

CoTiMA User's Guide:  
A package for R to perform  
Continuous Time Meta-Analysis

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# 1 General description

Continuous time meta-analysis (CoTiMA) performs meta-analyses of correlation matrices of repeatedly measured variables. Since variables are measured at discrete time points (e.g., today at 4pm, next week on Monday etc.) this imposes a problem for meta-analysis of longitudinal studies because the time intervals between measurement could vary across studies. However, so-called continuous time math can be used to extrapolate or interpolate the results from all studies to any desired time interval. By this, effects obtained in studies that used different time intervals can be meta-analyzed<sup>1</sup>.

A critical assumption is the validity of the underlying causal model that describes the investigated process. CoTiMA is based on a rather general model, which can be restricted on demand. For instance, for a causal system that describes how a single variable that is measured repeatedly (e.g.,  $x_1$ ,  $x_2$ ,  $x_3$ , etc.) develops over time, the default CoTiMA model assumes that  $x_1$  affects  $x_2$ ,  $x_2$  affects  $x_3$  and so forth. This is called a first order autoregressive structure. In a two-variable model of  $x$  and  $y$ , the underlying CoTiMA model is a cross-lagged model with autoregressive effects for  $x$  and  $y$  and, in addition, a cross-lagged effect of  $x_t$  on  $y_{t+1}$  and of  $y_t$  on  $x_{t+1}$ . More complex models (e.g., including  $x_t$  on  $y_{t+1}$  and  $x_t$  on  $y_{t+2}$ ) can also be meta-analyzed, but they require user-specific adaptations. Restricted versions of the default CoTiMA model (e.g.,  $x_t$  on  $y_{t+1}$  but not  $y_t$  on  $x_{t+1}$ ) are easier to implement and several specific models (e.g.,  $x_t$  on  $y_{t+1}$  exactly of the same size as  $y_t$  on  $x_{t+1}$ ) could be optionally requested. Correlations of primary studies serve as an input for CoTiMA and synthesized (i.e., meta-analytically aggregated) effect sizes represent the output of CoTiMA.

```
library(devtools)
install_github('CoTiMA/CoTiMA')
library(CoTiMA)
```

Figure 1: Installing CoTiMA from GitHub

CoTiMA is a package for R (R Core Team, 2020). It can be downloaded from CRAN (<https://cran.r-project.org>) using `install.packages('CoTiMA')`. After the devtools R package is installed (`install.packages('devtools')`), the latest version of the R package CoTiMA can be installed from our GitHub repository (Dormann & Homberg, 2020) using the code shown in Figure 1. All code and examples shown in the User's Guide were performed and tested with R version 4.1.0 and run using RStudio (RStudio Team, 2021).

The next six pages show how to conduct a CoTiMA. This involves several

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<sup>1</sup>In a nutshell, CoTiMA fits models to empirical data using the structural equation model (SEM) package `ctsem`. The effects specified in a SEM are related (constrained) to parameters that are not directly included in the model (i.e., *continuous time parameters*; together, they represent the *continuous time structural equation model*, CTSEM) which is done in a fashion similar to other SEM programs (e.g., like  $a = b \times c$  to test for mediation in MPLUS) using matrix algebra functions (e.g., matrix exponentiation, which is not available in MPLUS), and statistical model comparisons and significance tests are performed on the continuous time parameter estimates. For details see Dormann, Guthier, and Cortina (2020).

steps starting with entering primary study information (correlations etc.), initial fitting of a ctsem model to each primary study, fitting the CoTiMA, and plotting the results<sup>2</sup>.

## 2 A CoTiMA Example

To prepare a CoTiMA, users have to supply information about the primary studies to be meta-analyzed. Primary study information has to be stored into ‘objects’ (everything in R is an object). Some objects have pre-defined names and are either always mandatory (`delta_ti`), mostly mandatory (`sampleSizei`, `empcovi`), or optional (`pairwiseNi`, `studyNumberi`, `moderatori`, etc., with *i* indicating the study number). User-defined object names could be added (e.g., `criticalRemarki`).

```
empcov2 <- matrix(c(1.00, 0.45, 0.57, 0.18,
                   0.45, 1.00, 0.31, 0.66,
                   0.57, 0.31, 1.00, 0.40,
                   0.18, 0.66, 0.40, 1.00), nrow=4, ncol=4)

delta_t2 <- 12
sampleSize2 <- 148

empcov3 <- matrix(c(1.00, 0.43, 0.71, 0.37,
                   0.43, 1.00, 0.34, 0.69,
                   0.71, 0.34, 1.00, 0.50,
                   0.37, 0.69, 0.50, 1.00), nrow=4, ncol=4)

delta_t3 <- 12
sampleSize3 <- 88

empcov313 <- matrix(c(1.00, 0.38, 0.54, 0.34, 0.60, 0.28,
                    0.38, 1.00, 0.34, 0.68, 0.28, 0.68,
                    0.54, 0.34, 1.00, 0.47, 0.66, 0.39,
                    0.34, 0.68, 0.47, 1.00, 0.38, 0.72,
                    0.60, 0.28, 0.66, 0.38, 1.00, 0.38,
                    0.28, 0.68, 0.39, 0.72, 0.38, 1.00), nrow=6, ncol=6)

delta_t313 <- c(1.5, 1.5)
sampleSize313 <- 335
```

Figure 2: Entering information of three primary studies

The present example of a small but nevertheless full CoTiMA is based on two variables (Variable 1 = V1, Variable 2 = V2). They were measured in three primary studies. The cross-lagged effects of earlier V1 on later V2 (*V1toV2*) and

<sup>2</sup>When it is desired, all R objects created in the following examples (e.g., `empcov2`, `delta_t2`, etc. in Figure 2 or `CoTiMAstudyList_3` in Figure 3) can be created in the user’s R environment in two ways. First, the code could be copied directly from this User Guide and then run. Second, the objects are ‘invisible’ but actually available in the package:CoTiMA environment. For example, `empcov2 <- empcov2` copies `empcov2` into the global environment. Afterwards, `rm(empcov2)` removes `empcov2` from the global environment, but it still available in the package:CoTiMA environment. Objects that are available in the package:CoTiMA environment only, but not in the global environment, are not used when the user performs any CoTiMA analyses.

vice versa (*V1toV2*) are meant to be meta-analyzed. The first two studies, which are numbered '2' and '3' in our database, both comprise two variables measured at two measurement occasions, which are represented in a correlation matrix with four rows (`nrow=4`) and four columns (`ncol=4`; i.e., a  $4 \times 4$  correlation matrix; see Figure 2). The correlations reported in primary studies are stored in the objects `empcov2` and `empcov3`, respectively. The third Study 313 has three waves of measurements and the empirical correlation matrix of Study 313 has, therefore,  $6 \times 6$  entries. The order of the variables has to be V1 at Time 0, V2 at Time 0, V1 at Time 1, and V2 at Time 1 etc. Note that in the continuous time literature it is common to number time points starting with 0. In the automatically generated output files, these two variables are labeled "V1" and "V2". The matrices have to be symmetric. Lack of symmetry is automatically detected by CoTiMA, a warning is issued, and processing is interrupted.

In addition to correlation matrices, a CoTiMA requires further information. Researchers need to provide time intervals (`delta_ti`) and sample sizes (`sampleSizei`). Primary Study 2 has a time lag of 12 months, which is stored in the object `delta_t2` (see Figure 2). One could also use 1.0 to indicate a 1.0 year lag. Any time scale is possible, but it has to be used consistently across primary studies. It is recommended using a time scale that allows assigning a value of 6 or less to the longest of all time intervals. For example, if the longest time lag was 10 years, it is recommended to use the number of 5-year intervals as the time scale, and to assign the value 2 to `delta_ti` if Study *i* had a 10-year interval. Since Study 313 had three waves of observations, the corresponding two time intervals have to be provided as vector (`delta_t313 <- c(1.5, 1.5)`).

Primary Study 2 further had a sample size of 148, which is stored in the object `sampleSize2` (not `sampleSize02`). In cases, in which correlation matrices include correlations based on pairwise deletion of missing values, sample sizes vary between correlations, too. This could be specified as explained later.

```
activeDirectory <- "/Users/cdormann/CoTiMA Users Guide/"
CoTiMAstudyList_3 <- ctmaPrep(selectedStudies = c(2, 3, 313),
                               activeDirectory=activeDirectory)
```

Figure 3: Compiling a list of primary studies (`ctmaPrep`)

After all primary study information was entered, the next step is to compile them into a list<sup>3</sup> and store this list as an R object. This is done with the `ctmaPrep` function included in CoTiMA. The created list object (e.g., `CoTiMAstudyList_3` in Figure 3) could be inspected as we shall see later. For the moment, it is sufficient to just have it available. Note that all functions provided by the CoTiMA R package start with 'ctma' such as `ctmaPrep`. In general, we label the objects to store the results delivered by the ctma-functions starting with "CoTiMA", such as `CoTiMAstudyList_3`.

<sup>3</sup>A list is a particular R object that is useful to collect a variety of information such as values, vectors, matrices, names etc.)

```

activeDirectory <- "/Users/cdormann/CoTiMA Users Guide/"
coresToUse = 1 # SET THIS TO 1 INSTEAD OF -1 IF YOU ARE USING WINDOWS

CoTiMAInitFit_3 <- ctmaInit(primaryStudies = CoTiMAstudyList_3,
                           n.latent = 2,
                           activeDirectory = activeDirectory,
                           coresToUse = coresToUse)

summary(CoTiMAInitFit_3)
saveRDS(CoTiMAInitFit_3, paste0(activeDirectory, "CoTiMAInitFit_3.rds"))

```

Figure 4: Fitting a ctsem model to each primary study (ctmaInit).

After a list of primary study information has been compiled with `ctmaPrep`, the next step is to fit a ctsem model to each primary study in a series of separate models. This step is mandatory for subsequent CoTiMA for several reasons. One of the most important reason is that at this stage one could check the results and identify possible problems with the data entered.

The use of `ctmaInit` is shown in Figure 4. Before using `ctmaInit`, specify the `activeDirectory` (where to save results) and the number of computer cores to be used (-1 indicates all cores except 1). This can then be used in all subsequent function calls. `ctmaInit` requires the number of latent variables per measurement occasion (in most cases probably identical to the overall number of variables) to be provided by the user as well as an `activeDirectory`, which is where `ctmaInit` saves the fitted models. In this case, the fitted models are stored in an Init-Fit object named `CoTiMAInitFit_3`, which can be saved to disk with `saveRDS`. Using `summary(CoTiMAInitFit_3)` displays the results, of which we selected the most interesting results in Figure 5<sup>4</sup>, <sup>5</sup>.

|                 |                          |           |           |          |          |    |
|-----------------|--------------------------|-----------|-----------|----------|----------|----|
| ##              |                          |           | V1toV1    | SE       | V2toV1   | SE |
| ## Study No 2   | "Reference not provided" | "-0.0537" | "0.0111"  | "0.0117" | "0.0105" |    |
| ## Study No 3   | "Reference not provided" | "-0.0323" | "0.0134"  | "0.0049" | "0.0106" |    |
| ## Study No 313 | "Reference not provided" | "-0.4126" | "0.0452"  | "0.1453" | "0.0376" |    |
| ##              | V1toV2                   | SE        | V2toV2    | SE       |          |    |
| ## Study No 2   | "-0.0202"                | "0.009"   | "-0.0254" | "0.0078" |          |    |
| ## Study No 3   | "0.0102"                 | "0.0097"  | "-0.0358" | "0.0097" |          |    |
| ## Study No 313 | "0.0939"                 | "0.0377"  | "-0.2823" | "0.0359" |          |    |

Figure 5: ctsem results (`summary(CoTiMAInitFit_3)`).

<sup>4</sup>Note that if computations are reproduced, the results are unlikely to be exactly the same because parameters and their standard errors are drawn from 1.000 parameter samples by default for final results computation. Using the argument `finishsamples = 10000` or larger numbers would make results reproducible with any desired precision.

<sup>5</sup>Note that CoTiMA could handle a range of time intervals by default; we have experienced few problems with time intervals from .01 to 16. However depending on the time scale used, one has to use the argument `scaleTime = 1/t`, with  $t$  being a reasonable number. For instance, suppose one's time scale is one week. An average year has  $(365.25)/4 = 52.1786$  weeks. If the longest time interval among the primary studies was 16years, this would correspond to  $\text{delta\_ti} = 834.8576$ . Using `scaleTime = 1/52.1786` would probably ensure getting proper results. Contrary, without adapting the time scale, one would probably see several warning or error messages during the fitting process, and the results should not be trusted.

The output shown in Figure 5 displays the so-called drift effects. The two auto effects (*V1toV1* & *V2toV2*) are negative as one would expect in continuous time modeling - we explain this later in Section 6. The two cross effects are mostly positive. Note that an effect is regarded as significant if its size is more than 1.96 times its standard error (*SE*). However, confidence intervals (or credible intervals in case Bayesian estimation is chosen) are easily available, too, and should be preferred. All of this – and a bit more – is displayed after entering `summary(CoTiMAInitFit_3)`. We do not show the output here due to space reasons. The study numbers are repeated as row names. “Reference not provided” just indicates that, yes, we did not provide a reference for each study, which would improve readability of the table. We explain later how to provide references for labeling the output.

The fit object `CoTiMAInitFit_3` resulting from applying the `ctmaInit` function to the list of compiled studies `CoTiMAstudyList_3` can then be used for aggregating (i.e., meta-analyzing) drift effects, performing moderator analyses, estimating publication bias, calculation of expected power and required samples sizes for different time intervals, plotting, and much more. In virtually all cases, the CoTiMA functions to perform these tasks take `CoTiMAInitFit_3` as the first (and only required) argument.

A full CoTiMA, with ‘full’ indicating that all drift parameters are simultaneously aggregated, is conducted by the code in Figure 6. Note that the `activeDirectory` is copied from `CoTiMAInitFit` if not provided as an argument to `ctmaFit`.

```
CoTiMAFullFit_3 <- ctmaFit(ctmaInitFit = CoTiMAInitFit_3,
                          coresToUse = coresToUse)
summary(CoTiMAFullFit_3)
```

Figure 6: Conducting a full CoTiMA (`ctmaFit`)

The summary function displays a couple of results that we present here in reduced form and in two subsequent steps. Results not shown here are explained later in Section 7.

We reduced the `$estimates` section in Figure 7 compared to the actual output displayed on screen. Reason is that among the whole lot of estimates presented, only the four drift effects are of major interest. These are the meta-analytically aggregated effects as indicated by the additional label ‘invariant’. Invariant means that this effect does not vary among primary studies and only one overall effect is estimated. This is similar to fixed effect analysis, where it is also assumed that a single overall (true) effect exists. This is what one usually wants from CoTiMA. We are done. All drift effects are significant by means of the T-values as well as by virtue of their confidence intervals.

The second part of the output generated by `summary(CoTiMAFullFit_3)` is shown in Figure 8. It displays the minus 2 loglikelihood (-2ll) value and the number of estimated parameters (both are important if researchers want to compare nested models), and the optimal lag sensu Dormann and Griffin (2015), across which the effects become largest. The previous output in Figure

|                             | row | col | Mean    | sd     | 2.5%    | 50%     | 97.5%   | Tvalues |
|-----------------------------|-----|-----|---------|--------|---------|---------|---------|---------|
| ## DRIFT V1toV1 (invariant) | 1   | 1   | -0.3867 | 0.0464 | -0.4841 | -0.3841 | -0.3024 | -8.3280 |
| ## DRIFT V2toV1 (invariant) | 1   | 2   | 0.2291  | 0.0327 | 0.1657  | 0.2289  | 0.2942  | 7.0092  |
| ## DRIFT V1toV2 (invariant) | 2   | 1   | 0.1158  | 0.0350 | 0.0468  | 0.1156  | 0.1841  | 3.3087  |
| ## DRIFT V2toV2 (invariant) | 2   | 2   | -0.1378 | 0.0341 | -0.2142 | -0.1341 | -0.0824 | -4.0385 |

Figure 7: First part of summary(CoTiMAFullFit\_3)

```
## $minus211
## [1] 7325.971
##
## $n.parameters
## [1] 22
##
## $opt.lag
##      [,1] [,2]
## [1,]    NA    6
## [2,]    6   NA
##
## $max.effects
##      [,1] [,2]
## [1,]    NA 0.3656
## [2,] 0.1848    NA
```

Figure 8: Second part of summary(CoTiMAFullFit\_3)

7 informed us that the effect of *V1toV2* is located in Row 2 and Column 1 and, conversely, the effect of *V2toV1* is located in Row 1 and Column 2. In this case, the optimal lag is six months for both effects, where the effects (see `$max.effects`) become .3669 for *V2toV1* and .1850 for *V1toV2*. The latter seems to be much smaller than the former, and we explain later how to test this statistically.

Effects in continuous time are difficult to interpret. Therefore, they are usually back-translated into discrete time. More specifically, they are usually back-translated into the cross-lagged regression coefficients that can be expected across a range of different time intervals. This is achieved when plotting a CoTiMA fit object (or several of the CoTiMA fit objects in the same plot).

```
plot(ctmaFitList(CoTiMAInitFit_3, CoTiMAFullFit_3),
     timeUnit="Months",
     timeRange=c(1, 144, 1) )
```

Figure 9: Plotting a Full CoTiMA (plot)

Figure 9 shows how to plot both the effects of the three separately fitted primary studies and the aggregated effect into single figures. Actually, since there are four effects (auto effect *V1toV1*, auto effect *V2toV2*, cross effect *V1toV2*, and cross effect *V2toV1*), four figures will be created. To tell the plot function that these are multiple CoTiMA fit objects, they have to be combined using the CoTiMA function `ctmaFitList`. For labeling of the x-axis the time unit is specified by `timeUnit="Months"` ranging from 1 to 144 in 1-month steps (the smaller the steps, the smoother the plot). For the effect *V2toV1*, the resulting



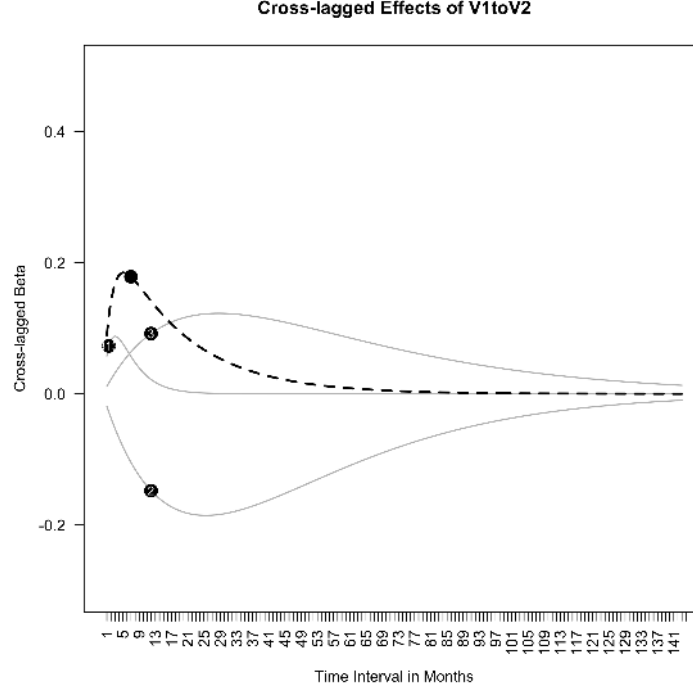


Figure 10: The cross-lagged effect  $V1toV2$  across 1 to 144 months.

plot is shown in Figure 10.

As can be seen, the dashed black line that represents the aggregated effect reaches its maximum across time intervals of 6 month, where it can be expected to be .3669 (see Figure 8), and then becomes smaller eventually approaching zero. It is noteworthy, albeit not occurring very often and probably limited to CoTiMAs with very few primary studies, that the aggregated effect does not always have to be somewhere in between the smallest and largest effects observed among the primary studies. CoTiMA does not aggregate by taking a (weighted) average of single effects. Rather, it optimizes estimates of all effects simultaneously by minimizing the loglikelihood value of the fit function, and the single set of the two auto effects and the two cross effects best explains the observed correlations across the three primary studies.

CoTiMA could be used for much more than demonstrated up to this point. Capabilities include traditional fixed and random effects analyses, analyses of publication biases, assessing heterogeneity, comparing effect sizes within models, moderator analysis, and analysis of statistical power. However, for CoTiMA like for any kind of meta-analysis, the most time consuming work is data collection and data management. Therefore, the two next sections deal with this topic. We make several recommendations of how to proceed and we introduce further functions and capabilities of CoTiMA which could make the life of a meta-

analyst more convenient. Subsequent sections then address additional types of analyses that could be conducted after a full CoTiMA.

### 3 EPIC-BiG-Power: A Recommended CoTiMA Workflow

Our recommended CoTiMA workflow can be summarized with the acronym EPIC-BiG-Power, which stands for **E**xtract, **P**repare, **I**nitFit, **C**oTiMAs, **B**ias & **G**eneralizability, and statistical **P**ower.

1. **EPIC**: **E**xtract correlations from the literature and save them to disk. There are no particular `ctma`-function available supporting this step. It is hard work! We make some suggestions in Section 4.
2. **EPIC**: In a **P**reparatory step, combine variables, correct correlations, add further study information, and add raw data if available. Finally, combine all information by compiling a 'list' of primary studies to be used for subsequent analysis using `ctmaPrep` (and `ctmaEmpCov` if useful). This is elaborated in Section 5.
3. **EPIC**: Perform a series of Initial fits, in which each primary study out of the list of primary studies is used to fit a `ctsem` model using `ctmaInit`. This is demonstrated in Section 6.
4. **EPIC**: The fit object delivered in Step 3 is typically used to perform a CoTiMA using `ctmaFit`. This is the core of CoTiMA!
  - (a) We show how to perform a full CoTiMA in Subsection 7.1, in which an entire drift matrix is aggregated.
  - (b) In Subsection 7.2 a partial CoTiMA is demonstrated, in which subsets of drift coefficients are aggregated.
  - (c) To address the question whether two (or more) drift effects (e.g., the 2 cross effects) estimated in Step 4(b) are identical, or if one effect is significantly larger than the other one, use the CoTiMA fit object delivered in Step 4(b) and `ctmaEqual` to test this, and see Subsection 7.3 for details.
  - (d) To address the question whether one (or more) drift effects are moderated by certain characteristics of the primary studies (e.g., the year when they were published), use the CoTiMA fit object delivered in Step 3 and `ctmaFit` to test this. See Subsection 7.4.
5. **BiG**: Analysis of publication **B**ias including possible corrections can also be performed. Further, various measure of heterogeneity, which allow answering the question if effects could be **G**eneralized, are reported. This also involves z-curve analysis. Classical fixed and random effects of each single drift effect (not as a set) are estimated, too. Use the CoTiMA fit

object delivered in Step 3 and `ctmaBiG` to test this. This is demonstrated in Section 8.

6. **Power:** Calculation of the statistical (post hoc) **Power** of the cross effects in each primary study (using the CoTiMA results as true effect estimates) as well as required sample sizes for future studies using a range of different time intervals could be performed, using by the CoTiMA fit object delivered in Step 3 and `ctmaPower`. This is demonstrated in Section 9.
7. Results of the different analyses could be plotted with `plot(CoTiMaFitObjects)`. Funnel and forest plots will be created if `CoTiMaFitObjects` is a CoTiMA fit object delivered by `ctmaBiG`. Plots of required sample sizes are delivered if `CoTiMaFitObjects` is a CoTiMA fit object delivered by `ctmaPower`. Discrete time cross-lagged and autoregressive effect size plots will be created if `CoTiMaFitObjects` is a CoTiMA fit object delivered by `ctmaInit` or `ctmaFit`. This is demonstrated throughout Section 6 – Section 9.

## 4 Extraction of Correlations from the Literature

In the previous example, we used only the mandatory objects (`delta_ti`) and objects that are probably required in most instances (`sampleSizei`, `empcovi`). We show later how data management can be improved by using further objects. This section starts, however, with some recommendations and helpful functions that can make data entry easier and that offer new possibilities.

One of the most laborious steps is entering the correlation matrices of primary studies. Although it would be less laborious to enter only lower triangular correlation matrices, the requirement to have full correlation matrices serves to double check if correlations are entered correctly. Small typographical errors could have large consequences such as time-consuming and poor convergence in fitting the model to the data. Although it is preferred to analyze correlation matrices in meta-analyses rather than covariances, the option to analyze covariances is available; CoTiMA automatically switches to the analysis of covariances if vectors of variances (`empVari`) are provided. This is, however, not recommended because different variances imply that effect sizes between studies are on different scales, making aggregated effects impossible to interpret. Similarly, empirical mean values for all variables (`empMeansi`) could be provided, but we do address these possibilities here.

Figure 11 shows an example of how to enter and save correlation matrices. We recommend entering them as they are published and not change any signs or skip variables. This could be easily done later. Although it is no formal requirement, we also recommend labeling the variables (i.e., the row names and column names of the matrices) as they are labelled by the authors of the primary studies. The correlation matrices including the labels are then saved. For demonstration purposes, we change the original matrix by deleting one variable from the matrix shown in Figure 11. In the original study (Childs &

```

empcov128 <- matrix(c(
  1.00, 0.48, 0.50,      0.50, 0.43, 0.40, 0.39, -0.51, -0.45,
  0.48, 1.00, 0.17,      0.23, 0.22, 0.00, 0.01, -0.10, -0.08,
  0.50, 0.17, 1.00,      0.63, 0.42, 0.45, 0.44, -0.52, -0.41,

  0.50, 0.23, 0.63,      1.00, 0.65, 0.59, 0.50, -0.50, -0.37,
  0.43, 0.22, 0.42,      0.65, 1.00, 0.49, 0.64, -0.41, -0.41,
  0.40, 0.00, 0.45,      0.59, 0.49, 1.00, 0.75, -0.54, -0.46,
  0.39, 0.01, 0.44,      0.50, 0.64, 0.75, 1.00, -0.48, -0.57,
  -0.51, -0.10, -0.52,   -0.50, -0.41, -0.54, -0.48, 1.00, 0.70,
  -0.45, -0.08, -0.41,   -0.37, -0.41, -0.46, -0.57, 0.70, 1.00), 9, 9)

pairwiseN128 <- matrix(c(
  100, 99, 88,      77, 66, 55, 44, 33, 22,
  99, 99, 99,      88, 77, 66, 55, 44, 33,
  88, 99, 88,      99, 88, 77, 66, 55, 44,

  77, 88, 99,      77, 99, 88, 77, 66, 55,
  66, 77, 88,      99, 66, 99, 88, 77, 66,
  55, 66, 77,      88, 99, 55, 99, 88, 77,
  44, 55, 66,      77, 88, 99, 44, 99, 88,
  33, 44, 55,      66, 77, 88, 99, 33, 99,
  22, 33, 44,      55, 66, 77, 88, 99, 22), 9, 9)

variableNames128 <- c("SPP_1", "SOP_1",
  "role stress_1",
  "exhaustion_1", "exhaustion_2",
  "cynicism_1", "cynicism_2", "efficacy_1", "efficacy_2")

dimnames(empcov128) <- list(variableNames128, variableNames128)
saveRDS(empcov128, file=paste0(activeDirectory, "empcov128.rds"))
saveRDS(pairwiseN128, file=paste0(activeDirectory, "pairwiseN128.rds"))

```

Figure 11: Entering correlation matrices

Stoeber, 2012, Study 1), the variable ‘role stress\_2’ was available, but sometimes researchers do not measure all variable at all time points. When conducting a CoTiMA one has to deal with missing data (correlations) then. To demonstrate how this could be achieved, we deleted ‘role stress\_2’ from the original matrix, which we visualize in Figure 11 by blanks after the column and row containing the correlations for ‘role stress\_1’.

A further possible challenge for CoTiMA are correlation matrices reported in primary studies that are based on pairwise deletion of missing values. One possible problem is that such matrices might not be suited at all for analysis if they or not positive definite. This cannot happen with listwise deletion. A not positive definite matrix is given, for example, if the correlation between A and B is  $r = .90$ , between A and C  $r = .80$ , and between B and C  $r = .10$  - given the two large correlations, such a small correlation is impossible if all correlations are based on identical samples. If a matrix is not positive definite, we recommend contacting the authors of the primary study and ask for a correlation matrix based on listwise deletion, or for raw data. Another option is to drop one or more variables from the correlation matrix. One could check if the matrix is positive definite after dropping variables; the code `eigen(empcov128)$values` should deliver only positive eigenvalues then.

A second challenge resulting from pairwise deletion of missing values in primary studies is the sample size to be used for CoTiMA. Sometimes, authors report the range of pairwise  $N$  (e.g., pairwise  $N = 22$  to 100) in a table note. We recommend using the smallest value then (e.g., `sampleSize128 = 22`). Sometimes, however, authors report pairwise  $N$  for each correlation. Thus, we also have a matrix of pairwise  $N$ , which we illustrate in Figure 11. Recall that we also have to deal with the entirely missing variable ‘role\_stress2’, which we again visualize by inserted blanks and an empty row in the matrix of pairwise  $N$ . Using a matrix of pairwise  $N$  rather than just the smallest of all  $N$  increases the statistical power of a CoTiMA. We recommend saving the matrix to disk. In case there is a matrix of pairwise  $N$  this could also be saved.

## 5 Preparatory Step (`ctmaEmpCov`, `ctmaCorRel`, `ctmaPrep`)

CoTiMA uses correlation matrices to generate ‘pseudo raw data’ using the MASS R package (Veneables & Ripley, 2002). Pseudo raw data exactly (!) reproduce the correlation matrices and offers a couple of interesting options. In the present section we show how data can be processed in terms of recoding variables, combining two or more variables into composite scores, and dealing with missing correlations. (The possibility to combine two or more correlations into a single correlation will be added soon.)

We turn now to processing the correlations shown in Figure 11. Our aim is to analyze the reciprocal effects between job demands and burnout. In particular, we (1) want to correct the correlations for unreliability (aka correction for attenuation, disattenuation). Further, we (2) want to drop the variables ‘SPP\_1’ and ‘SOP\_1’ because these variables do not exist in other primary studies and because they are not of particular interest. We also (3) want to recode ‘efficacy\_1’ and ‘efficacy\_2’ so that they represent lack of efficacy rather than efficacy. Lack of efficacy, cynicism, and exhaustion are the three burnout symptoms, and we (4) want to combine them into a single variable<sup>6</sup>. Whereas a measure of demands is available for the first measurement occasion (‘role stress 1’), such a measure is missing at the second measurement occasion. Thus, we (5) also have to deal with missing correlations.

First, to achieve our aims, we start with reading the previously saved correlation matrix and the matrix of pairwise  $N$  from disk (see Figure 12) and assign them to R objects `empcov128` and `pairwiseN128`. With `colnames(empcov128)` (not shown in Figure 12) we could recall the variable names, which are ‘SPP\_1’, ‘SOP\_1’, ‘role stress\_1’, ‘exhaustion\_1’, ‘exhaustion\_2’, ‘cynicism\_1’, ‘cynicism\_2’, ‘efficacy\_1’, and ‘efficacy\_2’. First, we do the corrections for unre-

---

<sup>6</sup>CoTiMA could also be used with measurement models, for example, with lack of efficacy, cynicism, and exhaustion as manifest indicators of a latent factor. However, in meta-analysis the most common case is that burnout would be measured using different (numbers of) variables. Therefore, combining the available variables for each primary study and then using a single manifest indicator in subsequent CoTiMA is frequently the only viable way.

```

empcov128 <- readRDS(file=paste0(activeDirectory, "empcov128.rds"))
pairwiseN128 <- readRDS(file=paste0(activeDirectory, "pairwiseN128.rds"))
delta_t128 <- c(6)
alphas128 <- c(.87, .88, .80, .94, .91, .88, .95, .81, .88)
empcov128 <- ctmaCorRel(empcov128, alphas128)
targetVariables128 <- c("role stress_1",
                        "exhaustion_1", "cynicism_1", "efficacy_1",
                        "exhaustion_2", "cynicism_2", "efficacy_2")
recodeVariables128 <- c("efficacy_1", "efficacy_2")
sampleSize128 <- mean(pairwiseN128)
combineVariables128 <- list("role stress_1",
                            c("exhaustion_1", "cynicism_1", "efficacy_1"),
                            c("exhaustion_2", "cynicism_2", "efficacy_2"))
combineVariablesNames128 <- c("Demands1", "Burnout1", "Burnout2")
missingVariables128 <- c(3)
results128 <- ctmaEmpCov(targetVariables=targetVariables128,
                        recodeVariables=recodeVariables128,
                        combineVariables=combineVariables128,
                        combineVariablesNames=combineVariablesNames128,
                        missingVariables=missingVariables128,
                        nlatents=2,
                        pairwiseN=pairwiseN128,
                        Tpoints=2,
                        empcov=empcov128)
empcov128 <- results128$r
pairwiseN128 <- results128$pairwiseNNew

```

Figure 12: Processing correlation matrices (ctmaCorRel, ctmaEmpCov)

liability. This has to be done first because, for example, reliabilities would be no longer available after two or more variables are combined. To correct for unreliability, a vector of reliabilities (`alpha128`) has to be provided, and then the `ctmaCorRel` is used to replace `empcov128` by its disattenuated counterpart<sup>7</sup>.

Second, we reduce the number of variables. All variables except the two we want to drop are assigned to `targetVariables128`. Note that a formal requirement of CoTiMA is that the variables are ordered in Time (Time 0 variables, Time 1 variables, etc.). This is also achieved by ordering the variables accordingly when creating `targetVariables128`.

Third, the two variables we want to recode are assigned to the object `recodeVariables128`. If an `empcovi` does not include variable names (no `dimnames`), one could use the variables' positions (i.e., `recodeVariables128 <- c(4, 7)`). Note that if numbers are used, they should correspond to the positions in the `targetVariablesi` object rather than the rows/columns in the `empcovi` object

<sup>7</sup>Correlations are disattenuated using the well-known formula developed by Spearman (1904). This formula is based on several assumptions. One of these assumptions is that the assumption underlying Cronbach's alpha (or any other estimate of reliability), which is usually used to measure reliability, are correct. While violations of the assumptions do usually not cause visible consequences when dealing with a single cross-sectional correlation coefficient, in the case of correlation matrices of longitudinal studies it might cause problems. One problem is that disattenuated test-retest correlations could become larger than 1.0, which is automatically corrected by `ctmaCorRel` (i.e., they are set to 1.0). Another problem is that the disattenuated matrices might not be positive definite and could not be analyzed then.

(i.e., recoding is done after `targetVariablesi` were selected from `empcovi`).

Although it is not necessary to assign any value to `sampleSize128`, we assigned the mean of the pairwise  $N$  (`mean(pairwiseN128)`). This is a reasonable value that will be used for descriptive statistics in the output of subsequent CoTiMAs. Other options could be `min(pairwiseN128)` or `max(pairwiseN128)`.

Fourth, we use a list (!) of variable names or vectors of variable names to specify the variables that should or should not be combined. This list is stored in the object `combineVariables128`. We keep the variable ‘role stress\_1’ as it is, whereas for the first and second measurement occasion the three burnout variables are combined into a single scale, respectively. The three final variables are then labeled as specified in `combineVariablesNames128`.

Fifth, since there is no variable for demands at the second time point, we declare it as missing. This is done by stating which variable is missing in the imagined set of ‘Demands1, Burnout1, Demands2, Burnout2’, which is the 3rd element. Thus, `missingVariables128 <- 3`.

```
## [1] empcov128
##      [,1]      [,2] [,3]      [,4]
## [1,] 1.0000000 0.7361878 NA 0.5809288
## [2,] 0.7361878 1.0000000 NA 0.8118634
## [3,]      NA      NA      NA      NA
## [4,] 0.5809288 0.8118634 NA 1.0000000
## [1] pairwiseN128
##      [,1] [,2] [,3] [,4]
## [1,] 88 77 0 44
## [2,] 77 55 0 44
## [3,] 0 0 0 0
## [4,] 44 44 0 22
```

Figure 13: Results of applying `ctmaEmpCov` to the specifications of Study 128

The CoTiMA package comes with the function `ctmaEmpCov` which performs the desired operations (recoding, combining etc.) and yields the final correlation matrix that we want to use for our subsequent CoTiMA. Since we have a matrix of pairwise  $N$ , this will be processed by `ctmaEmpCov`, too. The function `ctmaEmpCov` returns a new correlation matrix, which is then used to replace the `empcov128` from which we started. Further, `ctmaEmpCov` returns a new matrix of pairwise  $N$ , which is then used to replace the `pairwiseN128`. Figure 13 shows the new correlation matrix and matrix of pairwise  $N$ .

```
rawData128 <- list(fileName=paste0(activeDirectory, "rawdata128.txt"),
                  studyNumbers=128, missingValues=c(-99),
                  standardize=TRUE, header=FALSE, dec=".", sep=" ")
delta_t128 <- c(NA)
```

Figure 14: Using raw data

Instead of correlation matrices, raw data can be used as well, and the arguments required to read raw data from disc have to be stored in a `rawDatai` object. In R, a `list` is a list (sic!) that has elements, which have their own

labels (like in a shopping list, in which you summarize the planned purchases in subitems like "vegetables", "cheese" etc.). Unlike a vector, the elements of a list could be of different types, for example, characters, numbers, symbols, matrices etc. The list object created in Figure 14 has seven elements: `fileName`, `studyNumbers`, `missingValues`, `standardize`, `header`, `dec`, and `sep`.

| V1_T0   | V2_T0   | V1_T1   | V2_T1   | dT1 |
|---------|---------|---------|---------|-----|
| 0.835   | 2.328   | -0.778  | 2.969   | 11  |
| 1.555   | 2.634   | 1.977   | 1.807   | 12  |
| 3.209   | 1.849   | 2.291   | 2.795   | 12  |
| 0.416   | 2.351   | 0.127   | 1.705   | 13  |
| -99.000 | -99.000 | 0.476   | -99.000 | 13  |
| -99.000 | -99.000 | 0.854   | -99.000 | 11  |
| -99.000 | -99.000 | -99.000 | 2.987   | 12  |
| -99.000 | -99.000 | -99.000 | 2.087   | 12  |
| -99.000 | -99.000 | -99.000 | 0.927   | 13  |

Figure 15: Raw data file structure

The raw data have to be included in an ordinary text file, and the name of the file should be stored in the list element `fileName`. Possibly missing values should be specified, and only a single value is possible (-99 is assumed by default) and stored in the list element `missingValues`. Whether or not the raw data should be standardized, which implies the analysis of correlations, or not, which implies the analysis of covariance, could be specified by setting the list element `standardize` to either `TRUE` (default and recommended) or to `FALSE`. Whether or not the raw data files include a header with variable names (as for the example data below) could be specified by setting the element `header` to either `TRUE` (default) or to `FALSE`. Finally, a decimal delimiter (default = `'.'`) and the characters separating the values (default = `' '`) could be defined using the list elements `dec` and `sep`, respectively. Note that in meta-analysis, moderators are usually study characteristics (e.g., the average age of a sample) rather than characteristics of individual study participants. Therefore, moderator values are not taken from a raw data file, but they are defined directly for a primary study that does provide raw data by assigning values to the moderator object; this is explained later.

Raw data of a primary study has to be provided as a text (ascii) file. Data has to be in wide format (i.e., one row per individual). Assuming there are  $t$  measurement occasions, the order of the variables should be `V1_T0`, `V2_T0`,  $\dots$ , `V1_Tt`, `V2_Tt`, `dT1`, `dT2`,  $\dots$ , `dT(t-1)`, where `dTt` are the variables representing the time intervals (deltas) between measurements (see Figure 15; here with header). Note that if  $t$  measurement occasions exist, there are  $t-1$  time intervals. Compared to correlation matrices as input, raw data allow the time intervals to vary between the individuals within a study (average time intervals are automatically reported in CoTiMA fit objects). However, for studies that supply raw data, it is mandatory to specify the `delta_ti` object! It has to have as many NA as the largest number of possible time intervals in the respective



```

ageM2 <- 39.3
ageSD2 <- 8.7
malePercent2 <- .60
occupation2 <- c("Bank employees")
country2 <- c("Netherlands")
demands2 <- c("Workload")
burnout2 <- c("Emotional Exhaustion")
targetVariables2 <- c("Demands1", "Burnout1", "Demands1", "Burnout2")
source2 <- c("Houkes, I.", "Janssen, P, P, M.", "de Jonge, J", "& Bakker, A, B",
            "Study1", "2003")
moderator2 <- c(1, 0.72)

ageM3 <- 47.4
ageSD3 <- 5.8
malePercent3 <- .70
occupation3 <- c("Teachers for adults")
country3 <- c("Netherlands")
demands3 <- c("Workload")
burnout3 <- c("Emotional exhaustion")
targetVariables3 <- c("Demands1", "Burnout1", "Demands1", "Burnout2")
source3 <- c("Houkes, I.", "Janssen, P, P, M.", "de Jonge, J", "& Bakker, A, B",
            "Study2", "2003")
moderator3 <- c(1, 0.72)

ageM313 <- 30
ageSD313 <- 6
malePercent313 <- 0.30
occupation313 <- c("Wmployment agency employees")
country313 <- c("Netherlands")
demands313 <- c("Work pressure")
burnout313 <- c("Exhaustion")
targetVariables313 <- c("Demands1", "Burnout1", "Demands1", "Burnout2",
                      "Demands3", "Burnout3")
source313 <- c("Demerouti", "Bakker", "& Bulters", "2004")
moderator313 <- c(2, 0.72)

ageM128 <- 41
ageSD128 <- 11.4
malePercent128 <- 0.203
occupation128 <- c("Managerial employees in NHS trusts")
country128 <- c("UK")
demands128 <- c("Role Stress")
burnout128 <- c("Exhaustion", "Cynicism")
source128 <- c("Childs, J. H.", "& Stoeber, J.", "Study1", "2012")
moderator128 <- c(2, 0.66)

```

Figure 16: Additional information for study data entered before

study is, for example, in the case of not more than three intervals, `delta_ti` `<- c(NA, NA)`. In the example in Figure 15 there are only two time points and, thus, one interval `dt1`. Thus, `delta_ti` is indeed the only mandatory object because `rawDatai` could substitute `empcovi` and `pairwiseNi` could substitute `sampleSizei`.

So far, we introduced the objects `delta_ti`, `sampleSizei`, `empcovi`, `targetVariablesi`, `alphasi`, `pairwiseNi`, and `rawDatai`). Further pre-defined

object names are:

- **moderator*i***. A vector of numerical values either representing categorical or continuous variables, e.g., `moderator6 <- c(1, 2, 2, 0.76, 2.56, 2001)`
- **startValues*i***. A vector of start values, which was used in previous CoTiMA versions. Currently the use of start values is disabled, but this might change in the future.
- **empMeans*i***. Mean values of variables (default = 0). It is not recommended to change the default, but it is possible, e.g., `empMeans7 <- c(1, -2.5, 1.1, -2.4)`
- **empVars*i***. Variances of variables; (default = 1). It is not recommended to change the default, but it is possible, e.g., `empVars6 <- c(1, 2, 1.1, 1.9)`
- **studyNumber*i***. A special number used for labeling in the outputs of subsequently fitted CoTiMA models, e.g., `studyNumber6 <- 66`
- **source*i***. Useful to label the table displaying the estimated parameters for each primary study, rather than using the numbers used for the primary study objects (e.g., 128 from `empcov128`), e.g., `source6 <- c("De Jonge", "Dormann", "Janssen", "Dollard", "Landeweerd", "& Nijhuis", "2001")`
- **ageMi**. A value indicating the mean age of participants in a primary study, e.g., `ageM6 <- 31.78`
- **malePercent*i***. A value indicating the percentage of male participants in a primary study, e.g., `malePercent6 <- 0.11`
- **occupation*i***. A vector of character strings representing the occupations of participants in a primary study. Of course, this has not to be taken literally. For example it could be also used to represent the program in which student participants are enrolled and similar classifications, e.g., `occupation6 <- c("Health care workers")`
- **country*i***. A single character string representing the country in which a primary study was conducted, e.g., `country6 <- c("Netherlands")`

In addition to these pre-defined object names, user-defined object names could be added (e.g., `demandsi` and `burnouti`, to add information about the type of measurement scale used in primary studies). The difference between pre-defined and user-defined objects is twofold. First, pre-defined objects are included in the Excel workbook that summarizes primary study information (see. Figure 20). Second, user-defined objects have to be declared in `ctmaPrep` using the argument `addElements` (see Figure 18).

```

empcov18 <- matrix(c(1.00, 0.44, 0.62, 0.34,
                    0.44, 1.00, 0.41, 0.62,
                    0.62, 0.41, 1.00, 0.55,
                    0.34, 0.62, 0.55, 1.00), 4, 4)
variableNames18 <- c("Demands_1", "Burnout_1", "Demands_2", "Burnout_2")
dimnames(empcov18) <- list(variableNames18, variableNames18)
delta_t18 <- 12
sampleSize18 <- 174
ageM18 <- 41.33
ageSD18 <- 9.70
malePercent18 <- 0.03
occupation18 <- c("Service employees")
country18 <- c("Germany")
demands18 <- c("Workload")
burnout18 <- c("Emotional exhaustion", "Depersonalization")
source18 <- c("Diestel", "& Schmidt", "Study 1", "2012")
moderator18 <- c(1, 0.7)

empcov32 <- matrix(c(1.00, 0.45, 0.70, 0.40,
                    0.45, 1.00, 0.36, 0.66,
                    0.70, 0.36, 1.00, 0.43,
                    0.40, 0.66, 0.43, 1.00), 4, 4)
variableNames32 <- c("Demands_1", "Burnout_1", "Demands_2", "Burnout_2")
dimnames(empcov32) <- list(variableNames32, variableNames32)
delta_t32 <- 8
sampleSize32 <- 433
ageM32 <- 41.5
ageSD32 <- 10.2
malePercent32 <- 0.199
occupation32 <- c("Teachers")
country32 <- c("Canada")
demands32 <- c("classroom overload")
burnout32 <- c("Emotional exhaustion", "Depersonalization")
source32 <- c("Fernet", "Guay", "Senecal", "& Austin", "2012")
moderator32 <- c(1, NA)

```

Figure 17: Information for two further primary studies

To proceed further with the example, in a first step documented in Figure 16 we add information to those four primary studies data already entered before. In a second step, we add two further primary study information as shown in Figure 17.

The six studies are now compiled into a list as shown in Figure 18. We add the two user-defined object names `demandsi` and `burnouti`. We also provide a vector with the labels of the two moderators, and we provide a list of vectors to label the moderator values.

To get a convenient overview of the information stored in this list, one could use the `openxlsx` R package (see Figure 19). An example of what is displayed when opening the excel workbook with its several sheets with `openXL` is shown in Figure 20. The workbook could also be saved to disk using the `saveWorkbook` function of `openxlsx`.

```

activeDirectory <- "/Users/cdormann/CoTiMA Users Guide/"
CoTiMAstudyList_6 <- ctmaPrep(selectedStudies=c(2, 3, 313, 128, 18, 32),
                               activeDirectory = activeDirectory,
                               addElements = c("demands", "burnout"),
                               moderatorLabels=c("Burnout Measure",
                                                  "Control at Work"),
                               moderatorValues=list(c("1 = Emotional Exhaustion",
                                                      "2 = Exhaustion"),
                                                    "continuous"))

```

Figure 18: Compiling a list of primary studies with extended information (ctmaPrep)

```

openXL(CoTiMAstudyList_6$excelSheets)
saveWorkbook(CoTiMAstudyList_6$excelSheets, overwrite=TRUE,
             file=paste0(activeDirectory, "myExcelSheet.xlsx") )

```

Figure 19: Open an Excel sheet with summary information included in a compiled list of primary studies (requires package openxlsx)

| A             | B              | C             | D                     | E             | F             | G               | H                        | I               | J |
|---------------|----------------|---------------|-----------------------|---------------|---------------|-----------------|--------------------------|-----------------|---|
| Source Info 1 | Source Info 2  | Source Info 3 | Source Info 4         | Source Info 5 | Source Info 6 | Orig. Study No. | Moderator # 1            | Moderator # 2   |   |
| Houkes, I.    | Janssen, P, P. | de Jonge, J   | & Bakker, A, B Study1 | 2003          | 2             | 1               | 0.72                     |                 |   |
| Houkes, I.    | Janssen, P, P. | de Jonge, J   | & Bakker, A, B Study2 | 2003          | 3             | 1               | 0.72                     |                 |   |
| Demerouti     | Bakker         | & Bulters     | 2004                  |               | 313           | 2               | 0.72                     |                 |   |
| Childs, J. H. | & Stoeber, J.  | Study1        | 2012                  |               | 128           | 2               | 0.66                     |                 |   |
| Diestel       | & Schmidt      | Study 1       | 2012                  |               | 18            | 1               | 0.7                      |                 |   |
| Fernet        | Guay           | Senécal       | & Austin              | 2012          | 32            | 1               |                          |                 |   |
|               |                |               |                       |               |               |                 | Burnout Measure          | Control at Work |   |
|               |                |               |                       |               |               |                 | 1 = Emotional Exhaustion | continuous      |   |
|               |                |               |                       |               |               |                 | 2 = Exhaustion           |                 |   |

Figure 20: Excel sheet with summary information included in a compiled list of primary studies

## 6 Initial Fitting (ctmaInit)

Now the first two steps (**Extract & Prepare**) in the recommended EPIC-BiG-Power workflow are done and we can move forward to the ‘Init’ step, for which the previously compiled `CoTiMAstudyList_6` is required. Initial fitting is done with the code in Figure 21 (analogous to Figure 4), and the result is then displayed on the console (see Figure 22).

```
CoTiMAInitFit_6 <- ctmaInit(primaryStudies=CoTiMAstudyList_6,
                             n.latent = 2,
                             activeDirectory = activeDirectory,
                             coresToUse = 1)
```

Figure 21: Fitting a ctsem model for each primary study (ctmaInit)

| ##              |                                     |           | V1toV1    | SE        | V2toV1   |
|-----------------|-------------------------------------|-----------|-----------|-----------|----------|
| ## Study No 2   | "Houkes et al., Study1, 2003"       |           | "-0.0519" | "0.0106"  | "0.0096" |
| ## Study No 3   | "Houkes et al., Study2, 2003"       |           | "-0.0322" | "0.0107"  | "0.0052" |
| ## Study No 313 | "Demerouti et al., 2004"            |           | "-0.4156" | "0.0424"  | "0.1419" |
| ## Study No 128 | "Childs, & Stoeber, Study1, 2012"   |           | "0"       | "0"       | "5.9692" |
| ## Study No 18  | "Diestel, & Schmidt, Study 1, 2012" |           | "-0.0529" | "0.0103"  | "0.0253" |
| ## Study No 32  | "Fernet et al., 2012"               |           | "-0.0507" | "0.0075"  | "0.011"  |
| ##              | SE                                  | V1toV2    | SE        | V2toV2    | SE       |
| ## Study No 2   | "0.01"                              | "-0.0195" | "0.0086"  | "-0.0272" | "0.0095" |
| ## Study No 3   | "0.0104"                            | "0.0116"  | "0.0109"  | "-0.0378" | "0.0114" |
| ## Study No 313 | "0.0383"                            | "0.0937"  | "0.0359"  | "-0.2834" | "0.033"  |
| ## Study No 128 | "0"                                 | "0"       | "0"       | "-0.0384" | "0"      |
| ## Study No 18  | "0.0098"                            | "0.0128"  | "0.0095"  | "-0.0476" | "0.0103" |
| ## Study No 32  | "0.0076"                            | "0.0258"  | "0.0084"  | "-0.0654" | "0.0086" |

Figure 22: Some results for the primary studies (ctmaInit)

For Study 128, which we used to demonstrate how to deal with missing variables, some unusual estimates emerged that are not unexpected. In Study 128, which comprised two waves of measurement, the variable `V1_T1` was missing (demands T1, i.e., ‘role stress\_2’). Obviously, this makes it impossible to validly estimate and parameter involving `V1_T1`. These parameters are called *non-identified*. Thus, all estimates involving `V1_T1` are not trustworthy. And even if only a single parameter was not identified, consequently the entire model is not identified. Thus, even the seemingly reasonable drift effect *V2toV2* in Figure 22 is not trustworthy. We show later why Study 128 could nevertheless be used for CoTiMA. Anyway, we will use the current case to review some of the general principles of continuous time structural equation modeling (CTSEM).

First, in CTSEM any pair of subsequent measurement occasions is regarded as equivalent except the length of the time interval, which may vary. Therefore, continuous time coefficients do not describe, for example, the relations between demands at Time 0 and burnout at Time 1. Rather, *earlier* demands affect *later* burnout. Thus, in CoTiMA, the effect *V1toV1* means the auto effect of earlier V1 to later V1. Similarly, the effect *V1toV2* means the cross effect of earlier V1 to later V2. In continuous time, the terms *auto* effect and *cross*

effects are used, whereas in discrete time, the terms *auto-regressive* effect and *cross-lagged* effects are used. In a similar vein, the terms diffusion (variance) in continuous time substitutes the term error (variance) in discrete time, and the term continuous time intercepts substitutes the term intercept (for more details see Voelkle et al., 2012; Driver et al., 2017).

Between these pairs of continuous time and discrete time coefficients, well-defined mathematical relations exist. The only reason why continuous time coefficients are used is that the math is known to describe how coefficients change across time. To translate auto and cross effects into auto-regressive and cross-lagged effects, put the former into a matrix, multiply the matrix by length of time interval, and then apply the matrix (!) exponential function. This matrix contains the auto effect in the diagonal and the cross effects off the diagonal.

Figure 23 shows how the continuous time drift effects obtained for Study 313 (see Figure 22) relate to 1-month auto-regressive and cross-lagged effects in discrete time. Demands are slightly less stable (*V1toV1*) than Burnout (*V2toV2*). The negative auto effects in continuous time thus translate into positive auto-regressive effects in discrete time. Thus, in continuous time, the more negative an auto effect is, the less stable a variable is. Further, the effect of earlier demands on later burnout is smaller (*V1toV2*) than the effect of earlier burnout on later stressors (*V2toV1*). Note that multiplying the matrix with, for example, 2 (i.e., `expm(A313 * 2)`) yields the effects across a 2-month lag. This is the way how discrete time effect sizes are computed and plotted (see Figure 10).

```
## [1] library(expm)
## [1] A313 <- matrix(c(-0.4156, 0.1419, 0.0937, -0.2834), 2, 2, byrow=TRUE)
## [1] A313
##           [,1]      [,2]
## [1,] -0.4156  0.1419
## [2,]  0.0937 -0.2834
## [1] expm(A313 * 1)
##           [,1]      [,2]
## [1,] 0.66453654 0.1003401
## [2,] 0.06625697 0.7580176
```

Figure 23: Relation between continuous time drift coefficients of Study 313 and its discrete time effects

The result of applying the same transformation to the suspicious drift effects of Study 128 is shown in Figure 24. The non-identified auto effect *V1toV1* corresponds to an auto-regressive effect of 1.0 across 1 month: A person's level of demands at work does 'perfectly' predict the person's demands one month later, which one would usually regard as not very plausible. In fact, this out-of-range estimate is a consequence that in Study 128 later demands was a missing variable. Thus, we cannot expect meaningful results from fitting a ctsem model to Study 128.

Again, model results could also be opened as excel workbook with `openXL(CoTiMAInitFit_6$excelSheets)`. For example, effects, their standard errors and lower limit (LL) and upper limit (UL) credible intervals are shown in

```
## [1] library(expm)
## [1] A128 <- matrix(c(0, 5.9692, 0, -0.0384), 2, 2, byrow=TRUE)
## [1] A128
##      [,1]      [,2]
## [1,]      0 5.9692
## [2,]      0 -0.0384
## [1] expm(A128 * 1)
##      [,1]      [,2]
## [1,]      1 5.8560444
## [2,]      0 0.9623279
```

Figure 24: Relation between continuous time drift coefficients of Study 128 and its discrete time effects

Figure 24. From the workbook, coefficients could be easily copied into a word processing app to build proper results tables.

|                    | C        | D       | E      | F      | G       | H      | I       | J      | K         | L        | M        | N        |
|--------------------|----------|---------|--------|--------|---------|--------|---------|--------|-----------|----------|----------|----------|
|                    | V1toV1   | SE      | V2toV1 | SE     | V1toV2  | SE     | V2toV2  | SE     | V1toV1LL  | V1toV1UL | V2toV1LL | V2toV1UL |
| A, B, Study1, 2003 | -0.0514  | 0.011   | 0.0089 | 0.0099 | -0.0192 | 0.0091 | -0.0271 | 0.0091 | -0.0758   | -0.0332  | -0.0108  | 0.0283   |
| A, B, Study2, 2003 | -0.0328  | 0.011   | 0.0052 | 0.0104 | 0.0112  | 0.0107 | -0.0377 | 0.0113 | -0.0589   | -0.0165  | -0.0152  | 0.0254   |
|                    | -0.4162  | 0.063   | 0.1428 | 0.0395 | 0.0921  | 0.0347 | -0.2829 | 0.032  | -0.5064   | -0.3372  | 0.0658   | 0.2184   |
|                    | -19.3478 | 32.2561 | 1.5927 | 5.6399 | -0.0063 | 0.0185 | -0.0001 | 0.0023 | -110.3568 | 6        | -9.4899  | 12.588   |
|                    | -0.0536  | 0.0102  | 0.0257 | 0.0099 | 0.0125  | 0.0101 | -0.0477 | 0.0102 | -0.0761   | -0.0362  | 0.0085   | 0.0449   |
|                    | -0.0509  | 0.0075  | 0.0113 | 0.0076 | 0.0255  | 0.0081 | -0.0652 | 0.0085 | -0.0672   | -0.0376  | -0.0038  | 0.0262   |

Figure 25: Excel sheet with summary of model results

Doing the initial fitting of ctsem models to all primary studies allows setting several options (arguments) such as, for example, constraining some drift effects to be 0.0, or using different estimators such as Bayesian instead of maximum likelihood estimation. The arguments to select estimators are introduced as follows, and the entire list of possible arguments of the different CoTiMA functions are listed in the Appendix. Note that the `optimize` argument should be used and not be confused with `optimise`, which is used by ctsem.

One particular option is to use Bayesian estimation. Bayesian estimates are drawn from posterior probability distributions, for which different samplers could be used. The most robust sampler is the Hamiltonian Monte Carlo (HMC) sampler (Stan Developer Team, 2020a). However, it is the slowest one. The Stan Math library (Carpenter, Hoffman, Brubaker, Lee, Li & Betancourt, 2015), which is used by ctsem and CoTiMA for estimation, offers a No U-Turn Sampler (NUTS), which is a variant of the HMC sampler and usually works well and is faster. However, both samplers are much (!) slower than maximum likelihood estimation, which is the default estimator, or maximum a posteriori estimation. In fact, most desktop computers in 2021 probably would need a couple of weeks for a full CoTiMA with Bayesian estimation if 20 or more primary studies are analyzed. Table 1 gives an overview of how the different estimators can be requested by setting the `optimize` and the `nopriors` argument of all CoTiMA fitting functions (`ctmaInit`, `ctmaFit`, `ctmaEqual`, & `ctmaPower`).

Weakly informative priors for Bayesian estimation with the NUTS sampler

Table 1: Estimators available for CoTiMA

| optimize |   |   |
|----------|---|---|
|          | FALSE                                       | TRUE                                    |
| FALSE    | Bayesian estimation via Stan's NUTS sampler | Maximum a posteriori estimation         |
| nopriors | Bayesian estimation via HMC sampling        | maximum likelihood estimation (default) |
| TRUE     | (nopriors will be changed to FALSE)         |   |

*Note:* HMC = Hamiltonian Monte Carlos Sampler; NUTS = No U-Turn Sampler

and for maximum a posteriori estimation are provided by `ctsem`. They work well under most circumstances, however, sometimes they might not work well because the priors provided by `ctsem` have been optimized for time measured in years. For example, one could use the argument `scaleTime = 1/365.25` if time was measured in days and previous fitting attempts did not yield meaningful results.

Figure 26 shows how Bayesian estimates using the NUTS sampler could be obtained. Since estimation requires long time (expect several hours), it is recommended to save the model fits for each primary study using the `saveSingleStudyModelFit` argument. If further studies are added later, re-estimating these models could be avoided by the corresponding `readSingleStudyModelFit` argument. In the example in Figure 26, we used `chains = 2` and `coresToUse = 2`. Three chains and three cores are recommended before publishing results. Note that on Windows machines using more than one core may not work; use `coresToUse = 1` then (which doubles the time needed to fit the models). Since Bayesian estimation takes a long time, we want to take care that we get precise results in our first fitting attempt; we set `finishsamples = 10000` for this purpose. This means parameter estimates and the credible intervals will be sampled 10000 times from the estimated parameter distribution, rather than only 1000 sample, which is the default for `finishsamples`.

Part of the results obtained from the code in Figure 26 printed to the console with `summary(CoTiMAInitFit_6_NUTS)` is shown in Figure 26<sup>8</sup>. A comparison with the maximum likelihood effects and their standard errors in Figure 22 reveals no substantial differences except for Study 128, for which results are not trustworthy anyway. We should note, further, that Bayesian estimation is sensitive to priors, and default priors are only appropriate if the time scale is appropriately chosen, too. This could require using an appropriately chosen `scaleTime` argument (see Footnote 5).

<sup>8</sup>In addition, several warning messages are issued. They are all related to Study 128, for which we introduced missing data. This does not happen if doing the analysis again without Study 128.



```

CoTiMAInitFit_6_NUTS <- ctmaInit(primaryStudies=CoTiMAstudyList_6,
                                n.latent = 2,
                                activeDirectory=activeDirectory,
                                saveSingleStudyModelFit =
                                  c("InitFit_6_NUTS", 2, 3, 313, 128, 18, 32),
                                optimize=FALSE,
                                nopriors=FALSE,
                                chains = 2,
                                coresToUse = 2,
                                finishsamples = 10000)
saveRDS(CoTiMAInitFit_6_NUTS, file=paste0(activeDirectory,
                                           "CoTiMAInitFit_6_NUTS.rds"))
summary(CoTiMAInitFit_6_NUTS)

```

Figure 26: Using Bayesian estimation via Stan's NUTS sampler (ctmaInit)

|                 |                                     |           |          |           |          |           |
|-----------------|-------------------------------------|-----------|----------|-----------|----------|-----------|
| ##              |                                     |           |          | V1toV1    | SE       | V2toV1    |
| ## Study No 2   | "Houkes et al., Study1, 2003"       |           |          | "-0.0537" | "0.0117" | "0.0086"  |
| ## Study No 3   | "Houkes et al., Study2, 2003"       |           |          | "-0.0346" | "0.0113" | "0.0061"  |
| ## Study No 313 | "Demerouti et al., 2004"            |           |          | "-0.4204" | "0.0447" | "0.1459"  |
| ## Study No 128 | "Childs, & Stoeber, Study1, 2012"   |           |          | "-4.257"  | "2.4053" | "-0.0052" |
| ## Study No 18  | "Diestel, & Schmidt, Study 1, 2012" |           |          | "-0.0562" | "0.0108" | "0.0276"  |
| ## Study No 32  | "Fernet et al., 2012"               |           |          | "-0.0517" | "0.0079" | "0.0119"  |
| ##              | SE                                  | V1toV2    | SE       | V2toV2    | SE       |           |
| ## Study No 2   | "0.0103"                            | "-0.0193" | "0.0094" | "-0.0284" | "0.0086" |           |
| ## Study No 3   | "0.0111"                            | "0.0119"  | "0.0109" | "-0.0396" | "0.0116" |           |
| ## Study No 313 | "0.0404"                            | "0.0944"  | "0.034"  | "-0.284"  | "0.0308" |           |
| ## Study No 128 | "0.929"                             | "0.03"    | "0.3631" | "-0.0744" | "0.0754" |           |
| ## Study No 18  | "0.0104"                            | "0.014"   | "0.0111" | "-0.0506" | "0.0111" |           |
| ## Study No 32  | "0.0079"                            | "0.026"   | "0.0084" | "-0.0661" | "0.0088" |           |

Figure 27: Estimates for the primary studies using Bayesian estimation (ctmaInit)

## 7 CoTiMA (ctmaFit)

Now the first three steps (**Extract**, **Prepare**, & **InitFit**) in the recommended EPIC-BiG-Power workflow are done, and we can move forward to do CoTiMAs, for which the now available `CoTiMAInitFit_6` (or `CoTiMAInitFit_6_NUTS`) object is required. In the first subsection, we demonstrate how a *full CoTiMA* with all drift effects could be fitted. In the second subsection, we show how a *partial CoTiMA* could be fitted, and we use this subsection to introduce the possibilities to analyze (a) subsets of studies, specific (b) invariance constraints, and (c) hierarchical CoTiMA using clusters of studies. In the third subsection, we show how to statistically *test the equality* of drift effects, that is, a CoTiMA with equality constraints. In the fourth subsection, we show how a *moderated CoTiMA* can be performed.

### 7.1 Full CoTiMA (ctmaFit)

We shall note that the first full CoTiMA we present here is a very special case that is probably rarely applied, and we will move on to the regular case a bit

further below. The reason why the first full CoTiMA is a very special case is, again, Study 128, which was a 2-wave study with one missing variable. Such studies prevent applying the usually recommended CoTiMA.

### 7.1.1 Full CoTiMA as all-invariant model (ctmaFit)

Usually, CoTiMA aggregates the drift coefficients by constraining them to be invariant across primary studies, whereas the correlations at Time 0 and the diffusion terms (i.e., error (co-)variances) are freely estimated within each primary study. This is impossible with the current set of primary studies because for Study 128 demands (role stress) was measured at Time 0 only, so diffusions for demands cannot be estimated for Study 128. As we shall later, missing variables do not impose problems if each variable is measured at least twice, which is possible in studies comprising more than two waves, but Study 128 had only two waves. In such instances, one could either decide to exclude critical studies from CoTiMA, or one could estimate a very restrictive CoTiMA that restricts all parameters (Time 0 correlations, drift effects, diffusions) to be invariant across all studies. This is called an *all-invariant-model*, and estimating such a model can be achieved by using the argument `allInvModel = TRUE`. Usually, we do *not* recommend using this argument, but in this case there is no other option except excluding Study 128, which we do further below.

```
CoTiMAFullFit_6 <- ctmaFit(ctmaInitFit = CoTiMAInitFit_6_NUTS,
                          allInvModel = TRUE,
                          coresToUse = coresToUse)
saveRDS(CoTiMAFullFit_6, file=paste0(activeDirectory, "CoTiMAFullFit_6.rds"))
summary(CoTiMAFullFit_6)
```

Figure 28: Full CoTiMA with six studies (ctmaFit)

Fitting this type of a very restrictive CoTiMA is done with the code in Figure 28 and with `summary(CoTiMAFullFit_6)` the results are displayed<sup>9</sup>. The term ‘full CoTiMA’ is used to refer to a model in which all possible auto effects and all possible cross effects are simultaneously aggregated. Later, we show how some effects could be excluded from the model (i.e., fixed to 0.0), and how some effects could be exempted from being invariant across primary studies. It is noteworthy that the estimator used for initial fitting, which was NUTS, does not affect which estimator is used in a CoTiMA; it is maximum likelihood in the present example, which is the default estimator. Other estimators would have to be specified as shown in Table 1.

The results in Figure 29 show the names of all parameters of the full (and *all-invariant*) CoTiMA model, their respective row and column numbers in the matrices in which they are used, their estimated mean population values, their standard errors (labelled *sd*), their 2.5% lower credible interval, mean, and 97.5% upper credible interval, and the T-values.

<sup>9</sup>Fitting will issue a warning that an ‘approximate’ Hessian was used and standard errors are not trustworthy. This is caused by the missing variables in Study 128. Still, the credible intervals are not based on standard errors.

| ##                               | row | col | Mean    | sd     | 2.5%    | 50%     | 97.5%   | Tvalues  |
|----------------------------------|-----|-----|---------|--------|---------|---------|---------|----------|
| ## TOMEANS_1_1 (invariant)       | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## TOMEANS_2_1 (invariant)       | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## LAMBDA_1_1                    | 1   | 1   | 1.0000  | 0.0000 | 1.0000  | 1.0000  | 1.0000  | Inf      |
| ## LAMBDA_1_2                    | 1   | 2   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## LAMBDA_2_1                    | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## LAMBDA_2_2                    | 2   | 2   | 1.0000  | 0.0000 | 1.0000  | 1.0000  | 1.0000  | Inf      |
| ## DRIFT V1toV1 (invariant)      | 1   | 1   | -0.0512 | 0.0103 | -0.0741 | -0.0498 | -0.0344 | -4.9709  |
| ## DRIFT V2toV1 (invariant)      | 1   | 2   | 0.0087  | 0.0095 | -0.0090 | 0.0087  | 0.0274  | 0.9158   |
| ## DRIFT V1toV2 (invariant)      | 2   | 1   | -0.0197 | 0.0086 | -0.0371 | -0.0195 | -0.0027 | -2.2907  |
| ## DRIFT V2toV2 (invariant)      | 2   | 2   | -0.0270 | 0.0093 | -0.0490 | -0.0256 | -0.0129 | -2.9032  |
| ## MANIFESTMEANS_1_1 (invariant) | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## MANIFESTMEANS_2_1 (invariant) | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## CINT_1_1                      | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## CINT_2_1                      | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## asymCINT_1_1                  | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## asymCINT_2_1                  | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## asymDIFFUSIONcov_1_1          | 1   | 1   | 1.0087  | 0.1617 | 0.7318  | 1.0012  | 1.3419  | 6.2381   |
| ## asymDIFFUSIONcov_1_2          | 1   | 2   | 0.3700  | 0.1340 | 0.1155  | 0.3625  | 0.6613  | 2.7612   |
| ## asymDIFFUSIONcov_2_1          | 2   | 1   | 0.3700  | 0.1340 | 0.1155  | 0.3625  | 0.6613  | 2.7612   |
| ## asymDIFFUSIONcov_2_2          | 2   | 2   | 1.0514  | 0.2143 | 0.6609  | 1.0400  | 1.5214  | 4.9062   |
| ## DIFFUSIONcov_1_1 (invariant)  | 1   | 1   | 0.0935  | 0.0142 | 0.0686  | 0.0927  | 0.1241  | 6.5845   |
| ## DIFFUSIONcov_1_2 (invariant)  | 1   | 2   | 0.0387  | 0.0088 | 0.0228  | 0.0384  | 0.0573  | 4.3977   |
| ## DIFFUSIONcov_2_1 (invariant)  | 2   | 1   | 0.0387  | 0.0088 | 0.0228  | 0.0384  | 0.0573  | 4.3977   |
| ## DIFFUSIONcov_2_2 (invariant)  | 2   | 2   | 0.0679  | 0.0098 | 0.0504  | 0.0674  | 0.0876  | 6.9286   |
| ## MANIFESTcov_1_1               | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## MANIFESTcov_1_2               | 1   | 2   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## MANIFESTcov_2_1               | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## MANIFESTcov_2_2               | 2   | 2   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## TOcov_1_1 (invariant)         | 1   | 1   | 0.9922  | 0.1184 | 0.7787  | 0.9890  | 1.2405  | 8.3801   |
| ## TOcov_1_2 (invariant)         | 1   | 2   | 0.4481  | 0.0890 | 0.2822  | 0.4445  | 0.6354  | 5.0348   |
| ## TOcov_2_1 (invariant)         | 2   | 1   | 0.4481  | 0.0890 | 0.2822  | 0.4445  | 0.6354  | 5.0348   |
| ## TOcov_2_2 (invariant)         | 2   | 2   | 1.0019  | 0.1226 | 0.7807  | 0.9948  | 1.2676  | 8.1721   |
| ## dtDRIFT_1_1                   | 1   | 1   | 0.9500  | 0.0098 | 0.9284  | 0.9513  | 0.9662  | 96.9388  |
| ## dtDRIFT_1_2                   | 1   | 2   | 0.0084  | 0.0091 | -0.0087 | 0.0085  | 0.0265  | 0.9231   |
| ## dtDRIFT_2_1                   | 2   | 1   | -0.0189 | 0.0083 | -0.0356 | -0.0187 | -0.0026 | -2.2771  |
| ## dtDRIFT_2_2                   | 2   | 2   | 0.9733  | 0.0090 | 0.9522  | 0.9747  | 0.9869  | 108.1444 |

Figure 29: Results (Part 1) of a Full *all-invariant* CoTiMA with six studies (ctmaFit)

The four rows starting with DRIFT show the estimates for the continuous time drift coefficients, and their discrete time counterparts, that is, the autoregressive and cross-lagged effects, across one month are again shown closer to the bottom (dtDRIFT). As explained earlier, only the four rows containing the drift coefficients are usually important for reporting CoTiMA results. Nevertheless, we briefly explain what the other parameters stand for. For a more detailed description see Driver, Oud, and Voelkle (2017) and exact mathematical definitions can be found in Driver and Voelkle (2018).

TOMEANS at the top of Figure 29 represent the initial (T0) means of the latent variables. Closer to the bottom in Figure 29, TOcov shows correlation of the latent factors at T0, which is identical to their covariance because we deal with standardized variables here.

LAMBDA is a matrix with the factor loadings of the manifest variables on the latent factors. In the present example, this is a diagonal matrix in which the diagonal was fixed to 1.0. By this, each manifest variable loads on a single latent factor. Conversely, each latent factor is identified by a single manifest variable.

MANIFESTMEANS is a matrix (with a single column only) containing the means

of the intercepts of the manifest variables. Again, all values were fixed to 0.0 because we deal with standardized variables here.

CINT are the continuous time intercepts, which in case of standardized variables are usually zero. `asymCint` are the asymptotic continuous time intercepts. They reflect the intercept values to which the process converges after infinite time. These values should also be 0.0 in the case of CoTiMA, where we use standardized variables (correlations).

Similarly, `DIFFUSIONcov` are the continuous time error variances (usually referred to as diffusion term in the literature), and `asymDIFFUSIONcov` reflect asymptotic diffusion (error) variances and covariances. One might speculate that the asymptotic diffusion (error) variances should be 1.0 since one cannot explain any variance across infinite time. However these estimates are based on internal transformations. Asymptotic matrices are internally useful to reduce the time to fit the model and have no inherent meaning.

`MANIFESTcov` is a matrix of variances and covariances among the manifest variables at each measurement occasion. All values were fixed to 0.0 because we had only a single manifest indicator per latent factor.

```
## $randomEffects
## NULL
##
## $minus2ll
## [1] 1464.64
##
## $n.parameters
## [1] 10
##
## $opt.lag
##      [,1] [,2]
## [1,]   NA  19
## [2,]   19   NA
##
## $max.effects
##      [,1] [,2]
## [1,]    NA 0.0774
## [2,] 0.1752    NA
##
## $clus.effects
## NULL
##
## $message
## [1] "Mean time interval was 7.57142857142857. It is recommended to fit"
## [2] "the model again using the arguments scaleTime=1/12 and "
## [3] "customPar=FALSE. If the model fit (-2ll) is better (lower),"
## [4] "continue using, e.g., scaleTime=1/12 in all subsequent models."
```

Figure 30: Results (Part 2) of a Full *all-invariant* CoTiMA with six studies (`ctmaFit`)

Part 2 of the results generated by the code in Figure 28 is shown in Figure 30. A random effects model was not requested because it would require

raw data, which are usually not available<sup>10</sup>. The -2 loglikelihood values and number of estimated parameters are reported next. Then the optimal time interval according to Dormann and Griffin (2015) and the sizes of effects across the optimal interval are reported. Finally, CoTiMA allows to account for *hierarchically structured* (also called *nested* or *clustered*) primary studies. We will discuss this in the next example. Since no clusters were specified, cluster effects (`clus.effects`) do not exist. Finally, a warning message is issued that the average time intervals might have been too long to ensure proper fitting, and it is recommended to fit the model again using the `scaleTime=1/12` argument.

```
# Enter primary Study 201 with missing variables but each variable measured at least twice
empcov201 <- matrix(c(1.00, 0.43, 0.64, 0.32, 0.57, NA,
                    0.43, 1.00, 0.30, 0.61, 0.26, NA,
                    0.64, 0.30, 1.00, 0.48, 0.69, NA,
                    0.32, 0.61, 0.48, 1.00, 0.37, NA,
                    0.57, 0.26, 0.69, 0.37, 1.00, NA,
                    NA, NA, NA, NA, NA, NA), 6, 6)
variableNames201 <- c("Demands_1", "Burnout_1", "Demands_2", "Burnout_2",
                    "Demands_3", "Burnout_3")
dimnames(empcov201) <- list(variableNames201, variableNames201)
delta_t201 <- c(12, 12)
sampleSize201 <- 999
ageM201 <- 39.4
ageSD201 <- 10.55
malePercent201 <- .689
occupation201 <- c("different occupations")
country201 <- c("Switzerland")
demands201 <- c("Time Pressure")
burnout201 <- c("Exhaustion")
source201 <- c("Brauchli", "Schaufeli", "Jenny", "Fuelleman", "& Bauer", "2013")
moderator201 <- c(2, NA))

# Compiling a revised list of primary studies with Study 313 replacing Study 128
activeDirectory <- "/Users/cdormann/CoTiMA Users Guide/"
CoTiMAstudyList_6_new <- ctmaPrep(selectedStudies=c(2, 3, 313, 201, 18, 32),
                                activeDirectory = activeDirectory,
                                addElements = c("demands", "burnout"),
                                moderatorLabels=c("Burnout Measure", "Control at Work"),
                                moderatorValues=list(c("1 = Emotional Exhaustion",
                                                       "2 = Exhaustion"),
                                                       "continuous"))

# Initial Fitting of revised list of primary studies
CoTiMAInitFit_6_new <- ctmaInit(primaryStudies=CoTiMAstudyList_6_new,
                                n.latent = 2,
                                activeDirectory = activeDirectory)

# The Full CoTiMA
CoTiMAFullFit_6_new <- ctmaFit(ctmaInitFit = CoTiMAInitFit_6_new, coresToUse = coresToUse)
```

Figure 31: Workflow for replacing Study 128 by Study 201 and conducting a regular Full CoTiMA

### 7.1.2 Full CoTiMA as regular model (ctmaFit)

As noted in the last subsection, 2-wave studies with missing variables could be used, but they require constraining all parameters to be invariant across primary

<sup>10</sup>A ctsem model of a single primary study could be used to estimate random effects if raw data were available and the study comprises three or more waves.

| ##                          | row | col | Mean    | sd     | 2.5%    | 50%     | 97.5%   | Tvalues  |
|-----------------------------|-----|-----|---------|--------|---------|---------|---------|----------|
| ## TOMEANS_1_1              | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## TOMEANS_2_1              | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## LAMBDA_1_1               | 1   | 1   | 1.0000  | 0.0000 | 1.0000  | 1.0000  | 1.0000  | Inf      |
| ## LAMBDA_1_2               | 1   | 2   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## LAMBDA_2_1               | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## LAMBDA_2_2               | 2   | 2   | 1.0000  | 0.0000 | 1.0000  | 1.0000  | 1.0000  | Inf      |
| ## DRIFT V1toV1 (invariant) | 1   | 1   | -0.0408 | 0.0023 | -0.0452 | -0.0407 | -0.0364 | -18.0970 |
| ## DRIFT V2toV1 (invariant) | 1   | 2   | 0.0073  | 0.0023 | 0.0030  | 0.0074  | 0.0117  | 3.2125   |
| ## DRIFT V1toV2 (invariant) | 2   | 1   | 0.0115  | 0.0031 | 0.0054  | 0.0115  | 0.0173  | 3.7102   |
| ## DRIFT V2toV2 (invariant) | 2   | 2   | -0.0495 | 0.0032 | -0.0560 | -0.0495 | -0.0434 | -15.4945 |
| ## MANIFESTMEANS_1_1        | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## MANIFESTMEANS_2_1        | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## CINT_1_1                 | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## CINT_2_1                 | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## asymCINT_1_1             | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## asymCINT_2_1             | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## asymDIFFUSIONcov_1_1     | 1   | 1   | 1.1233  | 0.0886 | 0.9632  | 1.1182  | 1.3239  | 12.6813  |
| ## asymDIFFUSIONcov_1_2     | 1   | 2   | 0.3995  | 0.0659 | 0.2699  | 0.3984  | 0.5313  | 6.0593   |
| ## asymDIFFUSIONcov_2_1     | 2   | 1   | 0.3995  | 0.0659 | 0.2699  | 0.3984  | 0.5313  | 6.0593   |
| ## asymDIFFUSIONcov_2_2     | 2   | 2   | 1.0961  | 0.0854 | 0.9386  | 1.0911  | 1.2780  | 12.8383  |
| ## DIFFUSIONcov_1_1         | 1   | 1   | 0.0855  | 0.0060 | 0.0741  | 0.0854  | 0.0983  | 14.2011  |
| ## DIFFUSIONcov_1_2         | 1   | 2   | 0.0150  | 0.0045 | 0.0060  | 0.0152  | 0.0239  | 3.3134   |
| ## DIFFUSIONcov_2_1         | 2   | 1   | 0.0150  | 0.0045 | 0.0060  | 0.0152  | 0.0239  | 3.3134   |
| ## DIFFUSIONcov_2_2         | 2   | 2   | 0.0990  | 0.0068 | 0.0863  | 0.0990  | 0.1127  | 14.5060  |
| ## MANIFESTcov_1_1          | 1   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## MANIFESTcov_1_2          | 1   | 2   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## MANIFESTcov_2_1          | 2   | 1   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## MANIFESTcov_2_2          | 2   | 2   | 0.0000  | 0.0000 | 0.0000  | 0.0000  | 0.0000  | NaN      |
| ## TOcov_1_1                | 1   | 1   | 1.0029  | 0.0679 | 0.8790  | 1.0022  | 1.1444  | 14.7742  |
| ## TOcov_1_2                | 1   | 2   | 0.4507  | 0.0531 | 0.3486  | 0.4485  | 0.5540  | 8.4929   |
| ## TOcov_2_1                | 2   | 1   | 0.4507  | 0.0531 | 0.3486  | 0.4485  | 0.5540  | 8.4929   |
| ## TOcov_2_2                | 2   | 2   | 1.0015  | 0.0675 | 0.8793  | 0.9987  | 1.1433  | 14.8381  |
| ## dtDRIFT_1_1              | 1   | 1   | 0.9601  | 0.0022 | 0.9558  | 0.9601  | 0.9642  | 444.6937 |
| ## dtDRIFT_1_2              | 1   | 2   | 0.0070  | 0.0022 | 0.0029  | 0.0070  | 0.0112  | 3.2150   |
| ## dtDRIFT_2_1              | 2   | 1   | 0.0110  | 0.0030 | 0.0052  | 0.0110  | 0.0166  | 3.7187   |
| ## dtDRIFT_2_2              | 2   | 2   | 0.9517  | 0.0030 | 0.9456  | 0.9518  | 0.9575  | 313.1710 |

Figure 32: Results (Part 1) of a regular Full CoTiMA with six studies (ctmaFit)

studies. Such strict assumptions are not necessary if variables (correlations) are not missing, or if each variable in a primary studies is measured at least twice. When a variable is available at two measurement occasions and a primary study comprises more than two waves, it does not impose problems for CoTiMA if this variable is missing at further waves. Only two measurements are required, whenever they were carried out. This is demonstrated in the current section, where we add such a study (Study 201), which is then used in subsequent examples as replacement for Study 128.

The workflow for replacing Study 128 by Study 201 and conducting a Full CoTiMA is shown in Figure 31. Study 201 comprised three waves of measurement, and bunrout was not measured at the third measurement occasion so that the correlations were not available (NA). A new list of primary studies is compiled (CoTiMAstudyList\_6\_new), and the initial fitting of each primary study is re-done with the fit stored in the object CoTiMAInitFit\_6\_new. CoTiMAInitFit\_6\_new is then used as the ctmaInitFit argument to fit a regular full CoTiMA using ctmaFit.

The results of the full CoTiMA are shown in Figure 32 and Figure 33. The interpretation of results is analogous to the interpretation of the all-invariant

```
## $randomEffects
## NULL
##
## $minus2ll
## [1] 25461.29
##
## $n.parameters
## [1] 40
##
## $opt.lag
##      [,1] [,2]
## [1,]   NA  19
## [2,]   19  NA
##
## $max.effects
##      [,1] [,2]
## [1,]    NA 0.0586
## [2,] 0.0923    NA
##
## $clus.effects
## NULL
##
## $message
## [1] "Mean time interval was 8.875. It is recommended to fit"
## [2] "the model again using the arguments scaleTime=1/12 and "
## [3] "customPar=FALSE. If the model fit (-2ll) is better (lower),"
## [4] "continue using, e.g., scaleTime=1/12 in all subsequent models."
```

Figure 33: Results (Part 2) of a regular Full CoTiMA with six studies (ctmaFit)

CoTiMA discussed in Section 7.1.1<sup>11</sup>.

## 7.2 Partial CoTiMA (ctmaFit)

Figure 34 demonstrates some further possibilities for conducting a CoTiMA; additional capabilities are explained in Appendix A. The CoTiMA model specified in Figure 34 fixes the effect of  $V2toV1$  to 0.0 (which we do not generally recommend - let the evidence decide rather theoretical expectations), by labeling the according drift 0 or “0”. Further, only the effect  $V1toV2$  is invariant across primary studies as specified in the `invariantDrift` argument (which could be reasonable – and which could be decided based upon a statistical test). Finally, the first three primary studies were from The Netherlands, whereas studies 3, 4 and 5 (study numbers 128, 18 & 32), were from Switzerland, Germany, and

<sup>11</sup>There is one notable difference. Whereas in the all-invariant CoTiMA estimated T0 correlations and diffusions apply to the full sample of primary studies, in Figure 32 they apply to the last of the primary studies (i.e., Study 32). This is due to technical reasons inherent in the `ctsem` R-package used by CoTiMA. In `ctsem`,  $k - 1$  dummy variables for the overall  $k$  primary studies are used as so-called time independent predictors (TI), which modify (add or subtract values) the T0 correlations and the diffusion parameters estimated for the  $k$ th primary study. However, T0 correlations and diffusion parameters are usually of very little interest to researcher applying CoTiMA, so these technical details are only important in the probably rare case estimated T0 correlations and diffusions should be reported in publications.

Canada, respectively. This hierarchical structure is specified in the `cluster` argument. In the `cluster` argument, the studies that belong to one cluster receive the same number. Finally, `coresToUse` is specified here in negative notation, and -1 implies that all cores except 1 are used. As noted earlier, on Windows machines one should use 1 (not more than 1).

```
CoTiMAPart134Inv3Fit_6 <- ctmaFit(ctmaInitFit = CoTiMAInitFit_6_new,
                                drift=c("V1toV1", 0,
                                           "V1toV2", "V2toV2"),
                                invariantDrift=c("V1toV2"),
                                cluster=c(1,1,1,2,3,4),
                                coresToUse = -1)
saveRDS(CoTiMAPart134Inv3Fit_6, file=paste0(activeDirectory,
                                             "CoTiMAPart134Inv3Fit_6.rds"))
summary(CoTiMAPart134Inv3Fit_6)
```

Figure 34: A partial CoTiMA with a subset of primary studies, with one cross effect fixed to 0.0, with only a single effect invariant across primary studies, and with countries used as cluster variable (`ctmaFit`)

Parts of the summary are shown in Figure 35. The section `$estimates` shows the aggregated effect across all studies with country specific effects partialled out. Here, *V1toV2* is -.0093.

The section `$clus.effects` shows how the studies from The Netherlands (cluster 1) differ from the average effects, of which the drift effects are again of major importance. Note that cluster effects only exist for clusters comprising more than one single study; for all other studies it would be impossible to disentangle study-specific and cluster-specific effects. Each primary study (except the last one) is internally represented as a dummy variable, which affects the T0 variances and covariances, the diffusion parameters, and – not the drift parameters because they should be invariant (i.e., aggregated) across studies. Cluster dummies affect all of them. If a cluster would contain a single study only, its cluster dummy as well as its single study dummy would be perfectly correlated in affecting T0 variances and covariances and diffusion parameters. Thus, clusters have to contain more than a single study.

Additionally, the section `$clus.effects` show that the auto effect of demands (*V1toV1*) and the cross effect of demands on burnout (*V1toV2*) are significantly smaller in The Netherlands. Although it is not too important at this stage to know the country-specific effects (the main issue is that they are partialled out), they are shown in the section `cluster$specific$effect` in Figure 35. For instance, consider *V1toV2*. Since the cluster effect (-.0290) was significant because the credible interval excluded zero (LL = -.0470; UL = -.0107), one would conclude that there is no general effect of demands on burnout (-.0027, LL = -.0138, UL = .0086), but in The Netherlands the continuous time drift effect is significantly smaller and is  $-0.0027 - 0.029 \times 1.6767 = -.0513$ .



```

## $estimates
##               Mean      sd    2.5%    50%   97.5% Tvalues
## DRIFT V1toV1      -0.0603 0.0068 -0.0744 -0.0600 -0.0481  -8.9074
## DRIFT V2toV1       0.0000 0.0000  0.0000  0.0000  0.0000    NaN
## DRIFT V1toV2 (invariant) -0.0027 0.0058 -0.0138 -0.0026  0.0086  -0.4666
## DRIFT V2toV2      -0.0529 0.0034 -0.0599 -0.0528 -0.0466 -15.4273
##
## $clus.effects
## $clus.effects$effects
##               mean      sd    2.5%    50%   97.5% Tvalues
## Cluster_1_on__V1toV1      -0.0537 0.0161 -0.0886 -0.0525 -0.0260  -3.3386
## Cluster_1_on__V1toV2     -0.0290 0.0094 -0.0470 -0.0289 -0.0107  -3.0898
## Cluster_1_on__V2toV2     -0.0018 0.0044 -0.0105 -0.0017  0.0066  -0.4035
## Cluster_1_on__diff_eta1    0.1636 0.0310  0.1049  0.1629  0.2263   5.2737
## Cluster_1_on__diff_eta2_eta1 0.0601 0.1715 -0.2873  0.0663  0.3791   0.3504
## Cluster_1_on__diff_eta2     0.0739 0.0111  0.0525  0.0738  0.0958   6.6277
## Cluster_1_on__T0var_eta1   -0.0149 0.0775 -0.1572 -0.0182  0.1476  -0.1919
## Cluster_1_on__T0var_eta2_eta1 -0.0321 0.2563 -0.5758 -0.0107  0.4111  -0.1253
## Cluster_1_on__T0var_eta2    1.6013 3.5802 -0.6388  0.0836 12.4694   0.4473
##
## $clus.effects$weights
##           non Members Cluster Member
## 1_on__      -0.5961          1.6767
##
## $clus.effects$sizes
##           non Members Cluster Member
## N           1606          571
##
## $clus.effects$cluster.specific.effect
##           DRIFT V1toV1 DRIFT V2toV1 DRIFT V1toV2 (invariant) DRIFT V2toV2
## Cluster No. 1      -0.1503           NA           -0.0513           -0.0559
##
## $clus.effects$note
## [1] "The weights represent standardized cluster dummies. "
## [2] "They are used to multiply a cluster's TI effect and"
## [3] "this product is then added to the average effect shown in"
## [4] "$estimates, which overall yields the effects within a"
## [5] "cluster as shown in $cluster.specific.effect."
##
##
## $mod.effects
## NULL

```

Figure 35: Results of the partial CoTiMA specified in Figure 31 (ctmaFit)

### 7.3 CoTiMA with equality constraints (ctmaFit, ctmaEqual, ctmaCompFit)

To statistically test if two or more effects are equal is a bit complex and requires three steps: (1) ensure correct coding (polarity), (2) fit a partially invariant CoTiMA using `ctmaFit`, and (3) test equality using `ctmaEqual`. First, (1) one has to take care that the effects to be compared have equal signs. For example, consider a model with three latent variables such as demands, resources, and burnout. Work-related resources, such as supervisor support, can be supposed

to reduce burnout whereas demands increase burnout. To compare the effect sizes, one would need to go back to square one and re-start the EPIC part of the workflow. When preparing the correlations with `ctmaEmpCov`, one would need to use the `recode` argument to recode supervisor support so that it becomes lack of supervisor support. Then, one has to use `ctmaInit` again for initial fitting.

In the second step (2), one could start testing the equality of the effect sizes of supervisor support and of demands on burnout. This requires two CoTiMAs to be performed. The first CoTiMA has to specify those two or more effects as invariant across studies that should be tested for equality in the subsequent step. This is done with `ctmaFit`. We call this the *invariance model*.

```
CoTiMAFullInv23Fit_6 <- ctmaFit(ctmaInitFit = CoTiMAInitFit_6_new,
                              invariantDrift = c("V2toV1", "V1toV2") )
saveRDS(CoTiMAFullInv23Fit_6, file=paste0(activeDirectory,
                                           "CoTiMAFullInv23Fit_6.rds"))
summary(CoTiMAFullInv23Fit_6)

CoTiMAFullInvEq23Fit_6 <- ctmaEqual(CoTiMAFullInv23Fit_6)
saveRDS(CoTiMAFullInvEq23Fit_6, file=paste0(activeDirectory,
                                           "CoTiMAFullInvEq23Fit_6.rds"))
summary(CoTiMAFullInvEq23Fit_6)
```

Figure 36: Two-step procedure for testing the equality of two cross effects (`ctmaFit`, `ctmaEqual`)

Third (3), the CoTiMA fit object returned then serves as an argument for `ctmaEqual`. The code for Step 2 and 3 is shown in Figure 36.

We skip displaying the output returned from `summary(CoTiMAFullInv23Fit_6)` here because it is sufficient to note that  $V1toV2 = .0116$ ,  $V2toV1 = .0074$ ,  $-2ll = 25461.29$ , and the number of estimated parameters = 40.  $V1toV2$  and  $V2toV1$  were the only parameters that were aggregated, that is, invariant across primary studies. This is recognized by `ctmaEqual`, which, in addition to their invariance, constrains  $V1toV2$  and  $V2toV1$  to be equal. We call this the *equality model*. Again, we skip displaying the output returned from `summary(CoTiMAFullEq23Fit_6)` here because it is sufficient to note that  $V1toV2 = V2toV1 = .0089$ ,  $-2ll = 25462.47$ , and the number of estimated parameters = 39.

```
## [1] "   ###   NEXT MODEL COMPARISON   ###"
## [2] "Diff_Minus2LL:  1.18070136283495"
## [3] "Diff_df (= Diff_n.params):  1"
## [4] "prob:  0.277213258279257"
## [5] "Message1:  A prob value < .05 indicates a significant difference."
```

Figure 37: Result of the -2ll difference test comparing the fit of the invariance model with the fit of the equality to test if two cross effects are equal (`ctmaEqual`)

The -2ll difference test examines if the fit (-2ll value) of the equality model is not statistically worse than the fit of the invariance model. If this would be the

case, then the hypothesis that both effects are equal has to be rejected and the alternative hypothesis that one effect ( $V2toV1$  in this example) is significantly larger than the other one ( $V1toV2$  in this example), will be retained. The -2ll difference test is automatically performed by `ctmaEqual`, too, it is displayed at the end of the `summary(CoTiMAFullInv23Fit_6)`, and it is shown in Figure 37. In our example, the -2ll difference test was not significant. Thus, we could not reject the hypothesis that  $V1toV2 = V2toV1$ .

Finally, we shall mention the `ctmaCompFit` function that comes with the CoTiMA package. The `ctmaCompFit` function is automatically used by `ctmaEqual`. It can also be applied whenever researchers want to compare two model fits with a -2ll difference test by using `ctmaCompFit(CoTiMAFit1, CoTiMAFit2)`. Note, however, that the result is only valid if the two models are nested, that is, the second model is derived from the first model by constraining parameters. Such constraints are present, for example, if parameters are eliminated from a model by constraining them to be 0.0, or by constraining other parameters to be equal. The former is achieved by setting the desired drift effect to “0”, and the latter is achieved by assigning identical labels to the desired drift effects. This could be done with the `ctmaInit` and `ctmaFit` functions. For example, the argument `drift=c(“V1toV1”, 0, 0, “V1toV1”)` could be used to fit a model that has no cross effects and equal auto effects. This model is nested in a full CoTiMA model because it is more constrained.

## 7.4 Moderated CoTiMA (ctmaFit)

CoTiMA can handle multiple continuous moderators and multiple categorical moderators, however, it is not yet possible to mix categorical and continuous ones. In general, we recommend starting with a single moderator to foster understanding how they operate before analyzing multiple moderators combined.

```
CoTiMAMod1onFullFit_6 <- ctmaFit(ctmaInitFit = CoTiMAInitFit_6_new,
                                mod.number = 1,
                                mod.type = "cat",
                                mod.names = "Burnout Measure",
                                coresToUse = -1,
                                scaleMod = FALSE)
saveRDS(CoTiMAMod1onFullFit_6, file=paste0(activeDirectory,
                                             "CoTiMAMod1onFullFit_6.rds"))
summary(CoTiMAMod1onFullFit_6)
```

Figure 38: A full moderated CoTiMA with a single categorical moderator (`ctmaFit`)

Recalling from Figure 18, we entered information about two moderators. The first was the type of burnout measure applied in a primary study, which was either exhaustion or emotional exhaustion, and which was a categorical moderator. If there were two or more categorical moderators, the moderator numbers and moderator names would have to be provided as vectors (e.g., `mod.number = c(1, 3)`, `mod.names = c(“Burnout Measure”, “Study Quality”)`). How-

```

## $estimates
##               row col   Mean    sd   2.5%   50%  97.5%
## LAMBDA_2_1         2  1  0.0000 0.0000  0.0000  0.0000  0.0000
## LAMBDA_2_2         2  2  1.0000 0.0000  1.0000  1.0000  1.0000
## DRIFT V1toV1 (invariant) 1  1 -0.0473 0.0045 -0.0567 -0.0469 -0.0390
## DRIFT V2toV1 (invariant) 1  2  0.0120 0.0045  0.0029  0.0120  0.0204
##               Tvalues
## LAMBDA_2_1         NaN
## LAMBDA_2_2         Inf
## DRIFT V1toV1 (invariant) -10.4008
## DRIFT V2toV1 (invariant)  2.6633
##
## $randomEffects
## NULL
##
## $minus2ll
## [1] 25458.64
##
## $n.parameters
## [1] 44
##
## $opt.lag
##      [,1] [,2]
## [1,]   NA  19
## [2,]   19  NA
##
## $max.effects
##      [,1] [,2]
## [1,]   NA 0.0928
## [2,] 0.0727   NA
##
## $mod.effects
##
##               mean    sd   2.5%   50%
## 2 (category value) of Burnout Measure_on_V1toV1  0.0094 0.0064 -0.0015  0.0091
## 2 (category value) of Burnout Measure_on_V2toV1 -0.0063 0.0053 -0.0165 -0.0064
## 2 (category value) of Burnout Measure_on_V1toV2  0.0029 0.0063 -0.0098  0.0029
## 2 (category value) of Burnout Measure_on_V2toV2 -0.0034 0.0061 -0.0133 -0.0040
##               97.5% Tvalues
## 2 (category value) of Burnout Measure_on_V1toV1  0.0235  1.4735
## 2 (category value) of Burnout Measure_on_V2toV1  0.0038 -1.1808
## 2 (category value) of Burnout Measure_on_V1toV2  0.0142  0.4652
## 2 (category value) of Burnout Measure_on_V2toV2  0.0108 -0.5556

```

Figure 39: Part of the results moderated full CoTiMA (ctmaFit)

ever, in the present example, we use the first potential moderator variable only (`mod.number = 1` in Figure 38), which was categorical (`mod.type = "cat"` in Figure 38) representing two types of burnout measures (`mod.names = "Burnout Measures"` in Figure 38). By default CoTiMA does (!) standardize moderators from version 0.5.3 onwards. In the present example, we did overwrite the default this by including the argument `scaleMod = FALSE`. Thus, the  $k - 1$  dummy variables created from the  $k$  categories of the moderator variable use values 0 and 1. Note, while researcher frequently believe this facilitates interpretation of categorical moderator effects, it prevents disentangling effects between and

within the different categories (cf. Yaremych, Preacher, & Hedeker, 2021).

Part of the results are shown in Figure 39. The drift effects shown in the `$estimates` section are those in the reference group, which is always the group with the smallest category number. In the present example, these are the primary studies for which the moderator value was 1 (and internally recoded to 0 by CoTiMA) meaning they used an emotional exhaustion scale to measure burnout.

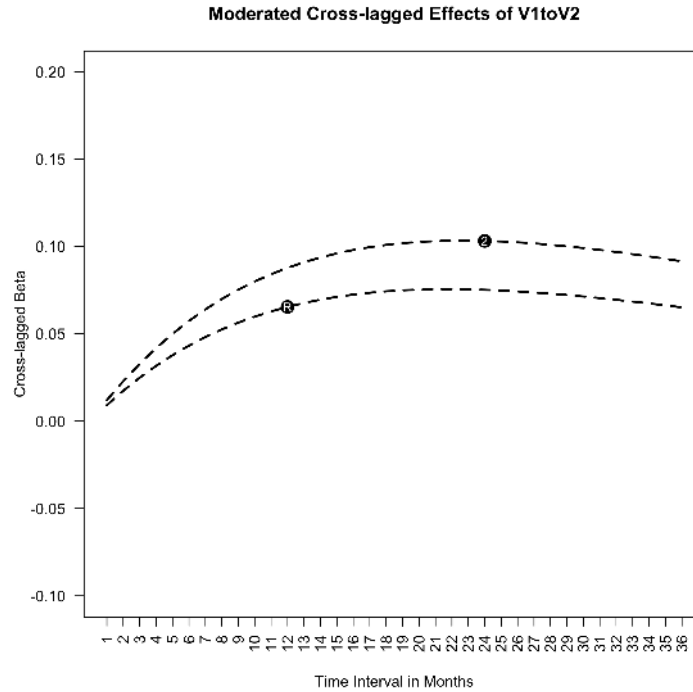


Figure 40: The cross-lagged effect  $V1toV2$  moderated by type of burnout measure (1 = emotional exhaustion, 2 = exhaustion) from 1 to 36 months. The horizontal location of the category indicators R (reference category) and 2 has no inherent meaning.

The section `$mod.effects` in Figure 39 show the effects belonging group with the 2nd category number. In case there were more categories, one would find here four additional rows starting with 3. `category number` etc. It is important to note that this section does not show the drift effects. Rather, it shows how in this category, which used an exhaustion compared to emotional exhaustion scale to measure burnout, the drift effects change compared to the reference group. Neither auto effects nor cross effects were significantly affected by the type of burnout measure. Leaving lack of significance aside, the effect of demands on burnout ( $V1toV2$ ) was increased if an exhaustion scale was used in primary studies and the effect of burnout on demands ( $V2toV1$ ) was reduced

if an exhaustion rather than emotional exhaustion scale was used. We call this a *positive moderating effect* and a *negative moderating effect* of the exhaustion scale, respectively<sup>12</sup>.

As always, the sizes of continuous time effects are virtually impossible to interpret. For example, the effect *V1toV2* is .0094 for emotional exhaustion and  $.0094 + .0029 = 0.0123$  (linearized; see footnote 12) for exhaustion. However, how these effects unfold over time also depends on the other three effects *V1toV1*, *V2toV2*, and *V2toV1*. We used `plot(CoTiMAMod1onFullFit_6, timeUnit = "Months", timeRange = c(1, 36, 1))` to plot the moderated discrete time effects. For *V1toV2*, the course of the moderated effect over discrete time is shown in Figure 43.

```
activeDirectory <- "/Users/cdormann/CoTiMA Users Guide/"
tmpStudyList <- ctmaPrep(selectedStudies=c(2, 3, 313, 18),
  activeDirectory = activeDirectory,
  addElements = c("demands", "burnout"),
  moderatorLabels=c("Burnout Measure",
    "Control at Work"),
  moderatorValues=list(c("1 = Emotional Exhaustion",
    "2 = Exhaustion"),
    "continuous"))

CoTiMAMod2on23Fit_6 <- ctmaFit(ctmaInitFit = CoTiMAInitFit_6_new,
  primaryStudyList = tmpStudyList,
  mod.number = 2,
  mod.type = "cont",
  mod.names = "Control",
  moderatedDrift = c("V1toV2", "V2toV1"),
  scaleMod=TRUE)

saveRDS(CoTiMAMod2on23Fit_6, file=paste0(activeDirectory,
  "CoTiMAMod2on23Fit_6.rds"))

summary(CoTiMAMod2on23Fit_6)
plot(CoTiMAMod2on23Fit_6, timeUnit = "Months", timeRange = c(1, 36, 1))
```

Figure 41: A partial moderated CoTiMA with a single continuous moderator (`ctmaFit`)

We have seen that the moderator did not have any significant effect. Leaving the lack of significance aside, researchers sometimes want to know if two or more categories have significantly *different* effects on drift parameters. In our example this is a trivial issue because we already know that Category 2 did not significantly change the drift effects obtained for Category 1 as the reference category. However, if a moderator has three or more categories, and some of them have significant effects, the questions could arise if two categories have significantly *different* effects. To test for this possibility, a further argument `catsToCompare` is available for the `ctmaFit` function, which allows contrasting

<sup>12</sup>Plotting the moderator effects is straightforward because for each time interval the change in the drift parameter introduced by the moderator can be depicted as shown in Figure 43. However, summarizing the effect of a moderator in continuous time is not as straightforward because of the non-linearities involved. To do so, the moderator effect is 'linearized' at the mean of the drift effect, and this linearized effect is reported in the `$mod.effects` section.

two categories.

```
CoTiMAModionFullFit_6_cats12 <- ctmaFit(ctmaInitFit = CoTiMAInitFit_6_new,
                                         mod.number = 1,
                                         mod.type = "cat",
                                         mod.names = "Burnout Measure",
                                         catsToCompare = c(1,2),
                                         scaleMod=FALSE)

saveRDS(CoTiMAModionFullFit_6_cats12,
        file=paste0(activeDirectory, "CoTiMAModionFullFit_6_cats12.rds"))

ctmaCompFit(CoTiMAModionFullFit_6_cats12, CoTiMAModionFullFit_6)
```

Figure 42: Comparing the effect of two categories of a categorical moderator (ctmaFit, ctmaCompFit)

Since only two categories exist, `catsToCompare = c(1, 2)` is the only viable option in the present example. In the actually fitted model the moderating effects of Category 1 and Category 2 are restricted to be invariant. If this assumption is valid (i.e., moderating effects are not different for the two categories), the minus 2 loglikelihood (-2ll) value of the restricted model should not be significantly different from the minus 2 loglikelihood (-2ll) value of the unrestricted model. This is tested with the `ctmaCompFit` function at the bottom of Figure 42, which shows (not displayed in a Figure) that the difference in the minus 2 loglikelihood values given 4 degrees of freedom is not significant ( $\Delta - 2ll = 2.6440$ ;  $\Delta df = 4$ ;  $p = 0.6191$ ). In fact, with only two categories available, restricting their effects to be invariant is conceptually identical to assuming there is no moderating effect. Hence, comparing the (unrestricted) moderator model with the full CoTiMA model estimated earlier (which had not moderator effect included), should yield virtually identical results, and indeed `ctmaCompFit(CoTiMAFullFit_6_new, CoTiMAModionFullFit_6)` yields ( $\Delta - 2ll = 2.6448$ ;  $\Delta df = 4$ ;  $p = 0.6189$ ). However, with three or more categories these two minus 2 loglikelihood (-2ll) difference tests will yield diverging results<sup>13</sup>.

The code for a partial moderated CoTiMA with a single *continuous* moderator is shown in Figure 41. Again, the types of primary studies we use in our example impose a difficulty that is likely to occur in many practical circumstances: For some studies the moderator variable is not available and the moderator has therefore be coded as NA. In our example, this was the case for

<sup>13</sup>Instead of `c(1, 2)`, it would also be possible to use indices such as `c(i, j)` and then use a double loop in R to compare all possible combinations of categories. For example:

```
for (i in 1:(numberOfCats-1)) {
  for (j in (i+1):numberOfCats) {
    tmpFit <- ctmaFit(ctmaInitFit = CoTiMAInitFit_object, mod.number = 1,
                     mod.type = "cat", catsToCompare=c(i, j))
    saveRDS(tmpFit, paste0(activeDirectory,
                           "CoTiMAModFit_cat", i, "_", j, ".rds"))
  }
}
```

Study 201 and Study 32. However, instead of going back to square one and compiling a reduced study list followed by applying `ctmaInit` again, we create a temporary study list using `ctmaPrep`, which does no longer include Study 201 and Study 32 (`tmpStudyList`). We use this temporary study list to specify an optional argument of the `ctmaFit` function (i.e., `primaryStudyList = tmpStudyList`). To conduct a moderated CoTiMA, further arguments have to be specified. In the current example in Figure 41 only the cross effects are specified to be moderated. It is recommended to standardize continuous moderators, which is achieved by `scaleMod = TRUE`. The summary (not shown) reveals that control does not significantly reduce  $V2toV1$  (i.e., the moderating effect) by  $-.0203$  from the average effect, which is  $V2toV1 = .2363$  (i.e., the main effect).

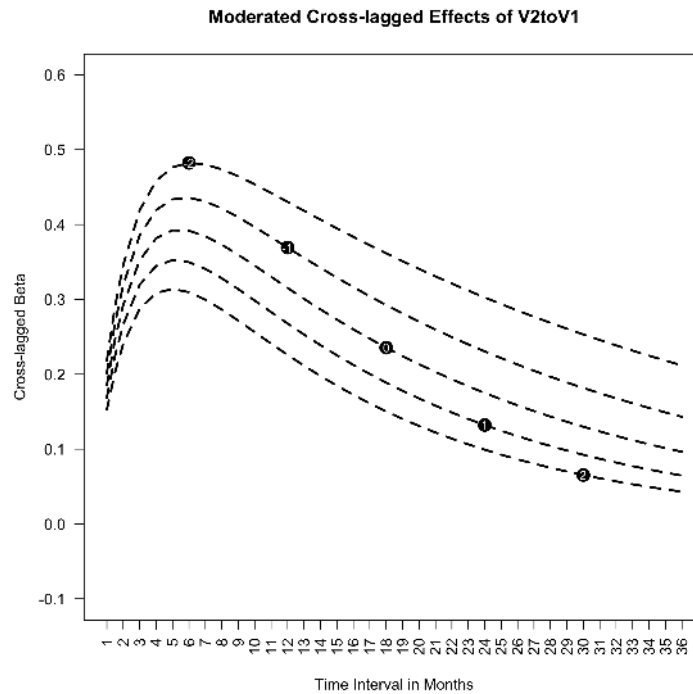


Figure 43: The cross-lagged effect  $V2toV1$  moderated (not significantly) by control at work from 1 to 30 months. The lines show the effect of  $V2toV1$  for control at  $-2SD$  below the mean of control (-2),  $-1SD$  below the mean of control (-1), at the mean of control (0),  $+1SD$  above the mean of control (1), and  $+2SD$  above the mean the mean of control (2). The horizontal location of the SD values has no inherent meaning.

The plot function shown in Figure 41 yields the plot shown in Figure 43. Across all time intervals, for people who have low levels of control at work, effects of demands on burnout are larger than for those with high levels of control. In



most empirical articles that visualize moderator effects for moderator values at  $+2SD$  and  $-2SD$  are not shown. This could be achieved by using `mod.values = c(-1, 0, 1)` as additional argument for the plot function in Figure 41.

## 8 Bias & Generalizability (ctmaBiG)

After finishing the EPIC part of the EPIC-BiG-Power workflow, we can now turn to the first part of the BiG workflow, which is done by using `ctmaBiG`. It performs Egger’s tests for drift coefficients (e.g., Sterne & Egger, 2001) and provides PET-PEESE corrections of fixed effect estimates (Stanley & Doucouliagos, 2014). Random effect estimates are also computed. Various measures of heterogeneity (cf. Borenstein, Hedges, Higgins, & Rothstein, 2009) as well as measures of expected replications rates (ERR) and expected discovery rates (EDR; Bartoš & Schimmack, 2020; Brunner & Schimmack, 2020) are also provided by `ctmaBiG`. The return object of `ctmaBiG` can be used to plot funnel plots and forest plots.

To proceed with `ctmaBiG`, we use the init fit-file published in the online repository of Dormann, Guthier, and Voelke (2020) that belongs to their CoTiMA of job stressors and burnout<sup>14</sup>. The file containing their init fit-object can be retrieved from the website of the Open Science Foundations with the code shown in Figure 44. Note that Guthier et al. (2020) used a preliminary CoTiMA version that was based on the OpenMx R-package (Boker et al., 2011), whereas the file we suggest downloading was created with the rstan R-package (Stan Development Team, 2020b). The latter samples parameter estimates from generated parameter distribution and results thus slightly change from analysis to analysis (unless the argument `finishsamples` is set to a large value, e.g., 10000). So one should expect minor differences compared to the results reported in Guthier et al. (2020). On the other hand, the init fit-object contains all information required to replicate all their results with minor deviations<sup>15</sup>. Note, however, computations would last several hours except of `ctmaBiG`. This is the major reason why we did not use their init fit-object before.

The analysis of bias and generalizability, summarizing the results, and plotting forest plots and funnel plots is achieved with the code in Figure 45. First, results of fixed effects analyses of *single* drift coefficients are displayed. Recall that in CoTiMA all drift effects (full CoTiMA) or a subset (partial CoTiMA) is aggregated simultaneously, thereby taking the entire causal system into account. Thus, CoTiMA estimates a *set* of fixed effects by a multi group SEM

<sup>14</sup>The data set of 6 primary studies we have been using up to this point is not really useful for the analyses presented in this section. First, we introduced missing values for study 128 in order to show how this could be done. This could be useful in full and partial CoTiMAs, but it is mathematically impossible to estimate all four cross effects in this study given that V1 at T1 was missing. The model is said to be mathematically not identified. Excluding study 128 would leave us with five studies only, which would not produce reliable results

<sup>15</sup>In addition to the fitted ctsem models of each primary study, it is possible to extract all information from an init fit-object that were originally compiled with `ctmaPrep` by, e.g., `originalStudyList <- initFitObject$primaryStudyList`. Thus, replicability of CoTiMA results is easily enabled by making one’s init fit-object available for download in a repository, for example, using the Open Science Framework <http://osf.io/>.

```

dl_link <- "https://osf.io/download/qhpae/"
target_file <- paste0(activeDirectory, "/CoTiMAInitFit_D_B0_stanct.rds")
download.file(dl_link, target_file)
CoTiMAInitFit_D_B0 <- readRDS(target_file)
saveRDS(CoTiMAInitFit_D_B0, paste0(activeDirectory, "CoTiMAInitFit_D_B0.rds"))

```

Figure 44: Downloading the Init-Fit file of Guthier et al. (2020)

```

CoTiMABiG_D_B0 <- ctmaBiG(CoTiMAInitFit_D_B0)
summary(CoTiMABiG_D_B0)
plot(CoTiMABiG_D_B0)

```

Figure 45: Analysis of bias and generalizability, summary of results, and plotting (ctmaBiG)

which constraints a set of drift effects to be invariant across groups (i.e., primary studies). Estimation is based on minimization of the discrepancy between the model implied covariance matrices and their empirical counterparts.

Contrary, in terms of a traditional fixed and random effects analysis, the drift effects of all primary studies, which resulted from the initial fitting of ctsem models one by one rather than as a set, are analyzed. Estimation is based on the standard errors of the drift effects rather than on minimizing discrepancies between implied and empirical covariance matrices. The fixed effect estimates of the two cross effects reported in the section **Fixed Effects of Drift Coefficients** of Figure 46 were  $V1toV2 = .0024$  ( $p < .001$ ) and  $V2toV1 = .0054$  ( $p < .001$ ).

The next section in Figure 46 is **Heterogeneity**. Here  $\tau^2$ ,  $H^2$ , and  $I^2$  are shown, of which  $I^2$  is usually of most interest. Note that estimates of  $\tau^2$  were small so even four decimal places are not sufficient to show this. Consequently, between study heterogeneity as indicated by  $I^2$  was larger with the exception of the (small) effect  $V1toV2$ .

The third section (**Random Effects of Drift Coefficients**) in Figure 46 displays the random effect estimates, their *SE*, confidence intervals (**Limit**), and the *z*-values with their associated probability levels. In addition, prediction intervals (**LimitPI**) also allow assessing the degree of heterogeneity. Prediction intervals describe a region in which about 95% of the true study effects are expected to be found (e.g., Guddat, Grouven, Bender, & Skipka, 2012). The effects  $V1toV2 = .0061$  ( $p < .001$ ) and  $V2toV1 = .0114$  ( $p < .001$ ) were larger than their fixed effects counterparts reported earlier. Note that the corresponding CoTiMA (fixed) effects reported by Guthier et al. (2020) were  $V1toV2 = .0039$  ( $p < .001$ ) and  $V2toV1 = .0084$  ( $p < .001$ ), and they were right in the middle between the traditional fixed and random effects estimates.

Part 2 of the results returned from ctmaBiG is shown in Figure 47. These results directly address possible publication bias. Egger's tests (e.g., Sterne & Egger, 2001) is a statistical test of funnel plot asymmetry. Significant results indicate that small-*N* studies produced larger effect sizes (i.e., more positive, if the true effect is positive & more negative, if the true effect is negative), suggest-

```

## $'Fixed Effects of Drift Coefficients'
##           V1toV1  V2toV1  V1toV2  V2toV2
## MeanOfDriftValues    -0.0590  0.0219  0.0112  -0.0539
## FixedEffect_Drift    -0.0219  0.0054  0.0024  -0.0133
## FixedEffect_DriftVariance  0.0000  0.0000  0.0000  0.0000
## FixedEffect_DriftSE      0.0004  0.0004  0.0003  0.0003
## FixedEffect_DriftUpperLimit -0.0211  0.0061  0.0030  -0.0128
## FixedEffect_DriftLowerLimit -0.0227  0.0047  0.0017  -0.0139
## FixedEffect_DriftZ     -54.3360  14.8412  7.4877  -46.5243
## FixedEffect_DriftProb      0.0000  0.0000  0.0000  0.0000
##
## $Heterogeneity
##           V1toV1  V2toV1  V1toV2  V2toV2
## tau2Drift      0.0001  0.0001  0.0000  0.0001
## Q_Drift      772.8459  534.4175  217.4290  1236.0298
## H2_Drift      16.4435  11.3706  4.6261  26.2985
## H2DriftUpperLimit 18.0367  12.6087  5.2890  28.4874
## H2DriftLowerLimit 14.9911  10.2540  4.0463  24.2778
## I2_Drift      93.9186  91.2054  78.3837  96.1975
## I2DriftUpperLimit 94.9455  92.8478  83.4626  96.7594
## I2DriftLowerLimit 92.6831  89.1858  71.7451  95.5382
##
## $'Random Effects of Drift Coefficients'
##           V1toV1  V2toV1  V1toV2  V2toV2
## RandomEffecttot_Drift    -0.0402  0.0114  0.0061  -0.0380
## RandomEffecttot_DriftVariance  0.0000  0.0000  0.0000  0.0000
## RandomEffecttot_DriftSE      0.0021  0.0017  0.0011  0.0021
## RandomEffecttot_DriftUpperLimit -0.0360  0.0147  0.0082  -0.0339
## RandomEffecttot_DriftLowerLimit -0.0444  0.0080  0.0039  -0.0420
## RandomEffecttot_DriftZ     -18.8203  6.6986  5.5511  -18.2134
## RandomEffecttot_DriftProb      0.0000  0.0000  0.0000  0.0000
## RandomEffecttot_DriftUpperLimitPI -0.0169  0.0289  0.0153  -0.0148
## RandomEffecttot_DriftLowerLimitPI -0.0635  -0.0062  -0.0032  -0.0611

```

Figure 46: Part 1 of results of `ctmaBiG`

ing that the aggregated effects are biased. Thus, the results in the `$'Egger's tests'` part of Figure 47 suggest that the cross effects are biased upwards, and the two auto effects are biased downwards. The latter means that demands and burnout in small- $N$  studies are less stable than in large- $N$  studies. This could have many reasons. For instance, if job stress studies with small- $N$  were based on single organizations or single occupations, variance might be restricted, implying lower test-retest correlations eventually resulting in smaller auto effects. Contrary, this reasoning would also imply smaller cross effects, which was not the case. Selective reporting might be a more plausible reason here.

Precision-effect test and precision effect estimates with standard errors (PET-PEESE; Stanley & Doucouliagos, 2014) removes small sample bias (selective reporting) from the fixed effect estimates in an 'aggressive' fashion (Stanley, Carter, & Doucouliagos, 2018, p. 1333). PET-PEESE involves a decision rule when PET or PEESE is more important. The result of this decision is the `PET_PEESE_Drift` row in the section `$'PET-PEESE corrections'` of Figure 43. The `WLS_Drift` estimates of the auto effects `V1toV1` and `V2toV2`, which are

```

## $'PET-PEESE corrections'
##           V1toV1 V2toV1 V1toV2 V2toV2
## PET_Drift      -0.0148 0.0031 0.0010 -0.0079
## PET_SE         0.0014 0.0015 0.0008 0.0010
## PEESE_Drift    -0.0206 0.0048 0.0021 -0.0126
## PEESE_SE       0.0013 0.0012 0.0007 0.0013
## PET_PEESE_Drift -0.0206 0.0048 0.0010 -0.0126
## PET_PEESE_SE   0.0013 0.0012 0.0008 0.0013
## WLS_Drift      -0.0219 0.0054 0.0024 -0.0133
## WLS_SE         0.0016 0.0012 0.0007 0.0015
##
## $'Egger's tests'
##           V1toV1 V2toV1 V1toV2 V2toV2
## Egger's b0 -3.9484 1.4749 1.0973 -4.9827
## SE(b0)     0.5032 0.5854 0.3510 0.5146
## T          -7.8459 2.5196 3.1259 -9.6831
## p          0.0000 0.0153 0.0031 0.0000

```

Figure 47: Part 2 of results of `ctmaBiG`

identical to the fixed effect estimates in Figure 46 (but have more appropriate *SE*), are more negative compared to their corrected `PET_PEESE_Drift` counterparts, but the differences are not very large. This also applies to the *V2toV1* cross effects, representing the effect of earlier burnout on later burnout. However, PET-PEESE of *V1toV2* = .0010, which is less than 1/5 of the fixed effect. Hence, the true effect of earlier demands on later burnout is probably much smaller than suggested by the fixed effect estimate.

Results of Z-Curve 2.0 (Bartoš & Schimmack, 2020) analyses including Expected Replication Rates (ERR) and Expected Discovery Rates (EDR) based are displayed in Figure 48. Figure 48 is limited to the auto effect *V1toV1* and the cross effect *V1toV2* for space reasons.

ERR is the probability of finding a significant effect in an exact replication study. ERR is also called conditional mean power, that is, the mean power of the *subset* of all conducted studies that produced significant effects. The unconditional power, that is, the mean power of *all* conducted studies, is called EDR. To put it differently, EDR is the proportion of all studies (published and unpublished) that found significant effects. EDR can be compared with the actually Observed Discovery Rate (ODR), that is, the proportion of significant effects in the subset of studies that have actually been published or otherwise identified as useful for CoTiMA. If ODR is high and EDR is low, publication bias is likely.

For the auto effect *V1toV1*, one might be tempted to believe that it should virtually always be replicated (some stability over one month should be present). However, the credible interval of *V1toV1* in the study by Jimenez and Dunkl (2017) included 0 (cf. Guthier et al., 2020, Table 1), so that only 47 out of 48 studies produced a significant effect, corresponding to the ODR of .98 in Figure 48. Still, ERR and EDR are very large and the CI always include 1.00. For *V1toV2*, the difference between ODR and EDR is not too large, either, but in this case EDR exceeds ODR. This could happen, especially if ODR is within

```
## $'Z-Curve 2.0 Results: '$'Z-Curve 2.0 analysis of
## V1toV1'
## Call:
## zcurve::zcurve(z = tmp1)
## model: EM via EM
##      Estimate  l.CI  u.CI
## ERR      0.979 0.905 1.000
## EDR      0.710 0.386 1.000
## Model converged in 24 + 69 iterations
## Fitted using 25 z-values. 48 supplied, 47 significant
## (ODR = 0.98, 95% CI [0.88, 1.00]).
## Q = -27.94, 95% CI[-36.08, -18.51]
## $'Z-Curve 2.0 Results: '$'Z-Curve 2.0 analysis of
## V1toV2'
## Call:
## zcurve::zcurve(z = tmp1)
## model: EM via EM
##      Estimate  l.CI  u.CI
## ERR      0.573 0.224 0.824
## EDR      0.507 0.050 0.795
## Model converged in 14 + 221 iterations
## Fitted using 20 z-values. 48 supplied, 21 significant
## (ODR = 0.44, 95% CI [0.30, 0.59]).
## Q = -19.87, 95% CI[-28.16, -9.05]
```

Figure 48: Expected Replication Rates (ERR) and Expected Discovery Rates (EDR) based on Z-Curve 2.0 analysis of *V1toV1* and of *V1toV2* by *ctmaBiG*.

the 95%CI of EDR, and in most instances it could occur simply due to sampling error when there is no publication bias.

Funnel plots and forest plots could be obtained with `plot(CoTiMABiG_D_B0)`. Funnel plots represent the graphical counterpart of Egger's tests, and they plot standard error of effects (an indicator of small  $N$ ; y-axis; large at the bottom & low at the top) against the effect size (x-axis). Without small- $N$  bias, funnel plots would be symmetric. Conversely, funnel plot asymmetry indicates small- $N$  bias. The funnel plot of *V1toV2*, for which Eggers's and PET-PEESE indicated large bias, is shown in Figure 49. Effect sizes are clearly asymmetrically distributed on the right hand side, particularly at the bottom where effect sizes of small- $N$  studies (with large  $SE$ ) are located.

A better impression of the effects obtained in all primary studies is provided in forest plots. The effects for each of the primary studies is represented by a square and their confidence intervals are represented by horizontal lines through these squares. A forest plot of the *V1toV2* effect is shown in Figure 46. The squares vary in size depending on their sample sizes, and they are sometimes small because sample sizes varied considerably across primary studies. The diamond at the bottom shows the aggregated fixed effect. There is no visible horizontal line for its confidence interval because the overall SE was very small and, thus, the confidence interval is rather narrow.

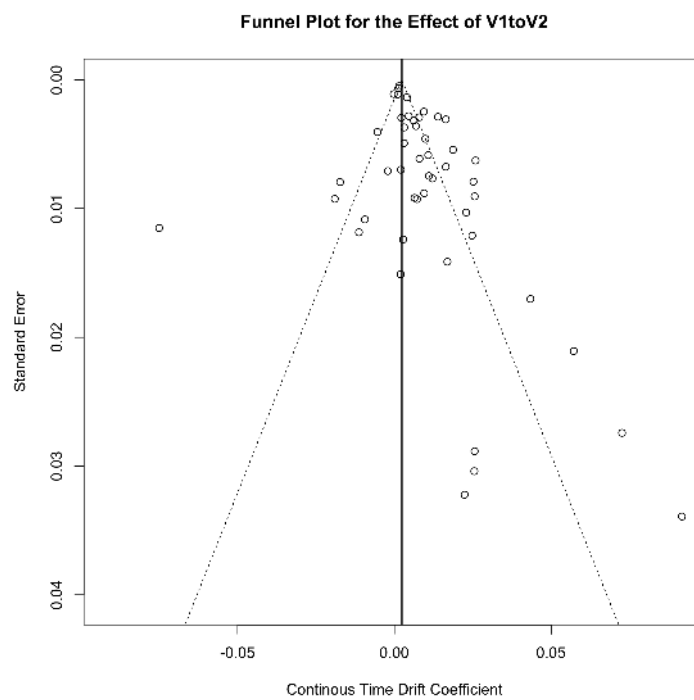


Figure 49: Funnel plot of the effect  $V1toV2$  of the fit object returned by `ctmaBiG` (`plot`)

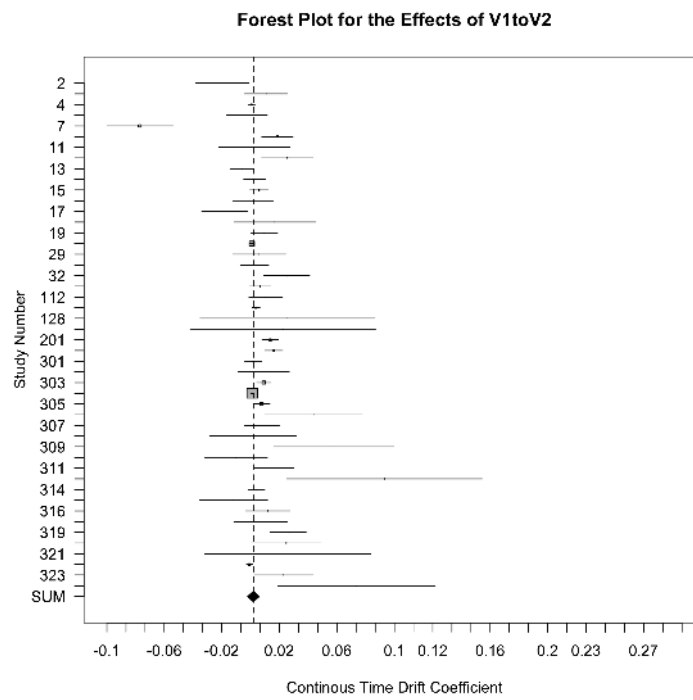


Figure 50: Forest plot of the effect  $V1toV2$  of the fit object returned by `ctmaBiG` (`plot`)

## 9 Statistical Power (ctmaPower)

Finally, we can turn to the Power part of the EPIC-BiG-Power workflow, which can be performed with `ctmaPower`. It conducts two types of analyses. First, it estimates required sample sizes for a range of different time intervals to achieve a desired statistical power. This is important for designing future studies. Second, it calculates the expected power for all primary studies (some-times also referred to as post hoc power or retrospective power). This is important to know if past studies might have failed to replicate effects with statistical significance because they were under-powered.

```
CoTiMAPower_D_BO <- ctmaPower(ctmaInitFit=CoTiMAInitFit_D_BO,
                             statisticalPower = c(.50, .80, .95),
                             coresToUse = -1,
                             finishsamples = 10000)
saveRDS(CoTiMAPower_D_BO, file=paste0(activeDirectory,
                                       "CoTiMAPower_D_BO.rds"))
summary(CoTiMAPower_D_BO)
```

Figure 51: Calculating expected (post hoc) power for three different probability levels (`ctmaPower`)

To calculate statistical power, a highly restrictive CoTiMA model has to be estimated. In the regular full CoTiMA, all drift effects are constrained to be invariant across primary studies. To calculate statistical power, a more restrictive model is required that, in addition, constraints the variance and covariances at T0 as well as the diffusion coefficients to be invariant. This model was previously used to include studies with two waves only and a missing variable (see Subsection 7.1.1). Stated differently, one has to assume all samples analyzed in the primary studies were drawn from the same population. There are several arguments that can be used with `ctmaPower`, and they are enumerated in the Appendix. In most cases, requesting the desired levels of power in addition to the init fit-object is probably sufficient. We used the code in Figure 51 for generating the subsequently discussed output and the figures.

|                            |  |         |        |          |        |          |        |        |
|----------------------------|--|---------|--------|----------|--------|----------|--------|--------|
| ##                         |  | V1toV1  | (SE)   | Tvalue   | V2toV1 | (SE)     | Tvalue | V1toV2 |
| ## Fixed Effects Drift     |  | -0.0525 | 0.0009 | -58.3333 | 0.0164 | 0.0008   | 20.5   | 0.0119 |
| ## Fixed Effects Diffusion |  | 0.0975  | 0.0013 | 75.0000  | 0.0096 | 0.0008   | 12.0   | 0.0096 |
| ## Fixed Effects T0Var     |  | 0.9982  | 0.0087 | 114.7356 | 0.3757 | 0.0065   | 57.8   | 0.3757 |
| ##                         |  | (SE)    | Tvalue | V2toV2   | (SE)   | Tvalue   |        |        |
| ## Fixed Effects Drift     |  | 0.0007  | 17.0   | -0.0428  | 0.0007 | -61.1429 |        |        |
| ## Fixed Effects Diffusion |  | 0.0008  | 12.0   | 0.0818   | 0.0010 | 81.8000  |        |        |
| ## Fixed Effects T0Var     |  | 0.0065  | 57.8   | 0.9984   | 0.0087 | 114.7586 |        |        |

Figure 52: Estimates of drift parameters using a model with all variance and covariances at T0, all drift effects, and all diffusion coefficients invariant across primary studies (`ctmaPower`)

Then, `summary(CoTiMAPower_D_BO)` creates a large output on the console that we again discuss in parts. Figure 52 displays the parameter estimates of



the model with *all* effects being invariant. These are the parameter estimates that are regarded as the *true* effects (mean of the distribution of true effects). In concert with the sample sizes and the time intervals of the primary studies (both are taken from `CoTiMAInitFit_D_B0` and do not need to be provided as arguments) the true effects determine the statistical power of the primary studies to achieve significance levels of  $\alpha = .05$  and  $\alpha = .01$ . Further, across a range of time intervals (could be provided with the argument `timeRange`; otherwise it is from 1 to 1.5 times the longest interval used in primary studies), the true effects determine the required sample sizes to and achieve the requested levels of statistical power.

| ##             | N    | Lag  | Power (.05) | Power (.01) | Lag  | Power (.05) | Power (.01) |
|----------------|------|------|-------------|-------------|------|-------------|-------------|
| ## Study_No_1  | 148  | 12   | 0.2068      | 0.0751      | <NA> | <NA>        | <NA>        |
| ## Study_No_2  | 188  | 12   | 0.2513      | 0.0983      | <NA> | <NA>        | <NA>        |
| ## Study_No_3  | 556  | 96   | 0.0527      | 0.0127      | <NA> | <NA>        | <NA>        |
| ## Study_No_4  | 261  | 12   | 0.3306      | 0.145       | <NA> | <NA>        | <NA>        |
| ## Study_No_5  | 1378 | 18   | 0.9461      | 0.839       | <NA> | <NA>        | <NA>        |
| ## ...         | ...  | ...  | ...         | ...         | ...  | ...         | ...         |
| ## Study_No_24 | 195  | 3    | 0.1343      | 0.0422      | <NA> | <NA>        | <NA>        |
| ## Study_No_25 | 999  | 12   | 0.8474      | 0.6581      | 12   | 0.8474      | 0.6581      |
| ## Study_No_26 | 668  | 12   | 0.6844      | 0.4449      | 12   | 0.6844      | 0.4449      |
| ## Study_No_27 | 370  | 12   | 0.4419      | 0.222       | 12   | 0.4419      | 0.222       |
| ## ...         | ...  | ...  | ...         | ...         | ...  | ...         | ...         |
| ## Study_No_48 | 171  | 3    | 0.1228      | 0.0375      | <NA> | <NA>        | <NA>        |
| ## Mean        | <NA> | <NA> | 0.3957      | 0.2407      | <NA> | <NA>        | <NA>        |
| ## Median      | <NA> | <NA> | 0.3142      | 0.1348      | <NA> | <NA>        | <NA>        |

Figure 53: Expected (post hoc) power across primary studies (`ctmaPower`)

The next section in the generated output reports the expected power of primary studies. For the effect of *V1toV2*, this is displayed in Figure 53. Note that in Guthier et al. (2020) we reported numerical problems in estimating the expected statistical power across short time intervals – since then we solved this issue. We left out several studies (6 to 23 & 28 to 47) for space reasons here. Assuming the aggregated effects in Figure 53 are the true effects, the probability values in Figure 53 represent the statistical power each primary study had to detect the focal true *V1toV2* effect (i.e., .0119; see Figure 52) with  $p < .05$  and  $p < .01$ . For those studies with more than two measurement occasions, the statistical power is reported for all adjacent time intervals. At the bottom, median and mean statistical power across all primary studies is shown. For instance, the median statistical power was .3142 to find a significant *V2toV1* effect with  $p < .05$ . As in most meta-analyses, this demonstrates that many primary studies are heavily under-powered and finding a significant effect is less likely than like getting heads-up when flipping a coin.

The generated output further shows the required samples sizes for (future) studies to obtain significant effects across different time intervals (Figure 54). Note that in Guthier et al. (2020) we reported numerical problems in estimating the required samples across short time intervals – since then we solved this issue. For most effects and most desired levels of statistical power, required sample sizes are lowest around 16-18 month intervals. We show how to plot

| ##       | V1toV2 | Power=0.5 | V1toV2 | Power=0.8 | V1toV2  | Power=0.95 |
|----------|--------|-----------|--------|-----------|---------|------------|
| ## 1     | 2737   |           | 5589   |           | 9251    |            |
| ## 1.5   | 1876   |           | 3830   |           | 6339    |            |
| ## 2     | 1447   |           | 2953   |           | 4888    |            |
| ## 3     | 1020   |           | 2082   |           | 3445    |            |
| ## 4     | 810    |           | 1652   |           | 2733    |            |
| ## ...   | ...    |           | ...    |           | ...     |            |
| ## 15    | 416    |           | 847    |           | 1400    |            |
| ## 16    | 415    |           | 844    |           | 1396    |            |
| ## 17    | 415    |           | 846    |           | 1399    |            |
| ## 18    | 418    |           | 851    |           | 1407    |            |
| ## 19    | 421    |           | 859    |           | 1420    |            |
| ## 20    | 427    |           | 869    |           | 1437    |            |
| ## 21    | 433    |           | 882    |           | 1459    |            |
| ## ...   | ...    |           | ...    |           | ...     |            |
| ## 142   | 345410 |           | 705741 |           | 1168433 |            |
| ## 143   | 368470 |           | 752857 |           | 1246439 |            |
| ## 144   | 393512 |           | 804022 |           | 1331148 |            |
| ## ---   | ---    |           | ---    |           | ---     |            |
| ## Min N | 415    |           | 844    |           | 1396    |            |

Figure 54: Required sample sizes to achieve requested levels of statistical power across a range of time intervals (**ctmaPower**)

required sample sizes against time interval later. Note that the output showing the required sample sizes would also display the expected (discrete time) effect sizes, which we omitted from Figure 54.

The last interesting output deals with combinations of possible time intervals and samples sizes, and it informs about the range of time intervals across which one could expect significant effects. If neither a sample size (**failSafeN**) nor a  $p$ -level (**failSaveP**) is provided as function argument, the average sample size of the primary studies is used (otherwise the values assigned to **failSafeN**) and  $p < .01$  (otherwise the values assigned to **failSaveP**) are used. As the **\$estimates\$'Range of significant effects'** section in Figure 55 reports, with  $N$  corresponding to the average  $N = 549$  across primary studies, one should select time intervals between 8-32 months to find a significant  $V2toV1$  effect. With the average  $N$  used in primary studies, one cannot expect finding a significant  $V1toV2$  effect across neither time interval.

Finally, required sample sizes can be plotted. We used `plot(CoTiMAPower-_D_B0, timeUnit="Months", timeRange=c(1, 84, 1) )` to generate the plot displayed in Figure 56. This figure is based on the values previously shown in parts in Figure 54

```

## [1] The shortest interval across which the effect (V2toV1) is
## significant with  $p < 0.01$  assuming  $N = 549$  (= avg.  $N$ ) is 8. The
## longest interval across which the effect (V2toV1) is significant with
##  $p < 0.01$  assuming  $N = 549$  (= avg.  $N$ ) is 32. Note that you have not
## provided an explicit time range for analysis of statistical power. The
## time intervals used ranged from 1 to 1.5 times the longest interval
## used in the primary studies, using integer steps of 1.0. These
## intervals were then augmented by time intervals found in primary
## studies that were non-integers.
## [2] There is no shortest interval across which the effect (V1toV2) is
## significant with  $p < 0.01$  assuming  $N = 549$  (= avg.  $N$ ). There is no
## longest interval across which the effect (V1toV2) is significant with
##  $p < 0.01$  assuming  $N = 549$ . Note that you have not provided an
## explicit time range for analysis of statistical power. The time
## intervals used ranged from 1 to 1.5 times the longest interval used in
## the primary studies, using integer steps of 1.0. These intervals were
## then augmented by time intervals found in primary studies that were
## non-integers.

```

Figure 55: Expected range across which significant effects could be expected (ctmaPower)

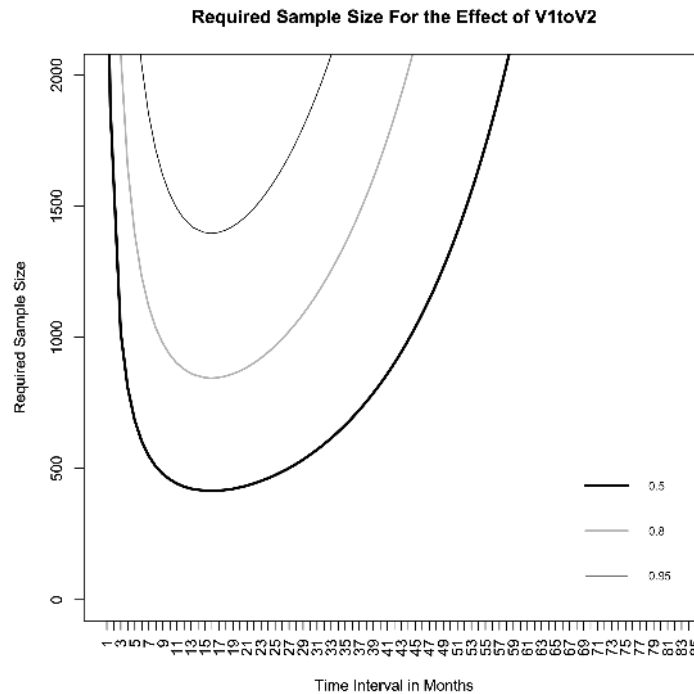


Figure 56: Required sample sizes across time to achieve a statistical power of .50, .80, and .95 (plot)

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## Appendix. Overview of CoTiMA Functions and their Arguments

| ctmaBiG (EPIC-BiG-Power) |   |                        | Performs fixed effect, random effect analysis, and analysis of publication bias (Egger's tests, PET-PEESE corrections, z.curve analysis). |
|--------------------------|---|------------------------|---|
| Argument                 | Default                                 | Possible Values        | Explanation   |
| ctmaInitFit              | NULL                                    | CoTiMA fit object      | CoTiMA fit object created with <b>ctmaInit</b> .  |
| activeDirectory          | path used to create ctmaInit-Fit object | character string       | Specifies the directory where required files are found and saved. Should end with "/". For example, <b>"/Users/GDC/CoTiMA/"</b>           |
| PETPEESEalpha            | .10                                     | values between 0 and 1 | Probability level (condition) below which to change from PET to PEESE.  |
| activateRPB              | FALSE                                   | FALSE/ TRUE            | Messages (warning, finished fitting) could be send to mobile phone if TRUE.   |
| digits                   | 4                                       | value > 0              | Rounding used in output.  |

| ctmaCompFit (EPIC-BiG-Power) |         |                   | Compares the fit of two nested CoTiMa models via -2ll difference test.                  |
|------------------------------|---------|-------------------|---|
| Argument                     | Default | Possible Values   | Explanation   |
| model1                       | NULL    | CoTiMA fit object | CoTiMA fit object created with <b>ctmaInit</b> , <b>ctmaFit</b> , or <b>ctmaEqual</b> . |
| model2                       | NULL    | CoTiMA fit object | CoTiMA fit object created with <b>ctmaInit</b> , <b>ctmaFit</b> , or <b>ctmaEqual</b> . |

| ctmaCorRel (EPIC-BiG-Power) |         |  | Corrects (disattenuates) correlation matrix for unreliabilities. |
|-----------------------------|---------|--|--|
| Argument                    | Default | Possible Values  | Explanation  |
| empcov                      | NULL    | symmetric correlation matrix                                 |  |
| alphas                      | NULL    | vector of the same length as dimensionality of <b>empcov</b> |  |

| ctmaEmpCov (EPIC-BiG-Power) |                  |  | Changes a full correlation matrix by selecting target variables, recode them, combine them (add), and add rows/columns with NA if focal variables are missing.   |
|-----------------------------|------------------|--|--|
| Argument                    | Default          | Possible Values                                | Explanation  |
| targetVariables             | NULL             | vector of variable positions or variable names | Selects desired variables in <code>empcov<i>i</i></code> (i.e., deletes those variables that should not be analyzed). For example, <code>c(1, 2, 4, 5)</code> deletes the 3rd and 6th row and column in a $6 \times 6$ <code>empcov<i>i</i></code> . Instead of positions, variable names could be used if <code>dimnames</code> were assigned to <code>empcov<i>i</i></code> .  |
| recodeVariables             | <code>c()</code> | vector of variable positions or variable names | Recodes desired variables in <code>empcov<i>i</i></code> (i.e., changes the signs of the correlations). For example, <code>c(1, 4)</code> changes the signs of the correlations in the 1st and 4th row of <code>empcov<i>i</i></code> . Instead of positions, variable names could be used if <code>dimnames</code> were assigned to <code>empcov<i>i</i></code> . Note that if numbers are used, they should correspond to the positions in the <code>targetVariables<i>i</i></code> object rather than the rows/columns in the <code>empcov<i>i</i></code> object (i.e., recoding is done after <code>targetVariables<i>i</i></code> were selected from <code>empcov<i>i</i></code> ). |
| combineVariables            | <code>c()</code> | list of (vectors of) variable positions        | Creates composite variables (i.e., means of one or more variables). Variables that should be combined have to be listed in a vector. Variables that should not be combined have to be listed, too. For example, <code>list(1, c(2, 3), 4, c(5, 6))</code> combines the 2nd and 4th as well as the 5th and 6th variables of <code>empcov<i>i</i></code> . and leaves the 1st and 4th variable untouched. Instead of positions, variable names could be used if they were also used in the argument <code>targetVariables</code> .   |
| combineVariables-Names      | <code>c()</code> | vector variable names for combined variables   | not yet operational  |
| missingVariables            | <code>c()</code> | vector of variable positions                   | Augments <code>empcov<i>i</i></code> and <code>pairwiseN<i>i</i></code> by rows and columns containing NA in order to create matrices of the desired dimension. For example, if the desired matrix should contain correlations of the four variables $x_0, y_0, x_1$ and $y_1$ , but a primary study did not measure $y_1$ , then the 4th variable is missing and the correlation matrix returned by <code>ctmaEmpCov</code> will be a $4 \times 4$ <code>empcov<i>i</i></code> and a $4 \times 4$ <code>pairwiseN<i>i</i></code> with NA in the 4th row and in the 4th column, respectively.  |

| ctmaEmpCov (EPIC-BiG-Power) |      |  | Changes a full correlation matrix by selecting target variables, recode them, combine them (add), and add rows/columns with NA if focal variables are missing. |
|-----------------------------|------|--|--|
| nlatents                    | NULL | value > 0  | The number of (latent) variables. Actually it is the number of all variables at T0. A distinction between latent and manifest variables is not made here.      |
| Tpoints                     | NULL | value > 1  | The number of time points.   |
| sampleSize                  | NULL | value > 0  | The sample size. It does not need to be specified if pairwiseN <sub>i</sub> is provided instead.   |
| pairwiseN                   | NULL | symmetrix matrix of same dimensions as empcov containing possible pairwiseN. | A matrix with sample sizes for each correlation of empcov <sub>i</sub> .   |
| empcov                      | NULL | symmetric correlations matrix  | Correlation matrix reported in a primary study.  |

| ctmaEqual (EPIC-BiG-Power) |   |                   | Statistically tests if the two or more invariant drift parameters in the Co-TiMAFit object supplied are equal   |
|----------------------------|---|-------------------|---|
| Argument                   | Default                                 | Possible Values   | Explanation   |
| ctmaInvariantFit           | NULL                                    | CoTiMA fit object | CoTiMA fit object thas was returned by ctmaFit. In most cases this is probably the fit of a model in which two effects were specified with the invariantDrift argument (e.g., two cross effects).                             |
| activeDirectory            | path used to create ctmaInit-Fit object | path to directory | Specifies the directory where required files are found and saved. Should end with “/”.  |
| activateRPB                | FALSE                                   | FALSE/ TRUE       | Messages (warning, finished fitting) could be send to mobile phone if TRUE.   |
| digits                     | 4                                       | value > 0         | Rounding used in output.  |
| coresToUse                 | 1                                       | value > 0 or < 0  | The number of cores (threads) to be used for fitting. If a negative values is specified, the value is subtracted from available cores, else the value sets the number of cores to be used. Should usually be 1 on Windows OS. |



| ctmaEx (-) |         |   | Loads R objects created in the examples (figures) of this User's Guide into the user's R environment   |
|------------|---------|---|--|
| Argument   | Default | Possible Values   | Explanation  |
| example    | NULL    | The figure in this User's Guide in which the desired R oibjects are created | The 'Figure' + number (e.g., 'Figure 2') which contains the R objects that should be loaded or fitted. For example, <code>ctmaEx('Figure 2')</code> loads <code>empocv2</code> , <code>delta_t2</code> in the user's R environment.                |
| do         | 'add'   | 'add' or 'remove'   | Specifies wether the desired R objects should be added or removed from the user's R environment. For example, <code>ctmaEx("Figure 3", fit=TRUE)</code> creates the <code>CoTiMAstudyList_3</code> by applying the <code>ctmaPrep</code> function. |
| fit        | FALSE   | FALSE/ TRUE   | Specifies of CoTiMA objects (i.e. objects created wi a <code>ctmaXxx</code> function) should only be loaded or actually be fitted  |

| ctmaFit (EPI $\mathcal{C}$ -BiG-Power) |  |  | Fits a CoTiMA model.   |
|--|--|--|--|
| Argument                               | Default  | Possible Values                                    | Explanation  |
| ctmaInitFit                            | NULL   | CoTiMA fit object                                  | Object to which all single ctsem fits of primary studies has been assigned to (i.e., what has been returned by <code>ctmaInit</code> )   |
| primaryStudyList                       | NULL   | list of primary studies                            | A list of primary studies compiled with <code>ctmaPrep</code> that contains a subset of studies included in <code>ctmaInitFit</code> . Useful to exclude studies without the need to use <code>ctmaInit</code> again.                      |
| cluster                                | NULL   | vector of same length as number of primary studies | Vector with cluster variables (e.g., countries), e.g., <code>c(1, 1, 1, 3, 3, 6, 7, 8)</code> . Has to be set up carfully. Will be included in <code>ctmaPrep</code> later.  |
| activeDirectory                        | path used to create <code>ctmaInit-Fit</code> object | path to directory                                  | Specifies the directory where required files are found and saved. Should end with <code>"/"</code> .   |
| activateRPB                            | FALSE  | FALSE/ TRUE  | Messages (warning, finished fitting) could be send to mobile phone if <code>TRUE</code> .  |
| digits                                 | 4  | value > 0  | Rounding used in output.   |
| drift                                  | NULL (=all)  | vector (!) of rowwise drift matrix elements        | Labels for drift effects that should or should not be included. Have to be either of the type <code>V1toV2</code> or 0 for effects to be excluded, which is usually not recommended, e.g., <code>c("V1toV1", "V2toV1", 0, "V2toV2")</code> |
| invariantDrift                         | NULL (=all)  | vector of drift effects                            | Labels for drift effects that should be aggregated. Have to be of the type <code>V1toV2</code> , e.g., <code>c("V2toV1")</code>  |

| ctmaFit (EPI $\mathcal{C}$ -BiG-Power) |                  |  | Fits a CoTiMA model.  |
|--|------------------|--|---|
| moderatedDrift                         | NULL<br>(=all)   | vector of drift effects                | Labels for drift effects that should be moderated. Have to be of the type V1toV2, e.g., c("V2toV1"). Is only used if moderators are specified.  |
| equalDrift                             | NULL             | vector of 0 or 2 or more drift effects | Labels for drift effects that should be set equal. Have to be of the type V1toV2, e.g., c("V2toV1", "V1toV2"). Is useful, for example, to test if the sizes of cross effects are statistically different.   |
| mod.number                             | NULL             | vector of positions of moderators      | The position(s) of the moderator(s) in the the vector of moderator values compiled with ctmaPrep, which should be used in a moderated CoTiMA, e.g., c(1, 3).  |
| mod.type                               | "cont"           | "cont" or "cat"                        | Type of moderator(s). Categorical and continuous moderators could not be used in combination, but more than one continuous or more than one categorical moderator is possible.  |
| mod.names                              | NULL             | (vector of) character object(s)        | Names used to label moderators in the output .  |
| indVarying                             | FALSE            | TRUE / FALSE                           | Specifies a random (manifest) intercept model. Still experimental.  |
| coresToUse                             | 1                | value > 0 or < 0                       | The number of cores (threads) to be used for fitting. If a negative values is specified, the value is subtracted from available cores, else the value sets the number of cores to be used. Should usually be 1 on Windows OS.   |
| scaleTI                                | NULL<br>(=FALSE) | TRUE / FALSE                           | With the move from the omx (OpenMX) version of ctsem to the stanct (stan) version, CoTiMA moved from fitting a multi group model to a model in which the groups are represented by dummy variables. These are internally handled as time independent (TI) predictors, and scaleTI specifies whether or not these dummy variables should be standardized. Recommended since version 0.5.3.1 and set to TRUE . Note that standardizing dummies for primary studies does not affect estimation of aggregated effects. However, without standardization the sutdy-specific effects (in which meta-analysist are usally <i>not</i> interested in) cannot be interpreted as within-study effects. |

| ctmaFit (EPI $\mathcal{C}$ -BiG-Power) |       |              | Fits a CoTiMA model.  |
|--|-------|--------------|---|
| scaleMod                               | FALSE | FALSE / TRUE | <p>Whether or not continuous moderators should be standardized or categorical moderators should be centered. Recommended for continuous moderators. The default value <b>FALSE</b> is taken from the <b>CoTiMAStanctArgs</b> list, which could also be used to specify more stanct fitting parameters.</p> <p>With categorical moderators, the argument <b>scaleMod=TRUE</b> leads to centring rather than standardization, which requires some explanation. Categorical moderators are internally transformed into dummy variables. The smallest category value represents the reference category. For instance, if 1 &amp; 2 are unused, 3 is &lt; 19 yrs old, 4 = 19-60 yrs, 5 = all ages mixed, two dummy variables are created. Dummy 1 is 1 if a primary study included people aged 19-60 only, and Dummy 1 is 0 in all other cases. Dummy 2 is 1 if a primary study included people with ages mixed, and dummy 2 is 0 in all other cases.</p> <p>If the argument <b>scaleMod=FALSE</b> is used in combination with categorical moderators, the resulting drift effects are those for the reference category, that is, for studies including people &lt; 19 yrs only. The effect of Dummy 1 the represents the changes that result if a study includes people aged 19-60 rather than &lt; 19 yrs. If this effect is significant, the interpretation is that the effect is significantly different compared to the effect found in studies using people &lt; 19 yrs only. Correspondingly, the effect of Dummy 2 the represents the changes that result if a study includes people with all ages mixed rather than &lt; 19 yrs.</p> <p>If the argument <b>scaleMod=TRUE</b> is used in combination with categorical moderators, the internally created dummy variables are centered (but not standardized; see the argument <b>transfMod</b> to circumnvent this default behavior and standardize them anyway). The resulting drift effects are not longer those for the reference category. Rather, they represent the average effetc across all studies and all moderator categories. The effect of the centred Dummy 1 now represents the mean difference between studies including people aged 19-60 and all other studies. If the effect of Dummy 1 is significant, its interpretation is that this category has a significantly different effect compared to all other categories. It does, however, no longer inform about the sizes of the drift effects resulting for this category.</p> <p>Since one is usually interested in both the size of a drift effect for a particular category and if it is significantly different, we recommend not centring the dummy variables representing categorical moderators (i.e., the argument <b>scaleMod=FALSE</b> should be used). See the argument <b>catsToCompare</b> to analyzed difference between catagories anyway.</p> |

| ctmaFit (EPI $\mathcal{C}$ -BiG-Power) |               |  | Fits a CoTiMA model.   |
|--|---------------|--|--|
| <b>transfMod</b>                       | NULL          | character vector applying R functions to x | Can be used as a replcement of <b>scaleMod</b> if more than one moderator is analyzed and standardization is not desired for all moderators. Then, it could take the form <b>transfMod=c("scale(x)", "x" "scale(x)").</b> Alternatively, users can define their own functions, e.g., <b>transfMode=("(x - mean(x))")</b> ; this function centralizes a single moderator without standardization. Another example is <b>transfMode=("scale(x) - min(x)")</b> , which standardizes x and then shif values to a scale beginning with 0.0. This yields the (unmoderated) drift effects for the reference group with them smallest moderator value.   |
| <b>scaleTime</b>                       | NULL (=FALSE) | value > 0                                  | Wether or not the time scale used for <b>delta_ti</b> should be changed.For example, <b>scaleTime=1/12</b> could change the time scale from months to years. It is usually recommended to avoid <b>delta_ti</b> larger than 6. The default value <b>FALSE</b> is taken from the <b>CoTiMAStanctArgs</b> list, which could also be used to specify more stanct fitting parameters.  |
| <b>scaleClus</b>                       | FALSE         | FALSE/TRUE                                 | The argument <b>scaleCLUS=TRUE</b> leads to centring of dummy variables representing different clusters. If the argument <b>scaleClus=FALSE</b> is used, the resulting drift effects are those for the reference cluster. The reference cluster either is a cluster that consists of all cluster values tha are unique (see main text for explanation) or the cluster with the larged number. If the argument <b>scaleClus=TRUE</b> is used, the internally created dummy variables are centered (but not standardized). The resulting drift effects are not longer those for the reference cluster. Rather, they represent the average effetc across all studies and all clusters. The effect of the centred cluster dummies now represent the mean difference between studies belonging to a particular cluster and all other studies. Since one is usually interested in both the size of a drift effect for a particular cluster , we recommend not centring the dummy variables representing clusters (i.e., the argument <b>scaleClus=FALSE</b> should be used). |

| ctmaFit (EPI $\mathcal{C}$ -BiG-Power) |              |              | Fits a CoTiMA model.   |
|--|--------------|--------------|--|
| optimize                               | TRUE         | TRUE / FALSE | The <b>optimize</b> argument is passed to ctStanFit. If <b>FALSE</b> , Bayesian estimations is used. The chosen sampler is conditional on the <b>nopriors</b> argument. Note that this works differently than the <b>optimise</b> argument of ctSatFit.  |
| nopriors                               | TRUE         | TRUE / FALSE | Consequences of <b>TRUE</b> or <b>FALSE</b> are conditional on the <b>optimize</b> argument. <b>optimize=TRUE &amp; nopriors=TRUE</b> implies maximum likelihood estimation, <b>optimize=TRUE &amp; nopriors=FALSE</b> implies maximum a posteriori estimation, <b>optimize=FALSE &amp; nopriors=TRUE</b> implies Bayesian estimation using HMC (Hamiltonian Monte Carlos sampler), and <b>optimize=FALSE &amp; nopriors=FALSE</b> implies Bayesian estimation using NUTS (No U-Turn Sampler). |
| finishesamples                         | NULL (=1000) | values > 0   | The <b>finishesamples</b> argument is passed to ctStanFit. It specifies the number of samples to draw for final results computation. Larger (e.g., 10.000) values make results more exactly replicable. Larger values are recommended before manuscripts are submitted. Very large values (e.g., 100.000) might be helpful if very small effects (e.g., 0.0002) result from estimation.  |
| iter                                   | NULL (=1000) |              | The <b>iter</b> argument is passed to ctStanFit. It specifies the number of iterations used for Bayesian estimation, half of which will be devoted to warmup.  |
| chains                                 | NULL (=2)    |              | The <b>chains</b> argument is passed to ctStanFit and specifies the number of chains to be used for Bayesian estimation.   |
| verbose                                | NULL         | 0, 1, or 2   | The <b>verbose</b> argument is passed to ctStanFit. Higher values print more information during model fit.   |
| allInvModel                            | FALSE        | TRUE / FALSE | Whether or not a model should be tested in which all (!) parameters are assumed to be invariant across primary studies. If set <b>TRUE</b> , other specifications (e.g., specified with the <b>equalDrift</b> argument) will be ignored. An all invariant model is also used by <b>ctmaPower</b> .   |

| <b>ctmaFit (EPI<math>\mathcal{C}</math>-BiG-Power)</b> |      |  | Fits a CoTiMA model.   |
|--|------|--|--|
| <b>customPar</b>                                       | TRUE | FALSE / TRUE   | If set TRUE some starting values usually used by ctSatFit will be used by CoTiMA specific settings. Not recommended to be used in combination with Bayesian estimation. It was introduced to improve handling of large values used in <b>delta_ti</b> . Setting it to FALSE and use <b>scaleTime</b> instead could be a better alternative if estimation problems will nevertheless occur.   |
| <b>modsToCompare</b>                                   | NULL | vector of positions of selected (!) moderators       | This argument is the 1st out of 3 used to specify contrast among categorical moderators. The values define the position(s) of the moderator(s) in the the vector of moderator values selected with the <b>mod.number</b> argument (see above). For example, if <b>mod.number=c(1, 4, 6)</b> was specified before, <b>modsToCompare=2</b> specifies that subsequent contrasts will be performed for the moderator at the 4th position of the moderator(s) in the the vector of moderator values compiled with <b>ctmaPrep</b> .   |
| <b>catsToCompare</b>                                   | NULL | vector of categories' values that should be compared | This argument is the 2nd out of 3 used to specify contrast among categorical moderators. Compared to an unconstrained moderator model, the effects of the categories of the vector specified are set equal. This will reduce the fit (i.e., increase the -2ll value), which can be used for comparing it with the unconstrained model. A significant difference indicates that the categories' effects are not equal. For example, <b>catsToCompare=c(2, 3)</b> sets the drift effects (see below) for categories 2 and 3 equal. Note that the smallest category selected will become the new comparison category (instead of the lowest of all category numbers) and the output will be labelled accordingly. |
| <b>driftsToCompare</b>                                 | NULL | string vector of drift names                         | This argument is the 3rd out of 3 used to specify contrasts among categorical moderators. The strings in the vector define which drift effects is analyzed for possible differences among categories of the moderator(s). For example, <b>driftsToCompare=c("V1toV2")</b> together with <b>catsToCompare=c(2, 3)</b> and <b>modsToCompare=2</b> fits a model in which the effect of category 2 and 3 on the drift parameter "V1toV2" of the second moderator is set equal.   |

| ctmaFitList (plotting) |         |  | Informes the plot function that more than a single CoTiMA fit object should be plotted. |
|------------------------|---------|--|---|
| Argument               | Default | Possible Values                        | Explanation   |
| ...                    | nothing | CoTiMA fit objects separated by commas | For example, <code>ctmaFitList(object1, object2)</code> .                               |

| ctmaGetPub (-)              |         |                                 | Retrieves publication and citation indices for authors from Google Scholar, which could be further processed with <code>ctmaPub</code> .  |
|-----------------------------|---------|---------------------------------|---|
| Argument                    | Default | Possible Values                 | Explanation   |
| <code>authorList</code>     | NULL    | List of vectors with 2 elements | Contains information about authors' names and their Google Scholar https address (or their user ID), e.g., <code>list(c("Wilmar B.; Schaufeli", "https://scholar.google.de/citations-hl=en&amp;user=w1tHcj4AAAAJ"), c("Maureen; Dollard", "user=J6oH3rgAAAAJ"))</code> . Authors' surnames are separated from given names or initials by a semicolon! |
| <code>flush</code>          | FALSE   | TRUE / FALSE                    | Argument is handed over to scholar R package. If TRUE, the cache will be cleared and the data reloaded from Google Scholar. Google Scholar will limit the retrieval of information or even suspend it for a while if the cache is flushed too frequently.   |
| <code>yearsToExclude</code> | NULL    | (vector of) years to exclude    | Recommended to leave as NULL. Years could be excluded later when using <code>ctmaPub</code> .   |

| ctmaOptimizeInit (-)         |         |                  | Initial fitting (i.e., applies <code>ctmaInit</code> ) to a primary study several times to capitalize on chance for obtaining a hard-to-find optimal fit.   |
|------------------------------|---------|------------------|---|
| Argument                     | Default | Possible Values  | Explanation   |
| <code>primaryStudies</code>  | NULL    | list             | A list created with <code>ctmaPrep</code> that contains all information (e.g., <code>empcovi</code> , <code>delta_ti</code> , <code>sampleSize</code> etc.) relevant for <code>ctmaInit</code> and subsequent analyses. |
| <code>activeDirectory</code> | NULL    | character string | Specifies the directory where required files are found and saved. Should end with <code>"/</code> . For example, <code>"/Users/GDC/CoTiMA/"</code>  |
| <code>problemStudy</code>    | NULL    | value > 0        | Number of the study (not the position) in the <code>primaryStudies</code> list that should be re-fitted.  |

| <b>ctmaOptimizeInit (-)</b>     |       |                  | Initial fitting (i.e., applies <code>ctmaInit</code> ) to a primary study several times to capitalize on chance for obtaining a hard-to-find optimal fit.   |
|---------------------------------|-------|------------------|---|
| <b>reFits</b>                   | NULL  | value > 0        | How many reFits should be done  |
| <b>n.latent</b>                 | NULL  | value > 0        | Number of latent variables.   |
| <b>coresToUse</b>               | 1     | value > 0 or < 0 | The number of cores (threads) to be used for fitting. If a negative values is specified, the value is subtracted from available cores, else the value sets the number of cores to be used. Should usually be 1 on Windows OS. |
| <b>activateRPB</b>              | FALSE | FALSE / TRUE     | Messages (warning, finished fitting) could be send to mobile phone if TRUE.   |
| <b>checkSingleStudy-Results</b> | FALSE | FALSE / TRUE     | If yes, displays estimates from single study ctsem models and waits for user input to continue. Useful to check estimates before they are saved.  |

| <b>ctmaInit (EPIC-BiG-Power)</b> |                              |   | Fits a ctsem model to a list of primary studies prepared by <code>ctmaPrep</code> .  |
|----------------------------------|------------------------------|---|--|
| Argument                         | Default                      | Possible Values   | Explanation  |
| <b>primaryStudies</b>            | NULL                         | list  | A list created with <code>ctmaPrep</code> that contains all information (e.g., <code>empcovi</code> , <code>delta_ti</code> , <code>sampleSizei</code> etc.) relevant for <code>ctmaInit</code> and subsequent analyses.                   |
| <b>activeDirectory</b>           | NULL                         | character string  | Specifies the directory where required files are found and saved. Should end with “/”. For example, “/Users/GDC/CoTiMA/”   |
| <b>activateRPB</b>               | FALSE                        | FALSE/ TRUE   | Messages (warning, finished fitting) could be send to mobile phone if TRUE.  |
| <b>checkSingleStudy-Results</b>  | TRUE                         | TRUE / FALSE  | If yes, displays estimates from single study ctsem models and waits for user input to continue. Useful to check estimates before they are saved.   |
| <b>digits</b>                    | 4                            | value > 0   | Rounding used in output.   |
| <b>n.latent</b>                  | NULL                         | value > 0   | Number of latent variables.  |
| <b>n.manifest</b>                | 0 (= <code>n.latent</code> ) | value $\geq$ <code>n.latent</code>                              | Number of manifest variables.  |
| <b>lambda</b>                    | NULL (= identity matrix)     | <code>n.latent</code> $\times$ <code>n.manifest</code> matrix   | Matrix with pattern of fixed (=1) or free (any string) loadings.   |
| <b>manifestVars</b>              | NULL (= 0)                   | <code>n.manifest</code> $\times$ <code>n.manifest</code> matrix | Matrix with error(co-)variances of manifest indicators.  |
| <b>drift</b>                     | NULL (=all)                  | vector (!) of rowwise drift matrix elements                     | Labels for drift effects that should or should not be included. Have to be either of the type <code>V1toV2</code> or 0 for effects to be excluded, which is usually not recommended, e.g., <code>c(“V1toV1”, “V2toV1”, 0, “V2toV2”)</code> |



| <b>ctmaInit (EPIC-BiG-Power)</b> |        |  | Fits a ctsem model to a list of primary studies prepared by <b>ctmaPrep</b> .   |
|----------------------------------|--------|--|---|
| <b>doPar</b>                     | 1      | integer value > 0  | Fits each model <b>doPar</b> times in parallel mode and returns best single model fit. In each of the parallel fit attempts, <b>coresToUse</b> is set to 1 to avoid conflicting processes. Probably does not work in Windows machines. The number of parallel processes is limited to all available threads (cores) minus 1, and if the value assigned to <b>doPar</b> is larger, multiple parallel fits are done sequentially. |
| <b>equalDrift</b>                | NULL   | vector of 0 or 2 or more drift effects   | Labels for drift effects that should be set equal. Have to be of the type <b>V1toV2</b> , e.g., <code>c("V2toV1", "V1toV2")</code> . Is useful, for example, to test if the sizes of cross effects are statistically different.   |
| <b>indVarying</b>                | FALSE  | TRUE / FALSE   | Specifies a random (manifest) intercept model. Works only if all primary studies have 3 or more waves and no missing values (i.e., variables) exist   |
| <b>saveRawData</b>               | list() | <code>list(saveRawData-\$studyNumbers, saveRawData\$fileName, saveRawData-\$row.names, saveRawData-\$col.names, saveRawData\$sep, saveRawData\$dec)</code> | A list with required information to save generated pseudo raw data. Might be useful for methodological research questions. For example, <code>list("saveRawData\$studyNumbers" = c(1:20), "saveRawData\$fileName" = "pseudoRaw", "saveRawData\$row.names" = FALSE, "saveRawData\$col.names" = TRUE, "saveRawData\$sep" = " ", "saveRawData\$dec" = ".")</code>  |
| <b>coresToUse</b>                | 1      | value > 0 or < 0   | The number of cores (threads) to be used for fitting. If a negative value is specified, the value is subtracted from available cores, else the value sets the number of cores to be used. Should usually be 1 on Windows OS.  |
| <b>silentOverwrite</b>           | FALSE  | TRUE / FALSE   | Whether or not to prompt user preventing undesired overwriting of existing single study fit files (requested via <b>saveSingleStudyModelFit</b> )   |
| <b>saveSingleStudy-ModelFit</b>  | c()    | vector with filename followed by the numbers of studies for which the fit is saved   | Save the fit of single study ctsem models (could save a lot of time afterwards if the fit is loaded, e.g. <code>saveSingleStudyModelFit=c("myModel", 1, 4, 5, 6:100)</code> )   |

| <b>ctmaInit (EPIC-BiG-Power)</b> |                  |  | Fits a ctsem model to a list of primary studies prepared by <b>ctmaPrep</b> .  |
|----------------------------------|------------------|--|--|
| <b>loadSingleStudy-ModelFit</b>  | <b>c()</b>       | vector with filename followed by the numbers of studies for which the fit is saved | Load the fit of single study ctsem models, e.g.<br><b>loadSingleStudyModelFit=c("myModel", 1, 4, 5, 6:100)</b> . This is useful, e.g, if primary studies are added to the pool of primary studies. Only the added studies will be fitted, the previously fitted models are loaded, and all is then stored in the resulting <b>ctmainit fit</b> object.   |
| <b>scaleTime</b>                 | NULL<br>(=FALSE) | value > 0  | Whether or not the time scale used for <b>delta_ti</b> should be changed. For example, <b>scaleTime=1/12</b> could change the time scale from months to years. It is usually recommended to avoid <b>delta_ti</b> larger than 6. The default value <b>FALSE</b> is taken from the <b>CoTiMAStancArgs</b> list, which could also be used to specify more stanc fitting parameters.  |
| <b>optimize</b>                  | TRUE             | TRUE / FALSE   | The <b>optimize</b> argument is passed to <b>ctStanFit</b> . If <b>FALSE</b> , Bayesian estimation is used. The chosen sampler is conditional on the <b>nopriors</b> argument. Note that this works differently than the <b>optimise</b> argument of <b>ctSatFit</b> .   |
| <b>nopriors</b>                  | TRUE             | TRUE / FALSE   | Consequences of <b>TRUE</b> or <b>FALSE</b> are conditional on the <b>optimize</b> argument. <b>optimize=TRUE &amp; nopriors=TRUE</b> implies maximum likelihood estimation, <b>optimize=TRUE &amp; nopriors=FALSE</b> implies maximum a posteriori estimation, <b>optimize=FALSE &amp; nopriors=TRUE</b> implies Bayesian estimation using HMC (Hamiltonian Monte Carlos sampler), and <b>optimize=FALSE &amp; nopriors=FALSE</b> implies Bayesian estimation using NUTS (No U-Turn Sampler). |
| <b>finishsamples</b>             | NULL<br>(=1000)  | values > 0   | The <b>finishsamples</b> argument is passed to <b>ctStanFit</b> . It specifies the number of samples to draw for final results computation. Larger (e.g., 10.000) values make results more exactly replicable. Larger values are recommended before manuscripts are submitted. Very large values (e.g., 100.000) might be helpful if very small effects (e.g., 0.0002) result from estimation.   |

| <b>ctmaInit (EPIC-BiG-Power)</b> |              |              | Fits a ctsem model to a list of primary studies prepared by <b>ctmaPrep</b> .  |
|----------------------------------|--------------|--------------|--|
| <b>chains</b>                    | NULL (=2)    | values > 0   | The <b>chains</b> argument is passed to <b>ctStanFit</b> and specifies the number of chains to be used for Bayesian estimation.  |
| <b>iter</b>                      | NULL (=1000) | values > 0   | The <b>iter</b> argument is passed to <b>ctStanFit</b> . It specifies the number of iterations used for Bayesian estimation, half of which will be devoted to warmup.  |
| <b>verbose</b>                   | NULL         | 0, 1, or 2   | The <b>verbose</b> argument is passed to <b>ctStanFit</b> . Higher values print more information during model fit.   |
| <b>customPar</b>                 | TRUE         | FALSE / TRUE | If set <b>TRUE</b> some starting values transformations used by <b>ctSatnFit</b> will be replaced by CoTiMA specific settings. Not recommended to be used in combination with Bayesian estimation. It was introduced to improve handling of large values used in <b>delta_ti</b> . Setting it to <b>FALSE</b> and use <b>scaleTime</b> instead could be a better alternative if estimation problems will nevertheless occur. |
| <b>useSV</b>                     | TRUE         | TRUE / FALSE | If set <b>TRUE</b> provided starting values will be used. These could be obtained via <b>ctmaSV</b> .  |

| <b>ctmaModDrift (-)</b> |         |  | Computes moderated drift matrices from CoTiMA Fit objects that were generated with <b>ctmaFit</b> . These are the same matrices that are internally used when generating moderator plots. <b>ctmaModDrift</b> can also handle <b>ctStanFit</b> objects. |
|-------------------------|---------|--|---|
| Argument                | Default | Possible Values                        | Explanation   |
| <b>CoTiMAFit</b>        | NULL    | CoTiMA fit object                      | Object to which all CoTiMA fit object has been assigned to (i.e., what has been returned by <b>ctmaFit</b> ).   |
| <b>ctStanFit</b>        | NULL    | ctsem fit object of type <b>ctStan</b> | A ctsem fit object created with <b>ctStanFit</b> .  |

| ctmaModDrift (-)        |                   |                 | Computes moderated drift matrices from CoTiMA Fit objects that were generated with <code>ctmaFit</code> . These are the same matrices that are internally used when generating moderator plots. <code>ctmaModDrift</code> can also handle <code>ctStanFit</code> objects.  |
|-------------------------|-------------------|-----------------|--|
| <code>transformm</code> | vector of strings | transformation  | Could be used to replace the transformations used during fitting by <code>ctsem</code> . Usually not required. For example, <code>transform=c("-(0.000001 + 2 * log1p_exp(-(2 * param)))", "param", "param", #' "-(0.000001 + 2 * log1p_exp(-(2 * param)))", "0.000001 + 10 * log1p_exp(2 * param)", #' "param", "0.000001 + 10 * log1p_exp(2 * param)", "0.000001 + 5 * log1p_exp(2 * param)", #' "param", "0.000001 + 5 * log1p_exp(2 * param)" )</code> . |
| <code>modValues</code>  | -2:2              | any value       | Values for which moderated drift matrices should be computed. Could be used to replace the values used in <code>CoTiMAFit</code> or in <code>ctStanFit</code> . Useful, if many moderator values exist.  |
| <code>mod.type</code>   | NULL              | "cont" or "cat" | Could be necessary if older versions of CoTiMA were used, in which the moderator type (continuous versus categorical) was not saved in the resulting CoTiMA fit object.  |
| <code>mod.number</code> | 1                 | value > 0       | In cases in which the fit object used more than a single moderator, <code>mod.number</code> specifies which moderated drift matrices should be computed.   |
| <code>scaleTime</code>  | 1                 | any value       | Re-scales the returned drift matrices to a different time interval than used when creating the CoTiMA Fit object or the <code>ctStanFit</code> object (i.e., a factor which is used to multiply the moderated drift matrices).   |

| ctmaPower (EPIC-BiG-Power)   |   |                   | Informs the plot function that more than a single CoTiMA fit object should be plotted.  |
|------------------------------|---|-------------------|---|
| Argument                     | Default   | Possible Values   | Explanation   |
| <code>ctmaInitFit</code>     | NULL  | CoTiMA fit object | Object to which all single <code>ctsem</code> fits of primary studies has been assigned to (i.e., what has been returned by <code>ctmaInit</code> ) |
| <code>activeDirectory</code> | path used to create <code>ctmaInitFit</code> object | path to directory | Specifies the directory where required files are found and saved. Should end with <code>"/</code> .   |

|                                   |       |                       |  |
|-----------------------------------|-------|-----------------------|--|
| <b>ctmaPower (EPIC-BiG-Power)</b> |       |                       | Informs the plot function that more than a single CoTiMA fit object should be plotted.   |
| <b>statisticalPower</b>           | c()   | vector                | Vector of requested statistical power values, e.g. c(.95, .80)   |
| <b>failSafeN</b>                  | NULL  | value > 0             | A sample size used to determine across which time intervals expected effects become not significant. If not specified, the average sample size of primary studies will be used.  |
| <b>failSafeP</b>                  | NULL  | value between 0 and 1 | A p-value used to determine across which time intervals expected effects become not significant. If not specified .01 will be used.  |
| <b>timeRange</b>                  | NULL  | vector with 3 values  | Specifies the time range across which statistical power etc will be computed. A vector with 3 values: starting point, end point, step width, e.g. c(0, 50, 1). if not specified, c(0, 1.5*maxDelta, 1) will be used, with 1.5*maxDelta indicating that the end point is 1.5 times the longest time interval among primary studies. |
| <b>useMBESS</b>                   | FALSE | TRUE / FALSE          | If TRUE, the MBESS package is used to calculate statistical power (slower). Otherwise, use the internal CoTiMA function (faster).  |
| <b>coresToUse</b>                 | 1     | value > 0 or < 0      | The number of cores (threads) to be used for fitting. If a negative value is specified, the value is subtracted from available cores, else the value sets the number of cores to be used. Should usually be 1 on Windows OS.   |
| <b>digits</b>                     | 4     | value > 0             | Rounding used in output.   |
| <b>indVarying</b>                 | FALSE | TRUE / FALSE          | Specifies a random (manifest) intercept model. Works only if all primary studies have 3 or more waves and no missing values (i.e., variables) exist  |
| <b>activateRPB</b>                | FALSE | FALSE/ TRUE           | Messages (warning, finished fitting) could be send to mobile phone if TRUE.  |
| <b>silentOverwrite</b>            | FALSE | TRUE / FALSE          | Whether or not to prompt user preventing undesired overwriting of existing fit files (requested via <code>saveAllInvFit</code> or <code>saveAllInvWOSingFit</code> )   |
| <b>loadAllInFit</b>               | c()   | character sting       | Load the fit of a CoTiMA model with all effects invariant across primary studies, e.g.<br><code>loadAllInvFit=c("myAllInvariantModel")</code>  |
| <b>saveAllInFit</b>               | c()   | character sting       | Save the fit of a CoTiMA model with all effects invariant across primary studies, e.g.<br><code>saveAllInvFit=c("myAllInvariantModel")</code>  |
| <b>loadAllInvWOSingFit</b>        | c()   | character sting       | not yet operational  |
| <b>saveAllInvWOSingFit</b>        | c()   | character sting       | not yet operational  |

| ctmaPower (EPIC-BiG-Power) |              |                         | <p>Informs the plot function that more than a single CoTiMA fit object should be plotted.</p>  |
|----------------------------|--------------|-------------------------|--|
| skipScaling                | TRUE         | FALSE / TRUE            | <p>If FALSE, combined raw data are standardized again. Although pseudo raw data for each primary study have variance = 1.0, this is not the case if they are combined into the single data set that is used to compute the model with all effects being invariant. This is because variance is computed with denominator <math>N - 1</math>. Could be corrected by setting skipScaling to FALSE, but usually has little practical consequences.</p>  |
| useSampleFraction          | NULL         | value between 100 and 0 | <p>Analyze only a fraction of the overall sample. Could help speeding up debugging. Provided as percent (e.g., useSampleFraction=30 uses 30% of the overall sample size)</p>   |
| optimize                   | TRUE         | TRUE / FALSE            | <p>The optimize argument is passed to ctStanFit. If FALSE, Bayesian estimations is used. The chosen sampler is conditional on the nopriors argument. Note that this works differently than the optimise argument of ctSatFit.</p>  |
| nopriors                   | TRUE         | TRUE / FALSE            | <p>Consequences of TRUE or FALSE are conditional on the optimize argument. optimize=TRUE &amp; nopriors=TRUE implies maximum likelihood estimation, optimize=TRUE &amp; nopriors=FALSE implies maximum a posteriori estimation, optimize=FALSE &amp; nopriors=TRUE implies Bayesian estimation using HMC (Hamiltonian Monte Carlos sampler), and optimize=FALSE &amp; nopriors=FALSE implies Bayesian estimation using NUTS (No U-Turn Sampler).</p> |
| finishsamples              | NULL (=1000) | values > 0              | <p>The finishsamples argument is passed to ctStanFit. It specifies the number of samples to draw for final results computation. Larger (e.g., 10.000) values make results more exactly replicable. Larger values are recommended before manuscripts are submitted. Very large values (e.g., 100.000) might be helpful if very small effects (e.g., 0.0002) result from estimation.</p>   |
| iter                       | NULL (=1000) | values > 0              | <p>The iter argument is passed to ctStanFit. It specifies the number of iterations used for Bayesian estimation, half of which will be devoted to warmup.</p>  |

| ctmaPower (EPIC-BiG-Power) |           |              | Informs the plot function that more than a single CoTiMA fit object should be plotted.   |
|----------------------------|-----------|--------------|--|
| chains                     | NULL (=2) | values > 0   | The <b>chains</b> argument is passed to ctStanFit and specifies the number of chains to be used for Bayesian estimation.   |
| verbose                    | NULL      | 0, 1, or 2   | The <b>verbose</b> argument is passed to ctStanFit. Higher values print more information during model fit.   |
| customPar                  | TRUE      | FALSE / TRUE | If set TRUE some starting values usually used by ctSatFit will be used by CoTiMA specific settings. Not recommended to be used in combination with Bayesian estimation. It was introduced to improve handling of large values used in <b>delta_ti</b> . Setting it to FALSE and use <b>scaleTime</b> instead could be a better alternative if estimation problems will nevertheless occur. |

| ctmaPub (-)     |                          |                                       | Computes publication indices for the group of authors of a study (augments ctmaGetPub).  |
|-----------------|--------------------------|---------------------------------------|--|
| Argument        | Default                  | Possible Values                       | Explanation  |
| getPubObj       | NULL                     | Object created with <b>ctmaPubGet</b> | Publication (and citation) information of authors.   |
| selectedStudies | NULL                     | Vector of study numbers               | Specifies the studies, for which the groups of authors' publication information should be computed.  |
| yearsToExclude  | NULL                     | (vector of) years to exclude          | Years to be excluded from computations. For example, the current year might be excluded because publication informations might not be very reliably. Early years (e.g., 1900-1960) might be excluded because they would cause invalid publications (sometimes this happens in Google Scholar). |
| targetYear      | NULL (=publication year) | a positive value                      | If left NULL, all publications before the year of the authors' publication count.  |
| recency         | 5                        | a positive value                      | <b>ctmaPub</b> computes 2 indices. For the first one (NEPP), all years before <b>targetYear</b> count. For the second one (NEPPrecency), the years between <b>targetYear</b> and <b>targetYear - recency</b> count.  |

| ctmaPub (-)           |                     |   | Computes publication indices for the group of authors of a study (augments <code>ctmaGetPub</code> ).   |
|-----------------------|---------------------|---|---|
| <code>indFUN</code>   | <code>"sum"</code>  | any of: <code>"mean"</code> , <code>"sum"</code> , <code>"max"</code> , <code>"min"</code> , <code>"var"</code> | Specifies the function used to aggregate an <i>individual</i> author's publication numbers, e.g., <code>sum</code> (recommended) computes the sum of an author's publication before <code>targetYear</code> , and <code>var</code> computes the variance of the number of publications for an author's first year of publication to <code>targetYear</code> .   |
| <code>colFUN</code>   | <code>"mean"</code> | any of: <code>"mean"</code> , <code>"sum"</code> , <code>"max"</code> , <code>"min"</code> , <code>"var"</code> | Specifies the function used to aggregate a group of authors ( <i>collective</i> ) publication numbers, e.g., <code>mean</code> computes the mean of all authors' publication scores (created with <code>indFUN</code> , e.g., the sums) before <code>targetYear</code> , and <code>max</code> takes largest of all authors' publication scores (created with <code>indFUN</code> , e.g., the sums) to <code>targetYear</code> . |
| <code>addAsMod</code> | <code>FALSE</code>  | <code>FALSE</code> / <code>TRUE</code>  | Currently disabled.   |

| ctmaPrep (EPIC-BiG-Power)    |                   |                      | Combines information of primary studies into a list object and returns this list.                                     |
|------------------------------|-------------------|----------------------|---|
| Argument                     | Default           | Possible Values      | Explanation   |
| <code>selectedStudies</code> | <code>NULL</code> | vector with integers | Vector of primary study numbers (numeric values with no leading 0; e.g., <code>'2'</code> but not <code>'02'</code> ) |



| ctmaPrep (EPIC-BiG-Power) |      |                      | Combines information of primary studies into a list object and returns this list.   |
|---------------------------|------|----------------------|---|
| excludedElements          | NULL | vector with integers | <p>Could be used to exclude some predefined objects from the results reported. Note that some predefined objects are strongly defined; they have to be used in a special way because they are actually used in subsequent analyses. Some other objects could be used at the researcher's convenience (information is just collected). Strongly predefined objects are <b>delta_t</b> (should be of the type <code>c(NA, NA)</code> in cases when raw data are provided, with the number of NAs corresponding to the number of time intervals), <b>sampleSize</b> (single number), <b>pairwiseN</b> (matrix of pairwise N; could be used if correlation matrix is based on pairwise N), <b>empcov</b> (correlation matrix), <b>moderator</b> (vector of numbers; could be continuous or categorical), <b>alphas</b> (vector of reliability estimates of the variables of a primary study), <b>startValues</b> (vector of start values), <b>rawData</b> (information about file name and structure of raw data), <b>empMeans</b> (means for variables; usually 0), and <b>empVars</b> (variances for variables; usually 1.0).</p> <p>Weakly predefined objects are <b>studyNumber</b> (intended as a special number used for the outputs of subsequently fitted CoTiMA models), <b>source</b> (intended as vector of authors' names and publication year), <b>ageM</b> value intended for indicating the mean age of participants in a primary study, <b>malePercen</b> (intended as value indicating the percentage of male participants in a primary study), <b>occupation</b> (intended as vector of character strings representing the occupations of participants in a primary study), <b>country</b> (intended as single character string representing the country in which a primary study was conducted), and <b>targetVariables</b> (intended as vector of character strings representing information about the variables used).</p> |

| ctmaPrep (EPIC-BiG-Power) |   |                             | Combines information of primary studies into a list object and returns this list.  |
|---------------------------|---|-----------------------------|--|
| activeDirectory           | path used to create ctmaInit-Fit object | path to directory           | Specifies the directory where required files are found and saved. Should end with “/”.   |
| addElements               | NULL                                    | vector of character strings | Could be use to add user-defined objects that are handled as the weakly predefined objects. The major purpose is to collect information a researcher regards as important, e.g. <code>c("Important", "Interesting")</code> |
| digits                    | 4                                       | value $\geq 0$              | Rounding used in output.   |
| moderatorLabels           | NULL                                    | vector of character strings | Vector of Names used to label moderators in the output e.g., <code>c("Mod1", "Control")</code>   |
| moderatorValues           | NULL                                    | list of vectors             | List of vector of Names (assignments) used to label moderators in the output e.g., <code>list(c(1="Emotional Exhaustion", "2=Exhaustion"), "continuous")</code>  |
| summary                   | TRUE                                    | TRUE / FALSE                | Requests summary table and xlsx workbook in return object. Could be set to FALSE to avoid reporting errors.  |

| ctmaSV (EPIC-BiG-Power) |   |                   | Computes new start values and returns an augmented list of primary studies that has 'inits' elements containing these start values. This list can then be used for the <code>primaryStudies</code> argument in subsequent <code>ctmaInit</code> applications. Starting values are obtained by using 'lavaan' to fit discrete time SEM to the primary studies provided. The discrete time estimates are then transformed into their continuous time counterparts and some specific transformations are applied (required by 'ctsem') before returned. In case of model with 3 or more waves of data, continuous time effects are computed for each intervals and then averaged. |
|-------------------------|---|-------------------|--|
| Argument                | Default                                 | Possible Values   | Explanation  |
| ctmaInitFit             | NULL                                    | CoTiMA fit object | Object to which all single ctsem fits of primary studies has been assigned to (i.e., what has been returned by <code>ctmaInit</code> )   |
| activeDirectory         | path used to create ctmaInit-Fit object | path to directory | Specifies the directory where required files are found and saved. Should end with “/”.   |

|                                |      |  |  |
|--------------------------------|------|--|--|
| <b>ctmaSV (EPIC-BiG-Power)</b> |      |  | Computes new start values and returns an augmented list of primary studies that has 'inits' elements containing these start values. This list can then be used for the <b>primaryStudies</b> argument in subsequent <b>ctmaInit</b> applications. Starting values are obtained by using 'lavaan' to fit discrete time SEM to the primary studies provided. The discrete time estimates are then transformed into their continuous time counterparts and some specific transformations are applied (required by 'ctsem') before returned. In case of model with 3 or more waves of data, continuous time effects are computed for each intervals and then averaged. |
| <b>coresToUse</b>              | 1    | value > 0 or < 0                               | The number of cores (threads) to be used for fitting. If a negative value is specified, the value is subtracted from available cores, else the value sets the number of cores to be used. Should usually be 1 on Windows OS.   |
| <b>primaryStudies</b>          | NULL | CoTiMA fit object created with <b>ctmaPrep</b> | In cases in which the CoTiMA fit object assigned to <b>ctmaInitFit</b> (possibly old fit files) does not contain the primaryStudies object created with <b>ctmaPrep</b> it could be added by assigning it to the <b>primaryStudies</b> argument.   |
| <b>replaceUV</b>               | TRUE | TRUE / FALSE                                   | The computed starting values could either replace existing starting values in the returned list of primary studies (TRUE; default) or save them as an additional list element <b>inits</b> .   |

The **plot** function, which is described next, works slightly different than other CoTiMA functions. Like all other CoTiMA functions, some arguments could be used as always. However, in addition, it is important to note that several plotting parameters ('fitAddSpecs') have to be assigned to the CoTiMA fit-object before plotting it, rather than using plotting parameters as arguments to the **plot** function (e.g., **CoTiMAInitFitObject\$XMax <- 200**). This is because the arguments have different effects conditional on the type of fit-object. The number of plotting parameters that can be changed in this way is still limited; we are working on extensions. Further, user-defined plotting parameters differ for fit objects created with **ctmaBiG** versus **ctmaInit** and **ctmaFit**). Finally, if problems with **plot** are encountered, we recommend trying **ctmaPlot** instead.

| <b>plot/ctmaPlot</b> |         |                 | Generates plots. |
|----------------------|---------|-----------------|------------------|
| Argument             | Default | Possible Values | Explanation      |

| plot/ctmaPlot     |  |   | Generates plots.   |
|-------------------|--|---|--|
| ctmaFitObject     | NULL   | vector with integers  | A CoTiMA fit-object created by <code>ctmaInit</code> , <code>ctmaFit</code> , or <code>ctmaBig</code> .  |
| activeDirectory   | path used to create <code>ctmaInit</code> -Fit object        | path to directory   | Specifies the directory where required files are found and saved. Should end with <code>"/</code> .  |
| saveFilePrefix    | <code>"ctmaPlot"</code>                                      | vector of character strings                                 | Labels for the generated plot, which might be automatically augmented by further information (e.g., <code>"ctmaplot V1toV1.png"</code> )   |
| activateRPB       | FALSE  | FALSE/ TRUE   | Messages (warning, finished fitting) could be send to mobile phone if TRUE.  |
| plotCrossEffects  | TRUE   | TRUE/ FALSE   | Affects plotting of <code>ctmaInit</code> or <code>ctmaFit</code> fit-objects only. Plotting of discrete time cross effects can be suspended.  |
| plotAutoEffects   | TRUE   | TRUE/ FALSE   | Affects plotting of <code>ctmaInit</code> or <code>ctmaFit</code> fit-objects only. Plotting of discrete time auto effects can be suspended.   |
| timeUnit          | <code>"timeUnit (not specified)"</code>                      | vector of character strings                                 | Affects plotting of <code>ctmaInit</code> or <code>ctmaFit</code> fit-objects only. Label used for the x-axis of discrete time plots.  |
| timeRange         | 1 to 1.5 times the longest interval used in primary studies  | vector with 3 values: <code>c(xMin, xMax, stepwidth)</code> | Affects plotting of <code>ctmaInit</code> or <code>ctmaFit</code> fit-objects only. The range across which discrete time effects are plotted, e.g., <code>c(10, 20, .01)</code> would plot effects from 10 units of time to 20 using steps of .01. Note that a <code>stepwidth &lt; 1</code> could be specified to obtain more fine-grained figures.         |
| yLimitsForEffects | values slightly exceeding min and max empirical effect sizes | vector with 2 values: <code>c(yMin, yMax)</code>            | Affects plotting of <code>ctmaInit</code> or <code>ctmaFit</code> fit-objects only. The min and max values for the y-axis. Setting explicit values could be better than relying on the automatically determined range, for example, to ensure identical y-axis across a larger set of plots.   |
| mod.values        | <code>c(-2-1, 0, 1, 2)</code>                                | vector with numbers   | Affects plotting of <code>ctmaFit</code> fit-objects only. The moderator values for which plots of continuous moderators should be generated. Correspondes to the standard deviations below and above the mean value if the continuous moderator has been standardized with <code>scaleMod=TRUE</code> . Does not affect plotting of categorical moderators. |

| plot/ctmaPlot  |                  |                     | Generates plots.  |
|----------------|------------------|---------------------|---|
| mod.number     | 1                | value > 0           | The number of the moderator effect that is plotted if more than a single moderator is included in the <code>ctmaFitObject</code> . Not that <code>mod.number</code> does not select the dummies used for categorical moderators (all dummy effects are plotted); rather it refers to the 1st, 2nd etc continuous or categorical moderator of an analysis.   |
| aggregateLabel | ""<br>(=nothing) | character(s)        | Affects plotting of <code>ctmaFit</code> fit-objects only. Symbol to be attached to the discrete time plot of a <code>ctmaFit</code> fit-object. In the case of <code>ctmaInit</code> fit-objects, each study is usually identified in the plot with a dot inside which the study number is shown. In the case of a <code>ctmaFit</code> fit-object with aggregated effects, one could use a symbol, e.g. <code>aggregateLabel="Σ"</code> . |
| xLabels        | NULL             | vector with numbers | Affects plotting of <code>ctmaFit</code> fit-objects only. The numbers indicating the time intervals on the x-axis are usually determined automatically. The could also directly specified, and the values provided are equally distributed across the time range used to plot the discrete time effects, e.g., <code>c(1, 3, 5, 7, 9)</code>   |

| Argument                                  | Default | Possible Values | Explanation   |
|---|---------|-----------------|---|
| <i>fitAddSpecs</i> (ctmaBias fit-objects) |         |                 |   |
| CoTiMAFit\$xMin                           | 0       | value $\geq 0$  | Internally, the x axis ranges from 0 to 300 (the values shown in the plot are irrelevant). Setting <code>xMin &gt; 0</code> creates a plot where the left part is left out. For example, if one wants to leave out the first quarter (i.e. 0 to $300/4 = 0$ to 75) you could set <code>xMin</code> to 75. If one wants extra space on the right hand side of the plot, one could lift <code>xMax</code> to values larger than 300, e.g., <code>c CoTiMAFit\$xMax &lt;- 400</code> . |
| CoTiMAFit\$xMax                           | 300     | value $\geq 0$  | see above   |

| <i>fitAddSpecs</i> (ctmaInit & ctmaFit fit-objects) |         |                 |             | Generates discrete time effect plots. |
|---|---------|-----------------|-------------|---------------------------------------|
| Argument  | Default | Possible Values | Explanation |                                       |

| <i>fitAddSpecs</i> (ctmaInit & ctmaFit fit-objects) |  |                               | Generates discrete time effect plots.  |
|---|--|-------------------------------|--|
| CoTiMAFit\$col                                      | “grey” & “black” for ctmaInit & ctmaFit fit-objects, respectively. | R-type color code             | Sepecifies the color of the curve showing the discrete time affects across time, e.g., CoTiMAFit\$col <- “red”   |
| CoTiMAFit\$lwd                                      | 1.5 & 2.5 for ctmaInit & ctmaFit fit-objects, respectively.        | value $\geq 0$                | Sepecifies the line width of the curve showing the discrete time affects across time, e.g., CoTiMAFit\$lwd <- 4  |
| CoTiMAFit\$lty                                      | 1 & 2 for ctmaInit & ctmaFit fit-objects, respectively.            | R-type integer value $\geq 0$ | Sepecifies the line type of the curve showing the discrete time affects across time, e.g., CoTiMAFit\$lty <- 1, with, e.g., 1 = solid, 2 = dashed, and 3 = dotted.   |
| CoTiMAFit\$xMin                                     | min of <b>timeRange</b>  | integer values                | Limits the displayed range of the discrete time effects plotted. Should only be used in combination with the <b>xLabels</b> argument. Overrides other setting if multiple fit-objects are supplied. This is experimental; it is recommended to set <b>timeRange</b> instead. |
| CoTiMAFit\$xMax                                     | max of <b>timeRange</b>  | integer values                | Limits the displayed range of the discrete time effects plotted. Should only be used in combination with the <b>xLabels</b> argument. Overrides other setting if multiple fit-objects are supplied. This is experimental; it is recommended to set <b>timeRange</b> instead. |
| CoTiMAFit\$dot.type                                 | “b”  | R-type characters             | Type of the plot. Use “p” for points, “l” for lines, “b” for both, “c” for the lines part alone of “b” etc.  |
| ... to be continued                                 |  |                               |  |