

Axel Mayer, Johannes Zimmermann, Jürgen Hoyer, Simone Salzer, Jörg Wiltink, Eric Leibling & Falk Leichsenring (2019) Interindividual Differences in Treatment Effects Based on Structural Equation Models with Latent Variables: An EffectLiteR Tutorial, Structural Equation Modeling: A Multidisciplinary Journal, DOI: 10.1080/10705511.2019.1671196

## Supplemental Materials

### Appendix A: Software Code

```
library(EffectLiteR) ## version number: 0.4-4
# d <- elrReadData("C:/PrivateData/Sophonet/sophonet_data_complete.rds") # real data
d <- sophonet_data_simulated # simulated data included in EffectLiteR

covs <- c("comorbid", "iip.lov", "iip.dom", "lsas.lt1", "bdi.lt1", "ecr.anx.lt1",
          "ecr.avoi.lt1", "hal", "tosca.shame.t1", "fskn.se.t1")
indicators <- list("lsas.lt2" = c("lsas.a.t2", "lsas.v.t2"),
                  "lsas.lt1" = c("lsas.a.t1", "lsas.v.t1"),
                  "bdi.lt1" = c("bdi.t1.i1", "bdi.t1.i2", "bdi.t1.i3"),
                  "ecr.anx.lt1" = c("ecr.anx.t1.i1", "ecr.anx.t1.i2", "ecr.anx.t1.i3"),
                  "ecr.avoi.lt1" = c("ecr.avoi.t1.i1", "ecr.avoi.t1.i2", "ecr.avoi.t1.i3"),
                  "hal" = c("tpq.ha.i1", "tpq.ha.i2", "tpq.ha.i3"),
                  "tosca.shame.t1" = c("tosca.shame.t1.i1", "tosca.shame.t1.i2"),
                  "fskn.se.t1" = c("fskn.se.t1.i1", "fskn.se.t1.i2"))

mm <- generateMeasurementModel(indicators=indicators, ncells=2)

model <- effectLite(y = "lsas.lt2", x = "tb", z = covs,
                   control = "CBT", data = d, missing = "fiml",
                   measurement = mm, homoscedasticity = FALSE)

model

## model with correction for multilevel structure (only works with real data)
# model2 <- effectLite(y = "lsas.lt2", x = "tb", z = covs,
#                      # control = "CBT", data = d, missing = "listwise",
#                      # measurement = mm, homoscedasticity = FALSE,
#                      # ids=~therap, fixed.cell=TRUE)
# model2
```

**Appendix B: Options in effectLite()**

y	Dependent variable (character string). Can be the name of a manifest variable or of a latent variable.
x	Treatment variable (character string) treated as categorical variable.
k	Vector of manifest variables treated as categorical covariates (character vector).
z	Vector of continuous covariates (character vector). Names of both manifest and latent variables are allowed.
data	A data frame.
method	Can be one of c("sem", "lm") and indicates which function is used to fit the model.
control	Value of x that is used as control group. If "default", takes the first entry of as.factor(x).
measurement	Measurement model. The measurement model is lavaan syntax (character string), that will be appended before the automatically generated lavaan input. It can be used to specify a measurement for a latent outcome variable and/or latent covariates. See also the example and <a href="#">generateMeasurementModel</a> .
fixed.cell	logical. If FALSE (default), the group sizes are treated as stochastic rather than fixed.
fixed.z	logical. If FALSE (default), the continuous covariates are treated as stochastic rather than fixed.
missing	Missing data handling. Will be passed on to sem or ignored for method="lm".
se	Type of standard errors. Will be passed on to sem or ignored for method="lm".
syntax.only	logical. If TRUE, only syntax is returned and the model will not be estimated.
interactions	character. Indicates the type of interaction. Can be one of "all (all interactions)", "2-way" (only two-way interactions), "X:K,X:Z" (only X:K and X:Z interactions), "X:K" (only X:K interactions), "X:Z" (only X:Z interactions), "none" (no treatment by covariate interactions, but potentially interactions between categorical and continuous covariates), or "no" (no interactions at all).
homoscedasticity	logical. If TRUE, residual variances of the dependent variable are assumed to be homogeneous across cells.
test.stat	character. Can be one of c("default", "Chisq", "Ftest") and indicates the statistic used for the hypothesis tests. The tests are either based on the large sample Chi-Squared statistic (Wald tests) or the finite sample F statistic with approximate F distribution. The default setting for method="sem" is "Chisq" and the default setting for method="lm" is "Ftest".
propscore	Vector of covariates (character vector) that will be used to compute (multiple) propensity scores based on a multinomial regression without interactions. Alternatively, the user can specify a formula with the treatment variable as dependent variable for more control over the propensity score model.
ids	Formula specifying cluster ID variables. Will be passed on to <a href="#">lavaan.survey</a> . See svydesign for details.

weights	Formula to specify sampling weights. Currently only one weight variable is supported. Will be passed on to <a href="#">lavaan.survey</a> . See <code>svydesign</code> for details. Note: Only use weights if you know what you are doing. For example, some conditional treatment effects may require different weights than average effects.
add	Character string that will be pasted at the end of the generated lavaan syntax. Can for example be used to add additional (in-) equality constraints or to compute user-defined conditional effects.
...	Further arguments passed to <a href="#">sem</a> .