Package: gconsensus (via r-universe)

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Type Package

Title Consensus Value Constructor

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Description An implementation of the generalized consensus estimators used to assign the reference value in a key comparison exercise. This can also be applied to any interlaboratory study. Given a set of different sources, primary laboratories or measurement methods this package provides an evaluation of the variance components according to the selected statistical method for consensus building. It also implements the comparison among different consensus builders and evaluates the participating method or sources against the consensus reference value. Based on a diverse set of references, DerSimonian-Laird (1986) <doi:10.1016/0197-2456(86)90046-2>, for a complete list of references look at the reference section in the package documentation.

Depends R (>= 3.4), graphics (>= 3.4), stats (>= 3.4), MASS (>= 7.0), utils (>= 3.4), rjags (>= 4-8), coda (>= 0.13)

License GPL (>= 3)

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NeedsCompilation no

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`gconsensus-package` *Consensus Value Constructor*

Description

An implementation of the generalized consensus estimators used to assign the reference value in a key comparison exercise. This can also be applied to any interlaboratory study. Given a set of different sources, primary laboratories or measurement methods this package provides an evaluation of the variance components according to the selected statistical method for consensus building. It also implements the comparison among different consensus builders and evaluates the participating method or sources against the consensus reference value. Based on a diverse set of references, DerSimonian-Laird (1986) <doi:10.1016/0197-2456(86)90046-2>, for a complete list of references look at the reference section in the package documentation. Partially based on the results published in Control clinical trials (1985). <https://doi.org/10.1016/0197-2456(86)90046-2> For a complete list of references see the reference section.

Details

The DESCRIPTION file:

Package:	gconsensus
Type:	Package
Title:	Consensus Value Constructor
Version:	0.3.2.1
Date:	2026-08-02
Authors@R:	person(given = "Hugo", family = "Gasca-Aragon", role = c("aut", "cre"), email = "hugo_gasca_aragon@
Maintainer:	Hugo Gasca-Aragon <hugo_gasca_aragon@hotmail.com>
Description:	An implementation of the generalized consensus estimators used to assign the reference value in a key c
Depends:	R (>= 3.4), graphics (>= 3.4), stats (>= 3.4), MASS (>= 7.0), utils (>= 3.4), rjags (>= 4-8), coda (>= 0.1

License:	GPL (>=3)
Encoding:	UTF-8
NeedsCompilation:	no
Author:	Hugo Gasca-Aragon [aut, cre] (ORCID: <https://orcid.org/0000-0002-5384-2530>)

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gconsensus	Generalized Consensus Contructor
gconsensus-package	Consensus Value Constructor
plot.comparison	Plot a gconsensus comparison object
plot.doe	Plot a degrees of equivalence (doe) object
plot.gconsensus	Plot a gconsensus object
print.comparison	Prints a Comparison Object.
print.doe	Prints a unilateral degrees of equivalence (doe) Object.
print.gconsensus	Prints a gconsensus object
toString.comparison	Builds a detailed description string of the comparison object.
toString.doe	Builds a detailed description string of the doe object.
toString.gconsensus	Builds a detailed description string of the gconsenus object.
vr.mle	Finds the maximum likelihood estimate solution described by Vangel-Rukhin for the one way random effects model.

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See Also

gconsensus

Examples

```
ilab <- list(
  data = data.frame(
    participant = c("BAM", "IRMM", "LGC", "NARL", "NIST", "NMIJ", "NRC"),
    code = paste0("p", c(1:7)),
    method = rep(1, 7),
    value = c(10.21, 10.9, 10.94, 10.58, 10.81, 9.62, 10.8),
    unit = rep("\\micro \\kilogram/\\kilogram", 7),
    expandedUnc = c(0.381, 0.250, 0.130, 0.410, 0.445, 0.196, 0.093),
    n = rep(1, 7),
    coverageFactor = rep(2, 7),
    coverageProbability = rep(0.95, 7),
```

```
 method.type = rep("p", 7),
    included = rep(1, 7)),
 symbol = rep(1, 7),
 symbol.Fillcolor = rep(1, 7),
 comments = rep("", 7),
 info = list(variable = c("Software", "Institute", "Exercise", "Author", "Date",
      "Measurand", "Units"),
    value = c("consensus", "BIPM", "CCQM-K25", "Michele Schantz & Stephen Wise",
      "12-12-2003", "PCB 105", "\\micro \\kilogram/\\kilogram"))
)

aConsensusDL <- gconsensus(ilab,
  method = "DL1",
  config = list(
              signif.digits = 2,
            display.order = "location",
            display.orientation = "horizontal",
            display.shownames = TRUE,
            tab.size = 12,
            alpha = 0.05,
               expansion.factor.type = "small.sample",
            tau = mad(ilab$data$value),
               unreliable.uncertainties = FALSE,
               MC_samples = 250000,
               MC_adaptive_optimizer = 1000,
               MC_burn_in = 125000,
               MC_thin = 10,
               MC_seed = 12345,
               MC_use.HKSJ.adjustment = TRUE,
            MC_interval.type = "symmetric",
            MC_use.parallel.computing = FALSE,
             filename = "hb_consensus_model.txt"
          )
)

print(aConsensusDL)

## Not run:
# to run this example you need to download and install JAGS >= 4.3.0
aConsensusHB <- gconsensus(ilab,
  method = "HB",
 build.model = jags.model,
 get.samples = coda.samples,
  config = list(
              signif.digits = 2,
            display.order = "location",
            display.orientation = "horizontal",
            display.shownames = TRUE,
            tab.size = 12,
            alpha = 0.05,
               expansion.factor.type = "small.sample",
            tau = mad(ilab$data$value),
               unreliable.uncertainties = FALSE,
```

```
                MC_samples = 250000,
                MC_adaptive_optimizer = 1000,
                MC_burn_in = 125000,
                MC_thin = 10,
                MC_seed = 12345,
                MC_use.HKSJ.adjustment = TRUE,
              MC_interval.type = "symmetric",
              MC_use.parallel.computing = FALSE,
               filename = "hb_consensus_model.txt"
            )
)

print(aConsensusHB)

## End(Not run)
```

`comparison.gconsensus` *Obtains a set of generalized consensus estimates by different statistical methods for comparison purposes.*

Description

Obtains a set of generalized consensus estimates.

Usage

```
comparison.gconsensus(x, methods, build.model = NULL, get.samples = NULL)
```

Arguments

`x`	consensus object, containing the definition of the participants' information.
`methods`	vector of strings, containing the statistical methods to be used in obtaining the consensus values.
`build.model`	function, NULL by default, the current function to build a JAGS measurand model.
`get.samples`	function, NULL by default, the current function to obtain CORA samples out of the JAGS model.

Details

The default function requires the default parameters (x, ...), the next version will replace the formal parameters with the default signature.

Value

`fit`	a data.frame object, consensus value estimates by the specified methods
`gconsensus`	the current estimated gconsensus as provided in the x parameter
`total.included.participants`	a numeric, the current number of included participating sources

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See Also

gconsensus, print.comparison, plot.comparison

---

doe.gconsensus *Obtains the unilateral degrees of equivalence (doe) out of a generalized consensus object.*

Description

Obtains the unilateral degrees of equivalence (doe) from a generalized consensus object.

Usage

```
doe.gconsensus(x)
```

Arguments

x	A generalized consensus object

Details

The unilateral doe are obtained from the participants data and the estimated generalized consensus value described in the gconsensus value. Computed as the difference between the participant's value and the consensus value.

Value

A doe object containing the unilateral doe.

fit	a data.frame with the source code, source lab name, value, expanded uncertainty, unit, coverage factor, probability coverage and tau.
gconsensus	the generalized consensus object the evaluation is based on.

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See Also

gconsensus, print.doe, plot.doe

gconsensus *Generalized Consensus Contructor*

Description

Compute a set of estimates for the generalized consensus value from a set of sources.

Usage

```
gconsensus(ilab, method = "mean",
  build.model = NULL, get.samples = NULL,
  config = list(alpha = 0.05,
    expansion.factor.type = "naive",
    tau = mad(ilab$data$value),
    unreliable.uncertainties = FALSE,
    MC_samples = 250000,
    MC_adaptive_optimizer = 1000,
    MC_burn_in = 125000,
    MC_thin = 10,
    MC_seed = NA,
    MC_use.HKSJ.adjustment = FALSE,
    filename = "hb_consensus_model.txt"))
```

Arguments

ilab	ilab object, containing the definition of the participating source/experts/laboratories.
method	string, the current statistical method for estimating the consensus value. The list of current valid methods is: mean [15], grand.mean [15], median [15], h15 for Huber estimator [15], MCM.mean for Monte Carlo mean, MCM.median for Monte Carlo median, GD1 for the original Graybill-Deal estimator [1], GD2 for the modified Graybill-Deal estimator as described by Sinha [13], GD3 for the modified Graybill-Deal estimator as described by Zhang [14], GD4 for the modified Graybill-Deal estimator as described by Zhang [14], DL1 for original DerSimonian-Laid estimator [2], DL2 for the modified DerSimonian-Laird estimator as described by Horn-Horn-Duncan [3], PM for original Paul-Mandel estimator [5], MPM for the modified Paul-Mandel estimator [6], VRMLE for Vangel-Rukhin MLE [7, 8, 9, 10, 11], BOB for the type B on Bias estimator [4], SE for the Schieller-Eberhardt [12], MCM.LP for linear pool, HB for Hierarchical Bayesian
build.model	a function (NULL by default) to build a JAGS model
get.samples	a function (NULL by dafault) to obtain the CODA samples based on the JAGS model
config	list, contains the configuration options used in the computational process. The complete list of options is: alpha for the significance level, default value = 0.05, expansion.factor.type for the type of coverage factor to be used: "naive" which use a coverage factor=2, "large sample" which uses a normal quantile,

"small sample" which uses a t quantile, `tau` initial estimate of between source uncertainty, by default it takes the mad of the reported values, `unreliable.uncertainties` an indicator for unreliables uncertainties, if TRUE then adjustment is used [15], `MC_samples` the number of cycles used in the simple Monte Carlo simulation, `MC_adaptive_optimizer` the number of cycles used in the optimizer to adapt the sampling strategy, `MC_burn_in` the number of initial cycles to be drop from Monte Carlo simulation. The Bayesian algorithm becomes stationary but in the begining it can be noisy, this is fixed by dropping the initial samples. `MC_thin` the number to set the thinning interval to monitor/keep the Monte Carlo Markov Chain variables. `MC_seed` the seed used to initializing the random number generator in the Monte Carlo simulation, `MC_use.HKSJ.adjustment` a flag indicating if small sample adjustments are required [16], `filename` a string containing the name of the file for communication with JAGS package.

Details

The consensus estimation will vary with the specified method. Display can be customized by using the options mechanism. Available options are: `display.signif.digits` an integer representing the number of significant digits to be obtained in the adaptative approach of the Monte Carlo simulation, `display.order` a string ("name", "code", "location", "dispersion") representing the order to be used for displaying the uncertainty contribution, `display.shownames` a boolean, if true source names are used otherwise source codes are used, `display.tab.size` an integer representing the column width used in formating data tables, `display.orientation` a string ("horizontal", "vertical"), plot orientation. `display.expandedUncertainty` a boolean, plot standard uncertainties or expanded uncertainties.

Value

`fit`	a data.frame with the value, expanded uncertainty, unit, expansion factor, probability coverage and tau, the between effect uncertainty.
`method`	statistical method used to estimate the consensus value.
`subset`	the subset of included values in the consensus value estimation.
`ilab`	the current participants' information.
`config`	the current configuration options provided for the consensus value estimation process.
`exercise`	the exercise the consensus belongs to.
`measurand`	the measurand the consensus belongs to.

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See Also

`doe.gconsensus`, `print.gconsensus`, `plot.gconsensus`

`plot.comparison` *Plot a gconsensus comparison object*

Description

Shows the confidence intervals associated with the different gconsensus values specified in the comparison.

Usage

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

Arguments

`x`	gconsensus comparison object, containing the estimates for a set of gconsensus value.
`...`	any additional graphical parameter.

Details

The plot contains the confidence intervals associated with the set of gconsensus values under comparison. Formating options of the plot: `display.order` a string, this is used to order the data source, valid values are: "location" for sorting based on the repoted means, "dispersion" for sorting based on reported variances, any other value for sorting based on typing order. Default value is "location". `display.shownames` a logical, if true then the participants names are used to identify the ploted values, otherwise the code value is used instead. Default value is FALSE. `display.orientation` a string, this is used to build the plot vertically or horizontally, valid values are: "horizontal" otherwise vertical is assumed, default value is "horizontal". `display.expandedUncertainty` a logical, if true then expanded uncertainty is used for plots, otherwise standard uncertainty is used. Default value is

Value

a plot object

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See Also

`comparison.gconsensus`, `print.comparison`, `plot`

`plot.doe` *Plot a degrees of equivalence (doe) object*

Description

Plots a char showing the confidence interval for the unilateral degrees of equivalance (doe) associated to each participating laboratory.

Usage

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

Arguments

`x`	A doe object
`...`	Any additional graphical parameter

Details

Plot a unilateral degree of equivalence (doe) object. Formating options of the plot: `display.order` a string, this is used to order the data source, valid values are: "location" for sorting based on the repoted means, "dispersion" for sorting based on reported variances, any other value for sorting based on typing order. Default value is "location". `display.shownames` a logical, if true then the participants names are used to identify the ploted values, otherwise the code value is used instead. Default value is FALSE. `display.orientation` a string, this is used to build the plot vertically or horizontally, valid values are: "horizontal" otherwise vertical is assumed, default value is "horizontal". `display.expandedUncertainty` a logical, if true then expanded uncertainty is used for plots, otherwise standard uncertainty is used. Default value is FALSE.

Value

A plot of the doe object using the options displor.order and display.shownames, showing the confidence interval for the unilateral degree of equivalence (doe) attached to each participant.

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See Also

`doe.gconsensus`, `plot`, `print.doe`

`plot.gconsensus` *Plot a gconsensus object*

Description

Shows the probability distribution of the estimated gconsensus value.

Usage

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

Arguments

`x`	gconsensus object, containing the estimated gconsensus value by the specified statistical method.
`...`	any additional graphical parameter

Details

The plot shows the confidence interval for each of the participants' values, the consensus value and its confidence interval, on the right side the probability distribution associated with the consensus value is showed and a normal distribution with the same expected value and variace. Formating options of the plot: `display.order` a string, this is used to order the data source, valid values are: "location" for sorting based on the repoted means, "dispersion" for sorting based on reported variances, any other value for sorting based on typing order. Default value is "location". `display.shownames` a logical, if true then the participants names are used to identify the ploted values, otherwise the code value is used instead. Default value is FALSE. `display.orientation` a string, this is used to build the plot vertically or horizontally, valid values are: "horizontal" otherwise vertical is assumed, default value is "horizontal". `display.length.out` a numeric, this represents the number of points to build the mixture distribution, default value = 101. `display.expandedUncertainty` a logical, if true then expanded uncertainty is used for plots, otherwise standard uncertainty is used. Default value is FALSE.

Value

a plot object.

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See Also

`gconsensus`, `print.gconsensus`, `plot`

print.comparison *Prints a Comparison Object.*

Description

Prints the consensus comparison object. One line for each selected gconsensus method.

Usage

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

Arguments

x	comparison, object to be described.
...	any additional parameters.

Value

A displayed text containing a summary of the selected gconsensus methods.

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See Also

comparison.gconsensus, plot.comparison, toString.comparison

print.doe *Prints a unilateral degrees of equivalence (doe) Object.*

Description

Prints a unilateral degrees of equivalence (doe)) object.

Usage

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

Arguments

x	doe, object to be described.
...	any additional parameters.

Value

A displayed text containg a detailed description of the object.

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See Also

`gconsensus`, `doe.gconsensus`, `toString.doe`

`print.gconsensus` *Prints a gconsensus object*

Description

Prints a gconsensus object

Usage

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

Arguments

`x`	a gconsensus object
`...`	any additional parameter

Details

option `digits` is used.

Value

A displayed text containing a detailed description of the object.

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See Also

`gconsensus`, `plot.gconsensus`, `toString.gconsensus`

`toString.comparison` *Builds a detailed description string of the comparison object.*

Description

This function converts a gconsensus comparison object into a string. The returned value contains a verbatim description of the object. This function is used to display the result of comparing several gconsensus values.

Usage

```
## S3 method for class 'comparison'
toString(x, ...)
```

Arguments

`x`	comparison, object to be described.
`...`	any additional parameters.

Value

string, it contains a verbatim description of the comparison object.

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See Also

`comparison.gconsensus`, `print.comparison`

`toString.doe` *Builds a detailed description string of the doe object.*

Description

This function converts a unilateral degrees of equivalence object into a string. The returned value contains a verbatim description of the object. This function is used to display the result of estimating the unilateral degrees of equivalence.

Usage

```
## S3 method for class 'doe'
toString(x, ...)
```

Arguments

x	doe, object to be described.
...	any additional parameters.

Value

string, it contains a verbatim description of the unilateral degrees of equivalence object.

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See Also

doe.gconsensus, print.doe

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toString.gconsensus *Builds a detailed description string of the gconsenus object.*

Description

This function converts a gconsensus object into a string. The returned value contains a verbatim description of the object. This function is used to display the result of estimating the gconsensus value.

Usage

```
## S3 method for class 'gconsensus'
toString(x, ...)
```

Arguments

x	gconsensus, object to be described.
...	any additional parameters.

Value

string, it contains a verbatim description of the gconsensus object.

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See Also

gconsensus, print.gconsensus

`vr.mle` *Finds the maximum likelihood estimate solution described by Vangel-Rukhin for the one way random effects model.*

Description

This function finds the mle solution to the one way random effects model.

Usage

```
vr.mle(xi, si2, ni, labi=c(1:length(xi)),
   max.iter=1000, tol=.Machine$double.eps^0.5,
   init.mu=mean(xi), init.sigma2=var(xi),
   trace=FALSE, alpha=0.05)
```

Arguments

`xi`	numeric vector, represents the mean values.
`si2`	numeric vector, represents the variances associated with a single measurement.
`ni`	integer vector, represents the number of observations associated with the reported mean values.
`labi`	vector, containing the associated labels of the participanting laboratories, source of the reported values (mean, variances, number of observations)
`max.iter`	integer, maximum number of iterations allowed.
`tol`	numeric, relative tolerance.
`init.mu`	numeric, initial consensus value.
`init.sigma2`	numeric, initial between variance.
`trace`	logic, indicates if traceable information must be shown during the execution.
`alpha`	numeric, significance level.

Value

`mu`	estimated consensus value by the method of maximum likelihood
`u.mu`	standard uncertainty estimation attached to the consensus value
`kp`	estimated expansion factor for the specified configuration options

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See Also

See also `gconsensus`

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