

# Package ‘quickpsy’

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**Type** Package

**Title** Fits Psychometric Functions for Multiple Groups

**Version** 0.1.4

**URL** <http://dlinares.org/quickpsy.html>

**Description** Quickly fits and plots psychometric functions (normal, logistic, Weibull or any or any function defined by the user) for multiple groups.

**Depends** R (>= 3.1.2), DEoptim, dplyr, ggplot2

**Imports** MPDiR

**Encoding** UTF-8

**License** MIT + file LICENSE

**LazyData** true

**RoxygenNote** 5.0.1

**NeedsCompilation** no

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---

aic

*Calculates the AICs*

---

### Description

aic calculates the AICs.

### Usage

aic(qp)

### Arguments

qp                      output from quickpsy

---

avbootstrap	<i>Creates bootstrap samples</i>
-------------	----------------------------------

---

**Description**

avbootstrap creates bootstrap samples

**Usage**

```
avbootstrap(qp, bootstrap = "parametric", B = 100)
```

**Arguments**

qp	output from quickpsy
bootstrap	'parametric' performs parametric bootstrap; 'nonparametric' performs non-parametric bootstrap; 'none' does not perform bootstrap (default is 'parametric').
B	number of bootstrap samples (default is 100 ONLY).

---

cum_normal_fun	<i>Cumulative normal function</i>
----------------	-----------------------------------

---

**Description**

Cumulative normal function.

**Usage**

```
cum_normal_fun(x, p)
```

**Arguments**

x	Vector of values of the explanatory variable.
p	Vector of parameters $p = c(\text{mean}, \text{standard\_deviation})$ .

**Value**

Probability at each x.

**See Also**

[inv\\_cum\\_normal\\_fun](#)

**Examples**

```
xseq <- seq(0,4, .01)
yseq <- cum_normal_fun(xseq, c(2, .5))
curve <- data.frame(x = xseq, y = yseq)
ggplot(curve, aes(x = x, y = y)) + geom_line()
```

deviance *Calculates the deviances*

---

**Description**

deviance calculates the deviances.

**Usage**

```
deviance(qp)
```

**Arguments**

qp                    output from quickpsy

**Examples**

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 20)
deviance(fit)
```

---

devianceboot *Calculates the bootstrap deviances*

---

**Description**

devianceboot calculates the bootstrap deviances.

**Usage**

```
devianceboot(qp)
```

**Arguments**

qp                    output from quickpsy

**Examples**

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 20)
devianceboot(fit)
```

---

get_functions	<i>Predefined functions</i>
---------------	-----------------------------

---

**Description**

getfunctions lists the predefined functions in quickpsy.

**Usage**

```
get_functions()
```

**See Also**

[cum\\_normal\\_fun](#), [logistic\\_fun](#), [weibull\\_fun](#)

---

inv_cum_normal_fun	<i>Inverse cumulative normal function</i>
--------------------	---

---

**Description**

Inverse cumulative normal function

**Usage**

```
inv_cum_normal_fun(prob, p)
```

**Arguments**

prob	Vector of probabilities.
p	Vector of parameters $p = c(\text{mean}, \text{standard\_deviation})$ .

**Value**

x at each probability. #' @seealso [cum\\_normal\\_fun](#)

**Examples**

```
yseq <- seq(0, 1, .01)
xseq <- inv_cum_normal_fun(yseq, c(2, .5))
curve <- data.frame(x = xseq, y = yseq)
ggplot(curve, aes(x = x, y = y)) + geom_line()
```

---

inv\_logistic\_fun      *Inverse logistic function*

---

**Description**

Inverse logistic function

**Usage**

```
inv_logistic_fun(q, p)
```

**Arguments**

q                      Vector of probabilities.  
p                      Vector of parameters  $p = c(\alpha, \beta)$ .

**Value**

x at each probability.

**See Also**

[logistic\\_fun](#)

**Examples**

```
yseq <- seq(0, 1, .01)  
xseq <- inv_logistic_fun(yseq, c(2, 4))  
curve <- data.frame(x = xseq, y = yseq)  
ggplot(curve, aes(x = x, y = y)) + geom_line()
```

---

inv\_weibull\_fun      *Inverse Weibull function*

---

**Description**

Inverse Weibull function

**Usage**

```
inv_weibull_fun(q, p)
```

**Arguments**

q                      Vector of probabilities.  
p                      Vector of parameters  $p = c(\alpha, \beta)$ .

**Value**

x at each probability.

**See Also**

[weibull\\_fun](#)

**Examples**

```
yseq <- seq(0, 1, .01)
xseq <- inv_weibull_fun(yseq, c(2, 4))
curve <- data.frame(x = xseq, y = yseq)
ggplot(curve, aes(x = x, y = y)) + geom_line()
```

---

logistic\_fun

*Logistic function*

---

**Description**

Logistic function of the form  $(1 + \exp(-\beta * (x - \alpha)))^{-1}$

**Usage**

```
logistic_fun(x, p)
```

**Arguments**

x                      Vector of values of the explanatory variable.  
p                      Vector of parameters  $p = c(\alpha, \beta)$ .

**Value**

Probability at each x.

**See Also**

[inv\\_logistic\\_fun](#)

**Examples**

```
xseq <- seq(0, 4, .01)
yseq <- logistic_fun(xseq, c(2, 4))
curve <- data.frame(x = xseq, y = yseq)
ggplot(curve, aes(x = x, y = y)) + geom_line()
```

logliks *Calculates the loglikelihoods* logliks *calculates the loglikelihoods.*

---

**Description**

Calculates the loglikelihoods logliks calculates the loglikelihoods.

**Usage**

```
logliks(qp)
```

**Arguments**

qp                    output from quickpsy

---

logliksboot *Calculates the bootstrap loglikelihoods*

---

**Description**

logliksboot calculates the bootstraploglikelihoods.

**Usage**

```
logliksboot(qp)
```

**Arguments**

qp                    output from quickpsy

**Examples**

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 20)
logliksboot(fit)
```

---

loglikssaturated *Calculates the bootstrap loglikelihoods for the saturated model*

---

**Description**

loglikssaturated calculates the bootstrap loglikelihoods for the saturated model.

**Usage**

```
loglikssaturated(qp)
```

**Arguments**

qp                    output from quickpsy

**Examples**

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 20)
loglikssaturated(fit)
```

---

loglikssaturated *Calculates the loglikelihoods of the saturated model*

---

**Description**

loglikssaturated calculates the loglikelihoods of the saturated model.

**Usage**

```
loglikssaturated(qp)
```

**Arguments**

qp                    output from quickpsy

**Examples**

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 20)
loglikssaturated(fit)
```

---

parbootstrap	<i>Creates bootstrap samples of the parameters</i>
--------------	--

---

**Description**

parbootstrap creates bootstrap samples of the parameters.

**Usage**

```
parbootstrap(qp)
```

**Arguments**

qp	output from quickpsy
----	----------------------

---

plotcurves	<i>Plot the curves</i>
------------	------------------------

---

**Description**

plotcurves plot the curves.

**Usage**

```
plotcurves(qp, panel = NULL, xpanel = NULL, ypanel = NULL, color = NULL,
  averages = T, curves = T, thresholds = T, ci = T)
```

**Arguments**

qp	output from quickpsy
panel	Name of the variable to be split in panels.
xpanel	Name of the variable to be split in horizontal panels.
ypanel	Name of the variable to be split in vertical panels.
color	Name of the variable coded by color.
averages	If FALSE averaged probabilities are not plotted (default is TRUE).
curves	If FALSE curves are not plotted (default is TRUE)
thresholds	If FALSE thresholds are not plotted (default is TRUE)
ci	If FALSE confidence intervals are not plotted (default is TRUE)

**See Also**

[plotcurves\\_](#)

**Examples**

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 5)
plotcurves(fit)
plotcurves(fit, xpanel = Direction)
plotcurves(fit, xpanel = Direction, color = WaveForm, ci = FALSE)
```

---

plotcurves\_                      *Plot the curves*

---

**Description**

plotcurves\_ is the standard evaluation SE function associated to the non-standard evaluation NSE function plotcurves. **SE functions can be more easily called from other functions.** In SE functions, you need to quote the names of the variables.

**Usage**

```
plotcurves_(qp, panel = NULL, xpanel = NULL, ypanel = NULL,
            color = NULL, averages = TRUE, curves = TRUE, thresholds = TRUE,
            ci = TRUE)
```

**Arguments**

qp	output from quickpsy
panel	Name of the variable to be split in panels.
xpanel	Name of the variable to be split in horizontal panels.
ypanel	Name of the variable to be split in vertical panels.
color	Name of the variable coded by color.
averages	If FALSE averaged probabilities are not plotted (default is TRUE).
curves	If FALSE curves are not plotted (default is TRUE)
thresholds	If FALSE thresholds are not plotted (default is TRUE)
ci	If FALSE confidence intervals are not plotted (default is TRUE)

**See Also**

[plotcurves](#)

**Examples**

```
library(MPDiR) # contains the Vernier data
data(Vernier) # ?Veniier for the reference
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 5)

plotcurves_(fit, xpanel = 'Direction')
plotcurves_(fit, color = 'Direction')
plotcurves_(fit, xpanel = 'Direction', color = 'WaveForm', ci = FALSE)
```

---

plotpar

*Plot the values of the parameters*


---

**Description**

plotpar plot the values of the parameters.

**Usage**

```
plotpar(qp, x = NULL, panel = NULL, xpanel = NULL, ypanel = NULL,
        color = NULL, geom = "bar", ci = T)
```

**Arguments**

qp	output from quickpsy.
x	Name of the variable to displayed in the x-axis.
panel	Name of the variable to be split in panels.
xpanel	Name of the variable to be split in horizontal panels.
ypanel	Name of the variable to be split in vertical panels.
color	Name of the variable coded by color.
geom	If 'bar' displays bars. If 'point' displays points (default is 'bar').
ci	If FALSE confidence intervals are not plotted (default is TRUE).

**See Also**

[plotpar\\_](#)

**Examples**

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 10)

plotpar(fit)
plotpar(fit, x = WaveForm)
plotpar(fit, xpanel = Direction)
plotpar(fit, color = Direction)
plotpar(fit, color = Direction, ypanel = WaveForm, geom = 'point')
```

---

`plotpar_`*Plot the values of the parameters*

---

### Description

`plotpar_` is the standard evaluation SE function associated to the non-standard evaluation NSE function `plotpar`. **SE functions can be more easily called from other functions.** In SE functions, you need to quote the names of the variables.

### Usage

```
plotpar_(qp, x = NULL, panel = NULL, xpanel = NULL, ypanel = NULL,
         color = NULL, geom = "bar", ci = T)
```

### Arguments

<code>qp</code>	output from <code>quickpsy</code> .
<code>x</code>	Name of the variable to displayed in the x-axis.
<code>panel</code>	Name of the variable to be split in panels.
<code>xpanel</code>	Name of the variable to be split in horizontal panels.
<code>ypanel</code>	Name of the variable to be split in vertical panels.
<code>color</code>	Name of the variable coded by color.
<code>geom</code>	If 'bar' displays bars. If 'point' displays points (default is 'bar').
<code>ci</code>	If FALSE confidence intervals are not plotted (default is TRUE).

### See Also

[plotpar](#)

### Examples

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), bootstrap = 'none')

plotpar_(fit, x = 'WaveForm')
plotpar_(fit, xpanel = 'Direction')
plotpar_(fit, color = 'Direction')
plotpar_(fit, color = 'Direction', ypanel = 'WaveForm', geom = 'point')
```

---

plotthresholds      *Plot the thresholds*

---

### Description

plotthresholds plot the thresholds.

### Usage

```
plotthresholds(qp, x = NULL, panel = NULL, xpanel = NULL, ypanel = NULL,
  color = NULL, geom = "bar", ci = T, sizeerrorbar = 0.5)
```

### Arguments

qp	output from quickpsy.
x	Name of the variable to displayed in the x-axis.
panel	Name of the variable to be split in panels.
xpanel	Name of the variable to be split in horizontal panels.
ypanel	Name of the variable to be split in vertical panels.
color	Name of the variable coded by color.
geom	If 'bar' displays bars.
ci	If FALSE confidence intervals are not plotted (default is TRUE).
sizeerrorbar	Line width of the error bars. If 'point' displays points (default is 'bar').

### See Also

[plotthresholds\\_](#)

### Examples

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
  grouping = .(Direction, WaveForm, TempFreq), B = 10)
plotthresholds(fit)
plotthresholds(fit, x = WaveForm)
plotthresholds(fit, xpanel = Direction)
plotthresholds(fit, color = Direction, ypanel = WaveForm, geom = 'point')
```

---

plotthresholds\_      *Plot the thresholds*

---

### Description

plotthresholds\_ is the standard evaluation SE function associated to the non-standard evaluation NSE function plotthresholds. **SE functions can be more easily called from other functions.** In SE functions, you need to quote the names of the variables.

### Usage

```
plotthresholds_(qp, x = NULL, panel = NULL, xpanel = NULL,
  ypanel = NULL, color = NULL, geom = "bar", ci = T,
  sizeerrorbar = 0.5)
```

### Arguments

qp	output from quickpsy.
x	Name of the variable to displayed in the x-axis.
panel	Name of the variable to be split in panels.
xpanel	Name of the variable to be split in horizontal panels.
ypanel	Name of the variable to be split in vertical panels.
color	Name of the variable coded by color.
geom	If 'bar' displays bars.
ci	If FALSE confidence intervals are not plotted (default is TRUE).
sizeerrorbar	Line width of the error bars. If 'point' displays points (default is 'bar').

### See Also

[plotthresholds](#)

### Examples

```
library(MPDiR) # contains the Vernier data
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
  grouping = .(Direction, WaveForm, TempFreq), B = 10)

plotthresholds_(fit, x = 'WaveForm')
plotthresholds_(fit, xpanel = 'Direction')
plotthresholds_(fit, color = 'Direction')
plotthresholds_(fit, color = 'Direction', ypanel = 'WaveForm', geom = 'point')
```

---

 qpdatt

*Data set for demonstration*


---

### Description

It is part of the data associated with the paper 'Motion signal and the perceived positions of moving objects'.

### Usage

qpdatt

### Format

An object of class `grouped_df` (inherits from `tbl_df`, `tbl`, `data.frame`) with 6240 rows and 8 columns.

### References

Linares, D., López-Moliner, J., & Johnston, A. (2007). Motion signal and the perceived positions of moving objects. *Journal of Vision*, 7(7), 1.

---

 quickpsy

*Fits psychometric functions*


---

### Description

quickpsy fits, by direct maximization of the likelihood (Prins and Kingdom, 2010; Knoblauch and Maloney, 2012), psychometric functions of the form

$$\psi(x) = \gamma + (1 - \gamma - \lambda) * fun(x)$$

where  $\gamma$  is the guess rate,  $\lambda$  is the lapse rate and *fun* is a sigmoidal-shape function with asymptotes at 0 and 1.

### Usage

```
quickpsy(d, x = x, k = k, n = n, grouping, random, within, between,
  xmin = NULL, xmax = NULL, log = FALSE, fun = cum_normal_fun,
  parini = NULL, guess = 0, lapses = 0, prob = NULL, thresholds = T,
  bootstrap = "parametric", B = 100, ci = 0.95, optimization = "optim")
```

**Arguments**

d	Data frame with the results of a Yes-No experiment to fit. It should have a <b>tidy</b> form in which each column corresponds to a variable and each row is an observation.
x	Name of the explanatory variable.
k	Name of the response variable. The response variable could be the number of trials in which a yes-type response was given or a vector of 0s (or -1s; no-type response) and 1s (yes-type response) indicating the response on each trial.
n	Only necessary if k refers to the number of trials in which a yes-type response was given. It corresponds to the name of the variable indicating the total number of trials.
grouping	Name of the grouping variables. It should be specified as <code>grouping = .(variable_name1, variable_name2)</code> .
random	Name of the random variable. It should be specified as <code>random = .(variable_name1, variable_name2)</code> . In the current version of quickpsy, the random variable has not special treatment. It does the same as <code>grouping</code> .
within	Name of the within variable. It should be specified as <code>within = .(variable_name1, variable_name2)</code> . In the current version of quickpsy, the within variable has not special treatment. It does the same as <code>grouping</code> .
between	Name of the between variable. It should be specified as <code>between = .(variable_name1, variable_name2)</code> . In the current version of quickpsy, the between variable has not special treatment. It does the same as <code>grouping</code> .
xmin	Minimum value of the explanatory variable for which the curves should be calculated (the default is the minimum value of the explanatory variable).
xmax	Maximum value of the explanatory variable for which the curves should be calculated (the default is the maximum value of the explanatory variable).
log	If TRUE, the logarithm of the explanatory variable is used to fit the curves (default is FALSE).
fun	Name of the shape of the curve to fit. It could be a predefined shape ( <code>cum_normal_fun</code> , <code>logistic_fun</code> , <code>weibull_fun</code> ) or the name of a function introduced by the user (default is <code>cum_normal_fun</code> ).
parini	Initial parameters. quickpsy calculates default initial parameters using probit analysis, but it is also possible to specify a vector of initial parameters or a list of the form <code>list(c(par1min, par1max), c(par2min, par2max))</code> to constraint the lower and upper bounds of the parameters (when <code>optimization = 'DE'</code> , <code>parini</code> should be also a list).
guess	Value indicating the guess rate $\gamma$ (default is 0). If TRUE, the guess rate is estimated as the $i + 1$ parameter where $i$ corresponds to the number of parameters of <code>fun</code> . If, for example, <code>fun</code> is a predefined shape with parameters $p_1$ and $p_2$ , then the guess rate corresponds to parameter $p_3$ .
lapses	Value indicating the lapse rate $\lambda$ (default is 0). If TRUE, the lapse rate is estimated as the $i + 1$ parameter where $i$ corresponds to the number of parameters of <code>fun</code> plus one if the guess rate is estimated. If, for example, <code>fun</code> is a predefined shape with parameters $p_1$ and $p_2$ , then the lapse rate corresponds to parameter $p_3$ . If the guess rate is also estimated, $p_3$ will be the guess rate and $p_4$ the lapse rate.

prob	Probability to calculate the threshold (default is $\text{guess} + .5 * (1 - \text{guess})$ ).
thresholds	If FALSE, thresholds are not calculated (default is TRUE).
bootstrap	'parametric' performs parametric bootstrap; 'nonparametric' performs non-parametric bootstrap; 'none' does not perform bootstrap (default is 'parametric').
B	number of bootstrap samples (default is 100 ONLY).
ci	Confidence intervals level based on percentiles (default is .95).
optimization	Method used for optimization. The default is 'optim' which uses the optim function. It can also be 'DE' which uses de function DEoptim from the package DEoptim, which performs differential evolution optimization. By using DEoptim, it is less likely that the optimization finishes in a local minimum, but the optimization is slow. When 'DE' is used, parini should be specified as a list with lower and upper bounds.

### Value

A list containing the following components:

- x, k, n
- groups The grouping variables.
- funname String with the name of the shape of the curve.
- psyfunguesslapses Curve including guess and lapses.
- limits Limits of the curves.
- parini Initial parameters.
- optimization Method to optimize.
- pariniset FALSE if initial parameters are not given.
- ypred Predicted probabilities at the values of the explanatory variable.
- curves Curves.
- par Fitted parameters and its confidence intervals.
- curvesbootstrap Bootstrap curves.
- thresholds Thresholds.
- thresholdsci Confidence intervals for the thresholds.
- logliks Log-likelihoods of the model.
- loglikssaturated Log-likelihoods of the saturated model.
- deviance Deviance of the model and the p-value calculated by bootstrapping.
- aic AIC of the model defined as

$$-2 * \text{loglik} + 2 * k$$

where k is the number of parameters of the model.

## References

- Burnham, K. P., & Anderson, D. R. (2003). Model selection and multimodel inference: a practical information-theoretic approach. Springer Science & Business Media.
- Knoblauch, K., & Maloney, L. T. (2012). Modeling Psychophysical Data in R. New York: Springer.
- Prins, N., & Kingdom, F. A. A. (2016). Psychophysics: a practical introduction. London: Academic Press.

## See Also

[quickpsy\\_](#)

## Examples

```
# make sure that all the requires packages are installed
# and loaded; instructions at https://github.com/danilinares/quickpsy
library(MPDiR) # contains the Vernier data; use ?Vernier for the reference
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 10)
plotcurves(fit)
plotpar(fit)
plotthresholds(fit, geom = 'point')
```

---

quickpsy\_

*Fits psychometric functions*

---

## Description

quickpsy\_ is the standard evaluation SE function associated to the non-standard evaluation NSE function quickpsy. **SE functions can be more easily called from other functions.** In SE functions, you need to quote the names of the variables.

## Usage

```
quickpsy_(d, x = "x", k = "k", n = "n", grouping, random, within, between,
          xmin = NULL, xmax = NULL, log = FALSE, fun = "cum_normal_fun",
          parini = NULL, guess = 0, lapses = 0, prob = NULL, thresholds = T,
          bootstrap = "parametric", B = 100, ci = 0.95, optimization = "optim")
```

## Arguments

- |   |  |
|---|--|
| d | Data frame with the results of a Yes-No experiment to fit. It should have a <b>tidy</b> form in which each column corresponds to a variable and each row is an observation.  |
| x | Name of the explanatory variable.  |
| k | Name of the response variable. The response variable could be the number of trials in which a yes-type response was given or a vector of 0s (or -1s; no-type response) and 1s (yes-type response) indicating the response on each trial. |

n	Only necessary if k refers to the number of trials in which a yes-type response was given. It corresponds to the name of the variable indicating the total number of trials.
grouping	Name of the grouping variables. It should be specified as <code>grouping = .(variable_name1, variable_name2)</code> .
random	Name of the random variable. It should be specified as <code>random = .(variable_name1, variable_name2)</code> . In the current version of quickpsy, the random variable has not special treatment. It does the same as grouping.
within	Name of the within variable. It should be specified as <code>within = .(variable_name1, variable_name2)</code> . In the current version of quickpsy, the within variable has not special treatment. It does the same as grouping.
between	Name of the between variable. It should be specified as <code>between = .(variable_name1, variable_name2)</code> . In the current version of quickpsy, the between variable has not special treatment. It does the same as grouping.
xmin	Minimum value of the explanatory variable for which the curves should be calculated (the default is the minimum value of the explanatory variable).
xmax	Maximum value of the explanatory variable for which the curves should be calculated (the default is the maximum value of the explanatory variable).
log	If TRUE, the logarithm of the explanatory variable is used to fit the curves (default is FALSE).
fun	Name of the shape of the curve to fit. It could be a predefined shape ( <code>cum_normal_fun</code> , <code>logistic_fun</code> , <code>weibull_fun</code> ) or the name of a function introduced by the user (default is <code>cum_normal_fun</code> ).
parini	Initial parameters. quickpsy calculates default initial parameters using probit analysis, but it is also possible to specify a vector of initial parameters or a list of the form <code>list(c(par1min, par1max), c(par2min, par2max))</code> to constraint the lower and upper bounds of the parameters (when <code>optimization = 'DE'</code> , <code>parini</code> should be also a list).
guess	Value indicating the guess rate $\gamma$ (default is 0). If TRUE, the guess rate is estimated as the $i + 1$ parameter where $i$ corresponds to the number of parameters of <code>fun</code> . If, for example, <code>fun</code> is a predefined shape with parameters $p_1$ and $p_2$ , then the guess rate corresponds to parameter $p_3$ .
lapses	Value indicating the lapse rate $\lambda$ (default is 0). If TRUE, the lapse rate is estimated as the $i + 1$ parameter where $i$ corresponds to the number of parameters of <code>fun</code> plus one if the guess rate is estimated. If, for example, <code>fun</code> is a predefined shape with parameters $p_1$ and $p_2$ , then the lapse rate corresponds to parameter $p_3$ . If the guess rate is also estimated, $p_3$ will be the guess rate and $p_4$ the lapse rate.
prob	Probability to calculate the threshold (default is <code>guess + .5 * (1 - guess)</code> ).
thresholds	If FALSE, thresholds are not calculated (default is TRUE).
bootstrap	'parametric' performs parametric bootstrap; 'nonparametric' performs non-parametric bootstrap; 'none' does not perform bootstrap (default is 'parametric').
B	number of bootstrap samples (default is 100 ONLY).
ci	Confidence intervals level based on percentiles (default is .95).

optimization Method used for optimization. The default is 'optim' which uses the optim function. It can also be 'DE' which uses de function DEoptim from the package DEoptim, which performs differential evolution optimization. By using DEoptim, it is less likely that the optimization finishes in a local minimum, but the optimization is slow. When 'DE' is used, parini should be specified as a list with lower and upper bounds.

### See Also

[quickpsy](#)

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quickreadfiles	<i>Reads several files</i>
----------------	----------------------------

---

### Description

quickreadfiles builds a data frame from several txt files. It assumes that in each file, the first row has the names of the variables.

### Usage

```
quickreadfiles(path = getwd(), extension = "txt", ...)
```

### Arguments

path	Path of the file (default is the working directory).
extension	Specify whether the file extension is 'txt' or 'csv'.
...	arguments of the form name_var = c('value1', 'value2',...). A new column with variable name name_var is added to the data frame.

### Examples

```
# download the 3 files in
# https://github.com/danilinares/quickpsy/tree/master/inst/extdata/example1
# and add them to your working directory
# dat <- quickreadfiles(subject = c('aa', 'bb', 'cc'), session = c('1', '2'))
# fit <- quickpsy(dat, phase, resp, grouping=.(subject), lapses = T, guess = T)
# plotcurves(fit)
```

---

sse	<i>Sum of squared errors of prediction</i>
-----	--

---

**Description**

ypred calculates the sum of squared errors of prediction

**Usage**

```
sse(qp)
```

**Arguments**

qp	output from quickpsy
----	----------------------

---

summary.quickpsy	<i>Plot the parameters and its confidence intervals summary Plot the parameters and its confidence intervals</i>
------------------	--

---

**Description**

Plot the parameters and its confidence intervals summary Plot the parameters and its confidence intervals

**Usage**

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

**Arguments**

object	An object for which a summary is desired.
...	Additional arguments affecting the summary produced.

---

weibull_fun	<i>Weibull function</i>
-------------	-------------------------

---

**Description**

Weibull function of the form  $(1 - \exp(-(x/\alpha)^\beta))$

**Usage**

```
weibull_fun(x, p)
```

**Arguments**

x                    Vector of values of the explanatory variable.  
p                    Vector of parameters  $p = c(\alpha, \beta)$ .

**Value**

Probability at each x.

**Examples**

```
xseq <- seq(0, 4, .01)
yseq <- weibull_fun(xseq, c(2, 4))
curve <- data.frame(x = xseq, y = yseq)
ggplot(curve, aes(x = x, y = y)) + geom_line()
```

---

ypred	<i>Predicted probabilities</i>
-------	--------------------------------

---

**Description**

ypred calculates the predicted probabilities at the values of the explanatory variable.

**Usage**

```
ypred(qp)
```

**Arguments**

qp                    output from quickpsy

**Examples**

```
library(MPDiR) # contains the Vernier data
data(Vernier) # ?Venier for the reference
fit <- quickpsy(Vernier, Phaseshift, NumUpward, N,
               grouping = .(Direction, WaveForm, TempFreq), B = 20)
ypred(fit)
```

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