

# Disinvestment example: code and output

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This document provides the code and output for model fitting for the disinvestment example presented in the main text. Data is available as a supplemental file (journal.pmed.1002412.s002.xlsx) for the paper published by Haines et al.<sup>1</sup> All calculations were done in R<sup>2</sup> version 3.6.1 with lme4<sup>3</sup> version 1.1-21.

## Set up data

```
#Load package for fitting mixed models  
library(lme4)
```

This data set contains information from two sequential SWTs; we're only examining the first one.

```
#Create a data set which contains only data from the first SWT  
study1 <- journal_pmed_1002412_s002[journal_pmed_1002412_s002$study1 == 1,]
```

Next, we prepare some variables to use in our model fitting.

```
#Create outcome: log length of stay, in days.  
study1$loglos <- log(study1$acute_los)  
#In this study, no_we_exposure is the treatment variable,  
#coded 1 when weekend services are removed (treatment) and 0 otherwise (control)  
study1$tx.var <- study1$no_we_exposure  
#Cluster ID, as a factor  
study1$cluster <- factor(study1$index_ward)  
#Time, as a factor; sw_step is the numerical time period ID (1 through 7)  
study1$time <- factor(study1$sw_step)  
#Interaction between time and cluster  
study1$clustime <- interaction(study1$cluster,study1$time)
```

## Fit models

Now, we fit the full model, random time model, and random treatment model. All warnings and messages are printed here.

### Full model

```
model.full <- lmer(loglos ~ sw_step + tx.var +  
                  (tx.var || cluster) + (1|clustime),data=study1)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(model.full)
```

```
## Linear mixed model fit by REML ['lmerMod']
```

```
## Formula:
```

```

## loglos ~ sw_step + tx.var + ((1 | cluster) + (0 + tx.var | cluster)) +
## (1 | clustime)
## Data: study1
##
## REML criterion at convergence: 42924.1
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -6.5606 -0.6783 -0.0015 0.6478 3.9854
##
## Random effects:
## Groups Name Variance Std.Dev.
## clustime (Intercept) 0.01368 0.1170
## cluster tx.var 0.00000 0.0000
## cluster.1 (Intercept) 0.07682 0.2772
## Residual 1.04670 1.0231
## Number of obs: 14834, groups: clustime, 84; cluster, 12
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 1.24562 0.08749 14.238
## sw_step -0.01499 0.01189 -1.261
## tx.var 0.12929 0.05454 2.371
##
## Correlation of Fixed Effects:
## (Intr) sw_stp
## sw_step -0.302
## tx.var 0.099 -0.761
## convergence code: 0
## boundary (singular) fit: see ?isSingular

```

## Random time model

```

model.time <- lmer(loglos ~ sw_step + tx.var +
  (1 | cluster) + (1|clustime),data=study1)

```

```

## Warning in checkConv(attr("opt", "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 0.00280268
## (tol = 0.002, component 1)

```

```

summary(model.time)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: loglos ~ sw_step + tx.var + (1 | cluster) + (1 | clustime)
## Data: study1
##
## REML criterion at convergence: 42924.1
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -6.5605 -0.6783 -0.0015 0.6478 3.9854
##
## Random effects:
## Groups Name Variance Std.Dev.
## clustime (Intercept) 0.01367 0.1169

```

```

## cluster (Intercept) 0.07680 0.2771
## Residual 1.04670 1.0231
## Number of obs: 14834, groups: clustime, 84; cluster, 12
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 1.24562 0.08747 14.240
## sw_step -0.01499 0.01188 -1.261
## tx.var 0.12929 0.05453 2.371
##
## Correlation of Fixed Effects:
## (Intr) sw_stp
## sw_step -0.302
## tx.var 0.099 -0.761
## convergence code: 0
## Model failed to converge with max|grad| = 0.00280268 (tol = 0.002, component 1)

```

## Random treatment model

```

model.treatment <- lmer(loglos ~ sw_step + tx.var +
                        (tx.var || cluster), data=study1)

```

```

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 0.00309531
## (tol = 0.002, component 1)

```

```

summary(model.treatment)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## loglos ~ sw_step + tx.var + ((1 | cluster) + (0 + tx.var | cluster))
## Data: study1
##
## REML criterion at convergence: 42987.5
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -6.4036 -0.6849 -0.0055 0.6495 3.9345
##
## Random effects:
## Groups Name Variance Std.Dev.
## cluster (Intercept) 0.078722 0.28057
## cluster.1 tx.var 0.009575 0.09785
## Residual 1.056125 1.02768
## Number of obs: 14834, groups: cluster, 12
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 1.245581 0.083440 14.928
## sw_step -0.010788 0.006492 -1.662
## tx.var 0.099265 0.041862 2.371
##
## Correlation of Fixed Effects:
## (Intr) sw_stp
## sw_step -0.168

```

```
## tx.var    0.031 -0.552
## convergence code: 0
## Model failed to converge with max|grad| = 0.00309531 (tol = 0.002, component 1)
```

## Compare fitted values

	Treatment effect	Treatment effect SE	Sigma	Tau	Gamma	Eta
Full model	0.129	0.055	1.023	0.277	0.117	0
Time model	0.129	0.055	1.023	0.277	0.117	NA
Treatment model	0.099	0.042	1.028	0.281	NA	0.098

## Addressing convergence messages

So far, for simplicity, we have been relying on all the default lme4 settings. However, even the two reduced models above have warnings that the model ‘failed to converge’. There are many things that can be done to improve convergence; here we simply use better starting values. In this case, this improves the fit enough to eliminate warning messages, but does not have a large impact on fitted values.

```
model.time.startingvals <- getME(model.time,c("theta","fixef"))
model.time.startingvals <- update(model.time,start=model.time.startingvals)
summary(model.time.startingvals)

## Linear mixed model fit by REML ['lmerMod']
## Formula: loglos ~ sw_step + tx.var + (1 | cluster) + (1 | clustime)
## Data: study1
##
## REML criterion at convergence: 42924.1
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -6.5606 -0.6783 -0.0015  0.6478  3.9854
##
## Random effects:
## Groups Name Variance Std.Dev.
## clustime (Intercept) 0.01368 0.1170
## cluster (Intercept) 0.07682 0.2772
## Residual 1.04670 1.0231
## Number of obs: 14834, groups: clustime, 84; cluster, 12
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 1.24562 0.08749 14.237
## sw_step -0.01499 0.01189 -1.261
## tx.var 0.12929 0.05453 2.371
##
## Correlation of Fixed Effects:
## (Intr) sw_stp
## sw_step -0.302
## tx.var 0.099 -0.761

model.treatment.startingvals <- getME(model.treatment,c("theta","fixef"))
model.treatment.startingvals <- update(model.treatment,start=model.treatment.startingvals)
```

```
summary(model.treatment.startingvals)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## loglos ~ sw_step + tx.var + ((1 | cluster) + (0 + tx.var | cluster))
## Data: study1
##
## REML criterion at convergence: 42987.5
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -6.4036 -0.6849 -0.0055  0.6495  3.9345
##
## Random effects:
##   Groups      Name                Variance Std.Dev.
## cluster  (Intercept)  0.078733  0.28059
## cluster.1 tx.var      0.009588  0.09792
## Residual                    1.056124  1.02768
## Number of obs: 14834, groups: cluster, 12
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  1.245584   0.083445  14.927
## sw_step      -0.010788   0.006492  -1.662
## tx.var        0.099261   0.041875   2.370
##
## Correlation of Fixed Effects:
##          (Intr) sw_stp
## sw_step -0.168
## tx.var   0.031 -0.552
```

Note that in practice, if a researcher believed the full model was appropriate they should also dedicate time and energy to improving the fit of that model (i.e. fitting a full model with nonzero variance components); in this case, the method of updating starting values is not sufficient. Further details are beyond the scope of this paper, but see Cheng et al.<sup>4</sup> for general guidance on improving model fit.

## References

1. Haines TP, Bowles K-A, Mitchell D, O'Brien L, Markham D, Plumb S, et al. Impact of disinvestment from weekend allied health services across acute medical and surgical wards: 2 stepped-wedge cluster randomised controlled trials. *PLoS Med.* 2017;14(10):e1002412.
2. R Core Team. *R: A language and environment for statistical computing.* Vienna, Austria: R Foundation for Statistical Computing; 2019.
3. Bates D, Maechler M, Bolker B, Walker S. Fitting Linear Mixed-Effects Models Using lme4. *Journal of Statistical Software.* 2015;67(1):1-48.
4. Cheng J, Edwards LJ, Maldonado-Molina MM, Komro KA, Muller KE. Real longitudinal data analysis for real people: building a good enough mixed model. *Stat Med.* 2010;29(4):504-520.