

Package ‘semlbci’

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Title Likelihood-Based Confidence Interval in Structural Equation Models

Version 0.11.2

Description Forms likelihood-based confidence intervals (LBCIs) for parameters in structural equation modeling, introduced in Cheung and Pesigan (2023) <[doi:10.1080/10705511.2023.2183860](https://doi.org/10.1080/10705511.2023.2183860)>. Currently implements the algorithm illustrated by Pek and Wu (2018) <[doi:10.1037/met0000163](https://doi.org/10.1037/met0000163)>, and supports the robust LBCI proposed by Falk (2018) <[doi:10.1080/10705511.2017.1367254](https://doi.org/10.1080/10705511.2017.1367254)>.

URL <https://sfcheung.github.io/semlbci/>

BugReports <https://github.com/sfcheung/semlbci/issues>

License GPL-3

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Author Shu Fai Cheung [aut, cre] (<<https://orcid.org/0000-0002-9871-9448>>),
Ivan Jacob Agaloos Pesigan [ctb]
(<<https://orcid.org/0000-0003-4818-8420>>)

Maintainer Shu Fai Cheung <shufai.cheung@gmail.com>

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cfa_evar_near_zero	<i>Dataset (CFA, Two Factors, One Standardized Error Variance Close to Zero)</i>
--------------------	--

Description

Generated from a two-factor model, with one standardized error variance close to zero.

Usage

cfa_evar_near_zero

Format

A data frame with 120 rows and six variables, x1 to x6

Details

This model is used for examples like this one:

```
# If fitted by the following model, the standardized
# error variance of `x3` is close to zero.
# Consequently, the R-square of `x3` is close to one:

library(lavaan)
mod <- "f1 =~ x1 + x2 + x3
       f2 =~ x4 + x5 + x6"
fit <- cfa(mod, cfa_evar_near_zero)
summary(fit, standardized = TRUE, rsquare = TRUE)
```

Examples

```
print(head(cfa_evar_near_zero), digits = 3)
nrow(cfa_evar_near_zero)
```

cfa_two_factors	<i>Dataset (CFA, Two Factors, Six Variables)</i>
-----------------	--

Description

Generated from a two-factor model with six variables, $n = 500$

Usage

```
cfa_two_factors
```

Format

A data frame with 500 rows and six variables, x1 to x6.

Details

This model is used for examples like this one:

```
library(lavaan)
mod <- "f1 =~ x1 + x2 + x3
       f2 =~ x4 + x5 + x6"
fit <- cfa(mod, cfa_two_factors)
summary(fit)
```

Examples

```
print(head(cfa_two_factors), digits = 3)
nrow(cfa_two_factors)
```

cfa_two_factors_mg *Dataset (CFA, Two Factors, Six Variables, Two Groups)*

Description

Generated from a two-factor model with six variables, n = 500, two groups, n = 250 each.

Usage

```
cfa_two_factors_mg
```

Format

A data frame with 500 rows, one grouping variable, gp, six variables, x1 to x6.

Details

This model is used for examples like this one:

```
library(lavaan)
mod <- "f1 =~ x1 + x2 + x3
       f2 =~ x4 + x5 + x6"
fit <- cfa(mod, cfa_two_factors_mg, group = "gp")
summary(fit)
```

Examples

```
print(head(cfa_two_factors_mg), digits = 3)
nrow(cfa_two_factors_mg)
table(cfa_two_factors_mg$gp)
```

check_sem_out	<i>Pre-analysis Check For 'semlbci'</i>
---------------	---

Description

Check the output passed to [semlbci\(\)](#)

Usage

```
check_sem_out(
  sem_out,
  robust = c("none", "satorra.2000"),
  multigroup_ok = TRUE
)
```

Arguments

sem_out	The output from an SEM analysis. Currently only supports a lavaan::lavaan object.
robust	Whether the LBCI based on robust likelihood ratio test is to be found. Only "satorra.2000" in lavaan::lavTestLRT() is supported for now. If "none", the default, then likelihood ratio test based on maximum likelihood estimation will be used.
multigroup_ok	If TRUE, will not check whether the model is a multiple-group model. Default is TRUE.

Details

It checks whether the model and the estimation method in the `sem_out` object passed to [semlbci\(\)](#) are supported by the current version of [semlbci\(\)](#). This function is to be used by [semlbci\(\)](#) but is exported such that the compatibility of an SEM output can be checked directly.

Estimation methods (estimator in [lavaan::lavaan\(\)](#)) currently supported:

- Maximum likelihood (ML) and its variants (e.g., MLM, MLR). For methods with robust test statistics (e.g., MLR), only robust LBCIs (`robust = "satorra.2000"` in calling [semlbci\(\)](#)) can be requested.

Estimation methods not yet supported:

- Generalized least squares (GLS).
- Weighted least squares (a.k.a. asymptotically distribution free) (WLS) and its variants (e.g., WLSMV).
- Unweighted least squares (ULS).
- Diagonally weighted least squares (DWLS).
- Other methods not listed.

Models supported:

- Single-group models with continuous variables.
- Multiple-group models with continuous variables.

Models not tested:

- Models with categorical variables.

Models not yet supported:

- Models with formative factors.
- Multilevel models.

Value

A numeric vector of one element. If 0, the model and estimation method are officially supported. If larger than zero, then the model and method are not officially supported but users can still try to use [semLbci\(\)](#) on it at their own risks. If less than zero, then the model and/or the method are officially not supported.

The attributes `info` contains the reason for a value other than zero.

See Also

[semLbci\(\)](#), [ci_i_one\(\)](#)

Examples

```
library(lavaan)
data(cfa_two_factors)
mod <-
"
f1 =~ x1 + x2 + x3
f2 =~ x4 + x5 + x6
"

fit <- sem(mod, cfa_two_factors)

# Should be 0
check_sem_out(fit)

fit2 <- sem(mod, cfa_two_factors, estimator = "DWLS")

# Should be negative because DWLS is officially not supported
check_sem_out(fit2)

fit3 <- sem(mod, cfa_two_factors, estimator = "MLR")

# Should be negative because MLR is supported only if
# robust is set to "satorra.2000"
check_sem_out(fit3)

# Should be zero because robust is set to "satorra.2000"
check_sem_out(fit3, robust = "satorra.2000")
```

ci_bound_ur

*Find a Likelihood-Based Confidence Bound By Root Finding***Description**

Find the lower or upper bound of the likelihood-based confidence interval (LBCI) for one parameter in a structural equation model fitted in `lavaan::lavaan()` using `uniroot()`.

Usage

```
ci_bound_ur(
  sem_out,
  func,
  ...,
  level = 0.95,
  which = c("lbound", "ubound"),
  interval = NULL,
  progress = FALSE,
  method = "uniroot",
  lrt_method = "default",
  tol = 5e-04,
  root_target = c("chisq", "pvalue"),
  d = 5,
  uniroot_extendInt = switch(which, lbound = "downX", ubound = "upX"),
  uniroot_trace = 0,
  uniroot_maxiter = 1000,
  use_callr = TRUE,
  rs = NULL
)

gen_est_i(i, sem_out, standardized = FALSE)
```

Arguments

<code>sem_out</code>	The fit object. Currently supports <code>lavaan::lavaan</code> objects only.
<code>func</code>	A function that receives a lavaan object and returns a scalar. This function is to be used by <code>gen_userp()</code> and so there are special requirements on it. Alternatively, it can be the output of <code>gen_est_i()</code> .
<code>...</code>	Optional arguments to be passed to <code>func</code> . Usually not used but included in case the function has such arguments.
<code>level</code>	The level of confidence of the confidence interval. Default is .95, or 95%.
<code>which</code>	Whether the lower bound or the upper bound is to be found. Must be "lbound" or "ubound".
<code>interval</code>	A numeric vector of two values, which is the initial interval to be searched. If NULL, the default, it will be determined internally using Wald or delta method confidence interval, if available.

progress	Whether progress will be reported on screen during the search. Default is FALSE.
method	The actual function to be used in the search. which can only be "uniroot", the default, for now. May include other function in the future.
lrt_method	The method used in <code>lavaan::lavTestLRT()</code> . Default is "default". It is automatically set to "satorra.2000" and cannot be overridden if a scaled test statistic is requested in <code>sem_out</code> .
tol	The tolerance used in <code>uniroot()</code> , default is .005.
root_target	Whether the chi-square difference ("chisq"), the default, or its <i>p</i> -value ("pvalue") is used as the function value in finding the root. Should have little impact on the results.
d	A value used to determine the width of the interval in the initial search. Larger this value, <i>narrow</i> the interval. Default is 5.
uniroot_extendInt	To be passed to the argument <code>extendInt</code> of <code>uniroot()</code> . Whether the interval should be extended if the root is not found. Default value depends on the bound to be searched. Refer to the help page of <code>uniroot()</code> for possible values.
uniroot_trace	To be passed to the argument <code>trace</code> of <code>uniroot()</code> . How much information is printed during the search. Default is 0, and no information is printed during the search. Refer to the help page of <code>uniroot()</code> for possible values.
uniroot_maxiter	The maximum number of iteration in the search. Default is 1000.
use_callr	Whether the <code>callr</code> package will be used to do the search in a separate R process. Default is TRUE. Should not set to FALSE if used in an interactive environment unless this is intentional.
rs	Optional. If set to a persistent R process created by <code>callr</code> , it will be used instead of starting a new one, and it will not be terminated on exit.
i	The position of the target parameter as appeared in the parameter table of an <code>lavaan</code> object, generated by <code>lavaan::parameterTable()</code> .
standardized	If TRUE, the standardized estimate is to be retrieved. Default is FALSE. Only support "std.all" for now.

Details

This function is called xby `ci_bound_ur_i()`. This function is exported because it is a stand-alone function that can be used directly for any function that receives a `lavaan` object and returns a scalar.

The function `ci_bound_ur_i()` is a wrapper of this function, with an interface similar to that of `ci_bound_wn_i()` and returns a `cibound`-class object. The user-parameter function is generated internally by `ci_bound_wn_i()`.

This function, on the other hand, requires users to supply the function directly through the `func` argument. This provides the flexibility to find the bound for any function of the model parameter, even one that cannot be easily coded in `lavaan` model syntax.

ci_bound_ur_i

Likelihood-Based Confidence Bound By Root Finding

Description

Using root finding to find the lower or upper bound of the likelihood-based confidence interval (LBCI) for one parameter in a structural equation model fitted in `lavaan::lavaan()`.

Usage

```
ci_bound_ur_i(
  i = NULL,
  npar = NULL,
  sem_out = NULL,
  f_constr = NULL,
  which = NULL,
  history = FALSE,
  perturbation_factor = 0.9,
  lb_var = -Inf,
  standardized = FALSE,
  wald_ci_start = !standardized,
  opts = list(),
  ciperc = 0.95,
  ci_limit_ratio_tol = 1.5,
  verbose = FALSE,
  sf = 1,
  sf2 = 0,
  p_tol = 5e-04,
  std_method = "internal",
  bounds = "none",
  xtol_rel_factor = 1,
  ftol_rel_factor = 1,
  lb_prop = 0.05,
  lb_se_k = 3,
  d = 5,
  ...
)
```

Arguments

<code>i</code>	The position of the target parameter as appeared in the parameter table of a lavaan object, generated by <code>lavaan::parameterTable()</code> .
<code>npar</code>	Ignored by this function. Included consistency in the interface.
<code>sem_out</code>	The fit object. Currently supports <code>lavaan::lavaan</code> objects only.
<code>f_constr</code>	Ignored by this function. Included consistency in the interface.

which	Whether the lower bound or the upper bound is to be found. Must be "lbound" or "ubound".
history	Not used. Kept for backward compatibility.
perturbation_factor	Ignored by this function. Included consistency in the interface.
lb_var	Ignored by this function. Included consistency in the interface.
standardized	If TRUE, the LBCI is for the requested estimate in the standardized solution. Default is FALSE.
wald_ci_start	Ignored by this function. Included consistency in the interface.
opts	Options to be passed to <code>stats::uniroot()</code> . Default is <code>list()</code> .
ciperc	The intended coverage probability for the confidence interval. Default is .95, and the bound for a 95% confidence interval will be sought.
ci_limit_ratio_tol	The tolerance for the ratio of a to b, where a is the distance between an LBCI limit and the point estimate, and the b is the distance between the original confidence limit (by default the Wald CI in <code>lavaan::lavaan()</code>) and the point estimate. If the ratio is larger than this value or smaller than the reciprocal of this value, a warning is set in the status code. Default is 1.5.
verbose	If TRUE, the function will store more diagnostic information in the attribute <code>diag</code> . Default is FALSE.
sf	Ignored by this function. Included consistency in the interface.
sf2	Ignored by this function. Included consistency in the interface.
p_tol	Tolerance for checking the achieved level of confidence. If the absolute difference between the achieved level and <code>ciperc</code> is greater than this amount, a warning is set in the status code and the bound is set to NA. Default is $5e-4$.
std_method	The method used to find the standardized solution. If equal to "lavaan", <code>lavaan::standardizedSolution()</code> will be used. If equal to "internal", an internal function will be used. The "lavaan" method should work in all situations, but the "internal" method is usually much faster. Default is "internal".
bounds	Ignored by this function. Included consistency in the interface.
xtol_rel_factor	Ignored by this function. Included consistency in the interface.
ftol_rel_factor	Ignored by this function. Included consistency in the interface.
lb_prop	Ignored by this function. Included consistency in the interface.
lb_se_k	Ignored by this function. Included consistency in the interface.
d	A value used to determine the width of the interval in the initial search. Larger this value, <i>narrow</i> the interval. Default is 5. Used by <code>ci_bound_ur()</code> .
...	Optional arguments. Not used.

Details

Important Notice:

This function is not supposed to be used directly by users in typical scenarios. Its interface is user-*unfriendly* because it should be used through `semlbci()`. It is exported such that interested users can examine how a confidence bound is found, or use it for experiments or simulations.

Usage:

This function is the lowest level function used by `semlbci()`. `semlbci()` calls this function once for each bound of each parameter.

For consistency in the interface, most of the arguments in `ci_bound_wn_i()` are also included in this function, even those not used internally.

Algorithm:

This function, unlike `ci_bound_wn_i()`, use a simple root finding algorithm. Basically, it tries fixing the target parameter to different values until the likelihood ratio test p -value, or the corresponding chi-square difference, is equal to the value corresponding to the desired level of confidence. (Internally, the difference between the p -value and the target p -value, that for the chi-square difference, is the function value.)

For finding the bound, this algorithm can be inefficient compared to the one proposed by Wu and Neale (2012). The difference can be less than one second versus 10 seconds. It is included as a backup algorithm for parameters which are difficult for the method by Wu and Neale.

Internally, it uses `uniroot()` to find the root.

Limitation(s):

This function does not handle an estimate close to an attainable bound using the method proposed by Wu and Neale (2012). Use it for such parameters with cautions.

Value

A `cibound`-class object which is a list with three elements:

- `bound`: A single number. The value of the bound located. NA is the search failed for various reasons.
- `diag`: A list of diagnostic information.
- `call`: The original call.

A detailed and organized output can be printed by the default print method (`print.cibound()`).

References

Wu, H., & Neale, M. C. (2012). Adjusted confidence intervals for a bounded parameter. *Behavior Genetics*, 42(6), 886-898. doi:10.1007/s105190129560z

See Also

`print.cibound()`, `semlbci()`, `ci_i_one()`; see `ci_bound_wn_i()` on the version for the method by Wu and Neale (2012).

Examples

```

library(lavaan)
data(simple_med)
dat <- simple_med
mod <-
"
m ~ x
y ~ m
"
fit_med <- sem(mod, simple_med, fixed.x = FALSE)
# Remove `opts` in real cases.
# The options are added just to speed up the example
out11 <- ci_bound_ur_i(i = 1,
                      sem_out = fit_med,
                      which = "lbound",
                      opts = list(use_callr = FALSE,
                                  interval = c(0.8277, 0.8278)))

out11

```

ci_bound_wn_i

Likelihood-based Confidence Bound By Wu-Neale-2012

Description

Use the method proposed by Wu and Neale (2012) to find the lower or upper bound of the likelihood-based confidence interval (LBCI) for one parameter in a structural equation model fitted in `lavaan::lavaan()`.

Usage

```

ci_bound_wn_i(
  i = NULL,
  npar = NULL,
  sem_out = NULL,
  f_constr = NULL,
  which = NULL,
  history = FALSE,
  perturbation_factor = 0.9,
  lb_var = -Inf,
  standardized = FALSE,
  wald_ci_start = !standardized,
  opts = list(),
  ciperc = 0.95,
  ci_limit_ratio_tol = 1.5,
  verbose = FALSE,
  sf = 1,
  sf2 = 0,
  p_tol = 5e-04,

```

```

    std_method = "internal",
    bounds = "none",
    xtol_rel_factor = 1,
    ftol_rel_factor = 1,
    lb_prop = 0.05,
    lb_se_k = 3,
    try_harder = 0,
    fit_lb = -Inf,
    fit_ub = +Inf,
    timeout = 300,
    ...
)

```

Arguments

<code>i</code>	The position of the target parameter as appeared in the parameter table of an lavaan object, generated by <code>lavaan::parameterTable()</code> .
<code>npar</code>	The number of free parameters, including those constrained to be equal.
<code>sem_out</code>	The fit object. Currently supports <code>lavaan::lavaan</code> objects only.
<code>f_constr</code>	The constraint function generated by <code>set_constraint()</code> .
<code>which</code>	Whether the lower bound or the upper bound is to be found. Must be "lbound" or "ubound".
<code>history</code>	Not used. Kept for backward compatibility.
<code>perturbation_factor</code>	A number multiplied to the parameter estimates in <code>sem_out</code> . Using the parameter estimates as starting values may lead to errors in the first few iterations. Default is .90. This argument is ignored if <code>wald_ci_start</code> is 'TRUE'.
<code>lb_var</code>	The lower bound for free parameters that are variances. If equal to <code>-Inf</code> , the default, <code>lb_prop</code> and <code>lb_se_k</code> will be used to set the lower bounds for free variances. If it is a number, it will be used to set the lower bounds for all free variances.
<code>standardized</code>	If TRUE, the LBCI is for the requested estimate in the standardized solution. Default is FALSE.
<code>wald_ci_start</code>	If TRUE, there are no equality constraints in the model, and the target parameter is not a user-defined parameter, the Wald confidence bounds will be used as the starting value.
<code>opts</code>	Options to be passed to <code>nloptr::nloptr()</code> , the current optimizer. Default is <code>list()</code> .
<code>ciperc</code>	The intended coverage probability for the confidence interval. Default is .95, and the bound for a 95% confidence interval will be sought.
<code>ci_limit_ratio_tol</code>	The tolerance for the ratio of a to b, where a is the distance between an LBCI limit and the point estimate, and the b is the distance between the original confidence limit (by default the Wald CI in <code>lavaan::lavaan()</code>) and the point estimate. If the ratio is larger than this value or smaller than the reciprocal of this value, a warning is set in the status code. Default is 1.5.

verbose	If TRUE, the function will store more diagnostic information in the attribute diag. Default is FALSE.
sf	A scaling factor. Used for robust confidence bounds. Default is 1. Computed by an internal function called by <code>semlbci()</code> when <code>robust = "satorra.2000"</code> .
sf2	A shift factor. Used for robust confidence bounds. Default is 0. Computed by an internal function called by <code>semlbci()</code> when <code>robust = "satorra.2000"</code> .
p_tol	Tolerance for checking the achieved level of confidence. If the absolute difference between the achieved level and <code>ciperc</code> is greater than this amount, a warning is set in the status code and the bound is set to NA. Default is $5e-4$.
std_method	The method used to find the standardized solution. If equal to "lavaan", <code>lavaan::standardizedSolution()</code> will be used. If equal to "internal", an internal function will be used. The "lavaan" method should work in all situations, but the "internal" method is usually much faster. Default is "internal".
bounds	Default is "" and this function will set the lower bounds to <code>lb_var</code> for variances. Other valid values are those accepted by <code>lavaan::lavaan()</code> . Ignored for now.
xtol_rel_factor	Multiply the default <code>xtol_rel</code> by a number, usually a positive number equal to or less than 1, to change the default termination criterion. Default is 1.
ftol_rel_factor	Multiply the default <code>ftol_rel</code> by a number, usually a positive number equal to or less than 1, to change the default termination criterion. Default is 1.
lb_prop	Used by an internal function to set the lower bound for free variances. Default is .05, setting the lower bound to $.05 * \text{estimate}$. Used only if the lower bound set by <code>lb_se_k</code> is negative.
lb_se_k	Used by an internal function to set the lower bound for free variances. Default is 3, the estimate minus 3 standard error. If negative, the lower bound is set using <code>lb_prop</code> .
try_harder	If error occurred in the optimization, how many more times to try. In each new attempt, the starting values will be randomly jittered. Default is 0.
fit_lb	The vector of lower bounds of parameters. Default is <code>-Inf</code> , setting the lower bounds to <code>-Inf</code> for all parameters except for free variances which are controlled by <code>lb_var</code> .
fit_ub	The vector of upper bounds of parameters. Default is <code>+Inf</code> , setting the lower bounds to <code>+Inf</code> for all parameters.
timeout	The approximate maximum time for the search, in second. Default is 300 seconds (5 minutes).
...	Optional arguments. Not used.

Details

Important Notice:

This function is not supposed to be used directly by users in typical scenarios. Its interface is *user-unfriendly* because it should be used through `semlbci()`. It is exported such that interested users can examine how a confidence bound is found, or use it for experiments or simulations.

Usage:

This function is the lowest level function used by `semlbci()`. `semlbci()` calls this function once for each bound of each parameter. To use it, `set_constraint()` needs to be called first to create the equality constraint required by the algorithm proposed by Wu and Neale (2012).

Algorithm:

This function implements the algorithm presented in Wu and Neale (2012; see also Pek & Wu, 2015, Equation 12) that estimates all free parameters in the optimization.

Limitation(s):

This function does not yet implement the method by Wu and Neale (2012) for an estimate close to an attainable bound.

Value

A `cibound`-class object which is a list with three elements:

- `bound`: A single number. The value of the bound located. NA is the search failed for various reasons.
- `diag`: A list of diagnostic information.
- `call`: The original call.

A detailed and organized output can be printed by the default print method (`print.cibound()`).

References

Pek, J., & Wu, H. (2015). Profile likelihood-based confidence intervals and regions for structural equation models. *Psychometrika*, 80(4), 1123-1145. doi:10.1007/s1133601594611

Wu, H., & Neale, M. C. (2012). Adjusted confidence intervals for a bounded parameter. *Behavior Genetics*, 42(6), 886-898. doi:10.1007/s105190129560z

See Also

`print.cibound()`, `semlbci()`, `ci_i_one()`

Examples

```
data(simple_med)
dat <- simple_med

mod <-
"
m ~ x
y ~ m
"

fit_med <- lavaan::sem(mod, simple_med, fixed.x = FALSE)

fn_constr0 <- set_constraint(fit_med)
```



```

out11 <- ci_bound_wn_i(i = 1,
                      npar = 5,
                      sem_out = fit_med,
                      f_constr = fn_constr0,
                      which = "lbound")

out11

```

ci_i_one

Likelihood-Based Confidence Bound for One Parameter

Description

Find the likelihood-based confidence bound for one parameter.

Usage

```

ci_i_one(
  i,
  which = NULL,
  sem_out,
  method = c("wn", "ur"),
  standardized = FALSE,
  robust = "none",
  sf_full = NA,
  sf_args = list(),
  sem_out_name = NULL,
  try_k_more_times = 0,
  ...
)

```

Arguments

i	The position (row number) of the target parameters as appeared in the parameter table of the <code>lavaan::lavaan</code> object.
which	Whether the lower bound or the upper bound is to be found. Must be "lbound" or "ubound".
sem_out	The SEM output. Currently supports <code>lavaan::lavaan</code> outputs only.
method	The approach to be used. Default is "wn" (Wu-Neale-2012 Method). Another method is "ur", root finding by <code>stats::uniroot()</code> .
standardized	Logical. Whether the bound of the LBCI of the standardized solution is to be searched. Default is FALSE.
robust	Whether the LBCI based on robust likelihood ratio test is to be found. Only "satorra.2000" in <code>lavaan::lavTestLRT()</code> is supported for now. If "none", the default, then likelihood ratio test based on maximum likelihood estimation will be used. For "ur", "satorra.2000" is automatically used if a scaled test statistic is requested in sem_out.

<code>sf_full</code>	A list with the scaling and shift factors. Ignored if <code>robust</code> is "none". If <code>robust</code> is "satorra.2000" and <code>sf_full</code> is supplied, then its value will be used. If <code>robust</code> is "satorra.2000" but <code>sf_full</code> is NA, then scaling factors will be computed internally.
<code>sf_args</code>	The list of arguments to be used for computing scaling factors if <code>robust</code> is "satorra.2000". Used only by <code>semlbci()</code> . Ignored if <code>robust</code> is not "satorra.2000".
<code>sem_out_name</code>	The name of the object supplied to <code>sem_out</code> . NULL by default. Originally used by some internal functions. No longer used in the current version but kept for backward compatibility.
<code>try_k_more_times</code>	How many more times to try if the status code is not zero. Default is 0.
<code>...</code>	Arguments to be passed to the function corresponds to the requested method (<code>ci_bound_wn_i()</code> for "wn").

Details

Important Notice:

This function is not supposed to be used directly by users in typical scenarios. Its interface is *user-unfriendly* because it should be used through `semlbci()`. It is exported such that interested users can examine how a confidence bound is found, or use it for experiments or simulations.

Usage:

`ci_i_one()` is the link between `semlbci()` and the lowest level function (currently `ci_bound_wn_i()`). When called by `semlbci()` to find the bound of a parameter, `ci_i_one()` calls a function (`ci_bound_wn_i()` by default) one or more times to find the bound (limit) for a likelihood-based confidence interval.

Value

A list of the following elements.

- `bound`: The bound located. NA if the search failed.
- `diags`: Diagnostic information.
- `method`: Method used. Currently only "wn" is the only possible value.
- `times`: Total time used in the search.
- `sf_full`: The scaling and shift factors used.
- `ci_bound_i_out`: The original output from `ci_bound_wn_i()`.
- `attempt_lb_var`: How many attempts used to reduce the lower bounds of free variances.
- `attempt_more_times`: How many additional attempts used to search for the bounds. Controlled by `try_k_more_times`.

See Also

`semlbci()`, `ci_bound_wn_i()`

Examples

```

data(simple_med)

library(lavaan)
mod <-
"
m ~ x
y ~ m
"
fit_med <- lavaan::sem(mod, simple_med, fixed.x = FALSE)

parameterTable(fit_med)

# Find the LBCI for the first parameter
# The method "wn" needs the constraint function.
# Use set_constraint() to generate this function:
fn_constr0 <- set_constraint(fit_med)

# Call ci_i to find the bound, the lower bound in this example.
# The constraint function, assigned to f_constr, is passed
# to ci_bound_wn_i().
# npar is an argument for ci_bound_wn_i().
out <- ci_i_one(i = 1,
               which = "lbound",
               sem_out = fit_med,
               npar = 5,
               f_constr = fn_constr0)

out$bounds

```

`ci_order`*Check The Order of Bounds in a List of semlbcI Objects*

Description

Check whether the LBCIs in a list of `semlbcI`-class of objects are consistent with their levels of confidence.

Usage

```

ci_order(semlbcI_list)

## S3 method for class 'ci_order'
print(x, digits = 3, ...)

```

Arguments

`semlbcI_list` An object of class `semlbcI_list`, such as the output of `nearby_levels()`.

`x` The output of `ci_order()`.

digits The number of decimal places in the printout.
 ... Additional arguments. Not used.

Value

A `ci_order`-class object with a print method `print.ci_order()`. The number of rows is equal to the number of parameters in `semlbci_list`, and the columns stores the confidence limits from the list, ordered according to the level of confidence.

`x` is returned invisibly. Called for its side effect.

Methods (by generic)

- `print(ci_order)`: The print method of the output of `ci_order()`.

Author(s)

Shu Fai Cheung <https://orcid.org/0000-0002-9871-9448>

See Also

[nearby_levels\(\)](#), [semlbci\(\)](#)

Examples

```
library(lavaan)
mod <-
"
m ~ x
y ~ m
"
fit_med <- sem(mod, simple_med, fixed.x = FALSE)
lbci_fit <- semlbci(fit_med)
lbci_fit_nb <- nearby_levels(lbci_fit,
                           cipercl_levels = c(-.050, .050))

# Check the order of the confidence bounds.
# A confidence interval with a higher level of confidence
# should enclose a confidence interval with
# a lower level of confidence.
ci_order(lbci_fit_nb)
```

confint.semlbci *Confidence Intervals for a 'semBci' Object*

Description

Return the confidence intervals of the parameters in the output of `semlbci()`.

Usage

```
## S3 method for class 'semlbci'  
confint(object, parm, level = 0.95, ...)
```

Arguments

<code>object</code>	The output of <code>semlbci()</code> .
<code>parm</code>	The parameters for which the confidence intervals are returned. Not used because parameters are defined by three or more columns (lhs, op, rhs, and group for multisample models).
<code>level</code>	Ignored. The level of confidence is determined when calling <code>semlbci()</code> and cannot be changed.
<code>...</code>	Optional arguments. Ignored.

Details

It returns the likelihood-based confidence intervals in the output of `semlbci()`.

Value

A two-column matrix of the confidence intervals.

Author(s)

Shu Fai Cheung <https://orcid.org/0000-0002-9871-9448>

See Also

`semlbci()`

Examples

```
library(lavaan)  
mod <-  
"  
m ~ a*x  
y ~ b*m  
ab := a * b  
"
```

```

fit_med <- sem(mod, simple_med, fixed.x = FALSE)
p_table <- parameterTable(fit_med)
p_table
lbc_med <- semlbc(fit_med,
                 pars = "ab :=")
lbc_med

confint(lbc_med)

```

gen_userp

Create a Wrapper To Be Used in 'lavaan' Models

Description

Make a function on lavaan object usable in a lavaan model syntax.

Usage

```

gen_userp(func, sem_out)

gen_sem_out_userp(
  userp,
  sem_out,
  userp_name = "semlbcuserp1234",
  fix = TRUE,
  control_args = list(),
  iter.max = 10000,
  max_attempts = 5
)

```

Arguments

func	A function that receives a lavaan-object and returns a scalar. See Details on the restriction on this function.
sem_out	A lavaan-class object to be modified.
userp	A function that is generated by gen_userp() .
userp_name	The name of the function userp to be used in the lavaan model. It does not have to be the name of the function in userp. Should be changed only if it conflicts with another object in the parent environment, which should not happen if the model is always fitted in a clean R session.
fix	If TRUE, the default, the function generated is used to fix the value of userp to a target value using an equality constraint. If FALSE, then the function simply fits the model to the data.
control_args	To be passed to the argument of the same name in <code>lavaan::lavaan()</code> . Default is <code>list()</code> . Can be used to set the default values of this argument in the generated function.

<code>iter.max</code>	The maximum number of iteration when the generated function fit the model. Default is 10000.
<code>max_attempts</code>	If the initial fit with the equality constraint fails, how many more attempts will be made by the generated function. Default is 5.

Details

gen_userp:

There are cases in which we want to create a user parameter which is a function of other free parameters, computed by a function. However such a function may work only on a lavaan object. If the target function works by extracting parameter estimates stored in the `Model` slot and/or the `implied` slot, then `gen_userp()` can be used to convert it to a function that retrieves the parameter estimates when being called by `lavaan::lavaan()` or its wrappers, modifies the stored lavaan object using `lavaan::lav_model_set_parameters()` and `lavaan::lav_model_implied()` to change the estimates, and call the target function.

Note that this is an unconventional way to define a user parameter and the generated function should always be checked to see whether it works as expected.

As shown in the examples, the parameter computed this may not have standard error nor p -value. The main purpose is for the point estimate, for searching the likelihood-based confidence bound using `ci_bound_ur()` and `ci_bound_ur_i()`.

Note that the target function specified in `func` should work directly on the parameter estimates stored in the `Model` slot and then get the estimates using `lavaan::lav_model_get_parameters()`. Functions that work on the unmodified output generated by `lavaan::lavaan()` usually do not work.

Users are not recommended to use `gen_userp()` and `gen_sem_out_userp()` directly because they require unconventional way to extract parameter estimates from a lavaan model. However, developers may use them to include functions they wrote in a lavaan model. This is the technique used by `ci_bound_ur_i()` to constrain any parameter in a model to an arbitrary value.

gen_sem_out_userp:

The function `gen_sem_out_userp()` is to be used internally for generating a function for searching a likelihood-based confidence bound. It is exported because it needs to be run in a fresh external R process, usually created by `callr` in other internal functions.

Value

gen_userp:

It returns a function that accepts a numeric vector of length equals to the number of free parameters in `sem_out`, and returns a scalar which is the output of `func`. If this vector is not supplied, it will try to find it in the `parent.frame()`. This is how it works inside a lavaan model.

gen_sem_out_userp:

If `fix` is TRUE, it returns a function with these arguments:

- `target`: The value to which the user-defined parameter will be fixed to.
- `verbose`: If TRUE, additional information will be printed when fitting the model.
- `control`: The values to be passed as a list to the argument of the same name in `lavaan::lavaan()`.

- `seed`: Numeric. If supplied, it will be used in `set.seed()` to initialize the random number generator. Necessary to reproduce some results because random numbers are used in some steps in lavaan. If NULL, the default, `set.seed()` will not be called.

If `fix` is `'FALSE'`, then it returns a function with optional arguments that will be ignored, Calling it will simply fit the modified model to the data. Useful for getting the value of the user-defined parameter.

Examples

```
library(lavaan)

data(simple_med)
dat <- simple_med
mod <-
"
m ~ a*x
y ~ b*m
ab := a*b
"

fit_med <- sem(mod, simple_med, fixed.x = FALSE)
parameterEstimates(fit_med)

# A trivial example for verifying the results
my_ab <- function(object) {
  # Need to use lav_model_get_parameters()
  # because the object is only a modified
  # lavaan-object, not one directly
  # generated by lavaan function
  est <- lavaan::lav_model_get_parameters(object@Model, type = "user")
  unname(est[1] * est[2])
}

# Check the function
my_ab(fit_med)
coef(fit_med, type = "user")["ab"]

# Create the function
my_userp <- gen_userp(func = my_ab,
                     sem_out = fit_med)
# Try it on the vector of free parameters
my_userp(coef(fit_med))

# Generate a modified lavaan model
fit_userp <- gen_sem_out_userp(userp = my_userp,
                              userp_name = "my_userp",
                              sem_out = fit_med)

# This function can then be used in the model syntax.

# Note that the following example only work when called inside the
# workspace or inside other functions such as ci_bound_ur()
# and ci_bound_ur_i() because lavaan::sem() will
```



```
# search `my_userp()` in the global environment.

# Therefore, the following lines are commented out.
# They should be run only in a "TRUE" interactive
# session.

# mod2 <-
# "
# m ~ x
# y ~ m
# ab := my_userp()
# "
# fit_med2 <- sem(mod2, simple_med, fixed.x = FALSE)
# parameterEstimates(fit_med2)
#
# # Fit the model with the output of the function, a*b
# # fixed to .50
#
# fit_new <- fit_userp(.50)
#
# # Check if the parameter ab is fixed to .50
# parameterEstimates(fit_new)
```

get_cibound

A 'cibound' Output From a 'semlbci' Object

Description

Get the cibound output of a bound from a semlbci object, the output of [semlbci\(\)](#).

Usage

```
get_cibound(x, row_id, which = c("lbound", "ubound"))
```

```
get_cibound_status_not_0(x)
```

Arguments

x	The output of semlbci() .
row_id	The row number in x. Should be the number on the left, not the actual row number, because some rows may be omitted in the printout of x.
which	The bound for which the ci_bound_wn_i() is to be extracted. Either "lbound" or "ubound".

Details

The function `get_cibound()` returns the original output of `ci_bound_wn_i()` for a bound. Usually for diagnosis.

The function `get_cibound_status_not_0()` checks the status code of each bound, and returns the cibound outputs of bounds with status code not equal to zero (i.e., something wrong in the search). Printing it can print the diagnostic information for all bounds that failed in the search.

Value

`get_cibound()` returns a cibound-class object. See `ci_bound_wn_i()` for details. `get_cibound_status_not_0()` returns a list of cibound-class objects with status not equal to zero. If all bounds have status equal to zero, it returns an empty list.

Author(s)

Shu Fai Cheung <https://orcid.org/0000-0002-9871-9448>

See Also

`semlbci()`

Examples

```
library(lavaan)
mod <-
"
m ~ a*x
y ~ b*m
ab := a * b
"

fit_med <- sem(mod, simple_med, fixed.x = FALSE)
p_table <- parameterTable(fit_med)
p_table
lbc_med <- semlbci(fit_med,
                  pars = c("ab :="))

lbc_med

# Get the output of ci_bound_wn_i() of the lower
# bound of the LBCI for the indirect effect:
get_cibound(lbc_med, row_id = 6, which = "lbound")

# Get the output of ci_bound_wn_i() of the upper
# bound of the LBCI for the indirect effect:
get_cibound(lbc_med, row_id = 6, which = "ubound")
```

loglike_compare	<i>Log Profile likelihood of a Parameter</i>
-----------------	--

Description

These functions compute the log profile likelihood of a parameter when it is fixed to a value or a range of values

Usage

```
loglike_compare(  
  sem_out,  
  semlbci_out = NULL,  
  par_i,  
  confidence = 0.95,  
  n_points = 21,  
  start = "default",  
  try_k_more = 5,  
  parallel = FALSE,  
  ncpus = parallel::detectCores(logical = FALSE) - 1,  
  use_pbapply = TRUE  
)
```

```
loglike_range(  
  sem_out,  
  par_i,  
  confidence = 0.95,  
  n_points = 21,  
  interval = NULL,  
  verbose = FALSE,  
  start = "default",  
  try_k_more = 5,  
  parallel = FALSE,  
  ncpus = parallel::detectCores(logical = FALSE) - 1,  
  use_pbapply = TRUE  
)
```

```
loglike_point(  
  theta0,  
  sem_out,  
  par_i,  
  verbose = FALSE,  
  start = "default",  
  try_k_more = 5  
)
```

```
loglike_quad_range(  
  theta0,  
  sem_out,  
  par_i,  
  verbose = FALSE,  
  start = "default",  
  try_k_more = 5  
)
```

```

    sem_out,
    par_i,
    confidence = 0.95,
    n_points = 21,
    interval = NULL,
    parallel = FALSE,
    ncpus = parallel::detectCores(logical = FALSE) - 1,
    use_pbapply = TRUE,
    try_k_more = 5,
    start = "default"
)

loglike_quad_point(theta0, sem_out, par_i)

```

Arguments

<code>sem_out</code>	The SEM output. Currently the outputs of <code>lavaan::lavaan()</code> or its wrappers, such as <code>lavaan::sem()</code> and <code>lavaan::cfa()</code> are supported.
<code>semlbci_out</code>	The output of <code>semlbci()</code> . If supplied, it will extract the likelihood-based confidence interval from the output. If not, it will call <code>semlbci()</code> .
<code>par_i</code>	The row number of the parameter in the output of <code>lavaan::parameterTable()</code> . Can also be a <code>lavaan::model.syntax</code> specification for a parameter, e.g., "y ~ x" or <code>ab := .</code> . It will be converted to the row number by <code>syntax_to_i()</code> . Refer to <code>syntax_to_i()</code> for details.
<code>confidence</code>	The level of confidence of the Wald-type confidence interval. If <code>interval</code> is <code>NULL</code> , this confidence is used to form the interval.
<code>n_points</code>	The number of points to be evaluated in the interval. Default is 21.
<code>start</code>	How the start values are set in <code>lavaan::lavaan()</code> . See <code>lavaan::lavOptions()</code> on this argument. Default is "default". If the plot is too irregular, try setting it to "simple".
<code>try_k_more</code>	How many more times to try finding the p-values, by randomizing the starting values. Default is 5. Try increasing this number if the plot is too irregular.
<code>parallel</code>	If <code>TRUE</code> , parallel processing will be used. A cluster will be created by <code>parallel::makeCluster()</code> , with the number of workers equal to <code>ncpus</code> . Parallel processing, though not enabled by default, is recommended because it can speed up the computation a lot.
<code>ncpus</code>	The number of workers if <code>parallel</code> is <code>TRUE</code> . Default is <code>parallel::detectCores(logical = FALSE) - 1</code> , the number of physical cores minus 1.
<code>use_pbapply</code>	If <code>TRUE</code> and <code>pbapply::pbapply</code> is installed, <code>pbapply::pbapply</code> will be used to display the progress in computing the log profile likelihood. Default is <code>TRUE</code> .
<code>interval</code>	A vector of numbers. If provided and has two elements, this will be used as the end points of the interval. If it has more than two elements, the elements will be used directly to form the values in the interval. Default is <code>NULL</code> .
<code>verbose</code>	Whether some diagnostic information will be printed. Default is <code>FALSE</code> .
<code>theta0</code>	The value at which the parameter is fixed to.

Details

It uses the methods presented in Pawitan (2013) to compute and visualize the log profile likelihood of a parameter in a structural equation model when this parameter is fixed to a value or a range of values. `loglike_range()` and `loglike_point()` compute the so-called "true" log profile likelihood, while `loglike_quad_range()` and `loglike_quad_point()` approximate the log profile likelihood by a quadratic function.

These functions are for creating illustrative examples and learning only, not for research use. Therefore, they are not as versatile as `sem1bci()` in the types of models and parameters supported. They can be used for free parameters and user-defined parameters not involved in any constraints. Only a model fitted by maximum likelihood is supported.

They will not check whether the computation is appropriate for a model. It is the responsibility of the users to ensure that the computation is appropriate for the model and parameter.

Value

`loglike_compare()` calls `loglike_range()` and `loglike_quad_range()` and returns their results in a `loglike_compare`-class object, a list with these elements:

- `quadratic`: The output of `loglike_quad_range()`.
- `loglikelihood`: The output of `loglike_range()`.
- `pvalue_quadratic`: The likelihood ratio test p -values at the quadratic approximation confidence bounds.
- `pvalue_loglikelihood`: The likelihood ratio test p -values at the likelihood-based confidence bounds.
- `est`: The point estimate of the parameter in `sem_out`.

`loglike_compare`-class object has a plot method (`plot.loglike_compare()`) that can be used to plot the log profile likelihood.

`loglike_point()` returns a list with these elements:

- `loglike`: The log profile likelihood of the parameter when it is fixed to `theta0`.
- `pvalue`: The p -values based on the likelihood ratio difference test between the original model and the model with the parameter fixed to `theta0`.
- `fit`: A `lavaan::lavaan` object. The original model with the parameter fixed to `theta0`.
- `lrt`: The output of `lavaan::lavTestLRT()`, comparing the original model to the model with the parameter fixed to `theta0`.

`loglike_quad_range()` returns a data frame with these columns:

- `theta`: The values to which the parameter is fixed to.
- `loglike`: The log profile likelihood values of the parameter using quadratic approximation.
- `pvalue`: The p -values based on the likelihood ratio difference test between the original model and the model with the parameter fixed to `theta`.

`loglike_quad_point()` returns a single number of the class `lavaan.vector` (because it is the output of `lavaan::fitMeasures()`). This number is the quadratic approximation of the log profile likelihood when the parameter is fixed to `theta0`.

`loglike_range()` returns a data frame with these columns:

- theta: The values to which the parameter is fixed to.
- loglike: The log profile likelihood at theta.
- pvalue: The p -values based on the likelihood ratio difference test between the original model and model with the parameter fixed to theta.

Functions

- loglike_compare(): Generates points for log profile likelihood and quadratic approximation, by calling the helper functions loglike_range() and loglike_quad_range().
- loglike_range(): Find the log profile likelihood for a range of values.
- loglike_point(): Find the log likelihood at a value.
- loglike_quad_range(): Find the approximated log likelihood for a range of values.
- loglike_quad_point(): Find the approximated log likelihood at a value.

References

Pawitan, Y. (2013). *In all likelihood: Statistical modelling and inference using likelihood*. Oxford University Press.

See Also

[plot.loglike_compare\(\)](#)

Examples

```
## loglike_compare

library(lavaan)
data(simple_med)
dat <- simple_med
mod <-
"
m ~ a * x
y ~ b * m
ab := a * b
"
fit <- lavaan::sem(mod, simple_med, fixed.x = FALSE)

# 4 points are used just for illustration
# At least 21 points should be used for a smooth plot
# Remove try_k_more in real applications. It is set
# to zero such that this example does not take too long to run.
# use_pbapply can be removed or set to TRUE to show the progress.
ll_a <- loglike_compare(fit, par_i = "m ~ x", n_points = 4,
                       try_k_more = 0,
                       use_pbapply = FALSE)

plot(ll_a)

# See the vignette "loglike" for an example for the
# indirect effect.
```

```
## loglike_range

# Usually not to be used directly.
# Used by loglike_compare().
# 3 points are used just for illustration
ll_1 <- loglike_range(fit, par_i = "y ~ m", n_points = 2)
head(ll_1)

## loglike_point

# Usually not to be used directly.
# Used by loglike_compare().
llp_1 <- loglike_point(theta0 = 0.3, sem_out = fit, par_i = "y ~ m")
llp_1$loglike
llp_1$pvalue
llp_1$lrt

## loglike_quad_range

# Usually not to be used directly.
# Used by loglike_compare().
# 2 points are used just for illustration
lq_1 <- loglike_quad_range(fit, par_i = "y ~ m", n_points = 2)
head(lq_1)

## loglike_quad_point

# Usually not to be used directly.
# Used by loglike_compare().
lqp_1 <- loglike_quad_point(theta0 = 0.3, sem_out = fit, par_i = "y ~ m")
lqp_1
```

mediation_latent	<i>Dataset (SEM, Three Factors, Nine Variables, Mediation)</i>
------------------	--

Description

Generated from a three-factor model with nine variables, $n = 150$

Usage

```
mediation_latent
```

Format

A data frame with 150 rows and nine variables:

```
x1 x1
x2 x2
x3 x3
x4 x4
x5 x5
x6 x6
x7 x7
x8 x8
x9 x9
```

Details

This model is used for examples like this one:

```
mod <-
"
fx =~ x1 + x2 + x3
fm =~ x4 + x5 + x6
fy =~ x7 + x8 + x9
fm ~ a*fx
fy ~ b*fm + cp*fx
ab := a*b
"
fit <- lavaan::sem(mod, mediation_latent)
```

Examples

```
print(head(mediation_latent), digits = 3)
nrow(mediation_latent)
```

mediation_latent_skewed

Dataset (SEM, Three Factors, Nine Variables, Mediation, Skewed)

Description

Generated from a three-factor model with nine variables, $n = 150$, with some observed variables positively skewed.

Usage

```
mediation_latent_skewed
```

Format

A data frame with 150 rows and nine variables:

```
x1 x1
```

```
x2 x2
```

```
x3 x3
```

```
x4 x4
```

```
x5 x5
```

```
x6 x6
```

```
x7 x7
```

```
x8 x8
```

```
x9 x9
```

Details

This model is used for examples like this one:

```
mod <-  
"  
fx =~ x1 + x2 + x3  
fm =~ x4 + x5 + x6  
fy =~ x7 + x8 + x9  
fm ~ a*fx  
fy ~ b*fm + cp*fx  
ab := a*b  
"  
fit <- lavaan::sem(mod, mediation_latent)
```

Examples

```
print(head(mediation_latent_skewed), digits = 3)  
nrow(mediation_latent_skewed)
```

nearby_levels *LBCI Bounds of Nearby Levels of Confidence*

Description

Find LBCIs with levels of confidence different from those stored in a `semlbci`-class object.

Usage

```
nearby_levels(x, cipercl_levels = c(-0.025, 0.025), cipercl_range = c(0.6, 0.99))
```

Arguments

<code>x</code>	The output of <code>semlbci()</code> .
<code>cipercl_levels</code>	A numeric vector of deviations from the original level of confidence. The default is <code>c(-.025, .025)</code> . Therefore, if the original level is <code>.95</code> , the levels to be used is <code>c(-.025, .025) + .95</code> or <code>c(.925, .975)</code> .
<code>cipercl_range</code>	A numeric vector of two numbers, which are the minimum and maximum levels of confidence to be used, respectively. Default is <code>c(.60, .99)</code> .

Details

It receives a `semlbci`-class object, gets the original level of confidence, generates one or more levels of confidence different from this level by certain amounts, and repeats the original call to `semlbci()` with these levels of confidence. The results are returned as a list of class `semlbci_list`, with the original `semlbci`-class included.

Value

A `semlbci_list`-class object, which is simply a named list of `semlbci`-class object, names being the levels of confidence.

Author(s)

Shu Fai Cheung <https://orcid.org/0000-0002-9871-9448>

See Also

`semlbci()`, `ci_order()`

Examples

```
library(lavaan)
mod <-
"
m ~ x
y ~ m
"
```

```

fit_med <- sem(mod, simple_med, fixed.x = FALSE)
lbc_fit <- semlbc_fit(fit_med)
lbc_fit_nb <- nearby_levels(lbc_fit,
                           ciper_levels = c(-.050, .050))

names(lbc_fit_nb)
# Check the order of the confidence bounds.
# A confidence interval with a higher level of confidence
# should enclose a confidence interval with
# a lower level of confidence.
ci_order(lbc_fit_nb)

```

plot.loglike_compare *Plot the Output of 'loglike_compare()'*

Description

Visualize the log profile likelihood of a parameter fixed to values in a range.

Usage

```

## S3 method for class 'loglike_compare'
plot(
  x,
  y,
  type = c("ggplot2", "default"),
  size_label = 4,
  size_point = 4,
  nd_theta = 3,
  nd_pvalue = 3,
  size_theta = 4,
  size_pvalue = 4,
  add_pvalues = FALSE,
  ...
)

```

Arguments

x	The output of <code>loglike_compare()</code> .
y	Not used.
type	Character. If "ggplot2", will use <code>ggplot2::ggplot()</code> to plot the graph. If "default", will use R base graphics. The ggplot2 version plots more information. Default is "ggplot2".
size_label	The relative size of the labels for thetas (and p -values, if requested) in the plot, determined by <code>ggplot2::rel()</code> . Default is 4.
size_point	The relative size of the points to be added if p -values are requested in the plot, determined by <code>ggplot2::rel()</code> . Default is 4.

nd_theta	The number of decimal places for the labels of theta. Default is 3.
nd_pvalue	The number of decimal places for the labels of p -values. Default is 3.
size_theta	Deprecated. No longer used.
size_pvalue	Deprecated. No longer used.
add_pvalues	If TRUE, likelihood ratio test p -values will be included for the confidence limits. Only available if type = "ggplot2".
...	Optional arguments. Ignored.

Details

Given the output of `loglike_compare()`, it plots the log profile likelihood based on quadratic approximation and that based on the original log-likelihood. The log profile likelihood is scaled to have a maximum of zero (at the point estimate) as suggested by Pawitan (2013).

Value

Nothing if type = "default", the generated `ggplot2::ggplot()` graph if type = "ggplot2".

References

Pawitan, Y. (2013). *In all likelihood: Statistical modelling and inference using likelihood*. Oxford University Press.

Examples

```
## loglike_compare

library(lavaan)
data(simple_med)
dat <- simple_med
mod <-
"
m ~ a * x
y ~ b * m
ab := a * b
"
fit <- lavaan::sem(mod, simple_med, fixed.x = FALSE)

# Four points are used just for illustration
# At least 21 points should be used for a smooth plot
# Remove try_k_more in real applications. It is set
# to run such that this example is not too slow.
# use_pbapply can be removed or set to TRUE to show the progress.
ll_a <- loglike_compare(fit, par_i = "m ~ x", n_points = 4,
                       try_k_more = 0,
                       use_pbapply = FALSE)

plot(ll_a)
plot(ll_a, add_pvalues = TRUE)
```

```
# See the vignette "loglike" for an example for the
# indirect effect.
```

```
print.cibound          Print Method of a 'cibound'-class Object
```

Description

Print the diagnostic information of a cibound-class object.

Usage

```
## S3 method for class 'cibound'
print(x, digits = 5, ...)
```

Arguments

x	The output of a <code>ci_bound_xx_i</code> function. Currently the only such function is <code>ci_bound_wn_i()</code> .
digits	The number of digits after the decimal point. To be passed to <code>round()</code> . Default is 5.
...	Other arguments. They will be ignored.

Details

This is the print method for the output of `ci_bound_wn_i()`, a cibound-class object. It prints the diagnostic information on the bound being found and the search process.

Value

x is returned invisibly. Called for its side effect.

Examples

```
data(simple_med)
dat <- simple_med

mod <-
"
m ~ x
y ~ m
"

fit_med <- lavaan::sem(mod, simple_med, fixed.x = FALSE)

fn_constr0 <- set_constraint(fit_med)
```

```

out11 <- ci_bound_wn_i(i = 1,
                      npar = 5,
                      sem_out = fit_med,
                      f_constr = fn_constr0,
                      which = "lbound")

# Print the output
out11

```

```

print.semlbci      Print Method of a 'semlbci' Object

```

Description

Prints the results of a `semlbci` object, the output of `semlbci()`.

Usage

```

## S3 method for class 'semlbci'
print(
  x,
  digits = 3,
  annotation = TRUE,
  time = FALSE,
  verbose = FALSE,
  verbose_if_needed = TRUE,
  drop_no_lbci = TRUE,
  output = c("table", "text", "lavaan"),
  sem_out = NULL,
  lbci_only = drop_no_lbci,
  ratio_digits = 1,
  se = TRUE,
  zstat = TRUE,
  pvalue = TRUE,
  boot.ci.type = "perc",
  ...
)

```

Arguments

<code>x</code>	The output of <code>semlbci()</code> .
<code>digits</code>	The number of digits after the decimal point. To be passed to <code>formatC()</code> . Default is 3.
<code>annotation</code>	If TRUE, print table notes. Default is TRUE.
<code>time</code>	If TRUE, print the time spent on each bound. Default is FALSE.

verbose	If TRUE, additional diagnostic information will always be printed. This argument overrides verbose_if_needed. Default is FALSE.
verbose_if_needed	If TRUE, additional diagnostic information will be printed only if necessary. If FALSE, additional diagnostic information will always be printed. Default is TRUE.
drop_no_lbci	If TRUE, parameters without LBCIs will be removed. Default is TRUE.
output	The type of printout. If "table", the default, the results will be printed in a table. If "text" or "lavaan", then the results will be printed in the lavaan style, as in the summary() method for the output of lavaan.
sem_out	If output is "text" or "lavaan", the original output of lavaan used in calling semlbci() needs to be supplied to this argument.
lbci_only	Used only if output is "text" or "lavaan". If TRUE, only the likelihood-based confidence intervals (LBCIs) will be printed. If FALSE, LBCIs will be printed alongside the confidence intervals by lavaan. Its default value depend on the argument drop_no_lbci. If drop_no_lbci is TRUE, then lbci_only is TRUE by default. If drop_no_lbci is FALSE, then lbci_only is FALSE by default.
ratio_digits	The number of digits after the decimal points for the ratios of distance from the confidence limits to the point estimates. Default is 1.
se	Logical. To be passed to lavaan::parameterEstimates() . Whether standard error (S.E.) will be printed. Only applicable if output is "text" or "lavaan".
zstat	Logical. To be passed to lavaan::parameterEstimates() . Whether z-values will be printed. Only applicable if output is "text" or "lavaan".
pvalue	Logical. To be passed to lavaan::parameterEstimates() . Whether p-values will be printed. Only applicable if output is "text" or "lavaan".
boot.ci.type	Logical. To be passed to lavaan::parameterEstimates() . The type of bootstrap confidence intervals to be printed if bootstrapping confidence intervals available. Possible values are "norm", "basic", "perc", or "bca.simple". The default value is "perc". Refer to the help of lavaan::parameterEstimates() for further information. Only applicable if output is "text" or "lavaan".
...	Other arguments. They will be ignored.

Details

Prints the results of [sem**l**bci\(\)](#) as a table.

Value

x is returned invisibly. Called for its side effect.

Author(s)

Shu Fai Cheung <https://orcid.org/0000-0002-9871-9448>

See Also[semlbci\(\)](#)**Examples**

```

library(lavaan)
mod <-
"
m ~ a*x
y ~ b*m
ab := a * b
"
fit_med <- sem(mod, simple_med, fixed.x = FALSE)
p_table <- parameterTable(fit_med)
p_table
lbc_med <- semlbci(fit_med,
                  pars = c("ab :="))
lbc_med

print(lbc_med, verbose_if_needed = FALSE)

print(lbc_med, verbose = TRUE)

print(lbc_med, time = TRUE)

print(lbc_med, annotation = FALSE)

print(lbc_med, digits = 4)

# Text output

print(lbc_med, output = "lavaan", sem_out = fit_med)

print(lbc_med, output = "lavaan", sem_out = fit_med, lbc_only = FALSE)

print(lbc_med, output = "lavaan", sem_out = fit_med, lbc_only = FALSE,
      se = FALSE, zstat = FALSE, pvalue = FALSE)

```

reg_cor_near_one

Dataset (Six Variables, One Correlation Close to One)

Description

Generated from a regression model six variables, $x_4 \sim x_5$ correlation close to one.

Usage

```
reg_cor_near_one
```


Format

A data frame with 100 rows and six variables:

x1 x1

x2 x2

x3 x3

x4 x4, with correlation with x5 nearly equal to 1

x5 x5, with correlation with x4 nearly equal to 1

y y, the dependent variable

Details

This model is used for examples like this one:

```
out <- lm(y ~ x1 + x2 + x3 + x4 + x5, reg_cor_near_one)
summary(out)
cor(reg_cor_near_one[, c("x4", "x5")])
```

Examples

```
print(head(reg_cor_near_one), digits = 3)
nrow(reg_cor_near_one)
```

 semIbci

Likelihood-Based Confidence Interval

Description

Find the likelihood-based confidence intervals (LBCIs) for selected free parameters in an SEM output.

Usage

```
semIbci(
  sem_out,
  pars = NULL,
  include_user_pars = TRUE,
  remove_variances = TRUE,
  remove_intercepts = TRUE,
  ciperc = 0.95,
  standardized = FALSE,
  method = c("wn", "ur"),
  robust = c("none", "satorra.2000"),
  try_k_more_times = 2,
```

```

semLbci_out = NULL,
check_fit = TRUE,
...,
parallel = FALSE,
ncpus = 2,
use_pbapply = TRUE,
loadbalancing = TRUE
)

```

Arguments

<code>sem_out</code>	The SEM output. Currently supports <code>lavaan::lavaan</code> outputs only.
<code>pars</code>	The positions of the parameters for which the LBCIs are to be searched. Use the position as appeared on the parameter tables of the <code>sem_out</code> . If <code>NULL</code> , the default, then LBCIs for all free parameters will be searched. Can also be a vector of strings to indicate the parameters on the parameter table. The parameters should be specified in <code>lavaan::lavaan()</code> syntax. The vector of strings will be converted by <code>syntax_to_i()</code> to parameter positions. See <code>syntax_to_i()</code> on how to specify the parameters.
<code>include_user_pars</code>	Logical. Whether all user-defined parameters are automatically included when <code>pars</code> is not set. Default is <code>TRUE</code> . If <code>pars</code> is explicitly set, this argument will be ignored.
<code>remove_variances</code>	Logical. Whether variances and error variances will be removed. Default is <code>TRUE</code> , removing all variances and error variances even if specified in <code>pars</code> .
<code>remove_intercepts</code>	Logical. Whether intercepts will be removed. Default is <code>TRUE</code> , removing all intercepts (parameters with operator <code>~1</code>). Intercepts are not yet supported in standardized solution and so will always be removed if <code>standardized = TRUE</code> .
<code>ciperc</code>	The proportion of coverage for the confidence interval. Default is <code>.95</code> , requesting a 95 percent confidence interval.
<code>standardized</code>	If <code>TRUE</code> , the LBCI is for the standardized estimates.
<code>method</code>	The method to be used to search for the confidence bounds. Supported methods are <code>"wn"</code> (Wu-Neale-2012), the default, and <code>"ur"</code> (root finding by <code>stats::uniroot()</code>).
<code>robust</code>	Whether the LBCI based on robust likelihood ratio test is to be found. Only <code>"satorra.2000"</code> in <code>lavaan::lavTestLRT()</code> is supported for now, implemented by the method proposed by Falk (2018). If <code>"none"</code> , the default, then likelihood ratio test based on maximum likelihood estimation will be used.
<code>try_k_more_times</code>	How many more times to try if failed. Default is 2.
<code>semLbci_out</code>	An <code>semLbci</code> -class object. If provided, parameters already with LBCIs formed will be excluded from <code>pars</code> .
<code>check_fit</code>	If <code>TRUE</code> (default), the input (<code>sem_out</code>) will be checked by <code>check_sem_out()</code> . If not supported, an error will be raised. If <code>FALSE</code> , the check will be skipped and the LBCIs will be searched even for a model or parameter not supported. Set to <code>TRUE</code> only for testing.

...	Arguments to be passed to <code>ci_bound_wn_i()</code> .
<code>parallel</code>	If TRUE, will use parallel processing to do the search.
<code>ncpus</code>	The number of workers, if <code>parallel</code> is TRUE. Default is 2. This number should not be larger than the number CPU cores.
<code>use_pbapply</code>	If TRUE and <code>pbapply</code> is installed, <code>pbapply::pbapply()</code> will be used to display a progress bar when finding the intervals. Default is TRUE. Ignored if <code>pbapply</code> is not installed.
<code>loadbalancing</code>	Whether load balancing is used when <code>parallel</code> is TRUE and <code>use_pbapply</code> is TRUE.

Details

`semlbci()` finds the positions of the selected parameters in the parameter table and then calls `ci_i_one()` once for each of them. For the technical details, please see `ci_i_one()` and the functions it calls to find a confidence bound, currently `ci_bound_wn_i()`. `ci_bound_wn_i()` uses the approach proposed by Wu and Neale (2012) and illustrated by Pek and Wu (2015).

It supports updating an output of `semlbci()` by setting `semlbci_out`. This allows forming LBCIs for some parameters after those for some others have been formed.

If possible, parallel processing should be used (see `parallel` and `ncpus`), especially for a model with many parameters.

If the search for some of the confidence bounds failed, with NA for the bounds, try increasing `try_k_more_times`.

The SEM output will first be checked by `check_sem_out()` to see whether the model and the estimation method are supported. To skip this test (e.g., for testing or experimenting with some models and estimators), set `check_fit` to FALSE.

Examples and technical details can be found at Cheung and Pesigan (2023), the website of the `semlbci` package (<https://sfcheung.github.io/semlbci/>), and the technical appendices at (<https://sfcheung.github.io/semlbci/appendices/>).

It currently supports `lavaan::lavaan` outputs only.

Value

A `semlbci`-class object similar to the parameter table generated by `lavaan::parameterEstimates()`, with the LBCIs for selected parameters added. Diagnostic information, if requested, will be included in the attributes. See `print.semlbci()` for options available.

Author(s)

Shu Fai Cheung <https://orcid.org/0000-0002-9871-9448>

References

Cheung, S. F., & Pesigan, I. J. A. (2023). *semlbci*: An R package for forming likelihood-based confidence intervals for parameter estimates, correlations, indirect effects, and other derived parameters. *Structural Equation Modeling: A Multidisciplinary Journal*, 30(6), 985–999. doi:10.1080/10705511.2023.2183860

Falk, C. F. (2018). Are robust standard errors the best approach for interval estimation with non-normal data in structural equation modeling? *Structural Equation Modeling: A Multidisciplinary Journal*, 25(2), 244-266. doi:10.1080/10705511.2017.1367254

Pek, J., & Wu, H. (2015). Profile likelihood-based confidence intervals and regions for structural equation models. *Psychometrika*, 80(4), 1123-1145. doi:10.1007/s1133601594611

Wu, H., & Neale, M. C. (2012). Adjusted confidence intervals for a bounded parameter. *Behavior Genetics*, 42(6), 886-898. doi:10.1007/s105190129560z

Pritikin, J. N., Rappaport, L. M., & Neale, M. C. (2017). Likelihood-based confidence intervals for a parameter with an upper or lower bound. *Structural Equation Modeling: A Multidisciplinary Journal*, 24(3), 395-401. doi:10.1080/10705511.2016.1275969

See Also

`print.semlbci()`, `confint.semlbci()`, `ci_i_one()`, `ci_bound_wn_i()`

Examples

```
library(lavaan)
mod <-
"
m ~ a*x
y ~ b*m
ab := a * b
"

fit_med <- sem(mod, simple_med, fixed.x = FALSE)
p_table <- parameterTable(fit_med)
p_table
lbc_med <- semlbc(fit_med,
                 pars = c("m ~ x",
                         "y ~ m",
                         "ab :="))

lbc_med
```

set_constraint

Equality Constraint for Finding the LBCI by Wu-Neale-2012

Description

Create the equality constraint for finding the likelihood-based confidence interval (LBCI) by the Wu-Neale-2012 method.

Usage

```
set_constraint(sem_out, ciper = 0.95)
```

Arguments

sem_out The SEM output. Currently supports `lavaan::lavaan` outputs only.
 ciperc The intended coverage probability of the confidence interval. Default is .95.

Details**Important Notice:**

This function is not supposed to be used directly by users in typical scenarios. Its interface is user-*unfriendly* because it should be used through `sem1bci()`. It is exported such that interested users can examine how a confidence bound is found, or use it for experiments or simulations.

Usage:

The Wu-Neale-2012 method uses a simple objective function that is optimized with an equality constraint. `set_constraint()` generates the equality constraint function to be used by `ci_bound_wn_i()`. It currently supports `lavaan::lavaan` outputs only.

Value

An equality constraint function to be used by `ci_bound_wn_i()`.

Examples

```
library(lavaan)
data(simple_med)
dat <- simple_med
mod <-
"
m ~ x
y ~ m
"
fit_med <- sem(mod, simple_med, fixed.x = FALSE)

fn_constr0 <- set_constraint(fit_med)
out <- fn_constr0(coef(fit_med), sem_out = fit_med)
out
lavTech(fit_med, "optim")$fx
```

simple_med

Dataset (Simple Mediation Model)

Description

Generated from a simple mediation model, n = 200

Usage

simple_med

Format

A data frame with 200 rows and three variables:

x x, the independent variable

m m, the mediator

y y, the dependent variable

Details

This model is used for examples like this one:

```
library(lavaan)
mod <- "m ~ x
       y ~ m"
fit <- cfa(mod, simple_med)
summary(fit)
```

Examples

```
print(head(simple_med), digits = 3)
nrow(simple_med)
```

simple_med_mg	<i>Dataset (Simple Mediation Model, Two Groups)</i>
---------------	---

Description

Generated from a simple mediation model, n = 200, two groups, n = 100 each.

Usage

```
simple_med_mg
```

Format

A data frame with 500 rows and four variables:

gp gp, the grouping variable

x x, the independent variable

m m, the mediator

y y, the dependent variable

Details

This model is used for examples like this one:

```
library(lavaan)
mod <- "m ~ x
      y ~ m"
fit <- sem(mod, simple_med_mg, gp = "group")
summary(fit)
```

Examples

```
print(head(simple_med_mg), digits = 3)
nrow(simple_med_mg)
table(simple_med_mg$gp)
```

syntax_to_i

Parameter Positions From lavaan Syntax

Description

Converts lavaan syntax to positions in the model parameter table.

Usage

```
syntax_to_i(syntax, sem_out)
```

Arguments

syntax	A vector of parameters, defined as in lavaan.
sem_out	The SEM output. Currently lavaan output only.

Details

`syntax_to_i()` converts a vector of strings, in lavaan syntax, to the positions in the parameter table of a `lavaan::lavaan` fit object.

Each element in the vector should have left hand side (lhs), operator (op), and/or right hand side (rhs). For example:all.x

- "m ~ x" denotes the coefficient of the path from x to m.
- "y ~~ x" denotes the covariance between y and x.

For user-defined parameters, only lhs and op will be interpreted. For example:

- To specify the user parameter ab, both "ab := ..." and "ab :=" will do, ... the definition of ab in the model. The right-hand side will be ignored.

To denote a labelled parameters, such as "y ~ a*x", treat it as a user-defined parameters and use :=, e.g., "a := " in this example.

For multiple-group models, if a parameter is specified as in a single-group models, then this parameter in all groups will be selected. For example:all.x

- If a model has three groups, "y ~ x" denotes this path parameter in all three groups, and it will be converted to three row numbers.

To select the parameter in a specific group, "multiply" the right-hand-side variable by the group number. For example:

- "y ~ 2*x" denotes the path coefficient from x to y in Group 2.

To denote the parameters in more than one group, multiply the right-hand side variable by a vector of number. For example:all.x

- "f1 =~ c(2,3)*x2" denotes the factor loading of x2 on f1 in Group 2 and Group 3.

Elements that cannot be converted to a parameter in the parameter table will be ignored.

Currently supports [lavaan::lavaan](#) outputs only.

Value

A numeric vector of positions (row numbers) in the parameter table.

Examples

```
library(lavaan)
data(simple_med)
mod <-
"
m ~ a*x
y ~ b*m
ab:= a*b
asq:= a^2
"
fit_med <- sem(mod, simple_med, fixed.x = FALSE)
p_table <- parameterTable(fit_med)

pars <- c("m ~ x",
         "y ~ m",
         "asq := 1",
         "ab := 2")
out <- syntax_to_i(pars, fit_med)
out
p_table[out, ]
```


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