Package 'powertools'

June 3, 2024

Type Package

Title powertools: Power and Sample Size Tools

Version 0.1.0

Description This package accompanies the book Power and Sample Size in R by
Catherine M. Crespi for calculating power and sample size requirements for designing studies.

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Suggests designsize,
longpower,
npsurvSS,
powerSurvEpi,
rPowerSampleSize,
ssanv,
testthat (>= 3.0.0)

Config/testthat/edition 3

Imports magrittr,
mvtnorm,
plyr,
PowerTOST,
Hmisc,
stats,
knitr

Depends R (>= 2.10)

R topics documented:

Index **58**

---

margin.sign *Margin Sign Table*

Description

A table documenting the sign of margin for tests comparing two parameters.

Usage

```
margin.sign
```

Format

'margin.sign' A data frame with 3 rows and 3 columns:

columns Whether the test is for noninferiority of superirority by a margin

rows Whether a higher or lower parameter value is better

xij The sign of delta given the row & column

---

pss.altprimary *Power calculations for multiple alternative (at least one) primary continuous endpoints assuming known covariance matrix*

Description

Power calculations for multiple alternative (at least one) primary continuous endpoints assuming known covariance matrix

Usage

```
pss.altprimary(
  K,
  n1 = NULL,
  n.ratio = 1,
  delta = NULL,
  Sigma,
  sd,
  rho,
  alpha = 0.025,
  power = NULL,
  tol = .Machine$double.eps^0.25
)
```

Arguments

K	The number of endpoints.
n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
delta	A vector of length K of the true mean differences mu1k - mu2k; must all be positive.
Sigma	The covariance matrix of the K outcomes, of dimension K x K.
sd	A vector of length K of the standard deviations of the K outcomes.
rho	A vector of length 0.5*K*(K-1) of the correlations among the K outcomes.
alpha	The significance level or type 1 error rate; defaults to 0.025. A one-sided test is assumed.
power	The specified level of power.

Value

A list of the arguments (including the computed one).

Examples

```
pss.altprimary(K = 2, n1 = 100, delta = c(0.4, 0.5), sd = c(1, 1), rho = 0.3,
alpha = 0.025, power = NULL)
```

---

pss.anova1way.c.bal	*Power calculations for one-way balanced analysis of variance contrast test*

Description

Power calculations for one-way balanced analysis of variance contrast test

Usage

```
pss.anova1way.c.bal(
  n = NULL,
  mvec = NULL,
  cvec = NULL,
  sd = 1,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  power = NULL,
  v = TRUE
)
```

Arguments

n	The sample size per group.
mvec	A vector of group means c(mu1, mu2, ...).
cvec	A vector of contrast coefficients c(c1, c2, ...).
sd	The estimated standard deviation within each group; defaults to 1.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.anova1way.c.bal(n = 20, mvec = c(5, 10, 12), cvec = c(1, -1, 0), sd = 10, alpha = 0.025)
pss.anova1way.c.bal(n = 20, mvec = c(5, 10, 12), cvec = c(1, 0, -1), sd = 10, alpha = 0.025)
```

---

pss.anova1way.c.unbal   *Power calculations for one-way unbalanced analysis of variance con-
                         trast test*

Description

Power calculations for one-way unbalanced analysis of variance contrast test

Usage

```
pss.anova1way.c.unbal(
  nvec = NULL,
  mvec = NULL,
  cvec = NULL,
  sd = NULL,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  v = TRUE
)
```

Arguments

nvec	A vector of group sample sizes c(n1, n2, ...).
mvec	A vector of group mvec c(mu1, mu2, ...).
cvec	A vector of contrast coefficients c(c1, c2, ...).
sd	The estimated standard deviation within each group.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.

ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed power).

Examples

```
pss.anova1way.c.unbal(nvec = c(20, 20, 20), mvec = c(5, 10, 12), cvec = c(1, -1, 0),
sd = 10, alpha = 0.025)
pss.anova1way.c.unbal(nvec = c(20, 20, 20), mvec = c(5, 10, 12), cvec = c(1, 0, -1),
sd = 10, alpha = 0.025)
```

| pss.anova1way.F.bal | *Power calculations for one-way balanced analysis of variance omnibus F test* |

Description

Power calculations for one-way balanced analysis of variance omnibus F test

Usage

```
pss.anova1way.F.bal(
  n = NULL,
  mvec = NULL,
  sd = 1,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  power = NULL,
  v = TRUE
)
```

Arguments

n	The sample size per group.
mvec	A vector of group means c(mu1, mu2, ...).
sd	The estimated standard deviation within each group; defaults to 1.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.anova1way.F.bal(n = 20, mvec = c(5, 10, 12), sd = 10)
pss.anova1way.F.bal(n = NULL, mvec = c(-0.25, 0.25), sd = 1, Rsq = 0.5^2, ncov = 1, power = 0.8)
```

---

pss.anova1way.F.unbal   *Power calculations for one-way unbalanced analysis of variance omnibus F test*

Description

Power calculations for one-way unbalanced analysis of variance omnibus F test

Usage

```
pss.anova1way.F.unbal(
  nvec = NULL,
  mvec = NULL,
  sd = NULL,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  v = TRUE
)
```

Arguments

nvec	A vector of group sample sizes c(n1, n2, ...).
mvec	A vector of group mvec c(mu1, mu2, ...).
sd	The estimated standard deviation within each group.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed power).

Examples

```
pss.anova1way.F.unbal(nvec = c(10, 20, 30), mvec = c(5, 10, 12), sd = 10)
```

---

pss.anova2way.c.bal   *Power calculations for two-way balanced analysis of variance con-*
                              trast test

Description

Power calculations for two-way balanced analysis of variance contrast test

Usage

```
pss.anova2way.c.bal(
  n = NULL,
  mmatrix = NULL,
  cvec = NULL,
  factor = c("a", "b"),
  sd = 1,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  power = NULL,
  v = TRUE
)
```

Arguments

n	The sample size per group.
mmatrix	A matrix of group means (see example).
cvec	A vector of contrast coefficients c(c1, c2, ...).
factor	Either "a" for rows or "b" for columns depending on which factor the contrast test is being made on.
sd	The estimated standard deviation within each group; defaults to 1.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.3), nrow = 2, byrow = TRUE)
pss.anova2way.c.bal(n = 30, mmatrix = mmatrix, cvec = c(1, 0, -1), factor = "b",
sd = 2, alpha = 0.05)
```

---

pss.anova2way.c.unbal	*Power calculations for two-way unbalanced analysis of variance contrast test*

Description

Power calculations for two-way unbalanced analysis of variance contrast test

Usage

```
pss.anova2way.c.unbal(
  nmatrix = nmatrix,
  mmatrix = NULL,
  cvec = NULL,
  factor = c("a", "b"),
  sd = NULL,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  v = TRUE
)
```

Arguments

nmatrix	A matrix of group sample sizes (see example).
mmatrix	A matrix of group means (see example).
cvec	A vector of contrast coefficients c(c1, c2, ...).
factor	Either "a" (rows) or "b" (columns) depending on which factor the contrast test is being made on.
sd	The estimated standard deviation within each group.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
nmatrix <- matrix(c(30, 30, 30, 30, 30, 30), nrow = 2, byrow = TRUE)
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.3), nrow = 2, byrow = TRUE)
pss.anova2way.c.unbal(nmatrix = nmatrix, mmatrix = mmatrix, cvec = c(1, 0, -1),
factor = "b", sd = 2, alpha = 0.05)
```

pss.anova2way.F.bal   *Power calculations for two-way balanced analysis of variance omnibus F test*

Description

Power calculations for two-way balanced analysis of variance omnibus F test

Usage

```
pss.anova2way.F.bal(
  n = NULL,
  mmatrix = NULL,
  sd = 1,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  power = NULL,
  v = TRUE
)
```

Arguments

n	The sample size per group.
mmatrix	A matrix of group means (see example).
sd	The estimated standard deviation within each group; defaults to 1.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.9), nrow = 2, byrow = TRUE)
pss.anova2way.F.bal(n = 30, mmatrix = mmatrix, sd = 2, alpha = 0.05)
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.3), nrow = 2, byrow = TRUE)
pss.anova2way.F.bal(n = 30, mmatrix = mmatrix, sd = 2, alpha = 0.05)
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.9), nrow = 2, byrow = TRUE)
pss.anova2way.F.bal(n = 30, mmatrix = mmatrix, sd = 2, Rsq = 0.4, ncov = 1, alpha = 0.05)
```

---

pss.anova2way.F.unbal   *Power calculations for two-way unbalanced analysis of variance omnibus F test*

Description

Power calculations for two-way unbalanced analysis of variance omnibus F test

Usage

```
pss.anova2way.F.unbal(
  nmatrix = NULL,
  mmatrix = NULL,
  sd = NULL,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  v = TRUE
)
```

Arguments

nmatrix	A matrix of group sample sizes (see example).
mmatrix	A matrix of group means (see example).
sd	The estimated standard deviation within each group.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed power).

Examples

```
nmatrix <- matrix(c(30, 30, 30, 30, 30, 30), nrow = 2, byrow = TRUE)
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.9), nrow = 2, byrow = TRUE)
pss.anova2way.F.unbal(nmatrix = nmatrix, mmatrix = mmatrix, sd = 2, alpha = 0.05)
nmatrix <- matrix(c(30, 30, 30, 30, 30, 30), nrow = 2, byrow = TRUE)
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.3), nrow = 2, byrow = TRUE)
pss.anova2way.F.unbal(nmatrix = nmatrix, mmatrix = mmatrix, sd = 2, alpha = 0.05)
nmatrix <- matrix(c(30, 30, 30, 30, 30, 30), nrow = 2, byrow = TRUE)
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.9), nrow = 2, byrow = TRUE)
pss.anova2way.F.unbal(nmatrix = nmatrix, mmatrix = mmatrix, sd = 2, Rsq = 0.4^2,
ncov = 1, alpha = 0.05)
```

---

pss.anova2way.se.bal   *Power calculations for two-way balanced analysis of variance simple effects test*

Description

Power calculations for two-way balanced analysis of variance simple effects test

Usage

```
pss.anova2way.se.bal(
  n = NULL,
  mmatrix = NULL,
  cmatrix = NULL,
  sd = 1,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  power = NULL,
  v = TRUE
)
```

Arguments

n	The sample size per group.
mmatrix	A matrix of group means (see example).
cmatrix	A matrix of contrast coefficients (see example).
sd	The estimated standard deviation within each group; defaults to 1.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.3), nrow = 2, byrow = TRUE)
cmatrix <- matrix(c(-1, 0, 0, 1, 0, 0), nrow = 2, byrow = TRUE)
pss.anova2way.se.bal(n = 30, mmatrix = mmatrix, cmatrix = cmatrix, sd = 2, alpha = 0.025)
```

---

pss.anova2way.se.unbal

Power calculations for two-way unbalanced analysis of variance simple effects test

---

Description

Power calculations for two-way unbalanced analysis of variance simple effects test

Usage

```
pss.anova2way.se.unbal(
  nmatrix = NULL,
  mmatrix = NULL,
  cmatrix = NULL,
  sd = 0,
  Rsq = 0,
  ncov = 0,
  alpha = 0.05,
  v = TRUE
)
```

Arguments

nmatrix	A matrix of sample sizes (see example).
mmatrix	A matrix of group means (see example).
cmatrix	A matrix of contrast coefficients (see example).
sd	The estimated standard deviation within each group.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
ncov	The number of covariates adjusted for in the model; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed power).

Examples

```
nmatrix <- matrix(c(30, 30, 30, 30, 30, 30), nrow = 2, byrow = TRUE)
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.3), nrow = 2, byrow = TRUE)
cmatrix <- matrix(c(-1, 0, 0, 1, 0, 0), nrow = 2, byrow = TRUE)
pss.anova2way.se.unbal(nmatrix = nmatrix, mmatrix = mmatrix, cmatrix = cmatrix,
sd = 2, alpha = 0.025)
```

---

pss.chisq.gof   *Power calculations for chi-square goodness-of-fit test*

Description

Power calculations for chi-square goodness-of-fit test

Usage

```
pss.chisq.gof(
  p0vec = NULL,
  p1vec = NULL,
  N = NULL,
  alpha = 0.05,
  power = NULL,
  v = TRUE
)
```

Arguments

p0vec	The first vector of probabilities (under the null).
p1vec	The second vector of probabilities (under the alternative hypothesis).
N	The number of total observations.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.chisq.gof(p0vec = c(0.5, 0.3, 0.2), p1vec = c(0.7, 0.2, 0.1), N = 50)
```

---

pss.chisq.indep   *Power calculations for chi-square test of independence*

Description

Power calculations for chi-square test of independence

Usage

```
pss.chisq.indep(pmatrix = NULL, N = NULL, alpha = 0.05, power = NULL, v = TRUE)
```

Arguments

pmatrix	The two-way probability table under the alternative hypothesis.
N	The number of total observations.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.chisq.indep(pmatrix = matrix(c(0.050, 0.350, 0.100, 0.075, 0.250, 0.175),
nrow = 2, byrow = TRUE), N = 230)
pss.chisq.indep(pmatrix = matrix(c(0.3, 0.2, 0.4, 0.1), nrow = 2, byrow = TRUE), N = 200)
```

---

pss.ci.mean   *Power calculations for precision analysis for one mean*

Description

Power calculations for precision analysis for one mean

Usage

```
pss.ci.mean(
  N = NULL,
  halfwidth = NULL,
  sd = 1,
  alpha = 0.05,
  power = NULL,
  cond = FALSE,
  v = TRUE
)
```

Arguments

N	The sample size.
halfwidth	The desired halfwidth.
sd	The estimated standard deviation; defaults to 1.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
cond	Specify using unconditional or conditional probability. Defaults to FALSE.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.ci.mean(N = NULL, halfwidth = 0.25, power = 0.8)
pss.ci.mean(N = 62, halfwidth = 0.25, power = NULL)
pss.ci.mean(N = 73, halfwidth = 0.25, cond = TRUE)
```

---

pss.ci.meandiff   *Power calculations for precision analysis for a difference between means*

Description

Power calculations for precision analysis for a difference between means

Usage

```
pss.ci.meandiff(
  n1 = NULL,
  n.ratio = 1,
  halfwidth = NULL,
  sd = 1,
  alpha = 0.05,
  power = NULL,
  cond = FALSE,
  v = TRUE
)
```

Arguments

n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
halfwidth	The desired halfwidth for the difference in means.
sd	The estimated standard deviation; defaults to 1.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
cond	Specify using unconditional or conditional probability. Defaults to FALSE.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.ci.meandiff(n1 = NULL, halfwidth = 0.25, power = 0.8)
pss.ci.meandiff(n1 = 134, halfwidth = 0.25, cond = TRUE)
```

| pss.coprimary.t | *Power calculations for multiple co-primary continuous endpoints assuming unknown covariance matrix* |

Description

Power calculations for multiple co-primary continuous endpoints assuming unknown covariance matrix

Usage

```
pss.coprimary.t(
  K,
  n1 = NULL,
  n.ratio = 1,
  delta = NULL,
  Sigma,
  sd,
  rho,
  alpha = 0.025,
  power = NULL,
  M = 10000,
  min.n = NULL,
  max.n = NULL,
  tol = .Machine$double.eps^0.25,
  use.uniroot = TRUE
)
```

Arguments

K	The number of endpoints.
n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
delta	A vector of length K of the true mean differences mu1k - mu2k; must all be positive.
Sigma	The covariance matrix of the K outcomes, of dimension K x K.
sd	A vector of length K of the standard deviations of the K outcomes.
rho	A vector of length 0.5*K*(K-1) of the correlations among the K outcomes.
alpha	The significance level or type 1 error rate; defaults to 0.025. A one-sided test is assumed.
power	The specified level of power.
M	The number of simulation.
min.n	Minimum value of n1; used in search for n1 to achieve desired power.
max.n	Maximum value of n1; used in search for n1 to achieve desired power.

Value

A list of the arguments (including the computed one).

Examples

```
pss.coprimary.t(K = 2, n1 = 100, delta = c(0.4, 0.5), sd = c(1, 1), rho = 0.3,
alpha = 0.025, power = NULL)
```

---

pss.coprimary.z	*Power calculations for multiple co-primary continuous endpoints assuming known covariance matrix*

Description

Power calculations for multiple co-primary continuous endpoints assuming known covariance matrix

Usage

```
pss.coprimary.z(
  K,
  n1 = NULL,
  n.ratio = 1,
  delta = NULL,
  Sigma,
  sd,
  rho,
  alpha = 0.025,
  power = NULL,
  tol = .Machine$double.eps^0.25
)
```

Arguments

K	The number of endpoints.
n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
delta	A vector of length K of the true mean differences mu1k - mu2k; must all be positive.
Sigma	The covariance matrix of the K outcomes, of dimension K x K.
sd	A vector of length K of the standard deviations of the K outcomes.
rho	A vector of length 0.5*K*(K-1) of the correlations among the K outcomes.
alpha	The significance level or type 1 error rate; defaults to 0.025. A one-sided test is assumed.
power	The specified level of power.

Value

A list of the arguments (including the computed one).

Examples

```
pss.coprimary.z(K = 2, n1 = 100, delta = c(0.4, 0.5), sd = c(1, 1), rho = 0.3,
alpha = 0.025, power = NULL)
```

---

pss.corr.1samp	*Power calculations for one correlation coefficient*

Description

Power calculations for one correlation coefficient

Usage

```
pss.corr.1samp(
  N = NULL,
  rho0 = 0,
  rhoA = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

N	The sample size.
rho0	The correlation coefficient under the null hypothesis; defaults to 0.
rhoA	The correlation coefficient under the alternative hypothesis.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.corr.1samp(N = 100, rhoA = 0.2, sides = 1)
pss.corr.1samp(N = 100, rho0 = 0.2, rhoA = 0.4, sides = 1)
```

---

pss.corr.2samp	*Power calculations for comparing two correlation coefficients*

Description

Power calculations for comparing two correlation coefficients

Usage

```
pss.corr.2samp(
  n1 = NULL,
  n.ratio = 1,
  rho1 = NULL,
  rho2 = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
rho1	The correlation coefficient in group 1.
rho2	The correlation coefficient in group 2.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.corr.2samp(n1 = 300, rho1 = 0.3, rho2 = 0.1, sides = 1)
```

---

pss.crt.long.cont	*Power for test of treatment effect in longitudinal cluster randomized trial with baseline measurement*

Description

Power for test of treatment effect in longitudinal cluster randomized trial with baseline measurement

Usage

```
pss.crt.long.cont(
  m = NULL,
  J1 = NULL,
  J.ratio = 1,
  delta = NULL,
  sd = 1,
  icc = 0,
```

```
    cac = 0,
    sac = 0,
    alpha = 0.05,
    power = NULL,
    sides = 2,
    v = TRUE
)
```

Arguments

m	The number of subjects measured during each cluster-period.
J1	The number of clusters in arm 1.
J.ratio	The ratio J2/J1 between the number of clusters in the two arms; defaults to 1 (equal clusters per arm).
delta	The difference between the intervention and control means under the alternative minus the difference under the null hypothesis.
sd	The total standard deviation of the outcome variable; defaults to 1.
icc	The within-cluster, within-period intraclass correlation coefficient; defaults to 0.
cac	The cluster autocorrelation; defaults to 0.
sac	The subject autocorrelation; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.crt.long.cont(m = 30, J1 = 8, delta = 0.3, icc = 0.05, cac = 0.4, sac = 0.5)
```

---

pss.crt.parallel.bin   *Power for a cluster randomized trial with a binary outcome*

Description

Power for a cluster randomized trial with a binary outcome

Usage

```
pss.crt.parallel.bin(
  m = NULL,
  m.sd = 0,
  J = NULL,
  pc = NULL,
  pt = NULL,
```

```
    sigma.u = NULL,
    alpha = 0.05,
    power = NULL,
    sides = 2,
    v = TRUE
)
```

Arguments

m	The number of subjects per cluster.
m.sd	The standard deviation of cluster sizes (provide if unequal number of participants per cluster); defaults to 0.
J	The number of clusters.
pc	The probability of the outcome in control clusters.
pt	The probability of the outcome in treatment clusters.
sigma.u	Standard deviation of the cluster random effect.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.crt.parallel.bin(m = 60, J = NULL, pc = 0.25, pt = 0.15, sigma.u = 0.3, power = 0.8)
pss.crt.parallel.bin(m = 60, m.sd = 1, J = NULL, pc = 0.25, pt = 0.15, sigma.u = 0.3, power = 0.8)
```

---

pss.crt.parallel.cont   *Power for a cluster randomized trial with a continuous outcome*

Description

Power for a cluster randomized trial with a continuous outcome

Usage

```
pss.crt.parallel.cont(
    m = NULL,
    m.sd = 0,
    J1 = NULL,
    J.ratio = 1,
    delta = NULL,
    sd = 1,
    icc1 = 0,
    icc2 = 0,
    ncov = 0,
```

```
    RsqB = 0,
    RsqW = 0,
    alpha = 0.05,
    power = NULL,
    sides = 2,
    v = TRUE
)
```

Arguments

m	The number of subjects per cluster or the mean cluster size (if unequal number of participants per cluster).
m.sd	The standard deviation of cluster sizes (provide if unequal number of participants per cluster); defaults to 0.
J1	The number of clusters in arm 1.
J.ratio	The ratio J2/J1 between the number of clusters in the two arms; defaults to 1 (equal clusters per arm).
delta	The difference between the intervention and control means under the alternative minus the difference under the null hypothesis.
sd	The total standard deviation of the outcome variable; defaults to 1.
icc1	The intraclass correlation coefficient in arm 1; defaults to 0.
icc2	The intraclass correlation coefficient in arm 2; defaults to 0.
ncov	The number of cluster-level and individual-level covariates; defaults to 0.
RsqB	The estimated proportion of total variance explained by cluster-level covariates; defaults to 0.
RsqW	The estimated proportion of total variance explained by individual-level covariates; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.crt.parallel.cont(m = 30, J1 = 8, delta = 0.4, icc1 = 0.05, icc2 = 0.05)
pss.crt.parallel.cont(m = NULL, J1 = 6, delta = 0.5, icc1 = 0.05, icc2 = 0.05, power = 0.8)
pss.crt.parallel.cont(m = 25, m.sd = 15, J1 = NULL, delta = 0.3, icc1 = 0.05,
icc2 = 0.05, power = 0.8)
pss.crt.parallel.cont(m = 20, J1 = 15, delta = 0.3, icc1 = 0.05, icc2 = 0.05,
RsqB = 0.1, ncov = 1, sides = 1)
pss.crt.parallel.cont(m = 20, J1 = 15, delta = 0.3, icc1 = 0.05, icc2 = 0.05,
RsqW = 0.5^2, ncov = 1, sides = 1)
pss.crt.parallel.cont(m = NULL, J1 = 6, delta = 0.5, icc1 = 0.05, icc2 = 0.05, power = 0.8)
```

pss.crt.r	*Correlation between a cluster mean at baseline and follow up*

Description

Correlation between a cluster mean at baseline and follow up

Usage

```
pss.crt.r(m, icc, cac, sac)
```

Arguments

m	The number of measurements in each cluster at baseline and follow up.
icc	The intraclass correlation coefficient.
cac	The cluster autocorrelation.
sac	The subject autocorrelation.

Value

The computed correlation.

Examples

```
pss.crt.r(m = 30, icc = 0.05, cac = 0.4, sac = 0.5)
```

pss.crt.varexplore	*Variance exploration for cluster randomized trials with binary outcomes*

Description

Variance exploration for cluster randomized trials with binary outcomes

Usage

```
pss.crt.varexplore(pc, pt)
```

Arguments

pc	The probability of the outcome in control clusters.
pt	The probability of the outcome in treatment clusters.

Value

A list of the arguments and a dataframe of outputs.

Examples

```
pss.crt.varexplore(pc = 0.25, pt = 0.15)
```

| pss.crt.xo.cont | *Power for test of treatment effect in 2x2 crossover cluster randomized trial* |

Description

Power for test of treatment effect in 2x2 crossover cluster randomized trial

Usage

```
pss.crt.xo.cont(
  m = NULL,
  J.arm = NULL,
  delta = NULL,
  sd = 1,
  icc = 0,
  iccb = NULL,
  xi = 0,
  cac = NULL,
  sac = 0,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

m	The number of subjects measured during each cluster-period.
J.arm	The number of clusters in each arm.
delta	The difference between the intervention and control means under the alternative minus the difference under the null hypothesis.
sd	The total standard deviation of the outcome variable; defaults to 1.
icc	The within-cluster, within-period intraclass correlation coefficient; defaults to 0.
iccb	The within-cluster, between-period intraclass correlation coefficient. Either iccb OR cac must be specified.
xi	The within-cluster, within-subject correlation (correlation between two measurements within the same subject); defaults to 0.
cac	The cluster autocorrelation. Either iccb OR cac must be specified.
sac	The subject autocorrelation; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.crt.xo.cont(m = 30, J.arm = 4, delta = 0.3, icc = 0.05, cac = 0.8, sac = 0.4)
pss.crt.xo.cont(m = 30, J.arm = 4, delta = 0.3, icc = 0.05, iccb = 0.04, xi = 0.42)
pss.crt.xo.cont(m = 30, J.arm = 4, delta = 0.3, icc = 0.05, cac = 0.5)
```

---

pss.es.anova.f   *Cohen's f effect size calculation for one- or two- way analysis of vari-*
                          ance

Description

Cohen's f effect size calculation for one- or two- way analysis of variance

Usage

```
pss.es.anova.f(means = NULL, sd = NULL, v = TRUE)
```

Arguments

means	A vector or matrix of group means.
sd	The estimated standard deviation within each group.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

Various calculated f effect sizes.

Examples

```
pss.es.anova.f(means = c(5, 10, 12), sd = 10)
mmatrix <- matrix(c(9.3, 8.9, 8.5, 8.7, 8.3, 7.9), nrow = 2, byrow = TRUE)
pss.es.anova.f(means = mmatrix, sd = 2)
```

---

pss.es.d   *Cohen's d effect size calculation for one or two means*

Description

Cohen's d effect size calculation for one or two means

Usage

```
pss.es.d(delta = NULL, sd = 1)
```

Arguments

delta	If one mean: muA (the true mean) - mu0 (the mean under the null). If two means: DeltaA (the true difference mu1 - mu2) - Delta0 (the difference under the null).
sd	The estimated standard deviation; defaults to 1.

Value

A list of the arguments and the d effect size.

Examples

```
pss.es.d(delta = 6.5 - 5.7, sd = 0.4)
```

---

pss.es.fsq   *Cohen's f^2 effect size calculation for overall F test*

Description

Cohen's f^2 effect size calculation for overall F test

Usage

```
pss.es.fsq(Rsq = 0.02)
```

Arguments

Rsq   The squared sample multiple correlation coefficient.

Value

A list of the arguments and the f^2 effect size.

Examples

```
pss.es.fsq(Rsq = 0.02)
```

---

pss.es.h   *Cohen's h effect size calculation for two proportions*

Description

Cohen's h effect size calculation for two proportions

Usage

```
pss.es.h(p1 = NULL, p2 = NULL)
```

Arguments

p1   The proportion in group 1.
p2   The proportion in group 2.

Value

A list of the arguments and the h effect size.

Examples

```
pss.es.h(p1 = 0.8, p2 = 0.6)
```

---

pss.es.q   *Cohen's q effect size calculation for two correlation coefficients*

Description

Cohen's q effect size calculation for two correlation coefficients

Usage

```
pss.es.q(rho1 = NULL, rho2 = NULL)
```

Arguments

rho1   The correlation coefficient in group 1.

rho2   The correlation coefficient in group 2.

Value

A list of the arguments and the q effect size.

Examples

```
pss.es.q(rho1 = 0.3, rho2 = 0.1)
```

---

pss.es.w   *Cohen's w effect size calculation for chi-square tests*

Description

Cohen's w effect size calculation for chi-square tests

Usage

```
pss.es.w(p0vec = NULL, p1vec = NULL, pmatrix = NULL)
```

Arguments

p0vec   The first vector of probabilities. Both p0vec and p1vec, or pmatrix must be
                specified.

p1vec   The second vector of probabilities. Both p0vec and p1vec, or pmatrix must be
                specified.

pmatrix   The two-way probability table. Both p0vec and p1vec, or pmatrix must be spec-
                ified.

Value

A list of the arguments and the w effect size.

Examples

```
pss.es.w(p0vec = c(0.5, 0.3, 0.2), p1vec = c(0.7, 0.2, 0.1))
pss.es.w(pmatrix = matrix(c(0.050, 0.350, 0.100, 0.075, 0.250, 0.175), nrow = 2, byrow = TRUE))
```

pss.irgtt.bin	*Power for an individual randomized group treatment trial with binary outcomes*

Description

Power for an individual randomized group treatment trial with binary outcomes

Usage

```
pss.irgtt.bin(
  m = NULL,
  J = NULL,
  n = NULL,
  p1 = NULL,
  p2 = NULL,
  icc = 0,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

m	The number of subjects per cluster in the treatment group.
J	The number of clusters in the treatment group.
n	The number of total participants in the control group.
p1	The probability of the outcome in the control group.
p2	The probability of the outcome in the intervention group.
icc	The intraclass correlation coefficient in the treatment group; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.irgtt.bin(m = 20, J = 5, n = 100, p1 = 0.8, p2 = 0.6, icc = 0.04, sides = 2)
pss.irgtt.bin(m = 20, J = 6, n = 120, p1 = 0.8, p2 = 0.6, icc = 0.04, sides = 2)
```

---

pss.irgtt.cont   *Power for individually randomized group treatment trial with continuous outcome*

Description

Power for individually randomized group treatment trial with continuous outcome

Usage

```
pss.irgtt.cont(
  m = NULL,
  J = NULL,
  n = NULL,
  delta = NULL,
  sd = 1,
  icc = 0,
  Theta = 1,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  tol = .Machine$double.eps^0.25,
  v = TRUE
)
```

Arguments

m	The number of subjects per cluster in the treatment group.
J	The number of clusters in the treatment group.
n	The number of total participants in the control group.
delta	The difference between the intervention and control means under the alternative minus the difference under the null hypothesis.
sd	The total standard deviation of the outcome variable in the control group; defaults to 1.
icc	The intraclass correlation coefficient in the treatment group; defaults to 0.
Theta	The ratio of the total variance between intervention and control groups; defaults to 1.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.irgtt.cont(m = 10, J = 12, n = 120, delta = 0.4, icc = 0.05, Theta = 1, power = NULL)
pss.irgtt.cont(m = 10, J = 12, n = NULL, delta = 0.4, icc = 0.05, Theta = 1, power = 0.8)
```

---

pss.mcnemar.test   *Power approximation for McNemar's test for two correlated proportions*

Description

Power approximation for McNemar's test for two correlated proportions

Usage

```
pss.mcnemar.test(
  N = NULL,
  p1 = NULL,
  p2 = NULL,
  phi = NULL,
  paid = NULL,
  dpr = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

N	The sample size; the number of pairs.
p1	The proportion in condition 1.
p2	The proportion in condition 2.
phi	The estimated correlation between the two conditions.
paid	The smaller of the two discordant probabilities. Either p1, p2, and phi, OR paid and dpr must be specified.
dpr	The discordant proportion ratio. Either p1, p2, and phi, OR paid and dpr must be specified.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.mcnemar.test(N = NULL, p1 = 0.8, p2 = 0.9, phi = 0, power = 0.9, sides = 2)
pss.mcnemar.test(N = NULL, paid = 0.08, dpr = 0.18 / 0.08, power = 0.9, sides = 2)
```

pss.mlrF.overall   *Power calculations for a multiple linear regression overall F test*

Description

Power calculations for a multiple linear regression overall F test

Usage

```
pss.mlrF.overall(
  N = NULL,
  p = NULL,
  Rsq = NULL,
  fsq = NULL,
  alpha = 0.05,
  power = NULL,
  random = FALSE,
  v = TRUE
)
```

Arguments

N	The sample size.
p	The number of predictors.
Rsq	The squared sample multiple correlation coefficient.
fsq	The squared f effect size. Either Rsq OR fsq must be specified.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
random	Whether the values of the predictors are random; defaults to FALSE.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.mlrF.overall(N = 400, p = 2, Rsq = 0.02)
pss.mlrF.overall(N = 400, p = 2, fsq = 0.02 / (1 - 0.02))
pss.mlrF.overall(N = 109, p = 1, Rsq = 0.3^2)
pss.mlrF.overall(N = 50, p = 1, Rsq = 0.2)
pss.mlrF.overall(N = 50, p = 3, Rsq = 0.2)
pss.mlrF.overall(N = 50, p = 5, Rsq = 0.2)
pss.mlrF.overall(N = 400, p = 2, Rsq = 0.02, random = TRUE)
```

---

pss.mlrF.partial *Power calculations for a multiple linear regression partial F test*

Description

Power calculations for a multiple linear regression partial F test

Usage

```
pss.mlrF.partial(
  N = NULL,
  p = NULL,
  q = NULL,
  pc = NULL,
  Rsq.red = NULL,
  Rsq.full = NULL,
  alpha = 0.05,
  power = NULL,
  v = TRUE
)
```

Arguments

N	The sample size.
p	The number of control predictors.
q	The number of test predictors.
pc	The partial correlation coefficient. Either both Rsq terms OR pc must be specified.
Rsq.red	The squared sample multiple correlation coefficient in the reduced model.
Rsq.full	The squared sample multiple correlation coefficient in the full model.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.mlrF.partial(N = 80, p = 3, q = 2, Rsq.red = 0.25, Rsq.full = 0.35)
pss.mlrF.partial(N = 150, p = 4, pc = 0.2)
```

---

pss.ms.varexplore   *Variance exploration for multisite trials with binary outcomes*

Description

Variance exploration for multisite trials with binary outcomes

Usage

```
pss.ms.varexplore(pc, pt)
```

Arguments

pc	The probability of the outcome in control clusters.
pt	The probability of the outcome in treatment clusters.

Value

A list of the arguments and a dataframe of outputs.

Examples

```
pss.ms.varexplore(pc = 0.1, pt = 0.2)
```

---

pss.multisite.bin   *Power for multisite trials with binary outcomes*

Description

Power for multisite trials with binary outcomes

Usage

```
pss.multisite.bin(
  m = NULL,
  alloc.ratio = 1,
  J = NULL,
  pc = NULL,
  pt = NULL,
  sigma.u = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

m	The total number of subjects per site.
alloc.ratio	The allocation ratio of intervention/control per site; defaults to 1.
J	The number of sites.
pc	The probability of the outcome in the control condition.
pt	The probability of the outcome in the treatment condition.
sigma.u	Standard deviation of the treatment effect across sites.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.multisite.bin(m = 30, J = 25, pc = 0.1, pt = 0.2, sigma.u = 0.4, power = NULL)
pss.multisite.bin(m = 30, J = NULL, pc = 0.1, pt = 0.2, sigma.u = 0.4, power = 0.9)
```

---

pss.multisite.cont   *Power for test of average treatment effect in a multisite trial*

Description

Power for test of average treatment effect in a multisite trial

Usage

```
pss.multisite.cont(
  m = NULL,
  m.sd = 0,
  alloc.ratio = 1,
  J = NULL,
  delta = NULL,
  sd = 1,
  icc0 = NULL,
  icc1 = NULL,
  Rsq = 0,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

m	The total number of subjects per site or the mean cluster size (if unequal number of participants per site).
m.sd	The standard deviation of cluster sizes (provide if unequal number of participants per site); defaults to 0.
alloc.ratio	The allocation ratio of intervention/control per site; defaults to 1.
J	The number of sites.
delta	The difference between the intervention and control means under the alternative minus the difference under the null hypothesis.
sd	The total standard deviation of the outcome variable; defaults to 1.
icc0	The proportion of total variance of the outcome attributable to variation in site-level means.
icc1	The proportion of total variance of the outcome attributable to variation in the treatment effect across sites.
Rsq	The estimated R^2 for regressing the outcome on the covariates; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.multisite.cont(m = 20, J = 10, delta = 3, sd = sqrt(40), icc0 = 0.1, icc1 = 0)
pss.multisite.cont(m = 20, J = 10, delta = 3, sd = sqrt(48), icc0 = 0.095, icc1 = 0.048)
pss.multisite.cont(m = 20, alloc.ratio = 1.5, J = 10, delta = 0.43, icc0 = 0.095, icc1 = 0.048)
pss.multisite.cont(m = 10, J = NULL, delta = 0.5, sd = 1, icc0 = 0, icc1 = 0.05, power = 0.8)
pss.multisite.cont(m = 20, m.sd = 5, J = 10, delta = 3, sd = sqrt(48), icc0 = 0.095, icc1 = 0.048)
pss.multisite.cont(m = 20, J = 10, delta = 3, sd = sqrt(48), icc0 = 0.095,
icc1 = 0.048, Rsq = 0.5^2)
```

---

pss.multisite.hte   *Power for test of heterogeneity of treatment effect in multisite trials*

Description

Power for test of heterogeneity of treatment effect in multisite trials

Usage

```
pss.multisite.hte(
  m = NULL,
  alloc.ratio = 1,
  J = NULL,
  VR = NULL,
  alpha = 0.05,
  v = TRUE
)
```

Arguments

m	The total number of subjects per site.
alloc.ratio	The allocation ratio of intervention/control per site; defaults to 1.
J	The number of sites.
VR	The variance ratio (site-level treatment effects / observations within sites) the under the alternative.
alpha	The significance level or type 1 error rate; defaults to 0.05.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed power).

Examples

```
pss.multisite.hte(m = 10, J = 30, VR = 8 / 36)
```

---

pss.prop.1samp	*Power calculations for one sample proportion tests*

Description

Power calculations for one sample proportion tests

Usage

```
pss.prop.1samp(
  N = NULL,
  p0 = NULL,
  pA = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

N	The sample size.
p0	The proportion under the null.
pA	The true proportion.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.prop.1samp(N = NULL, p0 = 0.2, pA = 0.3, power = 0.8, sides = 1)
pss.prop.1samp(N = NULL, p0 = 0.4, pA = 0.5, power = 0.8, sides = 1)
```

---

pss.prop.2samp   *Power calculations for two sample proportion tests*

Description

Power calculations for two sample proportion tests

Usage

```
pss.prop.2samp(
  n1 = NULL,
  n.ratio = 1,
  p1 = NULL,
  p2 = NULL,
  margin = 0,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
p1	The proportion in group 1.
p2	The proportion in group 2.
margin	The margin of noninferiority or superiority; defaults to 0. See margin.sign for guidance on the sign of margin.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.prop.2samp(n1 = NULL, p1 = 0.6, p2 = 0.8, alpha = 0.025, power = 0.9, sides = 1)
pss.prop.2samp(n1 = NULL, p1 = 0.25, p2 = 0.25, margin = 0.1, alpha = 0.025, power = 0.8, sides = 1)
```

pss.prop.test.equiv   *Power calculations for test of equivalence of two proportions*

Description

Power calculations for test of equivalence of two proportions

Usage

```
pss.prop.test.equiv(
  n1 = NULL,
  n.ratio = 1,
  p1 = NULL,
  p2 = NULL,
  margin = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
p1	The outcome proportion in group 1.
p2	The outcome proportion in group 2.
margin	The equivalence margin. See margin.sign for guidance on the sign of margin.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.prop.test.equiv(n1 = NULL, p1 = 0.5, p2 = 0.5, margin = 0.1, alpha = 0.05, power = 0.8,
sides = 1)
```

---

pss.propodds   *Power calculations for ordinal categorical variable under propor-*
                                tional odds assumption

Description

Power calculations for ordinal categorical variable under proportional odds assumption

Usage

```
pss.propodds(pC, OR, n1, n.ratio = 1, alpha = 0.05, power = NULL)
```

Arguments

pC	Vector of response probabilities in control group (group 1). Must sum to 1. Categories are ordered from best to worst.
OR	Odds ratio when the alternative is true. Must be greater than 1.
n1	Sample size for group 1 (control group).
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power; defaults to 0.8.

Value

A list of the arguments (including the computed one).

Examples

```
library(Hmisc)
pC <- c(0.2, 0.5, 0.2, 0.1)
pss.propodds(pC = pC, OR = 2.5, n1 = 65, n.ratio = 1, alpha = 0.05)
```

---

pss.ranksum   *Power calculations for rank-sum test*

Description

Power calculations for rank-sum test

Usage

```
pss.ranksum(
  n1 = NULL,
  n.ratio = 1,
  p = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2
)
```

Arguments

n1	The sample size in group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
p	The probability that an observation in group 2 is greater than an observation in group 1 (P(Y>X).
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two-sided hypothesis test.

Value

A list of the arguments (including the computed one).

Examples

```
pss.ranksum(n1 = 10, n.ratio = 1, p = 0.8, alpha = 0.05, power = NULL, sides = 2)
```

---

pss.re.crt.bin	*Relative efficiency for cluster randomized trials with binary outcomes*
	Relative efficiency of varying to equal cluster sizes

Description

Relative efficiency for cluster randomized trials with binary outcomes Relative efficiency of varying to equal cluster sizes

Usage

```
pss.re.crt.bin(m, m.sd, pc, pt, sigma.u)
```

Arguments

m	The number of subjects per cluster or the mean cluster size (if unequal number of participants per cluster).
m.sd	The standard deviation of cluster sizes (provide if unequal number of participants per cluster).
pc	The probability of the outcome in control clusters.
pt	The probability of the outcome in treatment clusters.
sigma.u	Standard deviation of the cluster random effect.

Value

The computed RE.

Examples

```
pss.re.crt.bin(m = 60, m.sd = 45, pc = 0.25, pt = 0.15, sigma.u = 0.3)
```

pss.rr	*Power calculations for relative risk*

Description

Power calculations for relative risk

Usage

```
pss.rr(
  n1 = NULL,
  n.ratio = 1,
  p1 = NULL,
  p2 = NULL,
  RR0 = 1,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
p1	The proportion in group 1.
p2	The proportion in group 2.
RR0	The relative risk under the null; defaults to 1.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.rr(n1 = NULL, n.ratio = 1/6, p1 = 0.1, p2 = 0.1 * 2, power = 0.8)
```

---

pss.signedrank   *Power calculations for signed-rank test*

Description

Power calculations for signed-rank test

Usage

```
pss.signedrank(N = NULL, ps = NULL, alpha = 0.05, power = NULL, sides = 2)
```

Arguments

N	The sample size; number of observations or paired differences.
ps	The probability that the sum of two values exceeds zero when the alternative hypothesis is true.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two-sided hypothesis test.

Value

A list of the arguments (including the computed one).

Examples

```
pss.signedrank(N = 20, p = 0.87, power = NULL, sides = 2)
```

---

pss.signtest   *Power calculations for sign test (one sample median)*

Description

Power calculations for sign test (one sample median)

Usage

```
pss.signtest(N = NULL, p = NULL, alpha = 0.05, power = NULL, sides = 2)
```

Arguments

N	The sample size.
p	The probability of a positive difference when the alternative hypothesis is true.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two-sided hypothesis test.

Value

A list of the arguments (including the computed one).

Examples

```
pss.signtest(N = 40, p = 0.7, power = NULL, alpha = 0.05, sides = 1)
```

---

pss.slr   *Power calculations for a simple linear regression*

Description

Power calculations for a simple linear regression

Usage

```
pss.slr(
  N = NULL,
  beta10 = 0,
  beta1A = NULL,
  sd.x.sq = NULL,
  sigma.e = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

N	The sample size.
beta10	The slope regression coefficient under the null hypothesis.
beta1A	The slope regression coefficient under the alternative hypothesis.
sd.x.sq	The sample variance of the covariate X.
sigma.e	The estimated standard deviation of the error terms.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
# Yi = beta0 + beta1 * Xi + ei, i = 1,...,N
pss.slr(N = 100, beta10 = 1, beta1A = 1.5, sd.x.sq = 25, sigma.e = 10, sides = 1)
```

Description

Power calculations for one sample t tests

Usage

```
pss.t.test.1samp(
  N = NULL,
  delta = NULL,
  sd = 1,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

N	The sample size.
delta	muA (the true mean) - mu0 (the mean under the null).
sd	The estimated standard deviation; defaults to 1.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.t.test.1samp(N = 36, delta = 4.9 - 5.7, sd = 2, sides = 1)
pss.t.test.1samp(N = 36, delta = 6.3 - 5.7, sd = 2, sides = 1)
pss.t.test.1samp(N = 36, delta = 4.9 - 5.7, sd = 2, sides = 2)
pss.t.test.1samp(delta = 0.6, sd = 1, power = 0.8, sides = 1)
```

pss.t.test.2samp	*Power calculations for two sample t tests allowing for unequal sample sizes and/or variances*

Description

Power calculations for two sample t tests allowing for unequal sample sizes and/or variances

Usage

```
pss.t.test.2samp(
  n1 = NULL,
  n.ratio = 1,
  delta = NULL,
  sd1 = 1,
  sd.ratio = 1,
  df.method = c("welch", "classical"),
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
delta	DeltaA (the true difference mu1 - mu2) - Delta0 (the difference under the null) - margin. See margin.sign for guidance on the sign of the margin.
sd1	The estimated standard deviation for group 1; defaults to 1 (equal standard deviations in the two groups).
sd.ratio	The ratio sd2/sd1 between the standard deviations of the two groups.
df.method	Method for calculating the degrees of freedom: "welch" (default) or "classical".
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.t.test.2samp(n1 = 50, delta = 2, sd1 = 5, sides = 1)
pss.t.test.2samp(n1 = NULL, n.ratio = 2, delta = 0.5, sd1 = 1, power = 0.8, sides = 2)
pss.t.test.2samp(n1 = 49, n.ratio = 2, delta = 0.5, sd1 = 1, power = NULL, sides = 2)
pss.t.test.2samp(n1 = 25, n.ratio = 3, delta = 3, sd1 = 4, sd.ratio = 1.5, alpha = 0.025, sides = 1)
pss.t.test.2samp(n1 = NULL, delta = 0.5, sd1 = 1, power = 0.8, sides = 2)
```

pss.t.test.paired *Power calculations for paired t tests*

Description

Power calculations for paired t tests

Usage

```
pss.t.test.paired(
  N = NULL,
  delta = NULL,
  sd1 = 1,
  sd2 = 1,
  rho = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

N	The sample size; the number of pairs.
delta	DeltaA (the true mean difference) - Delta0 (the mean difference under the null).
sd1	The estimated pre standard deviation; defaults to 1.
sd2	The estimated post standard deviation; defaults to 1.
rho	The estimated correlation between pre and post measurements on the same individual.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.t.test.paired(N = NULL, delta = 4, sd1 = 10, sd2 = 10, rho = 0.4, power = 0.8, sides = 2)
```

---

pss.varym.re   *Relative efficiency for cluster randomized or multisite trials due to*
                                varying cluster sizes

Description

Relative efficiency for cluster randomized or multisite trials due to varying cluster sizes

Usage

```
pss.varym.re(m, m.sd, icc)
```

Arguments

m	The number of subjects per cluster or the mean cluster size (if unequal number of participants per cluster).
m.sd	The standard deviation of cluster sizes (provide if unequal number of participants per cluster).
icc	The intraclass correlation coefficient. For a multisite trial this is icc1. For a CRT this is the average of the 2 icc's.

Value

The computed RE.

Examples

```
pss.varym.re(m = 25, m.sd = 15, icc = 0.05)
```

---

pss.z.test.1samp   *Power calculations for one sample z tests*

Description

Power calculations for one sample z tests

Usage

```
pss.z.test.1samp(
  N = NULL,
  delta = NULL,
  sd = 1,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

N	The sample size.
delta	muA (the true mean) - mu0 (the mean under the null).
sd	The estimated standard deviation; defaults to 1.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.z.test.1samp(N = NULL, delta = 6.5 - 5.7, sd = 2, power = 0.8, sides = 2)
pss.z.test.1samp(N = 40, delta = NULL, sd = 1, power = 0.9, sides = 2)
pss.z.test.1samp(N = NULL, delta = 0.6, sd = 1, power = 0.8, sides = 1)
```

---

pss.z.test.2samp	*Power calculations for two sample z tests allowing for unequal sample sizes and/or variances*

Description

Power calculations for two sample z tests allowing for unequal sample sizes and/or variances

Usage

```
pss.z.test.2samp(
  n1 = NULL,
  n.ratio = 1,
  delta = NULL,
  sd1 = 1,
  sd.ratio = 1,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

n1	The sample size for group 1.
n.ratio	The ratio n2/n1 between the sample sizes of two groups; defaults to 1 (equal group sizes).
delta	DeltaA (the true difference mu1 - mu2) - Delta0 (the difference under the null) - margin See margin.sign for guidance on the sign of the margin.

sd1	The estimated standard deviation for group 1; defaults to 1 (equal standard deviations in the two groups).
sd.ratio	The ratio sd2/sd1 between the standard deviations of the two groups.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.z.test.2samp(n1 = NULL, n.ratio = 1, delta = 0.5, sd1 = 1, power = 0.8, sides = 2)
```

---

pss.z.test.paired   *Power calculations for paired z tests*

Description

Power calculations for paired z tests

Usage

```
pss.z.test.paired(
  N = NULL,
  delta = NULL,
  sd1 = 1,
  sd2 = 1,
  rho = NULL,
  alpha = 0.05,
  power = NULL,
  sides = 2,
  v = TRUE
)
```

Arguments

N	The sample size; the number of pairs.
delta	DeltaA (the true mean difference) - Delta0 (the mean difference under the null).
sd1	The estimated pre standard deviation; defaults to 1.
sd2	The estimated post standard deviation; defaults to 1.
rho	The estimated correlation between pre and post measurements on the same individual; defaults to 0.
alpha	The significance level or type 1 error rate; defaults to 0.05.
power	The specified level of power.
sides	Either 1 or 2 (default) to specify a one- or two- sided hypothesis test.
v	Either TRUE for verbose output or FALSE to output computed argument only.

Value

A list of the arguments (including the computed one).

Examples

```
pss.z.test.paired(N = NULL, delta = 4, sd1 = 10, sd2 = 10, rho = 0.4, power = 0.8, sides = 2)
```

---

swd_1trt_power   *Stepped Wedge Design Power Calculation with 1 Treatment*

Description

Calculates power for stepped wedge design with one treatment and one control condition.

Usage

```
swd_1trt_power(alpha = 0.05, J, m, K, b, d, rho, rho_c, rho_s)
```

Arguments

alpha	The significance level or type 1 error rate
J	Number of clusters
m	The number of individuals in each cluster at each time period
K	The number of steps (if one baseline period, then this is periods - 1)
b	The number of baseline periods
d	The standardized effect size
rho	Intraclass correlation coefficient (ICC)
rho_c	Cluster autocorrelation (proportion of cluster-level variance that is time invariant)
rho_s	Subject autocorrelation (This is 0 in repeated cross sectional designs because people are measured only once)

Value

power

Examples

```
# closed cohort design as in Example 12.5
swd_1trt_power(alpha = 0.05, m = 30, J = 5, K = 5, b = 1, d = 0.4,
               rho = 0.05, rho_c = 0.2, rho_s = 0.4)
# repeated cross sectional design as in Example 12.5
swd_1trt_power(alpha = 0.05, m = 30, J = 5, K = 5, b = 1, d = 0.4,
               rho = 0.05, rho_c = 0.2, rho_s = 0)
```

---

swd_1trt_ss   *Stepped Wedge Design Sample Size Calculation with 1 Treatment*

Description

Calculates sample size requirements for stepped wedge design with one treatment and one control condition.

Usage

```
swd_1trt_ss(alpha, power, m, K, b, d, rho, rho_c, rho_s)
```

Arguments

alpha	The significance level or type 1 error rate
power	The specified level of power
m	The number of individuals in each cluster at each time period
K	The number of steps (if one baseline period, then this is periods - 1)
b	The number of baseline periods
d	The standardized effect size
rho	Intraclass correlation coefficient (ICC)
rho_c	Cluster autocorrelation (proportion of cluster-level variance that is time invariant)
rho_s	Subject autocorrelation (This is 0 in repeated cross sectional designs because people are measured only once)

Value

Calculated number of clusters required, adjusted number of clusters, and suggested number of clusters that includes the value of K

Examples

```
# Repeated Cross Sectional Stepped Wedge Sample Size Calculation
# with 3 steps, 1 baseline period, 80% power, 0.05 significance, 30 ppl per
# cluster, effect size of 0.4, ICC of 0.05, and cluster autocorrelation of 0.2
# Following Example 12.6 in text
swd_1trt_ss(alpha = 0.05, power = 0.8, m = 30, K = 3, b = 1, d = 0.4,
            rho = 0.05, rho_c = 0.2, rho_s = 0)
```

swd_2trt_additive_power

Additive Treatments Stepped Wedge Design Power Calculation

Description

Calculate power for detecting treatment effects in a two-treatment stepped wedge design with additive treatment effects. We only consider complete designs. This function is based on Power Analysis for Stepped Wedge Trials with Two Treatments published in Stat Med in 2022 by Phillip Sundin and Catherine Crespi. This manuscript uses the normal distribution and the Wald Test to derive power.

Usage

```
swd_2trt_additive_power(
  RhoW,
  ModelChoice,
  n.individuals,
  n.clusters,
  n.periods,
  delta_1,
  delta_2,
  RhoA,
  IAC,
  Sequence_Tx1,
  Sequence_Tx2,
  typeIerror
)
```

Arguments

RhoW	The intraclass correlation coefficient, which refers to the correlation between outcomes of two different individuals in the same cluster at the same time.
ModelChoice	A string indicating either a repeated cross sectional design ("RCS"), nested exchangeable ("NEC"), Cohort ("Cohort"), or any one of these three designs in their standardized form. Only one of "RCS Standardized", "RCS", "Cohort Standardized", "Cohort", "NEC Standardized", or "NEC" can be specified. The standardized design refers to dividing by the standard deviation of y (the outcome) in the covariance specification.
n.individuals	The number of individuals in each condition at one time period.
n.clusters	The number of clusters
n.periods	The number of time periods.
delta_1	The standardized effect size for treatment 1
delta_2	The standardized effect size for treatment 2
RhoA	The correlation between two observations in the same individual in the same cluster but different time periods. RCS models assume RhoW = RhoA, and Cohort models assume RhoA >= RhoW.
IAC	The individual auto-correlation, which is the proportion of the individual-level variance that is time-invariant. IAC = 0 in a RCS.

Sequence_Tx1   A vector representing the time points (periods) at which each cluster transitions
                 from control to treatment 1 (ie the first occurence).

Sequence_Tx2   A vector representing the time points (periods) at which each cluster transitions
                 from control to treatment 2 (ie the first occurence).

typeIerror   The significance level.

Value

A list with power for detecting treatment effect for treatment 1 and 2

Examples

```
## For example, the 3 cluster, 4 period SWD,
##      0 1 1   1
##      0 0 1+2 1+2
##      0 0 2   1+2
## where 0 denotes control condition, 1 denotes the condition with only
## treatment 1, 2 denote the condition with only treatment 2, and 1+2 denotes the condition
## where a cluster receives both treatment 1 and 2
## would have Sequence1 <- c(2,3,4) and Sequence2 <- c(NA,3,3)
## notice sequence 1 cluster 3 has time period 4 even though time period 3 had treatment 2,
## so it is the first occurrence of trt 1 in this cluster.


# 12-cluster concurrent repeated cross sectional design
# Sequencing has 2 clusters transition to treatment 1 at time 2,
# 2 clusters transition to treatment 1 at time 3, and 2 clusters transition
# to treatment 1 at time 3. These clusters never receive treatment 2
Sequence_Tx1 <- c(2, 2, 3, 3, 4, 4, NA, NA, NA, NA, NA, NA)
# similar sequencing for treatment 2
Sequence_Tx2 <- c(NA, NA, NA, NA, NA, NA, 4, 4, 3, 3, 2, 2)
swd_2trt_additive_power(RhoW = 0.05, ModelChoice = "RCS", RhoA = 0.2, IAC = 0,
        n.individuals = 30, n.clusters = 12, n.periods = 4, delta_1 = 0.4, delta_2 = 0.1,
            Sequence_Tx1 = Sequence_Tx1, Sequence_Tx2 = Sequence_Tx2,
            typeIerror = 0.05)
```

---

swd_2trt_interaction_power
                  Stepped Wedge Design Power Calculation for Interaction Term

---

Description

Calculate power for detecting interaction effects in a two-treatment stepped wedge design. We only
consider complete designs. This function is based on Power Analysis for Stepped Wedge Trials
with Two Treatments published in Stat Med in 2022 by Phillip Sundin and Catherine Crespi. This
manuscript uses the normal distribution and the Wald Test to derive power.

Usage

```
swd_2trt_interaction_power(
  RhoW,
  ModelChoice,
  n.individuals,
```

```
    n.clusters,
    n.periods,
    delta_1,
    delta_2,
    delta_3,
    RhoA,
    IAC,
    typeIerror,
    Sequence_Tx1,
    Sequence_Tx2
)
```

Arguments

RhoW
: The intraclass correlation coefficient, which refers to the correlation between outcomes of two different individuals in the same cluster at the same time.

ModelChoice
: A string indicating either a repeated cross sectional design ("RCS"), nested exchangeable ("NEC"), Cohort ("Cohort"), or any one of these three designs in their standardized form. Only one of "RCS Standardized", "RCS", "Cohort Standardized", "Cohort", "NEC Standardized", or "NEC" can be specified. The standardized design refers to dividing by the standard deviation of y (the outcome) in the covariance specification.

n.individuals
: The number of individuals in each condition at one time period.

n.clusters
: The number of clusters

n.periods
: The number of time periods.

delta_1
: The standardized effect size for treatment 1

delta_2
: The standardized effect size for treatment 2

delta_3
: The standardized effect size for the interaction effect.

RhoA
: The correlation between two observations in the same individual in the same cluster but different time periods. RCS models assume RhoW = RhoA, and Cohort models assume RhoA >= RhoW.

IAC
: The individual auto-correlation, which is the proportion of the individual-level variance that is time-invariant. IAC = 0 in a RCS.

typeIerror
: The significance level.

Sequence_Tx1
: A vector representing the time points (periods) at which each cluster transitions from control to treatment 1 (ie the first occurence).

Sequence_Tx2
: A vector representing the time points (periods) at which each cluster transitions from control to treatment 2 (ie the first occurence).

Value

A matrix with the standard error, statistic, and power for detecting effects for treatment 1, treatment 2, and interaction effects.

Examples

```
# 8 Cluster repeated cross sectional SWD with main and interaction effects assumed
# to be the same with 0.6 effect size.
swd_2trt_interaction_power(RhoW = 0.2, ModelChoice = "RCS", RhoA = 0.2, IAC = 0,
                n.individuals = 15, n.clusters = 8, n.periods = 5, delta_1 = 0.6,
```

```
          delta_2 = 0.6, delta_3 = 0.6, typeIerror = 0.05/3,
        Sequence_Tx1 = c(2,3,2,3,4,5,NA,NA), Sequence_Tx2 = c(NA,NA,2,3,4,5,3,2))
```

---

swd_2trt_linearcontrast_power

Stepped Wedge Design Power Calculation for Linear Contrasts of Treatment Effects

---

Description

Calculate the power for detecting linear contrasts of two treatment effects in a two-treatment stepped wedge design (SWD) with additive treatment effects. We only consider complete designs. This function is based on Power Analysis for Stepped Wedge Trials with Two Treatments published in Stat Med in 2022 by Phillip Sundin and Catherine Crespi. This manuscript uses the normal distribution and the Wald Test to derive power.

Usage

```
swd_2trt_linearcontrast_power(
  RhoW,
  ModelChoice,
  n.individuals,
  n.clusters,
  n.periods,
  delta_12,
  RhoA,
  IAC,
  Sequence_Tx1,
  Sequence_Tx2,
  typeIerror
)
```

Arguments

RhoW　　　　　　　The intraclass correlation coefficient, which refers to the correlation between outcomes of two different individuals in the same cluster at the same time.

ModelChoice　　　A string indicating either a repeated cross sectional design ("RCS"), nested exchangeable ("NEC"), Cohort ("Cohort"), or any one of these three designs in their standardized form. Only one of "RCS Standardized", "RCS", "Cohort Standardized", "Cohort", "NEC Standardized", or "NEC" can be specified. The standardized design refers to dividing by the standard deviation of y (the outcome) in the covariance specification.

n.individuals　The number of individuals in each condition at one time period.

n.clusters　　　The number of clusters

n.periods　　　　The number of time periods.

delta_12　　　　The standardized difference between the two treatment effects to be powered on.

RhoA　　　　　　　The correlation between two observations in the same individual in the same cluster but different time periods. RCS models assume RhoW = RhoA, and Cohort models assume RhoA >= RhoW.

IAC	The individual auto-correlation, which is the proportion of the individual-level variance that is time-invariant. IAC = 0 in a RCS.
Sequence_Tx1	A vector representing the time points (periods) at which each cluster transitions from control to treatment 1 (ie the first occurence).
Sequence_Tx2	A vector representing the time points (periods) at which each cluster transitions from control to treatment 2 (ie the first occurence).
typeIerror	The significance level.

Value

Power for detecting the difference of treatment effects

Examples

```
# Late factorial SWD design with 12 clusters
swd_2trt_linearcontrast_power(RhoW = 0.2, ModelChoice="RCS", IAC = 0,
                     RhoA = 0.2, n.individuals = 15, delta_12 = 0.4,
                     n.clusters = 12, n.periods = 4,
                     Sequence_Tx1 = c(2,2,3,3,4,4,4,4,4,4,4,4),
                     Sequence_Tx2 = c(4,4,4,4,4,4,2,2,3,3,4,4),
                     typeIerror = 0.05)

# Example where there are different potential designs to be considered #
#creating data frame for power as a function of rho_w
PowerTable <- data.frame(RhoW = c(rep(seq(0,0.4,by=0.01),times=3)))
PowerTable$DesignChoice <- c(rep('"Late" Factorial Design, 12 clusters',times=41),
                            rep('"Early" Factorial Design, 10 clusters',times=41),
                            rep("Concurrent Design, 12 clusters",times=41))

PowerTable$n.clusters <- c(rep(12,times=41), rep(10,times=41), rep(12,times=41))

PowerTable$Sequence1 <- c(rep(list(c(2,2,3,3,4,4,4,4,4,4,4,4)),times=41),
                    rep(list(c(2,2,2,3,4,4,3,4,4,4)),times=41),
                    rep(list(c(2,2,3,3,4,4,NA,NA,NA,NA,NA,NA)),times=41))

PowerTable$Sequence2 <- c(rep(list(c(4,4,4,4,4,4,2,2,3,3,4,4)),times=41),
                    rep(list(c(4,4,4,3,4,4,3,2,2,2)),times=41),
                    rep(list(c(NA,NA,NA,NA,NA,NA,4,4,3,3,2,2)),times=41))

PowerTable$Power <- mapply(swd_2trt_linearcontrast_power,
                    RhoW = PowerTable$RhoW,
                    ModelChoice="RCS",
                    IAC = 0, RhoA = PowerTable$RhoW,
                    n.individuals = 15, delta_12 = 0.4,
                    n.clusters = PowerTable$n.clusters,
                    n.periods = 4, typeIerror = 0.05,
                    Sequence_Tx1 = PowerTable$Sequence1,
                    Sequence_Tx2 = PowerTable$Sequence2)

##removing unnecessary columns of clusters
PowerTable <- PowerTable[ ,-which(names(PowerTable) %in%
            c("Sequence1","Sequence2","n.clusters"))]
PowerTable
```

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