Package: crt2power (via r-universe)

September 4, 2024

Type Package

Title Designing Cluster-Randomized Trials with Two Co-Primary Outcomes

Version 1.1.0

Description Provides methods for powering cluster-randomized trials
with two co-primary outcomes using five key design techniques.
Includes functions for calculating required sample size and
statistical power. For more details on methodology, see Li et
al. (2020) <doi:10.1111/biom.13212>, Pocock et al. (1987)
<doi:10.2307/2531989>, Vickerstaff et al. (2019)
<doi:10.1186/s12874-019-0754-4>, and Yang et al. (2022)
<doi:10.1111/biom.13692>.

License GPL-3

Encoding UTF-8

LazyData true

URL https://github.com/melodyaowen/crt2power

Depends R (>= 4.3)

Imports devtools (>= 2.4.5), knitr (>= 1.43), rootSolve (>= 1.8.2.3),
tidyverse (>= 2.0.0), tableone (>= 0.13.2), foreach (>= 1.5.2),
mvtnorm (>= 1.2), tibble (>= 3.2.1), dplyr (>= 1.1.4), tidyr
(>= 1.3.0), stats (>= 3.6.2)

RoxygenNote 7.3.1

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Repository https://melodyaowen.r-universe.dev

RemoteUrl https://github.com/melodyaowen/crt2power

RemoteRef HEAD

RemoteSha 15f9d94c537a5e015fa730a6befe692d268e7db5

Contents

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calc_K_comb_outcome	*Calculate required number of clusters per treatment group for a cluster-randomized trial with co-primary endpoints using a combined outcomes approach.*

Description

Allows user to calculate the number of clusters per treatment arm of a cluster-randomized trial with two co-primary outcomes given a set of study design input values, including the number of clusters in each trial arm, and cluster size. Uses a combined outcomes approach where the two outcome effects are summed together.

Usage

```
calc_K_comb_outcome(
  power,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
```

```
    r = 1
)
```

Arguments

power	Desired statistical power in decimal form; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A data frame of numerical values.

Examples

```
calc_K_comb_outcome(power = 0.8, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

---

calc_K_conj_test	*Calculate required number of clusters per treatment group for a cluster-randomized trial with co-primary endpoints using the conjunctive intersection-union test approach.*

Description

Allows user to calculate the required number of clusters per treatment group of a cluster-randomized trial with two co-primary outcomes given a set of study design input values, including the statistical power, and cluster size. Uses the conjunctive intersection-union test approach.Code is adapted from "calSampleSize_ttestIU()" from https://github.com/siyunyang/coprimary_CRT written by Siyun Yang.

Usage

```
calc_K_conj_test(
  power,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1,
  cv = 0,
  deltas = c(0, 0),
  dist = "T"
)
```

Arguments

power	Desired statistical power in decimal form; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.
cv	Cluster variation parameter, set to 0 if assuming all cluster sizes are equal; numeric.
deltas	Vector of non-inferiority margins, set to delta_1 = delta_2 = 0; numeric vector.
dist	Specification of which distribution to base calculation on, either 'T' for T-Distribution or 'MVN' for Multivariate Normal Distribution. Default is T-Distribution.

Value

A data frame of numerical values.

Examples

```
calc_K_conj_test(power = 0.8, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

---

calc_K_disj_2dftest	*Calculate required number of clusters per treatment group for a cluster-randomized trial with co-primary endpoints using a disjunctive 2-DF test approach.*

Description

Allows user to calculate the number of clusters per treatment arm of a cluster-randomized trial with two co-primary outcomes given a set of study design input values, including the statistical power, and cluster size. Uses the disjunctive 2-DF test approach. Code is adapted from "calSampleSize_omnibus()" from https://github.com/siyunyang/coprimary_CRT.

Usage

```
calc_K_disj_2dftest(
  dist = "Chi2",
  power,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1
)
```

Arguments

dist	Specification of which distribution to base calculation on, either 'Chi2' for Chi-Squared or 'F' for F-Distribution.
power	Desired statistical power in decimal form; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.

beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A data frame of numerical values.

Examples

```
calc_K_disj_2dftest(power = 0.8, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

---

calc_K_pval_adj	*Calculate required number of clusters per treatment group for a cluster-randomized trial with co-primary endpoints using three common p-value adjustment methods*

Description

Allows user to calculate the number of clusters per treatment arm of a cluster-randomized trial with two co-primary endpoints given a set of study design input values, including the statistical power, and cluster size. Uses three common p-value adjustment methods.

Usage

```
calc_K_pval_adj(
  power,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
```

```
    varY2,
    rho01,
    rho02,
    rho2,
    r = 1
)
```

Arguments

power	Desired statistical power in decimal form; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A data frame of numerical values.

Examples

```
calc_K_pval_adj(power = 0.8, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho2  = 0.05)
```

---

calc_K_single_1dftest   *Calculate required number of clusters per treatment group for a cluster-randomized trial with co-primary endpoints using the single 1-DF combined test approach.*

Description

Allows user to calculate the number of clusters per treatment arm of a cluster-randomized trial with two co-primary endpoints given a set of study design input values, including the statistical power, and cluster size. Uses the single 1-DF combined test approach for clustered data and two outcomes.

Usage

```
calc_K_single_1dftest(
  power,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1
)
```

Arguments

power	Desired statistical power in decimal form; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A data frame of numerical values.

Examples

```
calc_K_single_1dftest(power = 0.8, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

---

calc_m_comb_outcome | *Calculate cluster size for a cluster-randomized trial with co-primary endpoints using a combined outcomes approach.*

Description

Allows user to calculate the cluster size of a cluster-randomized trial with two co-primary endpoints given a set of study design input values, including the number of clusters in each trial arm, and statistical power. Uses a combined outcomes approach where the two outcome effects are summed together.

Usage

```
calc_m_comb_outcome(
  power,
  K,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1
)
```

Arguments

power	Desired statistical power in decimal form; numeric.
K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.

rho2   Correlation between the first and second outcomes for the same individual; nu-
                meric.

r   Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experi-
                mental group; numeric.

Value

A numerical value.

Examples

```
calc_m_comb_outcome(power = 0.8, K = 15, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

---

calc_m_conj_test   *Calculate cluster size for a cluster-randomized trial with co-primary*
                          endpoints using the conjunctive intersection-union test approach.

Description

Allows user to calculate the cluster size of a cluster-randomized trial with two co-primary endpoints
given a set of study design input values, including the number of clusters in each trial arm, and
statistical power. Uses the conjunctive intersection-union test approach.

Usage

```
calc_m_conj_test(
  power,
  K,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1,
  cv = 0,
  deltas = c(0, 0),
  dist = "T"
)
```

Arguments

power	Desired statistical power in decimal form; numeric.
K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.
cv	Cluster variation parameter, set to 0 if assuming all cluster sizes are equal; numeric.
deltas	Vector of non-inferiority margins, set to delta_1 = delta_2 = 0; numeric vector.
dist	Specification of which distribution to base calculation on, either 'T' for T-Distribution or 'MVN' for Multivariate Normal Distribution. Default is T-Distribution.

Value

A numerical value.

Examples

```
calc_m_conj_test(power = 0.8, K = 15, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

| calc_m_disj_2dftest | *Calculate cluster size for a cluster-randomized trial with co-primary endpoints using a disjunctive 2-DF test approach.* |

Description

Allows user to calculate the cluster size of a cluster-randomized trial with two co-primary outcomes given a set of study design input values, including the number of clusters in each trial arm, and statistical power. Uses the disjunctive 2-DF test approach.

Usage

```
calc_m_disj_2dftest(
  dist = "Chi2",
  power,
  K,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1
)
```

Arguments

dist	Specification of which distribution to base calculation on, either 'Chi2' for Chi-Squared or 'F' for F-Distribution.
power	Desired statistical power in decimal form; numeric.
K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.

rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A numerical value.

Examples

```
calc_m_disj_2dftest(power = 0.8, K = 15, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

| calc_m_pval_adj | *Calculate cluster size for a cluster-randomized trial with co-primary endpoints using three common p-value adjustment methods* |

Description

#' @description Allows user to calculate the cluster size of a cluster-randomized trial with two co-primary endpoints given a set of study design input values, including the number of clusters in each trial arm, and statistical power. Uses three common p-value adjustment methods.

Usage

```
calc_m_pval_adj(
  power,
  K,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho2,
  r = 1
)
```

Arguments

power	Desired statistical power in decimal form; numeric.
K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A data frame of numerical values.

Examples

```
calc_m_pval_adj(power = 0.8, K = 15, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho2  = 0.05)
```

---

calc_m_single_1dftest	*Calculate cluster size for a cluster-randomized trial with co-primary endpoints using the single 1-DF combined test approach.*

Description

Allows user to calculate the cluster size of a cluster-randomized trial with two co-primary endpoints given a set of study design input values, including the number of clusters in each trial arm, and statistical power. Uses the single 1-DF combined test approach for clustered data and two outcomes.

Usage

```
calc_m_single_1dftest(
  power,
  K,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1
)
```

Arguments

power	Desired statistical power in decimal form; numeric.
K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A numerical value.

Examples

```
calc_m_single_1dftest(power = 0.8, K = 15, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

| calc_ncp_chi2 | *Find the non-centrality parameter corresponding to Type I error rate and statistical power* |

Description

Allows user to find the corresponding non-centrality parameter for power analysis based on the Type I error rate, statistical power, and degrees of freedom.

Usage

```
calc_ncp_chi2(alpha, power, df = 1)
```

Arguments

alpha	Type I error rate; numeric.
power	Desired statistical power in decimal form; numeric.
df	Degrees of freedom; numeric.

Value

A number.

Examples

```
calc_ncp_chi2(alpha = 0.05, power = 0.8, df = 1)
```

| calc_pwr_comb_outcome | *Calculate statistical power for a cluster-randomized trial with co-primary endpoints using a combined outcomes approach.* |

Description

Allows user to calculate the statistical power of a cluster-randomized trial with two co-primary outcomes given a set of study design input values, including the number of clusters in each trial arm, and cluster size. Uses a combined outcomes approach where the two outcome effects are summed together.

Usage

```
calc_pwr_comb_outcome(
  dist = "Chi2",
  K,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1
)
```

Arguments

dist	Specification of which distribution to base calculation on, either 'Chi2' for Chi-Squared or 'F' for F-Distribution.
K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A numerical value.

Examples

```
calc_pwr_comb_outcome(K = 15, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

---

calc_pwr_conj_test	*Calculate statistical power for a cluster-randomized trial with co-primary endpoints using the conjunctive intersection-union test approach.*

Description

Allows user to calculate the statistical power of a cluster-randomized trial with two co-primary outcomes given a set of study design input values, including the number of clusters in each trial arm, and cluster size. Uses the conjunctive intersection-union test approach. Code is adapted from "calPower_ttestIU()" from https://github.com/siyunyang/coprimary_CRT written by Siyun Yang.

Usage

```
calc_pwr_conj_test(
  K,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1,
  cv = 0,
  deltas = c(0, 0),
  dist = "T"
)
```

Arguments

K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.

varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.
cv	Cluster variation parameter, set to 0 if assuming all cluster sizes are equal; numeric.
deltas	Vector of non-inferiority margins, set to delta_1 = delta_2 = 0; numeric vector.
dist	Specification of which distribution to base calculation on, either 'T' for T-Distribution or 'MVN' for Multivariate Normal Distribution. Default is T-Distribution.

Value

A numerical value.

Examples

```
calc_pwr_conj_test(K = 15, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

---

calc_pwr_disj_2dftest	*Calculate statistical power for a cluster-randomized trial with co-primary endpoints using a disjunctive 2-DF test approach.*

Description

Allows user to calculate the statistical power of a cluster-randomized trial with two co-primary outcomes given a set of study design input values, including the number of clusters in each trial arm, and cluster size. Uses the disjunctive 2-DF test approach. Code is adapted from "calPower_omnibus()" from https://github.com/siyunyang/coprimary_CRT written by Siyun Yang.

Usage

```
calc_pwr_disj_2dftest(
  dist = "Chi2",
  K,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1
)
```

Arguments

dist	Specification of which distribution to base calculation on, either 'Chi2' for Chi-Squared or 'F' for F-Distribution.
K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A numerical value.

Examples

```
calc_pwr_disj_2dftest(K = 15, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

---

calc_pwr_pval_adj	*Calculate statistical power for a cluster-randomized trial with co-primary endpoints using three common p-value adjustment methods*

Description

Allows user to calculate the statistical power of a cluster-randomized trial with two co-primary endpoints given a set of study design input values, including the number of clusters in each trial arm, and cluster size. Uses three common p-value adjustment methods.

Usage

```
calc_pwr_pval_adj(
  dist = "Chi2",
  K,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho2,
  r = 1
)
```

Arguments

dist	Specification of which distribution to base calculation on, either 'Chi2' for Chi-Squared or 'F' for F-Distribution.
K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.

rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A data frame of numerical values.

Examples

```
calc_pwr_pval_adj(K = 15, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho2  = 0.05)
```

---

calc_pwr_single_1dftest

Calculate statistical power for a cluster-randomized trial with co-primary endpoints using the single 1-DF combined test approach.

Description

Allows user to calculate the statistical power of a cluster-randomized trial with two co-primary endpoints given a set of study design input values, including the number of clusters in each trial arm, and cluster size. Uses the single 1-DF combined test approach for clustered data and two outcomes.

Usage

```
calc_pwr_single_1dftest(
  dist = "Chi2",
  K,
  m,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1
)
```

Arguments

dist	Specification of which distribution to base calculation on, either 'Chi2' for Chi-Squared or 'F' for F-Distribution.
K	Number of clusters in treatment arm, and control arm under equal allocation; numeric.
m	Individuals per cluster; numeric.
alpha	Type I error rate; numeric.
beta1	Effect size for the first outcome; numeric.
beta2	Effect size for the second outcome; numeric.
varY1	Total variance for the first outcome; numeric.
varY2	Total variance for the second outcome; numeric.
rho01	Correlation of the first outcome for two different individuals in the same cluster; numeric.
rho02	Correlation of the second outcome for two different individuals in the same cluster; numeric.
rho1	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
rho2	Correlation between the first and second outcomes for the same individual; numeric.
r	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A numerical value.

Examples

```
calc_pwr_single_1dftest(K = 15, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

---

run_crt2_design	*Find study design output specifications based on all five CRT co-primary design methods.*

Description

Allows user to calculate either statistical power, number of clusters per treatment group (K), or cluster size (m), given a set of input values for all five study design approaches.

Usage

```
run_crt2_design(
  output,
  power = NA,
  K = NA,
  m = NA,
  alpha = 0.05,
  beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1
)
```

Arguments

`output`	Parameter to calculate, either "power", "K", or "m"; character.
`power`	Desired statistical power; numeric.
`K`	Number of clusters in each arm; numeric.
`m`	Individuals per cluster; numeric.
`alpha`	Type I error rate; numeric.
`beta1`	Effect size for the first outcome; numeric.
`beta2`	Effect size for the second outcome; numeric.
`varY1`	Total variance for the first outcome; numeric.
`varY2`	Total variance for the second outcome; numeric.
`rho01`	Correlation of the first outcome for two different individuals in the same cluster; numeric.
`rho02`	Correlation of the second outcome for two different individuals in the same cluster; numeric.
`rho1`	Correlation between the first and second outcomes for two individuals in the same cluster; numeric.
`rho2`	Correlation between the first and second outcomes for the same individual; numeric.
`r`	Treatment allocation ratio - K2 = rK1 where K1 is number of clusters in experimental group; numeric.

Value

A data frame of numerical values.

Examples

```
run_crt2_design(output = "power", K = 15, m = 300, alpha = 0.05,
beta1 = 0.1, beta2 = 0.1, varY1 = 0.23, varY2 = 0.25,
rho01 = 0.025, rho02 = 0.025, rho1 = 0.01, rho2  = 0.05)
```

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