lavaan: a brief user's guide

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Contents

1 lavaan: a brief user's guide

1.1 Model syntax: specifying models

The four main formula types, and other operators

formula type	operator	mnemonic
latent variable	=~	is manifested by
regression	~	is regressed on
(residual) (co)variance	~~	is correlated with
intercept	~ 1	intercept
defined parameter	:=	is defined as
equality constraint	==	is equal to
inequality constraint	<	is smaller than
inequality constraint	>	is larger than

A typical model syntax

```
> myModel <- ' # regressions
               y1 + y2 ~ f1 + f2 + x1 + x2
                    f1 ~ f2 + f3
                    f2 ~ f3 + x1 + x2

             # latent variable definitions
               f1 =~ y1 + y2 + y3
               f2 =~ y4 + y5 + y6
               f3 =~ y7 + y8 +
                     y9 + y10

             # variances and covariances
               y1 ~~ y1
               y1 ~~ y2
               f1 ~~ f2

             # intercepts
               y1 ~ 1
               f1 ~ 1
           '
```

Fixing parameters, and overriding auto-fixed parameters

```
HS.model.bis <- ' visual  =~ NA*x1 + x2 + x3
                  textual =~ NA*x4 + x5 + x6
                  speed   =~ NA*x7 + x8 + x9
                  visual  ~~ 1*visual
                  textual ~~ 1*textual
                  speed   ~~ 1*speed
                '
```

- pre-multiplying a model parameter with a numeric value will keep the parameter fixed to that value
- pre-multiplying a model parameter with 'NA' will force the parameter to be free
- for this piece of code: using the `std.lv=TRUE` argument has the same effect

Labels and simple equality constraints

```
model.equal <- '
  # measurement model
    ind60 =~ x1 + x2 + x3
    dem60 =~ y1 + d1*y2 + d2*y3 + d3*y4
    dem65 =~ y5 + d1*y6 + d2*y7 + d3*y8

  # regressions
    dem60 ~ ind60
    dem65 ~ ind60 + dem60

  # residual covariances
    y1 ~~ y5
    y2 ~~ y4 + y6
    y3 ~~ y7
    y4 ~~ y8
    y6 ~~ y8
'
```

- pre-multiplying model parameters with a string gives the model parameter a custom ‘label’
- model parameters with the same label are considered to be equal

Defined parameters and mediation analysis

```
X <- rnorm(100); M <- 0.5*X + rnorm(100); Y <- 0.7*M + rnorm(100)
Data <- data.frame(X = X, Y = Y, M = M)

model <- ' # direct effect
             Y ~ c*X
           # mediator
             M ~ a*X
             Y ~ b*M
           # indirect effect (a*b)
             ab := a*b
           # total effect
             total := c + (a*b)
         '

fit <- sem(model, data=Data)
```

- the ":=" operator defines a new parameter, as a function of existing (free) parameters, but referring to their labels
- by default, the delta rule is used to compute standard errors for these defined parameters; bootstrapping may be a better option

Linear and nonlinear equality and inequality constraints

```
Data <- data.frame(y = rnorm(100), x1 = rnorm(100), x2 = rnorm(100),
                   x3 = rnorm(100))

model.constr <- ' # model with labeled parameters
                    y ~ b1*x1 + b2*x2 + b3*x3
                  # constraints
                    b1 == (b2 + b3)^2
                    b1 > exp(b2 + b3) '
fit <- sem(model.constr, data=Data)
```

- simple regression model, but with (nonlinear) constraints imposed on the regression coefficients
- can be used to force variances to be strictly positive
- can be used for testing interaction effects among latent variables
- for simple equality constraints (e.g. `b1 == b2`), it is much more efficient to simply provide the same label

1.2 Fitting functions: estimating models

User-friendly fitting functions

- `cfa()` for confirmatory factor analysis
- `sem()` for path analysis and SEM
- `growth()` for growth curve modeling

Arguments of the cfa() and sem() fitting functions

```
sem(model = NULL, meanstructure = "default", fixed.x = "default",
    orthogonal = FALSE, std.lv = FALSE, data = NULL, std.ov = FALS
    missing = "default", sample.cov = NULL, sample.mean = NULL,
    sample.nobs = NULL, group = NULL, group.equal = "",
    group.partial = "", constraints = '', estimator = "default",
    likelihood = "default", information = "default", se = "default
    test = "default", bootstrap = 1000L,
    mimic = "default", representation = "default",
    do.fit = TRUE, control = list(), start = "default",
    verbose = FALSE, warn = TRUE, debug = FALSE)
```

`model` A description of the user-specified model. Typically, the model is described using the lavaan model syntax. See `model.syntax` for more information. Alternatively, a parameter list (eg. the output of the `lavaanify()` function) is also accepted.

`meanstructure` If `TRUE`, the means of the observed variables enter the model. If `"default"`, the value is set based on the user-specified model, and/or the values of other arguments.

`fixed.x` If `TRUE`, the exogenous 'x' covariates are considered fixed variables and the means, variances and covariances of these variables are fixed to their sample values. If `FALSE`, they are considered random, and the means, variances and covariances are free parameters. If `"default"`, the value is set depending on the mimic option.

`orthogonal` If `TRUE`, the exogenous latent variables are assumed to be uncorrelated.

`orthogonal` If `TRUE`, the exogenous latent variables are assumed to be uncorrelated.

`std.lv` If `TRUE`, the metric of each latent variable is determined by fixing their variances to 1.0. If `FALSE`, the metric of each latent variable is determined by fixing the factor loading of the first indicator to 1.0.

`data` An optional data frame containing the observed variables used in the model.

`std.ov` If `TRUE`, all observed variables are standardized before entering the analysis.

`missing` If `"listwise"`, cases with missing values are removed listwise from the data frame before analysis. If `"direct"` or `"ml"` or `"fiml"` and the estimator

	is maximum likelihood, Full Information Maximum Likelihood (FIML) estimation is used using all available data in the data frame. This is only valid if the data are missing completely at random (MCAR) or missing at random (MAR). If `"default"`, the value is set depending on the estimator and the mimic option.
`sample.cov`	Numeric matrix. A sample variance-covariance matrix. The rownames must contain the observed variable names. For a multiple group analysis, a list with a variance-covariance matrix for each group.
`sample.mean`	A sample mean vector. For a multiple group analysis, a list with a mean vector for each group.
`sample.nobs`	Number of observations if the full data frame is missing and only sample moments are given. For a multiple group analysis, a list or a vector with the number of observations for each group.
`group`	A variable name in the data frame defining the groups in a multiple group analysis.
`group.equal`	A vector of character strings. Only used in a multiple group analysis. Can be one or more of the following: `"loadings"`, `"intercepts"`, `"means"`, `"regressions"`, `"residuals"`, `"residual.covariances"`, `"lv.vari` or `"lv.covariances"`, specifying the pattern of equality constraints across multiple groups.
`group.partial`	A vector of character strings containing the labels of the parameters which

	should be free in all groups (thereby overriding the group.equal argument for some specific parameters).
`constraints`	Additional (in)equality constraints not yet included in the model syntax. See `model.syntax` for more information.
`estimator`	The estimator to be used. Can be one of the following: `"ML"` for maximum likelihood, `"GLS"` for generalized least squares, `"WLS"` for weighted least squares (sometimes called ADF estimation), `"MLM"` for maximum likelihood estimation with robust standard errors and a Satorra-Bentler scaled test statistic, `"MLF"` for maximum likelihood estimation with standard errors based on first-order derivatives and a conventional test statistic, `"MLR"` for maximum likelihood estimation with robust 'Huber-White' standard errors and a scaled test statistic which is asymptotically equivalent to the Yuan-Bentler T2-star test statistic. Note that the `"MLM"`, `"MLF"` and `"MLR"` choices only affect the standard errors and the test statistic. They also imply `mimic="Mplus"`.
`likelihood`	Only relevant for ML estimation. If `"wishart"`, the wishart likelihood approach is used. In this approach, the covariance matrix has been divided by N-1, and both standard errors and test statistics are based on N-1. If `"normal"`, the normal likelihood approach is used. Here, the covariance matrix has been divided by N, and both standard errors and test statistics are based on N. If `"default"`, it depends on the mimic option: if `mimic="Mplus"`, normal likelihood is used; otherwise, wishart likelihood is used.
`information`	If `"expected"`, the expected information matrix is used (to compute the standard errors). If `"observed"`, the observed information matrix is used.

	If `"default"`, the value is set depending on the estimator and the mimic option.
`se`	If `"standard"`, conventional standard errors are computed based on inverting the (expected or observed) information matrix. If `"first.order"`, standard errors are computed based on first-order derivatives. If `"robust.mlm"`, conventional robust standard errors are computed. If `"robust.mlr"`, standard errors are computed based on the 'mlr' (aka pseudo ML, Huber-White) approach. If `"robust"`, either `"robust.mlm"` or `"robust.mlr"` is used depending on the estimator, the mimic option, and whether the data are complete or not. If `"boot"` or `"bootstrap"`, bootstrap standard errors are computed using standard bootstrapping (unless Bollen-Stine bootstrapping is requested for the test statistic; in this case bootstrap standard errors are computed using model-based bootstrapping). If `"none"`, no standard errors are computed.
`test`	If `"standard"`, a conventional chi-square test is computed. If `"Satorra-Bentl` a Satorra-Bentler scaled test statistic is computed. If `"Yuan-Bentler"`, a Yuan-Bentler scaled test statistic is computed. If `"boot"` or `"bootstrap"` or `"bollen.stine"`, the Bollen-Stine bootstrap is used to compute the bootstrap probability value of the test statistic. If `"default"`, the value depends on the values of other arguments.
`bootstrap`	Number of bootstrap draws, if bootstrapping is used.
`mimic`	If `"Mplus"`, an attempt is made to mimic the Mplus program. If `"EQS"`,

an attempt is made to mimic the EQS program. If `"default"`, the value is (currently) set to `"Mplus"`.

`representation` If `"LISREL"` the classical LISREL matrix representation is used to represent the model (using the all-y variant).

`do.fit` If `FALSE`, the model is not fit, and the current starting values of the model parameters are preserved.

`control` A list containing control parameters passed to the optimizer. By default, lavaan uses `"nlminb"`. See the manpage of `nlminb` for an overview of the control parameters. A different optimizer can be chosen by setting the value of `optim.method`. For unconstrained optimization (the model syntax does not include any ”==”, ”¿” or ”¡” operators), the available options are `"nlminb"` (the default), `"BFGS"` and `"L-BFGS-B"`. See the manpage of the `optim` function for the control parameters of the latter two options. For constrained optimization, the only available option is `"nlminb.constr"`.

`start` If it is a character string, the two options are currently `"simple"` and `"Mplus"`. In the first case, all parameter values are set to zero, except the factor loadings (set to one), the variances of latent variables (set to 0.05), and the residual variances of observed variables (set to half the observed variance). If `"Mplus"`, we use a similar scheme, but the factor loadings are estimated using the fabin3 estimator (tsls) per factor. If `start` is a fitted object of class `lavaan-class`, the estimated values of the corresponding parameters will be extracted. If it is a model list, for example the output of the

	paramaterEstimates() function, the values of the est or start or ustart column (whichever is found first) will be extracted.
verbose	If TRUE, the function value is printed out during each iteration.
warn	If TRUE, some (possibly harmless) warnings are printed out during the iterations.
debug	If TRUE, debugging information is printed out.

Power-user fitting functions

- the `lavaan()` function does NOT do anything automagically
  1. no model parameters are added to the parameter table
  2. no actions are taken to make the model identifiable (e.g. setting the metric of the latent variables

Example model syntax using the lavaan() function

```
HS.model.full <- ' # latent variables
                     visual  =~ 1*x1 + x2 + x3
                     textual =~ 1*x4 + x5 + x6
                     speed   =~ 1*x7 + x8 + x9

                   # factor variances
                     visual  ~~ visual
                     textual ~~ textual
                     speed   ~~ speed

                   # factor covariances
                     visual  ~~ textual
```

```
                   visual  ~~ speed
                   textual ~~ speed

                 # residual variances observed variables
                   x1 ~~ x1
                   x2 ~~ x2
                   x3 ~~ x3
                   x4 ~~ x4
                   x5 ~~ x5
                   x6 ~~ x6
                   x7 ~~ x7
                   x8 ~~ x8
                   x9 ~~ x9
                '
fit <- lavaan(HS.model.full, data=HolzingerSwineford1939)
```

Combining the lavaan() function with auto.* arguments

- several `auto.*` arguments are available to
  - automatically add a set of parameters (e.g. all (residual) variances)
  - take actions to make the model identifiable (e.g. set the metric of the latent variables)

Example using lavaan with an auto.* argument

```
HS.model.mixed <- ' # latent variables
                      visual  =~ 1*x1 + x2 + x3
                      textual =~ 1*x4 + x5 + x6
                      speed   =~ 1*x7 + x8 + x9
                    # factor covariances
                      visual  ~~ textual + speed
                      textual ~~ speed
                 '
fit <- lavaan(HS.model.mixed, data=HolzingerSwineford1939,
              auto.var=TRUE)
```

keyword	operator	parameter set
`auto.var`	~~	(residual) variances observed and latent variables
`auto.cov.y`	~~	(residual) covariances observed and latent endogenous variables
`auto.cov.lv.x`	~~	covariances among exogenous latent variables

keyword	default	action
`auto.fix.first`	TRUE	fix the factor loading of the first indicator to 1
`auto.fix.single`	TRUE	fix the residual variance of a single indicator to 0
`int.ov.free`	TRUE	freely estimate the intercepts of the observed variables (only if a mean structure is included)
`int.lv.free`	FALSE	freely estimate the intercepts of the latent variables (only if a mean structure is included)

1.3 Extractor functions: inspecting fitted models

Method	Description
`summary()`	print a long summary of the model results
`show()`	print a short summary of the model results
`coef()`	returns the estimates of the free parameters in the model as a named numeric vector
`fitted()`	returns the implied moments (covariance matrix and mean vector) of the model
`resid()`	returns the raw, normalized or standardized residuals (difference between implied and observed moments)
`vcov()`	returns the covariance matrix of the estimated parameters
`predict()`	compute factor scores
`logLik()`	returns the log-likelihood of the fitted model (if maximum likelihood estimation was used)
`AIC()`, `BIC()`	compute information criteria (if maximum likelihood estimation was used)
`update()`	update a fitted lavaan object
`inspect()`	peek into the internal representation of the model; by default, it returns a list of model matrices counting the free parameters in the model; can also be used to extract starting values, gradient values, and much more

1.4 Other functions

Function	Description
`lavaanify()`	converts a lavaan model syntax to a parameter table
`parameterTable()`	returns the parameter table
`parameterEstimates()`	returns the parameter estimates, including confidence intervals, as a data frame
`standardizedSolution()`	returns one of three types of standardized parameter estimates, as a data frame
`modindices()`	computes modification indices and expected parameter changes
`bootstrapLavaan()`	bootstrap any arbitrary statistic that can be extracted from a fitted lavaan object
`bootstrapLRT()`	bootstrap a chi-square difference test for comparing two alternative models

1.5 Meanstructures

- traditionally, SEM has focused on covariance structure analysis
- but we can also include the means
- typical situations where we would include the means are:
  - multiple group analysis
  - growth curve models
  - analysis of non-normal data, and/or missing data
- we have more data: the p-dimensional mean vector
- we have more parameters:
  - means/intercepts for the observed variables
  - means/intercepts for the latent variables (often fixed to zero)

Adding the means in lavaan

- when the `meanstructure` argument is set to `TRUE`, a meanstructure is added to the model

```
fit <- cfa(HS.model, data=HolzingerSwineford1939,
           meanstructure=TRUE)
```

- if no restrictions are imposed on the means, the fit will be identical to the non-meanstructure fit
- we add p datapoints (the mean vector)
- we add p free parameters (the intercepts of the observed variables)
- we fix the latent means to zero
- the number of degrees of freedom does not change

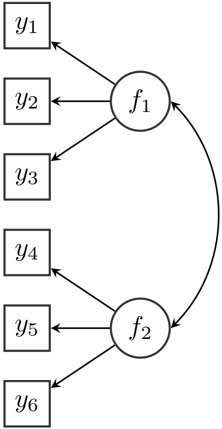
Output meanstructure=TRUE

```
lavaan (0.4-12) converged normally after 41 iterations

  Number of observations                           301

  Estimator                                         ML
  Minimum Function Chi-square                   85.306
  Degrees of freedom                                24
  P-value                                        0.000

Parameter estimates:

  Information                                 Expected
  Standard Errors                             Standard

                   Estimate  Std.err  Z-value  P(>|z|)
Latent variables:
  visual =~
    x1                1.000
    x2                0.553    0.100    5.554    0.000
    x3                0.729    0.109    6.685    0.000
  textual =~
    x4                1.000
    x5                1.113    0.065   17.014    0.000
    x6                0.926    0.055   16.703    0.000
  speed =~
    x7                1.000
```

```
    x8                  1.180    0.165    7.152    0.000
    x9                  1.082    0.151    7.155    0.000

Covariances:
  visual ~~
    textual             0.408    0.074    5.552    0.000
    speed               0.262    0.056    4.660    0.000
  textual ~~
    speed               0.173    0.049    3.518    0.000

Intercepts:
    x1                  4.936    0.067   73.473    0.000
    x2                  6.088    0.068   89.855    0.000
    x3                  2.250    0.065   34.579    0.000
    x4                  3.061    0.067   45.694    0.000
    x5                  4.341    0.074   58.452    0.000
    x6                  2.186    0.063   34.667    0.000
    x7                  4.186    0.063   66.766    0.000
    x8                  5.527    0.058   94.854    0.000
    x9                  5.374    0.058   92.546    0.000
    visual              0.000
    textual             0.000
    speed               0.000

Variances:
    x1                  0.549    0.114
    x2                  1.134    0.102
    ...
```

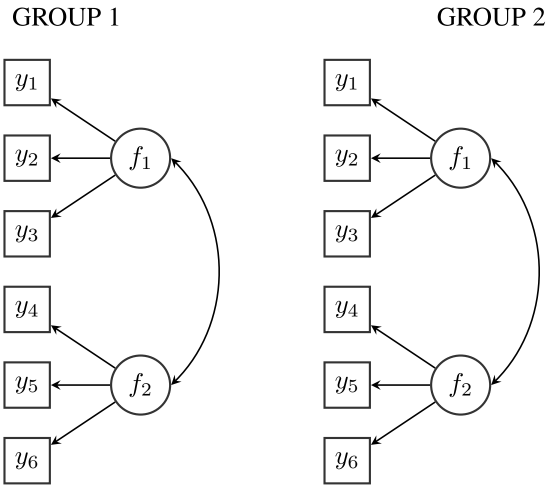
1.6 Multiple groups

Single group analysis (CFA)



- factor means typically fixed to zero

Multiple group analysis (CFA)



- can we compare the means of the latent variables?

Measurement Invariance in lavaan

```
# model 1: configural invariance
fit1 <- cfa(HS.model, data=HolzingerSwineford1939, group="school")

# model 2: weak invariance
fit2 <- cfa(HS.model, data=HolzingerSwineford1939, group="school",
            group.equal="loadings")

# model 3: strong invariance
fit3 <- cfa(HS.model, data=HolzingerSwineford1939, group="school",
            group.equal=c("loadings", "intercepts"))
```

Comparing two (nested) models: the anova() function

```
anova(fit1, fit2)

Chi Square Difference Test

     Df    AIC    BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit1 48 7484.4 7706.8 115.85
fit2 54 7480.6 7680.8 124.04     8.1922       6     0.2244
```

Measurement invariance tests – all together

```
> measurementInvariance(HS.model, data=HolzingerSwineford1939,
                        group="school", strict=FALSE)

Measurement invariance tests:

Model 1: configural invariance:
   chisq       df    pvalue       cfi     rmsea       bic
 115.851   48.000    0.000     0.923     0.097 7706.822

Model 2: weak invariance (equal loadings):
   chisq       df    pvalue       cfi     rmsea       bic
 124.044   54.000    0.000     0.921     0.093 7680.771

[Model 1 versus model 2]
  delta.chisq      delta.df delta.p.value     delta.cfi
        8.192         6.000         0.224         0.002

Model 3: strong invariance (equal loadings + intercepts):
   chisq       df    pvalue       cfi     rmsea       bic
 164.103   60.000    0.000     0.882     0.107 7686.588

[Model 1 versus model 3]
  delta.chisq      delta.df delta.p.value     delta.cfi
       48.251        12.000         0.000         0.041

...
```

1.7 Missing data in lavaan

- if the data contain missing values, the default behavior in **lavaan** is listwise deletion

- if the missing mechanism is MCAR or MAR, the **lavaan** package provides case-wise (or 'full information') maximum likelihood (FIML) estimation by specifying the argument `missing="ml"` (or its alias `missing="fiml"`):

```
fit <- sem(myModel, data=myIncompleteData, missing="ml")
```

- an unrestricted (h1) model will automatically be estimated (using the EM algorithm), so that all common fit indices are available

- robust standard errors are also available, as is a scaled ('Yuan-Bentler') test statistic if the data are both incomplete and non-normal (`estimator="MLR"`)

1.8 Standard errors

- the `se` argument can be used to switch between different types of standard errors
- setting `se="robust"` will produce robust standard errors
  - if data is complete, lavaan will use `se="robust.mlm"`
  - if data is incomplete, lavaan will use `se="robust.mlr"`
- setting `se="boot"` or `se="bootstrap` will produce bootstrap standard errors
- setting `se="none"` will NOT compute standard errors

1.9 Test statistics

- the `test` argument can be used to switch between different test statistics:
  - `test="standard"` (default)
  - `test="satorra.bentler"`
  - `test="yuan.bentler"`
  - `test="bootstrap"` or `test="bollen.stine"`
  - `test="none"`
- combine both robust standard errors and a scaled test statistic:
  - `estimator="MLM"`
  - `estimator="MLR"`

1.10 BootstrapLavaan

- once a lavaan model has been fitted, you can bootstrap any statistic that you can extract from a fitted lavaan object

- examples:

```
# bootstrap model parameters
PAR.boot <- bootstrapLavaan(fit, R=10, type="ordinary",
                            FUN="coef")


# bootstrap test statistic + compute p-value
T.boot <- bootstrapLavaan(fit, R=10, type="bollen.stine",
                          FUN=fitMeasures, fit.measures="chisq")

pvalue.boot <- length(which(T.boot > T.orig))/length(T.boot)


# bootstrap CFI
CFI.boot <-  bootstrapLavaan(fit, R=10, type="parametric",
                             FUN=fitMeasures, fit.measures="cfi",
                             parallel="multicore", ncpus=8)
```

1.11 Constraints and defined parameters

linear and nonlinear equality and inequality constraints

```
Data <- data.frame(   y = rnorm(100),
                     x1 = rnorm(100),
                     x2 = rnorm(100),
                     x3 = rnorm(100)  )

model.constr <- ' # model with labeled parameters
                    y ~ b1*x1 + b2*x2 + b3*x3

                  # constraints
                    b1 == (b2 + b3)^2
                    b1 > exp(b2 + b3)
                '

fit <- sem(model.constr, data=Data)
```

defined parameters and mediation analysis

```
X <- rnorm(100)
M <- 0.5*X + rnorm(100)
Y <- 0.7*M + rnorm(100)
Data <- data.frame(X = X, Y = Y, M = M)

model <- ' # direct effect
             Y ~ c*X
           # mediator
             M ~ a*X
             Y ~ b*M

           # indirect effect (a*b)
             ab := a*b
           # total effect
             total := c + (a*b)
         '

fit <- sem(model, data=Data)
```

1.12 Using a covariance matrix as input

```
lower <- '
 11.834,
  6.947,    9.364,
  6.819,    5.091,   12.532,
  4.783,    5.028,    7.495,    9.986,
 -3.839,   -3.889,   -3.841,   -3.625,   9.610,
-21.899,  -18.831,  -21.748,  -18.775,  35.522,  450.288 '

# classic wheaton et al model
wheaton.cov <- getCov(lower,
                      names=c("anomia67","powerless67", "anomia71",
                              "powerless71","education","sei"))

wheaton.model <- '
  # measurement model
    ses     =~ education + sei
    alien67 =~ anomia67 + powerless67
    alien71 =~ anomia71 + powerless71

  # equations
    alien71 ~ alien67 + ses
    alien67 ~ ses
```

```
   # correlated residuals
     anomia67 ~~ anomia71
     powerless67 ~~ powerless71
'

fit <- sem(wheaton.model, sample.cov=wheaton.cov, sample.nobs=932)
summary(fit, standardized=TRUE)
```

2 Some technical details

2.1 Default estimator: ML

- ML is the default estimator in all software packages for SEM
- the likelihood function is derived from the multivariate normal distribution (the 'normal' tradition) or the Wishart distribution (the 'Wishart' tradition)
- standard errors are usually based on the covariance matrix that is obtained by inverting the expected information matrix

$$
\begin{aligned}
n\text{Cov}(\hat{\theta}) &= A^{-1} \\
&= (\Delta' W \Delta)^{-1}
\end{aligned}
$$

  – Δ is a jacobian matrix and W is a function of Σ^{-1}
  – if no meanstructure:

$$
\begin{aligned}
\Delta &= \partial\hat{\Sigma}/\partial\hat{\theta}' \\
W &= 2D'(\hat{\Sigma}^{-1} \otimes \hat{\Sigma}^{-1})D
\end{aligned}
$$

- an alternative is to use the *observed* information matrix

$$
\begin{aligned}
n\text{Cov}(\hat{\theta}) &= A^{-1} \\
&= [-\text{Hessian}]^{-1} \\
&= \left[-\partial F(\hat{\theta})/(\partial\hat{\theta}\partial\hat{\theta}')\right]^{-1}
\end{aligned}
$$

where $F(\theta)$ is the function that is minimized

- overall model evaluation is based on the likelihood-ratio (LR) statistic (chi-square test): T_{ML}
  - (minus two times the) difference between loglikelihood of user-specified model H_0 and unrestricted model H_1
  - equals (in lavaan) $2 \times n$ times the minimum value of $F(\theta)$
  - T_{ML} follows (under regularity conditions) a chi-square distribution

2.2 Estimator MLM

- parameter estimates are standard ML estimates
- standard errors are robust to non-normality
  - standard errors are computed using a sandwich-type estimator:

$$\begin{aligned} n\text{Cov}(\hat{\theta}) &= A^{-1}BA^{-1} \\ &= (\Delta' W \Delta)^{-1}(\Delta' W \Gamma W \Delta)(\Delta' W \Delta)^{-1} \end{aligned}$$

  - A is usually the expected information matrix (but not in Mplus)
  - references: Huber (1967), Browne (1984), Shapiro (1983), Bentler (1983), …

- chi-square test statistic is robust to non-normality
  - test statistic is 'scaled' by a correction factor

$$T_{SB} = T_{ML}/c$$

  - the scaling factor c is computed by:

$$c = tr\left[U\Gamma\right]/\mathrm{df}$$

    where

$$U = (W^{-1} - W^{-1}\Delta(\Delta'W^{-1}\Delta)^{-1}\Delta'W^{-1})$$

  - correction method described by Satorra & Bentler (1986, 1988, 1994)
- estimator MLM: for complete data only

2.3 Estimator MLR

- parameter estimates are standard ML estimates
- standard errors are robust to non-normality
  - standard errors are computed using a (different) sandwich approach:

$$\begin{aligned} n\text{Cov}(\hat{\theta}) &= A^{-1}BA^{-1} \\ &= A_0^{-1}B_0A_0^{-1} = C_0 \end{aligned}$$

    where

$$A_0 = -\sum_{i=1}^{n} \frac{\partial \log L_i}{\partial\hat{\theta}\,\partial\hat{\theta}'} \quad \text{(observed information)}$$

    and

$$B_0 = \sum_{i=1}^{n} \left(\frac{\partial \log L_i}{\partial\hat{\theta}}\right) \times \left(\frac{\partial \log L_i}{\partial\hat{\theta}}\right)'$$

  - for both complete and incomplete data

- Huber (1967), Gourieroux, Monfort & Trognon (1984), Arminger & Schoenberg (1989)

- chi-square test statistic is robust to non-normality
  - test statistic is 'scaled' by a correction factor

$$T_{MLR} = T_{ML}/c$$

  - the scaling factor c is (usually) computed by

$$c = tr\left[M\right]$$

    where

$$M = C_1(A_1 - A_1\Delta(\Delta' A_1 \Delta)^{-1}\Delta' A_1)$$

  - A_1 and C_1 are computed under the unrestricted (H_1) model
  - correction method described by Yuan & Bentler (2000)

- information matrix (A) can be observed or expected

- for complete data, the MLR and MLM corrections are asymptotically equivalent