

Package ‘baystability’

March 13, 2018

Type Package

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

Version 0.1.0

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Description Performs general Bayesian estimation method of linear–bilinear models for genotype \times 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, ggfortify, lme4, magrittr, MASS, matrixStats, reshape2, rstiefel, rlang, scales, stats, tibble, tidyr, tidyverse

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2018-03-13 15:55:34 UTC

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

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

k <- fm2$k
alpha1 <- fm2$alphas
gamma1 <- fm2$gammas

alpha1 <- tibble::as_tibble(fm2$alphas)
gamma1 <- tibble::as_tibble(fm2$gammas)

```

```

# 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(gammasa)))
    , 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)

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

Mean_Alphas <- tibble::as_tibble(matrix(colMeans(fm3$alphas1), ncol = 11))
Mean_Gammas <- tibble::as_tibble(matrix(colMeans(fm3$gammas1), ncol = 11))

# 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)

```

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)

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](https://doi.org/10.1007/s13253-011-0063-9))

Examples

```
data(cultivo2009)
```

e_eff	<i>Environment Effects</i>
-------	----------------------------

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

<code>.data</code>	data.frame
<code>.y</code>	Response Variable
<code>.gen</code>	Genotypes Factor
<code>.env</code>	Environment Factor
<code>.rep</code>	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](https://doi.org/10.1007/s13253-011-0063-9))

Examples

```
data(cultivo2008)
fm1 <-
  ge_amm(
    .data = cultivo2008
    , .y = y
    , .gen = entry
```

```
, .env = site
, .rep = rep
)

data(cultivo2009)
fm2 <-
  ge_ammf(
    .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

<code>.data</code>	data.frame
<code>.y</code>	Response Variable
<code>.gen</code>	Genotypes Factor
<code>.env</code>	Environment Factor
<code>.rep</code>	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](https://doi.org/10.1007/s13253-011-0063-9))

orthnorm	<i>Orthogonal Normalization</i>
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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](https://doi.org/10.1007/s13253-011-0063-9))

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