Package ‘concurve’

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Type Package

Title Computes and Plots Compatibility (Confidence) Intervals, P-Values, S-Values, & Likelihood Intervals to Form Consonance, Surprisal, & Likelihood Functions

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Description Allows one to compute compatibility (confidence) intervals for various statistical tests along with their corresponding P-values, S-values, and likelihoods. The intervals can be plotted to create consonance, surprisal, and likelihood functions allowing one to see what effect sizes are compatible with the test model at various compatibility levels rather than being limited to one interval estimate such as 95% [.]. Functions can also be compared to one another to see how much they overlap with one another and differ. Results can also be exported for Word, Powerpoint, and TeX documents. The package currently supports bootstrapping, linear models, generalized linear models, linear mixed-effects models, survival analysis, and meta-analysis. These methods are discussed by Poole C. (1987) <doi:10.2105/AJPH.77.2.195>, Schweder T, Hjort NL. (2002) <doi:10.1111/1467-9469.00285>, Singh K, Xie M, Strawderman WE. (2007) <arXiv:0708.0976>, Rothman KJ, Greenland S, Lash TL. (2008, ISBN:9781451190052), Greenland S. (2019) <doi:10.1080/00031305.2018.1529625>, Chow ZR, Greenland S. (2019) <arXiv:1909.08579>, and Greenland S, Chow ZR. (2019) <arXiv:1909.08583>.

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BugReports https://github.com/zadrafi/concurve/issues

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\begin{verbatim}
curve_boot Generate Consonance Functions via Bootstrapping
\end{verbatim}

Description

Use the Bca bootstrap method and the t-boostrap method from the bcaboot and boot packages to generate consonance distributions.
Usage

curve_boot(data = data, func = func, method = "bca", t0, tt, bb,
replicates = 2000, steps = 1000, table = TRUE)

Arguments

data
Dataset that is being used to create a consonance function.

func
Custom function that is used to create parameters of interest that will be bootstrapped.

method
The bootstrap method that will be used to generate the functions. Methods include "bca" which is the default, "bcapar", which is parametric bootstrapping using the bca method and "t", for the t-bootstrap/percentile method.

t0
Only used for the "bcapar" method. Observed estimate of theta, usually by maximum likelihood.

tt
Only used for the "bcapar" method. A vector of parametric bootstrap replications of theta of length B, usually large, say B = 2000

bb
Only used for the "bcapar" method. A B by p matrix of natural sufficient vectors, where p is the dimension of the exponential family.

replicates
Indicates how many bootstrap replicates are to be performed. The default is currently 20000 but more may be desirable, especially to make the functions more smooth.

steps
Indicates how many consonance intervals are to be calculated at various levels. For example, setting this to 100 will produce 100 consonance intervals from 0 to 100. Setting this to 10000 will produce more consonance levels. By default, it is set to 1000. Increasing the number substantially is not recommended as it will take longer to produce all the intervals and store them into a dataframe.

table
Indicates whether or not a table output with some relevant statistics should be generated. The default is TRUE and generates a table which is included in the list object.

Value

A list with 7 items where the dataframe of standard values is in the first list and the table for it in the second if table = TRUE. The Bca intervals and table are found in the third and fourth list. The values for the density function are in the fifth object, while the Bca stats are in the sixth and seventh objects.

curve_compare

Compare Two Functions and Produces An AUC Score

Description

Compares the p-value/s-value, and likelihood functions and computes an AUC number.
Usage

curve_compare(data1, data2, type = "c", plot = TRUE, ...)

Arguments

data1 The first dataframe produced by one of the interval functions in which the intervals are stored.

data2 The second dataframe produced by one of the interval functions in which the intervals are stored.

type Choose whether to plot a "consonance" function, a "surprisal" function or "likelihood". The default option is set to "c". The type must be set in quotes, for example curve_compare (type = "s") or curve_compare(type = "c"). Other options include "pd" for the consonance distribution function, and "cd" for the consonance density function, "l1" for relative likelihood, "l2" for log-likelihood, "l3" for likelihood and "d" for deviance function.

plot by default it is set to TRUE and will use the plot_compare() function to plot the two functions.

... Can be used to pass further arguments to plot_compare().

Value

Computes an AUC score and returns a plot that graphs two functions.

See Also

plot_compare()
ggcurve()
curve_table()

Examples

library(concurve)
GroupA <- rnorm(50)
GroupB <- rnorm(50)
RandomData <- data.frame(GroupA, GroupB)
intervalsdf <- curve_mean(GroupA, GroupB, data = RandomData)
GroupA2 <- rnorm(50)
GroupB2 <- rnorm(50)
RandomData2 <- data.frame(GroupA2, GroupB2)
model <- lm(GroupA2 ~ GroupB2, data = RandomData2)
randomframe <- curve_gen(model, "GroupB2")
curve_compare(intervalsdf[[1]], randomframe[[1]])
curve_compare(intervalsdf[[1]], randomframe[[1]], type = "s")
Description

Computes consonance intervals to produce P- and S-value functions for correlational analyses using the cor.test function in base R and places the interval limits for each interval level into a data frame along with the corresponding p-values and s-values.

Usage

curve_corr(x, y, alternative, method, steps = 10000, table = TRUE)

Arguments

x A vector that contains the data for one of the variables that will be analyzed for correlational analysis.

y A vector that contains the data for one of the variables that will be analyzed for correlational analysis.

alternative Indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association.

method A character string indicating which correlation coefficient is to be used for the test. One of "pearson", "kendall", or "spearman", can be abbreviated.

steps Indicates how many consonance intervals are to be calculated at various levels. For example, setting this to 100 will produce 100 consonance intervals from 0 to 100. Setting this to 10000 will produce more consonance levels. By default, it is set to 1000. Increasing the number substantially is not recommended as it will take longer to produce all the intervals and store them into a dataframe.

table Indicates whether or not a table output with some relevant statistics should be generated. The default is TRUE and generates a table which is included in the list object.

Value

A list with 3 items where the dataframe of values is in the first object, the values needed to calculate the density function in the second, and the table for the values in the third if table = TRUE.

Examples

GroupA <- rnorm(50)
GroupB <- rnorm(50)
joe <- curve_corr(x = GroupA, y = GroupB, alternative = "two.sided", method = "pearson")
curve_gen

Consonance Functions For Linear Models, Generalized Linear Models, and Robust Linear Models

Description

Computes thousands of consonance (confidence) intervals for the chosen parameter in the selected model (ANOVA, ANCOVA, regression, logistic regression) and places the interval limits for each interval level into a data frame along with the corresponding p-values and s-values.

Usage

curve_gen(model, var, method = "lm", steps = 1000, table = TRUE)

Arguments

model

The statistical model of interest (ANOVA, regression, logistic regression) is to be indicated here.

var

The variable of interest from the model (coefficients, intercept) for which the intervals are to be produced.

method

Chooses the method to be used to calculate the consonance intervals. There are currently three methods: "lm", "rlm", "glm" and "aov". The "lm" method uses the profile likelihood method to compute intervals and can be used for models created by the 'lm' function. It is typically what most people are familiar with when computing intervals based on the calculated standard error. The "rlm" method is designed for usage with the "rlm" function from the MASS package. The "glm" method allows this function to be used for specific scenarios like logistic regression and the 'glm' function.

steps

Indicates how many consonance intervals are to be calculated at various levels. For example, setting this to 100 will produce 100 consonance intervals from 0 to 100. Setting this to 10000 will produce more consonance levels. By default, it is set to 1000. Increasing the number substantially is not recommended as it will take longer to produce all the intervals and store them into a dataframe.

table

Indicates whether or not a table output with some relevant statistics should be generated. The default is TRUE and generates a table which is included in the list object.

Value

A list with 3 items where the dataframe of values is in the first object, the values needed to calculate the density function in the second, and the table for the values in the third if table = TRUE.
Examples

# Simulate random data
GroupA <- rnorm(50)
GroupB <- rnorm(50)
RandomData <- data.frame(GroupA, GroupB)
rob <- lm(GroupA ~ GroupB, data = RandomData)
bob <- curve_gen(rob, "GroupB")

curve_lik

Compute Profile Likelihood Functions

Description

Compute Profile Likelihood Functions

Usage

curve_lik(likobject, data, table = TRUE)

Arguments

likobject          An object from the ProfileLikelihood package
data               The dataframe that was used to create the likelihood object in the ProfileLikelihood package.
table              Indicates whether or not a table output with some relevant statistics should be generated. The default is TRUE and generates a table which is included in the list object.

Value

A list with 2 items where the dataframe of values is in the first object, and the table for the values in the second if table = TRUE.

Examples

library(ProfileLikelihood)
data(dataglm)
xx <- profilelike.glm(y ~ x1 + x2, dataglm, profile.theta = "group", binomial("logit"))
lik <- curve_lik(xx, dataglm)
curve_lmer

Consonance Functions For Linear & Non-Linear Mixed-Effects Models.

Description

Computes thousands of consonance (confidence) intervals for the chosen parameter in the selected lme4 model and places the interval limits for each interval level into a data frame along with the corresponding p-values and s-values.

Usage

curve_lmer(object, parm, method = "profile", zeta = NULL, nsim = NULL, 
FUN = NULL, boot.type = NULL, steps = 1000, mc.cores = 1, 
table = FALSE)

Arguments

object The statistical model of interest from lme4 is to be indicated here.
parm The variable of interest from the model (coefficients, intercept) for which the intervals are to be produced.
method Chooses the method to be used to calculate the consonance intervals. There are currently four methods: "default", "wald", "lm", and "boot". The "default" method uses the profile likelihood method to compute intervals and can be used for models created by the 'lm' function. The "wald" method is typically what most people are familiar with when computing intervals based on the calculated standard error. The "lm" method allows this function to be used for specific scenarios like logistic regression and the 'glm' function. The "boot" method allows for bootstrapping at certain levels.
zeta (for method = "profile" only:) likelihood cutoff (if not specified, as by default, computed from level).
nsim number of simulations for parametric bootstrap intervals.
FUN function; if NULL, an internal function that returns the fixed-effect parameters as well as the random-effect parameters on the standard deviation/correlationscale will be used.
boot.type bootstrap confidence interval type, as described in boot.c i. Methods stud and bca are unavailable because they require additional components to be calculated.
steps Indicates how many consonance intervals are to be calculated at various levels. For example, setting this to 100 will produce 100 consonance intervals from 0 to 100. Setting this to 10000 will produce more consonance levels. By default, it is set to 1000. Increasing the number substantially is not recommended as it will take longer to produce all the intervals and store them into a data frame.
mc.cores For parallel processing. Defaults to 1 core.
table Indicates whether or not a table output with some relevant statistics should be generated. The default is TRUE and generates a table which is included in the list object.
\textit{curve\_mean}

\textbf{Value}

A list with 3 items where the dataframe of values is in the first object, the values needed to calculate the density function in the second, and the table for the values in the third if \texttt{table = TRUE}.

---

\textbf{Description}

Computes thousands of consonance (confidence) intervals for the chosen parameter in a statistical test that compares means and places the interval limits for each interval level into a data frame along with the corresponding p-values and s-values.

\textbf{Usage}

\begin{verbatim}
curve_mean(x, y, data, paired = F, method = "default", replicates = 1000, steps = 10000, table = TRUE)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{x} Variable that contains the data for the first group being compared.
  \item \texttt{y} Variable that contains the data for the second group being compared.
  \item \texttt{data} Data frame from which the variables are being extracted from.
  \item \texttt{paired} Indicates whether the statistical test is a paired difference test. By default, it is set to "F", which means the function will be an unpaired statistical test comparing two independent groups. Inserting "paired" will change the test to a paired difference test.
  \item \texttt{method} By default this is turned off (set to "default"), but allows for bootstrapping if "boot" is inserted into the function call.
  \item \texttt{replicates} Indicates how many bootstrap replicates are to be performed. The default is currently 20000 but more may be desirable, especially to make the functions more smooth.
  \item \texttt{steps} Indicates how many consonance intervals are to be calculated at various levels. For example, setting this to 100 will produce 100 consonance intervals from 0 to 100. Setting this to 10000 will produce more consonance levels. By default, it is set to 1000. Increasing the number substantially is not recommended as it will take longer to produce all the intervals and store them into a data frame.
  \item \texttt{table} Indicates whether or not a table output with some relevant statistics should be generated. The default is TRUE and generates a table which is included in the list object.
\end{itemize}

\textbf{Value}

A list with 3 items where the dataframe of values is in the first object, the values needed to calculate the density function in the second, and the table for the values in the third if \texttt{table = TRUE}. 

---
Examples

```r
# Simulate random data
GroupA <- runif(100, min = 0, max = 100)
GroupB <- runif(100, min = 0, max = 100)
RandomData <- data.frame(GroupA, GroupB)
bob <- curve_mean(GroupA, GroupB, RandomData)
```

Curve Meta

Consonance Functions For Meta-Analytic Data

Description

Computes thousands of consonance (confidence) intervals for the chosen parameter in the meta-
analysis done by the metafor package and places the interval limits for each interval level into a
data frame along with the corresponding p-values and s-values.

Usage

```r
curve_meta(x, measure = "default", method = "uni", robust = FALSE,
          cluster = NULL, adjust = FALSE, steps = 1000, table = TRUE)
```

Arguments

- **x**: Object where the meta-analysis parameters are stored, typically a list produced by 'metafor'
- **measure**: Indicates whether the object has a log transformation or is normal/default. The
default setting is "default. If the measure is set to "ratio", it will take logarithmically transformed values and convert them back to normal values in the
dataframe. This is typically a setting used for binary outcomes such as risk ratios, hazard ratios, and odds ratios.
- **method**: Indicates which meta-analysis metafor function is being used. Currently sup-
ports rma.uni ("uni"), which is the default, rma.mh ("mh"), and rma.peto ("peto")
- **robust**: a logical indicating whether to produce cluster robust interval estimates Default
  is FALSE.
- **cluster**: a vector specifying a clustering variable to use for constructing the sandwich
  estimator of the variance-covariance matrix. Default setting is NULL.
- **adjust**: logical indicating whether a small-sample correction should be applied to the
  variance-covariance matrix. Default is FALSE.
- **steps**: Indicates how many consonance intervals are to be calculated at various levels. For example, setting this to 100 will produce 100 consonance intervals from 0 to 100. Setting this to 10000 will produce more consonance levels. By default, it is set to 1000. Increasing the number substantially is not recommended as it will take longer to produce all the intervals and store them into a dataframe.
- **table**: Indicates whether or not a table output with some relevant statistics should be
  generated. The default is TRUE and generates a table which is included in the
  list object.
Value

A list with 3 items where the dataframe of values is in the first object, the values needed to calculate the density function in the second, and the table for the values in the third if table = TRUE.

Examples

```r
# Simulate random data for two groups in two studies
GroupAData <- runif(20, min = 0, max = 100)
GroupAMean <- round(mean(GroupAData), digits = 2)
GroupASD <- round(sd(GroupAData), digits = 2)

GroupBDData <- runif(20, min = 0, max = 100)
GroupBMean <- round(mean(GroupBDData), digits = 2)
GroupBSD <- round(sd(GroupBDData), digits = 2)

GroupCDData <- runif(20, min = 0, max = 100)
GroupCMean <- round(mean(GroupCDData), digits = 2)
GroupCSD <- round(sd(GroupCDData), digits = 2)

GroupDDData <- runif(20, min = 0, max = 100)
GroupDMean <- round(mean(GroupDDData), digits = 2)
GroupDSD <- round(sd(GroupDDData), digits = 2)

# Combine the data
StudyName <- c("Study1", "Study2")
MeanTreatment <- c(GroupAMean, GroupCMean)
MeanControl <- c(GroupBMean, GroupDMean)
SDTreatment <- c(GroupASD, GroupCSD)
SDControl <- c(GroupBSD, GroupDSD)
NTreatment <- c(20, 20)
NControl <- c(20, 20)

metadf <- data.frame(
  StudyName, MeanTreatment, MeanControl,
  SDTreatment, SDControl, NTreatment, NControl
)

# Use metafor to calculate the standardized mean difference
library(metafor)

dat <- escalc(
  measure = "SMD", m1i = MeanTreatment, sd1i = SDTreatment,
  n1i = NTreatment, m2i = MeanControl, sd2i = SDControl,
  n2i = NControl, data = metadf
)

# Pool the data using a particular method. Here "FE" is the fixed-effects model
res <- rma(yi, vi,
```

data = dat, slab = paste(StudyName, sep = " ", " "),
method = "FE", digits = 2
)

# Calculate the intervals using the metainterval function
metaf <- curve_meta(res)

---

**curve_rev**

Reverse Engineer Consonance / Likelihood Functions Using the Point Estimate and Confidence Limits

**Description**

Using the confidence limits and point estimates from a dataset, one can use these estimates to compute thousands of consonance intervals and graph the intervals to form a consonance and surprisal function. The intervals are calculated from the approximated normal distribution.

**Usage**

```r
curve_rev(point, LL, UL, type = "c", measure = "default", steps = 10000,
table = TRUE)
```

**Arguments**

- **point** The point estimate from an analysis. Ex: 1.20
- **LL** The lower confidence limit from an analysis Ex: 1.0
- **UL** The upper confidence limit from an analysis Ex: 1.4
- **type** Indicates whether the produced result should be a consonance function or a likelihood function. The default is "c" for consonance and likelihood can be set via "l".
- **measure** The type of data being used. If they involve mean differences, then the "default" option should be used, which is also the default setting. If the data are ratios, then the "ratio" option should be used.
- **steps** Indicates how many consonance intervals are to be calculated at various levels. For example, setting this to 100 will produce 100 consonance intervals from 0 to 100. Setting this to 10000 will produce more consonance levels. By default, it is set to 1000. Increasing the number substantially is not recommended as it will take longer to produce all the intervals and store them into a dataframe.
- **table** Indicates whether or not a table output with some relevant statistics should be generated. The default is TRUE and generates a table which is included in the list object.

**Value**

A list with 3 items where the dataframe of values is in the first object, the values needed to calculate the density function in the second, and the table for the values in the third if table = TRUE.
See Also
ggcurve()
curve_compare()
plot_compare()

Examples

# From a real published study. Point estimate of the result was hazard ratio of 1.61 and
# lower bound of the interval is 0.997 while upper bound of the interval is 2.59.
#
df <- curve_rev(point = 1.61, LL = 0.997, UL = 2.59, measure = "ratio")

curve_surv  Consonance Functions For Survival Data

Description

Computes thousands of consonance (confidence) intervals for the chosen parameter in the Cox
model computed by the 'survival' package and places the interval limits for each interval level into
a data frame along with the corresponding p-value and s-value.

Usage

curve_surv(data, x, steps = 10000, table = TRUE)

Arguments

data Object where the Cox model is stored, typically a list produced by the 'survival'
package.
x Predictor of interest within the survival model for which the consonance inter-
vals should be computed.
steps Indicates how many consonance intervals are to be calculated at various levels.
For example, setting this to 100 will produce 100 consonance intervals from 0
to 100. Setting this to 10000 will produce more consonance levels. By default,
it is set to 1000. Increasing the number substantially is not recommended as it
will take longer to produce all the intervals and store them into a dataframe.
table Indicates whether or not a table output with some relevant statistics should be
generated. The default is TRUE and generates a table which is included in the
list object.

Value

A list with 3 items where the dataframe of values is in the first object, the values needed to calculate
the density function in the second, and the table for the values in the third if table = TRUE.
Examples

```r
library(carData)
Rossi[1:5, 1:10]
library(survival)

mod.allison <- coxph(Surv(week, arrest) ~ fin + age + race + wexp + mar + paro + prio, data = Rossi)
mod.allison
z <- curve_surv(mod.allison, "prio")
```

---

### curve_table

**Produce Tables For concurve Functions**

Produces publication-ready tables with relevant statistics of interest for functions produced from the concurve package.

**Usage**

```r
curve_table(data, levels, type = "c", format = "data.frame")
```

**Arguments**

- **data**
  - Dataframe from a concurve function to produce a table for

- **levels**
  - Levels of the consonance intervals or likelihood intervals that should be included in the table.

- **type**
  - Indicates whether the table is for a consonance function or likelihood function. The default is set to "c" for consonance and can be switched to "l" for likelihood.

- **format**
  - The format of the tables. The options include "data.frame" which is the default, "docx" (which creates a table for a word document), "pptx" (which creates a table for powerpoint), "latex", (which creates a table for a TeX document), and "image", which produces an image of the table.

**See Also**

- `ggcurve()`
- `curve_compare()`
- `plot_compare()`
Examples

```r
library(concurve)

GroupA <- rnorm(500)
GroupB <- rnorm(500)

RandomData <- data.frame(GroupA, GroupB)

intervalsdf <- curve_mean(GroupA, GroupB, data = RandomData, method = "default")

(z <- curve_table(intervalsdf[[1]], format = "data.frame"))
(z <- curve_table(intervalsdf[[1]], format = "latex"))
(z <- curve_table(intervalsdf[[1]], format = "image"))
```

**Description**

Takes the dataframe produced by the interval functions and plots the p-values/s-values, consonance (confidence) levels, and the interval estimates to produce a p-value/s-value function using ggplot2 graphics.

**Usage**

```r
ggcurve(data, type = "c", measure = "default", levels = 0.95,
       nullvalue = FALSE, position = "pyramid", title = "Interval Function",
       subtitle = "The function displays intervals at every level.",
       xaxis = expression(Theta ~ "Range of Values"),
       yaxis = expression(paste(italic(p), "-value")), color = "#000000",
       fill = "#239a98")
```

**Arguments**

- `data` The dataframe produced by one of the interval functions in which the intervals are stored.
- `type` Choose whether to plot a "consonance" function, a "surprisal" function or "likelihood". The default option is set to "c". The type must be set in quotes, for example `ggcurve(type = "s")` or `ggcurve(type = "c")`. Other options include "pd" for the consonance distribution function, and "cd" for the consonance density function, "l1" for relative likelihood, "l2" for log-likelihood, "l3" for likelihood and "d" for deviance function.
- `measure` Indicates whether the object has a log transformation or is normal/default. The default setting is "default". If the measure is set to "ratio", it will take logarithmically transformed values and convert them back to normal values in the dataframe. This is typically a setting used for binary outcomes and their measures such as risk ratios, hazard ratios, and odds ratios.
levels
Indicates which interval levels should be plotted on the function. By default it is set to 0.95 to plot the 95% interval on the consonance function, but more levels can be plotted by using the c() function for example, levels = c(0.50, 0.75, 0.95).

nullvalue
Indicates whether the null value for the measure should be plotted. By default, it is set to FALSE, meaning it will not be plotted as a vertical line. Changing this to TRUE, will plot a vertical line at 0 when the measure is set to "default" and a vertical line at 1 when the measure is set to "ratio". For example, ggcurve(type = "c", data = df, measure = "ratio", nullvalue = "present"). This feature is not yet available for surprisal functions.

position
Determines the orientation of the P-value (consonance) function. By default, it is set to "pyramid", meaning the p-value function will stand right side up, like a pyramid. However, it can also be inverted via the option "inverted". This will also change the sequence of the y-axes to match the orientation. This can be set as such, ggcurve(type = "c", data = df, position = "inverted").

title
A custom title for the graph. By default, it is set to "Consonance Function". In order to set a title, it must be in quotes. For example, ggcurve(type = "c", data = x, title = "Custom Title").

subtitle
A custom subtitle for the graph. By default, it is set to "The function contains consonance/confidence intervals at every level and the P-values." In order to set a subtitle, it must be in quotes. For example, ggcurve(type = "c", data = x, subtitle = "Custom Subtitle").

xaxis
A custom x-axis title for the graph. By default, it is set to "Range of Values." In order to set a x-axis title, it must be in quotes. For example, ggcurve(type = "c", data = x, xaxis = "Hazard Ratio").

yaxis
A custom y-axis title for the graph. By default, it is set to "Consonance Level". In order to set a y-axis title, it must be in quotes. For example, ggcurve(type = "c", data = x, yaxis = "Confidence Level").

color
Item that allows the user to choose the color of the points and the ribbons in the graph. By default, it is set to color = "#555555". The inputs must be in quotes. For example, ggcurve(type = "c", data = x, color = "#333333").

fill
Item that allows the user to choose the color of the ribbons in the graph. By default, it is set to fill = "#239a98". The inputs must be in quotes. For example, ggcurve(type = "c", data = x, fill = "#333333").

Value
A plot with intervals at every consonance level graphed with their corresponding p-values and compatibility levels.

See Also
plot_compare()

Examples

# Simulate random data
library(concurve)

GroupA <- rnorm(500)
GroupB <- rnorm(500)

RandomData <- data.frame(GroupA, GroupB)

intervalsdf <- curve_mean(GroupA, GroupB, data = RandomData, method = "default")
gcurve(type = "c", intervalsdf[[1]], nullvalue = TRUE)

### Description

Graph and Compare Consonance, Surprisal, and Likelihood Functions

Comparing the p-value/s-value, and likelihood functions using ggplot2 graphics.

### Usage

plot_compare(data1, data2, type = "c", measure = "default",
nullvalue = FALSE, position = "pyramid", title = "Interval Functions",
subtitle = "The function displays intervals at every level.",
       xaxis = expression(Theta ~ "Range of Values"),
       yaxis = expression(paste(italic(p), ", "-value")), color = "#000000",
       fill1 = "#239a98", fill2 = "#EE6A50")

### Arguments

**data1**
The first dataframe produced by one of the interval functions in which the intervals are stored.

**data2**
The second dataframe produced by one of the interval functions in which the intervals are stored.

**type**
Choose whether to plot a "consonance" function, a "surprisal" function or "likelihood". The default option is set to "c". The type must be set in quotes, for example plot_compare(type = "s") or plot_compare(type = "c"). Other options include "pd" for the consonance distribution function, and "cd" for the consonance density function, "l1" for relative likelihood, "l2" for log-likelihood, "l3" for likelihood and "d" for deviance function.

**measure**
Indicates whether the object has a log transformation or is normal/default. The default setting is "default". If the measure is set to "ratio", it will take logarithmically transformed values and convert them back to normal values in the dataframe. This is typically a setting used for binary outcomes and their measures such as risk ratios, hazard ratios, and odds ratios.
**nullvalue**
Indicates whether the null value for the measure should be plotted. By default, it is set to FALSE, meaning it will not be plotted as a vertical line. Changing this to TRUE, will plot a vertical line at 0 when the measure is set to "default" and a vertical line at 1 when the measure is set to "ratio". For example, `plot_compare(type = "c", data = df, measure = "ratio", nullvalue = "present")`. This feature is not yet available for surprisal functions.

**position**
Determines the orientation of the P-value (consonance) function. By default, it is set to "pyramid", meaning the p-value function will stand right side up, like a pyramid. However, it can also be inverted via the option "inverted". This will also change the sequence of the y-axes to match the orientation. This can be set as such, `plot_compare(type = "c", data = df, position = "inverted")`.

**title**
A custom title for the graph. By default, it is set to "Consonance Function". In order to set a title, it must be in quotes. For example, `plot_compare(type = "c", data = x, title = "Custom Title")`.

**subtitle**
A custom subtitle for the graph. By default, it is set to "The function contains consonance/confidence intervals at every level and the P-values." In order to set a subtitle, it must be in quotes. For example, `plot_compare(type = "c", data = x, subtitle = "Custom Subtitle")`.

**xaxis**
A custom x-axis title for the graph. By default, it is set to "Range of Values. In order to set a x-axis title, it must be in quotes. For example, `plot_compare(type = "c", data = x, xaxis = "Hazard Ratio")`.

**yaxis**
A custom y-axis title for the graph. By default, it is set to "Consonance Level". In order to set a y-axis title, it must be in quotes. For example, `plot_compare(type = "c", data = x, yaxis = "Confidence Level")`.

**color**
Item that allows the user to choose the color of the points and the ribbons in the graph. By default, it is set to color = "#555555". The inputs must be in quotes. For example, `plot_compare(type = "c", data = x, color = "#333333")`.

**fill1**
Item that allows the user to choose the color of the ribbons in the graph for data1. By default, it is set to fill1 = "#239a98". The inputs must be in quotes. For example, `plot_compare(type = "c", data = x, fill1 = "#333333")`.

**fill2**
Item that allows the user to choose the color of the ribbons in the graph for data1. By default, it is set to fill2 = "#d46c5b". The inputs must be in quotes. For example, `plot_compare(type = "c", data = x, fill2 = "#333333")`.

**Value**
A plot that compares two functions.

**See Also**
- `ggcurve()`
- `curve_compare()`

**Examples**

```r
library(concurve)
```

GroupA <- rnorm(50)
GroupB <- rnorm(50)
RandomData <- data.frame(GroupA, GroupB)
intervalsdf <- curve_mean(GroupA, GroupB, data = RandomData)
GroupA2 <- rnorm(50)
GroupB2 <- rnorm(50)
RandomData2 <- data.frame(GroupA2, GroupB2)
model <- lm(GroupA2 ~ GroupB2, data = RandomData2)

randomframe <- curve_gen(model, "GroupB2")

plot_compare(intervalsdf[[1]], randomframe[[1]], type = "c")
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