Package 'concurve'

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Type Package

Title Computes & Plots Compatibility (Confidence), Surprisal, & Likelihood Distributions

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Description
Computes compatibility (confidence) distributions along with their corresponding P-values, S-values, and likelihoods. The intervals can be plotted to form the distributions themselves. Functions can be compared to one another to see how much they overlap. Results can be exported to Microsoft Word, Powerpoint, and TeX documents. The package currently supports resampling methods, computing differences, generalized linear models, mixed-effects models, survival analysis, and meta-analysis. These methods are discussed by Schweder T, Hjort NL. (2016, ISBN:9781316445051) and Rafi Z, Greenland S. (2020) <doi:10.1186/s12874-020-01105-9>.

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URL https://data.lesslikely.com/concurve/, https://github.com/zadrafi/concurve

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

Depends R (>= 4.0.0)

Imports methods, bcaboot, boot, dplyr, flextable, ggplot2, knitr, metafor, officer, parallel, pbmcapply, ProfileLikelihood, scales, colorspace, survival, survminer, tibble, tidyr

Suggests MASS, lme4, covr, roxygen2, spelling, testthat, rmarkdown, Lock5Data, carData, bench, rms, brms, rstan, rstanarm, bayesplot, vdiffr, ggtext, daewr, svglite, data.table, nlme, simstudy, patchwork, cowplot, reprex

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`concurve-package` *A description of the* `concurve` R *package*

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%.

Package: concurve

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Details

Accepts most modeling functions that produce confidence intervals to construct distributions.

See the following articles::

- **Comparison to Bayesian Posterior Distributions**
- **The Bootstrap and Consonance Functions**
- **Background Literature**
- **Customizing Plots**
- **Examples in R**
- **Logistic Regression in R**
- **Profile Likelihoods**
- **Meta-Analysis Examples**
- **Survival Modeling**
- **S-values**
- **Generating Tables**
- **Troubleshooting**
- **Consonance Functions for Linear Mixed-Effects Models**
- **Wish List**

Author(s)

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References

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See Also

curve_gen, ggcurve, curve_table

`curve_boot` *Generate Consonance Functions via Bootstrapping*

Description

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

Usage

```
curve_boot(data = data, func = func, method = "bca", t0, tt, bb,
  replicates = 2000, steps = 1000, cores = getOption("mc.cores", 1L),
  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 boostrap 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.
cores	Select the number of cores to use in order to compute the intervals The default is 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.

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

```
## Not run:
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]])

## End(Not run)
```

curve_corr *Consonance Functions for Correlations*

Description

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

Usage

```
curve_corr(x, y, alternative, method, steps = 10000,
  cores = getOption("mc.cores", 1L), 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.
cores	Select the number of cores to use in order to compute the intervals The default is 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.

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

```
## Not run:
GroupA <- rnorm(50)
GroupB <- rnorm(50)
joe <- curve_corr(x = GroupA, y = GroupB, alternative = "two.sided", method = "pearson")

## End(Not run)
```

---

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 (linear models, general linear models, robust linear models, and generalized least squares and places the interval limits for each interval level into a data frame along with the corresponding p-values and s-values. Can also adjust for multiple comparisons. It is generally recommended to wrap this function using suppressMessages() due to the long list of profiling messages.

Usage

```
curve_gen(model, var, method = "lm", log = FALSE, penalty = NULL,
  m = NULL, steps = 1000, cores = getOption("mc.cores", 1L),
  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 five methods: "lm", rms::ols objects can be used with the "lm" option, "rlm", "glm" and "aov", and "gls". 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 ols function from the rms package can also be used for this option. 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. Similarly, the Glm function from the rms package can also be used for this option. The gls method allows objects from gls() or from Gls() from the rms package.

log	Determines whether the coefficients will be exponentiated or not. By default, it is off and set to FALSE or F, but changing this to TRUE or T, will exponentiate the results which may be useful if trying to view the results from a logistic regression on a scale that is not logarithmic.
penalty	An input to specify whether the confidence intervals should be corrected for multiple comparisons. The default is NULL, so there is no correction. Other options include "bonferroni" and "sidak".
m	Indicates how many comparisons are being done and the number that should be used to correct for multiple comparisons. The default is NULL.
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.
cores	Select the number of cores to use in order to compute the intervals The default is 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.

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

```
## Not run:
# 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")

## End(Not run)
```

---

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.. It is generally recommended to wrap this function using suppressMessages() due to the long list of profiling messages

Usage

```
curve_lmer(object, parm, method = "profile", zeta = NULL, nsim = NULL,
  FUN = NULL, boot.type = NULL, steps = 1000,
  cores = getOption("mc.cores", 1L), 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 typicallywhat

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 dataframe.

`cores` Select the number of cores to use in order to compute the intervals The default is 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.

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.

`curve_mean` *Consonance Functions For Mean Differences*

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.

Usage

```
curve_mean(x, y, data, paired = F, method = "default", replicates = 1000,
  steps = 10000, cores = getOption("mc.cores", 1L), table = TRUE)
```

Arguments

x	Variable that contains the data for the first group being compared.
y	Variable that contains the data for the second group being compared.
data	Data frame from which the variables are being extracted from.
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.
method	By default this is turned off (set to "default"), but allows for bootstrapping if "boot" is inserted into the function call.
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.
cores	Select the number of cores to use in order to compute the intervals The default is 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.

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

```
## Not run:
# 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)

## End(Not run)
```

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

```
curve_meta(x, measure = "default", method = "uni", parm = NULL,
  robust = FALSE, cluster = NULL, adjust = FALSE, steps = 1000,
  cores = getOption("mc.cores", 1L), 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 supports rma.uni ("uni"), which is the default, rma.mh ("mh"), and rma.peto ("peto")
parm	Typically ignored, but needed sometimes in order to specify which variable to produce function for.
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
cores	Select the number of cores to use in order to compute the intervals The default is 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.

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

```
## Not run:
# 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)

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

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

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

## End(Not run)
```

---

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, surprisal, and likelihood functions. The intervals are calculated from the approximated normal distribution, however, users should be cautious as this this function is currently designed for similar situations (involving ratios and normal approximations), nevertheless the function also works for means but should be used skeptically, as it can break down in many situations and give implausible numbers. Computations of likelihood functions for means is currently not supported.

Usage

```
curve_rev(point, LL = NULL, UL = NULL, se = NULL, conf.level = 0.95,
  type = "c", measure = "ratio", steps = 10000,
  cores = getOption("mc.cores", 1L), 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
se	The standard error of the point estimate. Ex: 0.05
conf.level	Confidence level of the interval estimate.
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 "mean" option should be used. If the data are ratios, then the "ratio" option should be used. "ratio" is currently the default option. Currently, this function is designed to be used with ratios and normal approximations rather than means.

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.
cores	Select the number of cores to use in order to compute the intervals The default is 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.

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

```
## Not run:
# 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")

## End(Not run)
```

---

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, cores = getOption("mc.cores", 1L),
  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 intervals 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.
cores	Select the number of cores to use in order to compute the intervals The default is 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.

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

```
## Not run:
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")

## End(Not run)
```

---

curve_table *Produce Tables For concurve Functions*

Description

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

Usage

```
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

```
## Not run:
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"))

## End(Not run)
```

---

ggcurve *Plots Consonance, Surprisal, and Likelihood Functions*

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

```
ggcurve(data, type = "c", measure = "default", levels = 0.95,
  nullvalue = NULL, position = "pyramid", title = "Consonance Function",
  subtitle = "The function displays intervals at every level.",
  xaxis = expression(theta == ~"Range of Values"),
  yaxis1 = expression(paste(italic(p), "-value")),
  yaxis2 = "Levels for CI (%)", color = darken("#009E73", 0.5),
  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 NULL, meaning it will not be plotted as a vertical line. Changing this to a numerical vector will specify the region where a line should be plotted or an area that should be shaded. The input must be a numerical vector, for example c(-0.5, 0.5) or a single numerical vector such as 0 or 1.
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").

yaxis1	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, yxis1= "Confidence Level").
yaxis2	A custom y-axis title for the graph. By default, it is set to "Levels for CI". In order to set a y-axis title, it must be in quotes. For example, ggcurve(type = "c", data = x, yxis2= "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

```
## Not run:
# Simulate random data

library(concurve)

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

RandomData <- data.frame(GroupA, GroupB)

intervalsdf <- suppressMessages(curve_mean(GroupA, GroupB, data = RandomData, method = "default"))
ggcurve(type = "c", intervalsdf[[1]], nullvalue =c(0))

## End(Not run)
```

---

plot_compare *Graph and Compare Consonance, Surprisal, and Likelihood Functions*

Description

Compares 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"),
  yaxis1 = expression(paste(italic(p), "-value")),
  yaxis2 = "Levels for CI (%)", color1 = darken("#D55E00", 0.2),
  color2 = darken("#009E73", 0.2), fill1 = "#99c7c7", fill2 = "#d46c5b")
```

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").

yaxis1	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, yxis1= "Confidence Level").
yaxis2	A custom y-axis title for the graph. By default, it is set to "Levels for CI". In order to set a y-axis title, it must be in quotes. For example, ggcurve(type = "c", data = x, yxis2= "Confidence Level").
color1	Item that allows the user to choose the color of the points and the ribbons in the graph. By default, it is set to darken("#D55E00", 0.4). The inputs must be in quotes.
color2	Item that allows the user to choose the color of the points and the ribbons in the graph. By default, it is set to darken("#009E73", 0.4). 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

```
## Not run:
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")

## End(Not run)
```

RobustMax — *Robust Max, an alternative to max() that doesn't throw a warning*

Description

Robust Max, an alternative to max() that doesn't throw a warning

Usage

```
RobustMax(x)
```

Arguments

x	A vector to find the maximum value of

Value

The max value from a vector

RobustMin — *Robust Min, an alternative to max() that doesn't throw a warning*

Description

Robust Min, an alternative to max() that doesn't throw a warning

Usage

```
RobustMin(x)
```

Arguments

x	A vector find the minimum value of

Value

The minimum value from the vector

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