

# Technical Appendix: Details on the Power Calculations for Two- and Three-level Models with Missing Data

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This vignette details how the power calculations are implemented in **powerlmm**. We will focus on the fully *nested* three-level model, since the two- and partially nested three-level model are just reduced forms of the three-level model. Thus, in standard multilevel notation the fully nested three-level model is

Level 1

$$Y_{ijk} = \beta_{0jk} + \beta_{1jk}t_{ijk} + R_{ijk}$$

Level 2

$$\beta_{0jk} = \gamma_{00k} + U_{0jk}$$

$$\beta_{1jk} = \gamma_{10k} + U_{1jk}$$

Level 3

$$\gamma_{00k} = \delta_{000} + \delta_{001}TX_k + V_{0k}$$

$$\gamma_{10k} = \delta_{100} + \delta_{101}TX_k + V_{1k}$$

where we have  $i = 1, \dots, n_{1j}$  equally spaced time points for subject  $j = 1, \dots, N_2$ , where  $N_2$  is the total number of subjects in the treatment arm. Furthermore, the subjects are nested within  $k = 1, \dots, n_3$  clusters, where  $n_3$  is the total number of clusters in the treatment arm. To allow for varying cluster sizes we let each cluster have  $j = 1, \dots, n_{2[k]}$  subjects, where  $n_{2[k]}$  is the total number of subjects in cluster  $k$ .

The parameter of interest is  $\delta_{101}$ , i.e. the mean difference in slopes between the two treatment groups. However, in **powerlmm** the calculations are simplified by calculating the variance of the slope-coefficient separately for each treatment group. Since the slopes in the treatment and control group are independent, the variance of the interaction-term is simply

$$V(\delta_{101}) = V(\delta_{100[t_x]} - \delta_{100[c]}) = V(\delta_{100[t_x]}) + V(\delta_{100[c]}),$$

where  $\delta_{100[t_x]}$  and  $\delta_{100[c]}$  are the fixed time effects in the treatment and control group respectively. In order to calculate the variances we begin by formulating the three-level model for the complete data vector  $\mathbf{Y}$  from a single treatment arm,

$$\mathbf{Y} = \mathbf{XZW}\boldsymbol{\beta} + \mathbf{Xu} + \mathbf{XZv} + \boldsymbol{\epsilon}, \quad (1)$$

where  $\mathbf{Y}$  is the  $N_1 \times 1$  outcome vector containing all the observations from all the subjects in the treatment arm,  $\mathbf{X}$  is a  $N_1 \times 2N_2$  matrix containing co-variate information for all  $N_2$  subjects in the treatment arm,  $\mathbf{X}$  is also used as the design matrix for the second-level random effects.  $\mathbf{Z}$  is a  $2n_3 \times 2N_2$  matrix containing the level-three random effects design matrices for each  $k$ th cluster in the treatment arm.  $\mathbf{W}$  is a  $2n_3 \times 2$  matrix relating the third-level to the overall effects  $\boldsymbol{\beta}$ , and here  $\boldsymbol{\beta}$  is simply a  $2 \times 1$  vector with the population values for the fixed intercept and slope effects. Lastly,  $\mathbf{u}$  is a  $2N_2 \times 1$  vector with the level two random effects,  $\mathbf{v}$  is a  $2n_3 \times 1$  vector with the third-level random effects, and  $\boldsymbol{\epsilon}$  a  $N_1 \times 1$  vector with the level one residuals.

The random effects and residuals are distributed as follows,

$$\begin{aligned}\mathbf{u} &\sim \mathcal{N}(\mathbf{0}, \boldsymbol{\Psi}_2), \\ \mathbf{v} &\sim \mathcal{N}(\mathbf{0}, \boldsymbol{\Psi}_3), \\ \boldsymbol{\epsilon} &\sim \mathcal{N}(\mathbf{0}, \sigma^2 \mathbf{I}_{N_1}).\end{aligned}$$

With the second and third level variance components being

$$\boldsymbol{\Psi}_2 = \mathbf{I}_{N_2} \otimes \begin{pmatrix} u_0^2 & u_{01} \\ u_{01} & u_1^2 \end{pmatrix}, \boldsymbol{\Psi}_3 = \mathbf{I}_{n_3} \otimes \begin{pmatrix} v_0^2 & v_{01} \\ v_{01} & v_1^2 \end{pmatrix},$$

with  $\otimes$  denoting the Kronecker product. The co-variate matrix  $\mathbf{X}$  is block-diagonal containing a sub-matrix  $\mathbf{X}_{jk}$  for each subject (level-two unit), thus

$$\mathbf{X} = \begin{pmatrix} \mathbf{X}_1 & 0 & \cdots & 0 \\ 0 & \mathbf{X}_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \mathbf{X}_{N_2} \end{pmatrix}.$$

Since each subject can have a different number of observations due to dropout, each  $\mathbf{X}_{jk}$  will have dimension  $n_{1[j]} \times 2$ , where  $n_{1[j]}$  is the total number of observations for subject  $j$  in cluster  $k$ ,

$$\mathbf{X}_{jk} = \begin{pmatrix} 1 & T_0 \\ 1 & T_1 \\ \vdots & \vdots \\ 1 & T_{n_{1[j]}} \end{pmatrix}. \quad (2)$$

$\mathbf{Z}$  is a block-diagonal matrix containing the level-three design matrices for each cluster  $k$ ,

$$\mathbf{Z} = \begin{pmatrix} \mathbf{Z}_1 & 0 & \cdots & 0 \\ 0 & \mathbf{Z}_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \mathbf{Z}_{n_3} \end{pmatrix}.$$

With the sub-matrices  $\mathbf{Z}_k$  being stacks of  $2 \times 2$  matrices for each subject in cluster  $k$ ,

$$\mathbf{Z}_k = \mathbf{1}_{n_{2[k]}} \otimes \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix},$$

thus the dimension of  $\mathbf{Z}_k$  will be  $n_{2[k]} \times 2$ , where  $n_{2[k]}$  is the number of subjects in cluster  $k$ . This enables power calculations for designs with varying number of subjects per cluster.

The matrix  $\mathbf{W}$ , relates the cluster-level effects to the overall effects  $\boldsymbol{\beta}$ ,

$$\mathbf{W} = \mathbf{1}_{n_3} \otimes \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix},$$

and thus  $\mathbf{XZW}$  simply stacks all the  $N_2$  sub-matrices,  $\mathbf{X}_{jk}$ , into a  $N_1 \times 2$  matrix.

Then we can calculate the marginal variance-covariance matrix for  $\mathbf{Y}$  as

$$\mathbf{V}(\mathbf{Y}) = \mathbf{X}\boldsymbol{\Psi}_2\mathbf{X}^\top + \mathbf{XZ}\boldsymbol{\Psi}_3\mathbf{Z}^\top\mathbf{X}^\top + \boldsymbol{\epsilon}^2\mathbf{I}_{N_1},$$

and the variance of the population parameters in  $\beta$  as

$$V(\beta) = [(\mathbf{XZ}\mathbf{W})^\top V(\mathbf{Y})^{-1} \mathbf{XZ}\mathbf{W}]^{-1}. \quad (3)$$

The lower right corner of  $V(\beta)$  corresponds to the variance of the time-coefficient. As we noted earlier we can use the slope variances to calculate the variance of the time $\times$ treatment-interaction.

## Accounting for dropout

Dropout is accounted for by defining a dropout vector  $\mathbf{D} = (p_1, \dots, p_{n_1})^\top$ , where  $p_i$  is the proportion of participants that have dropped out at time point  $i$ , for the  $i, \dots, n_1$  scheduled time points, and  $p_0 = 0$  and  $p_i \leq p_{i+1}$ . The default in **powerlmm** is to treat the values in  $\mathbf{D}$  as known, i.e. exactly  $p_i$  subjects will have dropped out at time  $i$ . This is done by randomly sampling which  $p_i N_2$  participants should drop out a time  $i$ , then adjusting their design matrices  $\mathbf{X}_{ij}$  to be of size  $(i - 1) \times 2$ , thus their last time point will be  $i - 1$ . Since, it is random which subjects will dropout, the power calculations will differ slightly each time. It is also possible to treat  $\mathbf{D}$  as random (using the option `deterministic_dropout = FALSE`), then dropout will be sampled from a multinomial distribution, by converting the elements of  $\mathbf{D}$  to the probability  $p_i$  that a subject will have exactly  $i$  measurements. This approach is similar to Galbraith, Stat, and Marschner (2002), and Verbeke and Lesaffre (1999) who presents power calculations for two-level models with missing data.

## Speeding up the computation of $V(\mathbf{Y})^{-1}$

Doing the matrix inversion of  $V(\mathbf{Y})$ , which is of dimension  $N_1 \times N_1$ , can be extremely slow for some designs. De Leeuw and Kreft (1986) (where they credit Swamy (1971)) noted a more computationally efficient formulation, adopting it to the three-level formulation in Equation 1, lets us write

$$V(\mathbf{Y})^{-1} = \sigma^{-2} [\mathbf{I}_{N_1} - \mathbf{X}(\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top] + \mathbf{X}(\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{A}^{-1} (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X},$$

where,

$$\mathbf{A}^{-1} = [\sigma^2 (\mathbf{X}^\top \mathbf{X})^{-1} + \boldsymbol{\Psi}_2 + \mathbf{Z} \boldsymbol{\Psi}_3 \mathbf{Z}^\top].$$

Here  $\mathbf{A}$  of size  $2N_2 \times 2N_2$ . However, since  $\mathbf{A}$  is block-diagonal, with each block for cluster  $k$  being of size  $n_{2[k]}$ , the computation done in **powerlmm**, takes advantage of the sparse matrix functions from the **Matrix**-package. By using sparse matrix algebra the speed of computing  $\mathbf{A}^{-1}$  will depend greatly on the number of subjects per cluster. In most cases this solution is dramatically faster then directly solving  $V(\mathbf{Y})^{-1}$ . For instance, calculating  $V(\beta)$  for a study with  $n_1 = 10$ ,  $n_2 = 30$ ,  $n_3 = 20$  is approximately 50 times faster using this method.

## Changes in powerlmm 0.2

As of version 0.2,  $V(\beta)$  is now computed using the sparse Cholesky factorization used in **lme4**, and the implementation specifically borrows from **lme4pureR**. Thus,

$$V(\beta) = \sigma^2 \mathbf{R}_X^{-1} (\mathbf{R}_X^\top)^{-1}$$

where  $\mathbf{R}_X$  is the Cholesky factor of the fixed effects, see Eq. 54 in Bates et al. (2015).

## Power

To make the power calculations accurate for small samples sizes, power is calculated using the  $t$  distribution. Thus, we can define the power function as,

$$1 - \beta = P(t_{\nu,\lambda} > t_{\nu,1-\alpha/2}) + P(t_{\nu,\lambda} < t_{\nu,\alpha/2}),$$

where  $\lambda$  is the non-centrality parameter,

$$\lambda = \delta_{101} / \sqrt{V(\delta_{101})},$$

and  $\nu$  is the appropriate degrees of freedom of the  $t$  distribution. For the balanced fully nested three-level model, the degrees of freedom are  $N3 - 2$ , where  $N3$  is the total number of clusters in both treatment arms.

## Satterthwaite's degrees of freedom approximation

For small samples, the choice of degrees of freedom will potentially influence the accuracy of the power analysis a lot. In **powerlmm** it is therefore possible to use Satterthwaite's DF approximation in the power analysis. The degrees of freedom of the  $t$  distribution is approximated as,

$$\nu = \frac{2(\mathbf{L}^\top \mathbf{V}(\boldsymbol{\beta}) \mathbf{L})^2}{V(\mathbf{L}^\top \mathbf{V}(\boldsymbol{\beta}) \mathbf{L})},$$

and  $\mathbf{L}$  specifies the linear contrast we are testing. Moreover,  $V(\mathbf{L}^\top \mathbf{V}(\boldsymbol{\beta}) \mathbf{L})$  is approximated using the delta method

$$V(\mathbf{L}^\top \mathbf{V}(\boldsymbol{\beta}) \mathbf{L}) \cong [\Delta_{f(\boldsymbol{\theta})}(\boldsymbol{\theta})]^\top V(\boldsymbol{\theta}) [\Delta_{f(\boldsymbol{\theta})}(\boldsymbol{\theta})],$$

$\Delta_{f(\boldsymbol{\theta})}(\boldsymbol{\theta})$  is the gradient of  $\mathbf{L}^\top \mathbf{V}(\boldsymbol{\beta}) \mathbf{L}$  with respect to  $\boldsymbol{\theta}$ , where  $\boldsymbol{\theta}$  is the vector of variance components, and thus  $V(\boldsymbol{\theta})$  is the asymptotic covariance matrix of the random effects (including  $\sigma^2$ ), which is approximated as  $V(\boldsymbol{\theta}) = 2\mathcal{I}_E^{-1}$ , where  $\mathcal{I}_E$  is the expected information matrix for the variance parameters. The calculation of  $\mathcal{I}_E$  is described in Equation 25 in Halekoh and Højsgaard (2014). However, this implementation involves manipulating  $V(\mathbf{Y})$ , i.e. the full variance-covariance matrix including all  $N$  observations. For large sample sizes this will be very computationally intensive, and the computation time will depend mostly on  $n_1$  and  $n_2$ . For instance, for a fully nested model with  $n_1 = 10$ ,  $n_2 = 100$ ,  $n_3 = 4$ , computations will likely take 30-60 seconds, and be very RAM intensive.

## Partially nested designs

For the partially nested designs  $V(\delta_{100[t,x]})$  is calculated as above, and  $V(\delta_{100[c]})$  by setting the cluster-level random effects to zero. Degrees of freedom for this model is trickier, and I *recommend always* using Satterthwaite DFs whenever possible. If balanced DFs are requested, then currently  $n_3 - 1$  is used, where  $n_3$  is the number of clusters in the treatment group only.

## Two-level designs

For the two-level designs,  $V(\delta_{101})$  can be calculated using the three-level formulas with the cluster-level random effects set to zero. Deleting these terms reduces the model to the classical two-level formulation. Degrees of freedom for the balanced model is  $N_2 - 2$ , where  $N_2$  is the total number of subjects in both treatment arms.

## Standardized formulation

If there's no missing data and the clusters sizes are balanced, the variance of the slope can be calculated more simply as

$$V(\delta_{100}) = \frac{\sigma^2 + n_1\sigma_{u_1}^2 V(\mathbf{t}) + n_1n_2\sigma_{v_1}^2 V(\mathbf{t})}{n_1n_2n_3V(\mathbf{t})},$$

with,

$$V(\mathbf{t}) = \sum_{i=1}^{n_1} (t_i - \bar{t})^2.$$

By defining the amount of slope variance at the cluster-level as  $\rho_s = \sigma_{v_1}^2 / (\sigma_{v_1}^2 + \sigma_{u_1}^2)$ , and  $\text{ICC\_pre\_subjects} = \rho_1 = (\sigma_{u_0}^2 + \sigma_{v_0}^2) / (\sigma_{v_0}^2 + \sigma_{u_0}^2 + \sigma_e^2)$ , and the variance ratio as  $r_\tau = (\sigma_{v_1}^2 + \sigma_{u_1}^2) / \sigma_e^2$  we can then rewrite the formula using the relative parameters  $\rho_1$ ,  $\rho_s$  and  $r_\tau$ ,

$$V(\delta_1^*) = \frac{(1 - \rho_1) + n_1 \text{Var}(\mathbf{t})(1 - \rho_1)[n_2\rho_sr + (1 - \rho_s)r]}{n_1n_2n_3\text{Var}(\mathbf{t})},$$

which will yield the same non-centrality parameters as long as the interaction-coefficient corresponds to the same standardized value, e.g. Cohen's d. Thus, we see that power depends on  $n_1$ ,  $n_2$ ,  $n_3$ , the duration of the study, the proportion of intercept variance at baseline, the amount of slope variance at the third level, and the variance ratio.

## References

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