Package 'RGE'

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Type Package

Title Response from Genotype to Environment

Depends R (>= 3.5.0), Matrix, MatrixModels, coda

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Description Compute yield-stability index based on Bayesian methodology, which is useful for analyze multi-environment trials in plant breeding programs. References: Cotes Torres JM, Gonzalez Jaimes EP, and Cotes Torres A (2016) <`https://revistas.unimilitar.edu.co/index.php/rfcb/article/view/2037`> Seleccion de Genotipos con Alta Respuesta y Estabilidad Fenotipica en Pruebas Regionales: Recuperando el Concepto Biologico.

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`RGE-package` *Response from Genotype to Environment*

Description

RGE is a packages for analize regionals trials from plant breeding programs. The package simplify the analysis process in order to obtaind the more useful results to be consider for the resercher. The program perfomace a GIBBS sampler and finally obtain a bayesian yield stability index. Tools for obtain useful plot were developed in order to make the interpretation of results more easy.

Author(s)

Jose Miguel Cotes Torres <`jmcotes@unal.edu.co`>

References

Cotes Torres, J. M., Gonzalez Jaimes, E. P., & Cotes Torres, A. (2016). Seleccion de Genotipos con Alta Respuesta y Estabilidad Fenotipica en Pruebas Regionales: Recuperando el Concepto Biologico. Revista Facultad De Ciencias Basicas, 8(2), 226-243.

`bayes.posterior` *Summary of the posterior distribution*

Description

Obtaining the bayes estimative and the highest posterior density intervals at 95% from a object obtained by RGE function.

Usage

```
bayes.posterior(x, ...)
```

Arguments

`x`	An object obtained by the function RGE `"RGE"`
`...`	Further arguments to be passed

Value

Dataframe with the summary of the posterior distribution

Note

coda package is needed.

Author(s)

Jose Miguel Cotes Torres <`jmcotes@unal.edu.co`>

See Also

`coda`

Examples

```
data(m1)
bayes.posterior(m1)
```

`datos` *Potato regional trial in Colombia*

Description

Eleven trials with ten genotypes stablished in state of Narino-Colombia Cortesy: Professor Luis Ernesto Rodriguez Molano <`lerodriguezmo@unal.edu.co`>

Usage

```
data("datos")
```

Format

A data frame with 440 observations on the following 17 variables.

`Localidad`	a numeric vector
`Nlocalidad`	a character vector
`Semestre`	a numeric vector
`Bloque`	a numeric vector
`Genotipo`	a character vector
`RO`	a numeric vector
`R1`	a numeric vector
`Rcomercial`	a numeric vector
`RcTon`	a numeric vector
`R2`	a numeric vector
`R3`	a numeric vector
`RendimientoTotal`	a numeric vector
`RTton`	a numeric vector
`GE`	a numeric vector
`MS`	a numeric vector
`CF`	a numeric vector
`AR`	a numeric vector

References

Unpublished data.

Examples

```
data(datos)
```

`m1` *Samples of the posterior distribution by GIBBS sampler*

Description

Object obtained by function RGE

Usage

```
data("m1")
```

Format

The format is: num [1:20, 1:10000] 14.2 15.8 16.1 19.9 17.3 ... - attr(*, "dimnames")=List of 2 ..$: chr [1:20] "Predicted_T1" "Predicted_T2" "Predicted_UN 4" "Predicted_UN 50" ... ..$: NULL

Examples

```
data(m1)
```

`plot.RGE` *Plots for object obtained by RGE*

Description

This functions makes the plots of bayes estimate (mean) and the highest posterior density intervals at 95%, of predicted value of genotype, his stability variance, and his bayesian yield stability index.

Usage

```
## S3 method for class 'RGE'
plot(
    x,
    labelg = "Predicted value",
    labelsv = "Stability variance",
    labelby = "Bayesian yield stability index",
    margin = c(1, 0.8, 0, 0.8), ...)
```

Arguments

`x`	an object obtained by the function RGE `"RGE"`
`labelg`	Label to use in the plot of predicted value of genotype
`labelsv`	Label to use in the plot of stability variance
`labelby`	Label to use in the plot of bayesian yield stability index
`margin`	A numerical vector of the form c(bottom, left, top, right) which gives the margin size specified in inches.
`...`	Further arguments to be passed

Value

Plot of the predicted values, stability variance and bayesian yield stability index

Author(s)

Jose Miguel Cotes Torres `<jmcotes@unal.edu.co>`

See Also

`plot`,`plot.mcmc`,`par`

Examples

```
data(m1)
plot(m1)
```

`print.RGE` *Summary of the posterior distribution*

Description

Obtaining the bayes estimative and the highest posterior density intervals at 95% from predicted value of the genotypes, his stability variances and his bayesian yiled stability indexes.

Usage

```
## S3 method for class 'RGE'
print(x, ...)
```

Arguments

`x`	An object obtained by the function RGE `"RGE"`
`...`	Further arguments to be passed

Value

Do not return any value. It is a print version of summary.RGE

Note

coda package is needed.

Author(s)

Jose Miguel Cotes Torres <`jmcotes@unal.edu.co`>

See Also

`coda`

Examples

```
data(m1)
print(m1)
```

`RGEgibbs` *Response from Genotype to Environment*

Description

This function performance the GIBBS sampler for analyze reginals trials.

Usage

```
RGEgibbs(data, gen_c, env_c, blk_c, y_c, prior.g = NULL,
        prior.vg =NULL,prior.b = NULL, prior.dfb = NULL,
        prior.sv = NULL, prior.dfsv = NULL, prior.se = NULL,
        prior.dfse = NULL,
        burnin = 10, thin = 5, niter = 50, saveAt = 10)
```

Arguments

`data`	`data.frame`
`gen_c`	Number of the column from de data.frame with the genotypes information.
`env_c`	Number of the column from de data.frame with the environment information.
`blk_c`	Number of the column from de data.frame with the block information.
`y_c`	Number of the column from de data.frame with the phenotype information.
`prior.g`	Vector with prior information of the means of genotypes
`prior.vg`	Vector with prior information of the variances of the means of genotypes
`prior.b`	Vector with prior information of the variances of block within environment
`prior.dfb`	Vector with prior information of hyperparameter degree of credibility of the variances of block within environment.
`prior.sv`	Vector with prior information of the stability's variances

`prior.dfsv`	Vector with prior information of hyperparameter degree of credibility of the stability's variances.
`prior.se`	Vector with prior information of the error's variances
`prior.dfse`	Vector with prior information of hyperparameter degree of credibility of the variances of error.
`burnin`	Number of iteration to be consider as burn-in period. This period is not saved in the final result.
`thin`	The thinning interval between consecutive observations. This interval is not saved in the final result.
`niter`	Numbers of iterations to be saved
`saveAt`	Save object outtS4 with samples of the posterior distribution on the work directory each "saveAt" iteration

Value

Matrix with samples of the posterior distribution

Author(s)

Jose Miguel Cotes Torres `<jmcotes@unal.edu.co>`

References

Cotes Torres, J. M., Gonzalez Jaimes, E. P., & Cotes Torres, A. (2016). Seleccion de Genotipos con Alta Respuesta y Estabilidad Fenotipica en Pruebas Regionales: Recuperando el Concepto Biologico. Revista Facultad De Ciencias Basicas, 8(2), 226-243.

Examples

```
##data(datos)
##m<-RGEgibbs(data=datos,gen_c=5,env_c=1,blk_c=4,y_c=9,
##thin=5,burnin=100,niter=10000,saveAt=1000)
```

`summary.RGE` *Summary of the posterior distribution*

Description

Obtaining the bayes estimative and the highest posterior density intervals at 95% from predicted value of the genotypes, his stability variances and his bayesian yiled stability indexes.

Usage

```
## S3 method for class 'RGE'
summary(object, ...)
```

Arguments

`object`	An object obtained by the function RGE `"RGE"`
`...`	Further arguments to be passed

Value

Return a list with:

`mu`	Summary with predicted values of genotypes.
`sv`	Summary of the stability variances
`sv`	Summary of the bayesian yield stability indexes

Note

coda package is needed.

Author(s)

Jose Miguel Cotes Torres `<jmcotes@unal.edu.co>`

See Also

`coda`

Examples

```
data(m1)
summary(m1)
```

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