Package 'SteppedPower'

July 7, 2021

Type Package

Title Power Calculation for Stepped Wedge Designs

Version 0.2.0

Description Tools for power and sample size
calculation as well as design diagnostics for
longitudinal mixed model settings, with a focus on stepped wedge designs.
All calculations are oracle estimates i.e. assume random effect variances
to be known (or guessed) in advance.
The method is introduced in Hussey and Hughes (2007) <doi:10.1016/j.cct.2006.05.007>,
extensions are discussed in Li et al. (2020) <doi:10.1177/0962280220932962>.

Imports Matrix, plotly, grDevices, stats, utils

Suggests knitr, rmarkdown, swCRTdesign, testthat, pwr

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VignetteBuilder knitr

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R topics documented:

`alpha012_to_RandEff` *Correlation structure: transform alpha to random effects*

Description

Correlation structure: transform alpha to random effects

Usage

```
alpha012_to_RandEff(alpha012, sigResid = NULL, sigMarg = NULL)
```

Arguments

`alpha012`	A vector or a list of length 3. Each list element must have the same dimension.
`sigResid`	Residual standard deviation on individual level. Either residual sd or marginal sd needs to be specified.
`sigMarg`	Marginal standard deviation on individual level. Either residual sd or marginal sd needs to be specified.

Value

a list containing four named elements (possibly matrices): random cluster intercept ‘tau‘, random time effect ‘gamma‘, random subject intercept and residual standard deviation

Examples

```
alpha012_to_RandEff(alpha012=c(.1,.1,.1), sigMarg=1)
alpha012_to_RandEff(alpha012=c(.1,.1,.1), sigResid=.9486833)

## The function is vectorised:
alpha012_to_RandEff(alpha012=list(matrix(c(0,.1,.1,.2), 2, 2),
                                  matrix(c(0,0,.1,.2) , 2, 2),
                                  matrix(c(0,0,.2,.2) , 2, 2)),
                    sigMarg=1)
```

`compute_wlsPower` *Compute power via weighted least squares*

Description

This function is not intended to be used directly, but rather to be called by 'wlsPower' - the main function of this package. It expects the design matrix as an input argument 'DesMat' and construct the covariance matrix (if not given as well). These matrices are used to calculate the variance of the treatment effect estimator which is then used to calculate the power to detect the assumed treatment effect.

Usage

```
compute_wlsPower(
  DesMat,
  EffSize,
  sigma,
  tau = 0,
  eta = NULL,
  AR = NULL,
  rho = NULL,
  gamma = NULL,
  psi = NULL,
  N = NULL,
  CovMat = NULL,
  dfAdjust = "none",
  sig.level = 0.05,
  INDIV_LVL = FALSE,
  verbose = 1
)
```

Arguments

`DesMat`	object of class 'DesMat'.
`EffSize`	raw effect, i.e. difference between mean under control and mean under intervention

sigma	numeric, residual error of cluster means if no N given.
tau	numeric, standard deviation of random intercepts
eta	numeric (scalar or matrix), standard deviation of random slopes. If ‘eta‘ is given as scalar, ‘trtMat‘ is needed as well.
AR	numeric, vector containing up to three values, each between 0 and 1. Defaults to NULL. It defines the AR(1)-correlation of random effects. The first element corresponds to the cluster intercept, the second to the treatment effect and the third to subject specific intercept. If only one element is provided, autocorrelation of all random effects is assumed to be the same. *Currently not compatible with ‘rho‘!=0 !*
rho	numeric (scalar), correlation of ‘tau‘ and ‘eta‘
gamma	numeric (scalar), random time effect
psi	numeric (scalar), random subject specific intercept. Leads to a closed cohort setting
N	numeric, number of individuals per cluster. Either a scalar, vector of length #Clusters or a matrix of dimension #Clusters x timepoints. Defaults to 1 if not passed.
CovMat	numeric, a positive-semidefinite matrix with (#Clusters · timepoints) rows and columns. If ‘CovMat‘ is given, ‘sigma‘, ‘tau‘, ‘eta‘, ‘rho‘, ‘gamma‘ and ‘psi‘ as well as ‘alpha_0_1_2‘ must be NULL.
dfAdjust	character, one of the following: "none","between-within", "containment", "residual".
sig.level	numeric (scalar), significance level, defaults to 0.05
INDIV_LVL	logical, should the computation be conducted on an individual level? This leads to longer run time and is mainly for diagnostic purposes.
verbose	integer, how much information should the function return?

Value

The return depends on the ‘verbose‘ parameter. If ‘verbose‘=0, only the power is returned If ‘verbose‘=1 (the default), a list containing power and the parameters of the specific setting is returned. If requested (by ‘verbose‘=2) this list also contains relevant matrices.

---

construct_CovBlk *Construct a Single Block of the Covariance Matrix*

Description

Constructs the covariance matrix for multiple measurements of the same cluster. This function is usually called by ‘construct_CovMat‘ and is not designed to be used directly.

Usage

```
construct_CovBlk(sigma, tau = NULL, eta = NULL, AR = NULL, rho = NULL)
```

Arguments

sigma	numeric (vector of length ‘timepoints‘), residual error
tau	numeric (vector of length ‘timepoints‘), standard deviation of random intercepts
eta	numeric (vector of length ‘timepoints‘), standard deviation of random slope
AR	numeric, vector containing up to three values, each between 0 and 1. Defaults to NULL. It defines the AR(1)-correlation of random effects. The first element corresponds to the cluster intercept, the second to the treatment effect and the third to subject specific intercept. If only one element is provided, autocorrelation of all random effects is assumed to be the same. *Currently not compatible with ‘rho‘!=0 !*
rho	numeric (scalar), correlation of ‘tau‘ and ‘eta‘

Value

a block of a covariance matrix, corresponding to intra-cluster covariance over time for one cluster

Examples

```
construct_CovBlk(sigma=rep(2,5), tau=rep(1,5))

construct_CovBlk(sigma=rep(2,5),
                 tau=rep(.5,5), eta=c(0,0,1,1,1),
                 AR=c(.5, 1))
```

---

construct_CovMat *Construct a Covariance Matrix*

Description

constructs a (block diagonal) covariance matrix. This function calls ‘construct_CovBlk‘ (or ‘construct_CovSubMat‘ in case of repeated observations of the same individuals) for each block.

Usage

```
construct_CovMat(
  SumCl = NULL,
  timepoints = NULL,
  sigma,
  tau,
  eta = NULL,
  AR = NULL,
  rho = NULL,
  gamma = NULL,
  trtMat = NULL,
  N = NULL,
  CovBlk = NULL,
```

```
  psi = NULL,
  INDIV_LVL = FALSE
)
```

Arguments

SumCl	total number of clusters
timepoints	numeric (scalar or vector), number of timepoints (periods). If design is swd, timepoints defaults to length(Cl)+1. Defaults to 1 for parallel designs.
sigma	numeric, residual error of cluster means if no N given.
tau	numeric, standard deviation of random intercepts
eta	numeric (scalar or matrix), standard deviation of random slopes. If 'eta' is given as scalar, 'trtMat' is needed as well.
AR	numeric, vector containing up to three values, each between 0 and 1. Defaults to NULL. It defines the AR(1)-correlation of random effects. The first element corresponds to the cluster intercept, the second to the treatment effect and the third to subject specific intercept. If only one element is provided, autocorrelation of all random effects is assumed to be the same. *Currently not compatible with 'rho'!=0 !*
rho	numeric (scalar), correlation of 'tau' and 'eta'
gamma	numeric (scalar), random time effect
trtMat	a matrix of dimension *#Cluster* x *timepoints* as produced by the function 'construct_trtMat', indicating the cluster-periods that receive interventional treatment. Defaults to NULL. If trtMat is given, the arguments 'SumCl' and 'timepoints' are ignored (!).
N	numeric, number of individuals per cluster. Either a scalar, vector of length #Clusters or a matrix of dimension #Clusters x timepoints. Defaults to 1 if not passed.
CovBlk	a matrix of dimension *timepoints* x *timepoints*.
psi	numeric (scalar), random subject specific intercept. Leads to a closed cohort setting
INDIV_LVL	logical, should the computation be conducted on an individual level? This leads to longer run time and is mainly for diagnostic purposes.

Value

a covariance matrix

Examples

```
## Two clusters, three timepoints,
## residual standard error sd=3, random slope sd=1.
construct_CovMat(SumCl=2, timepoints=3, sigma=3, tau=1)
##
##
```

```
## ... with random slope as AR-1 process
construct_CovMat(SumCl=2, timepoints=3, sigma=3, tau=1, AR=.8)
##
##
## ... with sigma and tau variing over time and between clusters:
construct_CovMat(SumCl=2,timepoints=3,
                 sigma=matrix(c(1,2,2,1,1,2),nrow=2, byrow=TRUE),
                 tau=matrix(c(.2,.1,.1,.2,.2,.1),nrow=2, byrow=TRUE),
                 N=c(3,4))
```

`construct_CovSubMat` *Construct a Block of the Covariance Matrix*

Description

Constructs the covariance matrix for multiple measurements of the same cluster if the same individuals are observed at all time periods. This function is not designed to be used directly.

Usage

```
construct_CovSubMat(
  N,
  timepoints,
  sigma,
  tau,
  eta = NULL,
  AR = NULL,
  rho = NULL,
  gamma = NULL,
  trtMat = NULL,
  psi = NULL,
  INDIV_LVL = FALSE
)
```

Arguments

`N`	Number of individuals per cluster
`timepoints`	numeric (scalar or vector), number of timepoints (periods). If design is swd, timepoints defaults to length(Cl)+1. Defaults to 1 for parallel designs.
`sigma`	numeric (vector of length 'timepoints'), residual error
`tau`	numeric (vector of length 'timepoints'), standard deviation of random intercepts
`eta`	numeric (vector of length 'timepoints'), standard deviation of random slope
`AR`	numeric, vector containing up to three values, each between 0 and 1. Defaults to NULL. It defines the AR(1)-correlation of random effects. The first element corresponds to the cluster intercept, the second to the treatment effect and the third to subject specific intercept. If only one element is provided, autocorrelation of all random effects is assumed to be the same. *Currently not compatible with 'rho'!=0 !*

rho	numeric (scalar), correlation of ‘tau‘ and ‘eta‘
gamma	numeric (vector of length ‘timepoints‘), standard deviation of a random time effect.
trtMat	a matrix of dimension *#Cluster* x *timepoints* as produced by the function ‘construct_trtMat‘, indicating the cluster-periods that receive interventional treatment. Defaults to NULL. If trtMat is given, the arguments ‘SumCl‘ and ‘timepoints‘ are ignored (!).
psi	numeric (scalar), random subject specific intercept. Leads to a closed cohort setting
INDIV_LVL	logical, should the computation be conducted on an individual level? This leads to longer run time and is mainly for diagnostic purposes.

Value

a block of a covariance matrix with two levels of clustering, corresponding to intra-cluster covariance over time for one cluster

---

construct_DesMat *Construct the Design Matrix*

Description

Constructs the design matrix with one column for every (fixed) parameter to be estimated and one row for every cluster for every timepoint. This function calls ‘construct_trtMat‘ to construct a matrix that indicates treatment status for each cluster at each timepoint. This is then transformed into the first column of the design matrix. ‘construct_CovMat‘ further calls ‘construct_timeAdjust‘ to get the fixed effect(s) of the timepoints.

Note: Unlike the usual notation, the treatment effect is in the first column (for easier access by higher level functions).

Usage

```
construct_DesMat(
  Cl = NULL,
  trtDelay = NULL,
  dsntype = "SWD",
  timepoints = NULL,
  timeAdjust = "factor",
  period = NULL,
  trtmatrix = NULL,
  timeBlk = NULL,
  N = NULL,
  INDIV_LVL = FALSE
)
```

Arguments

Cl	integer (vector), number of clusters per sequence group (in SWD), or number in control and intervention (in parallel designs)
trtDelay	numeric (possibly vector), value(s) between 0 and 1 specifying the proportion of intervention effect in the first (second ...) intervention phase.
dsntype	character, defines the type of design. Options are "SWD", "parallel" and "parallel_baseline", defaults to "SWD".
timepoints	numeric (scalar or vector), number of timepoints (periods). If design is swd, timepoints defaults to length(Cl)+1. Defaults to 1 for parallel designs.
timeAdjust	character, specifies adjustment for time periods. One of the following: "factor", "linear", "none", "periodic". Defaults to "factor".
period	numeric (scalar)
trtmatrix	an optional user defined matrix to define treatment allocation
timeBlk	an optional user defined matrix that defines the time adjustment in one cluster. Is repeated for every cluster.
N	numeric, number of individuals per cluster. Either a scalar, vector of length #Clusters or a matrix of dimension #Clusters x timepoints. Defaults to 1 if not passed.
INDIV_LVL	logical, should the computation be conducted on an individual level? This leads to longer run time and is mainly for diagnostic purposes.

Value

an object of class DesMat

Examples

```
construct_DesMat(Cl=c(2,0,1))
construct_DesMat(Cl=c(2,0,1), N=c(1,3,2))

## manually defined time adjustment (same as above)
timeBlock <- matrix(c(1,0,0,0,
                      1,1,0,0,
                      1,0,1,0,
                      1,0,0,1), 4, byrow=TRUE)
construct_DesMat(Cl=c(2,0,1), timeBlk=timeBlock)
```

---

construct_timeAdjust *Construct the time period adjustment in the design matrix*

Description

Offers several options to adjust for secular trends.

Usage

```
construct_timeAdjust(
  Cl,
  timepoints,
  timeAdjust = "factor",
  period = NULL,
  timeBlk = NULL
)
```

Arguments

Cl	integer (vector), number of clusters per sequence group (in SWD), or number in control and intervention (in parallel designs)
timepoints	numeric (scalar or vector), number of timepoints (periods). If design is swd, timepoints defaults to length(Cl)+1. Defaults to 1 for parallel designs.
timeAdjust	character, specifies adjustment for time periods. One of the following: "factor", "linear", "none", "periodic". Defaults to "factor".
period	numeric (scalar)
timeBlk	an optional user defined matrix that defines the time adjustment in one cluster. Is repeated for every cluster.

Value

a matrix with one row for every cluster at every timepoint and number of columns depending of adjustment type.

---

construct_trtMat *Construct Treatment Matrix*

Description

Constructs a matrix of '#cluster' rows and '#timepoint' columns, indicating treatment status in each cluster at each timepoint.

Usage

```
construct_trtMat(Cl, trtDelay, dsntype, timepoints = NULL)
```

Arguments

Cl	integer (vector), number of clusters per sequence group (in SWD), or number in control and intervention (in parallel designs)
trtDelay	numeric (possibly vector), value(s) between 0 and 1 specifying the proportion of intervention effect in the first (second ...) intervention phase.
dsntype	character, defines the type of design. Options are "SWD", "parallel" and "parallel_baseline", defaults to "SWD".

timepoints	numeric (scalar or vector), number of timepoints (periods). If design is swd, timepoints defaults to length(Cl)+1. Defaults to 1 for parallel designs.

Value

a matrix trtMat, where rows and columns correspond to cluster and timepoints, respectively

Examples

```
construct_trtMat(Cl=c(1,2,1), trtDelay=c(.2,.8), dsntype="SWD")
```

`plot.DesMat` *plot.DesMat*

Description

plot.DesMat

Usage

```
## S3 method for class 'DesMat'
plot(x, show_colorbar = FALSE, ...)
```

Arguments

x	An object of class 'DesMat'
show_colorbar	logical, should the colorbar be shown?
...	Arguments to be passed to methods

Value

a plotly html widget, displaying the treatment status

Examples

```
x <- construct_DesMat(C=c(2,2,2,0,2,2,2),.5)
```

plot.wlsPower *plot an object of class 'wlsPower'*

Description

Up to three plots (selectable by 'which') that visualise: influence of each cluster for each timepoint, the treatment status for each cluster for each timepoint and the covariance matrix. By default, only the first plot is returned.

Usage

```
## S3 method for class 'wlsPower'
plot(x, which = 1, show_colorbars = NULL, ...)
```

Arguments

x	object of class wlsPower
which	Specify a subset of the numbers 1:3 to select plots
show_colorbars	logical, should the colorbars be shown?
...	Arguments to be passed to methods

Value

a list of plotly html widgets

plot_CovMat *Visualise a Covariance Matrix*

Description

Currently not exported.

Usage

```
plot_CovMat(CovMat, show_colorbar = TRUE)
```

Arguments

CovMat	A covariance matrix (possibly in sparse matrix notation)
show_colorbar	logical, should the colorbar be shown?

Value

a plotly object

print.DesMat *print.DesMat*

Description

print.DesMat

Usage

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

Arguments

x	An object of class 'DesMat
...	Arguments to be passed to methods

Value

Messages with information about the design.

print.wlsPower *Print an object of class 'wlsPower'*

Description

Print an object of class 'wlsPower'

Usage

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

Arguments

x	object of class wlsPower
...	Arguments to be passed to methods

Value

Messages, containing information about (at least) power and significance level

RandEff_to_alpha012 *Correlation structure: transform random effects to alpha*

Description

Correlation structure: transform random effects to alpha

Usage

```
RandEff_to_alpha012(sigResid, tau, gamma, psi)
```

Arguments

sigResid	Residual standard deviation on individual leve
tau	standard deviation of random cluster intercept
gamma	standard deviation of random time effect
psi	standard deviation of random subject specific intercept

Value

a list containing four named elements (possibly matrices): 'alpha0', 'alpha1', 'alpha2' specify a correlation structure and SigMarg denotes the marginal standard deviation

Examples

```
RandEff_to_alpha012(sigResid=sqrt(11), tau=4, gamma=3, psi=2)

## The function is vectorised:
RandEff_to_alpha012(sigResid = matrix(c(0,1,2,3,4,5), 2, 3),
                    tau      = matrix(c(1,1,1,0,0,0), 2, 3),
                    gamma    = matrix(c(0,0,1,0,0,1), 2, 3),
                    psi      = matrix(c(0,1,1,0,0,1), 2, 3))
```

SteppedPower-pkg *SteppedPower*

Description

SteppedPower offers tools for power and sample size calculation as well as design diagnostics for longitudinal mixed model settings, with a focus on stepped wedge designs. All calculations are oracle estimates i.e. assume random effect variances to be known (or guessed) in advance.

Author(s)

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tTestPwr *Compute Power of a Wald Test*

Description

Computes the power of a scaled Wald test given a standard error, an effect size, the degrees of freedom of the t-distribution and a significance level. Computes the exact power, see second example

Usage

```
tTestPwr(d, se, df, sig.level = 0.05)
```

Arguments

d	numeric, raw effect
se	numeric, standard error
df	numeric, degrees of freedom of the t-distribution
sig.level	numeric, significance level, defaults to 0.05

Value

a scalar

Examples

```
tTestPwr(4,1,10) ; tTestPwr(4,1,30) ; tTestPwr(4,1,Inf)
```

VarClosed_Kasza *Closed formula for treatment variance in open cohort settings*

Description

From Kasza et al "Sample size and power calculations for open cohort longitudinal cluster rondomized trials" 2020

Usage

```
VarClosed_Kasza(trtMat, tau, gamma = 0, psi = 0, sigma, N, chi)
```

Arguments

trtMat	a matrix trtMat to define treatment allocation, where rows and columns correspond to cluster and timepoints, respectively
tau	numeric, standard deviation of random intercepts
gamma	numeric, random time effect
psi	numeric, random subject specific intercept.
sigma	numeric, residual error on subject level.
N	numeric, number of individuals per cluster.
chi	Attrition factor

Value

numeric, variance of the estimator for treatment effect

Examples

```
##  test setting, from Hussey&Hughes 2007  ####
trtMat <- construct_DesMat(c(6,6,6,6))$trtMat
tau <- .025 ; sigma <- sqrt(.041*.959) ; N <- 100 ;
gamma <- 0.01 ; psi <- .1 ; chi <- .7

tmp <- VarClosed_Kasza(trtMat, tau=tau, sigma=sigma, gamma=0, psi=0, N=N, chi=0)
tTestPwr((.05-.032), sqrt(tmp), df = Inf)
wlsPower(Cl = rep(6,4), N=N, mu0=.05, mu1=.032, verbose=0,
        sigma=sigma, gamma=0, tau=tau, psi=0)

tmp <- VarClosed_Kasza(trtMat, tau=tau, sigma=sigma, gamma=gamma, psi=psi, N=N, chi=0)
tTestPwr((.05-.032), sqrt(tmp), df = Inf)
wlsPower(Cl = rep(6,4), N=N, mu0=.05, mu1=.032, verbose=0,
        sigma=sigma, gamma=gamma, tau=tau, psi=psi)

tmp <- VarClosed_Kasza(trtMat, tau=tau, sigma=sigma, gamma=gamma, psi=psi, N=N, chi=1)
tTestPwr((.05-.032), sqrt(tmp), df = Inf)
wlsPower(Cl = rep(6,4), N=N, mu0=.05, mu1=.032, verbose=0,
         sigma=sigma, gamma=sqrt(gamma^2+psi^2/N), tau=tau, psi=0)

tmp <- VarClosed_Kasza(trtMat, tau=tau, sigma=sigma, gamma=gamma, psi=psi, N=N, chi=chi)
tTestPwr((.05-.032), sqrt(tmp), df = Inf)
wlsPower(Cl = rep(6,4), N=N, mu0=.05, mu1=.032, verbose=0,
         sigma=sigma, gamma=sqrt(gamma^2+chi*psi^2/N), tau=tau, psi=sqrt(1-chi)*psi)
```

VarClosed_Li *Closed formula for treatment variance, with proportional decay*

Description

From Li et al "Design and analysis considerations for cohort stepped wedge cluster randomized trials with a decay correlation structure"

Usage

```
VarClosed_Li(trtMat, tau, psi, N, AR)
```

Arguments

trtMat	a matrix trtMat to define treatment allocation, where rows and columns correspond to cluster and timepoints, respectively
tau	numeric, standard deviation of random intercepts
psi	numeric, random subject specific intercept.
N	numeric, number of individuals per cluster.
AR	numeric (scalar), It defines the AR(1)-correlation of random effects.

Value

numeric, variance of the estimator for treatment effect

Examples

```
##  test setting, from Hussey&Hughes 2007  ####
trtMat <- construct_DesMat(c(6,6,6,6))$trtMat
tau <- .025 ; N <- 100 ; psi <- .1 ; AR <- .6
tmp <- VarClosed_Li(trtMat, tau=tau, psi=psi, N=N, AR=AR)
tTestPwr((.05-.032), se=sqrt(tmp), Inf)
wlsPower(Cl=rep(6,4), mu0=.05, mu1=.032, AR=AR,
         tau=tau, N=N, sigma=0, psi=psi, verbose=0)
```

---

wlsPower *Compute power via weighted least squares*

Description

This is the main function of the SteppedPower package. It calls the constructor functions for the design matrix and covariance matrix, and then calculates the variance of the intervention effect estimator. The latter is then used to compute the power of a Wald test of a (given) intervention effect.

Usage

```
wlsPower(
  Cl = NULL,
  timepoints = NULL,
  DesMat = NULL,
  trtDelay = NULL,
  incomplete = NULL,
  timeAdjust = "factor",
  period = NULL,
```

```
  dsntype = "SWD",
  mu0,
  mu1,
  marginal_mu = FALSE,
  sigma = NULL,
  tau = NULL,
  eta = NULL,
  AR = NULL,
  rho = NULL,
  gamma = NULL,
  psi = NULL,
  alpha_0_1_2 = NULL,
  CovMat = NULL,
  N = NULL,
  power = NULL,
  family = "gaussian",
  N_range = c(1, 1000),
  sig.level = 0.05,
  dfAdjust = "none",
  INDIV_LVL = FALSE,
  verbose = 1
)
```

Arguments

Cl	integer (vector), number of clusters per sequence group (in SWD), or number in control and intervention (in parallel designs)
timepoints	numeric (scalar or vector), number of timepoints (periods). If design is swd, timepoints defaults to length(Cl)+1. Defaults to 1 for parallel designs.
DesMat	Either an object of class 'DesMat' or a matrix indicating the treatment status for each cluster at each timepoint. If supplied, 'timepoints','Cl','trtDelay' are ignored.
trtDelay	numeric (possibly vector), value(s) between 0 and 1 specifying the proportion of intervention effect in the first (second ...) intervention phase.
incomplete	integer, either a scalar (only for SWD) or a matrix. A vector defines the number of periods before and after the switch from control to intervention that are observed. A matrix consists of 1's for observed clusterperiods and 0's for unobserved clusterperiods.
timeAdjust	character, specifies adjustment for time periods. One of the following: "factor", "linear", "none", "periodic". Defaults to "factor".
period	numeric (scalar)
dsntype	character, defines the type of design. Options are "SWD", "parallel" and "parallel_baseline", defaults to "SWD".
mu0	numeric (scalar), mean under control
mu1	numeric (scalar), mean under treatment

marginal_mu	logical. Only relevant for non-gaussian outcome. Indicates whether mu0 and mu1 are to be interpreted as marginal prevalence under control and under treatment, respectively, or whether they denote the prevalence conditional on random effects being 0 (It defaults to the latter). *(experimental!)*
sigma	numeric, residual error of cluster means if no N given.
tau	numeric, standard deviation of random intercepts
eta	numeric (scalar or matrix), standard deviation of random slopes. If ‘eta‘ is given as scalar, ‘trtMat‘ is needed as well.
AR	numeric, vector containing up to three values, each between 0 and 1. Defaults to NULL. It defines the AR(1)-correlation of random effects. The first element corresponds to the cluster intercept, the second to the treatment effect and the third to subject specific intercept. If only one element is provided, autocorrelation of all random effects is assumed to be the same. *Currently not compatible with ‘rho‘!=0 !*
rho	numeric (scalar), correlation of ‘tau‘ and ‘eta‘
gamma	numeric (scalar), random time effect
psi	numeric (scalar), random subject specific intercept. Leads to a closed cohort setting
alpha_0_1_2	numeric vector or list of length 2 or 3, that consists of alpha_0, alpha_1 and alpha_2. Can be used instead of random effects to define the correlation structure, following Li et al. (2018). When omitting alpha_2, this describes a cross-sectional design, where alpha_0 and alpha_1 define the intracluster correlation and cluster autocorrelation, respectively - as defined by Hooper et al. (2016).
CovMat	numeric, a positive-semidefinite matrix with (#Clusters · timepoints) rows and columns. If ‘CovMat‘ is given, ‘sigma‘, ‘tau‘, ‘eta‘, ‘rho‘, ‘gamma‘ and ‘psi‘ as well as ‘alpha_0_1_2‘ must be NULL.
N	numeric, number of individuals per cluster. Either a scalar, vector of length #Clusters or a matrix of dimension #Clusters x timepoints. Defaults to 1 if not passed.
power	numeric, a specified target power. If supplied, the minimal ‘N‘ is returned.
family	character, distribution family. One of "gaussian", "binomial". Defaults to "gaussian"
N_range	numeric, vector specifying the lower and upper bound for ‘N‘, ignored if ‘power‘ is NULL.
sig.level	numeric (scalar), significance level, defaults to 0.05
dfAdjust	character, one of the following: "none","between-within", "containment", "residual".
INDIV_LVL	logical, should the computation be conducted on an individual level? This leads to longer run time and is mainly for diagnostic purposes.
verbose	integer, how much information should the function return?

Details

Let $\theta := \mu_1 - \mu_0$ the treatment effect under investigation. The variance of the treatment effect estimator $\hat{\theta}$ can then be estimated via weighted least squares (see also vignette 'Getting Started').

Value

The return depends on the 'verbose' parameter. If 'verbose'=0, only the power is returned If 'verbose'=1 (the default), a list containing power and the parameters of the specific setting is returned. If requested (by 'verbose'=2) this list also contains relevant matrices.

Examples

```
## See also vignette for more examples
##
##
## stepped wedge design with 5 Clusters in 5 sequences,
## residual standard deviation 2,
## cluster effect sd = 0.33, and 10 individuals per cluster.
## Further, let the mean under the null and alternative hypothesis 0 and 1,
## respectively.
wlsPower(mu0=0, mu1=1, Cl=rep(1,5), sigma=2, tau=0.33, N=10)
##
##
## ... with auto-regressive cluster effect `AR=0.7`.
wlsPower(mu0=0, mu1=1, Cl=rep(1,5), sigma=2, tau=0.33, AR=0.7, N=10)
##
##
## ... with varying cluster size
wlsPower(mu0=0, mu1=1, Cl=rep(1,5), sigma=2, tau=0.33, N=c(12,8,10,9,14))
wlsPower(mu0=0, mu1=1, Cl=rep(1,5), sigma=2, tau=0.33,
              N=matrix(c(12,8,10,9,14,
                         11,8,10,9,13,
                         11,7,11,8,12,
                         10,7,10,8,11,
                          9,7, 9,7,11,
                          9,6, 8,7,11),5,6))
##
##
## ... with random treatment effect (with standard deviation 0.2),
## which is correlated with the cluster effect with `rho`=0.25.
wlsPower(mu0=0, mu1=1, Cl=rep(1,5), sigma=2, tau=0.33, eta=.2, rho=.25, N=10)
##
##
## ... with missing observations (a.k.a. incomplete stepped wedge design)
wlsPower(mu0=0, mu1=1, Cl=rep(1,5), sigma=2, tau=0.33, N=10, incomplete=3)
wlsPower(mu0=0, mu1=1, Cl=rep(1,5), sigma=2, tau=0.33, N=10,
             incomplete=matrix(c(1,1,1,0,0,
                                 1,1,1,1,0,
                                 1,1,1,1,1,
                                 1,1,1,1,1,
                                 0,1,1,1,1,
                                 0,0,1,1,1),5,6))
## -> the same.
##
## ... with two levels of clustering. This arises if the patients are
## observed over the whole  study period
## (often referred to as closed cohort design) or if subclusters exist
```

```
## (such as wards within clinics). For
mod_aggr  <- wlsPower(mu0=0, mu1=1, Cl=rep(1,5),
                         sigma=2, tau=0.33, psi=.25,
                         N=10, incomplete=3, verbose=2)
mod_indiv <- wlsPower(mu0=0, mu1=1, Cl=rep(1,5),
                         sigma=2, tau=0.33, psi=.25,
                         N=10, incomplete=3, verbose=2, INDIV_LVL=TRUE)
mod_aggr
mod_indiv
## Compare covariance matrices of first cluster
mod_aggr$CovarianceMatrix[1:6,1:6] ; mod_indiv$CovarianceMatrix[1:60,1:60]
##
##
## stepped wedge design with 5 Clusters in 5 sequences, residual sd = 2,
## cluster effect sd = 0.33. How many Individuals are needed to achieve a
## power of 80% ?
wlsPower(mu0=0, mu1=1, Cl=rep(1,5), sigma=2, tau=0.33, power=.8)
##
## ... How many are needed if we have a closed cohort design with a random
## individuum effect of .7?
wlsPower(mu0=0, mu1=1, Cl=rep(1,5), sigma=2, tau=0.33, psi=.7, power=.8)
##
##
## longitudinal parallel design, with 5 time periods, 3 clusters in treatment
## and control arm each.
wlsPower(mu0=0, mu1=1, Cl=c(3,3), sigma=2, tau=0.33, N=10,
              dsntype="parallel", timepoints=5)
##
##
##
## ... with one baseline period and four parallel periods
wlsPower(mu0=0, mu1=1, Cl=c(3,3), sigma=2, tau=0.33, N=10,
              dsntype="parallel_baseline", timepoints=c(1,4))
##
##
##
## cross-over design with two timepoints before and two after the switch
wlsPower(mu0=0, mu1=1, Cl=c(3,3), sigma=2, tau=0.33, N=10,
              dsntype="crossover", timepoints=c(2,2))
##
##
##
## stepped wedge design with 32 Individuals in 8 sequences, binomial outcome,
## 50% incidence under control, 25% incidence under interventional treatment.
## cluster effect sd = 0.5 (ICC of 1/3 under control),
## every individual is its own cluster.
## ... with incidences defined conditional on cluster effect=0
wlsPower(mu0=0.5, mu1=0.25, Cl=rep(4,8), tau=0.5, N=1,
             family="binomial")
##
##
## ... with  marginally defined proportions
wlsPower(mu0=0.5, mu1=0.25, Cl=rep(4,8), tau=0.5, N=1,
```

```
family="binomial", marginal_mu=TRUE)
```

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