The SAS %swdpwr Macro

Abstract:

The macro `%swdpwr` meets the needs of statistical power calculation for stepped wedge cluster randomized trials. Different parameters can be specified by users for different scenarios, including: cohort and cross-sectional settings, binary and continuous outcomes, marginal (GEE) and conditional (GLMM) methods, different link functions (identity, log, logit links), with and without time effect of treatment, etc. Technical details are given in Zhou et al. (2020) and Li et al. (2018).

Keywords: SAS, macro, statistical power, stepped wedge cluster design, cross-sectional, cohort study, repeated measures, correlation matrix, GEE, GLMM.

Contents

1. Description

This macro for statistical power calculations in stepped wedge cluster randomized trials is designed to use under the following scenarios:

1. Cohort and cross-sectional designs with/without time effect for continuous outcomes (`response=1`) supported by the marginal model (`model=2`) under linear link.
   1) For cohort designs, ICCs at three levels are not the same, satisfying $0 < \alpha_1 \leq \alpha_0 < 1, 0 < \alpha_1 \leq \alpha_2 < 1$. For cross-sectional designs, ICCs have $\alpha_1 = \alpha_2$.
   2) Time effect is specified by the value of `gammaJ`.
   3) `Sigma2` is a required argument for continuous outcomes.
2. Cohort and cross-sectional designs with/without time effect for binary outcomes (`response=2`) supported by the marginal model (`model=2`) under three link functions (`link=1,2,3`).
   1) For cohort designs, ICCs at three levels are not the same, satisfying $0 < \alpha_1 \leq \alpha_0 < 1, 0 < \alpha_1 \leq \alpha_2 < 1$. For cross-sectional designs, ICCs have $\alpha_1 = \alpha_2$.
   2) Time effect is specified by the value of `gammaJ`.
   3) Linear link (`link=1`), log link (`link=2`), logit link(`link=3`).
3. Cross-sectional designs with/without time effect for binary outcomes (`response=2`) supported by the conditional model (`model=1`) under three link functions (`link=1,2,3`).

1) For this cross-sectional model, ICCs at three levels are the same.
2) Time effect is specified by the value of `gammaJ`.
3) Linear link (`link=1`), log link (`link=2`), logit link(`link=3`).

4. Type I error can be specified to correct for multiple testing.

2. Invocation and details

You need to generate a dataset for the study design matrix via SAS data step. Please specify the name of each column (numofclusters, time1, time2, time3 etc.) for the header of the file.

The required and optional arguments for `%swdpwr` are summarized as follows:

```
%macro swdpwr
(
 I=, /*number of clusters*/
 J=, /*number of time steps*/
 K=, /*number of participants at each time step from every cluster*/
 dataset=, /*name of the generated SAS data set*/
 response=2,   /*choose continuous outcome(response=1) or binary
 outcome(response=2), with default value of 2*/
 model=2,   /*choose conditional model (model=1) or marginal
 model(model=2),with default value of 2*/
 link=1, /*choose link function (identity 1, log 2, logit 3),with default
 value of 1*/
 mu=, /*baseline effect in control groups*/
 beta=, /*treatment effect (the parameter we would like to test)*/
 gammaJ=0, /*time effect at time period J, with default value of 0*/
 sigma2=0,/* Marginal variance of the outcome (only needed by continuous
 outcomes)*/
 alpha=0.05, /*type one error rate,with default value of 0.05*/
 ICC0=0.1, /*Within-period correlation,alpha0,with default value of 0.1*/
 ICC1=ICC0/2, /*Inter-period correlation,alpha1, with default value of
 ICC0/2*/
 ICC2=, /*Within-individual,alpha2*/
 );
```

The objects returned are the summary features of the design as well as the power in this scenario.

3. Examples

Example 1: Comparing Standard of Care (HTN-Basic) to a new intervention (HTN-Plus) in a (**closed-cohort**) stepped wedge cluster randomized trial with a **continuous** outcome (eg. blood pressure). Participants will be enrolled into sites at baseline, and followed thereafter, with their blood pressure measured repeatedly.

The study design matrix `dataset` can be generated as follows:

```
data design2;
input numofclusters time1 time2 time3 time4;
cards;
6 0 1 1 1
6 0 0 1 1
6 0 0 0 1
;
run;
```

The model we utilized in this cohort trial is a GEE model specified in Li et al. (2018). Obtained the necessary parameters in practical settings, we get the power by calling the macro as:

```
%swdpwr(I = 18, J = 4, K = 15, dataset = design2, response = 1, model =
2, link = 1, mu = 0.3, beta = 0.098, gammaJ = 0.05, sigma2 = 0.06, alpha
= 0.05, ICC0 = 0.1, ICC1 = 0.05, ICC2 = 0.2)
```

We get power for 0.866 under this setting.

Example 2: Comparing Standard of Care (HTN-Basic) to a new intervention (HTN-Plus) in a (**closed-cohort**) stepped wedge cluster randomized trial with a **binary** outcome (eg. disease or not). Participants will be enrolled into sites at baseline, and followed thereafter, with their blood pressure measured repeatedly.

The study design matrix `dataset` can be generated as follows:

```
data design2;
input numofclusters time1 time2 time3 time4;
cards;
6 0 1 1 1
6 0 0 1 1
6 0 0 0 1
;
run;
```

The model we utilized in this cohort trial is a GEE model with **logit link** specified in Li et al. (2018). Obtained the necessary parameters in practical settings, we get the power by calling the macro as:

```
%swdpwr(I = 18, J = 4, K = 100, dataset = design2, response = 2, model =
2, link = 3, mu = 0.3, beta = 0.5, gammaJ = 0.01, alpha = 0.05, ICC0 =
0.1, ICC1 = 0.05, ICC2 = 0.2
```

We get power for 0.658 under this setting.

Example 3: The Tanzania PPIUD study utilized a stepped wedge design to assess the causal effect of PPIUD intervention on subsequent pregnancy. The **binary** outcome whether the participant is currently pregnant or has had a pregnancy that was terminated

will be obtained at 18 months postpartum. 6 hospitals were selected into the trial and the **cross-sectional** study lasted for 18 months with 4 time periods.

The study design matrix `dataset` can be generated as follows:

```
data PPIUD;
input numofclusters time1 time2 time3 time4;
cards;
3 0 1 1 1
3 0 0 0 1
;
```

A GLMM under **identity link** without time effects specified in Zhou et.al (2020) is employed for design. Obtained the necessary parameters in practical settings, we get the power by calling the macro as:

```
%swdpwr(I = 6, J = 4, K = 120, dataset = PPIUD, response = 2, model = 1,
link = 1, mu = 0.24, beta = -0.046, gammaJ = 0, alpha = 0.05, ICC0 = 0.15,
ICC1 = 0.15, ICC2 = 0.15)
```

We get power for 0.846 under this setting.

4. Warnings

When the input parameters such as correlation parameters, Type I error, and mean response for binary outcomes are out of range, an error message will return in the software. Here we list all scenarios that error might occur, and users could check the input parameters according to the error message and the suggestions about revision of them.

1. ICCs and Type I error have natural restrictions to be between 0 and 1.
2. The requirement that correlation matrix is positive-definite is violated when ICCs exceed plausible ranges. This error could occur for both types of outcomes in all models.
3. For binary outcomes, the marginal means limit the ranges of correlation (Qaqish 2013), thus we need additional restrictions for ICCs. This error occurs when they violate these restrictions.
4. For binary outcomes, the input parameters related to mean responses (mu, beta, gammaJ) may exceed the range for valid probability under identity and log link functions.

5. Reference

1) Zhou X, Liao X, Kunz LM, Normand ST, Wang M, Spiegelman D. A maximum likelihood approach to power calculations for stepped wedge designs of binary outcomes. *Biostatistics*. 2020;21(1):102-121.
2) Li F, Turner EL, Preisser JS. Sample size determination for GEE analyses of stepped wedge cluster randomized trials. *Biometrics*. 2018;74(4):1450-1458.
3) Qaqish B F. A family of multivariate binary distributions for simulating correlated binary variables with specified marginal means and correlations[J]. Biometrika, 2003, 90(2): 455-463.