

Package ‘longpower’

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Type Package

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Author Michael C. Donohue, Anthony C. Gamst, Steven D. Edland

Maintainer Michael C. Donohue <mtonohue@ucsd.edu>

Description The longpower package contains functions for computing power and sample size for linear models of longitudinal data based on the formula due to Liu and Liang (1997) and Diggle et al (2002). Either formula is expressed in terms of marginal model or Generalized Estimating Equations (GEE) parameters. This package contains functions which translate pilot mixed effect model parameters (e.g. random intercept and/or slope) into marginal model parameters so that the formulas of Diggle et al or Liu and Liang formula can be applied to produce sample size calculations for two sample longitudinal designs assuming known variance.

License GPL (>= 2)

Depends R (>= 3.0.0), Matrix, lme4 (>= 1.0), nlme, methods

Suggests knitr, gee

LazyLoad yes

VignetteBuilder knitr

URL <http://mtonohue.bitbucket.org/longpower>

Collate 'diggle.linear.power.R' 'edland.linear.power.R'
'liu.liang.linear.power.R' 'lmpower.R' 'power_mmr.R' 'print.power.longtest.R'

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longpower-package	<i>Sample size calculations for longitudinal data</i>
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Description

The longpower package contains functions for computing power and sample size for linear models of longitudinal data based on the formula due to Liu and Liang (1997) and Diggle et al (1994). Either formula is expressed in terms of marginal model or Generalized Estimating Equations (GEE) parameters. This package contains functions which translate pilot mixed effect model parameters (e.g. random intercept and/or slope) into marginal model parameters so that the formulas of Diggle et al or Liu and Liang formula can be applied to produce sample size calculations for two sample longitudinal designs assuming known variance. The package also handles the categorical time Mixed Model of Repeated Measures (MMRM) using the formula of Lu, Luo, and Chen (2008)

Details

Package:	longpower
Type:	Package
Version:	1.0
Date:	2013-05-22
License:	GPL (>= 2)
LazyLoad:	yes

Author(s)

Michael C. Donohue <mcdonohue@ucsd.edu> Anthony C. Gamst Steven D. Edland

References

Diggle PJ, Heagerty PJ, Liang K, Zeger SL. (2002) *Analysis of longitudinal data*. Second Edition. Oxford Statistical Science Series.

Liu, G., & Liang, K. Y. (1997). Sample size calculations for studies with correlated observations. *Biometrics*, 53(3), 937-47.

Lu, K., Luo, X., & Chen, P.-Y. (2008). Sample size estimation for repeated measures analysis in randomized clinical trials with missing data. *International Journal of Biostatistics*, 4, (1)

See Also

[lmpower](#), [power.mmrn](#), [power.mmrn.ar1](#), [lmpower](#), [diggle.linear.power](#), [edland.linear.power](#), [liu.liang.linear.power](#)

`diggle.linear.power` *Linear mixed model sample size calculations.*

Description

This function performs the sample size calculation for a linear mixed model. See Diggle et al (2002) for parameter definitions and other details.

Usage

```
diggle.linear.power(n = NULL, delta = NULL, t = NULL,
  sigma2 = 1, R = NULL, sig.level = 0.05, power = NULL,
  alternative = c("two.sided", "one.sided"))
```

Arguments

<code>n</code>	sample size per group
<code>delta</code>	group difference in slopes
<code>t</code>	the observation times
<code>sigma2</code>	the marginal model (GEE) scale parameter
<code>R</code>	the working correlation matrix (or variance-covariance matrix if <code>sigma2</code> is 1). If <code>R</code> is a scalar, an exchangeable working correlation matrix will be assumed.
<code>sig.level</code>	Type I error
<code>power</code>	power
<code>alternative</code>	one- or two-sided test

Details

The parameters `u`, `v`, and `Pi` are expected to be the same length and sorted with respect to each other. See Diggle, et al (1997) and package vignette for more details.

Value

The number of subject required per arm to attain the specified power given `sig.level` and the other parameter estimates.

Author(s)

Michael C. Donohue, Steven D. Edland

References

Diggle P.J., Heagerty P.J., Liang K., Zeger S.L. (2002) *Analysis of longitudinal data*. Second Edition. Oxford Statistical Science Series.

See Also

[lmpower](#), [diggle.linear.power](#)

Examples

```
## Not run:
browseVignettes(package = "longpower")

## End(Not run)

# Reproduces the table on page 29 of Diggle et al
n = 3
t = c(0,2,5)
rho = c(0.2, 0.5, 0.8)
sigma2 = c(100, 200, 300)
tab = outer(rho, sigma2,
  Vectorize(function(rho, sigma2){
    ceiling(diggle.linear.power(
      delta=0.5,
      t=t,
      sigma2=sigma2,
      R=rho,
      alternative="one.sided",
      power = 0.80)$n}))
colnames(tab) = paste("sigma2 =", sigma2)
rownames(tab) = paste("rho =", rho)
tab

# An Alzheimer's Disease example using ADAS-cog pilot estimates
# var of random intercept
sig2.i = 55
# var of random slope
sig2.s = 24
# residual var
sig2.e = 10
# covariance of slope and intercep
cov.s.i <- 0.8*sqrt(sig2.i)*sqrt(sig2.s)

cov.t <- function(t1, t2, sig2.i, sig2.s, cov.s.i){
  sig2.i + t1*t2*sig2.s + (t1+t2)*cov.s.i
}

t = seq(0,1.5,0.25)
```

```
n = length(t)
R = outer(t, t, function(x,y){cov.t(x,y, sig2.i, sig2.s, cov.s.i)})
R = R + diag(sig2.e, n, n)

diggle.linear.power(d=1.5, t=t, R=R, sig.level=0.05, power=0.80)
```

edland.linear.power *Linear mixed model sample size calculations.*

Description

This function performs the sample size calculation for a linear mixed model with random slope.

Usage

```
edland.linear.power(n = NULL, delta = NULL, t = NULL,
  sig2.s = 0, sig2.e = 1, sig.level = 0.05, power = NULL,
  alternative = c("two.sided", "one.sided"))
```

Arguments

n	sample size per group
delta	group difference in slopes
t	the observation times
sig2.s	variance of random slope
sig2.e	residual variance
sig.level	type one error
power	power
alternative	one- or two-sided test

Details

This function will also provide sample size estimates for linear mixed models with random intercept only simply by setting `sig2.s = 0`

Value

The number of subject required per arm to attain the specified power given `sig.level` and the other parameter estimates.

Author(s)

Michael C. Donohue, Steven D. Edland

References

Edland, S.D. (2009) Which MRI measure is best for Alzheimer's disease prevention trials: Statistical considerations of power and sample size. *Joint Stat Meeting Proceedings*. 4996-4999.

See Also

[lmpower](#), [diggle.linear.power](#), [liu.liang.linear.power](#)

Examples

```
## Not run:
browseVignettes(package = "longpower")

## End(Not run)
# Reproduces the table on page 29 of Diggle et al
n = 3
t = c(0,2,5)
rho = c(0.2, 0.5, 0.8)
sigma2 = c(100, 200, 300)
tab = outer(rho, sigma2,
  Vectorize(function(rho, sigma2){
    ceiling(edland.linear.power(
      delta=0.5,
      t=t,
      sig2.e=sigma2*(1-rho),
      alternative="one.sided",
      power=0.80)$n}))
colnames(tab) = paste("sigma2 =", sigma2)
rownames(tab) = paste("rho =", rho)
tab

# An Alzheimer's Disease example using ADAS-cog pilot estimates
t = seq(0,1.5,0.25)
n = length(t)

edland.linear.power(delta=1.5, t=t, sig2.s = 24, sig2.e = 10, sig.level=0.05, power = 0.80)
```

liu.liang.linear.power

Linear mixed model sample size calculations from Liu & Liang (1997).

Description

This function performs the sample size calculation for a linear mixed model. See Liu and Liang (1997) for parameter definitions and other details.

Usage

```
liu.liang.linear.power(N = NULL, delta = NULL, u = NULL,
  v = NULL, sigma2 = 1, R = NULL, R.list = NULL,
  sig.level = 0.05, power = NULL,
  Pi = rep(1/length(u), length(u)),
  alternative = c("two.sided", "one.sided"))
```

Arguments

N	The total sample size. This formula can accommodate unbalanced group allocation via Pi. See Liu and Liang (1997) for more details
delta	group difference (possibly a vector of differences)
u	a list of covariate vectors or matrices associated with the parameter of interest
v	a respective list of covariate vectors or matrices associated with the nuisance parameter
sigma2	the error variance
R	the variance-covariance matrix for the repeated measures
R.list	a list of variance-covariance matrices for the repeated measures, if assumed different in two groups
sig.level	type one error
power	power
Pi	the proportion of covariates of each type
alternative	one- or two-sided test

Details

The parameters u, v, and Pi are expected to be the same length and sorted with respect to each other. See Liu and Liang (1997) and package vignette for more details.

References

Liu, G. and Liang, K. Y. (1997) Sample size calculations for studies with correlated observations. *Biometrics*, 53(3), 937-47.

See Also

[lmpower](#)

Examples

```
## Not run:
browseVignettes(package = "longpower")

## End(Not run)
# Reproduces the table on page 29 of Diggle et al
n = 3
```

```

t = c(0,2,5)
u = list(u1 = t, u2 = rep(0,n))
v = list(v1 = cbind(1,1,rep(0,n)),
        v2 = cbind(1,0,t))
rho = c(0.2, 0.5, 0.8)
sigma2 = c(100, 200, 300)
tab = outer(rho, sigma2,
            Vectorize(function(rho, sigma2){
              ceiling(liu.liang.linear.power(
                delta=0.5, u=u, v=v,
                sigma2=sigma2,
                R=rho, alternative="one.sided",
                power=0.80)$N/2}))
colnames(tab) = paste("sigma2 =", sigma2)
rownames(tab) = paste("rho =", rho)
tab

# An Alzheimer's Disease example using ADAS-cog pilot estimates
# var of random intercept
sig2.i = 55
# var of random slope
sig2.s = 24
# residual var
sig2.e = 10
# covariance of slope and intercep
cov.s.i <- 0.8*sqrt(sig2.i)*sqrt(sig2.s)

cov.t <- function(t1, t2, sig2.i, sig2.s, cov.s.i){
  sig2.i + t1*t2*sig2.s + (t1+t2)*cov.s.i
}

t = seq(0,1.5,0.25)
n = length(t)
R = outer(t, t, function(x,y){cov.t(x,y, sig2.i, sig2.s, cov.s.i)})
R = R + diag(sig2.e, n, n)
u = list(u1 = t, u2 = rep(0,n))
v = list(v1 = cbind(1,1,rep(0,n)),
        v2 = cbind(1,0,t))

liu.liang.linear.power(delta=1.5, u=u, v=v, R=R, sig.level=0.05, power=0.80)
liu.liang.linear.power(N=416, u=u, v=v, R=R, sig.level=0.05, power=0.80)
liu.liang.linear.power(N=416, delta = 1.5, u=u, v=v, R=R, sig.level=0.05)
liu.liang.linear.power(N=416, delta = 1.5, u=u, v=v, R=R, power=0.80, sig.level = NULL)

# Reproduces total sample sizes, m, of Table 1 of Liu and Liang 1997
tab1 <- data.frame(cbind(
  n = c(rep(4, 4), rep(2, 4), 1),
  rho = c(0.0, 0.3, 0.5, 0.8)))
u = list(u1 = 1, u2 = 1) # intercept
v = list(v1 = 1, # treatment
        v2 = 0) # control
m <- c()
for(i in 1:nrow(tab1)){

```



```

R <- matrix(tab1$rho[i], nrow = tab1$n[i], ncol = tab1$n[i])
diag(R) <- 1
m <- c(m, liu.liang.linear.power(
  delta=0.5,
  u = list(u1 = rep(1, tab1$n[i]), u2 = rep(1, tab1$n[i])), # intercept
  v = list(v1 = rep(1, tab1$n[i]), # treatment
           v2 = rep(0, tab1$n[i])), # control
  sigma2=1,
  R=R, alternative="two.sided",
  power=0.90)$N)
}
cbind(tab1, m)

# Reproduces total sample sizes, m, of Table 3.a. of Liu and Liang 1997
# with unbalanced design
tab3 <- data.frame(cbind(
  rho = rep(c(0.0, 0.3, 0.5, 0.8), 2),
  pi1 = c(rep(0.8, 4), rep(0.2, 4))))
u = list(u1 = 1, u2 = 1) # intercept
v = list(v1 = 1, # treatment
         v2 = 0) # control
m <- c()
for(i in 1:nrow(tab3)){
  R <- matrix(tab3$rho[i], nrow = 4, ncol = 4)
  diag(R) <- 1
  m <- c(m, ceiling(liu.liang.linear.power(
    delta=0.5,
    u = list(u1 = rep(1, 4), u2 = rep(1, 4)), # intercept
    v = list(v1 = rep(1, 4), # treatment
             v2 = rep(0, 4)), # control
    sigma2=1,
    Pi = c(tab3$pi1[i], 1-tab3$pi1[i]),
    R=R, alternative="two.sided",
    power=0.90)$N))
}
cbind(tab3, m)

```

lmpower-methods

Sample size calculations for linear mixed models of rate of change based on lmer, lme, or gee "placebo" pilot estimates.

Description

These functions compute sample size for linear mixed models based on the formula due to Diggle (2002) or Liu and Liang (1997). These formulae are expressed in terms of marginal model or Generalized Estimating Equations (GEE) parameters. These functions translate pilot mixed effect model parameters (e.g. random intercept and/or slope, fixed effects, etc.) into marginal model parameters so that either formula can be applied to equivalent affect. Pilot estimates are assumed to be from an appropriate "placebo" group and the parameter of interest is assumed to be the rate of change over time of the outcome.

Usage

```
Immpower.default(object = NULL, n = NULL, parameter = 2, pct.change =
  NULL, delta = NULL, t = NULL, sig.level = 0.05, power =
  NULL, alternative = c("two.sided", "one.sided"),
  beta = NULL, beta.CI = NULL, delta.CI = NULL, sig2.i =
  NULL, sig2.s = NULL, sig2.e = NULL, cov.s.i = NULL, R
  = NULL, method = c("edland", "diggle", "liuliang"),
  ...)
```

```
Immpower.lme(object, n = NULL, parameter = 2, pct.change = NULL,
  delta = NULL, t = NULL, sig.level = 0.05, power =
  NULL, alternative = c("two.sided", "one.sided"), beta
  = NULL, beta.CI = NULL, delta.CI = NULL, sig2.i =
  NULL, sig2.s = NULL, sig2.e = NULL, cov.s.i = NULL,
  method = c("edland", "diggle", "liuliang"), ...)
```

```
Immpower.gee(object, n = NULL, parameter = 2, pct.change = NULL,
  delta = NULL, t = NULL, sig.level = 0.05, power =
  NULL, alternative = c("two.sided", "one.sided"), beta
  = NULL, beta.CI = NULL, delta.CI = NULL, method =
  c("diggle", "liuliang"), ...)
```

Arguments

n	sample size per group
object	an object returned by lme4 of a mixed-effects model object to placebo data assumed to have either a random intercept, or a random intercept and random effect for time (slope); and fixed effect representing the rate of change in a placebo group.
parameter	the name or position of the rate of change parameter of interest, e.g. ("time", "t", or 2 if it is the second specified fixed effect).
pct.change	the percent change in the pilot estimate of the parameter of interest (beta, the placebo/null effect)
delta	the change in the pilot estimate of the parameter of interest, computed from pct.change if left missing.
t	vector of time points
sig.level	Type I error
power	power
alternative	"two.sided" or "one.sided"
beta	pilot estimate of the placebo effect (slope or rate of change in the outcome)
beta.CI	95% confidence limits of the pilot estimate of beta
delta.CI	95% confidence limits of the effect size
sig2.i	pilot estimate of variance of random intercept
sig2.s	pilot estimate of variance of random slope

sig2.e	pilot estimate of residual variance
cov.s.i	pilot estimate of covariance of random slope and intercept
R	pilot estimate of a marginal model working correlation matrix
method	the formula to use. Defaults to "diggle" for Diggle et al (2002). Alternatively "liuliang" can be selected for Liu & Liang (1997).
...	other arguments

Details

Any parameters not explicitly stated are extracted from the fitted object.

Value

An object of class `power.htest` giving the calculated sample size, N, per group and other parameters.

Methods

```
signature(object = "ANY")
signature(object = "merMod")
```

Author(s)

Michael C. Donohue

References

Diggle P.J., Heagerty P.J., Liang K., Zeger S.L. (2002) *Analysis of longitudinal data*. Second Edition. Oxford Statistical Science Series.

Liu, G., and Liang, K. Y. (1997) Sample size calculations for studies with correlated observations. *Biometrics*, 53(3), 937-47.

See Also

[liu.liang.linear.power](#) [diggle.linear.power](#)

Examples

```
## Not run:
browseVignettes(package = "longpower")

## End(Not run)

lmpower(delta=1.5, t = seq(0,1.5,0.25),
sig2.i = 55, sig2.s = 24, sig2.e = 10, cov.s.i=0.8*sqrt(55)*sqrt(24), power = 0.80)
lmpower(n=208, t = seq(0,1.5,0.25),
sig2.i = 55, sig2.s = 24, sig2.e = 10, cov.s.i=0.8*sqrt(55)*sqrt(24), power = 0.80)
lmpower(beta = 5, pct.change = 0.30, t = seq(0,1.5,0.25),
sig2.i = 55, sig2.s = 24, sig2.e = 10, cov.s.i=0.8*sqrt(55)*sqrt(24), power = 0.80)
```

```
## Not run:
library(lme4)
fm1 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
lmpower(fm1, pct.change = 0.30, t = seq(0,9,1), power = 0.80)

library(nlme)
fm2 <- lme(Reaction ~ Days, random=~Days|Subject, sleepstudy)
lmpower(fm2, pct.change = 0.30, t = seq(0,9,1), power = 0.80)

# random intercept only
fm3 <- lme(Reaction ~ Days, random=~1|Subject, sleepstudy)
lmpower(fm3, pct.change = 0.30, t = seq(0,9,1), power = 0.80)

library(gee)
fm4 <- gee(Reaction ~ Days, id = Subject,
           data = sleepstudy,
           corstr = "exchangeable")
lmpower(fm4, pct.change = 0.30, t = seq(0,9,1), power = 0.80)

## End(Not run)
```

power.mmrn

Linear mixed model sample size calculations.

Description

This function performs the sample size calculation for a mixed model of repeated measures with general correlation structure. See Lu, Luo, & Chen (2008) for parameter definitions and other details. This function executes Formula (3) on page 4.

Usage

```
power.mmrn(N = NULL, Ra = NULL, ra = NULL, sigmaa = NULL,
           Rb = NULL, rb = NULL, sigmab = NULL, lambda = 1,
           delta = NULL, sig.level = 0.05, power = NULL,
           alternative = c("two.sided", "one.sided"))
```

Arguments

N	total sample size
Ra	correlation matrix for group a
ra	retention in group a
sigmaa	standard deviation of observation of interest in group a
Rb	correlation matrix for group a
rb	retention in group b

sigmab	standard deviation of observation of interest in group b. If NULL, sigmab is assumed same as sigmaa. If not NULL, sigmaa and sigmab are averaged.
lambda	allocation ratio
delta	effect size
sig.level	type one error
power	power
alternative	one- or two-sided test

Details

See Lu, Luo, & Chen (2008).

Value

The number of subject required per arm to attain the specified power given sig.level and the other parameter estimates.

Author(s)

Michael C. Donohue

References

Lu, K., Luo, X., Chen, P.-Y. (2008) Sample size estimation for repeated measures analysis in randomized clinical trials with missing data. *International Journal of Biostatistics*, 4, (1)

See Also

[power.mmrn.ar1](#), [lmpower](#), [diggle.linear.power](#)

Examples

```
# reproduce Table 1 from Lu, Luo, & Chen (2008)
phi1 <- c(rep(1, 6), 2, 2)
phi2 <- c(1, 1, rep(2, 6))
lambda <- c(1, 2, sqrt(1/2), 1/2, 1, 2, 1, 2)
ztest <- ttest1 <- c()
for(i in 1:8){
  Na <- (phi1[i] + lambda[i] * phi2[i])*(qnorm(0.05/2) + qnorm(1-0.90))^2*(0.5^-2)
  Nb <- Na/lambda[i]
  ztest <- c(ztest, Na + Nb)
  v <- Na + Nb - 2
  Na <- (phi1[i] + lambda[i] * phi2[i])*(qt(0.05/2, df = v) + qt(1-0.90, df = v))^2*(0.5^-2)
  Nb <- Na/lambda[i]
  ttest1 <- c(ttest1, Na + Nb)
}
data.frame(phi1, phi2, lambda, ztest, ttest1)

Ra <- matrix(0.25, nrow = 4, ncol = 4)
diag(Ra) <- 1
```

```

ra <- c(1, 0.90, 0.80, 0.70)
sigmaa <- 1
power.mmr(Ra = Ra, ra = ra, sigmaa = sigmaa, delta = 0.5, power = 0.80)
power.mmr(N = 174, Ra = Ra, ra = ra, sigmaa = sigmaa, delta = 0.5)
power.mmr(N = 174, Ra = Ra, ra = ra, sigmaa = sigmaa, power = 0.80)

power.mmr(Ra = Ra, ra = ra, sigmaa = sigmaa, delta = 0.5, power = 0.80, lambda = 2)
power.mmr(N = 174, Ra = Ra, ra = ra, sigmaa = sigmaa, delta = 0.5, lambda = 2)
power.mmr(N = 174, Ra = Ra, ra = ra, sigmaa = sigmaa, power = 0.80, lambda = 2)

```

power.mmr.ar1 *Linear mixed model sample size calculations.*

Description

This function performs the sample size calculation for a mixed model of repeated measures with AR(1) correlation structure. See Lu, Luo, & Chen (2008) for parameter definitions and other details.

Usage

```

power.mmr.ar1(N = NULL, rho = NULL, ra = NULL,
  sigmaa = NULL, rb = NULL, sigmab = NULL, lambda = 1,
  times = 1:length(ra), delta = NULL, sig.level = 0.05,
  power = NULL,
  alternative = c("two.sided", "one.sided"))

```

Arguments

N	total sample size
rho	AR(1) correlation parameter
ra	retention in group a
sigmaa	standard deviation of observation of interest in group a
rb	retention in group a (assumed same as ra if left blank)
sigmab	standard deviation of observation of interest in group b. If NULL, sigmab is assumed same as sigmaa. If not NULL, sigmaa and sigmab are averaged.
lambda	allocation ratio
times	observation times
delta	effect size
sig.level	type one error
power	power
alternative	one- or two-sided test

Details

See Lu, Luo, & Chen (2008).

Value

The number of subject required per arm to attain the specified power given sig. level and the other parameter estimates.

Author(s)

Michael C. Donohue

References

Lu, K., Luo, X., Chen, P.-Y. (2008) Sample size estimation for repeated measures analysis in randomized clinical trials with missing data. *International Journal of Biostatistics*, 4, (1)

See Also

[power.mmr](#), [lmpower](#), [diggle.linear.power](#)

Examples

```
# reproduce Table 2 from Lu, Luo, & Chen (2008)
tab <- c()
for(J in c(2,4))
for(aJ in (1:4)/10)
for(p1J in c(0, c(1, 3, 5, 7, 9)/10)){
  rJ <- 1-aJ
  r <- seq(1, rJ, length = J)
  # p1J = p^(J-1)
  tab <- c(tab, power.mmr.ar1(rho = p1J^(1/(J-1)), ra = r, sigmaa = 1,
    lambda = 1, times = 1:J,
    delta = 1, sig.level = 0.05, power = 0.80)$phi1)
}
matrix(tab, ncol = 6, byrow = TRUE)

# approximate simulation results from Table 5 from Lu, Luo, & Chen (2008)
ra <- c(100, 76, 63, 52)/100
rb <- c(100, 87, 81, 78)/100

power.mmr.ar1(rho=0.6, ra=ra, sigmaa=1, rb = rb,
  lambda = sqrt(1.25/1.75), power = 0.904, delta = 0.9
)
power.mmr.ar1(rho=0.6, ra=ra, sigmaa=1, rb = rb,
  lambda = 1.25/1.75, power = 0.910, delta = 0.9
)
power.mmr.ar1(rho=0.6, ra=ra, sigmaa=1, rb = rb,
  lambda = 1, power = 0.903, delta = 0.9
)
power.mmr.ar1(rho=0.6, ra=ra, sigmaa=1, rb = rb,
  lambda = 2, power = 0.904, delta = 0.9
)

power.mmr.ar1(N=81, ra=ra, sigmaa=1, rb = rb,
  lambda = sqrt(1.25/1.75), power = 0.904, delta = 0.9
```

```
)
power.mmr.ar1(N=87, rho=0.6, ra=ra, sigmaa=1, rb = rb,
  lambda = 1.25/1.75, power = 0.910
)
power.mmr.ar1(N=80, rho=0.6, ra=ra, sigmaa=1, rb = rb,
  lambda = 1, delta = 0.9
)
power.mmr.ar1(N=84, rho=0.6, ra=ra, sigmaa=1, rb = rb,
  lambda = 2, power = 0.904, delta = 0.9, sig.level = NULL
)
```

`print.power.longtest` *Print method for longitudinal data power calculation object*

Description

Print object of class "power.longtest" in nice layout.

Usage

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

Arguments

`x` Object of class "power.longtest".
`...` further arguments to be passed to or from methods.

Details

A `power.longtest` object is just a named list of numbers and character strings, supplemented with method and note elements. The method is displayed as a title, the note as a footnote, and the remaining elements are given in an aligned 'name = value' format.

Value

none

See Also

[liu.liang.linear.power](#), [diggle.linear.power](#), [lmmpower](#),

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