

# Package ‘GibbsACOV’

February 19, 2015

**Type** Package

**Title** Gibbs Sampler for One-Way Mixed-Effects ANOVA and ANCOVA Models

**Version** 1.1

**Date** 2013-05-05

**Author** Emily Goren and Quan Zhang

**Maintainer** Emily Goren <emily.goren@gmail.com>

**Description** Gibbs sampler for one-way linear mixed-effects models (ANOVA, ANCOVA) with homoscedasticity of errors and uniform priors.

**License** GPL (>= 2)

**Depends** MASS

**Collate** 'acovamcmc.R' 'plot.acovamcmc.R' 'print.acovamcmc.R'  
'summary.acovamcmc.R'

**NeedsCompilation** no

**Repository** CRAN

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## R topics documented:

GibbsACOV-package . . . . .	2
acovamcmc . . . . .	3
corn . . . . .	4
csection . . . . .	5
plot.acovamcmc . . . . .	6
print.acovamcmc . . . . .	6
summary.acovamcmc . . . . .	7
<b>Index</b>	<b>8</b>

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GibbsACOV-package

*Gibbs Sampler for One-Way Mixed-Effects ANOVA and ANCOVA Models*


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## Description

Gibbs sampler for one-way linear mixed-effects models (ANOVA, ANCOVA) with homoscedasticity of errors and uniform priors.

## Details

Package: GibbsACOV  
Type: Package  
Version: 1.1  
Date: 2013-05-05  
License: GPL (>= 2)

~~ An overview of how to use the package, including the most important functions ~~

## Author(s)

Emily Goren and Quan Zhang

Maintainer: Emily Goren <emily.goren@gmail.com>

## References

Gelman, A and Rubin, DB (1992) Inference from iterative simulation using multiple sequences, *Statistical Science*, 7, 457-511.

## Examples

```
## Not run:
# ANCOVA with 2 continuous predictors and 5 factor levels
data(corn)
init1 <- c(rep(0,7), 1, 1)
init2 <- c(rnorm(7), rgamma(2,2,1))
init3 <- c(rnorm(7), rgamma(2,2,1))
init4 <- c(rnorm(7), rgamma(2,2,1))
initval <- rbind(init1, init2, init3, init4)
acovamcmc(corn$yield, corn$variety, cbind((corn$nitrogen)^2, corn$nitrogen), 4, 10000 , initval)

# ANOVA with grand mean parameterization and 12 factor levels
data(csection)
init1 <- c(rep(0,13), 1, 1)
init2 <- c(rnorm(13), rgamma(2,2,1))
init3 <- c(rnorm(13), rgamma(2,2,1))
```

```

init4 <- c(rnorm(13), rgamma(2,2,1))
initval <- rbind(init1, init2, init3, init4)
Y = log(csection$rate / (1-csection$rate))
acovamcmc(Y, factor(csection$hospital), matrix(1,length(csection$hospital),1), 4, 10000, initval)

## End(Not run)

```

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acovamcmc	<i>Gibbs sampler for one-way mixed-effects ANOVA and ANCOVA models.</i>
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### Description

Gibbs sampler for one-way mixed-effects ANOVA and ANCOVA models using flat priors.

### Usage

```
acovamcmc(Y, trt, X, nochn, numIter, initval, credint = 0.95, Rthresh = 1.1)
```

### Arguments

Y	Vector of reponses of n subjects
trt	Vector of categorical factor levels for n subjects
X	Design matrix with dimension (n x p) where p is the number of continuous predictors (for ANOVA, p = 1 to include grand mean)
nochn	Number of chains to test convergence of the Gibbs sampler
numIter	Number of iterations in the Gibbs sampler
initval	Matrix of initial values for Gibbs sampler with dimension (nochn, (p + nlevels(trt) + 2))
credint	Coverage probability for parameter credible intervals
Rthresh	Gelman-Rubin diagnostic for test of convergence

### Value

S3 acovamcmc object; a list consisting of

beta	values of regression coefficients for each iteration
sig2a	values of mixed-effect variance for each iteration
sig2e	values of error variance for each iteration
Credible_Interval	lower bound, point estimate, and upper bound for parameters
Credible_Interval_Coverage	coverage percentage for credible intervals
Convergence_Diag	status of Gibbs sampler convergence using threshold set for Gelman and Rubin's diagnostic

Gelman\_Rubin\_Threshold      threshold set for Gelman and Rubin's diagnostic

Iterations                    number of iterations of Gibbs sampler

Run\_Time                      total elapsed seconds

## References

Gelman, A and Rubin, DB (1992) Inference from iterative simulation using multiple sequences, *Statistical Science*, 7, 457-511.

## Examples

```
## Not run:
# ANCOVA with 2 continuous predictors and 5 factor levels
data(corn)
init1 <- c(rep(0,7), 1, 1)
init2 <- c(rnorm(7), rgamma(2,2,1))
init3 <- c(rnorm(7), rgamma(2,2,1))
init4 <- c(rnorm(7), rgamma(2,2,1))
initval <- rbind(init1, init2, init3, init4)
acovamcmc(corn$yield, corn$variety, cbind((corn$nitrogen)^2, corn$nitrogen), 4, 10000, initval)
# ANOVA with grand mean parameterization and 12 factor levels
data(csection)
init1 <- c(rep(0,13), 1, 1)
init2 <- c(rnorm(13), rgamma(2,2,1))
init3 <- c(rnorm(13), rgamma(2,2,1))
init4 <- c(rnorm(13), rgamma(2,2,1))
initval <- rbind(init1, init2, init3, init4)
Y = log(csection$rate / (1-csection$rate))
acovamcmc(Y, factor(csection$hospital), matrix(1,length(csection$hospital),1), 4, 10000, initval)

## End(Not run)
```

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corn

*Example dataset: corn*

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## Description

Example 1-way mixed-effects ANCOVA dataset for acovamcmc. Classic agricultural experiment: corn yield by variety and level of nitrogen fertilizer.

## Usage

corn

**Format**

variety corn variety

nitrogen level of nitrogen fertilizer

yield corn yield

**Examples**

```
data(corn)
```

---

csection

*Example dataset: C-section rates*

---

**Description**

Example 1-way mixed-effects ANOVA dataset for acovamcmc. C-section rate for 10 randomly selected obstetricians at 12 randomly selected urban hospitals with at least 20 obstetricians associated with its maternity ward.

**Usage**

```
csection
```

**Format**

hospital one of 12 hospitals where C-section rate was recorded

rate rate of delivery of babies by C-section

**Examples**

```
data(csection)
```

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<code>plot.acovamcmc</code>	<i>plot.acovamcmc</i>
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**Description**

Plots for a acovamcmc object

**Usage**

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

**Arguments**

<code>x</code>	A acovamcmc object
<code>...</code>	Ignored

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<code>print.acovamcmc</code>	<i>print.acovamcmc</i>
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**Description**

Print for a acovamcmc object

**Usage**

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

**Arguments**

<code>x</code>	A acovamcmc object
<code>...</code>	Ignored

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summary.acovamcmc      *summary.acovamcmc*

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**Description**

Summary for a acovamcmc object

**Usage**

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

**Arguments**

object	A acovamcmc object
...	Ignored

# Index

\*Topic **GibbsACOV**

GibbsACOV-package, [2](#)

acovamcmc, [3](#)

corn, [4](#)

csection, [5](#)

GibbsACOV (GibbsACOV-package), [2](#)

GibbsACOV-package, [2](#)

plot (plot.acovamcmc), [6](#)

plot.acovamcmc, [6](#)

print (print.acovamcmc), [6](#)

print.acovamcmc, [6](#)

summary (summary.acovamcmc), [7](#)

summary.acovamcmc, [7](#)