = expression(PC[1]), y = expression(PC[2])) +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

print(BiplotBayes3)

Plot1Mu <-
  ggplot(data = fm3$mu1, mapping = aes(x = 1:nrow(fm3$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 = fm3$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 = fm3$tau1, mapping = aes(x = 1:nrow(fm3$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 = fm3$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 = fm3$tao1, mapping = aes(x = 1:nrow(fm3$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 = fm3$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 = fm3$tao1, mapping = aes(x = 1:nrow(fm3$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 = fm3$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 = fm3$delta1, mapping = aes(x = 1:nrow(fm3$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 = fm3$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 = fm3$delta1, mapping = aes(x = 1:nrow(fm3$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 = fm3$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 = fm3$delta1, mapping = aes(x = 1:nrow(fm3$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 = fm3$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)

## End(Not run)
```

cultivo2008

Data for Genotypes by Environment Interaction (GEI)

Description

cultivo2008 is used for performing Genotypes by Environment Interaction (GEI) Analysis.

Usage

```
data(cultivo2008)
```

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. Diego Jarquin (<diego.jarquin@gmail.com>)
3. Sergio Perez-Elizalde (<sergiop@colpos.mx>)
4. Juan Burgueño (<j.burgueno@cgiar.org>)
5. Jose Crossa (<j.crossa@cgiar.org>)

References

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. ([doi:10.1007/s13253-011-0063-9](https://doi.org/10.1007/s13253-011-0063-9))

Examples

```
data(cultivo2008)
```

cultivo2009

Data for Genotypes by Environment Interaction (GEI)

Description

cultivo2009 is used for performing Genotypes by Environment Interaction (GEI) Analysis.

Usage

```
data(cultivo2009)
```

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. Diego Jarquin (<diego.jarquin@gmail.com>)
3. Sergio Perez-Elizalde (<sergiop@colpos.mx>)
4. Juan Burgueño (<j.burgueno@cgiar.org>)
5. Jose Crossa (<j.crossa@cgiar.org>)

References

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. (doi:10.1007/s13253-011-0063-9)

Examples

```
data(cultivo2009)
```

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

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. (doi:10.1007/s13253-011-0063-9)

Examples

```
data(cultivo2008)
e_eff(
  .data = cultivo2008
  , .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

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. (doi:10.1007/s13253-011-0063-9)

Examples

```
data(cultivo2008)
fm1 <-
  ge_ami(
    .data = cultivo2008
    , .y = y
    , .gen = entry
    , .env = site
    , .rep = rep
  )
```

```
data(cultivo2009)
fm2 <-
  ge_ami(
    .data = cultivo2009
    , .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

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. (doi:10.1007/s13253-011-0063-9)

Examples

```
data(cultivo2008)
ge_eff(
  .data = cultivo2008
  , .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

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. (doi:10.1007/s13253-011-0063-9)

Examples

```
data(cultivo2008)
ge_mean(
  .data = cultivo2008
  , .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

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. (doi:10.1007/s13253-011-0063-9)

Examples

```
data(cultivo2008)
fm1 <-
  ge_model(
    .data = cultivo2008
    , .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

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. (doi:10.1007/s13253-011-0063-9)

Examples

```
data(cultivo2008)
ge_var(
  .data = cultivo2008
  , .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

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. ([doi:10.1007/s13253-011-0063-9](https://doi.org/10.1007/s13253-011-0063-9))

Examples

```
data(cultivo2008)
g_eff(
  .data = cultivo2008
  , .y = y
  , .gen = entry
  , .env = site
)
```

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

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. (doi:10.1007/s13253-011-0063-9)

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

Perez-Elizalde, S., Jarquin, D., and Crossa, J. (2011) A General Bayesian Estimation Method of Linear–Bilinear Models Applied to Plant Breeding Trials With Genotype \times Environment Interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17, 15–37. (doi:10.1007/s13253-011-0063-9)

Index

* datasets

cultivo2008, 9
cultivo2009, 10

bayes_amm, 2

cultivo2008, 9
cultivo2009, 10

e_eff, 11

g_eff, 17
ge_amm, 12
ge_eff, 13
ge_mean, 14
ge_model, 15
ge_var, 16

matrix_k, 18

orthnorm, 19