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 and/or raw data 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[1].

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}. Random intercepts cross-lagged panel models (RI-CLPM; e.g., Hamaker, Kuiper, & Grasman, 2015) can performed with the CoTiMA R package, too, but certain assumptions have to be met. 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 and/or raw data serve as 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, 2022) using the code shown in Figure 1. All code

[1] 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).

and examples shown in the User's Guide were performed and tested with R version 4.1.3 and run using RStudio (RStudio Team, 2021).

The next pages show how to conduct a CoTiMA. This involves several 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. We also highlight some common problems frequently encountered during the CoTiMA process [2].

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_t`i), mostly mandatory (`sampleSize`i, `empcov`i), or optional (`pairwiseN`i, `studyNumber`i, `moderator`i, etc., with i indicating the study number). User-defined object names could be added (e.g., `criticalRemark`i).

```
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

[2] When it is desired, all R objects created in the following examples (e.g., `empocv2`, `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` from the package:CoTiMA environment 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.

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 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 × 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 × 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_t`*i*) and sample sizes (`sampleSize`*i*). 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, which usually results in better model convergence as we show later. For example, if the longest time lag was 10 years, one could use the number of 5-year intervals as the time scale, and to assign the value 2 to `delta_t`*i* 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 `sampleSize`*0*`2`). 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[3] and store this list as an R object. This is done with the `ctmaPrep` function included in the CoTiMA R package. 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

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

general, we label the objects to store the results delivered by the ctma-functions starting with "CoTiMA", such as `CoTiMAstudyList_3`.

```
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 complied 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 as, for example, the choice of a time scale that makes model convergence difficult.

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 (`n.latent`) 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 intersting results in Figure 5[4].

The output shown in the first panel [[1]] of 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 full 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.

[4]Note that if you try to reproduce estimation, 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.

```
## [[1]]
##                                       V1toV1    SE       V2toV1    SE
## Study No 2   "Reference not provided" "-2.8223" "0.7516" "-0.0524" "1.2582"
## Study No 3   "Reference not provided" "-3.2862" "2.2722" "0.1611"  "1.0724"
## Study No 313 "Reference not provided" "-0.4144" "0.0419" "0.1418"  "0.0391"
##              V1toV2    SE       V2toV2    SE
## Study No 2   "-0.0423" "1.2204" "-2.8667" "0.764"
## Study No 3   "0.2741"  "1.2138" "-4.1591" "3.9813"
## Study No 313 "0.0912"  "0.0345" "-0.2819" "0.0321"
##
## [[2]]
##               discrete time           V1toV1 discrete time V2toV1 discrete time
## Study No 2   "Reference not provided" "0.0595"             "-0.003"
## Study No 3   "Reference not provided" "0.038"              "0.004"
## Study No 313 "Reference not provided" "0.6652"             "0.1004"
##              V1toV2 discrete time V2toV2 discrete time
## Study No 2   "-0.0025"            "0.057"
## Study No 3   "0.0069"             "0.0161"
## Study No 313 "0.0646"             "0.759"
```

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

The second panel [[2]] of Figure 5 displays the discrete time counterparts of the two auto and the two cross effects. We explain the relation between continuous time and dicrete time effects further below. The reason why we already show the discrete time effects here is that they can be interpreted as ordinary standardized lagged regression coefficients across 1 month. Inspecting the *V1toV1* and *V2toV2* auto-regressive effects shows that for Study 313 the effects is reasonble, but for Study 2 and Study 3 the auto-regressive effects are much smaller than one would usually expect. The reason is that the choice of months as time scale resulted in values for `delta_ti` of 1.5 (Study 131) and 12 (Study 2 & Study 3), and 12 is a bit too large to ensure proper convergence - it may sometimes work, but in this example it did not.

```
CoTiMAInitFit_3_st <- ctmaInit(primaryStudies = CoTiMAstudyList_3,
                           n.latent = 2,
                           activeDirectory = activeDirectory,
                           coresToUse = coresToUse,
                           scaleTime = 1/12)

summary(CoTiMAInitFit_3_st)
saveRDS(CoTiMAInitFit_3_st, paste0(activeDirectory, "CoTiMAInitFit_3_st.rds"))
```

Figure 6: Fitting a ctsem model to each primary study with time units re-scaled (`ctmaInit`).

In Figure 6 the argument scaleTime = 1/12 was added, which implies that the standard unit for time intervals changes from months to years, so that the `delta_ti` of 1.5 are now internally transformed to 1.5/12 and the `delta_ti` of 12 are transformed to 12/12 all being smaller than the largest recommend value 6. The estimated effects are shown in 7. They are now much more reasonable, although one might wonder if the autoregressive effects for Study 313 across 1

year are unreasonably small. They are not and we explain this in more detail in the section on CoTiMA with random intercepts. For the moment, it is sufficient to know that the the time-scaled model yielded a minus 2 loglikelihood (-2ll) value of 7137.718, which is smaller (better), then the -2ll value of the previous model without time scaling, where is was 7401.953. This indicates that the results of the time-scaled model fit are more trustworthy.

```
## [[1]]
##                                       V1toV1    SE       V2toV1   SE
## Study No 2   "Reference not provided" "-0.6083" "0.1306" "0.1019" "0.1171"
## Study No 3   "Reference not provided" "-0.3907" "0.1333" "0.0587" "0.1291"
## Study No 313 "Reference not provided" "-4.9717" "0.5126" "1.7061" "0.4668"
##              V1toV2    SE       V2toV2    SE
## Study No 2   "-0.2278" "0.1095" "-0.3277" "0.1043"
## Study No 3   "0.1366"  "0.1257" "-0.4548" "0.1433"
## Study No 313 "1.1245"  "0.4018" "-3.3813" "0.3943"
##
## [[2]]
##               discrete time           V1toV1 discrete time V2toV1 discrete time
## Study No 2   "Reference not provided" "0.5373"             "0.0638"
## Study No 3   "Reference not provided" "0.6792"             "0.0385"
## Study No 313 "Reference not provided" "0.0214"             "0.0388"
##              V1toV2 discrete time V2toV2 discrete time
## Study No 2   "-0.1426"            "0.713"
## Study No 3   "0.0896"             "0.6372"
## Study No 313 "0.0256"             "0.0576"
```

Figure 7: ctsem results after time units re-scaled (`summary(CoTiMAInitFit_3)`).

The fit object `CoTiMAInitFit_3` (or `CoTiMAInitFit_3_st`; both will do the same) 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 8. 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 8: 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 9 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.

```
##                           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 9: First part of summary(`CoTiMAFullFit_3`)

```
## $minus2ll
## [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 10: Second part of summary(`CoTiMAFullFit_3`)

The second part of the output generated by `summary(CoTiMAFullFit_3)` is shown in Figure 10. 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 9 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 totest if the difference between the two effects is statistically significant.

Effects in continuous time are difficult to interpret. Therefore, they are usually back-translated into discrete time effects. 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 11: Plotting a Full CoTiMA (`plot`)

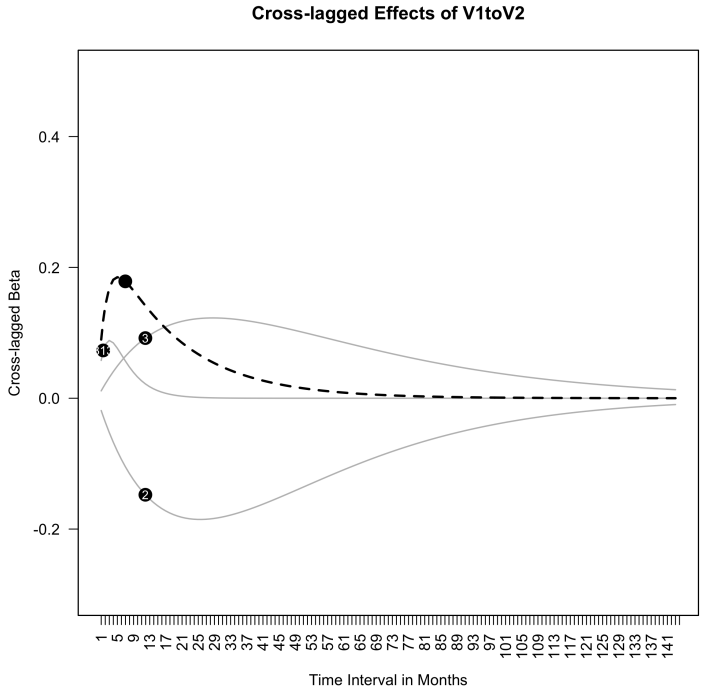


Figure 12: The cross-lagged effect *V1toV2* across 1 to 144 months.

Figure 11 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 plot is shown in Figure 12.

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 10), 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, **Bi**as & **G**eneralizability, and statistical **Power**.

1. **E**PIC: **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. E**P**IC: 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. EP**I**C: 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. EPI**C**: 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 **Bi**as 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) **P**ower 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_t`*i*) and objects that are probably required in most instances (`sampleSize`*i*, `empcov`*i*). 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

```
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 13: Entering correlation matrices

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 (`empVar`*i*) 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 (`empMeans`*i*) could be provided, but we do address these possibilities here.

Figure 13 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 13. In the original study (Childs & 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 13 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 13. 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 13. 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 re-

code '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[5]. 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.

```
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 14: Processing correlation matrices (`ctmaCorRel`, `ctmaEmpCov`)

First, to achieve our aims, we start with reading the previously saved correlation matrix and the matrix of pairwise N from disk (see Figure 14) and assign them to R objects `empcov128` and `pairwiseN128`. With `colnames(empcov128)` (not shown in Figure 14) 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 unreliability. 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[6].

[5] 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.

[6] Correlations are disattenuated using the well-known formula developed by Spearman

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 `empcov`*i* 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 `targetVariables`*i* object rather than the rows/columns in the `empcov`*i* object (i.e., recoding is done after `targetVariables`*i* were selected from `empcov`*i*).

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 15: Results of applying `ctmaEmpCov` to the specifications of Study 128

The CoTiMA package comes with the function `ctmaEmpCov` which performs

(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 positive definite and could not be analyzed then.

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 15 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 16: 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`. See the Appendix for the `ctmaShapeRawData` function, which can be helpful to get raw data organized in the way required by CoTiMA (or ctsem).

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 17: 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

```
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 18: Additional information for study data entered before

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, ..., V1_Tt, V2_Tt, dT1, dT2, ... dT(t-1), where dTt are the variables representing the time intervals (deltas) between measurements (see Figure 17; 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_t`i object! It has to have as many NA as the largest number of possible time intervals in the respective study is, for example, in the case of not more than three intervals, `delta_t`i `<- c(NA, NA)`. In the example in Figure 17 there are only two time points and, thus, one interval `dT1`. Thus, `delta_t`i is indeed the only mandatory object because `rawData`i could substitute `empcov`i and `pairwiseN`i could substitute `sampleSize`i.

So far, we introduced the objects `delta_t`i, `sampleSize`i, `empcov`i, `targetVariables`i, `alphas`i, `pairwiseN`i, and `rawData`i). 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")`
- `ageM`i. 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")`

```
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 19: Information for two further primary studies

In addition to these pre-defined object names, user-defined object names could be added (e.g., `demands`i and `burnout`i, 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

```
activeDirectory <- "/Users/cdormann/SynologyDrive/Synology Drive/CHRISTIAN/TEXTE/METHODEN/R/GitHub/CoTiMA Users G
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 20: Compiling a list of primary studies with extended information (`ctmaPrep`)

included in the Excel workbook that summarizes primary study information (see. Figure 22). Second, user-defined objects have to be declared in `ctmaPrep` using the argument `addElements` (see Figure 20).

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

Figure 21: Open an Excel sheet with summary information included in a compiled list of primary studies (requires package openxlsx)

To proceed further with the example, in a first step documented in Figure 18 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 19.

The six studies are now compiled into a list as shown in Figure 20. We add the two user-defined object names `demands`i and `burnout`i. We also provide a vector with the labels of the two moderators, and we provide a list of vectors to label the moderator values.

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		

Deltas | Sample Sizes | Correlations | **Moderators** | Countries | Occupations | +

Figure 22: Excel sheet with summary information included in a compiled list of primary studies

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.

6 Initial Fitting (`ctmaInit`)

Now the first two steps (**E**xtract & **P**repare) 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 23 (analogous to Figure 4), and the result is then displayed on the console (see Figure 24).

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

Figure 23: 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 24: 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. Thise 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 24 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 25 shows how the continuous time drift effects obtained for Study 313 (see Figure 24) 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 12).

```
## [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 25: Relation between continuous time drift coefficients of Study 313 and its discrete time effects

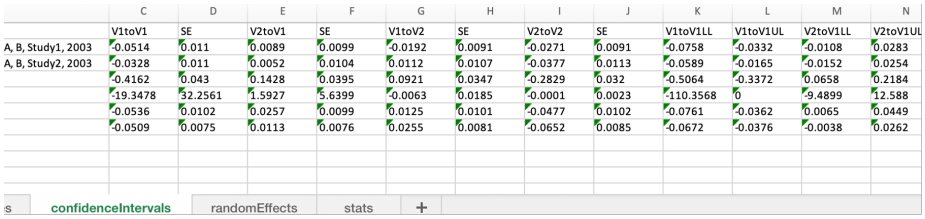
The result of applying the same transformation to the suspicious drift effects of Study 128 is shown in Figure 26. The non-identified auto effect *V1toV1* corresponds to an auto-regressive effect of 1.0 across 1 month: A person's level of demands at work does ´perfectly predict the person's demands one 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.

```
## [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 26: Relation between continuous time drift coefficients of Study 128 and its discrete time effects

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 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	0.043	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	0	9.4899	12.588
	-0.0536	0.0102	0.0257	0.0099	0.0125	0.0101	-0.0477	0.0102	-0.0761	-0.0362	0.0065	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

s | confidenceIntervals | randomEffects | stats | +

Figure 27: 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`).

Table 1: Estimators available for CoTiMA

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

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

Weakly informative priors for Bayesian estimation with the NUTS 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 28 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 28, 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 28 printed to the console with `summary(CoTiMAInitFit_6_NUTS)` is shown in Figure 26[7]. A comparison with the maximum likelihood effects and their standard errors in Figure 24 reveals no substantial differences except for Study 128, for which results are

[7]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 28: Using Bayesian estimation via Stan's NUTS sampler (ctmaInit)

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 **??**).

```
##                                                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 29: Estimates for the primary studies using Bayesian estimation (`ctmaInit`)

7 CoTiMA (`ctmaFit`)

Now the first three steps (**E**xtract, **P**repare, & **I**nitFit) 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 then 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 by 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 30: Full CoTiMA with six studies (ctmaFit)

Fitting this type of a very restrictive CoTiMA is done with the code in Figure 30 and with `summary(CoTiMAFullFit_6)` the results are displayed[8]. 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

[8]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.

the present example, which is the default estimator. Other estimators would have to be specified as shown in Table 1.

```
##                                row col    Mean     sd    2.5%     50%   97.5%  Tvalues
## T0MEANS_1_1 (invariant)          1   1  0.0000 0.0000  0.0000  0.0000  0.0000      NaN
## T0MEANS_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
## T0cov_1_1 (invariant)            1   1  0.9922 0.1184  0.7787  0.9890  1.2405   8.3801
## T0cov_1_2 (invariant)            1   2  0.4481 0.0890  0.2822  0.4445  0.6354   5.0348
## T0cov_2_1 (invariant)            2   1  0.4481 0.0890  0.2822  0.4445  0.6354   5.0348
## T0cov_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 31: Results (Part 1) of a Full *all-invariant* CoTiMA with six studies (`ctmaFit`)

The results in Figure 31 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.

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).

`T0MEANS` at the top of Figure 31 represent the initial (T0) means of the latent variables. Closer to the bottom in Figure 31, `T0cov` 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.

Part 2 of the results generated by the code in Figure 30 is shown in Figure 32. A random effects model was not requested because it would require raw data, which are usually not available[9]. 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.

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 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

[9] 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.

```
## $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 32: Results (Part 2) of a Full *all-invariant* CoTiMA with six studies (`ctmaFit`)

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 33. 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 34 and Figure 35. The interpretation of results is anaologous to the interpretation of the all-invariant CoTiMA discussed in Section 7.1.1[10].

[10]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 34they 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 kth

```r
# 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", "Fuellemann", "& Bauer", "2013")
moderator201 <- c(2, NA)

# Compiling a revised list of primary studies with Study 313 replacing Study 128
activeDirectory <- "/Users/cdormann/SynologyDrive/Synology Drive/CHRISTIAN/TEXTE/METHODEN/R/GitHub/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 33: Workflow for replacing Study 128 by Study 201 and conducting a regular Full CoTiMA

7.2 Partial CoTiMA (`ctmaFit`)

Figure 36 demonstrates some further possibilities for conducting a CoTiMA; additional capabilities are explained in Appendix A. The CoTiMA model specified in Figure 36 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 Canada, respectively. This hierarchical structure is specified in the `cluster` argument. In the `cluster` argument, the studies that belong to one cluster receive

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.

```
##                           row col    Mean     sd    2.5%     50%   97.5%  Tvalues
## T0MEANS_1_1                 1   1  0.0000 0.0000  0.0000  0.0000  0.0000      NaN
## T0MEANS_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
## T0cov_1_1                   1   1  1.0029 0.0679  0.8790  1.0022  1.1444  14.7742
## T0cov_1_2                   1   2  0.4507 0.0531  0.3486  0.4485  0.5540   8.4929
## T0cov_2_1                   2   1  0.4507 0.0531  0.3486  0.4485  0.5540   8.4929
## T0cov_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 34: Results (Part 1) of a regular Full CoTiMA with six studies (`ctmaFit`)

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).

Parts of the summary are shown in Figure 37. 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.

```
## $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 35: Results (Part 2) of a regular Full CoTiMA with six studies (`ctmaFit`)

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 37. 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 × 1.6767 = – .0513.

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

```
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 36: 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`)

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*.

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 38.

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.

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 39. 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`.

```
## $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 37: Results of the partial CoTiMA specified in Figure 31 (`ctmaFit`)

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

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

```
## [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 39: 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`)

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

Recalling from Figure 20, we entered information about two moderators. The fist 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

```
## $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 41: Part of the results moderated full CoTiMA (`ctmaFit`)

and moderator names would have to be provided as vectors (e.g., `mod.number = c(1, 3)`, `mod.names = c(''Burnout Measure'', ''Study Quality'')`). However, in the present example, we use the first potential moderator variable only (`mod.number = 1` in Figure 40), which was categorial (`mod.type = ''cat''` in Figure 40) representing two types of burnout measures (`mod.names = ''Burnout Measures''` in Figure 40). 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 41. 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.

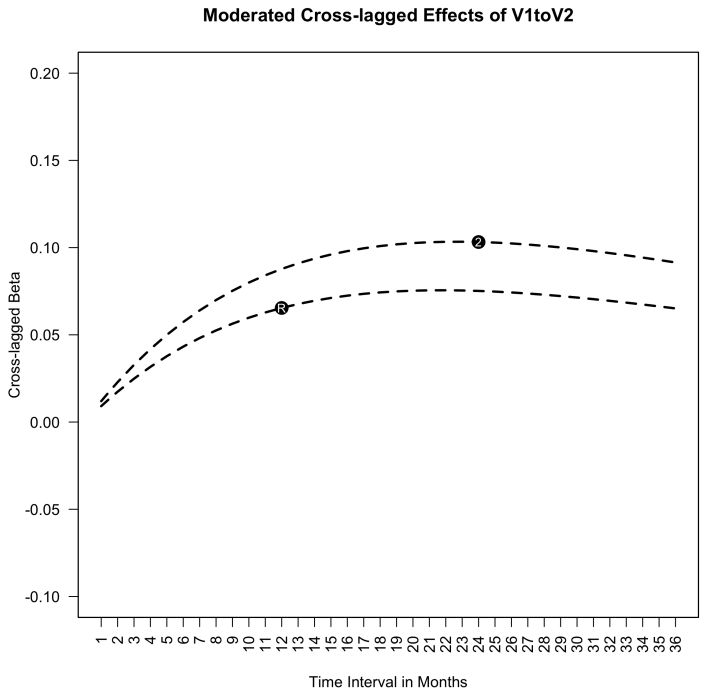


Figure 42: The cross-lagged effect *V1toV2* moderated by type of burnout measure (1 = emotional exhaustion, 2 = exhaustion) from 1 to 36 months. The horizontal location of the category indicators R (reference category) and 2 has no inherent meaning.

The section `$mod.effects` in Figure 41 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 bunrout 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[11].

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 11) 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 45.

```
activeDirectory <- "/Users/cdormann/SynologyDrive/Synology Drive/CHRISTIAN/TEXTE/METHODEN/R/GitHub/CoTiMA Users G
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 43: 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

[11] 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 45. 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 efect is reported in the `$mod.effects` section.

significantly *different* effects. To test for this possibility, a further argument `catsToCompare` is available for the `ctmaFit` function, which allows contrasting two categories.

```
CoTiMAMod1onFullFit_6_cats12 <- ctmaFit(ctmaInitFit = CoTiMAInitFit_6_new,
                                        mod.number = 1,
                                        mod.type = "cat",
                                        mod.names = "Burnout Measure",
                                        catsToCompare = c(1,2),
                                        scaleMod=FALSE)
saveRDS(CoTiMAMod1onFullFit_6_cats12,
        file=paste0(activeDirectory, "CoTiMAMod1onFullFit_6_cats12.rds"))

ctmaCompFit(CoTiMAMod1onFullFit_6_cats12, CoTiMAMod1onFullFit_6)
```

Figure 44: 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 if Figure 44, which shows (not displayed in a Figure) that the difference in the minus 2 loglikelihood values given 4 degrees of freedom is not significant ($\triangle -2ll = 2.6440$; $\triangle df = 4$; $p = 0.6191$). 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, CoTiMAMod1onFullFit_6)` yields ($\triangle -2ll = 2.6448$; $\triangle df = 4$; $p = 0.6189$). However, with three or more categories these two minus 2 loglikelihood (-2ll) difference tests will yield diverging results[12].

The code for a partial moderated CoTiMA with a single *continuous* moderator is shown in Figure 43. Again, the types of primary studies we use in

[12]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"))
 }
}
```

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 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 43only the cross effects are 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).

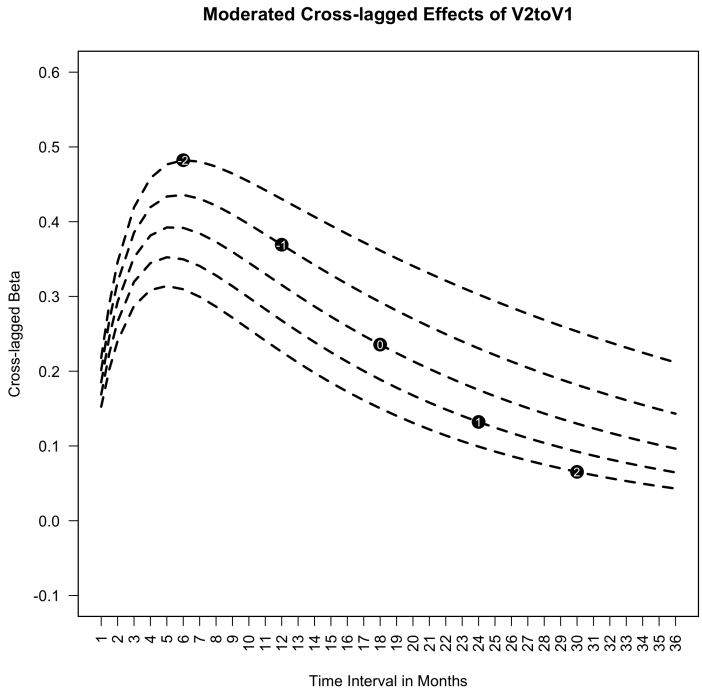


Figure 45: The cross-lagged effect *V2toV1* moderated (not significantly) by control at work from 1 to 30 months. The lines show the effect of *V2toV1* for control at -2*SD* below the mean of control (-2), -1*SD* below the mean of control (-1), at the mean of control (0), +1*SD* above the mean of control (1), and +2*SD* 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 43 yields the plot shown in Figure 45. 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 43 .

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; Barto? & 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 Voelkle (2020) that belongs to their CoTiMA of job stressors and burnout[13]. The file containing their init fit-object can be retrieved from the website of the Open Science Foundations with the code shown in Figure 46. 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[14]. 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 47. First, results of fixed effects analyses of *single* drift coefficients are displayed. Recall

[13]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

[14]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 complied 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 an repository, for example, using the Open Science Framework http://osf.io/.

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

Figure 46: Downloading the Init-Fit file of Guthier et al. (2020)

```
CoTiMABiG_D_BO <- ctmaBiG(CoTiMAInitFit_D_BO)
summary(CoTiMABiG_D_BO)
plot(CoTiMABiG_D_BO)
```

Figure 47: Analysis of bias and generalizability, summary of results, and plotting (`ctmaBiG`)

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 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 48 were $V1toV2 = .0024$ ($p < .001$) and $V2toV1 = .0054$ ($p < .001$).

The next section in Figure 48 is `$Heterogeneity`. Here τ^2, H^2, and I^2 are shown, of which I^2 is usually of most interest. Note that estimates of τ^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 48 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 49. These results directly address possible publication bias. Egger's tests (e.g., Sterne &

```
## $`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 48: Part 1 of results of `ctmaBiG`

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), suggesting that the aggregated effects are biased. Thus, the results in the `$‘Egger’s tests‘` part of Figure 49 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

```
## $`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 49: Part 2 of results of `ctmaBiG`

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 identical to the fixed effect estimates in Figure 48 (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 50. Figure 50 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

```
## $`Z-Curve 2.0 Results:`$`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 50: Expected Replication Rates (ERR) and Expected Discovery Rates (EDR) based on Z-Curve 2.0 analysis of *V1toV1* and of *V1toV2* by `ctmaBiG`.

50. 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 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_BO)`. 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 51. 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

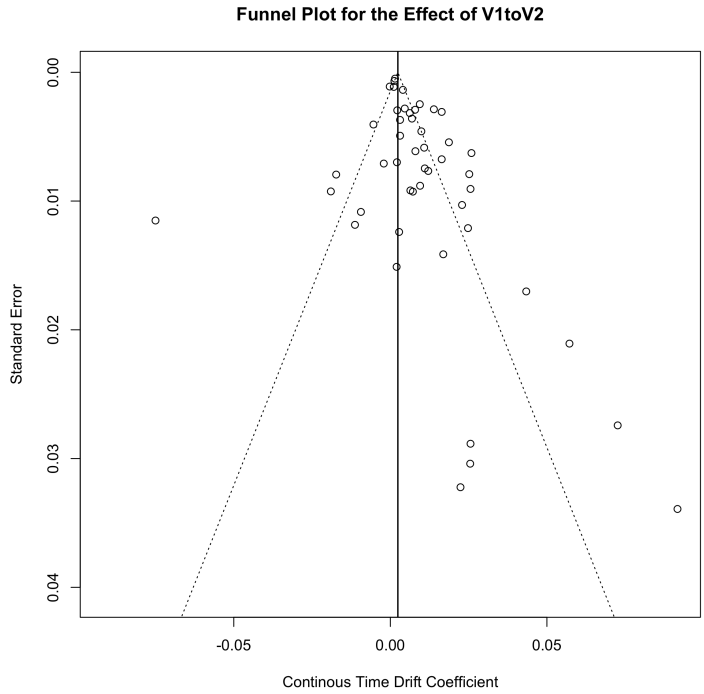


Figure 51: Funnel plot of the effect *V1toV2* of the fit object returned by `ctmaBiG` (`plot`)

and, thus, the confidence interval is rather narrow.

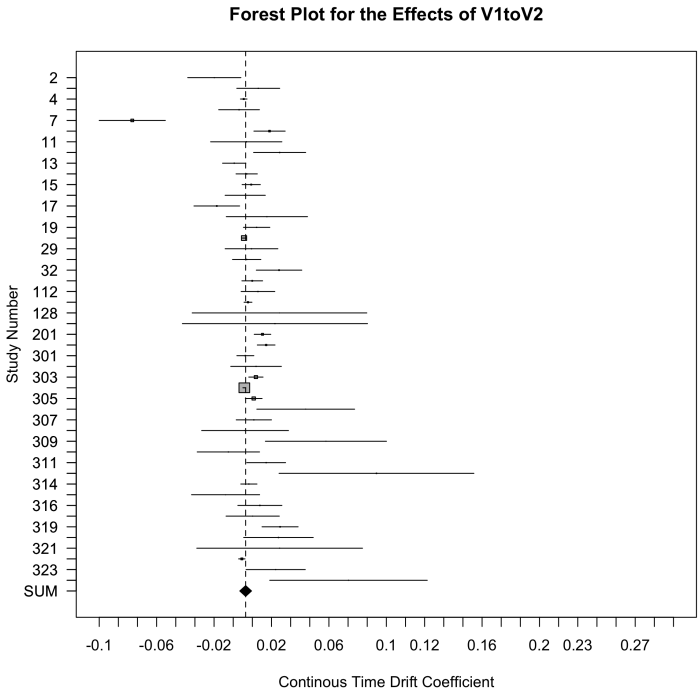


Figure 52: Forest plot of the effect *V1toV2* of the fit object returned by `ctmaBiG` (`plot`)

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 53: 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 previoulsy 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 53 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 54: 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 54 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_BO` 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.

The next section in the generated output reports the expected power of primary studies. For the effect of *V1toV2*, this is displayed in Figure 55. 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 55 are the true effects, the probability values in Figure 55 represent the statistical power each primary study had to detect the focal true *V1toV2* effect (i.e., .0119; see Figure 54) 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,

```
##             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 55: Expected (post hoc) power across primary studies (`ctmaPower`)

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.

```
##       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 56: Required sample sizes to achieve requested levels of statistical power across a range of time intervals (`ctmaPower`)

The generated output further shows the required samples sizes for (future) studies to obtain significant effects across different time intervals (Figure 56). 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

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 56.

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 57 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.

```
## [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 57: Expected range across which significant effects could be expected (`ctmaPower`)

Finally, required sample sizes can be plotted. We used `plot(CoTiMAPower_D_BO, timeUnit="Months", timeRange=c(1, 84, 1) )` to generate the plot displayed in Figure 58. This figure is based on the values previously shown in parts in Figure 56

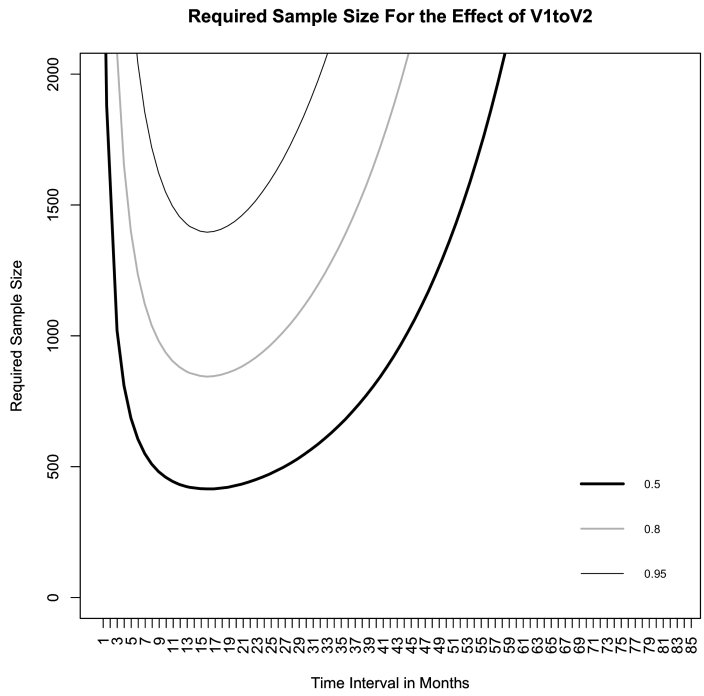


Figure 58: Required sample sizes across time to achieve a statistical power of .50, .80, and .95 (`plot`)

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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 `ctmaInit`.
`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, `"/Users/GDC/CoTiMA/"`
`activateRPB`	`FALSE`	`FALSE/ TRUE`	Messages (warning, finished fitting) could be send to mobile phone if TRUE.
`digits`	4	value > 0	Rounding used in output.
`PETPEESEalpha`	`.10`	values between `0` and `1`	Probability level (condition) below which to change from PET to PEESE.
`undoTimeScaling`	`TRUE`	`TRUE/FALSE/`	Uses the time scale specified in the Extract-Step (i.e., as specified in the `delta_ti` objects when TRUE.
`dT`	`NULL`	value > 0	Not yet implemented: Performs all analyses for discrete time intervals, too, using the interval assigned to `dT`.

ctmaCompFit (EPI*C*-BiG-Power)			Compares the fit of two nested CoTiMa models (libreal model1 on the left, restricted model2 on the right) via -2ll difference test. Note that the nested structure of the two models is assumed to be given and not checked.
Argument	Default	Possible Values	Explanation
`model1`	`NULL`	CoTiMA fit object	CoTiMA fit object created with `ctmaInit`, `ctmaFit`, or `ctmaEqual`.
`model2`	`NULL`	CoTiMA fit object	CoTiMA fit object created with `ctmaInit`, `ctmaFit`, or `ctmaEqual`.

ctmaCorRel (E*P*IC-BiG-Power)			Corrects (disattenuates) correlation matrix for unreliabilities.
Argument	Default	Possible Values	Explanation

ctmaCorRel (EPIC-BiG-Power)			Corrects (disattenuates) correlation matrix for unreliabilities.
alphas	NULL	vector of the same length as dimensionality of empcov	
empcov	NULL	symmetric correlation matrix	

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
combineVariables	c()	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, list(1, c(2, 3), 4, c(5, 6)) combines the 2nd and 4rd as well as the 5th and 6th variables of empcov*i*. and leaves the 1st and 4th variable untouched. Instead of positions, variable names could be used if they were also used in the argument targetVariables.
combineVariables-Names	c()	vector variable names for combined variables	not yet operational
empcov	NULL	symmetric correlations matrix	Correlation matrix reported in a primary study.
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.
missingVariables	c()	vector of variable positions	Augments empcov*i* and pairwiseN*i* 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 ctmaEmpCov will be a 4×4 empcov*i* and a 4×4 pairwiseN*i* 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.
pairwiseN	NULL	symmetrix matrix of same dimensions as empcov containing possible pairwiseN.	A matrix with sample sizes for each correlation of empcov*i*.
recodeVariables	c()	vector of variable positions or variable names	Recodes desired variables in empcov*i* (i.e., changes the signs of the correlations). For example, c(1, 4) changes the signs of the correlations in the 1st and 4th row of empcov*i*. Instad of positions, variable names could be used if dimnames were assigned to empcov*i*. Note that if numbers are used, they should correspond to the positions in the targetVariables*i* object rather than the ros/columns in the empcov*i* object (i.e., recoding is done after targetVariables*i* were selected from empcov*i*).
sampleSize	NULL	value > 0	The sample size. It does not need to be specified if pairwiseN*i* is provided instead.
targetVariables	NULL	vector of variable positions or variable names	Selects desired variables in empcov*i* (i.e., deletes those variables that should not be analyzed). For example, c(1, 2, 4, 5) deletes the 3rd and 6th row and column in a 6×6 empcov*i*. Instad of positions, variable names could be used if dimnames were assigned to empcov*i*.
Tpoints	NULL	value > 1	The number of time points.

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
			.
activateRPB	FALSE	FALSE/ TRUE	Messages (warning, finished fitting) could be send to mobile phone if TRUE.
activeDirectory	path used to create ctmaInit-Fit object	path to directory	Specifies the directory where required files are found and saved. Should end with "/".

ctmaEqual (EPI*C*-BiG-Power)			Statistically tests if the two or more invariant drift parameters in the Co-TiMAFit object supplied are equal
`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.
`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).
`digits`	4	value > 0	Rounding used in output.

Argument	Default	Possible Values	Explanation

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
`activateRPB`	`FALSE`	`FALSE/ TRUE`	Messages (warning, finished fitting) could be send to mobile phone if `TRUE`.
`activeDirectory`	path used to create ctmaInit-Fit object	path to directory	Specifies the directory where required files are found and saved. Should end with "/".
`allInvModel`	`FALSE`	TRUE / FALSE	Whether or not a model should be tested in which all (!) parameters are assumed to be invariant across primiary studies. If set TRUE, other specifications (e.g., speficied with the `equalDrift` argument) will be ignored. An all invariant model is also used by `ctmaPower`.

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
`catsToCompare`	`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, `catsToCompare=c(2, 3)` 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.
`chains`	`NULL (=2)`		The `chains` argument is passed to ctStanFit and specifies the number of chains to be used for Bayesian estimation.
`cint`	`0`	string vector of names of means of continuous time intercepts	Usually, CoTiMA assumes that standardized varibales (correlations) are analyzed, which should result in estimates of manifestMeans (and T0mean) to be 0.0. To facilitate convergence, these parameters are set to 0.0 by default. They can be set free by providing names. Note that this is automatically done if `indVarying='cint'` is specified.
`cluster`	`NULL`	vector of same length as number of primary studies	Vector with cluster variables (e.g., countries), e.g., `c(1, 1, 1, 3, 3, 6, 7, 8)`. Has to be set up carfully. Will be included in `ctmaPrep` later.
`coresToUse`	2	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.
`CoTiMAStanctArgs`	`NULL`	list of further fitting parameters	All fitting parameters that are allowed in `ctStanFit` can be specified here, too.
`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 `ctmaInit`)

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
customPar	FALSE	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 delta_ti. Setting it to FALSE and use scaleTime instead could be a better alternative if estimation problems will nevertheless occur.
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 V1toV2 or 0 for effects to be excluded, which is usually not recommended, e.g., c(“V1toV1”, “V2toV1”, 0, “V2toV2”)
driftsToCompare	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, driftsToCompare=c(“V1toV2”) together with catsToCompare=c(2, 3) and modsToCompare=2 fits a model in which the effect of category 2 and 3 on the drift parameter “V1toV2” of the second moderator is set equal.
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”). LaConstrains all listed effects to be equal (e.g., equalDrift = c("V1toV2", "V2toV1")). Note that this is not required for testing the assumtion that two effects are equal in the population. use the invariantDrift argument and then ctmaEqual.
finishsamples	NULL (=1000)	values > 0	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 befor manuscripts are submitted. Very large values (e.g., 100.000) might be helpful if very small effects (e.g., 0.0002) result from estimation.

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.

ind.mod.names	NULL	string vector of names	Vector of names for individual level (!) moderators used in output. Can only be used with primary studies providing raw data.
			Individual level moderators are usually provided as last columns in raw data files, and this is the specified in rawDataï objects by adding the number of individual level moderators, e.g.,
			rawData2 <-
			list(fileName=paste0(activeDirectory,
			"rawData2.txt"),
			studyNumbers=6,
			missingValues=c(-99),
			standardize=TRUE, header=TRUE,
			dec=".", sep=" ", n.ind.mod=2)
			However, individual level moderators can also be added later to existing cmtaInit fit objects. In the following example, rawdata are extracted from an existing cmtaInit fit object, then the mean of all time intervals per individual is computed, which is then added to a copy of the cmtaInit fit object and saved. Time interval length as study-level of individual-level moderator could indicate that qualitatively different processes are captured by different sets of discrete time points.
			CoTiMAInitFit <-
			readRDS(file=paste0(activeDirectory,
			"CoTiMAInitFit.rds"))
			ind.mod.List <- list()
			for (i in
			1:length(CoTiMAInitFit$studyFitList))
			{
			wide <-
			CoTiMAInitFit$studyFitList[[i]]$empraw
			dtCols <- grep("dT",
			colnames(wide))
			naPos <- which(wide[,dtCols] <=
			.001, arr.ind=TRUE)
			wide[,dtCols][naPos] <- NA #
			replace missing (coded as <.001) by
			NA
			ind.mod.List[[i]] <-
			data.frame(matrix(NA, ncol=1,
			nrow=nrow(wide)))
			colnames(ind.mod.List[[i]]) <-
			"TI1"
			ind.mod.List[[i]]$TI1 <-
			c(apply(as.matrix(wide[, dtCols],
			nrow=nrow(wide)), 1, mean,
			na.rm=TRUE))
			}
			CoTiMAInitFit_iml <- CoTiMAInitFit
			CoTiMAInitFit_iml$ind.mod.List <-
			ind.mod.List
			saveRDS(CoTiMAInitFit_iml,
			paste0(activeDirectory,
			"CoTiMAInitFit_iml.rds"))

ind.mod.number	NULL	vector of positions of moderators	Which moderator (in the vector of individual level (!) moderators) shall be used (e.g., 2 for a single moderator or 1:3 for 3 moderators simultaneously). Can only be used with primary studies providing raw data.
ind.mod.types	'cont'	''cont'' or ''cat''	'cont' or 'cat' of the individual level (!) moderators (mixing them in a single model not yet possible). Can only be used with primary studies providing raw data.

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
indVarying	FALSE	TRUE / FALSE/'cint'	Specifies a random intercept (RI) model. RI models could be specified using individually varying ct intercepts (indVarying=='cint') or individually varying manifests (indVarying==TRUE). In case n-manifest=n.latent, both models are algebraically identical. However, numerically, models with individually varying manifests are easier to fit. Note that 'random intercept' models are referred to as 'fixed effect' models in the econometric literature.
indVaryingT0	NULL (automatically set to TRUE if indVarying=TRUE or indVarying='cint')	TRUE / FALSE	Random intercept models are estimated by CTSEM by correlating ct intercepts (or manifests) with all latents at T0. This automatically sets the effect of the dummy variables, which accounts for the nesting of data within primary studies, on T0 (co-)variances to 0. This is not expected to cause serious problems because the dummy variables can be expected to have only very small effects on T0 variables if the T0 variables are allowed to vary randomly, which makes indvaryingT0=TRUE the better option. However, overall, there could be many (k - 1) small effects of dummy variabls on T0 variables, which overall reduce the -2ll value more than the randomly varying intercepts. Thus, expect indVaryingT0=TRUE to yield worse model fit than indVaryingT0=FALSE, but prefer the former over the later.
invariantDrift	NULL (=all)	vector of drift effects or ''none''	Labels for drift effects that should be aggregated. Have to be of the type V1toV2, e.g., c(''V2toV1''). When ''none'' is used, ctmaFit mimics a ctmaInit model, which is only required if the reduction in heterogeneity by means of introducing moderators should be computed (see ctmaRedHet).
iter	NULL (=1000)	values > 0	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.
lambda	NULL (= identity matrix)	n.latent $\times$ n.manifest matrix	Matrix with pattern of fixed (=1) or free (any string) loadings.

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
manifestMeans	0	string vector of names of means of manifest variables	Usually, CoTiMA assumes that standardized varibales (correlations) are analyzed, which should result in estimates of manifestMeans (and T0mean) to be 0.0. To facilitate convergence, these parameters are set to 0.0 by default. They can be set free by providing names. Note that this is automatically done if `indVarying=TRUE` is specified. When many(!) waves of data exist, it could be possible to separate latent means from manifest means by setting either of them free.
manifestVars	0	0 or `n.manifest` × `n.manifest` matrix with values or strings	Lower triangular matrix with error(co-)variances of manifest indicators. Usually, CoTiMA assumes that a single indicator is used per latent. This typically requires to assume eror variances to be 0.0. Alternatively, they can be assigent a particular value, e.g., 1- Cronbach's alpha. In case s where many waves of observation are available, the error variance of single manifest indicators cann be estimated, too. This is achieved by assginging labels.
mod.names	NULL	(vector of) character object(s)	Names used to label moderators in the output .
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.
moderatedDrift	NULL (=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.

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
modsToCompare	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 mod.number argument (see above). For example, if mod.number=c(1, 4, 6) was specified before, modsToCompare=2 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 ctmaPrep.
nopriors	NA	TRUE / FALSE	Deprecated, but still working as of August 2023. Consequences of TRUE or FALSE are conditional on the optimize argument. optimize=TRUE & nopriors=TRUE implies maximum likelihood estimation, optimize=TRUE & nopriors=FALSE implies maximum a posteriori estimation, optimize=FALSE & nopriors=TRUE implies Bayesian estimation using HMC (Hamiltonian Monte Carlos sampler), and optimize=FALSE & nopriors=FALSE implies Bayesian estimation using NUTS (No U-Turn Sampler).
optimize	TRUE	TRUE / FALSE	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.
primaryStudyList	NULL	list of primary studies	A list of primary studies compiled with ctmaPrep that containes a subset of studies included in ctmaInitFit. Useful to exclude studies without the need to use ctmaInit again.
priors	FALSE	FALSE/TRUE	Replaces previously used nopriors argument. Consequences of TRUE or FALSE are conditional on the optimize argument. optimize=TRUE & priors=FALSE implies maximum likelihood estimation, optimize=TRUE & priors=TRUE implies maximum a posteriori estimation, optimize=FALSE & priors=FALSE implies Bayesian estimation using HMC (Hamiltonian Monte Carlos sampler), and optimize=FALSE & priors=TRUE implies Bayesian estimation using NUTS (No U-Turn Sampler).

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
scaleClus	TRUE	TRUE/FALSE	The argument scaleCLUS=TRUE leads to centring of dummy variables representing different clusters. If the argument scaleClus=FALSE 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 scaleClus=TRUE 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 scaleClus=FALSE should be used).

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
scaleMod	NULL	FALSE / TRUE	Whether or not continuous moderators should be standardized or categorical moderators should be centered. Recommended for continuous moderators. The default value FALSE is taken from the CoTiMAStanctArgs list, which could also be used to specify more stanct fitting parameters. With categorical moderators, the argument scaleMod=TRUE 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 & 2 are unused, 3 is < 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. If the argument scaleMod=FALSE is used in combination with categorical moderators, the resulting drift effects are those for the reference category, that is, for studies including people < 19 yrs only. The effect of Dummy 1 the represents the changes that result if a study includes people aged 19-60 rather than < 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 < 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 < 19 yrs. If the argument scaleMod=TRUE is used in combination with categorical moderators, the internally created dummy variables are centered (but not standardized; see the argument transfMod 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 categoy. 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 scaleMod=FALSE shoudl be used). See the argument catsToCompare to analyzed difference between catagories anyway.

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
scaleTI	TRUE	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 *not* interested in) cannot be interpreted as within-study effects.
scaleTime	NULL (=FALSE)	value > 0	Wether or not the time scale used for delta_ti should be changed.For example, scaleTime=1/12 could change the time scale from months to years. It is usually recommended to avoid delta_ti larger than 6. The default value FALSE is taken from the CoTiMAStanctArgs list, which could also be used to specify more stanct fitting parameters.
transfMod	NULL	character vector applying R functions to x	Can be used as a replcement of scaleMod if more than one moderator is analyzed and standardization is not desired for all moderators. Then, it could take the form transfMod=c(‘‘scale(x)‘‘, ‘‘x‘‘ ‘‘scale(x)‘‘). Alternativey, users can define their own functions, e.g., transfMode=(‘‘(x - mean(x))‘‘); this function centralizes a single moderator without standardization. Another example is transfMode=(‘‘scale(x) - min(x)‘‘), 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.

ctmaFit (EPI*C*-BiG-Power)			Fits a CoTiMA model.
T0means	0	string vector of names of means of T0 latents	Usually, CoTiMA assumes that standardized varibales (correlations) are analyzed, which should result in estimates of T0mean (and manifestMeans) to be 0.0. To facilitate convergence, these parameters are set to 0.0 by default. They can be set free by providing names. Note that this is automatically done if `indVarying= TRUE` is specified.
T0var	'auto'		
useSampleFraction	NULL	< value > 1	To speed up debugging. Provided as fraction (e.g., 1/10).
verbose	NULL	0, 1, or 2	The `verbose` argument is passed to ctStanFit. Higher values print more information during model fit.

ctmaFitList (plotting)			Informs 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, `ctmaFitList(object1, object2)`.

ctmaGetPub (-)			Retrieves publication and citation indices for authors from Google Scholar, which could be further processed with `ctmaPub`.
Argument	Default	Possible Values	Explanation
authorList	NULL	List of vectors with 2 elements	Contains information about authors' names and their Google Scholar https address (or their user ID), e.g., `list( c("Wilmar B.; Schaufeli", "https://scholar.google.de/citations-?hl=en&user=w1tHcj4AAAAJ"), c("Maureen; Dollard", "user=J6oH3rgAAAAJ") )`. Authors' surnames are separated from given names or initials by a semicolon!
flush	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.
yearsToExclude	NULL	(vector of) years to exclude	Recommended to leave as `NULL`. Years could be excluded later when using `ctmaPub`.

ctmaInit (EP*I*C-BiG-Power)			Fits a ctsem model to a list of primary studies prepared by `ctmaPrep`.
Argument	Default	Possible Values	Explanation
`activateRPB`	`FALSE`	`FALSE/ TRUE`	Messages (warning, finished fitting) could be send to mobile phone if TRUE.
`activeDirectory`	`NULL`	character string	Specifies the directory where required files are found and saved. Should end with "/". For example, `''/Users/GDC/CoTiMA/''`
`chains`	`NULL (=2)`	values > 0	The `chains` argument is passed to ctStanFit and specifies the number of chains to be used for Bayesian estimation.
`checkSingleStudy-Results`	`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.
`cint`	`0`	string vector of names of means of continuous time intercepts	Usually, CoTiMA assumes that standardized varibales (correlations) are analyzed, which should result in estimates of manifestMeans (and T0mean) to be 0.0. To facilitate convergence, these parameters are set to 0.0 by default. They can be set free by providing names. Note that this is automatically done if `indVarying='cint'` is specified.
`coresToUse`	`2`	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.
`CoTiMAStanctArgs`	`NULL`	list of further fitting parameters	All fitting parameters that are allowed in `ctStanFit` can be specified here, too.
`customPar`	`FALSE`	FALSE / TRUE	If set `TRUE` some starting values transformations used by ctSatnFit 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 `delta_ti`. Setting it to `FALSE` and use `scaleTime` instead could be a better alternative if estimation problems will nevertheless occur.
`digits`	4	value > 0	Rounding used in output.

ctmaInit (EP*I*C-BiG-Power)			Fits a ctsem model to a list of primary studies prepared by `ctmaPrep`.
`doPar`	1	`integer value > 0`	Fits each model `doPar` times in parallel mode and returns best single model fit. In each of the parellel fit attempts, `coresToUse` 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 `doPar` is larger, multiple parallel fits are done sequentially.
`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 `V1toV2` or `0` for effects to be excluded, which is usually not recommended, e.g., `c("V1toV1", "V2toV1", 0, "V2toV2")`
`finishsamples`	`NULL` `(=1000)`	values > 0	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 befor manuscripts are submitted. Very large values (e.g., 100.000) might be helpful if very small effects (e.g., 0.0002) result from estimation.
`indVarying`	`FALSE`	TRUE / FALSE	Specifies a random intercept RI model. Works only if all primary studies have 3 or more waves and no missing values (i.e., variables) exist! RI models could be specified using individually varying ct intercepts (`indVarying=='cint'`) or individually varying manifests (`indVarying==TRUE`). In case n-manifest=n.latent, both models are algebraically identical. However, numerically, models with individually varying manifests are easier to fit. Note that 'random intercept' models are referred to as 'fixed effect' models in the econometric literature.

ctmaInit (EP*I*C-BiG-Power)			Fits a ctsem model to a list of primary studies prepared by `ctmaPrep`.
`indVaryingT0`	`TRUE` (if indVarying=TRUE or 'cint')	TRUE / FALSE	Random intercept models are estimated by CTSEM by correlating ct intercepts (or manifests) with all latents at T0. This automatically sets the effect of the dummy variables, which accounts for the nesting of data within primary studies, on T0 (co-)variances to 0. This is not expected to cause serious problems because the dummy variables can be expected to have only very small effects on T0 variables if the T0 variables are allowed to vary randomly, which makes indvaryingT0=TRUE the better option. However, overall, there could be many (k - 1) small effects of dummy variabls on T0 variables, which overall reduce the -2ll value more than the randomly varying intercepts. Thus, expect `indVaryingT0=TRUE` to yield worse model fit than `indVaryingT0=FALSE`, but prefer the former over the later.
`iter`	`NULL` (=1000)	values > 0	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.
`lambda`	`NULL` (= identity matrix)	`n.latent` × `n.manifest` matrix	Matrix with pattern of fixed (=1) or free (any string) loadings.
`loadSingleStudy-ModelFit`	`c()`	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. `loadSingleStudyModelFit=c("myModel", 1, 4, 5, 6:100)`. This is useful, e.g, if primary studies aree 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 `ctmainit fit` object.
`manifestMeans`	`0`	string vector of names of means of T0 latents	Usually, CoTiMA assumes that standardized varibales (correlations) are analyzed, which should result in estimates of manifestMeans (and T0mean) to be 0.0. To facilitate convergence, these parameters are set to 0.0 by default. They can be set free by providing names. Note that this is automatically done if `indVarying= TRUE` is specified.

ctmaInit (EP*I*C-BiG-Power)			Fits a ctsem model to a list of primary studies prepared by `ctmaPrep`.
`manifestVars`	`0`	`0` or `n.manifest` × `n.manifest` matrix with values or strings	Lower triangular matrix with error(co-)variances of manifest indicators. Usually, CoTiMA assumes that a single indicator is used per latent. This typically requires to assume eror variances to be 0.0. Alternatively, they can be assigent a particular value, e.g., 1- Cronbach's alpha. In case s where many waves of observation are available, the error variance of single manifest indicators cann be estimated, too. This is achieved by assginging labels.
`n.latent`	`NULL`	value > 0	Number of latent variables.
`n.manifest`	0 (= `n.latent`)	value $\geq$ `n.latent`	Number of manifest variables.
`nopriors`	`TRUE`	TRUE / FALSE	Consequences of `TRUE` or `FALSE` are conditional on the optimize argument. optimize=`TRUE` & nopriors=`TRUE` implies maximum likelihood estimation, optimize=`TRUE` & nopriors=`FALSE` implies maximum a posteriori estimation, optimize=`FALSE` & nopriors=`TRUE` implies Bayesian estimation using HMC (Hamiltonian Monte Carlos sampler), and optimize=`FALSE` & nopriors=`FALSE` implies Bayesian estimation using NUTS (No U-Turn Sampler).
`optimize`	`TRUE`	TRUE / FALSE	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.
`primaryStudies`	`NULL`	list	A list created with ctmaPrep that containes all information (e.g., `empcovi`, `delta_ti`, `sampleSizei` etc.) relevant for ctmaInit and subsequent analyses.
`priors`	`FALSE`	`FALSE/TRUE`	Replaces previously used `nopriors` argument. Consequences of `TRUE` or `FALSE` are conditional on the optimize argument. optimize=`TRUE` & priors=`FALSE` implies maximum likelihood estimation, optimize=`TRUE` & priors=`TRUE` implies maximum a posteriori estimation, optimize=`FALSE` & priors=`FALSE` implies Bayesian estimation using HMC (Hamiltonian Monte Carlos sampler), and optimize=`FALSE` & priors=`TRUE` implies Bayesian estimation using NUTS (No U-Turn Sampler).

ctmaInit (EP*I*C-BiG-Power)			Fits a ctsem model to a list of primary studies prepared by `ctmaPrep`.
`saveRawData`	`list()`	`list(saveRawData$studyNumbers, saveRawData$fileName, saveRawData$row.names, saveRawData$col.names, saveRawData$sep, saveRawData$dec)`	A list with required information to save generated pseudo raw data. Might be usefull for methodological research questions. For example, `list("saveRawData$studyNumbers = c(1:20), "saveRawData$fileName" = "pseudoRaw", "saveRawData$row.names" = FALSE, "saveRawData$col.names" = TRUE, "saveRawData$sep" = " ", "saveRawData$dec" = ".")`
`saveSingleStudyModelFit`	`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. `saveSingleStudyModelFit=c("myModel", 1, 4, 5, 6:100)`
`scaleTI`	`NULL` (=TRUE)	`TRUE/FALSE`	Wether or not the to standardize the TI predictors that represent the primary study dummies.
`scaleTime`	`NULL` (=FALSE)	value > 0	Wether or not the time scale used for `delta_ti` should be changed.For example, scaleTime=1/12 could change the time scale from months to years. It is usually recommended to avoid `delta_ti` larger than 6. The default value `FALSE` is taken from the `CoTiMAStanctArgs` list, which could also be used to specify more stanct fitting parameters.
`silentOverwrite`	`FALSE`	`TRUE / FALSE`	Whether or not to prompt user preventing undesired overwriting of existing single study fit files (requested via `saveSingleStudyModelFit`)
`T0means`	`0`	string vector of names of means of T0 latents	Usually, CoTiMA assumes that standardized varibales (correlations) are analyzed, which should result in estimates of T0mean (and manifestMeans) to be 0.0. To facilitate convergence, these parameters are set to 0.0 by default. They can be set free by providing names. Note that this is automatically done if `indVarying= TRUE` is specified.
`T0var`	`'auto'`	`0` or n.manifest $\times$ n.manifest matrix with values or strings	
`useSV`	`TRUE`	TRUE / FALSE	If set `TRUE` provided starting values will be used. These could be obtained via `ctmaSV`.
`verbose`	`NULL`	`0`, `1`, or `2`	The `verbose` argument is passed to ctStanFit. Higher values print more information during model fit.

ctmaLCS (-)			Takes a CoTiMA fit object or CTSEM fit and transforms estimates into those estimates typically reported when fitting (dual) latent change score models. The fit object has to include random intercepts (either randomly varying ct intercepts obtained with `indVarying='cint'` or manifest means obtained with or randomly varying manifest means obtained with `indVarying=TRUE`). The function could also be used to transform estimates produced with `indVarying=TRUE` into estimates that would be obtained with `indVarying='cint.`
Argument	Default	Possible Values	Explanation
`CoTiMAFit`	`NULL`	CoTiMA fit object (or ctsem fit object)	Object to which all CotiMA fit object has been assigned to (i.e., what has been returned by `ctmaFit`). Also takes fit objects delivered by CTSEM.
`undoTimeScaling`	`TRUE`	`TRUE/FALSE or` any values	Undos possible time scaling achieve in ctmaInit or ctmaFit by setting the argument `scaleTime.` When a number is provided instead of a logical argument, the number is used to multiply the obtained effects (e.g., when time is scaled in days in a study, and `scaleTime=30.5` is used, the returned effect correspond to 1-month intervals).
`activateRPB`	`FALSE`	`FALSE/ TRUE`	Messages (warning, finished fitting) could be send to mobile phone if TRUE.
`checkSingleStudy-Results`	`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.
`digits`	4	value > 0	Rounding used in output.

ctmaOptimizeFit (-)			Repeated Initial fitting (i.e., applies `ctmaInit`} to a primary study or repeated Full Fitting (i.e., applies `ctmaFit`} several times to capitalize on chance for obtaining a hard-to-find optimal fit.
Argument	Default	Possible Values	Explanation
`activateRPB`	`FALSE`	`FALSE / TRUE`	Messages (warning, finished fitting) could be send to mobile phone if TRUE.
`activeDirectory`	`NULL`	character string	Specifies the directory where required files are found and saved. Should end with "/". For example, `''/Users/GDC/CoTiMA/''`

ctmaOptimizeFit (-)			Repeated Initial fitting (i.e., applies `ctmaInit`} to a primary study or repeated Full Fitting (i.e., applies `ctmaFit`} several times to capitalize on chance for obtaining a hard-to-find optimal fit.
`checkSingleStudy-Results`	`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.
`coresToUse`	`2`	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.
`CoTiMAStanctArgs`	`NULL`	list of further fitting parameters	All fitting parameters that are allowed in `ctStanFit` can be specified here, too.
`ctmaFitFit`	`NULL`	CoTiMA Fit object created with `ctmaFit`	The CoTiMA Full Fit object of which the fit should be improved.
`ctmaInitFit`	`NULL`	CoTiMA Init Fit object created with `ctmaInit`	The CoTiMA Init Fit object that was used when creating the CoTiMA Full Fit object
`customPar`	`FALSE`	`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 `delta_ti`. Setting it to `FALSE` and use `scaleTime` instead could be a better alternative if estimation problems will nevertheless occur.
`finishsamples`	`NULL` (=1000)	values > 0	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 befor manuscripts are submitted. Very large values (e.g., 100.000) might be helpful if very small effects (e.g., 0.0002) result from estimation.

ctmaOptimizeFit (-)			Repeated Initial fitting (i.e., applies ctmaInit} to a primary study or repeated Full Fitting (i.e., applies ctmaFit} several times to capitalize on chance for obtaining a hard-to-find optimal fit.
indVarying	FALSE	TRUE / FALSE	Note: Only if ctmaOptimizeFit is used to re-fit primary studies (i.e., when poor fit was obtained with ctmaInit) , indvarying=TRUE specifies a random intercept model. It then works only if all primary studies have 3 or more waves and no missing values (i.e., variables) exist. When ctmaOptimizeFit is used to re-fit a full CoTiMA (i.e., when a poor fit was obtained with ctmaFit), the indVarying argument has no effect because its value (TRUE/FALSE) is taken from the ctmeFitFit object (see 4 rows above).
lambda	NULL (= identity matrix)	n.latent × n.manifest matrix	Matrix with pattern of fixed (=1) or free (any string) loadings. Only relevant if ctmaOptimizeFit is used to re-fit primary studies (i.e., when poor fit was obtained with ctmaInit). When ctmaOptimizeFit is used to re-fit a full CoTiMA (i.e., when a poor fit was obtained with ctmaFit), the lambda argument has no effect because its values are taken from the ctmeFitFit object.
manifestMeans	0	string vector of names of means of T0 latents	Only relevant if ctmaOptimizeFit is used to re-fit primary studies (i.e., when poor fit was obtained with ctmaInit). When ctmaOptimizeFit is used to re-fit a full CoTiMA (i.e., when a poor fit was obtained with ctmaFit), the manifestMeans argument has no effect because ite value is taken from the ctmeFitFit object.
manifestVars	0	0 or n.manifest × n.manifest matrix with values or strings	Only relevant if ctmaOptimizeFit is used to re-fit primary studies (i.e., when poor fit was obtained with ctmaInit). When ctmaOptimizeFit is used to re-fit a full CoTiMA (i.e., when a poor fit was obtained with ctmaFit), the manifestVars argument has no effect because ite value is taken from the ctmeFitFit object.

ctmaOptimizeFit (-)			Repeated Initial fitting (i.e., applies `ctmaInit`} to a primary study or repeated Full Fitting (i.e., applies `ctmaFit`} several times to capitalize on chance for obtaining a hard-to-find optimal fit.
`n.latent`	`NULL`	value > 0	Only relevant if `ctmaOptimizeFit` is used to re-fit primary studies (i.e., when poor fit was obtained with `ctmaInit`). When `ctmaOptimizeFit` is used to re-fit a full CoTiMA (i.e., when a poor fit was obtained with `ctmaFit`), the `n.latent` argument has no effect because ite value is taken from the ctmeFitFit object..
`primaryStudies`	`NULL`	list	A list created with `ctmaPrep` that containes all information (e.g., `empcovi`, `delta_ti`, `sampleSizei` etc.). Relevant for `ctmaInit` only. In a typical workflow, one would create new new list with `ctmaPrep` that only contains the primary studies that were previously identified to yield improper fits.
`problemStudy`	`NULL`	value > 0	Number of the study (not the position) in the `primaryStudies` list that should be re-fitted.
`reFits`	`NULL`	value > 0	How many reFits should be done
`randomScaleTime`	`c(1,1)`	a pair of positive values	From a uniform distribution within the provided limits a value (rounded to 2 decimals) is drawn for each refit attempt.
`T0means`	`0`	string vector of names of means of T0 latents	Usually, CoTiMA assumes that standardized varibales (correlations) are analyzed, which should result in estimates of T0mean (and manifestMeans) to be 0.0. To facilitate convergence, these parameters are set to 0.0 by default. They can be set free by providing names. Note that this is automatically done if `indVarying= TRUE` is specified.
`randomPar`	`FALSE`	`FALSE / TRUE`	If set to `TRUE`, it overrides the `customPar` argument used to create the CoTiMA Full Fit object. Instead, `customPar` varies randomly between `TRUE` and `FALSE` during the number of fit attempts specified with `reFits`.

ctmaPlotCtsemMod (-)			Auxiliary function to plot moderator effects estimated with CTSEM using ctStanFit.
Argument	Default	Possible Values	Explanation
ctStanFitObject	NULL	CTSEM (ctstan) fit object	CTSEm fit object in which a single moderator (= time independent predictor TIpred) moderates drift 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 "/".
mod.sd.to.plot	c(-1, 0, 1)	vector	The standard deviation values of the moderator (default -1, 0, +1) for which the drift effects are plotted. The argument is ignored if the moderator is categoricl.
timeUnit	"timeUnit (not specified)"	vector of character strings	Affects plotting of ctmaInit or ctmaFit 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: c(xMin, xMax, stepwidth)	Affects plotting of ctmaInit or ctmaFit fit-objects only. The range across which discrete time effects are plotted, e.g., c(10,. 20, .01) would plot effects from 10 units of time to 20 using steps of .01. Note that a stepwidth < 1 could be specified to obtain more fine-grained figures.
yLimitsForEffects	values slightly exceeding min and max empirical effect sizes	vector with 2 values: c(yMin, yMax)	Affects plotting of ctmaInit or ctmaFit fit-objects only. The min and max values for the y-axis. Setting explicit values couod be better than relying on the automatically determined range, for example, to ensure identical y-axis across a larger set of plots.
mod.values	c(-2-1, 0, 1, 2)	vector with numbers	Affects plotting of ctmaFit 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 was standardized with scaleMod=TRUE. Does not affect plotting of categorical moderators.
mod.type	'cont'	'cont' or 'cat'	The type of moderator.
no.mod.cats	NULL	value > 0	Need to be specified if type = "cat". The number of categories should usually be equal the number of dummy variables used to represent the categorical moderator + 1.
n.x.labels	NULL	value > 0	How many values to be used for indicating time points on the x-axis (0 is automatically added and should not be counted).
plot.xMin	0	value $\geqq 0$	

ctmaPlotCtsemMod (-)			Auxiliary function to plot moderator effects estimated with CTSEM using ctStanFit.
plot.xMax	NULL	value > 0	
plot.yMin	-1	value	
plot.yMax	1	value	
plot..type	''l''	Any letter that can be used to represent the type of plot in R	Two dots (..) should be used. Points, lines, both etc.
plot.lty	1	Any letter that can be used to represent the type of lines in R	solid, dotted, dashed etc. lines.
plot.col	''grey''	Any color names or color number that can be used to represent the type of lines in R	Line color.
plot.lwd	1.5	value > 0	Line width.
dot.plot.type	''b''	Any letter that can be used to represent the type of plot in R	Sets the type of symbol used to show the moderator values along their trajectories.
dot.plot.col	''black''	Any color names or color number that can be used to represent the type of lines in R	Sets the color of the symbol used to show the moderator values.
dot.plot.lwd	0.5	value > 0	Sets the size of the symbol used to show the moderator values.
dot.plot.lty	1.5	Any letter that can be used to represent the type of lines in R	solid, dotted, dashed etc. lines.
dot.plot.pch	16	Any integer that can be used to represent the type of lines in R	Sets the shape of the symbol used to show the moderator values.
dot.plot.cex	3	value > 0	Magnifier for the symbol used to show the moderator values.

ctmaPower (EPIC-BiG-*Power*)			Informs the plot function that more than a single CoTiMA fit object should be plotted.
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 ctmaInit)

ctmaPower (EPIC-BiG-*Power*)			Informs the plot function that more than a single CoTiMA fit object should be plotted.
`activeDirectory`	path used to create ctmaInit-Fit object	path to directory	Specifies the directory where required files are found and saved. Should end with "/".
`statisticalPower`	`c()`	vector	Vector of requested statistical power values, e.g. `c(.95, .80)`
`failSafeN`	NULL	value > 0	A sample size used to determine across which time intervals expected effects become not significant. If not specified, the avergae sample size of primary studies will be used.
`failSafeP`	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.
`timeRange`	`NULL`	vector with 3 values	Specifies the time range across which statistical power etc will be computed. A vector with 3 values: sarting point, end point, step witdh, 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.
`useMBESS`	`FALSE`	TRUE / FALSE	If `TRUE`, the MBESS package is used to calculate statistical power (slower). Otherwise, use the internal CoTiMA function (faster).
`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.
`digits`	`4`	value > 0	Rounding used in output.
`indVarying`	`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
`activateRPB`	`FALSE`	`FALSE/ TRUE`	Messages (warning, finished fitting) could be send to mobile phone if `TRUE`.
`silentOverwrite`	`FALSE`	`TRUE / FALSE`	Whether or not to prompt user preventing undesired overwriting of existing fit files (requested via `saveAllInvFit` or `saveAllInvWOSingFit`)
`loadAllInFit`	`c()`	character sting	Load the fit of a CoTiMA model with all effects invaraint across primary studies, e.g. `loadAllInvFit=c("myAllInvariantModel")`
`saveAllInFit`	`c()`	character sting	Save the fit of a CoTiMA model with all effects invaraint across primary studies, e.g. `saveAllInvFit=c("myAllInvariantModel")`

ctmaPower (EPIC-BiG-*Power*)			Informs the plot function that more than a single CoTiMA fit object should be plotted.
loadAllInvWOSingFit	c()	character sting	not yet operational
saveAllInvWOSingFit	c()	character sting	not yet operational
skipScaling	TRUE	FALSE / TRUE	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 N - 1. Could be corrected by setting skipScaling to FALSE, but usually has little practical consequences.
useSampleFraction	NULL	value between 100 and 0	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)
optimize	TRUE	TRUE / FALSE	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.
nopriors	TRUE	TRUE / FALSE	Consequences of TRUE or FALSE are conditional on the optimize argument. optimize=TRUE & nopriors=TRUE implies maximum likelihood estimation, optimize=TRUE & nopriors=FALSE implies maximum a posteriori estimation, optimize=FALSE & nopriors=TRUE implies Bayesian estimation using HMC (Hamiltonian Monte Carlos sampler), and optimize=FALSE & nopriors=FALSE implies Bayesian estimation using NUTS (No U-Turn Sampler).
finishsamples	NULL (=1000)	values > 0	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 befor manuscripts are submitted. Very large values (e.g., 100.000) might be helpful if very small effects (e.g., 0.0002) result from estimation.

ctmaPower (EPIC-BiG-*Power*)			Informs the plot function that more than a single CoTiMA fit object should be plotted.
iter	NULL (=1000)	values > 0	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.
chains	NULL (=2)	values > 0	The chains argument is passed to ctStanFit and specifies the number of chains to be used for Bayesian estimation.
verbose	NULL	0, 1, or 2	The verbose 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 delta_ti. Setting it to FALSE and use scaleTime 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 ctmaPubGet	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 infromations might not be very reliably. Early years (e.g., 1900-1960) might be excluded because they would cause invalid publications (sometimes this happens in Goofle Scholar).
targetYear	NULL (=publication year)	a positive value	If left NULL, all publications before the year of the authors' publication count.

ctmaPub (-)			Computes publication indices for the group of authors of a study (augments ctmaGetPub).
recency	5	a positive value	ctmaPub computes 2 indices. For the first one (NEPP), all years before targetYear count. For the second one (NEPPrecency), the years between targetYear and targetYear - recency count.
indFUN	‘‘sum’’	any of: "mean", "sum", "max", "min", "var"	Specifies the function used to aggregate an *ind*ividual author's publication numbers, e.g., sum (recommended) computes the sum of an author's publication before targetYear, and var computes the variance of the number of publications for an author's first year of publication to targetYear.
colFUN	‘‘mean’’	any of: "mean", "sum", "max", "min", "var"	Specifies the function used to aggregate a group of authors (*col*lective) publication numbers, e.g., mean computes the mean of all authors' publication scores (created with indFUN, e.g., the sums) before targetYear, and max takes largest of all authors' publication scores (created with indFUN, e.g., the sums) to targetYear.
addAsMod	FALSE	FALSE / TRUE	Currently disabled.

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

ctmaPrep (EPIC-BiG-Power)			Combines information of primary studies into a list object and returns this list.
excludedElements	NULL	vector with integers	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 delta_t (should be of the type c(NA, NA) in cases when raw data are provided, with the number of NAs corresponding to the number of time intervals), sampleSize (single number), pairwiseN (matrix of pairwise N; could be used if correlation matrix is based on pairwise N), empcov (correlation matrix), moderator (vector of numbers; could be continuous or categorical), alphas (vector of reliability estimates of the variables of a primary study), startValues (vector of start values), rawData (information about file name and structure of raw data), empMeans (means for variables; usually 0), and empVars (variances for variables; usually 1.0). Weakly predefined objects are studyNumber (intended as a special number used for the outputs of subsequently fitted CoTiMA models), source (intended as vector of authors' names and publication year), ageM value intended for indicating the mean age of participants in a primary study, malePercen' (intended as value indicating the percentage of male participants in a primary study), occupation (intended as vector of character strings representing the occupations of participants in a primary study), country (intended as single character string representing the country in which a primary study was conducted), and targetVariables (intended as vector of character strings representing information about the variables used).
activeDirectory	path used to create ctmaInit-Fit object	path to directory	Specifies the directory where required files are found and saved. Should end with "/".

ctmaPrep (EPIC-BiG-Power)			Combines information of primary studies into a list object and returns this list.
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. c("Important", "Interesting")
digits	4	value ≥ 0	Rounding used in output.
moderatorLabels	NULL	vector of character strings	Vector of Names used to label moderators in the output e.g., c("Mod1", "Control")
moderatorValues	NULL	list of vectors	List of vector of Names (assignments) used to label moderators in the output e.g., list(c(1"=Emotional Exhaustion", "2=Exhaustion"), "continuous")
summary	TRUE	TRUE / FALSE	Requests summary table and xlsx workbook in return object. Could be set to FLASE to avoid reporting errors.

ctmaRedHet (-)			Computes the reduction in heterogeneity of drift effects after moderators are taken into account. The function takes two CoTiMA Fit objects as arguments. Both models should mimic the ctmaInit fit function, by using ctmaFit with the argument invariantDrift = c('none'). The first model should yield exactly the same fill (-2ll) as the ctmaInit fit because it is algebraically identical (all drift effects are moderated by dummy variables representing the primary studie). The second model includes moderator variables in addition. Mimicing ctmaInit by using ctmaFit is necessary because moderators are study-level variables that cannot be modelled if each primary study ist fitted seperately as in ctmaFit. For example, fit1 <- ctmaFit(ctmaInitFit=fitObject, scaleTI = FALSE, invariantDrift = c('none')) and fit2 <- ctmaFit(ctmaInitFit=fitObject, scaleTI = FALSE, invariantDrift = c('none'), mod.numer=1, mod.type='cont') and then results <- ctmaRedHet(ctmaFitObject=fit1, ctmaFitObjectMod=fit2) summary(results).
Argument	Default	Possible Values	Explanation
activateRPB	FALSE	FALSE / TRUE	Messages (warning, finished fitting) could be send to mobile phone if TRUE.
activeDirectory	NULL	character string	Specifies the directory where required files are found and saved. Should end with "/". For example, "/Users/GDC/CoTiMA/"

ctmaRedHet (-)			Computes the reduction in heterogeneity of drift effects after moderators are taken into account. The function takes two CoTiMA Fit objects as arguments. Both models should mimic the `ctmaInit` fit function, by using `ctmaFit` with the argument `invariantDrift = c('none')`. The first model should yield exactly the same fill (-2ll) as the `ctmaInit` fit because it is algebraically identical (all drift effects are moderated by dummy variables representing the primary studie). The second model includes moderator variables in addition. Mimicing `ctmaInit` by using `ctmaFit` is necessary because moderators are study-level variables that cannot be modelled if each primary study ist fitted seperately as in `ctmaFit`. For example,
			`fit1 <-`
			`ctmaFit(ctmaInitFit=fitObject,`
			`scaleTI = FALSE, invariantDrift =`
			`c('none'))`
			and
			`fit2 <-`
			`ctmaFit(ctmaInitFit=fitObject,`
			`scaleTI = FALSE, invariantDrift =`
			`c('none'), mod.numer=1,`
			`mod.type='cont')`
			and then
			`results <-`
			`ctmaRedHet(ctmaFitObject=fit1,`
			`ctmaFitObjectMod=fit2)`
			`summary(results).`

`ctmaFitObject`	`NULL`	CoTiMA fit object.	A CoTiMA fit object created with `ctmaFit` using the argument `invariantDrift = c('none')`.
`ctmaFitObjectMod`	`NULL`	CoTiMA fit object	A CoTiMA fit object created with `ctmaFit` using the argument `invariantDrift = c('none')` and at least one moderating effect.
`digits`	4	value > 0	Rounding used in output.
`dt`	`NULL`	value > 0	Not yet implemented. A scalar indicating a time interval across which discrete time effects should be estimated and then used for estimating the reduction heterogeneity.
`undoTimeScaling`	`TRUE`	`TRUE/FALSE` or any values	Undos possible time scaling achieved in ctmaFit by setting the argument `scaleTime`. When a number is provided instead of a logical argument, the number is used to multiply the obtained effects (e.g., when time is scaled in days in a study, and `scaleTime=30.5` is used, the returned effect correspond to 1-month intervals).

ctmaShapeRawData (E*P*IC-BiG-Power)			Transform raw data into the form required by ctsem or CoTiMA.
Argument	Default	Possible Values	Explanation

ctmaShapeRawData (EPIC-BiG-Power)			Transform raw data into the form required by ctsem or CoTiMA.
dataFrame	NULL	R object	An (typicallly pre-processed) R object containing data. For example, using the 'foreign' R-package a SPSS data file can be imported using 'tmpData <- data.frame(read.spss(X.sav"), use.value.labels = FALSE))', by which time stamps are translated into number of seconds since October 14, 1582 (i.e., the internal SPSS format). The can be change with the argument scaleTime (see beloe)
inputDataFrameFormat	NULL	''wide'' or ''long''	Specifies if the dataFrame object contains data in wide or long (not yet enabled) format.
inputTimeFormat	''time''	''time'' or ''delta''	Wether time points (time) or time intervals (delta) are included in the dataFrame object.
missingValues	NA	single value	Value that indicates missing values in the dataFrame object (default = NA).
n.manifest	NULL	single value > 0	Number of process variables in the dataFrame object (i.e., exluding possible moderators (for CoTiMA) or time dependent (TDpreds) and time independent (TIpreds; for ctsem) per time point. Possibly 2 for CoTiMA in most instances (i.e., a bivariate model).
Tpoints	NULL	single value > 0	Number of time points in the dataFrame object.
allInputVariablesNames	NULL	vector of character strings	Vector of all process variable names, time dependent predictor names, time independent predictor names, and names of times/deltas. Only required if the dataFrame does not have column names. Used to identify the variables that should be selected later.
orderInputVariablesNames	NULL	''names'' or ''time''	When names is specified, the process variables are expected to be in the order X1, X1, X3, Y1, Y2, X3 etc. When time is specified, the expected order is X1, Y1, X2, Y2, etc. "names" vs "time". For ctsem/CoTiMA, the output file will order them by time.
targetInputVariablesNames	NULL	vector of character strings	The process variables in the dataFrame that should be used (in names or in times order as specified with the argument orderInputVariablesNames). This is used to delete variables from the data frame that are not required.

ctmaShapeRawData (EPIC-BiG-Power)			Transform raw data into the form required by ctsem or CoTiMA.
targetInputTDpredNames	NULL	vector of character strings	Not really important for CoTiMA, but perhaps for fitting ctsem models. The vector of character strings should contain the actual TDpred labels, e.g, 3, or 6, or 9, ... names if Tpoints = 3. Each of the 3, 6, etc represents one TDpred. One typically does *not* have TD predictors in a CoTiMA.
targetInputTIpredNames	NULL	vector of character strings	Time independet (TI) predictor names names in the dataFrame. One typically does *not* have TI predictors in CoTiMA except it uses raw data only, where TIpreds are avalaible for individual cases. (In case data are prepared for CoTiMA, TIpreds could be preresented by moderator variables, which have to be specivied using `ctmaPrep`) , In case data are prepared for ctsem, each TIpred is feasible, and the vector of character strings should contain the actual TIpred labels in the `dataFrame` object.
targetTimeVariablesNames	NULL	vector of character strings	The labels of the time variables and time variables in the `dataFrame` that should be used, e.g., `c(''time2'', ''time4'')` or `c(''dT0'', ''dT1'')`.
outputDataFrameFormat	''long''	''long'' or ''wide''	The output format of the returned R object. Should be usually `wide` for CoTiMA and `long` for ctsem.
outputVariablesNames	''Y''	vector of character strings	The defaul value `"Y"` will results in variable labels Y1_T0, Y2_T0, Y3_T0 etc. with numbers representing the `n.manifest` variables . When, e.g., `n.manifest=3` one oculd also specify, e.g., `c("X", "Y", ''Z'')`, which will results in Y_T0, X_T0, Z_T0 etc.
outputTDpredNames	NULL	vector of character strings	Not really important for CoTiMA, but perhaps for fitting ctsem models. The defaul value `"TD"` will results in TDpred labels TD1_T0, TD2_T0, TD3_T0 etc. with numbers representing the number of TDpred . When, e.g., three TD labels per time point are specficied with the argument `targetInputTDpredNames`, one oculd also specify, e.g., `c("A", "B", ''C'')`, which will results in A_T0, B_T0, C_T0 etc.
outputTIpredNames	NULL	vector of character strings	Not really important for CoTiMA, but perhaps for fitting ctsem models. The defaul value `"TI"` will results in TIpred labels TI1, TI2, TI3 etc. with numbers representing the number of TDpred .

ctmaShapeRawData (EPIC-BiG-Power)			Transform raw data into the form required by ctsem or CoTiMA.
outputTimeVariablesNames	''time''	character string	Not really important for CoTiMA, but perhaps for fitting ctsem models. The defaul value "time" will results in time varibles labeled time0, time1, time2 etc.
outputTimeFormat	''time''	''time'' or ''delta''	Whether time is stored in absolute time or deltaas (time intervals). Note the CoTiMA requires ''delta'' (and ''wide'' format), whereas ctsem requires ''time'' (and ''long'' format).
scaleTime	1	any positive value	Scales time in the returned data frame by a scalar that is used to multiply the time variable. Typical use is rescaling primary study time to the time scale use in other primary studies. For example, scaleTime=1/(60 x 60 x 24 x 365.25) rescales time provided in seconds (frequent case when imported from SPSS) into years (60sec x 60min x 24hrs x 365.25days incl. leap years).
minInterval	.0001	single value > .00001	A parameter (default = 0.0001) supplied to ctIntervalise. Set to smaller values than any possible observed measurement interval, but larger than 0.0001. The value is used for indicating unavailable time interval information (caused by missing values) because NA is technically not possible for time intervals..
minTolDelta	NULL	single value > 0	The shortest time interval to be tolerated. Could be useful to eliminate invalid data, e.g., because primary researchers coded time wrongly or participants filled in invalid values to time questions or did not adhere to the research protocol. For example, assuming time is coded in months in a study that was supposed to have approximate 12-month (1-year) intervals, a value of 6 would delete values at a time point that was closer to the preceeding one than 6 months. Note that minTolDelta applies to the time intervals *after* the scaleTime argument has applied (i.e., scaleTime may need adaptation for each primary study, but minTolDelta does not).

ctmaShapeRawData (EPIC-BiG-Power)			Transform raw data into the form required by ctsem or CoTiMA.
maxTolDelta	NULL	single value > 0	The loingest time interval to be tolerated. Could be useful to eliminate invalid data, e.g., because primary researchers coded time wrongly or participants filled in invalid values to time questions or did not adhere to the research protocol. For example, assuming time is coded in months in a study that was supposed to sample 6 times within a 6-month (1/2-year) time frame, a value of 6 would delete values at aall (!!) time points that were farer away from any other one than 6 months.. Note that maxTolDelta applies to the time intervals *after* the scaleTime argument has applied (i.e., scaleTime may need adaptation for each primary study, but minTolDelta does not).
min.val.n.vars	1	any integer value between 0 and n.manifst	Specifies the minimum no. of valid variables (i.e., non NA) that has to be available per participant.. Default = 1 (retaines cases with only 1 valid variable), 0 would retain cases will all variables missing (not very useful). Retaining participants who provide a single valid variable is technically possible, but these participants contribute to the estimation of the variance/mean of this variable only. Since variance/mean are 1/0 in most CoTiMA applications, this is not very informative but at the cost of additional computational burden. Setting min.val.n.Vars = 2 is recommended..
min.val.Tpoints	1	any integer value between 1 and Tpoints	Minimum no. of valid Tpoints (i.e. Tpoints where min.val.n.Vars is met). Default = 1 retains participants with full set of valid variables at least at one single Tpoint (which will become T0). Setting min.val.Tpoints = 2 or higher values retains participants which provide longitudinal information. Since T0 covariances are usually not too interesting, min.val.Tpoints = 2 may be more reasonable then the default = 1..
experimental	FALSE	FALSE / TRUE	Deprecated.

ctmaSV (EP*I*C-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 `primaryStudies` argument in subsequent `ctmaInit` 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, cotinuous time effects are computed for each intervals and then aversaged.
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 `ctmaInit`)
`activeDirectory`	path used to create ctmaInit-Fit object	path to directory	Specifies the directory where required files are found and saved. Should end with "/".
`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.
`primaryStudies`	`NULL`	CoTiMA fit object created with `ctmaPrep`	In cases in which the CoTiMA fit object assigned to `ctmaInitFit` (possibly old fit files) does not contain the primaryStudies object created with `ctmaPrep` it could be added by assgining it to the `primaryStudies` argument.
`replaceUV`	`TRUE`	TRUE / FALSE	The computed starting values could either replace exiting starting values in the returned list of primary studie (`TRUE`; default) or save them as an addition list element `inits`.

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 paramters 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 lim-

ited; 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.

`plot/ctmaPlot`			Generates plots.
Argument	Default	Possible Values	Explanation
`ctmaFitObject`	`NULL`	vector with integers	A CoTiMA fit-object created by `ctmaInit`, `cmtaFit`, or `ctmaBig`.
`activeDirectory`	path used to create ctmaInit-Fit object	path to directory	Specifies the directory where required files are found and saved. Should end with "/".
`saveFilePrefix`	`"ctmaPlot"`	vector of character strings	Labels for the generated plot, which might be automatically augmented by further information (e.g., "ctmaplot V1toV1,png")
`activateRPB`	`FALSE`	`FALSE/ TRUE`	Messages (warning, finished fitting) could be send to mobile phone if `TRUE`.
`plotCrossEffects`	`TRUE`	`TRUE/ FALSE`	Affects plotting of `ctmaInit` or `ctmaFit` fit-objects only. Plotting of discrete time cross effects can be suspended.
`plotAutoEffects`	`TRUE`	`TRUE/ FALSE`	Affects plotting of `ctmaInit` or `ctmaFit` fit-objects only. Plotting of discrete time auto effects can be suspended.
`timeUnit`	`"timeUnit (not specified)"`	vector of character strings	Affects plotting of `ctmaInit` or `ctmaFit` 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: c(xMin, xMax, stepwidth)	Affects plotting of `ctmaInit` or `ctmaFit` fit-objects only. The range across which discrete time effects are plotted, e.g., `c(10,. 20, .01)` would plot effects from 10 units of time to 20 using steps of .01. Note that a stepwidth < 1 could be specified to obtain more fine-grained figures.
`yLimitsForEffects`	values slightly exceeding min and max empirical effect sizes	vector with 2 values: c(yMin, yMax)	Affects plotting of `ctmaInit` or `ctmaFit` fit-objects only. The min and max values for the y-axis. Setting explicit values couod be better than relying on the automatically determined range, for example, to ensure identical y-axis across a larger set of plots.
`mod.values`	`c(-2-1, 0, 1, 2)`	vector with numbers	Affects plotting of `ctmaFit` 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 was standardized with `scaleMod=TRUE`. 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 `ctmaFitObject`. Not that `mod.number` does not select the dummies used for categorical moderators (all dummy effects are ploted); rather it refers to the 1st, 2nd etc continuous or categorical moderator of an analysis.
`aggregateLabel`	`""` (=nothing)	character(s)	Affects plotting of `ctmaFit` fit-objects only. Symbol to be attached to the discrete time plot of a `ctmaFit` fit-object. In the case of `ctmaInit` fit-objects, each study is usually idetified in the plot with a dot inside which the study number is shown. In the case of a `ctmaFit` fit-object with aggregated effects, one could use a symbol, e.g. `aggregateLabel="Σ"`.
`xLabels`	`NULL`	vector with numbers	Affects plotting of `ctmaFit` 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., `c(1, 3, 5, 7, 9)`

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

fitAddSpecs `(ctmaInit & ctmaFit fit-objects)`			Generates discrete time effect plots.
Argument	Default	Possible Values	Explanation

fitAddSpecs (ctmaInit & ctmaFit fit-objects)			Generates discrete time effect plots.
CoTiMAFit$col	"grey" & "black" for ctmaInit & ctmaFit fit-objects, respectively.	R-type color code	Sepcifies the color of the curve showing the discrete time affects across time, e.g., CoTiMAFit$col <- ''red''
CoTiMAFit$lwd	1.5 & 2.5 for ctmaInit & ctmaFit fit-objects, respectively.	value ≥ 0	Sepcifies the line width of the curve showing the discrete time affects across time, e.g., CoTiMAFit$lwd <- 4
CoTiMAFit$lty	1 & 2 for ctmaInit & ctmaFit fit-objects, respectively.	R-type integer value ≥ 0	Sepcifies the line type of the curve showing the discrete time affects across time, e.g., CoTiMAFit$lty <- 1, with, e.g., 1 = solid, 2 = dashed, and 3 = dotted.
CoTiMAFit$xMin	min of timeRange	integer values	Limits the displayed range of the discrete time effects plotted. Should only be used in combination with the xLabels argument. Overrides other setting if multiple fit-objects are supplied. This is experimental; it is recommended to set timeRange instead.
CoTiMAFit$xMax	max of timeRange	integer values	Limits the displayed range of the discrete time effects plotted. Should only be used in combination with the xLabels argument. Overrides other setting if multiple fit-objects are supplied. This is experimental; it is recommended to set timeRange 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			