metaSEM: An **R** Package for Meta-Analysis using Structural Equation Modeling

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Abstract

The **metaSEM** package provides functions to conducting univariate and multivariate meta-analysis using a structural equation modeling (SEM) approach via the **OpenMx** package. It also implemented the two-stage SEM approach to conducting fixed- and random-effects meta-analytic SEM on correlation or covariance matrices. This paper outlines the basic theories and its implementations. Several examples are used to illustrate the procedures.

Keywords:˜meta-analysis, structural equation modeling, meta-analytic structural equation modeling, **metaSEM**, R.

1. Introduction

Meta-analysis is a popular technique to synthesizing research findings in social, behavioral, educational and medical sciences (e.g., Borenstein, Hedges, Higgins, and Rothstein 2009; Hedges and Olkin 1985; Hunter and Schmidt 2004; Whitehead 2002). There are several standalone programs to conduct meta-analysis, e.g., Comprehensive Meta-Analysis (Borenstein, Hedges, and Rothstein 2005) and Review Manager (The Nordic Cochrane˜Centre 2011). There are also macros or packages to fitting some meta-analytic models in standard statistical packages, for instance, Lipsey and Wilson (2000) for SPSS (Corp. 2012), Arthur, Bennett, and Huffcutt (2001) for SAS (SAS Institute˜Inc. 2003) and Sterne (2009) for Stata (StataCorp 2011). Even in the R (R Development Core˜Team 2012) community, there are already several R packages to conduct meta-analysis, for instance, **meta** (Schwarzer 2012), **rmeta** (Lumley 2009), **mvmeta** (Gasparrini 2012), **metaLik** (Guolo and Varin 2012) and **metafor** (Viechtbauer 2010).

The **metaSEM** package is yet another R package to conduct univariate and multivariate meta-analysis. It formulates meta-analytic models as structural equation models (Cheung 2008, 2011) via the OpenMx package (Boker, Neale, Maes, Wilde, Spiegel, Brick, Spies, Estabrook, Kenny, Bates, Mehta, and Fox 2011). It also implemented the two-stage structural equation modeling (TSSEM) approach (Cheung and Chan 2005b, 2009) to fit fixed- and random-effects meta-analytic structural equation modeling (MASEM) on correlation or covariance matrices. The main functions in this package are:

- `meta()` and `reml()`: `meta()` fits univariate and multivariate meta-analysis with maximum likelihood (ML) estimation method while `reml()` estimates the variance com-

ponents of the random-effects with restricted (residual) maximum likelihood (REML)
estimation method. Mixed-effects meta-analysis can be fitted by using study character-
istics as predictors. Equality constraints on the intercepts, regression coefficients and
variance components can be imposed.

- `meta3()`, `meta3X()` and `reml3()`: They fit three-level meta-analysis by considering
  cluster effect. `meta3()` fits the three-level meta-analysis with ML estimation method,
  whereas `meta3X()` fits the same three-level meta-analysis that can handle missing co-
  variates with (full information) ML estimation method. `reml3()` estimates the variance
  components with REML estimation method.

- `tssem1()` and `tssem2()`: `tssem1()` fits the first stage analysis of TSSEM by pooling cor-
  relation or covariance matrices with either a fixed- or random-effects model. `tssem2()`,
  which is a wrapper of `wls()`, conducts the second stage analysis by fitting structural
  models on the pooled correlation or covariance matrix.

- `wls()`: It fits a correlation or covariance structure analysis with weighted least squares
  (WLS) estimation method.

This paper was based on the **metaSEM** package version 0.8-4, the **OpenMx** package version
1.3.2-2301 and R version 3.0.0. The remaining sections are organized as follows. The next
section presents basic ideas on structural equation models and how they are linked to meta-
analytic models. Basic theory in TSSEM are then presented. Several examples are used to
illustrate these procedures. How to install the package is finally mentioned.

2. Structural equation modeling based meta-analysis

In this section, basic theories in structural equation modeling (SEM) are introduced. Univari-
ate and multivariate meta-analysis are then formulated as special cases in SEM (see Cheung
2008, 2011).

2.1. Structural equation model

Structural equation modeling is a multivariate technique to fit and test hypothesized models.
Let $\mathbf{y}$ be a $p \times 1$ vector of sample of continuous data where p is the number of variables. It is
hypothesized that the model for the first and the second moments are functions of θ where θ
is a vector of parameters that can be regression coefficients, error variances, factor loadings
and factor variances, i.e., $\mu = \mu(\theta)$ and $\mathbf{\Sigma} = \mathbf{\Sigma}(\theta)$ where μ and $\mathbf{\Sigma}$ are the population mean
vector and covariance matrix, respectively .

The -2*log-likelihood of the ith case is:

$$-2 * logL_i(\theta; \mathbf{y}_i)_{\mathrm{ML}} = p_i * log(2\pi) + log|\mathbf{\Sigma}_i(\theta)| + (\mathbf{y}_i - \mu_i(\theta))^{\top}\mathbf{\Sigma}_i(\theta)^{-1}(\mathbf{y}_i - \mu_i(\theta)), \quad (1)$$

where p_i is the number of filtered variables with complete data in the ith case, $\mu_i(\theta)$ and $\mathbf{\Sigma}_i(\theta)$
are the model implied mean vector and the model implied covariance matrix for the ith case,
respectively. Since there is a subscript i in Equation~1, the model implied mean vector and the
model implied covariance matrix may vary across cases. In order words, it handles incomplete

data automatically by selecting only the complete data in the log-likelihood function (Enders 2010).

To obtain the parameter estimates, we may take the sum of the -2*log-likelihood over all cases and minimize it. This is known as the full information maximum likelihood (FIML or simply ML) estimation method. Iterative methods are used to obtain the parameter estimates. When it is convergent, the asymptotic sampling covariance matrix of the parameter estimates may be obtained from the inverse of the Hessian matrix. The standard errors (*SE*s) of the parameter estimates are calculated by taking the square root of the diagonal elements. The parameter estimates divided by their *SE*s follow a z distribution under the null hypothesis. Likelihood ratio statistic may also be used to compare nested models.

2.2. Univariate fixed-effects model

Let us assume that there is only one effect size y_i in the ith study. y_i can be any effect size, such as odds ratio, raw mean difference, standardized mean difference, correlation coefficient or its Fisher's z transformed score. When the sample sizes are reasonably large, y_i can be assumed to be normally distributed with a variance of v_i (see e.g., Borenstein *et al.* 2009, for the formulas of common effect sizes). The univariate fixed-effects model for the ith study is:

$$y_i = \beta_{\text{fixed}} + e_i, \tag{2}$$

where β_{fixed} is the common effect under a fixed-effects model and $\mathsf{VAR}(e_i) = v_i$ is the known sampling variance.

To conduct a univariate fixed-effects meta-analysis in SEM, we may fit the following model implied moments:

$$\mu_i(\theta) = \beta_{\text{fixed}} \tag{3}$$

and

$$\mathbf{\Sigma}_i(\theta) = v_i. \tag{4}$$

Since v_i is known in Equations~3 and~4, the only parameter in the model is β_{fixed} .

2.3. Univariate random-effects model

A random-effects model allows studies to have their own study specific effect. The model for the ith study is:

$$y_i = \beta_{\text{random}} + u_i + e_i, \tag{5}$$

where β_{random} is the average effect under a random-effects model and $\mathsf{VAR}(u_i) = \tau^2$ is the heterogeneity variance that has to be estimated. To fit the univariate random-effects meta-analysis in SEM, we may consider the following model implied moments:

$$\mu_i(\theta) = \beta_{\text{random}} \tag{6}$$

and

$$\mathbf{\Sigma}_i(\theta) = \tau^2 + v_i. \tag{7}$$

v_i and $\tau^2 + v_i$ are known as the conditional and the unconditional variances in the literature of meta-analysis, respectively. In Equations~6 and~7 we have to estimate both β_{random} and τ^2.

Quantifying heterogeneity   To test the homogeneity of the effect sizes, we may compute a Q statistic (Cochran 1954):

$$Q = \sum_{i=1}^{k} w_i (y_i - \hat{\beta}_{\text{fixed}})^2, \tag{8}$$

where $w_i = 1/v_i$. Under the null hypothesis of homogeneity of effect sizes, the Q statistic has an approximate chi-square distribution with $(k-1)$ degrees of freedom.

Although the Q statistic may be used to test the homogeneity of effect sizes, it does not indicate the degree of heterogeneity. The Q statistic may be significant simply due to the large number of studies. Conversely, a large Q statistic may be non-significant because of the small number of studies. One popular index to quantifying the degree of heterogeneity of effect sizes is the I^2 proposed by Higgins and Thompson (2002). The general formula is:

$$I^2 = \frac{\hat{\tau}^2}{\hat{\tau}^2 + \tilde{v}}, \tag{9}$$

where $\tilde{v}$ is a *typical* within-study sampling variance. I^2 can be interpreted as the proportion of the total variation of the effect size that is due to the between study heterogeneity.

As v_i likely varies across studies, there are several possible definitions of *typical* within-study sampling variance. Takkouche, Cadarso-SuÃąrez, and Spiegelman (1999) suggested to use the harmonic mean of v_i as the *typical* within-study sampling variance in Equation˜9, i.e.,

$$\tilde{v}_{\text{HM}} = \frac{k}{\sum_{i=1}^{k} 1/v_i}. \tag{10}$$

Higgins and Thompson (2002) preferred to define the *typical* within-study sampling variance in Equation˜9 using the Q statistic:

$$\tilde{v}_{\text{Q}} = \frac{(k-1) \sum_{i=1}^{k} 1/v_i}{(\sum_{i=1}^{k} 1/v_i)^2 - \sum_{i=1}^{k} 1/v_i^2}. \tag{11}$$

One advantage of using $\tilde{v}_{\text{Q}}$ as the *typical* within-study sampling variance is that the I^2 can be simplified to $I_{\text{Q}}^2 = Q - (k-1)/Q$.

Besides these two estimators, Xiong, Miller, and Morris (2010) also discussed an estimator on I^2 that is based on the arithmetic mean:

$$\tilde{v}_{\text{AM}} = \sum_{i=1}^{k} v_i/k. \tag{12}$$

2.4. Univariate mixed-effects model

The mixed-effects meta-analysis extends the random-effects meta-analysis by using study characteristics as predictors. Assuming that $\mathbf{x}_i$ is a $(m+1) \times 1$ vector of predictors including a constant of 1 where m is the number predictors in the ith study, the mixed-effects model is:

$$y_i = \mathbf{x}_i^{\top} \beta + u_i + e_i, \tag{13}$$

where β is a a $(m+1) \times 1$ vector of regression coefficients including the intercept. To fit the univariate mixed-effects meta-analysis in SEM, we may use the following model implied conditional mean and variance:

$$\mu_i(\theta|\mathbf{x}_i) = \mathbf{x}_i^\top \beta \tag{14}$$

and

$$\mathbf{\Sigma}_i(\theta|\mathbf{x}_i) = \tau^2 + v_i. \tag{15}$$

Since $\mathbf{x}_i$ is specified via definition variables (see e.g., Cheung 2010), $\mathbf{x_i}$ is treated as a design matrix rather than random variables. This approach is consistent with conventional meta-analysis. An alternative approach is to treat $\mathbf{x_i}$ as random variables with their own means and covariance matrix that have to be estimated (see Cheung 2008). This approach is more similar to conventional SEM.

Explained variance   Besides testing whether the predictors are significant, researchers may want to quantify the degree of prediction. The percentage of explained variance by the inclusion of predictors can be calculated by comparing the $\hat{\tau}_0^2$ without predictor and the $\hat{\tau}_1^2$ with predictors (Raudenbush 2009):

$$R^2 = \frac{\hat{\tau}_0^2 - \hat{\tau}_1^2}{\hat{\tau}_0^2}. \tag{16}$$

By definition, R^2 is non-negative in Equation~16. When the calculated R^2 is negative, it is truncated to zero.

2.5. Multivariate mixed-effects model

Let us assume that there are p effect sizes with m predictors in k studies. The model for the multivariate effect sizes in the ith study is:

$$\mathbf{y}_i = \mathbf{B}\mathbf{x}_i + \mathbf{u}_i + \mathbf{e}_i, \tag{17}$$

where $\mathbf{y}_i$ is a $p \times 1$ effect sizes, $\mathbf{B}$ is a $p \times (m+1)$ regression coefficients including the intercepts, $\mathbf{x}_i$ is a $(m+1) \times 1$ predictors including 1 in the first column, $\mathbf{u}_i$ is a $p \times 1$ study specific random effects, and $\mathbf{e}_i$ is a $p \times 1$ sampling error. We assume that $\mathsf{VAR}(\mathbf{e}_i) = \mathbf{V}_i$ is known and given in the ith study and $\mathsf{VAR}(\mathbf{u}_i) = \mathbf{T}^2$ is the variance component of the between-study heterogeneity that has to be estimated.

The -2*log-likelihood of the above model is:

$$-2*logL_i(\mathbf{B}, \mathbf{T}^2; \mathbf{y}_i)_{\mathrm{ML}} = p_i*log(2\pi) + log|\mathbf{T}^2 + \mathbf{V}_i| + (\mathbf{y}_i - \mathbf{B}\mathbf{x}_i)^\top (\mathbf{T}^2 + \mathbf{V}_i)^{-1}(\mathbf{y}_i - \mathbf{B}\mathbf{x}_i), \tag{18}$$

where p_i is the number of complete effect sizes in the ith study.

In applied research, different studies may report different numbers of effect sizes, that is, p_i may vary across studies. The above -2*log-likelihood may handle missing effect sizes by selecting the complete effect sizes only in the above equation. It is expected that there is no missing data in $\mathbf{x}_i$. When there are missing data in $\mathbf{x}_i$, the whole study will be deleted before the analysis.

To fit the multivariate mixed-effects meta-analysis in SEM, we may use the following model implied conditional mean vector and covariance matrix:

$$\mu_i(\theta|\mathbf{x}_i) = \mathbf{B}\mathbf{x}_i \tag{19}$$

and

$$\mathbf{\Sigma}_i(\theta|\mathbf{x}_i) = \mathbf{T}^2 + \mathbf{V}_i. \tag{20}$$

The I^2 and R^2 in univariate meta-analysis are also calculated for each effect size in multivariate meta-analysis.

2.6. Restricted maximum likelihood (REML) estimation method

Since both the fixed- and the random-effects are estimated simultaneously, it is well-known that $\hat{\mathbf{T}}^2_{\mathrm{ML}}$ based on the ML estimation in Equation~18 is negatively biased. When estimating $\hat{\mathbf{T}}^2_{\mathrm{ML}}$, it does not take the uncertainty in estimating $\hat{\mathbf{B}}_{\mathrm{ML}}$ into account. If the unbiasedness of the variance component is crucial to the research questions, we may obtain the variance component $\hat{\mathbf{T}}^2_{\mathrm{REML}}$ based on the REML estimation method (Cheung 2013a; Harville 1977; Patterson and Thompson 1971).

The -2*log-likelihood of the model is:

$$-2*logL_i(\mathbf{T}^2;\mathbf{y}_i)_{\mathrm{REML}} = p_i*log(2\pi)+log|\mathbf{T}^2+\mathbf{V}_i|+(\mathbf{y}_i-\alpha\mathbf{X}_i)^\top(\mathbf{T}^2+\mathbf{V}_i)^{-1}(\mathbf{y}_i-\alpha\mathbf{X}_i)+|\mathbf{X}_i^\top\mathbf{V}_i^{-1}\mathbf{X}_i|, \tag{21}$$

where $\alpha = (\mathbf{X}^\top\mathbf{V}^{-1}\mathbf{X})^{-1}\mathbf{X}^\top\mathbf{V}^{-1}\mathbf{y}$, and $\mathbf{X}$, $\mathbf{V}$ and $\mathbf{y}$ are the stacked matrices and vector of the correspondent matrices and vectors.

Since the fixed effects $\mathbf{B}_{REML}$ is not involved in the above -2*log-likelihood function, it has to be calculated later. We may estimate $\mathbf{B}_{REML}$ by treating $\hat{\mathbf{T}}^2_{\mathrm{REML}}$ as fixed in Equations~19 and~20.

2.7. Three-level meta-analysis

Observed effect sizes may be related or dependent. For example, effect sizes reported by the same research team may be more similar when compared to effect sizes reported by other research teams. Effect sizes reported by studies in the same country may be more similar when compared to studies across countries. If the degree of dependence is known, multivariate meta-analysis introduced before may be applied.

When the degree of dependence is unknown, a three-level meta-analytic model may be used (e.g., Cheung 2013b; Konstantopoulos 2011). The model is:

$$y_{ij} = \mathbf{x}_{ij}^\top\beta + u_{(2)ij} + u_{(3)j} + e_{ij}, \tag{22}$$

where y_{ij} is the effect size for the ith effect size in the jth cluster, β is a $(m+1) \times 1$ vector of regression coefficients including the intercept, $\mathbf{x}_{ij}$ is the $(m+1) \times 1$ predictors including 1 in the first element for the ith study at the jth cluster, $u_{(2)ij}$ and $u_{(3)j}$ are the random-effects at level-2 and level-3, respectively, and e_{ij} is the known sampling variance of the effect size.

To fit the three-level meta-analytic model in SEM, we may use the following model implied moments for the conditional mean and variance:

$$\mu_{ij}(\theta|\mathbf{x}_{ij}) = \mathbf{x}_{ij}^\top\beta \tag{23}$$

and

$$\mathbf{\Sigma}_{ij}(\theta|\mathbf{x}_{ij}) = \tau^2_{(2)} + \tau^2_{(3)} + v_{ij}, \tag{24}$$

where $\mathsf{VAR}(u_{(2)ij}) = \tau^2_{(2)}$ and $\mathsf{VAR}(u_{(3)j}) = \tau^2_{(3)}$ are the heterogeneity at level-2 and level-3, respectively. Similar to those listed in Equation~21, $\tau^2_{(2)}$ and $\tau^2_{(3)}$ may also be estimated with REML estimation method. This approach is implemented in `reml3()`.

Quantifying heterogeneity and explained variance Similar to the I^2 defined in Equation~9 for random-effects meta-analysis, we may define the degree of heterogeneity for three-level meta-analysis in level 2 and level 3 as:

$$I^2_{(2)} = \frac{\hat{\tau}^2_{(2)}}{\hat{\tau}^2_{(2)} + \hat{\tau}^2_{(3)} + \tilde{v}} \tag{25}$$

and

$$I^2_{(3)} = \frac{\hat{\tau}^2_{(3)}}{\hat{\tau}^2_{(2)} + \hat{\tau}^2_{(3)} + \tilde{v}}, \tag{26}$$

where $\tilde{v}$ is the *typical* within-study sampling variance defined in Equations~10,~11 and~12. $I^2_{(2)}$ and $I^2_{(3)}$ can be interpreted as the proportion of the total variation of the effect size that is due to the level-2 and level-3 study heterogeneity, respectively.

When there are predictors, we may calculate the R^2 for the level 2 and level 3 similar to that defined in Equation~16:

$$R^2_{(2)} = \frac{\hat{\tau}^2_{(2)0} - \hat{\tau}^2_{(2)1}}{\hat{\tau}^2_{(2)0}}, \tag{27}$$

and

$$R^2_{(3)} = \frac{\hat{\tau}^2_{(3)0} - \hat{\tau}^2_{(3)1}}{\hat{\tau}^2_{(3)0}}. \tag{28}$$

When the estimates are negative, they are truncated to zero.

2.8. Examples

Three example data sets are used to demonstrate the procedures of fitting univariate and multivariate meta-analyses. The first data set was taken from Becker (1983) who reported 10 studies on sex differences in conformity using the fictitious norm group paradigm. *di* and *vi* are the standardized mean difference and its sampling variance, respectively. Becker hypothesized that the logarithm of the number of items (*items*) predicted the effect size.

The second data set is adapted from Berkey, Hoaglin, Antczak-Bouckoms, Mosteller, and Colditz (1998). They summarized five published trials comparing surgical and non-surgical treatments for medium-severity periodontal disease, one year after treatment. Publication year *pub_year* was hypothesized as a predictor.

The third data set was reported by Konstantopoulos (2011) that was based on Cooper, Valentine, Charlton, and Melson (2003). It described fifty-six effect sizes clustered in 11 districts. *Year* of publication was used as a predictor.

Univariate random-effects model We may load the **metaSEM** library and show the first few cases of `Becker83` by the following syntax:

```
R> library("metaSEM")
R> head(Becker83)
```

```
  study    di   vi percentage items
1     1 -0.33 0.03         25     2
2     2  0.07 0.03         25     2
3     3 -0.30 0.02         50     2
4     4  0.35 0.02        100    38
5     5  0.69 0.07        100    30
6     6  0.81 0.22        100    45
```

The function `meta()` is used to conduct the analyses. The arguments `y` and `v` are used to specify the effect sizes and its sampling variances (and covariances for multivariate meta-analysis), respectively. By default, a random-effects meta-analysis is fitted. After running the analysis, `summary()` is used to extract the results. The estimated fixed- and random-effects are represented by the `Intercept1` to `Intercept`p and by the `Tau2_1_1` to `Tau2`$\_p\_p$ parameters where p is the number of effect sizes, especially. `coef()` and `vcov()` may be used to extract the parameter estimates and their asymptotic sampling covariance matrix, respectively.

Before interpreting the results, it is necessary to check whether the optimization is successful. The `OpenMx status1` returns the status from the optimizer. The optimization can be considered as fine if the code is either 0 or 1. Users may refer to OpenMx's Common Errors (and how to avoid them) for more details.

```
R> summary( random1 <- meta(y = di, v = vi, data = Becker83) )


Running Meta analysis with ML


Call:
meta(y = di, v = vi, data = Becker83)


95% confidence intervals: z statistic approximation
Coefficients:
           Estimate Std.Error    lbound     ubound z value Pr(>|z|)
Intercept1 0.174734  0.113378 -0.047482   0.396950  1.5412   0.1233
Tau2_1_1   0.077376  0.054108 -0.028674   0.183426  1.4300   0.1527


Q statistic on homogeneity of effect sizes: 30.64949
Degrees of freedom of the Q statistic: 9
P value of the Q statistic: 0.0003399239
Heterogeneity indices (based on the estimated Tau2):
                         Estimate
Intercept1: I2 (Q statistic)   0.6718
```

```
Number of studies (or clusters): 10
Number of observed statistics: 10
Number of estimated parameters: 2
Degrees of freedom: 8
-2 log likelihood: 7.928307
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

From the above analyses, the Q statistic ($df = 9$) is 30.65, $p < .001$. The estimated heterogeneity variance is 0.0774 while the I^2 based on the Q statistic is .6718. The average effect size with its 95% Wald confidence interval (CI) based on the random-effects model is 0.1747 (-0.0475, 0.3970).

Univariate mixed-effects model We may conduct a mixed-effects meta-analysis by including predictors. The argument x is used to specify the predictors. If there are more than one predictor, cbind() is used to specify them. The estimated regression coefficients are represented by the Slopei_j parameter where i and j represent the ith effect size and the jth predictor.

```
R> summary( meta(y = di, v = vi, x = log(items), data = Becker83) )


Running Meta analysis with ML

Call:
meta(y = di, v = vi, x = log(items), data = Becker83)

95% confidence intervals: z statistic approximation
Coefficients:
              Estimate    Std.Error       lbound       ubound z value
Intercept1 -3.2015e-01  1.0981e-01  -5.3539e-01  -1.0492e-01  -2.9154
Slope1_1    2.1088e-01  4.5084e-02   1.2251e-01   2.9924e-01   4.6774
Tau2_1_1    1.0000e-10  2.0095e-02  -3.9386e-02   3.9386e-02   0.0000
            Pr(>|z|)
Intercept1  0.003552 **
Slope1_1    2.905e-06 ***
Tau2_1_1    1.000000
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q statistic on homogeneity of effect sizes: 30.64949
Degrees of freedom of the Q statistic: 9
P value of the Q statistic: 0.0003399239
Explained variances (R2):
                           y1
Tau2 (no predictor)    0.0774
Tau2 (with predictors) 0.0000
R2                     1.0000
```

```
Number of studies (or clusters): 10
Number of observed statistics: 10
Number of estimated parameters: 3
Degrees of freedom: 7
-2 log likelihood: -4.208024
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

The above analysis indicates that $log(items)$ is a significant predictor with the estimated regression coefficient and its 95% CI of 0.2109 (0.1225, 0.2992) with $R^2 = 1$.

Univariate fixed-effects model   Mathematically, fixed-effects meta-analysis is a special case of the random-effects meta-analysis by fixing the heterogeneity variance of the random-effects at 0. The argument `RE.constraints`, which expects a matrix as input, is used to constrain the variance component of the random effects. The following analysis shows that the estimated common effect and its 95% Wald CI under a fixed-effects model is 0.1006 (-0.0180, 0.2192).

```
R> summary( meta(y = di, v = vi, data = Becker83,
+                RE.constraints = matrix(0, ncol = 1, nrow = 1)) )

Running Meta analysis with ML

Call:
meta(y = di, v = vi, data = Becker83, RE.constraints = matrix(0,
    ncol = 1, nrow = 1))

95% confidence intervals: z statistic approximation
Coefficients:
            Estimate Std.Error    lbound    ubound z value Pr(>|z|)
Intercept1  0.100640  0.060510 -0.017957  0.219237  1.6632  0.09627 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q statistic on homogeneity of effect sizes: 30.64949
Degrees of freedom of the Q statistic: 9
P value of the Q statistic: 0.0003399239
Heterogeneity indices (based on the estimated Tau2):
                            Estimate
Intercept1: I2 (Q statistic)       0

Number of studies (or clusters): 10
Number of observed statistics: 10
Number of estimated parameters: 1
Degrees of freedom: 9
-2 log likelihood: 17.86043
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

Multivariate random-effects model Multivariate meta-analysis can be fitted by specifying the multivariate effect sizes and its sampling covariance matrix in the arguments `y` and `v` with `cbind()`, respectively. Only the lower triangle of the sampling covariance matrix arranged by column major is used in `v`. For example, if $\mathbf{V} = \begin{bmatrix} V_{11} & & \\ V_{21} & V_{22} & \\ V_{31} & V_{32} & V_{33} \end{bmatrix}$, we may use `meta(v=cbind(V11,V21,V31,V22,V32,V33), ...)`. The following syntax first shows the content of `Berkey98` and then conducts a multivariate random-effects meta-analysis:

```
R> Berkey98
```

```
  trial pub_year no_of_patients   PD    AL var_PD cov_PD_AL var_AL
1     1     1983             14 0.47 -0.32 0.0075    0.0030 0.0077
2     2     1982             15 0.20 -0.60 0.0057    0.0009 0.0008
3     3     1979             78 0.40 -0.12 0.0021    0.0007 0.0014
4     4     1987             89 0.26 -0.31 0.0029    0.0009 0.0015
5     5     1988             16 0.56 -0.39 0.0148    0.0072 0.0304
```

```
R> summary( meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
+                data = Berkey98) )
```

```
Running Meta analysis with ML

Call:
meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
    data = Berkey98)

95% confidence intervals: z statistic approximation
Coefficients:
             Estimate  Std.Error     lbound     ubound z value
Intercept1  0.3448390  0.0536312  0.2397238  0.4499542  6.4298
Intercept2 -0.3379383  0.0812479 -0.4971813 -0.1786953 -4.1593
Tau2_1_1    0.0070020  0.0090497 -0.0107351  0.0247391  0.7737
Tau2_2_1    0.0094607  0.0099698 -0.0100797  0.0290010  0.9489
Tau2_2_2    0.0261445  0.0177409 -0.0086270  0.0609161  1.4737
             Pr(>|z|)
Intercept1 1.278e-10 ***
Intercept2 3.192e-05 ***
Tau2_1_1      0.4391
Tau2_2_1      0.3427
Tau2_2_2      0.1406
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q statistic on homogeneity of effect sizes: 128.2267
Degrees of freedom of the Q statistic: 8
P value of the Q statistic: 0
```

```
Heterogeneity indices (based on the estimated Tau2):
                                Estimate
Intercept1: I2 (Q statistic)    0.6021
Intercept2: I2 (Q statistic)    0.9250

Number of studies (or clusters): 5
Number of observed statistics: 10
Number of estimated parameters: 5
Degrees of freedom: 5
-2 log likelihood: -11.68131
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

The Q statistic ($df = 8$) of the above example is 128.2267, $p < .001$. The estimated variance component is $\begin{bmatrix} 0.0070 & \\ 0.0095 & 0.02614 \end{bmatrix}$. The I^2 based on the Q statistic for PD and AL are .6021 and .9250, respectively. The pooled effect sizes with their 95% Wald CIs based on the random-effects model for PD and AL are 0.3448 (0.2397, 0.4500) and -0.3379 (-0.4972, -0.1787), respectively.

Multivariate mixed-effects model   As an illustration, we use *pub_year* as a predictor. To make the intercept more interpretable, we center the publication year at 1979, the first record for publication year in the data set.

```
R> mult2 <- meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
+               data = Berkey98, x = scale(pub_year, center = 1979),
+               model.name = "No constraint")

Running No constraint

R> summary(mult2)

Call:
meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
    x = scale(pub_year, center = 1979), data = Berkey98, model.name = "No constraint")

95% confidence intervals: z statistic approximation
Coefficients:
             Estimate  Std.Error      lbound      ubound z value
Intercept1  0.3440001  0.0857659   0.1759021   0.5120982  4.0109
Intercept2 -0.2918175  0.1312796  -0.5491208  -0.0345141 -2.2229
Slope1_1    0.0063540  0.1078235  -0.2049761   0.2176842  0.0589
Slope2_1   -0.0705888  0.1620965  -0.3882921   0.2471146 -0.4355
Tau2_1_1    0.0080405  0.0101206  -0.0117955   0.0278766  0.7945
Tau2_2_1    0.0093413  0.0105515  -0.0113392   0.0300218  0.8853
Tau2_2_2    0.0250135  0.0170788  -0.0084603   0.0584873  1.4646
            Pr(>|z|)
```

```
Intercept1 6.048e-05 ***
Intercept2   0.02622 *
Slope1_1     0.95301
Slope2_1     0.66322
Tau2_1_1     0.42692
Tau2_2_1     0.37599
Tau2_2_2     0.14303
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q statistic on homogeneity of effect sizes: 128.2267
Degrees of freedom of the Q statistic: 8
P value of the Q statistic: 0
Explained variances (R2):
                               y1        y2
Tau2 (no predictor)     0.0070020 0.0261
Tau2 (with predictors) 0.0080405 0.0250
R2                      0.0000000 0.0433


Number of studies (or clusters): 5
Number of observed statistics: 10
Number of estimated parameters: 7
Degrees of freedom: 3
-2 log likelihood: -12.00859
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

The estimated regression coefficients and their 95% CIs on PD and AL are 0.0064 (-0.2050, 0.2177) and -0.0706 (-0.3883, 0.2471), respectively. The R^2 in predicting PD and AL are .0000 and .0433, respectively.

When there are multiple parameters, it is preferable to test the significance of all parameters simultaneously. We may formulate two nested models and compare them with the `anova()` function. The following analysis indicates that the likelihood ratio statistic on comparing both regression coefficient is $\chi^2(df = 2) = 0.3273, p = .8490$. Thus, the null hypothesis of both regression coefficients are zero is not rejected.

```
R> mult0 <- meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
+                data = Berkey98, x = scale(pub_year, center = 1979),
+                model.name = "Both regression coefficients fixed at 0",
+                coef.constraints = matrix(c("0", "0"), nrow = 2))

Running Both regression coefficients fixed at 0

R> summary(mult0)

Call:
meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
```

```
    x = scale(pub_year, center = 1979), data = Berkey98, coef.constraints = matrix(c("0",
        "0"), nrow = 2), model.name = "Both regression coefficients fixed at 0")
```

```
95% confidence intervals: z statistic approximation
Coefficients:
             Estimate  Std.Error     lbound      ubound z value
Intercept1  0.3448390  0.0536312  0.2397238   0.4499542  6.4298
Intercept2 -0.3379383  0.0812479 -0.4971813  -0.1786953 -4.1593
Tau2_1_1    0.0070020  0.0090497 -0.0107351   0.0247391  0.7737
Tau2_2_1    0.0094607  0.0099698 -0.0100797   0.0290010  0.9489
Tau2_2_2    0.0261445  0.0177409 -0.0086270   0.0609161  1.4737
            Pr(>|z|)
Intercept1 1.278e-10 ***
Intercept2 3.192e-05 ***
Tau2_1_1      0.4391
Tau2_2_1      0.3427
Tau2_2_2      0.1406
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q statistic on homogeneity of effect sizes: 128.2267
Degrees of freedom of the Q statistic: 8
P value of the Q statistic: 0
Explained variances (R2):
                           y1       y2
Tau2 (no predictor)    0.007002 0.0261
Tau2 (with predictors) 0.007002 0.0261
R2                     0.000000 0.0000

Number of studies (or clusters): 5
Number of observed statistics: 10
Number of estimated parameters: 5
Degrees of freedom: 5
-2 log likelihood: -11.68131
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

R> anova(mult2, mult0)

```
          base                                   comparison ep  minus2LL
1 No constraint                                        <NA>  7 -12.00859
2 No constraint Both regression coefficients fixed at 0     5 -11.68131
  df      AIC    diffLL diffdf         p
1  3 -18.00859       NA     NA        NA
2  5 -21.68131 0.3272789      2 0.8490481
```

Sometimes, we may want to test the equality of regression coefficients and see if they are different. We may impose the equality constraint on the regression coefficients by using the

same label in the argument `coef.constraints`. The following analysis indicates that the average regression coefficient is 0.0017 (-0.1991, 0.2025). The likelihood ratio statistic on testing the equality of the regression coefficients is $\chi^2(df = 1) = 0.3270, p = .5674$. There is no evidence that one regression coefficient is stronger than the other.

```
R> mult3 <- meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
+               data = Berkey98, x = scale(pub_year, center = 1979),
+               model.name = "With equality constraint",
+               coef.constraints = matrix(c("0.3*Equal_Slope",
+                                           "0.3*Equal_Slope"), nrow = 2))

Running With equality constraint

R> summary(mult3)

Call:
meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
    x = scale(pub_year, center = 1979), data = Berkey98, coef.constraints = matrix(c("0.3*
        "0.3*Equal_Slope"), nrow = 2), model.name = "With equality constraint")

95% confidence intervals: z statistic approximation
Coefficients:
              Estimate  Std.Error      lbound     ubound z value
Equal_Slope  0.0016748  0.1024443 -0.1991123  0.2024619  0.0163
Intercept1   0.3437612  0.0849828  0.1771979  0.5103245  4.0451
Intercept2  -0.3390010  0.1041005 -0.5430344 -0.1349677 -3.2565
Tau2_1_1     0.0070474  0.0094638 -0.0115013  0.0255962  0.7447
Tau2_2_1     0.0095165  0.0105668 -0.0111940  0.0302269  0.9006
Tau2_2_2     0.0261979  0.0180773 -0.0092330  0.0616288  1.4492
             Pr(>|z|)
Equal_Slope  0.986956
Intercept1   5.231e-05 ***
Intercept2   0.001128 **
Tau2_1_1     0.456471
Tau2_2_1     0.367800
Tau2_2_2     0.147278
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q statistic on homogeneity of effect sizes: 128.2267
Degrees of freedom of the Q statistic: 8
P value of the Q statistic: 0
Explained variances (R2):
                             y1        y2
Tau2 (no predictor)     0.0070020 0.0261
Tau2 (with predictors)  0.0070474 0.0262
R2                      0.0000000 0.0000
```

```
Number of studies (or clusters): 5
Number of observed statistics: 10
Number of estimated parameters: 6
Degrees of freedom: 4
-2 log likelihood: -11.68158
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

```
R> anova(mult2, mult3)
```

```
             base                  comparison ep  minus2LL df        AIC
1 No constraint                          <NA>  7 -12.00859  3 -18.00859
2 No constraint With equality constraint  6 -11.68158  4 -19.68158
      diffLL diffdf          p
1         NA     NA         NA
2 0.3270107      1 0.5674246
```

Multivariate fixed-effects model   A multivariate fixed-effects meta-analysis can be conducted by fixing the variance component at a zero matrix. The following code illustrates the syntax. The pooled effect sizes with their 95% Wald CIs based on the fixed-effects model for PD and AL are 0.3072 (0.2512, 0.3632) and -0.3944 (-0.4310, -0.3578), respectively. It should be noted that the CIs on fixed-effects model are usually shorter than those on random-effects model when the heterogeneity is ignored in the analysis.

```
R> summary( meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
+               data = Berkey98,
+               RE.constraints = matrix(0, nrow = 2, ncol = 2)) )
```

```
Running Meta analysis with ML
```

```
Call:
meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
    data = Berkey98, RE.constraints = matrix(0, nrow = 2, ncol = 2))
```

```
95% confidence intervals: z statistic approximation
Coefficients:
            Estimate Std.Error    lbound    ubound z value  Pr(>|z|)
Intercept1  0.307219  0.028575  0.251212  0.363225  10.751 < 2.2e-16
Intercept2 -0.394377  0.018649 -0.430929 -0.357825 -21.147 < 2.2e-16
```

```
Intercept1 ***
Intercept2 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Q statistic on homogeneity of effect sizes: 128.2267
```

```
Degrees of freedom of the Q statistic: 8
P value of the Q statistic: 0
Heterogeneity indices (based on the estimated Tau2):
                                 Estimate
Intercept1: I2 (Q statistic)         0
Intercept2: I2 (Q statistic)         0

Number of studies (or clusters): 5
Number of observed statistics: 10
Number of estimated parameters: 2
Degrees of freedom: 8
-2 log likelihood: 90.88326
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

REML The `reml()` function may be used to estimate the variance component with the REML estimation method. The following analysis shows that the estimated heterogeneity using the REML method on the `Becker93` is 0.0914 while the estimated heterogeneity using the ML method in the previous analysis is 0.0774. Generally, variance component based on REML is larger than that based on ML.

```
R> summary( VarComp <- reml(y = di, v = vi, data = Becker83) )

Running Variance component with REML

Call:
reml(y = di, v = vi, data = Becker83)

95% confidence intervals: z statistic approximation
Coefficients:
          Estimate Std.Error    lbound    ubound z value Pr(>|z|)
Tau2_1_1  0.091445  0.064228 -0.034439  0.217329  1.4238   0.1545

Number of studies (or clusters): 10
Number of observed statistics: 9
Number of estimated parameters: 1
Degrees of freedom: 8
-2 log likelihood: -6.110579
OpenMx status: 0 ("0" and "1": considered fine; other values indicate problems)
```

It should be noted that it does not estimate the fixed-effects. The fixed-effects estimates can be obtained via the `meta()` function by specifying the estimated variance component from `reml()` as fixed values in the `RE.constraints` argument. This approach is consistent with the idea of REML that removes the fixed-effects parameter when estimating the variance component.

```
R> VarComp_REML <- matrix( coef(VarComp), ncol = 1, nrow = 1 )
R> summary( meta(y = di, v = vi, data = Becker83,
+               RE.constraints = VarComp_REML) )
```

```
Running Meta analysis with ML

Call:
meta(y = di, v = vi, data = Becker83, RE.constraints = VarComp_REML)

95% confidence intervals: z statistic approximation
Coefficients:
            Estimate Std.Error    lbound     ubound z value Pr(>|z|)
Intercept1  0.180189  0.117535 -0.050176  0.410555  1.5331   0.1253

Q statistic on homogeneity of effect sizes: 30.64949
Degrees of freedom of the Q statistic: 9
P value of the Q statistic: 0.0003399239
Heterogeneity indices (based on the estimated Tau2):
                                Estimate
Intercept1: I2 (Q statistic)    0.7075

Number of studies (or clusters): 10
Number of observed statistics: 10
Number of estimated parameters: 1
Degrees of freedom: 9
-2 log likelihood: 7.986161
OpenMx status1: 1 ("0" and "1": considered fine; other values indicate problems)
```

Plots of multivariate effect sizes   If multivariate meta-analysis is conducted, pairwise plots on the pooled effect sizes and their confidence ellipses can be obtained via the `plot()` function. By default, 95% confidence intervals on the average effect sizes and confidence ellipses on the random effects are plotted (see Cheung 2011). For example, Figure~1 plots the effect sizes in the `Berkey98` example. It is plotted with the following syntax:

```
R> Berkey98.fit <- meta(y = cbind(PD, AL), v = cbind(var_PD, cov_PD_AL, var_AL),
+                        data = Berkey98)
R> plot(Berkey98.fit, main = "", axis.label = c("PD", "AL"))
```

By combining with the forest plots provided by the **metafor** package, we may combine the univariate and multivariate natures of the effect sizes in a single figure. This will be very useful in displaying results of multivariate meta-analysis. Figure~2 shows the plot of multivariate effect sizes with two forest plots in the same figure. It is plotted with the following syntax:

```
R> library("metafor")
R> plot(Berkey98.fit, diag.panel = TRUE, main = "",
+       axis.label = c("PD", "AL"))
R> forest( rma(yi = PD, vi = var_PD, data = Berkey98) )
R> title("Forest plot for PD")
R> forest( rma(yi = AL, vi = var_AL, data = Berkey98) )
R> title("Forest plot for AL")
```
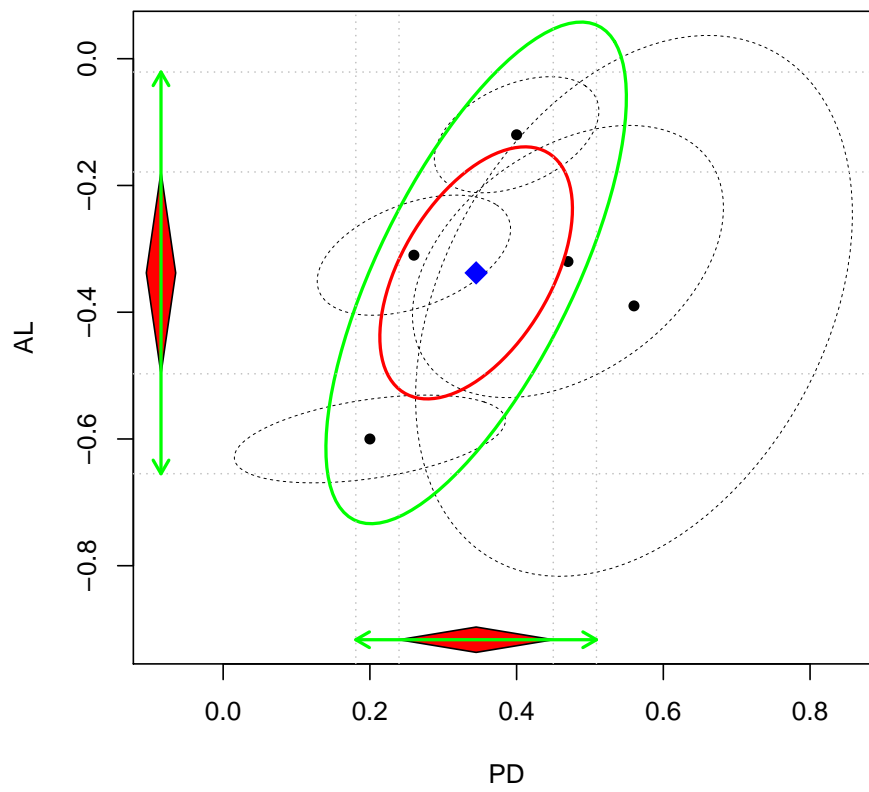
Figure 1: Multivariate meta-analysis with two effect sizes.

Forest plot for PD

Study 1	0.47 [0.30 , 0.64]
Study 2	0.20 [0.05 , 0.35]
Study 3	0.40 [0.31 , 0.49]
Study 4	0.26 [0.15 , 0.37]
Study 5	0.56 [0.32 , 0.80]
RE Model	0.36 [0.24 , 0.48]

0.00   0.40   0.80

Forest plot for AL

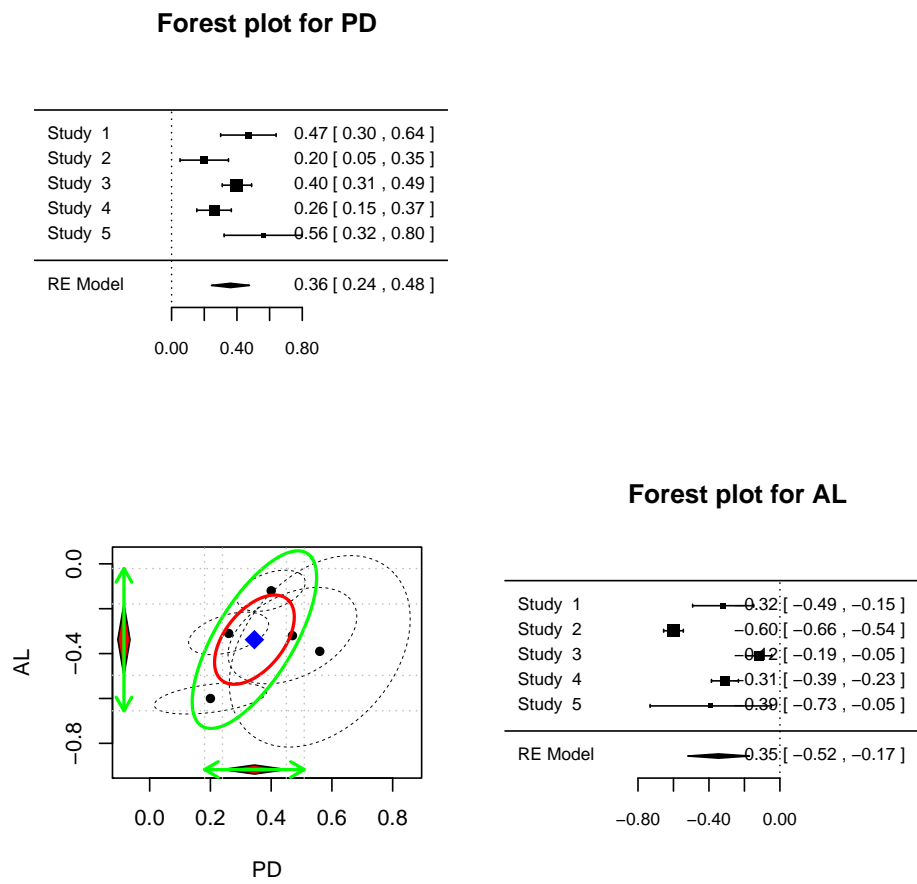| Study 1 | −0.32 [−0.49 , −0.15] |
Study 2	−0.60 [−0.66 , −0.54]
Study 3	−0.12 [−0.19 , −0.05]
Study 4	−0.31 [−0.39 , −0.23]
Study 5	−0.39 [−0.73 , −0.05]
RE Model	−0.35 [−0.52 , −0.17]

−0.80   −0.40   0.00

Figure 2: Multivariate meta-analysis with two effect sizes and forest plots.

Three-level meta-analysis The `meta3()` function may be used to fit three-level meta-analytic models. It is assumed that effect sizes within `cluster` are dependent. The following analysis shows that the $Q(df = 55) = 578.86, p < .001$. The I^2 based on the Q statistic at level-2 and level-3 are .3440 and .6043, respectively. The average effect and its 95% CI under a random-effects model is 0.1845 (0.0266, 0.3423).

```
R> summary( meta3(y = y, v = v, cluster = District, data = Cooper03) )


Running Meta analysis with ML

Call:
meta3(y = y, v = v, cluster = District, data = Cooper03)

95% confidence intervals: z statistic approximation
Coefficients:
             Estimate  Std.Error      lbound     ubound z value
Intercept  0.1844554  0.0805411   0.0265977  0.3423130  2.2902
Tau2_2     0.0328648  0.0111397   0.0110314  0.0546982  2.9502
Tau2_3     0.0577384  0.0307423  -0.0025154  0.1179921  1.8781
           Pr(>|z|)
Intercept 0.022010 *
Tau2_2    0.003175 **
Tau2_3    0.060362 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q statistic on homogeneity of effect sizes: 578.864
Degrees of freedom of the Q statistic: 55
P value of the Q statistic: 0
Heterogeneity indices (based on the estimated Tau2):
                            Estimate
I2_2 (Typical v: Q statistic)   0.3440
I2_3 (Typical v: Q statistic)   0.6043

Number of studies (or clusters): 11
Number of observed statistics: 56
Number of estimated parameters: 3
Degrees of freedom: 53
-2 log likelihood: 16.78987
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

We may use $Year$ of publication as a predictor. To make the intercept more meaningful, we may center the predictor. The estimated coefficient of $Year$ of publication in the following analysis is 0.0051, $p = .5518$. The R^2 at level-2 and level-3 are .0000 and .0221, respectively.

```
R> summary( meta3(y = y, v = v, cluster = District,
+                 x = scale(Year, scale = FALSE), data = Cooper03) )
```

```
Running Meta analysis with ML

Call:
meta3(y = y, v = v, cluster = District, x = scale(Year, scale = FALSE),
    data = Cooper03)

95% confidence intervals: z statistic approximation
Coefficients:
            Estimate  Std.Error      lbound      ubound z value
Intercept  0.1780268  0.0805219   0.0202067   0.3358469  2.2109
Slope_1    0.0050737  0.0085266  -0.0116382   0.0217856  0.5950
Tau2_2     0.0329390  0.0111620   0.0110618   0.0548162  2.9510
Tau2_3     0.0564628  0.0300330  -0.0024007   0.1153264  1.8800
           Pr(>|z|)
Intercept 0.027042 *
Slope_1   0.551814
Tau2_2    0.003168 **
Tau2_3    0.060104 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q statistic on homogeneity of effect sizes: 578.864
Degrees of freedom of the Q statistic: 55
P value of the Q statistic: 0
Explained variances (R2):
                       Level 2 Level 3
Tau2 (no predictor)   0.032865  0.0577
Tau2 (with predictors) 0.032939  0.0565
R2                    0.000000  0.0221

Number of studies (or clusters): 11
Number of observed statistics: 56
Number of estimated parameters: 4
Degrees of freedom: 52
-2 log likelihood: 16.43629
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

3. Meta-analytic structural equation modeling

MASEM combines ideas of meta-analysis and SEM by pooling correlation (or covariance) matrices and testing structural equation models on the pooled correlation (or covariance) matrix. There are two stages of analyses. In the first stage analysis, the correlation (or covariance) matrices are pooled together. In the second stage analysis, the pooled correlation (or covariance) matrix is used to fit structural equation models.

Cheung and Chan (2005b, 2009) proposed a TSSEM based on a fixed-effects model. The **metaSEM** package implemented this TSSEM approach. Moreover, the TSSEM approach has been extended to the random-effects model by using a multivariate meta-analysis (Cheung 2011) in the first stage analysis. Regardless of whether a fixed- or random-effects model is used, the `tssem2()` function will handle this automatically. In other words, parameter estimates, *SE*s and goodness-of-fit indices in the stage 2 analysis have already taken the stage 1 model into account.

3.1. Stage 1 analysis

The objective of the stage 1 analysis is to obtain a pooled correlation (or covariance) matrix. Under the fixed-effects model, it is assumed that all population correlation (or covariance) matrices are the same while there are study specific correlation (or covariance matrices) under the random-effects model. To simplify the presentation, I will mainly focus on the analysis of correlation matrices. Generalization to analysis of covariance matrices is straight forward (see Cheung and Chan 2009)

Fixed-effects model   The population correlation matrix in the ith study can be decomposed as:

$$\Sigma_i(\theta) = \mathbf{D}_i \mathbf{P}_i \mathbf{D}_i \tag{29}$$

where $\Sigma_i(\theta)$ is the model implied covariance matrix, $\mathbf{D}_i$ is the diagonal matrix of standard deviations, and $\mathbf{P}_i$ is the correlation matrix. Under the assumption of homogeneity of correlation matrices, we may obtain a common correlation matrix by imposing the constraint $P = P_1 = P_2 = \ldots = P_k$ where D_i may vary across studies. When there are missing correlations, the missing data are filtered out. If we want to obtain a common covariance matrix under the assumption of homogeneity of covariance matrices, we may also add the constraint $D = D_1 = D_2 = \ldots = D_k$.

Random-effects model   When a random-effects model is used, the correlation matrices are treated as vectors of multivariate effect sizes. Let $\mathbf{r}_i = vechs(\mathbf{R}_i)$ be the $p * (p-1)/2 \times 1$ vector of sample correlation for p variables by taking the column-wise non-redundant elements from $\mathbf{R}_i$. If the input is a covariance matrix $\mathbf{S}_i$, the $p * (p+1)/2 \times 1$ vectorized multivariate effect sizes become $\mathbf{s}_i = vech(\mathbf{S}_i)$. The model for the sample correlation vector $\mathbf{r}_i$ is:

$$\mathbf{r}_i = \rho_{\mathrm{random}} + \mathbf{u}_i + \mathbf{e}_i, \tag{30}$$

where ρ_{random} is the average correlation vector under a random-effects model, $\mathsf{VAR}(\mathbf{u}_i) = \mathbf{T}^2$ is the variance components of the random effects, and $\mathsf{VAR}(\mathbf{e}_i) = V_i$ is the conditional sampling covariance matrix. Multivariate meta-analysis listed in Equations~17 and~18 are used to conduct the stage 1 analysis with random-effects model.

3.2. Stage 2 analysis

After the stage 1 analysis with either a fixed- or a random-effects model, a vector of pooled correlations $\bar{\mathbf{r}}$ and its asymptotic covariance matrix $\mathbf{V}$ are estimated. A correlation structural model $\rho(\hat{\gamma})$ is fitted with WLS estimation method by minimizing the following fit function

(Cheung and Chan 2005b, 2009):

$$F(\hat{\gamma}) = (\bar{\mathbf{r}} - \rho(\hat{\gamma}))^{\top} \mathbf{V}^{-1} (\bar{\mathbf{r}} - \rho(\hat{\gamma})). \tag{31}$$

Likelihood-ratio statistics and various goodness-of-fit indices may be used to judge whether the proposed structural model is appropriate while *SE*s may be used to test the significance of individual parameter estimates.

3.3. Examples

An example from Cheung (2009b) is used to illustrate the procedures. In this example, Digman (1997) reported a second-order factor analysis on a five-factor model with 14 studies. He proposed that there were two second-order factors on the five-factor model: **alpha** factor for *agreeableness*, *conscientiousness*, and *emotional stability*, and **beta** factor for *extroversion* and *intellect*.

Fixed-effects model The correlation matrices and the sample sizes are stored in `Digman97$data` and `Digman97$n`, respectively.

```
R> head(Digman97$data, n = 2)


$`Digman 1 (1994)`
       A     C   ES     E    I
A   1.00  0.62 0.41 -0.48 0.00
C   0.62  1.00 0.59 -0.10 0.35
ES  0.41  0.59 1.00  0.27 0.41
E  -0.48 -0.10 0.27  1.00 0.37
I   0.00  0.35 0.41  0.37 1.00


$`Digman 2 (1994)`
       A    C   ES     E     I
A   1.00 0.39 0.53 -0.30 -0.05
C   0.39 1.00 0.59  0.07  0.44
ES  0.53 0.59 1.00  0.09  0.22
E  -0.30 0.07 0.09  1.00  0.45
I  -0.05 0.44 0.22  0.45  1.00


R> head(Digman97$n, n = 2)


[1] 102 149
```

The `tssem1()` function is used to pool the correlation matrices with a fixed-effects model in the first stage analysis by specifying `method="FEM"` in the argument:

```
R> fixed1 <- tssem1(Digman97$data, Digman97$n, method = "FEM")


Running TSSEM1 Analysis of Correlation Matrix
```

```
R> summary(fixed1)


Call:
tssem1FEM(my.df = my.df, n = n, cor.analysis = cor.analysis,
    model.name = model.name, cluster = cluster, suppressWarnings = suppressWarnings)


Coefficients:
        Estimate Std.Error z value  Pr(>|z|)
S[1,2] 0.363116  0.013391 27.1171 < 2.2e-16 ***
S[1,3] 0.390176  0.012903 30.2388 < 2.2e-16 ***
S[1,4] 0.103751  0.015070  6.8846 5.796e-12 ***
S[1,5] 0.092246  0.015071  6.1207 9.318e-10 ***
S[2,3] 0.415999  0.012540 33.1741 < 2.2e-16 ***
S[2,4] 0.135208  0.014799  9.1363 < 2.2e-16 ***
S[2,5] 0.141213  0.014891  9.4834 < 2.2e-16 ***
S[3,4] 0.244505  0.014175 17.2488 < 2.2e-16 ***
S[3,5] 0.138167  0.014858  9.2992 < 2.2e-16 ***
S[4,5] 0.424514  0.012396 34.2468 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


Goodness-of-fit indices:
                                       Value
Sample size                       4496.0000
Chi-square of target model        1499.7340
DF of target model                 130.0000
p value of target model              0.0000
Chi-square of independence model 4454.5995
DF of independence model           140.0000
RMSEA                                0.1812
SRMR                                 0.1750
TLI                                  0.6581
CFI                                  0.6825
AIC                               1239.7340
BIC                                406.3114
OpenMx status: 0 ("0" and "1": considered fine; other values indicate problems)
```

The fit indices on testing the homogeneity of the correlation matrices in the Stage 1 analysis are $\chi^2(df = 130, N = 4,496) = 1,499.73, p < .001$, CFI=0.6825, TLI=0.6581, SRMR=0.1750 and RMSEA=0.1812. These indicate that it is not reasonable to assume that the correlation matrices are homogeneous. Sub-group analysis or random-effects model that will be illustrated later are more appropriate. As an exercise, we continue to fit the stage 2 model even though the homogeneity assumption of the correlation matrices is questionable.

The `tssem2()` function is then used to fit a factor analytic model on the pooled correlation matrix with the inverse of its asymptotic covariance matrix as the weight matrix. When a correlation structure is fitted, it is necessary to ensure that the diagonals of the model implied

matrix are all fixed at ones. The error variances are usually treated as computed values so that the diagonals of the implied correlation matrix are always ones.

The structural model in the stage 2 analysis is specified via the reticular action model (RAM) formulation (McArdle and McDonald 1984). Structural models are specified via three matrices. **A** and **S** are used to specify the asymmetric paths and the symmetric variance covariance matrices, respectively. **F** is a selection matrix used to filter observed variables.

The following syntax specifies the **A** matrix:

```
R> Lambda <-  matrix(c(".3*Alpha_A", ".3*Alpha_C", ".3*Alpha_ES",
+                     rep(0,5),".3*Beta_E", ".3*Beta_I"), ncol = 2, nrow = 5)
R> A1 <- rbind( cbind(matrix(0, ncol = 5, nrow = 5), Lambda),
+              matrix(0, ncol = 7, nrow = 2) )
R> dimnames(A1) <- list(c("A", "C", "ES", "E", "I", "Alpha", "Beta"),
+                       c("A", "C", "ES", "E", "I", "Alpha", "Beta"))
R> A1
```

```
      A   C   ES  E   I   Alpha          Beta
A     "0" "0" "0" "0" "0" ".3*Alpha_A"   "0"
C     "0" "0" "0" "0" "0" ".3*Alpha_C"   "0"
ES    "0" "0" "0" "0" "0" ".3*Alpha_ES"  "0"
E     "0" "0" "0" "0" "0" "0"            ".3*Beta_E"
I     "0" "0" "0" "0" "0" "0"            ".3*Beta_I"
Alpha "0" "0" "0" "0" "0" "0"            "0"
Beta  "0" "0" "0" "0" "0" "0"            "0"
```

```
R> A1 <- as.mxMatrix(A1)
```

The following syntax specifies the **S** matrix:

```
R> Phi <- matrix(c(1, "0.3*cor", "0.3*cor",1), ncol=2, nrow=2)
R> S1 <- bdiagMat(list(Diag(c(".2*e1", ".2*e2", ".2*e3", ".2*e4", ".2*e5")), Phi))
R> dimnames(S1) <- list(c("A", "C", "ES", "E", "I", "Alpha", "Beta"),
+                       c("A", "C", "ES", "E", "I", "Alpha", "Beta"))
R> S1
```

```
      A       C       ES      E       I       Alpha     Beta
A     ".2*e1" "0"     "0"     "0"     "0"     "0"       "0"
C     "0"     ".2*e2" "0"     "0"     "0"     "0"       "0"
ES    "0"     "0"     ".2*e3" "0"     "0"     "0"       "0"
E     "0"     "0"     "0"     ".2*e4" "0"     "0"       "0"
I     "0"     "0"     "0"     "0"     ".2*e5" "0"       "0"
Alpha "0"     "0"     "0"     "0"     "0"     "1"       "0.3*cor"
Beta  "0"     "0"     "0"     "0"     "0"     "0.3*cor" "1"
```

```
R> S1 <- as.mxMatrix(S1)
```

The following syntax specifies the **F** matrix:

```
R> F1 <- create.Fmatrix(c(1, 1, 1, 1, 1, 0, 0), name = "F1")
```

We may then fit the structural model via `tssem2`:

```
R> fixed2 <- tssem2(fixed1, Amatrix = A1, Smatrix = S1, Fmatrix = F1,
+                   model.name = "TSSEM2 Digman97")

Running TSSEM2 Digman97

R> summary(fixed2)

Call:
wls(Cov = tssem1.obj$pooledS, asyCov = tssem1.obj$acovS, n = tssem1.obj$total.n,
    Amatrix = Amatrix, Smatrix = Smatrix, Fmatrix = Fmatrix,
    diag.constraints = diag.constraints, cor.analysis = cor.analysis,
    intervals.type = intervals.type, mx.algebras = mx.algebras,
    model.name = model.name, suppressWarnings = suppressWarnings)

95% confidence intervals: z statistic approximation
Coefficients:
             Estimate Std.Error   lbound   ubound z value  Pr(>|z|)
Amatrix[1,6] 0.562577  0.015409 0.532376 0.592777  36.510 < 2.2e-16
Amatrix[2,6] 0.605125  0.015353 0.575034 0.635216  39.415 < 2.2e-16
Amatrix[3,6] 0.719129  0.015716 0.688326 0.749931  45.758 < 2.2e-16
Amatrix[4,7] 0.782002  0.034345 0.714687 0.849316  22.769 < 2.2e-16
Amatrix[5,7] 0.550886  0.026073 0.499785 0.601988  21.129 < 2.2e-16
Smatrix[7,6] 0.362613  0.022427 0.318656 0.406569  16.169 < 2.2e-16

Amatrix[1,6] ***
Amatrix[2,6] ***
Amatrix[3,6] ***
Amatrix[4,7] ***
Amatrix[5,7] ***
Smatrix[7,6] ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Goodness-of-fit indices:
                                          Value
Sample size                            4496.0000
Chi-square of target model               65.0610
DF of target model                        4.0000
p value of target model                   0.0000
Number of constraints imposed on "Smatrix"  0.0000
DF manually adjusted                      0.0000
Chi-square of independence model       3100.6516
DF of independence model                 10.0000
```

```
RMSEA                                         0.0583
SRMR                                          0.0284
TLI                                           0.9506
CFI                                           0.9802
AIC                                          57.0610
BIC                                          31.4172
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

The fit indices on the Stage 2 structural model are $\chi^2(df = 4, N = 4496) = 65.06, p < .001$, CFI=0.9802, TLI=0.9506, SRMR=0.0284 and RMSEA=0.0583. Although the goodness-of-fit indices look good, we should be cautious in interpreting them because of the poor goodness-of-fit indices in Stage 1 analysis.

Fixed-effects model with sub-group analysis Studies may not share the same population correlation matrix. If the studies can be grouped into various subgroups, we may pool the correlation matrices separately for each subgroup (Cheung and Chan 2005a). This is similar to the sub-group analysis in conventional meta-analysis (Hedges and Olkin 1985). For example, Digman (1997) grouped the 14 studies according to their sample characteristics. These include children, adolescents, young adults, and mature adults. This information is stored in the variable `Digman97$cluster`.

First, we classify these studies into younger participants versus older participants.

```
R> ( sample <- ifelse(Digman97$cluster %in% c("Children","Adolescents"),
+                      yes = "Younger participants", no = "Older participants") )

 [1] "Younger participants" "Younger participants"
 [3] "Younger participants" "Younger participants"
 [5] "Younger participants" "Older participants"
 [7] "Older participants"   "Older participants"
 [9] "Older participants"   "Older participants"
[11] "Older participants"   "Older participants"
[13] "Older participants"   "Older participants"
```

We may run the Stage 1 by specifying the `cluster=sample` argument. The goodness-of-fit indices for these two clusters are not very good.

```
R> fixed1.cluster <- tssem1(Digman97$data, Digman97$n, method = "FEM",
+                           cluster = sample)

Running TSSEM1 Analysis of Correlation Matrix
Running TSSEM1 Analysis of Correlation Matrix

R> summary(fixed1.cluster)

$`Older participants`
```

```
Call:
tssem1FEM(my.df = data.cluster[[i]], n = n.cluster[[i]], cor.analysis = cor.analysis,
    model.name = model.name, suppressWarnings = suppressWarnings)

Coefficients:
        Estimate Std.Error z value  Pr(>|z|)
S[1,2] 0.297484  0.015455 19.2489 < 2.2e-16 ***
S[1,3] 0.370088  0.014552 25.4322 < 2.2e-16 ***
S[1,4] 0.137688  0.016423  8.3838 < 2.2e-16 ***
S[1,5] 0.097971  0.016744  5.8510 4.886e-09 ***
S[2,3] 0.393709  0.014163 27.7984 < 2.2e-16 ***
S[2,4] 0.182984  0.016075 11.3831 < 2.2e-16 ***
S[2,5] 0.092664  0.016664  5.5609 2.685e-08 ***
S[3,4] 0.260756  0.015573 16.7444 < 2.2e-16 ***
S[3,5] 0.096063  0.016594  5.7890 7.080e-09 ***
S[4,5] 0.411753  0.013917 29.5858 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Goodness-of-fit indices:
                                      Value
Sample size                        3658.0000
Chi-square of target model          823.8769
DF of target model                   80.0000
p value of target model               0.0000
Chi-square of independence model   2992.9294
DF of independence model             90.0000
RMSEA                                 0.1513
SRMR                                  0.1528
TLI                                   0.7117
CFI                                   0.7437
AIC                                 663.8769
BIC                                 167.5032
OpenMx status: 0 ("0" and "1": considered fine; other values indicate problems)


$`Younger participants`

Call:
tssem1FEM(my.df = data.cluster[[i]], n = n.cluster[[i]], cor.analysis = cor.analysis,
    model.name = model.name, suppressWarnings = suppressWarnings)

Coefficients:
        Estimate Std.Error z value  Pr(>|z|)
S[1,2]  0.604396  0.022188 27.2392 < 2.2e-16 ***
S[1,3]  0.465441  0.027579 16.8769 < 2.2e-16 ***
S[1,4] -0.030869  0.036047 -0.8563   0.39181
S[1,5]  0.061581  0.034650  1.7772   0.07553 .
```

```
S[2,3]   0.501309  0.026431 18.9668 < 2.2e-16 ***
S[2,4]  -0.060834  0.034660 -1.7552   0.07923 .
S[2,5]   0.321019  0.031157 10.3034 < 2.2e-16 ***
S[3,4]   0.175422  0.033776  5.1937 2.061e-07 ***
S[3,5]   0.305214  0.031679  9.6345 < 2.2e-16 ***
S[4,5]   0.478573  0.026966 17.7474 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


Goodness-of-fit indices:
                                    Value
Sample size                       838.0000
Chi-square of target model        344.1826
DF of target model                 40.0000
p value of target model             0.0000
Chi-square of independence model 1461.6701
DF of independence model           50.0000
RMSEA                               0.2131
SRMR                                0.1508
TLI                                 0.7307
CFI                                 0.7845
AIC                               264.1826
BIC                                74.9419
OpenMx status: 0 ("0" and "1": considered fine; other values indicate problems)
```

Separate fixed-effects analyses on the Stage 2 analysis are then applied automatically. Please note that the estimates for the younger participants are problematic.

```
R> fixed2.cluster <- tssem2(fixed1.cluster, Amatrix = A1, Smatrix = S1,
+                         Fmatrix = F1)

Running TSSEM2 (Fixed Effects Model) Analysis of Correlation Structure
Running TSSEM2 (Fixed Effects Model) Analysis of Correlation Structure

R> summary(fixed2.cluster)

$`Older participants`

Call:
wls(Cov = tssem1.obj$pooledS, asyCov = tssem1.obj$acovS, n = tssem1.obj$total.n,
    Amatrix = Amatrix, Smatrix = Smatrix, Fmatrix = Fmatrix,
    diag.constraints = diag.constraints, cor.analysis = cor.analysis,
    intervals.type = intervals.type, mx.algebras = mx.algebras,
    model.name = model.name, suppressWarnings = suppressWarnings)

95% confidence intervals: z statistic approximation
Coefficients:
```

```
           Estimate Std.Error    lbound    ubound z value  Pr(>|z|)
Amatrix[1,6] 0.512525  0.018230 0.476794 0.548256  28.114 < 2.2e-16
Amatrix[2,6] 0.550049  0.017969 0.514829 0.585268  30.610 < 2.2e-16
Amatrix[3,6] 0.732091  0.018954 0.694941 0.769241  38.624 < 2.2e-16
Amatrix[4,7] 0.967545  0.058900 0.852102 1.082987  16.427 < 2.2e-16
Amatrix[5,7] 0.430459  0.029681 0.372285 0.488634  14.503 < 2.2e-16
Smatrix[7,6] 0.349090  0.028161 0.293895 0.404286  12.396 < 2.2e-16

Amatrix[1,6] ***
Amatrix[2,6] ***
Amatrix[3,6] ***
Amatrix[4,7] ***
Amatrix[5,7] ***
Smatrix[7,6] ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Goodness-of-fit indices:
                                                Value
Sample size                                3658.0000
Chi-square of target model                   21.9236
DF of target model                            4.0000
p value of target model                       0.0002
Number of constraints imposed on "Smatrix"    0.0000
DF manually adjusted                          0.0000
Chi-square of independence model           2267.5641
DF of independence model                     10.0000
RMSEA                                         0.0350
SRMR                                          0.0160
TLI                                           0.9802
CFI                                           0.9921
AIC                                          13.9236
BIC                                         -10.8951
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)


$`Younger participants`

Call:
wls(Cov = tssem1.obj$pooledS, asyCov = tssem1.obj$acovS, n = tssem1.obj$total.n,
    Amatrix = Amatrix, Smatrix = Smatrix, Fmatrix = Fmatrix,
    diag.constraints = diag.constraints, cor.analysis = cor.analysis,
    intervals.type = intervals.type, mx.algebras = mx.algebras,
    model.name = model.name, suppressWarnings = suppressWarnings)

95% confidence intervals: z statistic approximation
Coefficients:
            Estimate Std.Error    lbound    ubound z value Pr(>|z|)
```

```
Amatrix[1,6]  0.747634  0.023954  0.700686  0.794583 31.2116   <2e-16
Amatrix[2,6]  0.911957  0.019924  0.872907  0.951008 45.7719   <2e-16
Amatrix[3,6]  0.677210  0.025947  0.626354  0.728066 26.0994   <2e-16
Amatrix[4,7]  0.152354  0.159815 -0.160877  0.465585  0.9533   0.3404
Amatrix[5,7]  3.289775  3.388684 -3.351923  9.931473  0.9708   0.3316
Smatrix[7,6]  0.117068  0.125919 -0.129728  0.363865  0.9297   0.3525

Amatrix[1,6] ***
Amatrix[2,6] ***
Amatrix[3,6] ***
Amatrix[4,7]
Amatrix[5,7]
Smatrix[7,6]
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Goodness-of-fit indices:
                                              Value
Sample size                                 838.0000
Chi-square of target model                  144.8650
DF of target model                            4.0000
p value of target model                       0.0000
Number of constraints imposed on "Smatrix"    0.0000
DF manually adjusted                          0.0000
Chi-square of independence model           2469.5247
DF of independence model                     10.0000
RMSEA                                         0.2051
SRMR                                          0.1051
TLI                                           0.8568
CFI                                           0.9427
AIC                                         136.8650
BIC                                         117.9409
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

Random-effects model   TSSEM using a random-effects model may be requested by specifying the `method="REM"` argument in `tssem1()`. By default (`RE.type="Symm"`), a positive definite symmetric covariance matrix among the random-effects is used. For practical reasons, e.g., there are not enough studies, it may not be feasible to estimate the full variance components of the random effects. A diagonal matrix on the random effects may be specified by using `RE.type="Diag"`. Researchers may also specify `RE.type="Zero"`. Since the variance component of the random effects is zero, it becomese a fixed-effects model. This model is similar to the Generalized Least Squares (GLS) approach proposed by Becker (1992).

Since the `tssem1(method="REM", ...)` indeed calls `meta()`, I^2 on the correlations elements are also reported. For example, the following analysis shows that the I^2 based on the Q statistic varies from .85 to .95 indicating a high degree of heterogeneity on the correlation elements.

```
R> random1 <- tssem1(Digman97$data, Digman97$n, method = "REM",
+                    RE.type = "Diag")

Running TSSEM1 (Random Effects Model) Analysis of Correlation Matrix

R> summary(random1)

Call:
meta(y = ES, v = acovR, RE.constraints = Diag(x = paste(RE.startvalues,
    "*Tau2_", 1:no.es, "_", 1:no.es, sep = "")), RE.lbound = RE.lbound,
    I2 = I2, model.name = model.name)

95% confidence intervals: z statistic approximation
Coefficients:
               Estimate   Std.Error       lbound      ubound z value
Intercept1   3.9465e-01  5.4223e-02   2.8837e-01  5.0092e-01  7.2782
Intercept10  4.4413e-01  3.2547e-02   3.8034e-01  5.0792e-01 13.6460
Intercept2   4.4009e-01  4.1258e-02   3.5923e-01  5.2096e-01 10.6668
Intercept3   5.4542e-02  6.1716e-02  -6.6418e-02  1.7550e-01  0.8838
Intercept4   9.8668e-02  4.6219e-02   8.0808e-03  1.8926e-01  2.1348
Intercept5   4.2966e-01  4.0156e-02   3.5096e-01  5.0836e-01 10.6999
Intercept6   1.2851e-01  4.0816e-02   4.8514e-02  2.0851e-01  3.1486
Intercept7   2.0526e-01  4.9591e-02   1.0806e-01  3.0245e-01  4.1390
Intercept8   2.3994e-01  3.1924e-02   1.7737e-01  3.0251e-01  7.5159
Intercept9   1.8910e-01  4.3014e-02   1.0480e-01  2.7341e-01  4.3963
Tau2_10_10   1.1151e-02  5.0467e-03   1.2592e-03  2.1042e-02  2.2095
Tau2_1_1     3.7207e-02  1.5000e-02   7.8080e-03  6.6607e-02  2.4805
Tau2_2_2     2.0305e-02  8.4348e-03   3.7735e-03  3.6837e-02  2.4073
Tau2_3_3     4.8220e-02  1.9723e-02   9.5632e-03  8.6876e-02  2.4448
Tau2_4_4     2.4610e-02  1.0624e-02   3.7873e-03  4.5434e-02  2.3164
Tau2_5_5     1.8725e-02  8.2474e-03   2.5602e-03  3.4889e-02  2.2704
Tau2_6_6     1.8256e-02  8.7889e-03   1.0302e-03  3.5482e-02  2.0772
Tau2_7_7     2.9424e-02  1.2263e-02   5.3894e-03  5.3459e-02  2.3995
Tau2_8_8     9.6512e-03  4.8825e-03   8.1723e-05  1.9221e-02  1.9767
Tau2_9_9     2.0934e-02  9.1280e-03   3.0430e-03  3.8824e-02  2.2933
             Pr(>|z|)
Intercept1   3.384e-13 ***
Intercept10  < 2.2e-16 ***
Intercept2   < 2.2e-16 ***
Intercept3    0.376823
Intercept4    0.032777 *
Intercept5   < 2.2e-16 ***
Intercept6    0.001641 **
Intercept7   3.488e-05 ***
Intercept8   5.662e-14 ***
Intercept9   1.101e-05 ***
Tau2_10_10    0.027142 *
```

```
Tau2_1_1      0.013120 *
Tau2_2_2      0.016069 *
Tau2_3_3      0.014492 *
Tau2_4_4      0.020534 *
Tau2_5_5      0.023184 *
Tau2_6_6      0.037785 *
Tau2_7_7      0.016419 *
Tau2_8_8      0.048075 *
Tau2_9_9      0.021829 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q statistic on homogeneity of effect sizes: 2381.01
Degrees of freedom of the Q statistic: 130
P value of the Q statistic: 0
Heterogeneity indices (based on the estimated Tau2):
                             Estimate
Intercept1: I2 (Q statistic)   0.9487
Intercept2: I2 (Q statistic)   0.9082
Intercept3: I2 (Q statistic)   0.9414
Intercept4: I2 (Q statistic)   0.8894
Intercept5: I2 (Q statistic)   0.9005
Intercept6: I2 (Q statistic)   0.8537
Intercept7: I2 (Q statistic)   0.9093
Intercept8: I2 (Q statistic)   0.7714
Intercept9: I2 (Q statistic)   0.8746
Intercept10: I2 (Q statistic)  0.8431


Number of studies (or clusters): 14
Number of observed statistics: 140
Number of estimated parameters: 20
Degrees of freedom: 120
-2 log likelihood: -110.8449
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

The Stage 2 analysis is conducted as usual via the `tssem2()` function. The fit indices on the Stage 2 structural model in Stage 2 with `RE.type="Diag"` are $\chi^2(df = 4, N = 4,496) = 8.51, p < .001$, CFI=0.9911, TLI=0.9776, SRMR=0.0463 and RMSEA=0.0158. This indicates that the model fits the data quite well. From the **Amatrix**, the factor loadings on the **alpha** factor are 0.5726, 0.5901 and 0.7705 while the factor loadings on the **beta** factor are 0.6934 and 0.6401. The factor correlation between these two factors is 0.3937.

```
R> random2 <- tssem2(random1, Amatrix = A1, Smatrix = S1, Fmatrix = F1)


Running TSSEM2 (Random Effects Model) Analysis of Correlation Structure


R> summary(random2)
```

```
Call:
wls(Cov = pooledS, asyCov = asyCov, n = tssem1.obj$total.n, Amatrix = Amatrix,
    Smatrix = Smatrix, Fmatrix = Fmatrix, diag.constraints = diag.constraints,
    cor.analysis = cor.analysis, intervals.type = intervals.type,
    mx.algebras = mx.algebras, model.name = model.name, suppressWarnings = suppressWarning

95% confidence intervals: z statistic approximation
Coefficients:
             Estimate Std.Error   lbound   ubound z value  Pr(>|z|)
Amatrix[1,6] 0.572551  0.051605 0.471408 0.673694 11.0950 < 2.2e-16
Amatrix[2,6] 0.590104  0.051834 0.488511 0.691697 11.3844 < 2.2e-16
Amatrix[3,6] 0.770456  0.061032 0.650836 0.890076 12.6239 < 2.2e-16
Amatrix[4,7] 0.693404  0.074788 0.546822 0.839987  9.2715 < 2.2e-16
Amatrix[5,7] 0.640111  0.068852 0.505163 0.775060  9.2969 < 2.2e-16
Smatrix[7,6] 0.393657  0.047568 0.300425 0.486889  8.2756  2.22e-16

Amatrix[1,6] ***
Amatrix[2,6] ***
Amatrix[3,6] ***
Amatrix[4,7] ***
Amatrix[5,7] ***
Smatrix[7,6] ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Goodness-of-fit indices:
                                              Value
Sample size                              4496.0000
Chi-square of target model                  8.5118
DF of target model                          4.0000
p value of target model                     0.0745
Number of constraints imposed on "Smatrix"  0.0000
DF manually adjusted                        0.0000
Chi-square of independence model          514.5581
DF of independence model                   10.0000
RMSEA                                        0.0158
SRMR                                         0.0463
TLI                                          0.9776
CFI                                          0.9911
AIC                                          0.5118
BIC                                        -25.1320
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

4. Other useful functions

4.1. Analysis of correlation or covariance structure with weighted least squares

The `wls()` function may be used to fit a correlation (or covariance) structure with WLS estimation method. The following example fits a one-factor CFA model on the correlation matrix with WLS estimation method.

```
R> R1 <- matrix(c(1.00, 0.22, 0.24, 0.18,
+                 0.22, 1.00, 0.30, 0.22,
+                 0.24, 0.30, 1.00, 0.24,
+                 0.18, 0.22, 0.24, 1.00), ncol = 4, nrow = 4)
R> n <- 1000
R> acovR1 <- asyCov(R1, n)
R> (A1 <- cbind(matrix(0, nrow = 5, ncol = 4),
+               matrix(c("0.2*a1", "0.2*a2", "0.2*a3", "0.2*a4", 0),
+               ncol=1)))

     [,1] [,2] [,3] [,4] [,5]
[1,] "0"  "0"  "0"  "0"  "0.2*a1"
[2,] "0"  "0"  "0"  "0"  "0.2*a2"
[3,] "0"  "0"  "0"  "0"  "0.2*a3"
[4,] "0"  "0"  "0"  "0"  "0.2*a4"
[5,] "0"  "0"  "0"  "0"  "0"

R> A1 <- as.mxMatrix(A1)
R> (S1 <- Diag(c("0.2*e1", "0.2*e2", "0.2*e3", "0.2*e4",1)))

     [,1]     [,2]     [,3]     [,4]     [,5]
[1,] "0.2*e1" "0"      "0"      "0"      "0"
[2,] "0"      "0.2*e2" "0"      "0"      "0"
[3,] "0"      "0"      "0.2*e3" "0"      "0"
[4,] "0"      "0"      "0"      "0.2*e4" "0"
[5,] "0"      "0"      "0"      "0"      "1"

R> S1 <- as.mxMatrix(S1)
R> (F1 <- create.Fmatrix(c(1, 1, 1, 1, 0), name = "F1"))

FullMatrix 'F1'

@labels: No labels assigned.

@values
     [,1] [,2] [,3] [,4] [,5]
[1,]    1    0    0    0    0
[2,]    0    1    0    0    0
[3,]    0    0    1    0    0
[4,]    0    0    0    1    0
```

```
@free: No free parameters.

@lbound: No lower bounds assigned.

@ubound: No upper bounds assigned.

R> wls.fit1 <- wls(Cov = R1, asyCov = acovR1, n = n, Fmatrix = F1,
+                  Smatrix = S1, Amatrix = A1, cor.analysis = TRUE)

Running WLS Analysis of Correlation Structure

R> summary(wls.fit1)

Call:
wls(Cov = R1, asyCov = acovR1, n = n, Amatrix = A1, Smatrix = S1,
    Fmatrix = F1, cor.analysis = TRUE)

95% confidence intervals: z statistic approximation
Coefficients:
            Estimate Std.Error   lbound   ubound z value  Pr(>|z|)
Amatrix[1,5] 0.421591  0.039595 0.343987 0.499195  10.648 < 2.2e-16
Amatrix[2,5] 0.523764  0.040240 0.444895 0.602633  13.016 < 2.2e-16
Amatrix[3,5] 0.570921  0.041109 0.490348 0.651494  13.888 < 2.2e-16
Amatrix[4,5] 0.421591  0.039595 0.343987 0.499195  10.648 < 2.2e-16

Amatrix[1,5] ***
Amatrix[2,5] ***
Amatrix[3,5] ***
Amatrix[4,5] ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Goodness-of-fit indices:
                                            Value
Sample size                             1000.0000
Chi-square of target model                 0.0134
DF of target model                         2.0000
p value of target model                    0.9933
Number of constraints imposed on "Smatrix" 0.0000
DF manually adjusted                       0.0000
Chi-square of independence model         207.8704
DF of independence model                   6.0000
RMSEA                                      0.0000
SRMR                                       0.0012
TLI                                        1.0295
CFI                                        1.0000
```

```
AIC                                              -3.9866
BIC                                             -13.8021
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

4.2. Likelihood-based confidence interval

Most CIs are based on the estimated *SE*s. These are known as Wald CIs. Wald CIs are symmetric around the estimates. The Wald CIs might be outside of the meaningful boundaries, for example, a negative lower limit for the variance or larger than 1 for a correlation coefficient. A preferable approach is to construct the CIs based on the likelihood. This is known as the likelihood-based CI (Cheung 2009a; Neale and Miller 1997). Likelihood-based CIs on the parameter estimates can be requested by specifying `intervals.type='LB'` argument. This is especially useful in constructing confidence intervals for the variance components. For example, we may request LBCI on the `Becker83` example by:

```
R> summary( meta(y = di, v = vi, data = Becker83, intervals.type = "LB") )


Running Meta analysis with ML


Call:
meta(y = di, v = vi, data = Becker83, intervals.type = "LB")


95% confidence intervals: Likelihood-based statistic
Coefficients:
            Estimate Std.Error    lbound    ubound z value Pr(>|z|)
Intercept1  0.174734        NA -0.052165  0.437627      NA       NA
Tau2_1_1    0.077376        NA  0.015124  0.302999      NA       NA


Q statistic on homogeneity of effect sizes: 30.64949
Degrees of freedom of the Q statistic: 9
P value of the Q statistic: 0.0003399239
Heterogeneity indices (I2) and their 95% likelihood-based CIs:
                              lbound Estimate ubound
Intercept1: I2 (Q statistic) 0.28410  0.67182 0.8888


Number of studies (or clusters): 10
Number of observed statistics: 10
Number of estimated parameters: 2
Degrees of freedom: 8
-2 log likelihood: 7.928307
OpenMx status1: 0 ("0" and "1": considered fine; other values indicate problems)
```

4.3. Reading external data files

Data sets are most likely stored externally. The **metaSEM** package reads three types of data formats. The first type is full correlation/covariance matrices, for example, fullmat.dat is the

same as the built-in data set `Cheung09`. Missing values are represented by `NA` (the default option). Suppose you have saved it at d:\fullmat.dat, you may read it by using the following command in R:

```
my.df <- readFullMat(file = "d:/fullmat.dat")
```

The second type is lower triangle correlation/covariance matrices, for example, lowertriangle.dat. Missing values are represented by the strings NA. Suppose you have saved it at d:\lowertriangle.dat, you may read it by using the following command in R:

```
my.df <- readLowTriMat(file = "d:/lowertriangle.dat", no.var = 9,
                       na.strings = "NA")
```

The third type is vectors of correlation/covariance elements based on column vectorization. One row represents one study, for example, stackvec.dat. Suppose you have saved it at d:\stackvec.dat, you may read it by using the following R command:

```
my.df <- readStackVec(file = "d:/stackvec.dat")
```

5. Installation

First of all, you need R to run it. The **metaSEM** package depends on the **OpenMx** package. Since **OpenMx** is not available at CRAN yet, both **OpenMx** and **metaSEM** packages have to be installed separately. To install **OpenMx**, run the following command inside an R session:

```
install.packages("OpenMx", repos = 'http://openmx.psyc.virginia.edu/packages/')
```

See http://openmx.psyc.virginia.edu/installing-openmx for the details on how to install **OpenMx**. Moreover, **metaSEM** also depends on the **ellipse** and the **MASS** packages that can be installed by the following command inside an R session:

```
install.packages(c('ellipse', 'MASS'))
```

5.1. Windows platform

Download the Windows binary of **metaSEM**. If the file is saved at d:\. Run the following command inside an R session:

```
install.packages(pkgs = "d:/metaSEM_0.8-4.zip", repos = NULL)
```

Please note that d:\ in Windows is represented by either d:/ or d:\\ in R.

5.2. Linux and Mac OS X platform

Download the source package of **metaSEM**. Run the following command (as Root) inside an R session:

```
install.packages(pkgs = "metaSEM_0.8-4.tar.gz", repos = NULL, type = "source")
```

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This package cannot be written without R and **OpenMx**. Contributions by the R Development Core Team and the **OpenMx** Core Development Team are highly appreciated.

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