

Package ‘zcurve’

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Title An Implementation of Z-Curves

Version 1.0.9

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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, 2020, <doi:10.15626/MP.2018.874>). 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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control_density	<i>Control settings for the z-curve 2.0 density algorithm</i>
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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 BartoÅj and Schimmack (2020). In order to fit the z-curve 1.0 density algorithm, set `model = "KD1"` and go to [control_density_v1](#)

Arguments

<code>version</code>	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 .
<code>model</code>	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)
<code>sig_level</code>	An alpha level of the test statistics, defaults to .05
<code>a</code>	A beginning of fitting interval, defaults to <code>qnorm(sig_level/2, lower.tail = F)</code>
<code>b</code>	An end of fitting interval, defaults to 6
<code>mu</code>	Means of the components, defaults to <code>seq(0, 6, 1)</code>
<code>sigma</code>	A standard deviation of the components, "Don't touch this" \- Ulrich Schimmack, defaults to 1
<code>theta_min</code>	Lower limits for weights, defaults to <code>rep(0, length(mu))</code>
<code>theta_max</code>	Upper limits for weights, defaults to <code>rep(1, length(mu))</code>
<code>max_iter</code>	A maximum number of iterations for the nlminb optimization for fitting mixture model, defaults to 150
<code>max_eval</code>	A maximum number of evaluation for the nlminb optimization for fitting mixture model, defaults to 1000

criterion	A criterion to terminate <code>nlminb</code> optimization, defaults to <code>1e-03</code>
bw	A bandwidth of the kernel density estimation, defaults to <code>.10</code>
aug	Augment truncated kernel density, defaults to <code>TRUE</code>
aug.bw	A bandwidth of the augmentation, defaults to <code>.20</code>
n.bars	A resolution of density function, defaults to <code>512</code>
density_dbc	Use <code>bckden</code> to estimate a truncated kernel density, defaults to <code>FALSE</code> , in which case <code>density</code> is used
compute_FDR	Whether to compute FDR, leads to noticeable increase in computation, defaults to <code>FALSE</code>
criterion_FDR	A criterion for estimating the maximum FDR, defaults to <code>.02</code>
criterion_FDR_dbc	A criterion for estimating the maximum FDR using the <code>bckden</code> function, defaults to <code>.01</code>
precision_FDR	A maximum FDR precision, defaults to <code>.05</code>

References

BartoÅ; F, Schimmack U (2020). "Z-curve. 2.0: Estimating Replication Rates and Discovery Rates." doi: [10.31219/osf.io/wr93f](https://doi.org/10.31219/osf.io/wr93f), submitted for publication, <https://doi.org/10.31219/osf.io/wr93f>.

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(OSC.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 (2020).

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 <code>qnorm(sig_level/2, lower.tail = F)</code>
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 (2020). "Estimating population mean power under conditions of heterogeneity and selection for significance." *Meta-Psychology*, 4. doi: [10.15626/MP.2018.874](https://doi.org/10.15626/MP.2018.874), <https://doi.org/10.15626/MP.2018.874>.

See Also

[zcurve\(\)](#), [control_density](#), [control_EM](#)

Examples

```
# to increase the number of iterations
ctrl <- list(
  version = 1,
  max_iter = 300
)
zcurve(OSC.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 Bartoň 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 <code>qnorm(sig_level/2, lower.tail = F)</code>
b	An end of fitting interval, defaults to 5
mu	Means of the components, defaults to <code>0:6</code>
sigma	A standard deviation of the components, defaults to <code>rep(1, length(mu))</code>
theta_alpha	A vector of alpha parameters of a Dirichlet distribution for generating random starting values for the weights, defaults to <code>rep(.5, length(mu))</code>
theta_max	Upper limits for weights, defaults to <code>rep(1, length(mu))</code>
criterion	A criterion to terminate the EM algorithm, defaults to <code>1e-6</code>
criterion_start	A criterion to terminate the starting phase of the EM algorithm, defaults to <code>1e-3</code>
criterion_boot	A criterion to terminate the bootstrapping phase of the EM algorithm, defaults to <code>1e-5</code>
max_iter	A maximum number of iterations of the EM algorithm (not including the starting iterations) defaults to <code>10000</code>
max_iter_start	A maximum number of iterations for the starting phase of EM algorithm, defaults to <code>100</code>
max_iter_boot	A maximum number of iterations for the booting phase of EM algorithm, defaults to <code>100</code>
fit_reps	A number of starting fits to get the initial position for the EM algorithm, defaults to <code>100</code>

References

BartoÅ; F, Schimmack U (2020). "Z-curve. 2.0: Estimating Replication Rates and Discovery Rates." doi: [10.31219/osf.io/wr93f](https://doi.org/10.31219/osf.io/wr93f), submitted for publication, <https://doi.org/10.31219/osf.io/wr93f>.

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(OSC.z, method = "EM", control = ctrl)
```

<code>is.zcurve</code>	<i>Reports whether x is a zcurve object</i>
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Description

Reports whether x is a zcurve object

Usage

```
is.zcurve(x)
```

Arguments

x	an object to test
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<code>OSC.z</code>	<i>Z-scores from subset of original studies featured in OSC 2015 reproducibility project</i>
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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](https://doi.org/10.1126/science.aac4716), <https://doi.org/10.1126/science.aac4716>.

plot.zcurve	<i>Plot fitted z-curve object</i>
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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 z-score corresponding to a power

Description

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

Usage

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

Arguments

<code>power</code>	A vector of powers
<code>alpha</code>	Level of significance $alpha$
<code>a</code>	Or, alternatively a z-score corresponding to $alpha$
<code>two.sided</code>	Whether directionality of the effect size should be taken into account.
<code>nleqslv_control</code>	A named list of control parameters passed to the <code>nleqslv</code> function used for solving the inverse of <code>z_to_power</code> function.

Examples

```
# z-scores corresponding to the (approximate) power of components of EM2
power_to_z(c(0.05, 0.20, 0.40, 0.60, 0.80, 0.974, 0.999), alpha = .05)
```

print.estimate.zcurve

Prints estimates from z-curve object

Description

Prints estimates from z-curve object

Usage

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

Arguments

x Estimate of a z-curve object
... Additional arguments

See Also

[zcurve\(\)](#)

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	<i>Fit a z-curve</i>
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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 Bartoň and Schimmack (2020). For the original z-curve (Brunner and Schimmack 2020), referred to as KD1, specify `'control = "density", control = list(model = "KD1")'`.

Value

The fitted z-curve object

References

Bartoň F, Schimmack U (2020). “Z-curve. 2.0: Estimating Replication Rates and Discovery Rates.” doi: [10.31219/osf.io/wr93f](https://doi.org/10.31219/osf.io/wr93f), submitted for publication, <https://doi.org/10.31219/osf.io/wr93f>.

Brunner J, Schimmack U (2020). “Estimating population mean power under conditions of heterogeneity and selection for significance.” *Meta-Psychology*, **4**. doi: [10.15626/MP.2018.874](https://doi.org/10.15626/MP.2018.874), <https://doi.org/10.15626/MP.2018.874>.

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 bootstrapped 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
```

zcurve.estimate	<i>z-curve estimate</i>
-----------------	-------------------------

Description

The following functions extract estimates from the z-curve object.

Usage

```
ERR(object, round.coef = 3)
EDR(object, round.coef = 3)
ODR(object, round.coef = 3)
Soric(object, round.coef = 3)
file_drawer_ratio(object, round.coef = 3)
expected_n(object, round.coef = 0)
missing_n(object, round.coef = 0)
significant_n(object)
included_n(object)
```

Arguments

object	the z-curve object
round.coef	rounding for the printed values

Details

Technically, ODR, significant n, and included n are not z-curve estimates but they are grouped in this category for convenience.

See Also

[zcurve\(\)](#)

`z_to_power`*Compute power corresponding to z-scores*

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),  
  two.sided = TRUE  
)
```

Arguments

<code>z</code>	A vector of z-scores
<code>alpha</code>	Level of significance <code>alpha</code>
<code>a</code>	Or, alternatively a z-score corresponding to <code>alpha</code>
<code>two.sided</code>	Whether directionality of the effect size should be taken into account.

Examples

```
# mean powers corresponding to the mean components of KD2  
z_to_power(0:6, alpha = .05)
```

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