

# Package ‘RGE’

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**Type** Package

**Title** Response from Genotype to Environment

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

**Version** 1.0

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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>> Selección de Genotipos con Alta Respuesta y Estabilidad Fenotípica en Pruebas Regionales: Recuperando el Concepto Biológico.

**License** GPL (>= 2)

**NeedsCompilation** no

**Repository** CRAN

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RGE-package

*Response from Genotype to Environment*

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**Description**

RGE is a packages for analyze regionals trials from plant breeding programs. The package simplify the analysis process in order to obtained 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). Selecccion de Genotipos con Alta Respuesta y Estabilidad Fenotipica en Pruebas Regionales: Recuperando el Concepto Biologico. Revista Facultad De Ciencias Basicas, 8(2), 226-243.

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bayes.posterior

*Summary of the posterior distribution*

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**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)
```

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datos	<i>Potato regional trial in Colombia</i>
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**Description**

Eleven trials with ten genotypes established 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  
R0 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	<i>Samples of the posterior distribution by GIBBS sampler</i>
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**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	<i>Plots for object obtained by RGE</i>
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**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 <jmccotes@unal.edu.co>

**References**

Cotes Torres, J. M., Gonzalez Jaimes, E. P., & Cotes Torres, A. (2016). Selecccion 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@una1.edu.co>

**See Also**

coda

**Examples**

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



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