Package 'BayesRepDesign'

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Title Bayesian Design of Replication Studies

Description Provides functionality for determining the sample size of replication studies using Bayesian design approaches in the normal-normal hierarchical model (Pawel et al., 2022) <doi:10.48550/arXiv.2211.02552>.

License GPL-3

Encoding UTF-8

Imports methods, lamW

Suggests roxygen2, tinytest

RoxygenNote 7.2.3

NeedsCompilation no

URL https://github.com/SamCH93/BayesRepDesign

BugReports https://github.com/SamCH93/BayesRepDesign/issues

Repository CRAN

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Contents

`density.designPrior` *Density method for class* `"designPrior"`

Description

Density method for class `"designPrior"`

Usage

```
## S3 method for class 'designPrior'
density(x, ...)
```

Arguments

`x`	Object of class `"designPrior"`
`...`	Other arguments passed to `stats::dnorm`

Value

Returns the density function of the design prior

Author(s)

Samuel Pawel

Examples

```
dp <- designPrior(to = 2.3123, so = 0.1, mu = 1.1, tau = 0.2)
f <- density(dp)
tseq <- seq(1, 3.5, 0.01)
plot(tseq, f(theta = tseq), type = "l", xlab = "theta", ylab = "Design prior density")
```

`designPrior` *Design prior for effect size*

Description

Creates a design prior for the effect size which can then be used for power and sample size calculations of a replication study. The design prior is obtained from updating an initial prior for the effect size by the data from the original study. A normal-normal hierarchical model is assumed, see Pawel et al. (2022) for details.

Usage

```
designPrior(
  to,
  so,
  mu = 0,
  sp = Inf,
  tau = 0,
  g = sp^2/(tau^2 + so^2),
  h = tau^2/so^2,
  type = c(NA, "conditional", "predictive", "EB")
)
```

Arguments

`to`	Effect estimate from original study
`so`	Standard error of effect estimate from original study
`mu`	The initial prior mean. Defaults to `0`
`sp`	The initial prior standard deviation. Defaults to `Inf` (an improper uniform prior)
`tau`	The initial prior heterogeneity standard deviation. Defaults to `0` (no heterogeneity)
`g`	The relative initial prior variance `g = sp^2/(tau^2 + so^2)` (alternative parametrization of prior standard deviation `sp`)
`h`	The relative initial prior heterogeneity variance `h = tau^2/so^2` (alternative parametrization of prior heterogeneity standard deviation `tau`)
`type`	Shortcut for special parameter combinations. The available options are `NA`, `"conditional"`, `"predictive"`, and `"EB"` (see details). Defaults to `NA`

Details

The `"conditional"` design prior corresponds to a point mass at the original effect estimate, i.e., assuming that the true effect size is equal to the original effect estimate. The `"predictive"` design prior is obtained from updating a uniform initial prior by the likelihood of the original data. The `"EB"` design prior is obtained by empirical Bayes estimation of the variance of the normal prior and induces adaptive shrinkage that depends on the p-value of the original effect estimate.

Value

Returns an object of class `"designPrior"` which is a list containing:

`dpMean`	The computed mean of the design prior
`dpVar`	The computed variance of the design prior
`to`	The specified original effect estimate
`so`	The specified original standard error
`mu`	The specified mean of the initial prior
`sp`	The specified standard deviation of the initial prior
`tau`	The specified heterogeneity variance

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

See Also

`pors`, `ssd`

Examples

```
designPrior(to = 1.1, so = 1)
```

`plot.designPrior` *Plot method for class* `"designPrior"`

Description

Plot method for class `"designPrior"`

Usage

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

Arguments

`x`	Object of class `"designPrior"`
`...`	Other arguments passed to `plot`

Value

Plots the density of the design prior

Author(s)

Samuel Pawel

Examples

```
dp <- designPrior(to = 2.3123, so = 0.1, mu = 1.1, tau = 0.2)
plot(dp)
plot(dp, xlim = c(0, 5), length.out = 500)
```

`pors` *Compute probability of replication success*

Description

This function computes the probabiliy of replication success based on a success region for the replication effect estimate, a design prior, and a replication standard error. If the specified number of sites is larger than 1, the supplied success region has to be formulated in terms of the meta-analytic replication effect estimate across sites.

Usage

```
pors(sregion, dprior, sr, nsites = 1)
```

Arguments

`sregion`	Success region for replication effect estimate
`dprior`	Design prior object
`sr`	Standard error of replication effect estimate
`nsites`	Number of sites, defaults to `1`. The sites are assumed to have the same standard error sr

Value

The probability of replication success

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Examples

```
dprior <- designPrior(to = 1.1, so = 1)
sregion <- successRegion(intervals = cbind(1.96, Inf))
pors(sregion = sregion, dprior = dprior, sr = 1)
```

`porsBF01` *Probability of replication success based on Bayes factor*

Description

This function computes the probability to achieve replication success based on a Bayes factor. The Bayes factor is oriented so that values above one indicate evidence for the null hypothesis of the effect size being zero, whereas values below one indicate evidence for the hypothesis of the effect size being non-zero (with normal prior assigned to it).

Usage

```
porsBF01(level, dprior, sr, priormean = 0, priorvar = 1)
```

Arguments

`level`	Bayes factor level below which replication success is achieved
`dprior`	Design prior object
`sr`	Replication standard error
`priormean`	Mean of the normal prior under the alternative. Defaults to `0`
`priorvar`	Variance of the normal prior under the alternative. Defaults to `1`

Value

The probability to achieve replication success

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Examples

```
## specify design prior
to1 <- 2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.03)
porsBF01(level = 1/10, dprior = dprior, sr = c(0.05, 0.04))
```

`porsBFr` *Probability of replication success based on replication Bayes factor*

Description

This function computes the probability to achieve replication success based on the replication Bayes factor. The replication Bayes factor is assumed to be oriented so that values below one indicate replication success, whereas values above one indicate evidence for the null hypothesis.

Usage

```
porsBFr(level, dprior, sr, paradox = TRUE)
```

Arguments

`level`	Bayes factor level below which replication success is achieved
`dprior`	Design prior object
`sr`	Replication standard error
`paradox`	Should the probability of replication success be computed allowing for the replication paradox (replication success when the effect estimates from original and replication study have a different sign)? Defaults to `TRUE`

Value

The probability to achieve replication success

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Verhagen, J. and Wagenmakers, E. J. (2014). Bayesian tests to quantify the result of a replication attempt. Journal of Experimental Psychology: General, 145:1457-1475. doi:10.1037/a0036731

Ly, A., Etz, A., Marsman, M., & Wagenmakers, E.-J. (2018). Replication Bayes factors from evidence updating. Behavior Research Methods, 51(6), 2498-2508. doi:10.3758/s134280181092x

Examples

```
## specify design prior
to1 <- 0.2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.03)
porsBFr(level = 1/10, dprior = dprior, sr = c(0.05, 0.04))
```

`porsBFs` *Probability of replication success based on the sceptical Bayes factor*

Description

This function computes the probability to achieve replication success based on the sceptical Bayes factor. The sceptical Bayes factor is assumed to be oriented so that values below one indicate replication success.

Usage

```
porsBFs(level, dprior, sr, paradox = TRUE)
```

Arguments

`level`	Threshold for the sceptical Bayes factor below which replication success is achieved
`dprior`	Design prior object
`sr`	Replication standard error
`paradox`	Should the probability of replication success be computed allowing for the replication paradox (replication success when the effect estimates from original and replication study have a different sign)? Defaults to `TRUE`

Value

The probability to achieve replication success

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Pawel, S. and Held, L. (2020). The sceptical Bayes factor for the assessement of replication success. Journal of the Royal Statistical Society: Series B (Statistical Methodology), 84(3), 879-911. doi:10.1111/rssb.12491

Examples

```
## specify design prior
to1 <- 0.2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1)
porsBFs(level = 1/3, dprior = dprior, sr = 0.05)
```

`porsEqu` *Probability of replication success based on effect size equivalence*

Description

This function computes the probability to achieve replication success on equivalence of original and replication effect size. Effect size equivalence is defined by the confidence interval for the difference between the original and replication effect sizes falling within an equivalence region around zero defined by the specified margin.

Usage

```
porsEqu(level, dprior, margin, sr)
```

Arguments

`level`	1 - confidence level of confidence interval for effect size difference
`dprior`	Design prior object
`margin`	The equivalence margin > 0 for the symmetric equivalence region around zero
`sr`	Replication standard error

Value

The probability to achieve replication success

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Anderson, S. F. and Maxwell, S. E. (2016). There's more than one way to conduct a replication study: Beyond statistical significance. Psychological Methods, 21(1), 1-12. doi:10.1037/met0000051

Examples

```
## specify design prior
to1 <- 2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.1)
porsEqu(level = 0.1, dprior = dprior, margin = 0.3, sr = c(0.05, 0.03))
```

`porsMeta` *Probability of replication success based on meta-analytic significance*

Description

This function computes the probability to achieve replication success on statistical significance of the fixed-effects meta-analytic effect estimate obtained from combining original and replication effect estimates.

Usage

```
porsMeta(level, dprior, sr)
```

Arguments

`level`	Significance level for p-value of the meta-analytic effect estimate (one-sided and in the same direction as the original effect estimate)
`dprior`	Design prior object
`sr`	Replication standard error

Value

The probability to achieve replication success

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Examples

```
## specify design prior
to1 <- 2
so1 <- 1
dprior <- designPrior(to = to1, so = so1, tau = 0.1)
porsMeta(level = 0.025^2, dprior = dprior, sr = c(0.2, 0.1))
```

`porsPs` *Probability of replication success based on the sceptical p-value*

Description

This function computes the probability to achieve replication success based on the sceptical p-value.

Usage

```
porsPs(level, dprior, sr)
```

Arguments

`level`	Threshold for the (one-sided) sceptical p-value below which replication success is achieved
`dprior`	Design prior object
`sr`	Replication standard error

Details

The sceptical p-value is assumed to be uncalibrated as in Held (2020). The package ReplicationSuccess allows for sample size and power calculations with the recalibrated sceptical p-value (`https://CRAN.R-project.org/package=ReplicationSuccess`).

Value

The probability to achieve replication success

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Held, L. (2020). A new standard for the analysis and design of replication studies (with discussion). Journal of the Royal Statistical Society: Series A (Statistics in Society), 183(2), 431-448. doi:10.1111/rssa.12493

Examples

```
## specify design prior
to1 <- 0.2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1)
porsPs(level = 0.025, dprior = dprior, sr = c(0.05, 0.01))
```

`porsSig` *Probability of replication success based on significance*

Description

This function computes the probability to achieve replication success on statistical significance of the replication effect estimate.

Usage

```
porsSig(level, dprior, sr)
```

Arguments

`level`	Significance level for p-value of the replication effect estimate (one-sided and in the same direction as the original effect estimate)
`dprior`	Design prior object
`sr`	Replication standard error

Value

The probability to achieve replication success

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Examples

```
## specify design prior
to1 <- 2
so1 <- 1
dprior <- designPrior(to = to1, so = so1, tau = 0.1)
porsSig(level = 0.025, dprior = dprior, sr = c(0.5, 0.3))
```

`porsTOST` *Probability of replication success based on TOST equivalence*

Description

This function computes the probability to achieve replication success based on establishing the absence of a practically relevant effect size with the Two One-Sided Tests (TOST) procedure in the replication study.

Usage

```
porsTOST(level, dprior, margin, sr)
```

Arguments

`level`	Significance level for the TOST p-value
`dprior`	Design prior object
`margin`	The equivalence margin > 0 for the equivalence region around zero that defines a region of practically irrelevant effect sizes
`sr`	Replication standard error

Value

The probability to achieve replication success

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Anderson, S. F. and Maxwell, S. E. (2016). There's more than one way to conduct a replication study: Beyond statistical significance. Psychological Methods, 21(1), 1-12. doi:10.1037/met0000051

Examples

```
## specify design prior
to1 <- 2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.1)
porsTOST(level = 0.1, dprior = dprior, margin = 0.3, sr = c(0.05, 0.03))
```

`print.designPrior` *Print method for class* `"designPrior"`

Description

Print method for class `"designPrior"`

Usage

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

Arguments

`x`	Object of class `"designPrior"`
`...`	Other arguments (for consistency with the generic)

Value

Prints text summary in the console and invisibly returns the `"designPrior"` object

Author(s)

Samuel Pawel

Examples

```
dp <- designPrior(to = 0.5, so = 0.05, sp = 0.2, tau = 0.1)
print(dp)
```

`print.ssdRS` *Print method for class* `"ssdRS"`

Description

Print method for class `"ssdRS"`

Usage

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

Arguments

`x`	Object of class `"ssdRS"`
`...`	Other arguments (for consistency with the generic)

Value

Prints text summary in the console and invisibly returns the `"ssdRS"` object

Author(s)

Samuel Pawel

Examples

```
## specify design prior
to1 <- 2
so1 <- 1
dprior <- designPrior(to = to1, so = so1)

## compute required standard error for significance at one-sided 2.5%
sregionfunSig <- function(sr, alpha = 0.025) {
    successRegion(intervals = cbind(stats::qnorm(p = 1- alpha)*sr, Inf))
}
ssd1 <- ssd(sregionfun = sregionfunSig, dprior = dprior, power = 0.8)
print(ssd1)
```

`print.successRegion` *Print method for class* `"successRegion"`

Description

Print method for class `"successRegion"`

Usage

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

Arguments

`x`	Object of class `"successRegion"`
`...`	Other arguments

Value

Prints text summary in the console and invisibly returns the `"successRegion"` object

Author(s)

Samuel Pawel

Examples

```
## success region for two-sided significance test
successRegion(intervals = rbind(c(1.96, Inf), c(-Inf, -1.96)))
## success region for one-sided significance test
successRegion(intervals = rbind(c(1.96, Inf)))
```

`se2n` *Sample size related to standard error and unit standard deviation*

Description

This function computes the sample size related to a specified standard error σ and unit standard deviation `unitSD`, which is the standard deviation of one effective unit (one measurement, one pair of measurements, one event, etc.). The relationship $\sigma = \texttt{unitSD}/\sqrt{n}$ is assumed. The unit standard deviation depends on the parameter type and the assumptions underlying the standard error calculation. The default is `unitSD = 2` which is, under some assumptions, a reasonable approximation to the unit standard deviation for standardized mean differences and log odds/hazard/rate ratios, see Section 2.4 in Spiegelhalter et al. (2004).

Usage

```
se2n(se, unitSD = 2)
```

Arguments

`se`	Standard error
`unitSD`	Unit standard deviation. Defaults to 2

Value

The sample size corresponding to the specified standard error and unit standard deviation

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Spiegelhalter, D.J., Abrams, K.R., Myles, J.P. (2004). Bayesian approaches to clinical trials and health care evaluation. Wiley. doi:10.1002/0470092602

Examples

```
smd1 <- 0.3
so1 <- 0.05
dprior <- designPrior(to = smd1, so = so1)
ssd1 <- ssdSig(level = 0.025, dprior = dprior, power = 0.8)
se2n(se = ssd1$sr, unitSD = 2) # required n
```

`ssd` *Sample size determination for replication success*

Description

This function computes the standard error of the replication effect estimate required to achieve replication success with a certain probability and based on a certain type of success region.

Usage

```
ssd(
  sregionfun,
  dprior,
  power,
  nsites = 1,
  searchInt = c(.Machine$double.eps^0.5, 4),
  ...
)
```

Arguments

`sregionfun`	Function that returns the success region for replication effect estimate as a function of the replication standard error
`dprior`	Design prior object
`power`	Desired probability of replication success
`nsites`	Number of sites. Defaults to `1`. The sites are assumed to have the same sample size
`searchInt`	Search interval for standard errors
`...`	Other arguments passed to `uniroot`

Value

Returns an object of class `"ssdRS"` which is a list containing:

`designPrior`	The specified `"designPrior"` object
`power`	The specified power
`powerRecomputed`	The recomputed power
`sr`	The required replication standard error
`c`	The required relative sample size `c = nr/no` (assuming `so = unitSD/no` and `sr = unitSD/nr`)

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Examples

```
## specify design prior
to1 <- 2
so1 <- 1
dprior <- designPrior(to = to1, so = so1)

## compute required standard error for significance at one-sided 2.5%
sregionfunSig <- function(sr, alpha = 0.025) {
    successRegion(intervals = cbind(stats::qnorm(p = 1- alpha)*sr, Inf))
}
ssd(sregionfun = sregionfunSig, dprior = dprior, power = 0.8)
```

`ssdBF01` *Sample size determination for replication success based on Bayes factor*

Description

This function computes the standard error required to achieve replication success with a certain probability and based on the Bayes factor under normality. The Bayes factor is oriented so that values above one indicate evidence for the null hypothesis of the effect size being zero, whereas values below one indicate evidence for the hypothesis of the effect size being non-zero (with normal prior assigned to it).

Usage

```
ssdBF01(
  level,
  dprior,
  power,
  priormean = 0,
  priorvar = 1,
  searchInt = c(.Machine$double.eps^0.5, 2)
)
```

Arguments

`level`	Bayes factor level below which replication success is achieved
`dprior`	Design prior object
`power`	Desired probability of replication success
`priormean`	Mean of the normal prior under the alternative. Defaults to `0`
`priorvar`	Variance of the normal prior under the alternative. Defaults to 1
`searchInt`	Interval for numerical search over replication standard errors

Value

Returns an object of class `"ssdRS"`. See `ssd` for details.

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Examples

```
## specify design prior
to1 <- 0.2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.03)
ssdBF01(level = 1/10, dprior = dprior, power = 0.8)
```

`ssdBFr` *Sample size determination for replication success based on replication Bayes factor*

Description

This function computes the standard error required to achieve replication success with a certain probability and based on the replication Bayes factor under normality. The replication Bayes factor is assumed to be oriented so that values below one indicate replication success, whereas values above one indicate evidence for the null hypothesis.

Usage

```
ssdBFr(
  level,
  dprior,
  power,
  searchInt = c(.Machine$double.eps^0.5, 2),
  paradox = TRUE
)
```

Arguments

`level`	Bayes factor level below which replication success is achieved
`dprior`	Design prior object
`power`	Desired probability of replication success

`searchInt`	Interval for numerical search over replication standard errors
`paradox`	Should the probability of replication success be computed allowing for the replication paradox (replication success when the effect estimates from original and replication study have a different sign)? Defaults to `TRUE`

Value

Returns an object of class `"ssdRS"`. See `ssd` for details.

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Verhagen, J. and Wagenmakers, E. J. (2014). Bayesian tests to quantify the result of a replication attempt. Journal of Experimental Psychology: General, 145:1457-1475. doi:10.1037/a0036731

Ly, A., Etz, A., Marsman, M., and Wagenmakers, E.-J. (2018). Replication Bayes factors from evidence updating. Behavior Research Methods, 51(6), 2498-2508. doi:10.3758/s134280181092x

Examples

```
## specify design prior
to1 <- 0.2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.03)
ssdBFr(level = 1/10, dprior = dprior, power = 0.8)
```

`ssdBFs` *Sample size determination for replication success based on the sceptical Bayes factor*

Description

This function computes the standard error required to achieve replication success with a certain probability and based on the sceptical Bayes factor. The sceptical Bayes factor is assumed to be oriented so that values below one indicate replication success.

Usage

```
ssdBFs(
  level,
  dprior,
  power,
  searchInt = c(.Machine$double.eps^0.5, 2),
  paradox = TRUE
)
```

Arguments

`level`	Threshold for the sceptical Bayes factor below which replication success is achieved
`dprior`	Design prior object
`power`	Desired probability of replication success
`searchInt`	Interval for numerical search over replication standard errors
`paradox`	Should the probability of replication success be computed allowing for the replication paradox (replication success when the effect estimates from original and replication study have a different sign)? Defaults to `TRUE`

Value

Returns an object of class `"ssdRS"`. See `ssd` for details.

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Pawel, S. and Held, L. (2020). The sceptical Bayes factor for the assessement of replication success. Journal of the Royal Statistical Society: Series B (Statistical Methodology), 84(3), 879-911. doi:10.1111/rssb.12491

Examples

```
## specify design prior
to1 <- 0.2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.03)
ssdBFs(level = 1/10, dprior = dprior, power = 0.9)
```

`ssdEqu` *Sample size determination for replication success based on effect size equivalence*

Description

This function computes the standard error required to achieve replication success with a certain probability and based on effect size equivalence of original and replication effect size. Effect size equivalence is defined by the confidence interval for the difference between the original and replication effect sizes falling within an equivalence region around zero defined by the specified margin.

Usage

```
ssdEqu(level, dprior, power, margin, searchInt = c(0, 2))
```

Arguments

`level`	1 - confidence level of confidence interval for effect size difference
`dprior`	Design prior object
`power`	Desired probability of replication success
`margin`	The equivalence margin > 0 for the symmetric equivalence region around zero
`searchInt`	Interval for numerical search over replication standard errors

Value

Returns an object of class `"ssdRS"`. See `ssd` for details.

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Anderson, S. F. and Maxwell, S. E. (2016). There's more than one way to conduct a replication study: Beyond statistical significance. Psychological Methods, 21(1), 1-12. doi:10.1037/met0000051

Examples

```
## specify design prior
to1 <- 0.2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.05)
ssdEqu(level = 0.1, dprior = dprior, power = 0.8, margin = 0.2)
```

`ssdMeta` *Sample size determination for replication success based on meta-analytic significance*

Description

This function computes the standard error required to achieve replication success with a certain probability and based on statistical significance of the fixed-effects meta-analytic effect estimate obtained from combining original and replication effect estimates.

Usage

```
ssdMeta(level, dprior, power, searchInt = c(0, 10))
```

Arguments

`level`	Significance level for the replication effect estimate (one-sided and in the same direction as the original effect estimate)
`dprior`	Design prior object
`power`	Desired probability of replication success
`searchInt`	Interval for numerical search over replication standard errors

Value

Returns an object of class `"ssdRS"`. See `ssd` for details.

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Examples

```
## specify design prior
to1 <- 2
so1 <- 1
dprior <- designPrior(to = to1, so = so1, tau = 0.25, sp = Inf)
ssdMeta(level = 0.025^2, dprior = dprior, power = 0.95)
```

`ssdPs` *Sample size determination for replication success based on the sceptical p-value*

Description

This function computes the standard error required to achieve replication success with a certain probability and based on the sceptical p-value.

Usage

```
ssdPs(level, dprior, power)
```

Arguments

`level`	Threshold for the (one-sided) sceptical p-value below which replication success is achieved
`dprior`	Design prior object
`power`	Desired probability of replication success

Details

The sceptical p-value is assumed to be uncalibrated as in Held (2020). The package ReplicationSuccess allows for sample size and power calculations with the recalibrated sceptical p-value (`https://CRAN.R-project.org/package=ReplicationSuccess`).

Value

Returns an object of class `"ssdRS"`. See `ssd` for details.

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Held, L. (2020). A new standard for the analysis and design of replication studies (with discussion). Journal of the Royal Statistical Society: Series A (Statistics in Society), 183(2), 431-448. doi:10.1111/rssa.12493

Examples

```
## specify design prior
to1 <- 0.2
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.03)
ssdPs(level = 0.05, dprior = dprior, power = 0.9)
```

`ssdSig` *Sample size determination for replication success based on significance*

Description

This function computes the standard error required to achieve replication success with a certain probability and based on statistical significance of the replication effect estimate.

Usage

```
ssdSig(level, dprior, power)
```

Arguments

`level`	Significance level for the replication effect estimate (one-sided and in the same direction as the original effect estimate)
`dprior`	Design prior object
`power`	Desired probability of replication success

Value

Returns an object of class `"ssdRS"`. See `ssd` for details.

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Examples

```
## specify design prior
to1 <- 2
so1 <- 0.5
dprior <- designPrior(to = to1, so = so1, tau = 0.1)
ssdSig(level = 0.025, dprior = dprior, power = 0.9)
```

`ssdTOST` *Sample size determination for replication success based on TOST equivalence*

Description

This function computes the standard error required to achieve replication success with a certain probability and based on establishing the absence of a practically relevant effect size with the Two One-Sided Tests (TOST) procedure in the replication study.

Usage

```
ssdTOST(level, dprior, power, margin, searchInt = c(0, 2))
```

Arguments

`level`	Significance level for the TOST p-value
`dprior`	Design prior object
`power`	Desired probability of replication success
`margin`	The equivalence margin > 0 for the equivalence region around zero that defines a region of practically irrelevant effect sizes
`searchInt`	Interval for numerical search over replication standard errors

Value

Returns an object of class `"ssdRS"`. See `ssd` for details.

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Anderson, S. F. and Maxwell, S. E. (2016). There's more than one way to conduct a replication study: Beyond statistical significance. Psychological Methods, 21(1), 1-12. doi:10.1037/met0000051

Examples

```
## specify design prior
to1 <- 0.05
so1 <- 0.05
dprior <- designPrior(to = to1, so = so1, tau = 0.05)
ssdTOST(level = 0.05, dprior = dprior, power = 0.9, margin = 0.3)
```

`successRegion` *Success region for replication effect estimate*

Description

Creates a success region object which can then be used for computing the probability of replication success with `pors`.

Usage

```
successRegion(intervals)
```

Arguments

`intervals`	A 2xN matrix containing N disjoint intervals, the first column containing the lower and the second column containing the upper limits

Value

Returns an object of class `"successRegion"` which is a matrix containing the success intervals sorted in ascending order

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

See Also

`pors`, `ssd`

Examples

```
successRegion(intervals = rbind(c(1.96, Inf), c(-Inf, -1.96)))
successRegion(intervals = cbind(1.96, Inf))
```

`successRegionSig` *Success region based on significance*

Description

This function returns the success region for the (meta-analytic) replication effect estimate to achieve significance

Usage

```
successRegionSig(sr, to, tau = 0, nsites = 1, level)
```

Arguments

`sr`	Replication standard error
`to`	Original effect estimate
`tau`	Heterogeneity standard deviation used in the calculation of the meta-analytic replication effect estimate and its standard error. Defaults to `0` (fixed effects analysis)
`nsites`	nsites Number of sites, defaults to `1`. The effect estimates from all sites are assumed to have the same standard error `sr`
`level`	Significance level for p-value of the (average) replication effect estimate (one-sided and in the same direction as the original effect estimate)

Value

An object of class `"successRegion"`. See `successRegion` for details.

Author(s)

Samuel Pawel

References

Pawel, S., Consonni, G., and Held, L. (2022). Bayesian approaches to designing replication studies. arXiv preprint. doi:10.48550/arXiv.2211.02552

Examples

```
successRegionSig(sr = 0.05, to = 0.2, tau = 0.01, nsites = 3, level = 0.025)
```

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