Package 'zcurve'

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Title An Implementation of Z-Curves

Version 1.0.0

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Description An implementation of z-curves - a method for estimating expected discovery
and replicability rates on the bases of test-statistics of published studies. The package
provides functions for fitting the new density and EM version
(Bartoš & Schimmack, 2020, <doi:10.31234/osf.io/urgtn>) as well as the original density
z-curve (Brunner & Schimmack, 2017, <doi:10.31219/osf.io/wr93f>). Furthermore, the package
provides summarizing and plotting functions for the fitted z-curve objects. See the
aforementioned articles for more information about the z-curves, expected discovery
and replicability rates, validation studies, and limitations.

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Encoding UTF-8

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Imports Rcpp (>= 1.0.2), nleqslv, stats, evmix, graphics, Rdpack

LinkingTo Rcpp

Suggests spelling

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R topics documented:

1

control_density	*Control settings for the z-curve 2.0 density algorithm*

Description

All settings are passed to the density fitting algorithm. All unspecified settings are set to the default value. Setting model = ″KD2″ sets all settings to the default value irrespective of any other setting and fits z-curve as describe in BartoĹˇ and Schimmack (2020). In order to fit the z-curve 1.0 density algorithm, set model = ″KD1″ and go to [control_density_v1](#)

Arguments

version	Which version of z-curve should be fitted. Defaults to 2 = z-curve 2.0. Set to 1 in order to fit the original version of z-curve. For its settings page go to [control_density_v1](#).
model	A type of model to be fitted, defaults to ″KD2″ (another possibility is ″KD1″ for the original z-curve 1.0, see [control_density_v1](#) for its settings)
sig_level	An alpha level of the test statistics, defaults to .05
a	A beginning of fitting interval, defaults to qnorm(sig_level/2,lower.tail = F)
b	An end of fitting interval, defaults to 6
mu	Means of the components, defaults to seq(0,6,1)
sigma	A standard deviation of the components, "Don't touch this" \- Ulrich Schimmack, defaults to 1
theta_min	Lower limits for weights, defaults to rep(0,length(mu))
theta_max	Upper limits for weights, defaults to rep(1,length(mu))
max_iter	A maximum number of iterations for the [nlminb](#) optimization for fitting mixture model, defaults to 150
max_eval	A maximum number of evaluation for the [nlminb](#) optimization for fitting mixture model, defaults to 1000
criterion	A criterion to terminate [nlminb](#) optimization, defaults to 1e-03
bw	A bandwidth of the kernel density estimation, defaults to .10

aug	Augment truncated kernel density, defaults to TRUE
aug.bw	A bandwidth of the augmentation, defaults to .20
n.bars	A resolution of density function, defaults to 512
density_dbc	Use bckden to estimate a truncated kernel density, defaults to FALSE, in which case density is used
compute_FDR	Whether to compute FDR, leads to noticeable increase in computation, defaults to FALSE
criterion_FDR	A criterion for estimating the maximum FDR, defaults to .02
criterion_FDR_dbc	
	A criterion for estimating the maximum FDR using the bckden function, defaults to .01
precision_FDR	A maximum FDR precision, defaults to .05

References

BartoĹˇ F, Schimmack U (2020). "Z-curve. 2.0: Estimating Replication Rates and Discovery Rates." doi: 10.31219/osf.io/wr93f, submitted for publication.

See Also

zcurve(), control_density_v1, control_EM

Examples

```
# to decrease the criterion and increase the number of iterations
ctrl <- list(
   max_iter  = 300,
   criterion = 1e-4
)
zcurve(z, method = "density", control = ctrl)
```

---

control_density_v1 *Control settings for the original z-curve density algorithm*

Description

All settings are passed to the density fitting algorithm. All unspecified settings are set to the default value. Setting model = "KD1" sets all settings to the default value irrespective of any other setting and fits z-curve as described in Brunner and Schimmack (in press).

Arguments

version	Set to 1 to fit the original version of z-curve. Defaults to 2 = the updated version of z-curve. For its settings page go to control_density.
model	A type of model to be fitted, defaults to ″KD1″ (the only possibility)
sig_level	An alpha level of the test statistics, defaults to .05
a	A beginning of fitting interval, defaults to qnorm(sig_level/2,lower.tail = F)
b	An end of fitting interval, defaults to 6
K	Number of mixture components, defaults to 3
max_iter	A maximum number of iterations for the nlminb optimization for fitting mixture model, defaults to 150
max_eval	A maximum number of evaluation for the nlminb optimization for fitting mixture model, defaults to 300
criterion	A criterion to terminate nlminb optimization, defaults to 1e-10
bw	A bandwidth of the kernel density estimation, defaults to ″nrd0″

References

Brunner J, Schimmack U (in press). "Estimating population mean power under conditions of heterogeneity and selection for significance." *Meta-Psychology*. doi: 10.31234/osf.io/urgtn.

See Also

zcurve(), control_density, control_EM

Examples

```
# to increase the number of iterations
ctrl <- list(
   version  = 1,
   max_iter = 300
)
zcurve(z, method = "density", control = ctrl)
```

---

control_EM	*Control settings for the zcurve EM algorithm*

Description

All these settings are passed to the Expectation Maximization fitting algorithm. All unspecified settings are set to the default value. Setting model = ″EM″ sets all settings to the default value irrespective of any other setting and fits z-curve as described in BartoĹˇ and Schimmack (2020)

Arguments

model	A type of model to be fitted, defaults to "EM" for a z-curve with 7 z-scores centered components.
sig_level	An alpha level of the test statistics, defaults to .05
a	A beginning of fitting interval, defaults to qnorm(sig_level/2,lower.tail = F)
b	An end of fitting interval, defaults to 5
mu	Means of the components, defaults to 0:6
sigma	A standard deviation of the components, defaults to rep(1,length(mu))
theta_alpha	A vector of alpha parameters of a Dirichlet distribution for generating random starting values for the weights, defaults to rep(.5,length(mu))
theta_max	Upper limits for weights, defaults to rep(1,length(mu))
criterion	A criterion to terminate the EM algorithm, defaults to 1e-6
criterion_start	A criterion to terminate the starting phase of the EM algorithm, defaults to 1e-3
criterion_boot	A criterion to terminate the bootstrapping phase of the EM algorithm, defaults to 1e-5
max_iter	A maximum number of iterations of the EM algorithm (not including the starting iterations) defaults to 10000
max_iter_start	A maximum number of iterations for the starting phase of EM algorithm, defaults to 100
max_iter_boot	A maximum number of iterations for the booting phase of EM algorithm, defaults to 100
fit_reps	A number of starting fits to get the initial position for the EM algorithm, defaults to 100

References

BartoĹˇ F, Schimmack U (2020). "Z-curve. 2.0: Estimating Replication Rates and Discovery Rates." doi: 10.31219/osf.io/wr93f, submitted for publication.

See Also

zcurve(), control_density

Examples

```
# to increase the number of starting fits
# and change the means of the mixture components

ctrl <- list(
   fit_reps  = 50,
   mu = c(0, 1.5, 3, 4.5, 6)
)
zcurve(z, method = "EM", control = ctrl)
```

OSC.z	*Z-scores from subset of original studies featured in OSC 2015 repro-ducibility project*

Description

The dataset contains z-scores from subset of original studies featured in psychology reproducibility project (Collaboration and others 2015). Only z-scores from studies with unambiguous original outcomes are supplied (eliminating 7 studies with marginally significant results). The real replication rate for those studies is 35/90 (the whole project reports 36/97).

Usage

```
OSC.z
```

Format

A vector with 90 observations

References

Collaboration OS, others (2015). "Estimating the reproducibility of psychological science." *Science*, **349**(6251). doi: 10.1126/science.aac4716.

plot.zcurve	*Plot fitted z-curve object*

Description

Plot fitted z-curve object

Usage

```
## S3 method for class 'zcurve'
plot(
  x,
  annotation = FALSE,
  CI = FALSE,
  extrapolate = FALSE,
  y.anno = c(0.95, 0.88, 0.78, 0.71, 0.61, 0.53, 0.43, 0.35),
  x.anno = 0.6,
  cex.anno = 1,
  ...
)
```

Arguments

x	Fitted z-curve object
annotation	Add annotation to the plot. Defaults to FALSE.
CI	Plot confidence intervals for the estimated z-curve. Defaults to FALSE.
extrapolate	Scale the chart to the extrapolated area. Defaults to FALSE.
y.anno	A vector of length 8 specifying the y-positions of the individual annotation lines relative to the figure's height. Defaults to c(.95,.88,.78,.71,.61,.53,.43,.35)
x.anno	A number specifying the x-position of the block of annotations relative to the figure's width.
cex.anno	A number specifying the size of the annotation text.
...	Additional arguments including main, xlab, ylab, cex.axis, cex.lab

See Also

zcurve()

Examples

```
# simulate some z-statistics and fit a z-curve
z <- abs(rnorm(300,3))
m.EM <- zcurve(z, method = "EM", bootstrap = 100)

# plot the z-curve
plot(m.EM)

# add annotation text and model fit CI
plot(m.EM, annotation = TRUE, CI = TRUE)

# change the location of the annotation to the left
plot(m.EM, annotation = TRUE, CI = TRUE, x_text = 0)
```

---

power_to_z	*Compute power corresponding to z-scores*

Description

A function for computing z-scores of two-sided tests corresponding to power for a given significance level.

Usage

```
power_to_z(
  power,
  alpha = 0.05,
  a = stats::qnorm(alpha/2, lower.tail = FALSE),
  nleqslv_control = list(xtol = 1e-15, maxit = 300, stepmax = 0.5)
)
```

Arguments

`power`	A vector of z-scores
`alpha`	Level of significance alpha
`a`	Or, alternatively a z-score corresponding to `alpha`
`nleqslv_control`	
	A named list of control parameters passed to the nleqslv function used for solving the inverse of z_to_power function.

Examples

```
# z-scores corresponding to the (aproximate) power of components of EM7p
power_to_z(c(0.05, 0.20, 0.40, 0.60, 0.80, 0.974, 0.999), alpha = .05)
```

---

print.summary.zcurve   *Prints summary object for z-curve method*

Description

Prints summary object for z-curve method

Usage

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

Arguments

`x`	Summary of a z-curve object
`...`	Additional arguments

See Also

zcurve()

---

print.zcurve   *Prints a fitted z-curve object*

Description

Prints a fitted z-curve object

Usage

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

Arguments

x	Fitted z-curve object
...	Additional arguments

See Also

zcurve()

---

summary.zcurve   *Summarize fitted z-curve object*

Description

Summarize fitted z-curve object

Usage

```
## S3 method for class 'zcurve'
summary(
  object,
  type = "results",
  all = FALSE,
  ERR.adj = 0.03,
  EDR.adj = 0.05,
  round.coef = 3,
  ...
)
```

Arguments

object	A fitted z-curve object.
type	Whether the results "results" or the mixture mode parameters "parameters" should be returned. Defaults to "results".
all	Whether additional results, such as file drawer ration, expected and missing number of studies, and Soric FDR be returned. Defaults to FALSE
ERR.adj	Confidence intervals adjustment for ERR. Defaults to .03 as proposed by Bartos & Schimmack (in preparation).
EDR.adj	Confidence intervals adjustment for EDR. Defaults to .05 as proposed by Bartos & Schimmack (in preparation).
round.coef	To how many decimals should the coefficient be rounded. Defaults to 3.
...	Additional arguments

Value

Summary of a z-curve object

See Also

zcurve()

---

zcurve	*Fit a z-curve*

Description

zcurve is used to fit z-curve models. The function takes input of z-statistics or two-sided p-values and returns object of class "zcurve" that can be further interrogated by summary and plot function. It default to EM model, but different version of z-curves can be specified using the method and control arguments. See 'Examples' and 'Details' for more information.

Usage

```
zcurve(z, p, method = "EM", bootstrap = 1000, control = NULL)
```

Arguments

z	a vector of z-scores.
p	a vector of two-sided p-values, internally transformed to z-scores.
method	the method to be used for fitting. Possible options are Expectation Maximization "EM" and density "density", defaults to "EM".
bootstrap	the number of bootstraps for estimating CI. To skip bootstrap specify FALSE.
control	additional options for the fitting algorithm more details in control EM or control density.

Details

The function returns the EM method by default and changing method = "density" gives the KD2 version of z-curve as outlined in BartoĹˇ and Schimmack (2020). For the original z-curve (Brunner and Schimmack in press), referred to as KD1, specify 'control = "density", control = list(model = "KD1")'.

Value

The fitted z-curve object

References

BartoĹˇ F, Schimmack U (2020). "Z-curve. 2.0: Estimating Replication Rates and Discovery Rates." doi: 10.31219/osf.io/wr93f, submitted for publication.

Brunner J, Schimmack U (in press). "Estimating population mean power under conditions of heterogeneity and selection for significance." *Meta-Psychology*. doi: 10.31234/osf.io/urgtn.

See Also

summary.zcurve(), plot.zcurve(), control_EM, control_density

Examples

```
# load data from OSC 2015 reproducibility project
OSC.z

# fit an EM z-curve (with disabled bootstrap due to examples times limits)
m.EM <- zcurve(OSC.z, method = "EM", bootstrap = FALSE)
# a version with 1000 boostraped samples would looked like:
m.EM <- zcurve(OSC.z, method = "EM", bootstrap = 1000)

# or KD2 z-curve (use larger bootstrap for real inference)
m.D <- zcurve(OSC.z, method = "density", bootstrap = FALSE)

# inspect the results
summary(m.EM)
summary(m.D)
# see '?summary.zcurve' for more output options

# plot the results
plot(m.EM)
plot(m.D)
# see '?plot.zcurve' for more plotting options

# to specify more options, set the control arguments
# ei. increase the maximum number of iterations and change alpha level
ctr1 <- list(
  "max_iter" = 9999,
  "alpha"    = .10
  )
```

```
m1.EM <- zcurve(OSC.z, method = "EM", bootstrap = FALSE, control = ctr1)
# see '?control_EM' and '?control_density' for more information about different
# z-curves specifications
```

---

z_to_power   *Compute z-score corresponding to power*

Description

A function for computing power of two-sided tests corresponding to z-scores for a given significance level. alpha (or corresponding cut-off z-score a)

Usage

```
z_to_power(z, alpha = 0.05, a = stats::qnorm(alpha/2, lower.tail = FALSE))
```

Arguments

z	A vector of z-scores
alpha	Level of significance alpha
a	Or, alternatively a z-score corresponding to alpha

Examples

```
# mean powers corresponding to the mean components of EM7z and 19.9
z_to_power(0:6, alpha = .05)
```

Index