

# Package ‘convRJMCMC’

January 21, 2021

**Type** Package

**Title** Convergence assessment of RJMCMC algorithms

**Version** 0.1.0

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**Description** This package on version 0.1.0 has four functions to evaluate the convergence of RJMCMC outputs by using a modified version of Castellote and Zimmerman (2002) criteria.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Imports** Rdpack

**RdMacros** Rdpack

**RoxygenNote** 7.1.1

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CZ_ANOVA	<i>RJMCMC convergence assessment of a single parameter</i>
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## Description

This function creates an object of class CZ\_ANOVA with the necessary information to plot the diagnostic graphics proposed by the Castellote and Zimmerman (2002) criteria for a single parameter.

## Usage

```
CZ_ANOVA(theta, chains, models, mcmciterations, nbatches, batchsize, confidence, division)
```

## Arguments

theta	Observed values for the parameter in the different chains.
chains	Chain index for the observed parameter value. The number of iterations per chain must be equal.
models	Model index for the observed parameter value.
mcmciterations	For a given chain is the iteration index value.
nbatches	Numbers of batches. The standard value is 20.
batchsize	It is the size of a batch given by iterations in a chain/nbatches consecutive integer. The function disregard nbatches value in case both are available. There is only a need to supply the nbatches or batchsize value.
confidence	It is the confidence level for the upper bound of both potential scale reduction factors. The standard value is 0.95.
division	Division criteria to make the batches. If division="Batch" the batches are partitions with size=batchsize of the iterations set. If division="Sequential" all the batches will have size=number of iterations/2, with the first batch starting at first iteration and the others at iteration 1+(number of iterations/2)/nbatches. Standard is division="Batch".

## Details

The function output can be different from Castellote and Zimmerman (2002) criteria in cases that at least one model is visited only for some chains as the degrees of freedom are automatically calculated by aov function. We recommend not to use the original criteria from Castellote and Zimmerman (2002) in the situation above and to use this function instead.

## Value

An object of class CZ\_ANOVA which saves a list for every batch with the summary of the ANOVA 1 model, the summary of the ANOVA 2 Model, the summary of the ANOVA 3 model, PSRF1, PSRF2, the upper bound of PSRF1, the upper bound of PSRF2, V, Wc, Wm, and WcWm. For more details see Castellote and Zimmerman (2002) article.

## Author(s)

Tiago Pereira Marques and Miriam Harumi Tsunemi

## References

Castellote JM, Zimmerman DL (2002). "Convergence assessment for reversible jump MCMC samplers." *Department of Statistics and Actuarial Science, University of Iowa, Technical Report*, **313**.

## Examples

```
#Example 1

set.seed(634963)
#Create parameters observations for the 3 chains
#theta 1 - chains 1 ...
theta1<-rnorm(100000,mean=20,sd=1.5)
theta2<-rnorm(100000,mean=20,sd=1.5)
theta3<-rnorm(100000,mean=20,sd=1.5)
#Merge generate observations in theta object
```

```

theta<-c(theta1,theta2,theta3)
#Create chain index
chains<-c(rep(1,100000),rep(2,100000),rep(3,100000))
#Create model index
  #In these configuration there will be 3 models in
  #proportions 1:2:1
models<-factor(sample(c(1,2,3),300000,TRUE,c(0.25,0.5,0.25)))
#Create iterations index
mcmciterations<-rep(seq(1:100000),3)
#Create CZ_ANOVA object and save to test 1
teste_1<-CZ_ANOVA(theta,chains,models,mcmciterations)

```

CZ\_MANOVA

*RJMCMC convergence assessment of multiple parameters*

## Description

This function creates an object of class `CZ_MANOVA` with the necessary information to plot the diagnostic graphics proposed by the Castellote and Zimmerman (2002) criteria for multiple parameters.

## Usage

```
CZ_MANOVA(theta,chains,models,mcmciterations,nbatches,batchsize,confidence,division)
```

## Arguments

theta	Matrix with parameters observations, different parameters must be on different columns. For some iteration, chain, and model in a row, there must be a vector of the observed parameters.
chains	Chain index for the observed parameters. The number of iterations per chain must be equal.
models	Model index for the observed parameters.
mcmciterations	For a given chain is the iteration index value.
nbatches	Numbers of batches. The standard value is 20.
batchsize	It is the size of a batch given by iterations in a chain/nbatches consecutive integer. The function disregard nbatches value in case both are available. There is only a need to supply the nbatches or batchsize value.
confidence	It is the confidence level for the upper bound of both potential scale reduction factors. The standard value is 0.95.
division	Division criteria to make the batches. If division="Batch" the batches are partitions with size=batchsize of the iterations set. If division="Sequential" all the batches will have size=number of iterations/2, with the first batch starting at first iteration and the others at iteration 1+(number of iterations/2)/nbatches. Standard is division="Batch".

## Details

The function output can be different from Castellote and Zimmerman (2002) criteria in cases that at least one model is visited only for some chains as the degrees of freedom are automatically calculated by the manova function. We recommend not to use the original criteria from Castellote and Zimmerman (2002) in the situation above and to use this function instead.

**Value**

An object of class CZ\_MANOVA which saves a list for every batch with the V matrix, the Wc matrix, the Wm matrix, the WmWc matrix, MPSRF1, MPSRF2, the V matrix largest eigenvalue, the Wc matrix largest eigenvalue, the Wm matrix largest eigenvalue, and the WmWc matrix largest eigenvalue. For more details see Castellote and Zimmerman (2002) article.

**Author(s)**

Tiago Pereira Marques and Miriam Harumi Tsunemi

**References**

Castellote JM, Zimmerman DL (2002). "Convergence assessment for reversible jump MCMC samplers." *Department of Statistics and Actuarial Science, University of Iowa, Technical Report*, **313**.

**Examples**

```
#Example 1

set.seed(500)

chains<-c(rep(1,100000),rep(2,100000),rep(3,100000))
models<-factor(sample(c(1,2,3),300000,TRUE,c(0.25,0.5,0.25)))
mcmciterations<-rep(seq(1:100000),3)

{
  theta1a<-rnorm(100000,mean=0,sd=1)
  theta2a<-rnorm(100000,mean=1,sd=2)
  theta3a<-rnorm(100000,mean=1,sd=3)
  thetaa<-cbind(theta1a,theta2a,theta3a)

  theta1b<-rnorm(100000,mean=0,sd=1)
  theta2b<-rnorm(100000,mean=1,sd=2)
  theta3b<-rnorm(100000,mean=1,sd=3)
  thetab<-cbind(theta1b,theta2b,theta3b)

  theta1c<-rnorm(100000,mean=0,sd=1)
  theta2c<-rnorm(100000,mean=1,sd=2)
  theta3c<-rnorm(100000,mean=1,sd=3)
  thetac<-cbind(theta1c,theta2c,theta3c)

  theta<-rbind(thetaa,thetab,thetac)
}

teste_2<-CZ_MANOVA(theta,chains,models,mcmciterations)
```

---

plot.CZ\_ANOVA

*Diagnostic graphics proposed by Castellote and Zimmerman (2002)  
for a single parameter*

---

**Description**

This function plots the 3 diagnostic graphics proposed by Castellote and Zimmerman (2002) for a single parameter: 1 - PSRF1 and PSRF2 plus their upper bounds against batch; 2 - V and Wc against batch; 3 - Wm and WmWc against batch.

**Usage**

```
## S3 method for class 'CZ_ANOVA'
plot(x,...)
```

**Arguments**

x                      Object of class CZ\_ANOVA created by CZ\_ANOVA function.  
 ...                    Extra arguments to be parsed in the function.

**Details**

The plots are created in the currently active device. Users must press enter to see other plots.

**Note**

Axis and legend labels are in Brazilian Portuguese in this preliminary version. Future versions will have English labels as standard and allow user-defined labels.

**Author(s)**

Tiago Pereira Marques and Miriam Harumi Tsunemi

**References**

Castelloe JM, Zimmerman DL (2002). “Convergence assessment for reversible jump MCMC samplers.” *Department of Statistics and Actuarial Science, University of Iowa, Technical Report*, **313**.

**Examples**

```
#Example 1

set.seed(634963)
theta1<-rnorm(100000,mean=20,sd=1.5)
theta2<-rnorm(100000,mean=20,sd=1.5)
theta3<-rnorm(100000,mean=20,sd=1.5)
theta<-c(theta1,theta2,theta3)
chains<-c(rep(1,100000),rep(2,100000),rep(3,100000))
models<-factor(sample(c(1,2,3),300000,TRUE,c(0.25,0.5,0.25)))
mcmciterations<-rep(seq(1:100000),3)

#CZ_ANOVA object is saved on teste_1
teste_1<-CZ_ANOVA(theta,chains,models,mcmciterations)
plot(teste_1)
```

---

plot.CZ\_MANOVA

*Diagnostic graphics proposed by Castelloe and Zimmerman (2002)  
for a single parameter*

---

**Description**

This function plots the 3 diagnostic graphics proposed by Castelloe and Zimmerman (2002) for multiple parameters: 1 - MPSRF1 and MPSRF2 against batch; 2 - Largest eigenvalue of V and largest eigenvalue of Wc against batch; 3 - Largest eigenvalue of Wm and largest eigenvalue of WmWc against batch.

**Usage**

```
## S3 method for class 'CZ_MANOVA'
plot(x,...)
```

**Arguments**

x                      Object of class CZ\_MANOVA created by CZ\_MANOVA function.  
 ...                    Extra arguments to be parsed in the function.

**Details**

The plots are created in the currently active device. Users must press enter to see other plots.

**Note**

Axis and legend labels are in Brazilian Portuguese in this preliminary version. Future versions will have English labels as standard and allow user-defined labels.

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**References**

Castelloe JM, Zimmerman DL (2002). “Convergence assessment for reversible jump MCMC samplers.” *Department of Statistics and Actuarial Science, University of Iowa, Technical Report*, **313**.

**Examples**

```
#Example 1

set.seed(500)

chains<-c(rep(1,100000),rep(2,100000),rep(3,100000))
models<-factor(sample(c(1,2,3),300000,TRUE,c(0.25,0.5,0.25)))
mcmciterations<-rep(seq(1:100000),3)

{
  theta1a<-rnorm(100000,mean=0,sd=1)
  theta2a<-rnorm(100000,mean=1,sd=2)
  theta3a<-rnorm(100000,mean=1,sd=3)
  thetaa<-cbind(theta1a,theta2a,theta3a)

  theta1b<-rnorm(100000,mean=0,sd=1)
  theta2b<-rnorm(100000,mean=1,sd=2)
  theta3b<-rnorm(100000,mean=1,sd=3)
  thetab<-cbind(theta1b,theta2b,theta3b)

  theta1c<-rnorm(100000,mean=0,sd=1)
  theta2c<-rnorm(100000,mean=1,sd=2)
  theta3c<-rnorm(100000,mean=1,sd=3)
  thetac<-cbind(theta1c,theta2c,theta3c)

  theta<-rbind(thetaa,thetab,thetac)
}
```

```
#CZ_MANOVA object is saved on test_2  
teste_2<-CZ_MANOVA(theta,chains,models,mcmciterations)  
plot(teste_2)
```

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