

Package ‘PowerUpR’

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Type Package

Title Power Analysis Tools for Multilevel Randomized Experiments

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Description

Includes tools to calculate statistical power, minimum detectable effect size (MDES), MDES difference (MDESD), and minimum required sample size for various multilevel randomized experiments with continuous outcomes. Some of the functions can assist with planning two- and three-level cluster-randomized trials (CRTs) sensitive to multilevel moderation and mediation (2-1-1, 2-2-1, and 3-2-1). See 'PowerUp!' Excel series at <<https://www.causalevaluation.org/>>.

Suggests knitr, rmarkdown

VignetteBuilder knitr

License GPL (>= 3)

NeedsCompilation no

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PowerUpR-package	<i>Power Analysis Tools for Multilevel Randomized Experiments</i>
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Description

PowerUp! series consist of three excel-based applications to design various multilevel randomized experiments to detect main treatment effects, and to design two- and three-level cluster-randomized trials (CRTs) to detect multilevel moderation and mediation. For more information please refer to <http://www.causalevaluation.org/>.

bcra3f2	<i>Three-Level Blocked (Fixed) Cluster-level Random Assignment Design, Treatment at Level 2</i>
---------	---

Description

Use `mdes.bcra3f2()` to calculate the minimum detectable effect size, `power.bcra3f2()` to calculate the statistical power, and `mrss.bcra3f2()` to calculate the minimum required sample size.

Usage

```
mdes.bcra3f2(power=.80, alpha=.05, two.tailed=TRUE,
             rho2, p=.50, g2=0, r21=0, r22=0,
             n, J, K)

power.bcra3f2(es=.25, alpha=.05, two.tailed=TRUE,
              rho2, p=.50, g2=0, r21=0, r22=0,
              n, J, K)

mrss.bcra3f2(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
              n, J, K0=10, tol=.10,
              rho2, p=.50, g2=0, r21=0, r22=0)
```

Arguments

power	statistical power ($1 - \beta$).
es	effect size.
alpha	probability of type I error.
two.tailed	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
rho2	proportion of variance in the outcome between level 2 units (unconditional ICC2).
p	average proportion of level 2 units randomly assigned to treatment within level 3 units.
g2	number of covariates at level 2.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.
r22	proportion of level 2 variance in the outcome explained by level 2 covariates.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	harmonic mean of level 2 units across level 3 units (or simple average).
K	number of level 3 units.
K0	starting value for K.
tol	tolerance to end iterative process for finding K.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power ($1 - \beta$).
mde	minimum detectable effect size.
K	number of level 3 units.

Examples

```
# cross-checks
mde.bcra3f2(rho2=.10, n=20, J=44, K=5)
power.bcra3f2(es = .145, rho2=.10, n=20, J=44, K=5)
mrss.bcra3f2(es = .145, rho2=.10, n=20, J=44)
```

bcra3r2 *Three-Level Blocked Cluster-level Random Assignment Design, Treatment at Level 2*

Description

Use `mdes.bcra3r2()` to calculate the minimum detectable effect size, `power.bcra3r2()` to calculate the statistical power, and `mrss.bcra3r2()` to calculate the minimum required sample size.

Usage

```
mdes.bcra3r2(power=.80, alpha=.05, two.tailed=TRUE,
             rho2, rho3, omega3, p=.50, g3=0, r21=0, r22=0, r2t3=0,
             n, J, K)

power.bcra3r2(es=.25, alpha=.05, two.tailed=TRUE,
              rho2, rho3, omega3, p=.50, g3=0, r21=0, r22=0, r2t3=0,
              n, J, K)

mrss.bcra3r2(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
              n, J, K0=10, tol=.10,
              rho2, rho3, omega3, p=.50, g3=0, r21=0, r22=0, r2t3=0)
```

Arguments

<code>power</code>	statistical power ($1 - \beta$).
<code>es</code>	effect size.
<code>alpha</code>	probability of type I error.
<code>two.tailed</code>	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
<code>rho2</code>	proportion of variance in the outcome between level 2 units (unconditional ICC2).
<code>rho3</code>	proportion of variance in the outcome between level 3 units (unconditional ICC3).
<code>omega3</code>	treatment effect heterogeneity as ratio of treatment effect variance among level 3 units to the residual variance at level 3.
<code>p</code>	average proportion of level 2 units randomly assigned to treatment within level 3 units.
<code>g3</code>	number of covariates at level 3.
<code>r21</code>	proportion of level 1 variance in the outcome explained by level 1 covariates.
<code>r22</code>	proportion of level 2 variance in the outcome explained by level 2 covariates.
<code>r2t3</code>	proportion of treatment effect variance among level 3 units explained by level 3 covariates.
<code>n</code>	harmonic mean of level 1 units across level 2 units (or simple average).
<code>J</code>	harmonic mean of level 2 units across level 3 units (or simple average).

K	number of level 3 units.
K0	starting value for K.
tol	tolerance to end iterative process for finding K.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power $(1 - \beta)$.
mdes	minimum detectable effect size.
K	number of level 3 units.

See Also

[cosa.bcrd3r2](#)

Examples

```
# cross-checks
mdes.bcra3r2(rho3=.13, rho2=.10, omega3=.4,
             n=10, J=6, K=24)
power.bcra3r2(es = .246, rho3=.13, rho2=.10, omega3=.4,
              n=10, J=6, K=24)
mrss.bcra3r2(es = .246, rho3=.13, rho2=.10, omega3=.4,
             n=10, J=6)
```

bcra4f3	<i>Four-Level Blocked (Fixed) Cluster-level Random Assignment Design, Treatment at Level 3</i>
---------	--

Description

Use `mdes.bcra4f3()` to calculate the minimum detectable effect size, `power.bcra4f3()` to calculate the statistical power, and `mrss.bcra4f3()` to calculate the minimum required sample size.

Usage

```
mdes.bcra4f3(power=.80, alpha=.05, two.tailed=TRUE,
             rho2, rho3, p=.50, r21=0, r22=0, r23=0, g3=0,
             n, J, K, L)

power.bcra4f3(es=.25, alpha=.05, two.tailed=TRUE,
             rho2, rho3, p=.50, r21=0, r22=0, r23=0, g3=0,
             n, J, K, L)
```

```
mrss.bcra4f3(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
             n, J, K, L0=10, tol=.10,
             rho2, rho3, p=.50, g3=0, r21=0, r22=0, r23=0)
```

Arguments

power	statistical power ($1 - \beta$).
es	effect size.
alpha	probability of type I error.
two.tailed	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
rho2	proportion of variance in the outcome between level 2 units (unconditional ICC2).
rho3	proportion of variance in the outcome between level 3 units (unconditional ICC3).
p	average proportion of level 3 units randomly assigned to treatment within level 4 units.
g3	number of covariates at level 3.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.
r22	proportion of level 2 variance in the outcome explained by level 2 covariates.
r23	proportion of level 3 variance in the outcome explained by level 3 covariates.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	harmonic mean of level 2 units across level 3 units (or simple average).
K	harmonic mean of level 3 units across level 4 units (or simple average).
L	number of level 4 units.
L0	starting value for L.
tol	tolerance to end iterative process for finding L.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power ($1 - \beta$).
mdes	minimum detectable effect size.
L	number of level 4 units.

Examples

```
# cross-checks
mdes.bcra4f3(rho3=.15, rho2=.15,
             n=10, J=4, K=4, L=15)
power.bcra4f3(es=0.339, rho3=.15, rho2=.15,
             n=10, J=4, K=4, L=15)
mrss.bcra4f3(es=0.339, rho3=.15, rho2=.15,
             n=10, J=4, K=4)
```

bcra4r2 *Four-Level Blocked Cluster-level Random Assignment Design, Treatment at Level 2*

Description

Use `mdes.bcra4r2()` to calculate the minimum detectable effect size, `power.bcra4r2()` to calculate the statistical power, and `mrss.bcra4r2()` to calculate the minimum required sample size.

Usage

```
mdes.bcra4r2(power=.80, alpha=.05, two.tailed=TRUE,
             rho2, rho3, rho4, omega3, omega4,
             p=.50, r21=0, r22=0, r2t3=0, r2t4=0, g4=0,
             n, J, K, L)
```

```
power.bcra4r2(es=.25, alpha=.05, two.tailed=TRUE,
              rho2, rho3, rho4, omega3, omega4,
              p=.50, r21=0, r22=0, r2t3=0, r2t4=0, g4=0,
              n, J, K, L)
```

```
mrss.bcra4r2(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
              n, J, K, L0=10, tol=.10,
              rho2, rho3, rho4, omega3, omega4,
              p=.50, r21=0, r22=0, r2t3=0, r2t4=0, g4=0)
```

Arguments

<code>power</code>	statistical power ($1 - \beta$).
<code>es</code>	effect size.
<code>alpha</code>	probability of type I error.
<code>two.tailed</code>	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
<code>rho2</code>	proportion of variance in the outcome between level 2 units (unconditional ICC2).
<code>rho3</code>	proportion of variance in the outcome between level 3 units (unconditional ICC3).
<code>rho4</code>	proportion of variance in the outcome between level 4 units (unconditional ICC4).
<code>omega3</code>	treatment effect heterogeneity as ratio of treatment effect variance among level 3 units to the residual variance at level 3.
<code>omega4</code>	treatment effect heterogeneity as ratio of treatment effect variance among level 4 units to the residual variance at level 4.
<code>p</code>	average proportion of level 2 units randomly assigned to treatment within level 3 units.
<code>g4</code>	number of covariates at level 4.
<code>r21</code>	proportion of level 1 variance in the outcome explained by level 1 covariates.

r22	proportion of level 2 variance in the outcome explained by level 2 covariates.
r2t3	proportion of treatment effect variance among level 3 units explained by level 3 covariates.
r2t4	proportion of treatment effect variance among level 4 units explained by level 4 covariates.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	harmonic mean of level 2 units across level 3 units (or simple average).
K	harmonic mean of level 3 units across level 4 units (or simple average).
L	number of level 4 units.
L0	starting value for L.
tol	tolerance to end iterative process for finding L.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power $(1 - \beta)$.
mdes	minimum detectable effect size.
L	number of level 4 units.

See Also

[cosa.bcrd4r2](#)

Examples

```
# cross-checks
mdes.bcra4r2(rho4=.05, rho3=.15, rho2=.15,
             omega4=.50, omega3=.50, n=10, J=4, K=4, L=20)
power.bcra4r2(es = .206, rho4=.05, rho3=.15, rho2=.15,
              omega4=.50, omega3=.50, n=10, J=4, K=4, L=20)
mrss.bcra4r2(es = .206, rho4=.05, rho3=.15, rho2=.15,
             omega4=.50, omega3=.50, n=10, J=4, K=4)
```

bcra4r3	<i>Four-Level Blocked Cluster-level Random Assignment Design, Treatment at Level 3</i>
---------	--

Description

Use `mdes.bcra4r3()` to calculate the minimum detectable effect size, `power.bcra4r3()` to calculate the statistical power, and `mrss.bcra4r3()` to calculate the minimum required sample size.

Usage

```
mdes.bcra4r3(power=.80, alpha=.05, two.tailed=TRUE,
             rho2, rho3, rho4, omega4,
             p=.50, r21=0, r22=0, r23=0, r2t4=0, g4=0,
             n, J, K, L)
```

```
power.bcra4r3(es=.25, alpha=.05, two.tailed=TRUE,
              rho2, rho3, rho4, omega4,
              p=.50, r21=0, r22=0, r23=0, r2t4=0, g4=0,
              n, J, K, L)
```

```
mrss.bcra4r3(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
              n, J, K, L0=10, tol=.10,
              rho2, rho3, rho4, omega4,
              p=.50, r21=0, r22=0, r23=0, r2t4=0, g4=0)
```

Arguments

power	statistical power ($1 - \beta$).
es	effect size.
alpha	probability of type I error.
two.tailed	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
rho2	proportion of variance in the outcome between level 2 units (unconditional ICC2).
rho3	proportion of variance in the outcome between level 3 units (unconditional ICC3).
rho4	proportion of variance in the outcome between level 4 units (unconditional ICC4).
omega4	treatment effect heterogeneity as ratio of treatment effect variance among level 4 units to the residual variance at level 4.
p	average proportion of level 3 units randomly assigned to treatment within level 4 units.
g4	number of covariates at level 4.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.
r22	proportion of level 2 variance in the outcome explained by level 2 covariates.

r23	proportion of level 3 variance in the outcome explained by level 3 covariates.
r2t4	proportion of treatment effect variance among level 4 units explained by level 4 covariates.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	harmonic mean of level 2 units across level 3 units (or simple average).
K	harmonic mean of level 3 units across level 4 units (or simple average).
L	number of level 4 units.
L0	starting value for L.
tol	tolerance to end iterative process for finding L.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power $(1 - \beta)$.
mdes	minimum detectable effect size.
L	number of level 4 units.

See Also

[cosa.bcrd4r3](#)

Examples

```
# cross-checks
mdes.bcra4r3(rho4=.05, rho3=.15, rho2=.15,
             omega4=.50, n=10, J=4, K=4, L=20)
power.bcra4r3(es = .316, rho4=.05, rho3=.15, rho2=.15,
              omega4=.50, n=10, J=4, K=4, L=20)
mrss.bcra4r3(es = .316, rho4=.05, rho3=.15, rho2=.15,
             omega4=.50, n=10, J=4, K=4)
```

bira2c1

Two-Level Blocked (Constant Treatment Effect) Individual-level Random Assignment Design, Treatment at Level 1

Description

Use `mdes.bira2c1()` to calculate the minimum detectable effect size, `power.bira2c1()` to calculate the statistical power, and `mrss.bira2c1()` to calculate the minimum required sample size.

Usage

```
mdes.bira2c1(power=.80, alpha=.05, two.tailed=TRUE,
             p=.50, g1=0, r21=0,
             n, J)

power.bira2c1(es=.25, alpha=.05, two.tailed=TRUE,
              p=.50, g1=0, r21=0,
              n, J)

mrss.bira2c1(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
              n, J0=10, tol=.10,
              p=.50, g1=0, r21=0)
```

Arguments

power	statistical power ($1 - \beta$).
es	effect size.
alpha	probability of type I error.
two.tailed	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
p	average proportion of level 1 units randomly assigned to treatment within level 2 units.
g1	number of covariates at level 1.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	level 2 sample size.
J0	starting value for J.
tol	tolerance to end iterative process for finding J.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power ($1 - \beta$).
mdes	minimum detectable effect size.
J	number of level 2 units.

Examples

```
# cross-checks
mdes.bira2c1(n=15, J=20)
power.bira2c1(es=.325, n=15, J=20)
mrss.bira2c1(es=.325, n=15)
```

bira2f1	<i>Two-Level Blocked (Fixed) Individual-level Random Assignment Design, Treatment at Level 1</i>
---------	--

Description

Use `mdes.bira2f1()` to calculate the minimum detectable effect size, `power.bira2f1()` to calculate the statistical power, and `mrss.bira2f1()` to calculate the minimum required sample size.

Usage

```
mdes.bira2f1(power=.80, alpha=.05, two.tailed=TRUE,
            p=.50, g1=0, r21=0, n, J)
```

```
power.bira2f1(es=.25, alpha=.05, two.tailed=TRUE,
             p=.50, g1=0, r21=0, n, J)
```

```
mrss.bira2f1(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
            n, J0=10, tol=.10,
            p=.50, g1=0, r21=0)
```

Arguments

<code>power</code>	statistical power ($1 - \beta$).
<code>es</code>	effect size.
<code>alpha</code>	probability of type I error.
<code>two.tailed</code>	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
<code>p</code>	average proportion of level 1 units randomly assigned to treatment within level 2 units.
<code>g1</code>	number of covariates at level 1.
<code>r21</code>	proportion of level 1 variance in the outcome explained by level 1 covariates.
<code>n</code>	harmonic mean of level 1 units across level 2 units (or simple average).
<code>J</code>	level 2 sample size.
<code>J0</code>	starting value for J.
<code>tol</code>	tolerance to end iterative process for finding J.

Value

<code>fun</code>	function name.
<code>parms</code>	list of parameters used in power calculation.
<code>df</code>	degrees of freedom.
<code>ncp</code>	noncentrality parameter.

power	statistical power ($1 - \beta$).
mdes	minimum detectable effect size.
J	number of level 2 units.

Examples

```
# cross-checks
mdes.bira2f1(n=15, J=20)
power.bira2f1(es=.325, n=15, J=20)
mrss.bira2f1(es=.325, n=15)
```

bira2r1	<i>Two-Level Blocked Individual-level Random Assignment Design, Treatment at Level 1</i>
---------	--

Description

Use `mdes.bira2r1()` to calculate the minimum detectable effect size, `power.bira2r1()` to calculate the statistical power, and `mrss.bira2r1()` to calculate the minimum required sample size.

Usage

```
mdes.bira2r1(power=.80, alpha=.05, two.tailed=TRUE,
             rho2, omega2, p=.50, g2=0, r21=0, r2t2=0,
             n, J)

power.bira2r1(es=.25, alpha=.05, two.tailed=TRUE,
              rho2, omega2, g2=0, p=.50, r21=0, r2t2=0,
              n, J)

mrss.bira2r1(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
             n, J0=10, tol=.10,
             rho2, omega2, g2=0, p=.50, r21=0, r2t2=0)
```

Arguments

power	statistical power ($1 - \beta$).
es	effect size.
alpha	probability of type I error.
two.tailed	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
rho2	proportion of variance in the outcome between level 2 units (unconditional ICC2).
omega2	treatment effect heterogeneity as ratio of treatment effect variance among level 2 units to the residual variance at level 2.
p	average proportion of level 1 units randomly assigned to treatment within level 2 units.

g2	number of covariates at level 2.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.
r2t2	proportion of treatment effect variance among level 2 units explained by level 2 covariates.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	level 2 sample size.
J0	starting value for J.
tol	tolerance to end iterative process for finding J.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power $(1 - \beta)$.
mdes	minimum detectable effect size.
J	number of level 2 units.

See Also

[cosa.bird2r1](#)

Examples

```
# cross-checks
mdes.bira2r1(rho2=.17, omega2=.50, n=15, J=20)
power.bira2r1(es=.366, rho2=.17, omega2=.50, n=15, J=20)
mrss.bira2r1(es=.366, rho2=.17, omega2=.50, n=15)
```

bira3r1

*Three-Level Blocked Individual-level Random Assignment Design,
Treatment at Level 1*

Description

Use `mdes.bira3r1()` to calculate the minimum detectable effect size, `power.bira3r1()` to calculate the statistical power, and `mrss.bira3r1()` to calculate the minimum required sample size.

Usage

```
mde.bira3r1(power=.80, alpha=.05, two.tailed=TRUE,
            rho2, rho3, omega2, omega3,
            p=.50, r21=0, r2t2=0, r2t3=0, g3=0,
            n, J, K)
```

```
power.bira3r1(es=.25, alpha=.05, two.tailed=TRUE,
              rho2, rho3, omega2, omega3,
              p=.50, r21=0, r2t2=0, r2t3=0, g3=0,
              n, J, K)
```

```
mrss.bira3r1(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
             n, J, K0=10, tol=.10,
             rho2, rho3, omega2, omega3,
             p=.50, r21=0, r2t2=0, r2t3=0, g3=0)
```

Arguments

power	statistical power ($1 - \beta$).
es	effect size.
alpha	probability of type I error.
two.tailed	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
rho2	proportion of variance in the outcome between level 2 units (unconditional ICC2).
rho3	proportion of variance in the outcome between level 3 units (unconditional ICC3).
omega2	treatment effect heterogeneity as ratio of treatment effect variance among level 2 units to the residual variance at level 2.
omega3	treatment effect heterogeneity as ratio of treatment effect variance among level 3 units to the residual variance at level 3.
p	average proportion of level 1 units randomly assigned to treatment within level 2 units.
g3	number of covariates at level 3.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.
r2t2	proportion of treatment effect variance among level 2 units explained by level 2 covariates.
r2t3	proportion of treatment effect variance among level 3 units explained by level 3 covariates.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	harmonic mean of level 2 units across level 3 units (or simple average).
K	number of level 3 units.
K0	starting value for K.
tol	tolerance to end iterative process for finding K.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power ($1 - \beta$).
mdes	minimum detectable effect size.
K	number of level 3 units.

See Also

[cosa.bird3r1](#)

Examples

```
# cross-checks
mdes.bira3r1(rho3=.20, rho2=.15,
             omega3=.10, omega2=.10,
             n=69, J=10, K=100)
power.bira3r1(es = .045, rho3=.20, rho2=.15,
              omega3=.10, omega2=.10,
              n=69, J=10, K=100)
mrss.bira3r1(es = .045, rho3=.20, rho2=.15,
             omega3=.10, omega2=.10,
             n=69, J=10)
```

bira4r1	<i>Four-Level Blocked Individual-level Random Assignment Design, Treatment at Level 1</i>
---------	---

Description

Use `mdes.bira4r1()` to calculate the minimum detectable effect size, `power.bira4r1()` to calculate the statistical power, and `mrss.bira4r1()` to calculate the minimum required sample size.

Usage

```
mdes.bira4r1(power=.80, alpha=.05, two.tailed=TRUE,
             rho2, rho3, rho4, omega2, omega3, omega4,
             p=.50, r21=0, r2t2=0, r2t3=0, r2t4=0, g4=0,
             n, J, K, L)

power.bira4r1(es=.25, alpha=.05, two.tailed=TRUE,
             rho2, rho3, rho4, omega2, omega3, omega4,
             p=.50, r21=0, r2t2=0, r2t3=0, r2t4=0, g4=0,
             n, J, K, L)
```



```

mrss.bira4r1(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
             n, J, K, L0=10, tol=.10,
             rho2, rho3, rho4, omega2, omega3, omega4,
             p=.50, r21=0, r2t2=0, r2t3=0, r2t4=0, g4=0)

```

Arguments

power	statistical power ($1 - \beta$).
es	effect size.
alpha	probability of type I error.
two.tailed	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
rho2	proportion of variance in the outcome between level 2 units (unconditional ICC2).
rho3	proportion of variance in the outcome between level 3 units (unconditional ICC3).
rho4	proportion of variance in the outcome between level 4 units (unconditional ICC4).
omega2	treatment effect heterogeneity as ratio of treatment effect variance among level 2 units to the residual variance at level 2.
omega3	treatment effect heterogeneity as ratio of treatment effect variance among level 3 units to the residual variance at level 3.
omega4	treatment effect heterogeneity as ratio of treatment effect variance among level 4 units to the residual variance at level 4.
p	average proportion of level 1 units randomly assigned to treatment within level 2 units.
g4	number of covariates at level 4.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.
r2t2	proportion of treatment effect variance among level 2 units explained by level 2 covariates.
r2t3	proportion of treatment effect variance among level 3 units explained by level 3 covariates.
r2t4	proportion of treatment effect variance among level 4 units explained by level 4 covariates.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	harmonic mean of level 2 units across level 3 units (or simple average).
K	harmonic mean of level 3 units across level 4 units (or simple average).
L	number of level 4 units.
L0	starting value for L.
tol	tolerance to end iterative process for finding L.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power ($1 - \beta$).
mdes	minimum detectable effect size.
L	number of level 4 units.

See Also

[cosa.bird4r1](#)

Examples

```
# cross-checks
mdes.bira4r1(rho4=.05, rho3=.15, rho2=.15,
             omega4=.50, omega3=.50, omega2=.50,
             n=10, J=4, K=4, L=27)
power.bira4r1(es = 0.142, rho4=.05, rho3=.15, rho2=.15,
              omega4=.50, omega3=.50, omega2=.50,
              n=10, J=4, K=4, L=27)
mrss.bira4r1(es = 0.142, rho4=.05, rho3=.15, rho2=.15,
             omega4=.50, omega3=.50, omega2=.50,
             n=10, J=4, K=4)
```

conversion

Object Conversion

Description

Use `mrss.to.mdes()` to convert an object returned from MRSS functions into an object returned from MDES functions, `mrss.to.power()` to convert an object returned from MRSS functions into an object returned from power functions, `power.to.mdes()` to convert an object returned from power functions into an object returned from MDES functions, `mdes.to.power()` to convert an object returned from MDES functions into an object returned from power functions, and `mdes.to.pctl()` to convert effect sizes or an object returned from MDES functions into percentiles.

Usage

```
mrss.to.mdes(object)
mrss.to.power(object)
power.to.mdes(object)
mdes.to.power(object)
mdes.to.pctl(object)
```

Arguments

object an object returned from one of the functions in **PowerUpR** package.

Examples

```
design1 <- power.bira2r1(es=.15, rho2=.35, omega2=.10, n=83, J=10)
design2 <- power.to.mdes(design1)
mdes.to.pctl(design2)
```

cra2r2 *Two-level Cluster-randomized Trials to Detect Main, Moderation and Mediation Effects*

Description

Use `mdes.<design>()` to calculate minimum detectable effect size for the main effect, `mdesd.<design>()` to calculate minimum detectable effect size difference for the moderation effect, `power.<design>()` to calculate the statistical power, and `mrss.<design>()` to calculate the minimum required sample size. Use `<output>.cra2r2()` for the main effect, `<output>.mod221()` for the moderator at level 1, `<output>.mod222()` for the moderator at level 2. Use `power.med211()` for 2-1-1 mediation, and `power.med221()` for 2-2-1 mediation.

Usage

```
mdes.cra2r2(power=.80, alpha=.05, two.tailed=TRUE,
            rho2, p=.50, g2=0, r21=0, r22=0,
            n, J)

mdesd.mod221(power=.80, alpha=.05, two.tailed=TRUE,
             rho2, omegam2, g1=0, r21=0, r2m2=0,
             p=.50, q=NULL, n, J)

mdesd.mod222(power=.80, alpha=.05, two.tailed=TRUE,
             rho2, g2=0, r21=0, r22=0,
             p=.50, q=NULL, n, J)

power.cra2r2(es=.25, alpha=.05, two.tailed=TRUE,
            rho2, g2=0, p=.50, r21=0, r22=0,
            n, J)

power.mod221(es=.25, alpha=.05, two.tailed=TRUE,
            rho2, omegam2, g1=0, r21=0, r2m2=0,
            p=.50, q=NULL, n, J)

power.mod222(es=.25, alpha=.05, two.tailed=TRUE,
            rho2, g2=0, r21=0, r22=0,
            p=.50, q=NULL, n, J)
```

```

power.med211(esa, esb1, esB, escp, two.tailed = TRUE, alpha = .05,
             mc = FALSE, nsims = 1000, ndraws = 1000,
             rhom2, rho2, r21, r22, r2m1, r2m2,
             p, n, J)

power.med221(esa, esb, escp, two.tailed = TRUE, alpha = .05,
             mc = FALSE, nsims = 1000, ndraws = 1000,
             rho2, r22, r21, r2m2,
             p = .50, n, J)

mrss.cra2r2(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
            n, J0=10, tol=.10,
            rho2, g2=0, p=.50, r21=0, r22=0)

mrss.mod221(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
            n, J0=10, tol=.10, rho2, omegam2, g1=0, r21=0, r2m2=0,
            p=.50, q=NULL)

mrss.mod222(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
            n, J0=10, tol=.10, rho2, g2=0, r21=0, r22=0,
            p=.50, q=NULL)

mrss.mod222(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
            n, J0=10, tol=.10, rho2, g2=0, r21=0, r22=0,
            p=.50, q=NULL)

```

Arguments

power	statistical power ($1 - \beta$)
es, esa, esb, esb1, esB, escp	effect size for main/moderator effects, or for path coefficients a (treatment - mediator), b (level 2 mediator - outcome), b1 (level 1 mediator - outcome), B (overall mediator - outcome) or cp (direct treatment - outcome) in the mediation model.
alpha	probability of type I error.
two.tailed	logical; FALSE for one-tailed hypothesis testing.
rho2	proportion of variance in the outcome between level 2 units (unconditional ICC2).
rhom2	proportion of variance in the mediator between level 2 units.
omegam2	ratio of the unconditional variance in the moderator effect that is between level 2 units to the residual variance between level 2 units in the null model.
p	proportion of level 2 units randomly assigned to treatment.
q	proportion of level 1 or level 2 units in the moderator subgroup.
g1	number of covariates at level 1.
g2	number of covariates at level 2.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.

r22	proportion of level 2 variance in the outcome explained by level 2 covariates.
r2m1	proportion of mediator variance at level 1 explained by level 1 covariates.
r2m2	proportion of variance in the moderator (or mediator) effect that is explained by level 2 predictors. For the mediation model, proportion of mediator variance at level 2 explained by level 2 predictors.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	level 2 sample size.
J0	starting value for J.
tol	tolerance to end iterative process for finding J.
mc	logical; TRUE for monte carlo simulation based power.
nsims	number of replications, if mc = TRUE.
ndraws	number of draws from the distribution of the path coefficients for each replication, if mc = TRUE.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power $(1 - \beta)$.
mdes	minimum detectable effect size.
J	number of level 2 units.

See Also

For a more flexible sample size determination see [cosa.crd2r2](#).

Examples

```
# cross-checks for the main effect
mdes.cra2r2(rho2=.17, n=15, J=20)
power.cra2r2(es=.629, rho2=.17, n=15, J=20)
mrss.cra2r2(es=.629, rho2=.17, n=15)

# cross-checks for the randomly varying cont. L1 moderator effect
mdesd.mod221(rho2=.17, omegam2=.10, n=15, J=20)
power.mod221(es=.3563, rho2=.17, omegam2=.10, n=15, J=20)
mrss.mod221(es=.3563, rho2=.17, omegam2=.10, n=15)

# cross-checks for the non-randomly varying cont. L1 moderator effect
mdesd.mod221(rho2=.17, omegam2=0, n=15, J=20)
power.mod221(es=0.2957, rho2=.17, omegam2=0, n=15, J=20)
mrss.mod221(es=0.2957, rho2=.17, omegam2=0, n=15)

# cross-checks for the randomly varying bin. L1 moderator effect
```

```

mdesd.mod221(rho2=.17, omegam2=.10, q=.50, n=15, J=20)
power.mod221(es=.647, rho2=.17, omegam2=.10, q=.50, n=15, J=20)
mrss.mod221(es=.647, rho2=.17, omegam2=.10, q=.50, n=15)

# cross-checks for the non-randomly varying bin. L1 moderator effect
mdesd.mod221(rho2=.17, omegam2=0, q=.50, n=15, J=20)
power.mod221(es=0.5915, rho2=.17, omegam2=0, q=.50, n=15, J=20)
mrss.mod221(es=0.5915, rho2=.17, omegam2=0, q=.50, n=15)

# cross-checks for the cont. L2 moderator effect
mdesd.mod222(rho2=.17, n=15, J=100)
power.mod222(es=0.2742, rho2=.17, n=15, J=100)
mrss.mod222(es=0.2742, rho2=.17, n=15)

# cross-checks for the bin. L2 moderator effect
mdesd.mod222(rho2=.17, q=.50, n=15, J=100)
power.mod222(es=0.5485, rho2=.17, q=.50, n=15, J=100)
mrss.mod222(es=0.5485, rho2=.17, q=.50, n=15)

# 2-2-1 mediation
power.med221(esa=0.6596, esb=0.1891, escp=.1,
             rho2=.15, r22=.52, r21=.40, r2m2=.50,
             n=100, J=40, p=.5)

# 2-1-1 mediation
power.med211(esa=0.4135, esb1=0.0670, esB=0.3595, escp=.1,
             rhom2=.3, rho2=.3, r22=.6, r21=.6, r2m2=.6, r2m1=.6,
             n=30, J=80, p=.1)

```

cra3r3

*Three-level Cluster-randomized Trials to Detect Main, Moderation,
and Mediation Effects*

Description

Use `mdes.<design>()` to calculate the minimum detectable effect size for the main effect, `mdesd.<design>()` to calculate the minimum detectable effect size difference for the moderation effect, `power.<design>()` to calculate the statistical power, and `mrss.<design>()` to calculate the minimum required sample size. Use `<output>.cra3r3()` for the main effect, `<output>.mod331()` for the moderator at level 1, `<output>.mod332()` for the moderator at level 2, `<output>.mod333()` for the moderator at level 3. Use `power.med321()` for 3-2-1 mediation.

Usage

```

mdes.cra3r3(power=.80, alpha=.05, two.tailed=TRUE,
            rho2, rho3, p=.50, g3=0, r21=0, r22=0, r23=0,
            n, J, K)

mdesd.mod331(power=.80, alpha=.05, two.tailed=TRUE,

```

```

rho2, rho3, omegam2=0, omegam3=0,
g1=0, r21=0, r2m2=0, r2m3=0,
p=.50, q=NULL, n, J, K)

mdesd.mod332(power=.80, alpha=.05, two.tailed=TRUE,
rho2, rho3, omegam3, g2=0, r21=0, r22=0, r2m3=0,
p=.50, q=NULL, n, J, K)

mdesd.mod333(power=.80, alpha=.05, two.tailed=TRUE,
rho2, rho3, g3=0, r21=0, r22=0, r23=0,
p=.50, q=NULL, n, J, K)

power.cra3r3(es=.25, alpha=.05, two.tailed=TRUE,
rho2, rho3, g3=0, r21=0, r22=0, r23=0,
p=.50, n, J, K)

power.mod331(es=.25, alpha=.05, two.tailed=TRUE,
rho2, rho3, omegam2, omegam3,
g1=0, r21=0, r2m2=0, r2m3=0,
p=.50, q=NULL, n, J, K)

power.mod332(es=.25, alpha=.05, two.tailed=TRUE,
rho2, rho3, omegam3, g2=0, r21=0, r22=0, r2m3=0,
p=.50, q=NULL, n, J, K)

power.mod333(es=.25, alpha=.05, two.tailed=TRUE,
rho2, rho3, g3=0, r21=0, r22=0, r23=0,
p=.50, q=NULL, n, J, K)

power.med321(esa, esB, two.tailed=TRUE, alpha=.05,
mc=FALSE, nsims=1000, ndraws=1000,
rhom3, rho2, rho3, r2m2, r2m3, r21, r22, r23,
p=.50, n, J, K)

mrss.cra3r3(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
n, J, K0=10, tol=.10,
rho2, rho3, p=.50, g3=0, r21=0, r22=0, r23=0)

mrss.mod331(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
rho2, rho3, omegam2, omegam3,
g1=0, r21=0, r2m2=0, r2m3=0,
p=.50, q=NULL, n, J, K0=10, tol=.10)

mrss.mod332(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
rho2, rho3, omegam3, g2=0, r21=0, r22=0, r2m3=0,
p=.50, q=NULL, n, J, K0=10, tol=.10)

mrss.mod333(es=.25, power=.80, alpha=.05, two.tailed=TRUE,

```

rho2, rho3, g3=0, r21=0, r22=0, r23=0,
p=.50, q=NULL, n, J, K0=10, tol=.10)

Arguments

power	statistical power $(1 - \beta)$.
es, esa, esB	effect size for main/moderator effects, or for path coefficients a (treatment - mediator), or B (overall mediator - outcome) in the mediation model.
alpha	probability of type I error.
two.tailed	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
rho2	proportion of variance in the outcome between level 2 units (unconditional ICC2).
rho3	proportion of variance in the outcome between level 3 units (unconditional ICC3).
rhom3	proportion of variance in the mediator between level 3 units.
omegam2	ratio of the unconditional variance in the moderator effect that is between level 2 units to the residual variance between level 2 units in the null model.
omegam3	ratio of the unconditional variance in the moderator effect that is between level 3 units to the residual variance between level 3 units in the null model.
p	proportion of level 3 units randomly assigned to treatment.
q	proportion of level 1, level 2, or level 3 units in the moderator subgroup.
g1	number of covariates at level 1.
g2	number of covariates at level 2.
g3	number of covariates at level 3.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.
r22	proportion of level 2 variance in the outcome explained by level 2 covariates.
r23	proportion of level 3 variance in the outcome explained by level 3 covariates.
r2m2	proportion of variance in the moderator (or mediator) effect that is explained by level 2 predictors. For the mediation model, proportion of mediator variance at level 2 explained by level 2 predictors.
r2m3	proportion of variance in the moderator (or mediator) effect that is explained by level 3 predictors. For the mediation model, proportion of aggregated mediator variance at level 3 explained by level 3 predictors.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	harmonic mean of level 2 units across level 3 units (or simple average).
K	level 3 sample size.
K0	starting value for K.
tol	tolerance to end iterative process for finding K.
mc	logical; TRUE for monte carlo simulation based power.
nsims	number of replications, if mc = TRUE.
ndraws	number of draws from the distribution of the path coefficients for each replication, if mc = TRUE.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power ($1 - \beta$).
mdes	minimum detectable effect size.
K	number of level 3 units.

See Also

For a more flexible sample size determination see [cosa.crd3r3](#).

Examples

```
# cross-checks for the main effect
mdes.cra3r3(rho3=.06, rho2=.17, n=15, J=3, K=60)
power.cra3r3(es=.269, rho3=.06, rho2=.17, n=15, J=3, K=60)
mrss.cra3r3(es=.269, rho3=.06, rho2=.17, n=15, J=3)

# cross-checks for the randomly varying cont. L1 moderator effect
mdes.mod331(power=.80, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=.10, omegam3=.10,
            q=NULL, n=15, J=3, K=60)
power.mod331(es=0.1248, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=.10, omegam3=.10,
            q=NULL, n=15, J=3, K=60)
mrss.mod331(es=0.1248, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=.10, omegam3=.10,
            q=NULL, n=15, J=3)

# cross-checks for the non-randomly varying cont. L1 moderator effect
mdesd.mod331(power=.80, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=0, omegam3=0,
            q=NULL, n=15, J=3, K=60)
power.mod331(es=.0946, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=0, omegam3=0,
            q=NULL, n=15, J=3, K=60)
mrss.mod331(es=.0946, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=0, omegam3=0,
            q=NULL, n=15, J=3)

# cross-checks for the randomly varying bin. L1 moderator effect
mdesd.mod331(power=.80, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=.10, omegam3=.10,
            q=.50, n=15, J=3, K=60)
power.mod331(es=.2082, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=.10, omegam3=.10,
            q=.50, n=15, J=3, K=60)
```

```

mrss.mod331(es=.2082, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=.10, omegam3=.10,
            q=.50, n=15, J=3)

# cross-checks for the non-randomly varying bin. L1 moderator effect
mdesd.mod331(power=.80, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=0, omegam3=0,
            q=.50, n=15, J=3, K=60)
power.mod331(es=.1893, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=0, omegam3=0,
            q=.50, n=15, J=3, K=60)
mrss.mod331(es=.1893, alpha=.05, two.tailed=TRUE,
            rho2=.17, rho3=.06, omegam2=0, omegam3=0,
            q=.50, n=15, J=3)

# 3-2-1 mediation
power.med321(esa= .51, esB = .30, rhom3 = 0.27, rho2 = .15, rho3 = .19,
            r2m2 = .07, r2m3 = .16, r21 = .02, r22 = .41, r23 = .38,
            p = .50, n = 20, J = 4, K = 60)

```

cra4r4

Four-Level Cluster-randomized Trial

Description

use `mdes.cra4r4()` calculate the minimum detectable effect size, `power.cra4r4()` to calculate the statistical power, and `mrss.cra4r4()` to calculate the minimum required sample size.

Usage

```

mdes.cra4r4(power=.80, alpha=.05, two.tailed=TRUE,
            rho2, rho3, rho4, p=.50, r21=0, r22=0, r23=0, r24=0, g4=0,
            n, J, K, L)

power.cra4r4(es=.25, alpha=.05, two.tailed=TRUE,
            rho2, rho3, rho4, p=.50, r21=0, r22=0, r23=0, r24=0, g4=0,
            n, J, K, L)

mrss.cra4r4(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
            n, J, K, L0=10, tol=.10,
            rho2, rho3, rho4, p=.50,
            r21=0, r22=0, r23=0, r24=0, g4=0)

```

Arguments

<code>power</code>	statistical power ($1 - \beta$).
<code>es</code>	effect size.
<code>alpha</code>	probability of type I error.

two.tailed	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
rho2	proportion of variance in the outcome between level 2 units (unconditional ICC2).
rho3	proportion of variance in the outcome between level 3 units (unconditional ICC3).
rho4	proportion of variance in the outcome between level 4 units (unconditional ICC4).
p	proportion of level 4 units randomly assigned to treatment.
g4	number of covariates at level 4.
r21	proportion of level 1 variance in the outcome explained by level 1 covariates.
r22	proportion of level 2 variance in the outcome explained by level 2 covariates.
r23	proportion of level 3 variance in the outcome explained by level 3 covariates.
r24	proportion of level 4 variance in the outcome explained by level 4 covariates.
n	harmonic mean of level 1 units across level 2 units (or simple average).
J	harmonic mean of level 2 units across level 3 units (or simple average).
K	harmonic mean of level 3 units across level 4 units (or simple average).
L	number of level 4 units.
L0	starting value for L.
tol	tolerance to end iterative process for finding L.

Value

fun	function name.
parms	list of parameters used in power calculation.
df	degrees of freedom.
ncp	noncentrality parameter.
power	statistical power ($1 - \beta$).
mdes	minimum detectable effect size.
L	number of level 4 units.

See Also

[cosa.crd4r4](#)

Examples

```
# cross-checks
mdes.cra4r4(rho4=.05, rho3=.05, rho2=.10,
            n=10, J=2, K=3, L=20)
power.cra4r4(es = .412, rho4=.05, rho3=.05, rho2=.10,
            n=10, J=2, K=3, L=20)
mrss.cra4r4(es = .412, rho4=.05, rho3=.05, rho2=.10,
            n=10, J=2, K=3)
```

ira1r1

*Individual-level Random Assignment Design***Description**

Use `mdes.ira1r1()` to calculate minimum detectable effect size, `power.ira1r1()` to calculate statistical power, and `mrss.ira1r1()` to calculate minimum required sample size.

Usage

```
mdes.ira1r1(power=.80, alpha=.05, two.tailed=TRUE,
            p=.50, g1=0, r21=0, n)
```

```
power.ira1r1(es=.25, alpha=.05, two.tailed=TRUE,
             p=.50, g1=0, r21=0, n)
```

```
mrss.ira1r1(es=.25, power=.80, alpha=.05, two.tailed=TRUE,
            n0=10, tol=.10,
            p=.50, g1=0, r21=0)
```

Arguments

<code>power</code>	statistical power ($1 - \beta$).
<code>es</code>	effect size.
<code>alpha</code>	probability of type I error.
<code>two.tailed</code>	logical; TRUE for two-tailed hypothesis testing, FALSE for one-tailed hypothesis testing.
<code>p</code>	proportion of units randomly assigned to treatment.
<code>g1</code>	number of covariates.
<code>r21</code>	proportion of variance in the outcome explained by covariates.
<code>n</code>	sample size.
<code>n0</code>	starting value for n.
<code>tol</code>	tolerance to end iterative process for finding n.

Value

<code>fun</code>	function name.
<code>parms</code>	list of parameters used in power calculation.
<code>df</code>	degrees of freedom.
<code>ncp</code>	noncentrality parameter.
<code>power</code>	statistical power ($1 - \beta$).
<code>mdes</code>	minimum detectable effect size.
<code>n</code>	sample size.

See Also[power.ird1r1](#)**Examples**

```
# cross-checks
mdes.ird1r1(n=250)
power.ird1r1(es=.356, n=250)
mrss.ird1r1(es=.356)
```

plots

*Plots***Description**

Plots statistical power, minimum detectable effect size (MDES), or MDES difference (MDESD) curves with $(1-\alpha) \times 100$ % confidence interval.

Usage

```
## S3 method for class 'power'
plot(x, ypar = "mdes", xpar = NULL,
      xlim = NULL, ylim = NULL,
      xlab = NULL, ylab = NULL,
      main = NULL, sub = NULL,
      locate = FALSE, ...)

## S3 method for class 'mdes'
plot(x, ypar = "mdes", xpar = NULL,
      xlim = NULL, ylim = NULL,
      xlab = NULL, ylab = NULL,
      main = NULL, sub = NULL,
      locate = FALSE, ...)

## S3 method for class 'mrss'
plot(x, ypar = "mdes", xpar = NULL,
      xlim = NULL, ylim = NULL,
      xlab = NULL, ylab = NULL,
      main = NULL, sub = NULL,
      locate = FALSE, ...)
```

Arguments

x an object returned from one of the PowerUpR functions.

ypar character; "mdes" or "power" on y axis .

xpar character; one of the sample sizes on x axis.

<code>xlim</code>	limits for <code>xpar</code> .
<code>ylim</code>	limits for <code>ypar</code> .
<code>xlab</code>	x axis label (ignored for objects returned from <code>power.med211()</code> , <code>power.med221()</code> , and <code>power.med321()</code> functions).
<code>ylab</code>	y axis label (ignored for objects returned from <code>power.med211()</code> , <code>power.med221()</code> , and <code>power.med321()</code> functions).
<code>main</code>	title for the plot (ignored for objects returned from <code>power.med221()</code> and <code>power.med211()</code> functions).
<code>sub</code>	subtitle for the plot (ignored for objects returned from <code>power.med221()</code> and <code>power.med211()</code> functions).
<code>locate</code>	logical; TRUE locates parameter values for design <code>x</code> on the plot.
<code>...</code>	other graphical parameters to pass to <code>plot.new()</code> .

Examples

```
design1 <- mdes.cra3r3(rho3=.06, rho2=.17, n=15, J=3, K=60)
plot(design1, ypar = "mdes", xpar = "K", xlim = c(30, 100))
plot(design1, ypar = "power", xpar = "K", xlim = c(30, 100))

design2 <- power.cra3r3(es=.269, rho3=.06, rho2=.17, n=15, J=3, K=60)
plot(design2, ypar = "mdes", xpar = "K", xlim = c(30, 100))
plot(design2, ypar = "power", xpar = "K", xlim = c(30, 100))
```

PowerUpR-deprecated *Deprecated and Defunct functions in PowerUpR*

Description

Experimental MDES functions for 2-1-1 and 2-2-1 mediations are removed.

Format

Deprecated or defunct functions are no longer documented.

Details

Defunct functions:

- `mdes.med211` is defunct, there is no replacement function
- `mdes.med221` is defunct, there is no replacement function

`t1t2.error`*Plots Type I and Type II Error Rates*

Description

`t1t2.error` plots Type I (α) and Type II (β) error rates using central and noncentral t distributions for any objects returned from one of the PowerUpR functions.

Usage

```
t1t2.error(object)
```

Arguments

`object` an object returned from one of the PowerUpR functions.

Examples

```
## Not run:  
  
design1 <- mdes.bira2r1(rho2=.35, omega2=.10,  
                      n=83, J=480)  
t1t2.error(design1)  
  
## End(Not run)
```

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