

# Package ‘lcc’

April 29, 2019

**Type** Package

**Title** Longitudinal Concordance Correlation

**Version** 1.0.2

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**Description** Estimates the longitudinal concordance correlation to access the longitudinal agreement profile. The estimation approach implemented is variance components approach based on polynomial mixed effects regression model, as proposed by Oliveira, Hinde and Zocchi (2018) <doi:10.1007/s13253-018-0321-1>. In addition, non-parametric confidence intervals were implemented using percentile method or normal-approximation based on Fisher Z-transformation.

**Date** 2019-04-26

**Depends** R (>= 3.2.3), nlme (>= 3.1-124), ggplot2 (>= 2.2.1), grid (>= 3.2.3), gdata (>= 2.18.0), gridExtra (>= 2.3)

**Suggests** roxygen2 (>= 3.0.0), covr, testthat, MASS

**License** GPL (>= 2)

**Encoding** UTF-8

**Repository** CRAN

**NeedsCompilation** yes

**LazyData** true

**RoxygenNote** 6.1.1

**Date/Publication** 2019-04-29 08:10:03 UTC

## R topics documented:

hue . . . . .	2
lcc . . . . .	3

lccPlot . . . . .	7
simulated_hue . . . . .	9
simulated_hue_block . . . . .	9
summary.lcc . . . . .	10

<b>Index</b>	<b>12</b>
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hue	<i>Hue color data</i>
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### Description

An observational study conducted at the Vegetable Production Department at "Luiz de Queiroz" College of Agriculture/University of São Paulo in 2010/2011 to evaluate the peel color of 20 papaya fruits cv. Sunrise Solo over time. The color hue was measured on the equatorial region of each fruit using four points observed by the colorimeter and 1,000 points observed by the scanner. Thus, the circular mean hue was calculated for each fruit by each device at time  $t$ . The aim of the agreement study was to assess how well the colorimeter agreed with the scanner over time.

### Usage

data(hue)

### Format

A data frame with 554 observations on the mean hue variable. The format is:

H_mean	numeric; mean hue of papaya's peel
Method	a factor with levels Colorimeter, Scanner
Time	integer; time in days
Fruit	a factor with 20 levels; from 1 to 20 where each level is represented by one fruit.

### Source

Oliveira, T.P.; Hinde, J.; Zocchi S.S. Longitudinal Concordance Correlation Function Based on Variance Components: An Application in Fruit Color Analysis. *Journal of Agricultural, Biological, and Environmental Statistics*, v. 23, n. 2, 233–254, 2018.

Oliveira, T.P.; Zocchi S.S.; Jacomino, A.P. Measuring color hue in 'Sunrise Solo' papaya using a flatbed scanner. *Rev. Bras. Frutic.*, v. 39, n. 2, e-911, 2017.

### References

Oliveira, T.P.; Hinde, J.; Zocchi S.S. Longitudinal Concordance Correlation Function Based on Variance Components: An Application in Fruit Color Analysis. *Journal of Agricultural, Biological, and Environmental Statistics*, v. 23, n. 2, 233–254, 2018.

**See Also**[lcc](#).**Examples**

```

data(hue)
summary(hue)
str(hue)
## Second degree polynomial model with random intercept, slope and
## quadratic term including an exponential variance function using
## time as covariate.
model<-lcc(dataset = hue, subject = "Fruit", resp = "H_mean",
           method = "Method", time = "Time", qf = 2, qr = 2,
           components = TRUE, time_lcc = list(from = min(hue$Time),
           to = max(hue$Time), n=40), var.class=varExp,
           weights.form="time")
summary(model, type="model")
summary(model, type="lcc")
## for discussion on the analysis of complete data set,
## see Oliveira et al. (2018)

```

lcc

*Longitudinal Concordance Correlation (LCC) estimated by fixed effects and variance components of polynomial mixed-effects regression model*

**Description**

The `lcc` function gives fitted values and non-parametric bootstrap confidence intervals for LCC, longitudinal Pearson correlation (LPC), and longitudinal accuracy (LA) statistics. These statistics can be estimated using different structures for the variance-covariance matrix for random effects and variance functions to model heteroscedasticity among the within-group errors using or not the time as a covariate.

**Usage**

```

lcc(dataset, resp, subject, method, time, interaction, qf,
     qr, covar, pdmat, var.class, weights.form, time_lcc, ci,
     percentileMet, alpha, nboot, show.warnings, components,
     REML, lme.control)

```

**Arguments**

dataset	an object of class <code>data.frame</code> .
resp	character string. Name of the response variable in the data set.
subject	character string. Name of the subject variable in the data set.
method	character string. Name of the method variable in the data set. The first level of method is used as the gold-standard method.

<code>time</code>	character string. Name of the time variable in the data set.
<code>interaction</code>	an option to estimate the interaction effect between <code>method</code> and <code>time</code> . If TRUE, the default, interaction effect is estimated. If FALSE only the main effects of <code>time</code> and <code>method</code> are estimated.
<code>qf</code>	an integer specifying the degree time polynomial trends, normally 1, 2 or 3. (Degree 0 is not allowed).
<code>qr</code>	an integer specifying random effects terms to account for subject-to-subject variation. Note that <code>qr=0</code> specifies a random intercept (form <code>~ 1 subject</code> ); <code>qr=1</code> specifies random intercept and slope (form <code>~ time subject</code> ). If <code>qr=qf=q</code> , with $q \geq 1$ , random effects at subject level are added to all terms of the time polynomial regression (form <code>~ time + time^2 + ... + time^q subject</code> ).
<code>covar</code>	character vector. Name of the covariates to be included in the model as fixed effects. Default to NULL, never include.
<code>pdmat</code>	standard classes of positive-definite matrix structures defined in the <code>pdClasses</code> function. The different positive-definite matrices structures available in the <code>lcc</code> function are <code>pdSymm</code> , the default, <code>pdLogChol</code> , <code>pdDiag</code> , <code>pdIdent</code> , <code>pdCompSymm</code> , and <code>pdNatural</code> .
<code>var.class</code>	standard classes of variance functions to model the variance structure of within-group errors using covariates, see <code>varClasses</code> . Default to NULL, correspond to homoscedastic within-group errors. Available standard classes: <b>varIdent:</b> allows different variances according to the levels of the stratification variable. <b>varExp:</b> exponential function of the variance covariate; see <code>varExp</code> .
<code>weights.form</code>	character string. An one-sided formula specifying a variance covariate and, optionally, a grouping factor for the variance parameters in the <code>var.class</code> . If <code>var.class=varIdent</code> , the option “method”, form <code>~1 method</code> or “time.ident”, form <code>~1 time</code> , must be used in the <code>weights.form</code> argument. If <code>var.class=varExp</code> , the option “time”, form <code>~time</code> , or “both”, form <code>~time method</code> , must be used in the <code>weights.form</code> argument.
<code>time_lcc</code>	regular sequence for time variable merged with specific or experimental time values used for LCC, LPC, and LA predictions. Default is NULL. The list may contain the following components: <b>time:</b> a vector of specific or experimental time values of given length. The experimental time values are used as default. <b>from:</b> the starting (minimum) value of time variable. <b>to:</b> the end (maximum) value of time variable. <b>n:</b> an integer specifying the desired length of the sequence. Generally, <code>n</code> between 30 and 50 is adequate.
<code>ci</code>	an optional non-parametric bootstrap confidence interval calculated for the LCC, LPC and LA statistics. If TRUE confidence intervals are calculated and printed in the output. Default is FALSE.
<code>percentileMet</code>	an optional method for calculating the non-parametric bootstrap intervals. If FALSE, the default, is the normal approximation method. If TRUE, the percentile method is used instead.

alpha	significance level. Default is 0.05.
nboot	an integer specifying the number of bootstrap samples. Default is 5,000.
show.warnings	an optional argument that shows the number of convergence errors in the bootstrap samples. If TRUE shows in which bootstrap sample the error occurred. If FALSE, the default, shows the total number of convergence errors.
components	an option to print LPC and LA statistics. If TRUE the estimates and confidence intervals for LPC and LA are printed in the output. If FALSE, the default, provides estimates and confidence interval only for the LCC statistic.
REML	if TRUE, the default, the model is fit by maximizing the restricted log-likelihood. If FALSE the log-likelihood is maximized.
lme.control	a list of control values for the estimation algorithm to replace the default values of the function <code>lmeControl</code> available in the <code>nlme</code> package. Defaults to an empty list. The returned list is used as the control argument for the <code>lme</code> function.

### Value

an object of class `lcc`. The output is a list with the following components:

model	summary of the polynomial mixed-effects regression model.
summary.lcc	summary of the fitted and sampled values, and the concordance correlation coefficient between them as goodness of fit (gof)
dataset	the input dataset.

### Author(s)

Thiago de Paula Oliveira, <thiago.paula.oliveira@usp.br>, Rafael de Andrade Moral, John Hinde, Silvio Sandoval Zocchi, Clarice Garcia Borges Demetrio

### References

Lin, L. A Concordance Correlation Coefficient to Evaluate Reproducibility. *Biometrics*, 45, n. 1, 255-268, 1989.

Oliveira, T.P.; Hinde, J.; Zocchi S.S. Longitudinal Concordance Correlation Function Based on Variance Components: An Application in Fruit Color Analysis. *Journal of Agricultural, Biological, and Environmental Statistics*, v. 23, n. 2, 233–254, 2018.

### See Also

[summary.lcc](#), [lccPlot](#), [lmeControl](#)

### Examples

```
data(hue)
## Second degree polynomial model with random intercept, slope and
## quadratic term
fm1<-lcc(dataset = hue, subject = "Fruit", resp = "H_mean",
         method = "Method", time = "Time", qf = 2, qr = 2)
summary(fm1)
```

```
summary(fm1, type="model")
lccPlot(fm1)

## Estimating longitudinal Pearson correlation and longitudinal
#accuracy
fm2<-lcc(dataset = hue, subject = "Fruit", resp = "H_mean",
         method = "Method", time = "Time", qf = 2, qr = 2,
         components = TRUE)
summary(fm2)
lccPlot(fm2)

## Not run:
## A grid of points as the Time variable for prediction
fm3<-lcc(dataset = hue, subject = "Fruit", resp = "H_mean",
         method = "Method", time = "Time", qf = 2, qr = 2,
         components = TRUE, time_lcc = list(from = min(hue$Time),
         to = max(hue$Time), n=40))
summary(fm3)
lccPlot(fm3)

## End(Not run)

## Including an exponential variance function using time as a
#covariate.
fm4<-lcc(dataset = hue, subject = "Fruit", resp = "H_mean",
         method = "Method", time = "Time", qf = 2, qr = 2,
         components = TRUE, time_lcc = list(from = min(hue$Time),
         to = max(hue$Time), n=40), var.class=varExp,
         weights.form="time")
summary(fm4)
lccPlot(fm4)

## Not run:
## Non-parametric confidence interval with 500 bootstrap samples
fm5<-lcc(dataset = hue, subject = "Fruit", resp = "H_mean",
         method = "Method", time = "Time", qf = 2, qr = 2,
         ci = TRUE, nboot = 500)
summary(fm5)
lccPlot(fm5)

## End(Not run)

## Considering three methods of color evaluation
## Not run:
data(simulated_hue)
attach(simulated_hue)
fm6<-lcc(dataset = simulated_hue, subject = "Fruit",
         resp = "Hue", method = "Method", time = "Time",
         qf = 2, qr = 1, components = TRUE,
         time_lcc = list(n=50, from=min(Time), to=max(Time)))
summary(fm6)
lccPlot(fm6)
detach(simulated_hue)
```

```
## End(Not run)

## Including an additional covariate in the linear predictor
## (randomized block design)
## Not run:
data(simulated_hue_block)
attach(simulated_hue_block)
fm7<-lcc(dataset = simulated_hue_block, subject = "Fruit",
         resp = "Hue", method = "Method", time = "Time",
         qf = 2, qr = 1, components = TRUE, covar = c("Block"),
         time_lcc = list(n=50, from=min(Time), to=max(Time)))
summary(fm7)
lccPlot(fm7)
detach(simulated_hue_block)

## End(Not run)
```

---

lccPlot

*Plot an lcc object*


---

### Description

A plot of predictions versus the time covariate is generated. Predicted values are joined by lines while sampled observations are represented by circles. If the argument `components=TRUE` is considered in the `lcc` object, single plots of each statistics are returned on different pages.

### Usage

```
lccPlot(obj, type, control, ...)
```

### Arguments

<code>obj</code>	an object inheriting from class "lcc", representing a fitted lcc model.
<code>type</code>	character string. If <code>type = "lcc"</code> , the output is the LCC plot; if <code>type = "lpc"</code> , the output is the LPC plot; and if <code>type = "la"</code> the output is the LA plot. Types "lpc" and "la" are available only if <code>components = TRUE</code> .
<code>control</code>	a list of control values or character strings returned by the function <code>plotControl</code> . Defaults to an empty list. The list may contain the following components: <ul style="list-style-type: none"> <li><code>shape</code>: draw points considering a shape parameter. Possible shape values are the numbers 0 to 25, and 32 to 127; see <a href="#">aes_linetype_size_shape</a>. Default is 1.</li> <li><code>colour</code>: specification for lines color. Default is "black".</li> <li><code>size</code>: specification for lines size. Should be specified with a numerical value (in millimetres); see <a href="#">aes_linetype_size_shape</a>. Default is 0.5.</li> <li><code>xlab</code>: title for the x axis. Default is "Time".</li> </ul>

`ylab`: title for the y axis. Default is "LCC", "LPC", or "LA"  
`scale_y_continuous`: numeric vector of length two providing limits of the scale. Default is `c(0,1)`.  
`all.plot`: viewport functions for the lcc class. If TRUE, the default, returns an object created by the `viewport` function with multiple plots on a single page. If FALSE returns a single `ggplot` object by different pages using the `marrangeGrob` function.  
`...` not used.

### Author(s)

Thiago de Paula Oliveira, <thiago.paula.oliveira@usp.br>

### References

Lin, L. A Concordance Correlation Coefficient to Evaluate Reproducibility. *Biometrics*, 45, n. 1, 255-268, 1989.  
 Oliveira, T.P.; Hinde, J.; Zocchi S.S. Longitudinal Concordance Correlation Function Based on Variance Components: An Application in Fruit Color Analysis. *Journal of Agricultural, Biological, and Environmental Statistics*, v. 23, n. 2, 233–254, 2018.

### See Also

[lcc](#).

### Examples

```

data(hue)
## Second degree polynomial model with random intercept, slope and
## quadratic term
fm1<-lcc(dataset = hue, subject = "Fruit", resp = "H_mean",
         method = "Method", time = "Time", qf = 2, qr = 2,
         components=TRUE)
lccPlot(fm1, type="lcc")
lccPlot(fm1, type="lpc")
lccPlot(fm1, type="la")

## Runing all.plots = FALSE and saving plots as pdf
## Not run:
data(simulated_hue_block)
attach(simulated_hue_block)
fm2<-lcc(dataset = simulated_hue_block, subject = "Fruit",
         resp = "Hue", method = "Method", time = "Time",
         qf = 2, qr = 1, components = TRUE, covar = c("Block"),
         time_lcc = list(n=50, from=min(Time), to=max(Time)))
ggsave("myplots.pdf",
       lccPlot(fm2, type="lcc", control=list(all.plot=FALSE)))

## End(Not run)
  
```



---

simulated_hue	<i>Hue color simulated data</i>
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---

**Description**

Simulated hue data set based on papaya's maturation over time considering three methods of measurement.

**Usage**

```
data(simulated_hue)
```

**Format**

A simulated data frame with 6,000 observations on the mean hue variable. The format is:

Hue	numeric; mean hue of papaya's peel
Method	a factor with levels labelled from Method 1 to Method 3
Time	integer; time in days from 0 to 19
Fruit	a factor with 100 levels labelled from 1 to 100 where each level is represented by one fruit.

**Details**

A total of 100 fruits were observed over 20 days by three methods to evaluate the mean hue of fruit's peel. The aim of the agreement study was to assess how well the methods 2, and 3 agreed with method 1 over time.

**See Also**

[lcc](#).

**Examples**

```
data(simulated_hue)
summary(simulated_hue)
str(simulated_hue)
```

---

simulated_hue_block	<i>Hue color simulated data in a randomized block design</i>
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---

**Description**

Simulated hue data set based on papaya's maturation over time considering four methods of measurement in a randomized block design.

**Usage**

```
data(simulated_hue_block)
```

**Format**

A simulated data frame with 24,000 observations on the mean hue variable. The format is:

Hue	numeric; mean hue of papaya's peel
Block	factor with levels labelled from 1 to 3
Method	a factor with levels labelled from Method 1, to Method 4
Time	integer; time in days from 0 to 19
Fruit	a factor with 300 levels labelled from 1 to 300 where each level is represented by one fruit.

**Details**

A total of 100 fruits by block were observed over 20 days by four methods to evaluate the mean hue of fruit's peel. We considered three blocks in this simulation. The aim of the agreement study was to assess how well the methods 2, 3, and 4 agreed with method 1 over time.

**See Also**

[lcc](#).

**Examples**

```
data(simulated_hue_block)
summary(simulated_hue_block)
str(simulated_hue_block)
```

---

summary.lcc

*Summarize an lcc object*

---

**Description**

Additional information about the fit of longitudinal concordance correlation, longitudinal Pearson correlation, and longitudinal accuracy represented by an object of class [lcc](#). The returned object has a [print](#) method.

**Usage**

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

**Arguments**

object	an object inheriting from class <code>lcc</code> , representing a fitted longitudinal concordance correlation function.
type	an optional character string specifying the type of output to be returned. If <code>type="model"</code> , prints the summary of the polynomial mixed-effects regression model. If <code>type="lcc"</code> , prints the summary of the fitted and sampled values for LCC, LPC, and LA as well as the concordance correlation coefficient between fitted LCC values and sampled values as goodness of fit (gof). Defaults to <code>type="lcc"</code> .
...	not used.

**Value**

an object inheriting from class `summary.lcc` including:

fitted	the fitted values extracted from the <code>lcc</code> object.
sampled	the sampled values extracted from the <code>lcc</code> object.
gof	goodness of fit value based on concordance correlation coefficient between fitted and sampled values.

**Author(s)**

Thiago de Paula Oliveira, <thiago.paula.oliveira@usp.br>, Rafael de Andrade Moral

**References**

Lin, L. A Concordance Correlation Coefficient to Evaluate Reproducibility. *Biometrics*, 45, n. 1, 255-268, 1989.

Oliveira, T.P.; Hinde, J.; Zocchi S.S. Longitudinal Concordance Correlation Function Based on Variance Components: An Application in Fruit Color Analysis. *Journal of Agricultural, Biological, and Environmental Statistics*, v. 23, n. 2, 233–254, 2018.

**See Also**

[lcc](#).

**Examples**

```
data(hue)
## Second degree polynomial model with random intercept, slope and
## quadratic term
fm1<-lcc(dataset = hue, subject = "Fruit", resp = "H_mean",
         method = "Method", time = "Time", qf = 2, qr = 2)
summary(fm1, type="model")
summary(fm1, type="lcc")
```

# Index

- \*Topic **datasets**
  - hue, [2](#)
  - simulated\_hue, [9](#)
  - simulated\_hue\_block, [9](#)
- \*Topic **ggplot2**
  - lcc, [3](#)
- \*Topic **nlme**
  - lcc, [3](#)
  
- aes\_linetype\_size\_shape, [7](#)
  
- ggplot, [8](#)
  
- hue, [2](#)
  
- lcc, [3](#), [3](#), [8–11](#)
- lccPlot, [5](#), [7](#)
- lmeControl, [5](#)
  
- marrangeGrob, [8](#)
  
- nlme, [5](#)
  
- pdClasses, [4](#)
- plotControl, [7](#)
- print, [10](#)
  
- simulated\_hue, [9](#)
- simulated\_hue\_block, [9](#)
- summary.lcc, [5](#), [10](#)
  
- varClasses, [4](#)
- varExp, [4](#)
- viewport, [8](#)