## Package 'crt2power'

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#### Type Package

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

Version 1.2.1

Description Provides methods for powering cluster-randomized trials with two continuous coprimary outcomes using five key design techniques. Includes functions for calculating required sample size and statistical power. For more details on methodology, see Owen et al. (2025) <doi:10.1002/sim.70015>, Yang et al. (2022) <doi:10.1111/biom.13692>, Pocock et al. (1987) < erstaff et al. (2019) <doi:10.1186/s12874-019-0754-4>, and Li et al. (2020) <doi:10.1111/biom.13212>.

License GPL-3

#### Encoding UTF-8

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

#### **Depends** R (>= 4.3)

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**26** 

## Contents

| calc_K_comb_outcome     |
|-------------------------|
| calc_K_conj_test        |
| calc_K_disj_2dftest     |
| calc_K_pval_adj         |
| calc_K_single_1dftest   |
| calc_m_comb_outcome     |
| calc_m_conj_test        |
| calc_m_disj_2dftest     |
| calc_m_pval_adj 1       |
| calc_m_single_1dftest 1 |
| calc_ncp_chi2           |
| calc_pwr_comb_outcome   |
| calc_pwr_conj_test      |
| calc_pwr_disj_2dftest   |
| calc_pwr_pval_adj       |
| calc_pwr_single_1dftest |
| run_crt2_design         |
|                         |

## Index

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.

```
calc_K_comb_outcome(
   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-<br>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_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(
  dist = T'',
  power,
 m,
  alpha = 0.05,
 beta1,
  beta2,
  varY1,
  varY2,
  rho01,
  rho02,
  rho1,
  rho2,
  r = 1,
  cv = 0,
  deltas = c(0, 0),
  two_sided = FALSE
)
```

| dist  | Specification of which distribution to base calculation on, either 'T' for T-Distribution or 'MVN' for Multivariate Normal Distribution. Default is T-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.                   |
| 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.   |
| two_sided | Specification of whether to conduct two 2-sided tests, 'TRUE', or two 1-sided tests, 'FALSE', default is FALSE; boolean. |

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 disjunc- |
|                     | tive 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.

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

| dist  | Specification of which distribution to base calculation on, either 'Chi2' for Chi-<br>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 clus-<br>ter; 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. |

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.

```
calc_K_single_1dftest(
    dist = "Chi2",
    power,
    m,
    alpha = 0.05,
    beta1,
    beta2,
    varY1,
    varY2,
    rho01,
    rho02,
    rho1,
    rho2,
    r = 1
)
```

| 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_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(
    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.  |
| К     | 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.

10

calc\_m\_conj\_test

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

| dist  | Specification of which distribution to base calculation on, either 'T' for T-Distribution or 'MVN' for Multivariate Normal Distribution. Default is T-Distribution. |
|-------|---|
| power | Desired statistical power in decimal form; numeric.   |
| К     | 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.                                      |
| two_sided | Specification of whether to conduct two 2-sided tests, 'TRUE', or two 1-sided tests, 'FALSE', default is FALSE; boolean. |

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.

calc\_m\_disj\_2dftest

## 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.  |
| К     | 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 coprimary 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(
    dist = "Chi2",
    power,
    K,
    alpha = 0.05,
    beta1,
    beta2,
    varY1,
    varY2,
    rho01,
    rho02,
    rho2,
    r = 1
)
```

| 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.  |
| К     | 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. |

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.

```
calc_m_single_1dftest(
    dist = "Chi2",
    power,
    K,
    alpha = 0.05,
    beta1,
    beta2,
    varY1,
    varY2,
    rho01,
    rho02,
    rho1,
    rho2,
    r = 1
)
```

| 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.  |
| К     | 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)

| 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 coprimary 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.

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

| dist  | Specification of which distribution to base calculation on, either 'Chi2' for Chi-Squared or 'F' for F-Distribution. |
|-------|--|
| К     | 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.

calc\_pwr\_conj\_test

## Usage

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

```
)
```

| dist  | Specification of which distribution to base calculation on, either 'T' for T-Distribution or 'MVN' for Multivariate Normal Distribution. Default is T-Distribution. |
|-------|---|
| К     | 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.                                      |
|-----------|--|
| two_sided | Specification of whether to conduct two 2-sided tests, 'TRUE', or two 1-sided tests, 'FALSE', default is FALSE; boolean. |

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 coprimary 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.

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

| dist  | Specification of which distribution to base calculation on, either 'Chi2' for Chi-Squared or 'F' for F-Distribution. |
|-------|--|
| К     | 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. |
|-------|--|
| К     | 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)
```

22

calc\_pwr\_single\_1dftest

Calculate statistical power for a cluster-randomized trial with coprimary 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
)
```

| dist  | Specification of which distribution to base calculation on, either 'Chi2' for Chi-Squared or 'F' for F-Distribution. |
|-------|--|
| К     | 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 clus-<br>ter; 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. |

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.

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

| output | Parameter to calculate, either "power", "K", or "m"; character.  |
|--------|--|
| power  | Desired statistical power; numeric.  |
| К      | 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)
```

# Index

calc\_K\_comb\_outcome, 2 calc\_K\_conj\_test, 4 calc\_K\_disj\_2dftest, 5 calc\_K\_pval\_adj,7 calc\_K\_single\_1dftest, 8 calc\_m\_comb\_outcome, 9 calc\_m\_conj\_test, 11 calc\_m\_disj\_2dftest, 12 calc\_m\_pval\_adj, 14 calc\_m\_single\_1dftest, 15 calc\_ncp\_chi2, 16  $calc_pwr_comb_outcome, 17$ calc\_pwr\_conj\_test, 18 calc\_pwr\_disj\_2dftest, 20 calc\_pwr\_pval\_adj, 21 calc\_pwr\_single\_1dftest, 23

run\_crt2\_design, 24