

# Package: ClusterBootstrap (via r-universe)

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**Title** Analyze Clustered Data with Generalized Linear Models using the Cluster Bootstrap

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**Version** 1.1.2

**Description** Provides functionality for the analysis of clustered data using the cluster bootstrap.

**Depends** R (>= 3.0), stats, utils, graphics, parallel, magrittr, dplyr

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**URL** <https://github.com/mathijsdeen/ClusterBootstrap>

**BugReports** <https://github.com/mathijsdeen/ClusterBootstrap/issues>

**Maintainer** Mathijs Deen <m.l.deen@fsw.leidenuniv.nl>

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clusbootglm	<i>Fit generalized linear models with the cluster bootstrap</i>
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**Description**

Fit a generalized linear model with the cluster bootstrap for analysis of clustered data.

**Usage**

```
clusbootglm(  
  model,  
  data,  
  clusterid,  
  family = gaussian,  
  B = 5000,  
  confint.level = 0.95,  
  n.cores = 1  
)
```

**Arguments**

model	generalized linear model to be fitted with the cluster bootstrap. This should either be a formula (or be able to be interpreted as one) or a glm / lm object. From the (g)lm objects, the formula will be used.
data	dataframe that contains the data.
clusterid	variable in data that identifies the clusters.
family	error distribution to be used in the model, e.g. gaussian or binomial.
B	number of bootstrap samples.
confint.level	level of confidence interval.
n.cores	number of CPU cores to be used.

**Details**

Some useful methods for the obtained clusbootglm class object are [summary.clusbootglm](#), [coef.clusbootglm](#), and [clusbootsample](#).

**Value**

clusbootglm produces an object of class "clusbootglm", containing the following relevant components:

coefficients	A matrix of B rows, containing the parameter estimates for all bootstrap samples.
bootstrap.matrix	n*B matrix, of which each column represents a bootstrap sample; each value in a column represents a unit of subjectid.
lm.coefs	Parameter estimates from a single (generalized) linear model.
boot.coefs	Mean values of the parameter estimates, derived from the bootstrap coefficients.
boot.sds	Standard deviations of cluster bootstrap parameter estimates.
ci.level	User defined confidence interval level.
percentile.interval	Confidence interval based on percentiles, given the user defined confidence interval level.
parametric.interval	Confidence interval based on lm.coefs and column standard deviations of coefficients, given the user defined confidence interval level.
BCa.interval	Confidence interval based on percentiles with bias correction and acceleration, given the user defined confidence interval level.
samples.with.NA.coef	Cluster bootstrap sample numbers with at least one coefficient being NA.
failed.bootstrap.samples	For each of the coefficients, the number of failed bootstrap samples are given.

**Author(s)**

Mathijs Deen, Mark de Rooij

**Examples**

```
## Not run:
data(opposites)
clusbootglm(SCORE~Time*COG,data=opposites,clusterid=Subject)
## End(Not run)
```

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clusbootsample	<i>Return data for specified bootstrap sample</i>
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**Description**

Returns the full data frame for a specified bootstrap sample in a clusbootglm object.

**Usage**

```
clusbootsample(object, samplenr)
```

**Arguments**

object	object of class clusbootglm, created with the clusbootglm function.
samplenr	sample number for which the data frame should be returned.

**Author(s)**

Mark de Rooij, Mathijs Deen

**Examples**

```
## Not run:
data(opposites)
cbglm.1 <- clusbootglm(SCORE~Time*COG,data=opposites,clusterid=Subject)
clusbootsample(cbglm.1, samplenr=1)
## End(Not run)
```

---

coef.clusbootglm	<i>Obtain coefficients from cluster bootstrap object</i>
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**Description**

Returns the coefficients of an object of class clusbootglm.

**Usage**

```
## S3 method for class 'clusbootglm'
coef(object, estimate.type = "bootstrap", ...)
```

**Arguments**

object	object of class clusbootglm.
estimate.type	type of coefficient (bootstrap or GLM).
...	other arguments.

**Author(s)**

Mathijs Deen

**Examples**

```
## Not run:
data(opposites)
cbglm.1 <- clusbootglm(SCORE~Time*COG,data=opposites,clusterid=Subject)
coef(cbglm.1, estimate.type="bootstrap")
## End(Not run)
```

---

confint.clusbootglm      *Confidence intervals for cluster bootstrap model parameters*

---

### Description

Computes confidence intervals for one or more parameters in a fitted GLM with the cluster bootstrap.

### Usage

```
## S3 method for class 'clusbootglm'
confint(object, parm = "all", level = 0.95, interval.type = "BCa", ...)
```

### Arguments

object	object of class clusbootglm.
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. Defaults to all parameters.
level	the required confidence level
interval.type	type of confidence level. Options are BCa, percentile, and parametric.
...	other arguments.

### Author(s)

Mathijs Deen

### Examples

```
## Not run:
data(opposites)
cbglm.1 <- clusbootglm(SCORE~Time*COG,data=opposites,clusterid=Subject)
confint(cbglm.1,parm=c("Time","COG"), level=.90, interval.type="percentile")
## End(Not run)
```

---

emm      *Calculate estimated marginal means for a cluster bootstrap GLM*

---

### Description

Returns the estimated marginal means of an clusbootglm object. This function works with a maximum of one between-subjects and one within-subjects variable.

### Usage

```
emm(object, confint.level = 0.95)
```

**Arguments**

object                object of class `clusbootglm`.  
 confint.level       level of the confidence interval.

**Value**

`emmeans` returns an object of class `clusbootemm`, containing the following components:

`grid`                Grid with estimated marginal means for each combination of levels of the variables.  
`bootstrapsample.emm`        $p \times B$  matrix, with  $p$  being the number of estimates and  $B$  being the number of bootstrap samples.

**Author(s)**

Mathijs Deen

**Examples**

```
## Not run:
medication <- medication[medication$time %% 1 == 0,]
medication$time_f <- as.factor(medication$time)
set.seed(1)
model.1 <- clusbootglm(pos~time_f*treat, clusterid = id, data = medication)
emm.1 <- emm(object = model.1)
summary(object = emm.1)
## End(Not run)
```

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medication

*Medication data*

---

**Description**

The medication dataframe consists of 1242 observations within 73 individuals that were part of a placebo controlled clinical trial, as reported in Tomarken, Shelton, Elkins, and Anderson (1997).

The data were retrieved from the accompanied website of Singer & Willett (2003), at <https://stats.idre.ucla.edu/other/examples>

**Usage**

medication

**Format**

the following variables are available:

- `id`: subject indicator
- `treat`: either placebo (0) or antidepressant (1)
- `time`: number of days since trial start.
- `pos`: positive affect. Higher scores indicate a more positive mood.

## References

- Singer, J.D., & Willett, J.B. (2003). *Applied longitudinal data analysis. Modeling change and event occurrence*. NY: Oxford University Press, Inc.
- Tomarken, A.J., Shelton, R.C., Elkins, L., & Anderson, T (1997). *Sleep deprivation and anti-depressant medication: Unique effects on positive and negative affect*. Poster session presented at the 9th annual meeting of the American Psychological Society, Washington, DC.

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opposites

*Opposites naming data*

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## Description

The opposites dataframe consists of 144 observations within 36 individuals that completed an inventory that assesses their performance on a timed cognitive task called "opposites naming".

The dataset does not contain the empirical data within 35 individuals from the experiment by Willett (1988), but a simulation based on the multilevel model from Singer & Willett (2003) within 36 individuals.

## Usage

opposites

## Format

the following variables are available:

- Subject: subject indicator
- Time: a time variable, ranging 0-3
- COG: cognitive skill, measured once (at time=0)
- SCORE: score on opposites naming task

## References

- Willett, J.B. (1988). Questions and answers in the measurement of change. In: E. Rothkopf (Ed.), *Review of research in education (1988-89)* (pp. 345-422). Washington, DC: American Educational Research Association.
- Singer, J.D., & Willett, J.B. (2003). *Applied longitudinal data analysis. Modeling change and event occurrence*. NY: Oxford University Press, Inc.

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plot.clusbootemm	<i>Plot estimated marginal means for a cluster bootstrap GLM</i>
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---

### Description

Plots the estimated marginal means of an `clusbootglm` object. Works with one within-subjects and/or one between-subjects variable.

### Usage

```
## S3 method for class 'clusbootemm'
plot(
  x,
  within,
  between,
  pch,
  lty,
  ylab = "Estimated marginal mean",
  xlab = "Within subject",
  ...
)
```

### Arguments

<code>x</code>	object of class <code>clusbootemm</code> .
<code>within</code>	within-subjects variable. Should be numeric or numerically labeled factor.
<code>between</code>	between-subjects variable.
<code>pch</code>	point character. Length must be equal to the number of between-subjects levels.
<code>lty</code>	linetype. Length must be equal to the number of between-subjects levels.
<code>ylab</code>	label for y-axis.
<code>xlab</code>	label for x-axis.
<code>...</code>	other arguments to be passed to the <code>plot</code> function (see <a href="#">par</a> ).

### Author(s)

Mathijs Deen

### Examples

```
## Not run:
medication <- medication[medication$time %% 1 == 0,]
medication$time_f <- as.factor(medication$time)
set.seed(1)
model.1 <- clusbootglm(pos~time_f*treat, clusterid=id, data=medication)
emm.1 <- emm(object = model.1)
plot(x = emm.1, within = time_f, between = treat, pch = c(15,17), lty = c(1,2))
## End(Not run)
```



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plot.clusbootptest	<i>Plot results of a permutation test</i>
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---

**Description**

Plot results of a permutation test performed with ptest

**Usage**

```
## S3 method for class 'clusbootptest'
plot(x, pcol = "red", pty = 1, mfrow = c(1, 1), ...)
```

**Arguments**

x	object of class clusbootptest
pcol	color of vertical line indicating the observed Welch t test statistic
pty	type of vertical line indicating the observed Welch t test statistic
mfrow	vector of length 2 indicating the numbers of rows and columns in which the histograms will be drawn on the device.
...	other arguments to be passed into the hist function.

**Author(s)**

Mathijs Deen, Mark de Rooij

**Examples**

```
## Not run:
medication <- medication[medication$time % 1 == 0,]
set.seed(1)
permtest.1 <- ptest(data = meds, outcome = pos, within = time, between = treat,
                    at.within = c(0,2,4,6), at.between = c(0,1), pn = 2000)
plot(permtest.1, pcol = "red", pty=2, mfrow = c(2,2), breaks="FD")
## End(Not run)
```

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ptest	<i>Permutation test for group differences at within-subject levels</i>
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---

**Description**

Perform permutation tests for differences between two groups at given within-subject levels in a long-formatted dataframe

**Usage**

```
ptest(
  data,
  outcome,
  within,
  between,
  at.within,
  at.between,
  pn = 1000,
  progress.bar = TRUE
)
```

**Arguments**

<code>data</code>	dataframe that contains the data in long format.
<code>outcome</code>	outcome variable (i.e., the variable for which the difference should be tested).
<code>within</code>	within-subject variable.
<code>between</code>	between-subjects variable.
<code>at.within</code>	determine for which within-subject levels (e.g., which timepoint) the difference should be tested.
<code>at.between</code>	determine the groups in the difference test (should always be of length 2).
<code>pn</code>	the number of permutations that should be performed.
<code>progress.bar</code>	indicates whether a progress bar will be shown.

**Details**

In every permutation cycle, the outcome variable gets permuted and the Welch t test statistic is calculated.

**Value**

ptest produces an object of class "clusbootptest", containing the following relevant components:

<code>perm.statistics</code>	A matrix of <code>length(at.within)</code> rows and <code>pn</code> columns, containing the Welch t-test statistics for all permutations within the <code>at.within</code> level in the columns. The first column contains the t statistic for the observed data.
<code>pvalues</code>	Data frame containing the p values for every <code>at.within</code> level.

**Author(s)**

Mathijs Deen, Mark de Rooij

**See Also**

A useful method for the obtained `clusbootptest` class object is [plot.clusbootptest](#).

**Examples**

```
## Not run:
medication <- medication[medication$time %% 1 == 0,]
set.seed(1)
permtest.1 <- ptest(data = meds, outcome = pos, within = time, between = treat,
                    at.within = c(0,2,4,6), at.between = c(0,1), pn = 2000)
permtest.1$pvalues
## End(Not run)
```

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summary.clusbootemm	<i>Summarize estimated marginal means for cluster bootstrap GLM into a grid</i>
---------------------	---

---

**Description**

Returns the summary of the EMM for a clusbootglm class object.

**Usage**

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

**Arguments**

object	object of class clusbootemm.
...	other arguments.

**Author(s)**

Mathijs Deen

**Examples**

```
## Not run:
medication <- medication[medication$time %% 1 == 0,]
medication$time_f <- as.factor(medication$time)
set.seed(1)
model.1 <- clusbootglm(pos~time_f*treat, clusterid=id, data=medication)
emm.1 <- emm(object = model.1)
summary(object = emm.1)
## End(Not run)
```

---

summary.clusbootglm	<i>Summarize output of cluster bootstrap GLM</i>
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---

**Description**

Returns the summary of an object of class clusbootglm.

**Usage**

```
## S3 method for class 'clusbootglm'  
summary(object, estimate.type = "bootstrap", interval.type = "BCa", ...)
```

**Arguments**

object	object of class clusbootglm.
estimate.type	specify which type of estimate should be returned, either bootstrap means (default) or GLM estimates from model fitted on original data.
interval.type	which confidence interval should be used. Options are parametric, percentile, and BCa intervals.
...	other arguments.

**Author(s)**

Mathijs Deen

**Examples**

```
## Not run:  
data(opposites)  
cbglm.1 <- clusbootglm(SCORE~Time*COG,data=opposites,clusterid=Subject)  
summary(cbglm.1, interval.type="percentile")  
## End(Not run)
```

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