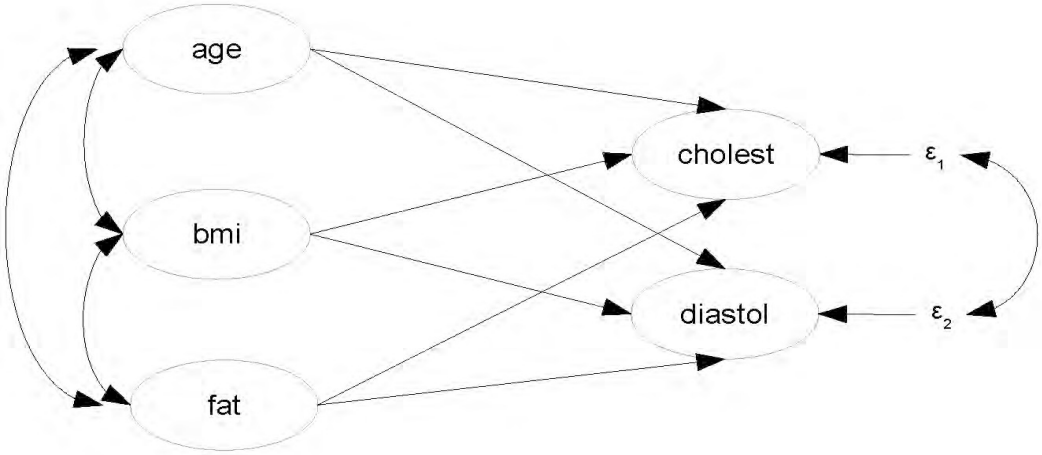
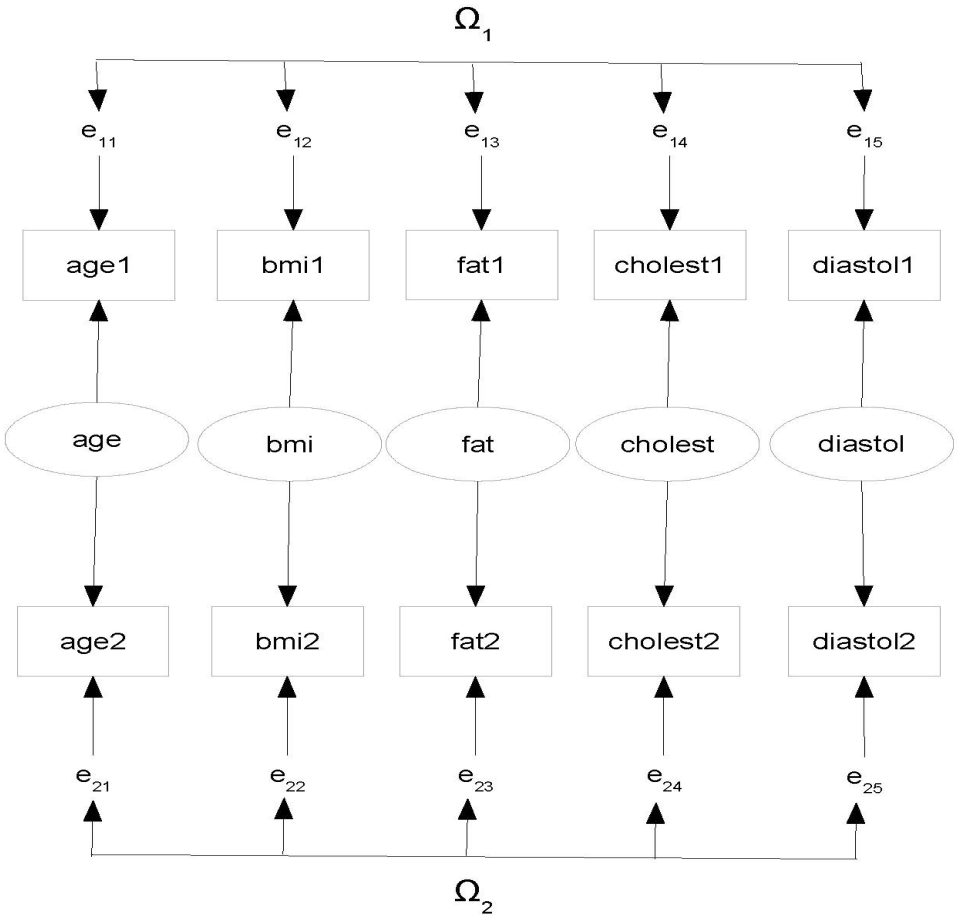
The BMI Health Study*





*This handout was prepared by Jerry Brunner, Department of Statistical Sciences, University of Toronto. It is licensed under a Creative Commons Attribution - ShareAlike 3.0 Unported License. Use any part of it as you like and share the result freely. The OpenOffice.org document is available from the course website:

http://www.utstat.toronto.edu/brunner/oldclass/431s23

```
> rm(list=ls()); options(scipen=999)
> bmidata =
read.table("http://www.utstat.toronto.edu/~brunner/openSEM/data/bmi.data.txt")
>
> head(bmidata)
  age1 bmi1 fat1 cholest1 diastol1 age2 bmi2 fat2 cholest2 diastol2
1   63 24.5 16.5    195.4       38   60 23.9 20.1    203.5       66
2   42 13.0  1.9    184.3       86   44 14.8  2.6    197.3       78
3   32 22.5 14.6    354.1      104   33 21.7 20.4    374.3       73
4   59 25.5 19.0    214.6       93   58 28.5 20.0    203.7      106
5   45 26.5 17.8    324.8       97   43 25.0 12.3    329.7       92
6   31 19.4 17.1    280.7       92   42 19.9 19.9    276.7       87
> dim(bmidata)
[1] 500  10
>
> ###################################
> # Naive surface regression        #
> ###################################
>
> bmi = within(bmidata,{
+ age = (age1+age2)/2; bmi = (bmi1+bmi2)/2; fat = (fat1+fat2)/2
+ cholest = (cholest1+cholest2)/2; diastol = (diastol1+diastol2)/2
+ })
> dim(bmi)
[1] 500  15
> fullmod = lm( cbind(cholest,diastol) ~ age + fat + bmi, data=bmi)
> summary(fullmod)
Response cholest :

Call:
lm(formula = cholest ~ age + fat + bmi, data = bmi)

Residuals:
     Min       1Q   Median       3Q      Max
-148.550  -34.243    2.626   33.661  165.582

Coefficients:
            Estimate Std. Error t value             Pr(>|t|)
(Intercept) 220.0610    21.0109  10.474 < 0.0000000000000002 ***
age          -0.2714     0.2002  -1.356              0.17578
fat           2.2334     0.5792   3.856              0.00013 ***
bmi           0.5164     1.0154   0.509              0.61128
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 52.43 on 496 degrees of freedom
Multiple R-squared:  0.09701, Adjusted R-squared:  0.09155
F-statistic: 17.76 on 3 and 496 DF,  p-value: 0.00000000005762

Response diastol :

Call:
lm(formula = diastol ~ age + fat + bmi, data = bmi)

Residuals:
    Min      1Q  Median      3Q     Max
-44.841  -7.140  -0.408   7.612  41.377
```

```
Coefficients:
            Estimate Std. Error t value             Pr(>|t|)
(Intercept) 49.69194    4.52512  10.981 < 0.0000000000000002 ***
age          0.12648    0.04311   2.934             0.003504 **
fat          0.64056    0.12474   5.135          0.000000406 ***
bmi          0.82627    0.21869   3.778             0.000177 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 11.29 on 496 degrees of freedom
Multiple R-squared:  0.3333,  Adjusted R-squared:  0.3293
F-statistic: 82.67 on 3 and 496 DF,  p-value: < 0.00000000000000022
>
> restrictedmod = update(fullmod, . ~ . - bmi) # Remove var(s) being tested
> anova(fullmod,restrictedmod) # Gives multivariate test.
Analysis of Variance Table

Model 1: cbind(cholest, diastol) ~ age + fat + bmi
Model 2: cbind(cholest, diastol) ~ age + fat
  Res.Df Df Gen.var.  Pillai approx F num Df den Df    Pr(>F)
1    496      591.89
2    497  1   599.36 0.02869   7.3106      2    495 0.0007431 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

>
> ###################################
> # Structural equation model       #
> ###################################
> # install.packages("lavaan", dependencies = TRUE) # Only need to do this once
> library(lavaan)
This is lavaan 0.6-11
lavaan is FREE software! Please report any bugs.
>
```

```
bmimodel1 =
    ###########################################################
    # Latent variable model
    # ---------------------
   'Lcholest ~ beta11*Lage + beta12*Lbmi + beta13*Lfat
    Ldiastol ~ beta21*Lage + beta22*Lbmi + beta23*Lfat
    #
    # Measurement model
    # -----------------
    Lage =~ 1*age1 + 1*age2
    Lbmi =~ 1*bmi1 + 1*bmi2
    Lfat =~ 1*fat1 +1*fat2
    Lcholest =~ 1*cholest1 + 1*cholest2
    Ldiastol =~ 1*diastol1 + 1*diastol2
    #
    # Variances and covariances
    # -------------------------
    # Of latent explanatory variables
    Lage ~~ phi11*Lage; Lage ~~ phi12*Lbmi; Lage ~~ phi13*Lfat
                        Lbmi ~~ phi22*Lbmi; Lbmi ~~ phi23*Lfat
                                            Lfat ~~ phi33*Lfat
    # Of error terms in latent the regression (epsilon_ij)
    Lcholest ~~ psi11*Lcholest; Lcholest ~~ psi12*Ldiastol
                                Ldiastol ~~ psi22*Ldiastol
    # Of measurement errors (e_ijk) for measurement set 1
    age1 ~~ w111*age1; age1 ~~ w112*bmi1; age1 ~~ w113*fat1;
    age1 ~~ w114*cholest1; age1 ~~ w115*diastol1
            bmi1 ~~ w122*bmi1; bmi1 ~~ w123*fat1; bmi1 ~~ w124*cholest1; bmi1 ~~ w125*diastol1
                    fat1 ~~ w133*fat1; fat1 ~~ w134*cholest1; fat1 ~~ w135*diastol1
                            cholest1 ~~ w144*cholest1; cholest1 ~~ w145*diastol1
                                                       diastol1 ~~ w155*diastol1
    # Of measurement errors (e_ijk) for measurement set 2
    age2 ~~ w211*age2; age2 ~~ w212*bmi2; age2 ~~ w213*fat2;
    age2 ~~ w214*cholest2; age2 ~~ w215*diastol2
            bmi2 ~~ w222*bmi2; bmi2 ~~ w223*fat2; bmi2 ~~ w224*cholest2; bmi2 ~~ w225*diastol2
                    fat2 ~~ w233*fat2; fat2 ~~ w234*cholest2; fat2 ~~ w235*diastol2
                            cholest2 ~~ w244*cholest2; cholest2 ~~ w245*diastol2
                                                       diastol2 ~~ w255*diastol2
   ' ################## End of bmimodel1 ##################

  > fit1 = lavaan(bmimodel1, data=bmidata)
  Warning messages:
  1: In lav_model_vcov(lavmodel = lavmodel, lavsamplestats = lavsamplestats,  :
    lavaan WARNING:
      Could not compute standard errors! The information matrix could
      not be inverted. This may be a symptom that the model is not
      identified.
  2: In lav_object_post_check(object) :
    lavaan WARNING: some estimated lv variances are negative
```

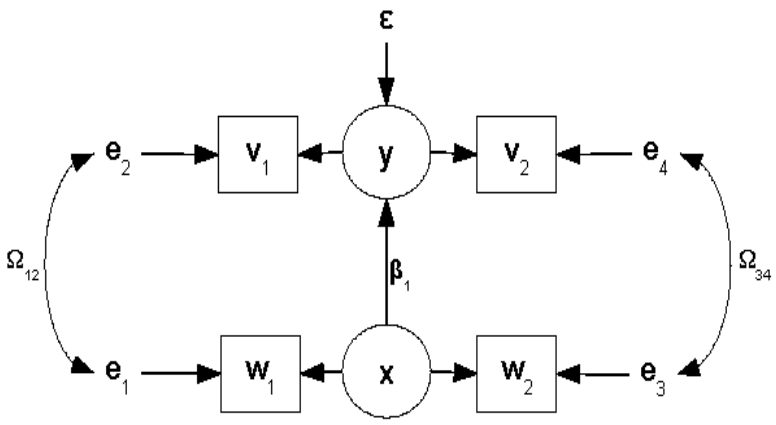
```
> summary(fit1)
lavaan 0.6-11 ended normally after 4241 iterations

  Estimator                                         ML
  Optimization method                           NLMINB
  Number of model parameters                        45

  Number of observations                           500

Model Test User Model:

  Test statistic                                89.369
  Degrees of freedom                                10
  P-value (Chi-square)                           0.000

Parameter Estimates:

  Standard errors                             Standard
  Information                                 Expected
  Information saturated (h1) model          Structured

Latent Variables:
                   Estimate   Std.Err  z-value  P(>|z|)
  Lage =~
    age1              1.000
    age2              1.000
  Lbmi =~
    bmi1              1.000
    bmi2              1.000
  Lfat =~
    fat1              1.000
    fat2              1.000
  Lcholest =~
    cholest1          1.000
    cholest2          1.000
  Ldiastol =~
    diastol1          1.000
    diastol2          1.000

Regressions:
                   Estimate   Std.Err  z-value  P(>|z|)
  Lcholest ~
    Lage    (bt11)   -26.391       NA
    Lbmi    (bt12)  -354.932       NA
    Lfat    (bt13)   203.432       NA
  Ldiastol ~
    Lage    (bt21)   -28.583       NA
    Lbmi    (bt22)  -390.464       NA
    Lfat    (bt23)   221.685       NA

Covariances:
                   Estimate   Std.Err  z-value  P(>|z|)
  Lage ~~
    Lbmi    (ph12)     3.288       NA
    Lfat    (ph13)    24.865       NA
  Lbmi ~~
    Lfat    (ph23)    22.225       NA
 .Lcholest ~~
   .Ldiastl (ps12) -2633.270       NA
 .age1 ~~
   .bmi1    (w112)     4.361       NA
   .fat1    (w113)     0.994       NA
   .cholst1 (w114)     3.102       NA
   .diastl1 (w115)    12.808       NA
```

```
 .bmi1 ~~
   .fat1    (w123)     7.385       NA
   .cholst1 (w124)    -0.497       NA
   .diastl1 (w125)    12.340       NA
 .fat1 ~~
   .cholst1 (w134)     7.835       NA
   .diastl1 (w135)    -6.960       NA
 .cholest1 ~~
   .diastl1 (w145)     0.038       NA
 .age2 ~~
   .bmi2    (w212)     0.752       NA
   .fat2    (w213)    -4.120       NA
   .cholst2 (w214)    -2.601       NA
   .diastl2 (w215)     5.903       NA
 .bmi2 ~~
   .fat2    (w223)    -3.043       NA
   .cholst2 (w224)    -3.469       NA
   .diastl2 (w225)     6.602       NA
 .fat2 ~~
   .cholst2 (w234)   -10.098       NA
   .diastl2 (w235)    -9.933       NA
 .cholest2 ~~
   .diastl2 (w245)   -10.026       NA

Variances:
                   Estimate   Std.Err  z-value  P(>|z|)
    Lage    (ph11)   146.720       NA
    Lbmi    (ph22)    12.318       NA
    Lfat    (ph33)    42.615       NA
   .Lcholst (ps11)   169.820       NA
   .Ldiastl (ps22) -2785.532       NA
   .age1    (w111)    18.767       NA
   .bmi1    (w122)     9.177       NA
   .fat1    (w133)    18.669       NA
   .cholst1 (w144)   200.123       NA
   .diastl1 (w155)   204.316       NA
   .age2    (w211)     8.326       NA
   .bmi2    (w222)     2.460       NA
   .fat2    (w233)     9.975       NA
   .cholst2 (w244)   344.031       NA
   .diastl2 (w255)    59.441       NA
```

```
> p1 = parTable(fit1); p1
   id      lhs op      rhs user block group free ustart exo  label plabel    start       est se
1   1 Lcholest  ~     Lage    1     1     1    1     NA   0 beta11   .p1.    0.000   -26.391 NA
2   2 Lcholest  ~     Lbmi    1     1     1    2     NA   0 beta12   .p2.    0.000  -354.932 NA
3   3 Lcholest  ~     Lfat    1     1     1    3     NA   0 beta13   .p3.    0.000   203.432 NA
4   4 Ldiastol  ~     Lage    1     1     1    4     NA   0 beta21   .p4.    0.000   -28.583 NA
5   5 Ldiastol  ~     Lbmi    1     1     1    5     NA   0 beta22   .p5.    0.000  -390.464 NA
6   6 Ldiastol  ~     Lfat    1     1     1    6     NA   0 beta23   .p6.    0.000   221.685 NA
7   7     Lage =~     age1    1     1     1    0      1   0          .p7.    1.000     1.000  0
8   8     Lage =~     age2    1     1     1    0      1   0          .p8.    1.000     1.000  0
9   9     Lbmi =~     bmi1    1     1     1    0      1   0          .p9.    1.000     1.000  0
10 10     Lbmi =~     bmi2    1     1     1    0      1   0         .p10.    1.000     1.000  0
11 11     Lfat =~     fat1    1     1     1    0      1   0         .p11.    1.000     1.000  0
12 12     Lfat =~     fat2    1     1     1    0      1   0         .p12.    1.000     1.000  0
13 13 Lcholest =~ cholest1    1     1     1    0      1   0         .p13.    1.000     1.000  0
14 14 Lcholest =~ cholest2    1     1     1    0      1   0         .p14.    1.000     1.000  0
15 15 Ldiastol =~ diastol1    1     1     1    0      1   0         .p15.    1.000     1.000  0
16 16 Ldiastol =~ diastol2    1     1     1    0      1   0         .p16.    1.000     1.000  0
17 17     Lage ~~     Lage    1     1     1    7     NA   0  phi11  .p17.    0.050   146.720 NA
18 18     Lage ~~     Lbmi    1     1     1    8     NA   0  phi12  .p18.    0.000     3.288 NA
19 19     Lage ~~     Lfat    1     1     1    9     NA   0  phi13  .p19.    0.000    24.865 NA
20 20     Lbmi ~~     Lbmi    1     1     1   10     NA   0  phi22  .p20.    0.050    12.318 NA
21 21     Lbmi ~~     Lfat    1     1     1   11     NA   0  phi23  .p21.    0.000    22.225 NA
```

```
22 22     Lfat ~~     Lfat    1     1     1   12     NA   0  phi33  .p22.     0.050    42.615 NA
23 23 Lcholest ~~ Lcholest    1     1     1   13     NA   0  psi11  .p23.     0.050   169.820 NA
24 24 Lcholest ~~ Ldiastol    1     1     1   14     NA   0  psi12  .p24.     0.000 -2633.270 NA
25 25 Ldiastol ~~ Ldiastol    1     1     1   15     NA   0  psi22  .p25.     0.050 -2785.532 NA
26 26     age1 ~~     age1    1     1     1   16     NA   0   w111  .p26.    83.763    18.767 NA
27 27     age1 ~~     bmi1    1     1     1   17     NA   0   w112  .p27.     0.000     4.361 NA
28 28     age1 ~~     fat1    1     1     1   18     NA   0   w113  .p28.     0.000     0.994 NA
29 29     age1 ~~ cholest1    1     1     1   19     NA   0   w114  .p29.     0.000     3.102 NA
30 30     age1 ~~ diastol1    1     1     1   20     NA   0   w115  .p30.     0.000    12.808 NA
31 31     bmi1 ~~     bmi1    1     1     1   21     NA   0   w122  .p31.    10.925     9.177 NA
32 32     bmi1 ~~     fat1    1     1     1   22     NA   0   w123  .p32.     0.000     7.385 NA
33 33     bmi1 ~~ cholest1    1     1     1   23     NA   0   w124  .p33.     0.000    -0.497 NA
34 34     bmi1 ~~ diastol1    1     1     1   24     NA   0   w125  .p34.     0.000    12.340 NA
35 35     fat1 ~~     fat1    1     1     1   25     NA   0   w133  .p35.    30.023    18.669 NA
36 36     fat1 ~~ cholest1    1     1     1   26     NA   0   w134  .p36.     0.000     7.835 NA
37 37     fat1 ~~ diastol1    1     1     1   27     NA   0   w135  .p37.     0.000    -6.960 NA
38 38 cholest1 ~~ cholest1    1     1     1   28     NA   0   w144  .p38.  1548.559   200.123 NA
39 39 cholest1 ~~ diastol1    1     1     1   29     NA   0   w145  .p39.     0.000     0.038 NA
40 40 diastol1 ~~ diastol1    1     1     1   30     NA   0   w155  .p40.   162.507   204.316 NA
41 41     age2 ~~     age2    1     1     1   31     NA   0   w211  .p41.    76.888     8.326 NA
42 42     age2 ~~     bmi2    1     1     1   32     NA   0   w212  .p42.     0.000     0.752 NA
43 43     age2 ~~     fat2    1     1     1   33     NA   0   w213  .p43.     0.000    -4.120 NA
44 44     age2 ~~ cholest2    1     1     1   34     NA   0   w214  .p44.     0.000    -2.601 NA
45 45     age2 ~~ diastol2    1     1     1   35     NA   0   w215  .p45.     0.000     5.903 NA
46 46     bmi2 ~~     bmi2    1     1     1   36     NA   0   w222  .p46.     7.156     2.460 NA
47 47     bmi2 ~~     fat2    1     1     1   37     NA   0   w223  .p47.     0.000    -3.043 NA
48 48     bmi2 ~~ cholest2    1     1     1   38     NA   0   w224  .p48.     0.000    -3.469 NA
49 49     bmi2 ~~ diastol2    1     1     1   39     NA   0   w225  .p49.     0.000     6.602 NA
50 50     fat2 ~~     fat2    1     1     1   40     NA   0   w233  .p50.    27.528     9.975 NA
51 51     fat2 ~~ cholest2    1     1     1   41     NA   0   w234  .p51.     0.000   -10.098 NA
52 52     fat2 ~~ diastol2    1     1     1   42     NA   0   w235  .p52.     0.000    -9.933 NA
53 53 cholest2 ~~ cholest2    1     1     1   43     NA   0   w244  .p53.  1608.286   344.031 NA
54 54 cholest2 ~~ diastol2    1     1     1   44     NA   0   w245  .p54.     0.000   -10.026 NA
55 55 diastol2 ~~ diastol2    1     1     1   45     NA   0   w255  .p55.    88.049    59.441 NA

> fit1B = lavaan(bmimodel1, data=bmidata, start = 'Mplus')
Warning messages:
1: In lav_model_vcov(lavmodel = lavmodel, lavsamplestats = lavsamplestats,  :
  lavaan WARNING:
    Could not compute standard errors! The information matrix could
    not be inverted. This may be a symptom that the model is not
    identified.
2: In lav_object_post_check(object) :
  lavaan WARNING: some estimated lv variances are negative
> # Same warnings, 4241 iterations again
```

Try starting at Method of Moments estimates



$$\boldsymbol{\Sigma} = cov\begin{pmatrix} \mathbf{w}_{i,1} \\ \mathbf{v}_{i,1} \\ \mathbf{w}_{i,2} \\ \mathbf{v}_{i,2} \end{pmatrix}$$

$$= \left(\begin{array}{c|c|c|c} \Sigma_{11} & \Sigma_{12} & \Sigma_{13} & \Sigma_{14} \\ \hline & \Sigma_{22} & \Sigma_{23} & \Sigma_{24} \\ \hline & & \Sigma_{33} & \Sigma_{34} \\ \hline & & & \Sigma_{44} \end{array}\right)$$

$$= \left(\begin{array}{c|c|c|c} \Phi + \Omega_{11} & \Phi\beta^\top + \Omega_{12} & \Phi & \Phi\beta^\top \\ \hline & \beta\Phi\beta^\top + \Psi + \Omega_{22} & \beta\Phi & \beta\Phi\beta^\top + \Psi \\ \hline & & \Phi + \Omega_{33} & \Phi\beta^\top + \Omega_{34} \\ \hline & & & \beta\Phi\beta^\top + \Psi + \Omega_{44} \end{array}\right)$$

```
> # Start at Method of Moment estimates.
>
> head(bmidata)
  age1 bmi1 fat1 cholest1 diastol1 age2 bmi2 fat2 cholest2 diastol2
1   63 24.5 16.5    195.4       38   60 23.9 20.1    203.5       66
2   42 13.0  1.9    184.3       86   44 14.8  2.6    197.3       78
3   32 22.5 14.6    354.1      104   33 21.7 20.4    374.3       73
4   59 25.5 19.0    214.6       93   58 28.5 20.0    203.7      106
5   45 26.5 17.8    324.8       97   43 25.0 12.3    329.7       92
6   31 19.4 17.1    280.7       92   42 19.9 19.9    276.7       87
> W1 = as.matrix(bmidata[,1:3])  # age1 bmi1 fat1
> V1 = as.matrix(bmidata[,4:5])  # cholest1 diastol1
> W2 = as.matrix(bmidata[,6:8])  # age2 bmi2 fat2
> V2 = as.matrix(bmidata[,9:10]) # cholest2 diastol2
> var(W1,W2) # Matrix of sample covariances
           age2      bmi2     fat2
age1 148.220782  3.621581 25.29808
bmi1   5.035726 13.194016 21.42201
fat1  23.542289 20.613490 45.13296
> # Using S as short for Sigmahat, and not worrying about n vs. n-1,
> S11 = var(W1); S12 = var(W1,V1); S13 = var(W1,W2); S14 = var(W1,V2)
>                S22 = var(V1);    S23 = var(V1,W2); S24 = var(V1,V2)
>                                  S33 = var(W2);    S34 = var(W2,V2)
>                                                    S44 = var(V2)
> # The matrices below should all have "hat" in the name, because they are estimates
> Phi = (S13+t(S13))/2
> rownames(Phi) = colnames(Phi) = c('Lage','Lbmi','Lfat'); Phi
           Lage      Lbmi     Lfat
Lage 148.220782  4.328654 24.42019
Lbmi   4.328654 13.194016 21.01775
Lfat  24.420185 21.017749 45.13296
> # To my surprise, these are quite close to the MLEs from the first run.
> Beta = 0.5*(t(S14)+S23) %*% solve(Phi)
> rownames(Beta) = c('Lcholest','Ldiastol')
> colnames(Beta) = c('Lage','Lbmi','Lfat'); Beta
               Lage       Lbmi     Lfat
Lcholest -0.3851327 -0.1885072 2.968322
Ldiastol  0.0224190 -0.3556138 1.407425
> # These are miles away from the supposed MLEs
> # Can just say some of the rest are close and others are not.
>
> Psi = S24 - Beta %*% Phi %*% t(Beta)
> rownames(Psi) = colnames(Psi) = c('Lcholest','Ldiastol') # epsilon1, epsilon2
> Psi
           Lcholest  Ldiastol
Lcholest 2548.17303 -44.56069
Ldiastol  -28.70087  57.64153
> # Oops, it should be symmetric.
> Psi = ( Psi+t(Psi) )/2; Psi
           Lcholest  Ldiastol
Lcholest 2548.17303 -36.63078
Ldiastol  -36.63078  57.64153
> # Again, far away.
> Omega11 = S11 - Phi; Omega11
          age1     bmi1      fat1
age1 19.640040 4.610807  1.634183
bmi1  4.610807 8.699533  8.754484
fat1  1.634183 8.754484 15.033932
> # Supposed MLEs are pretty close here.
> Omega12 = S12 - ( S14+t(S23) )/2; Omega12 # Not too bad
      cholest1  diastol1
age1  4.499017 12.164192
bmi1 -1.517733 10.671443
fat1  3.888565 -2.196681
```

```
> Omega22 = S22-S24 # A little rough but consistent
> Omega22 = (Omega22 + t(Omega22)  )/2
> Omega22 # Variances okay, covariance off.
          cholest1  diastol1
cholest1 213.76117  11.24971
diastol1  11.24971 196.44520
> Omega33 = S33 - Phi; Omega33 # Not too bad
          age2      bmi2      fat2
age2  5.862661 -1.219843 -2.155736
bmi2 -1.219843  1.146991 -1.714769
fat2 -2.155736 -1.714769 10.033984
> Omega34 = S34 - ( S14+t(S23) )/2; Omega34 # Not too bad
      cholest2   diastol2
age2 -2.978041  0.7795992
bmi2 -1.206256  2.1081739
fat2 -6.422983 -4.9125882
> Omega44 = S44 - S24 ; Omega44 = ( Omega44 + t(Omega44) )/2
> Omega44 # Not terrible
          cholest2  diastol2
cholest2 333.45335 -21.65923
diastol2 -21.65923  47.23065
>
> # Carefully assemble the MOM estimates into a vector, same order as p1 = parTable(fit1)
>
> mom = c(Beta[1,1], Beta[1,2], Beta[1,3], Beta[2,1], Beta[2,2], Beta[2,3],
+         1,1,1,1,1,1,1,1,1,1,
+         Phi[1,1], Phi[1,2], Phi[1,3], Phi[2,2], Phi[2,3], Phi[3,3],
+         Psi[1,1], Psi[1,2], Psi[2,2],
+         Omega11[1,1], Omega11[1,2], Omega11[1,3], Omega12[1,1], Omega12[1,2],
+         Omega11[2,2], Omega11[2,3], Omega12[2,1], Omega12[2,2],
+         Omega11[3,3], Omega12[3,1], Omega12[3,2],
+         Omega22[1,1], Omega22[1,2], Omega22[2,2],
+         Omega33[1,1], Omega33[1,2], Omega33[1,3], Omega34[1,1], Omega34[1,2],
+         Omega33[2,2], Omega33[2,3], Omega34[2,1], Omega34[2,2],
+         Omega33[3,3], Omega34[3,1], Omega34[3,2],
+         Omega44[1,1], Omega44[1,2], Omega44[2,2]      )
> length(mom)
[1] 55
>
> p1mom = p1; p1mom[,14] = mom # Replace column 14 (est) with mom

> fit2 = lavaan(bmimodel1, data=bmidata, start = p1mom); fit2
lavaan 0.6-11 ended normally after 242 iterations

  Estimator                                         ML
  Optimization method                           NLMINB
  Number of model parameters                        45

  Number of observations                           500

Model Test User Model:

  Test statistic                                 4.654
  Degrees of freedom                                10
  P-value (Chi-square)                           0.913
```

```
> summary(fit2)
lavaan 0.6-11 ended normally after 242 iterations

  Estimator                                         ML
  Optimization method                           NLMINB
  Number of model parameters                        45

  Number of observations                           500

Model Test User Model:

  Test statistic                                 4.654
  Degrees of freedom                                10
  P-value (Chi-square)                           0.913

Parameter Estimates:

  Standard errors                             Standard
  Information                                 Expected
  Information saturated (h1) model          Structured

Latent Variables:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lage =~
    age1              1.000
    age2              1.000
  Lbmi =~
    bmi1              1.000
    bmi2              1.000
  Lfat =~
    fat1              1.000
    fat2              1.000
  Lcholest =~
    cholest1          1.000
    cholest2          1.000
  Ldiastol =~
    diastol1          1.000
    diastol2          1.000

Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lcholest ~
    Lage     (bt11)  -0.320    0.228   -1.404    0.160
    Lbmi     (bt12)   0.393    1.708    0.230    0.818
    Lfat     (bt13)   2.774    0.980    2.829    0.005
  Ldiastol ~
    Lage     (bt21)   0.020    0.050    0.407    0.684
    Lbmi     (bt22)  -0.480    0.419   -1.145    0.252
    Lfat     (bt23)   1.480    0.235    6.312    0.000

Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lage ~~
    Lbmi     (ph12)   4.160    2.141    1.944    0.052
    Lfat     (ph13)  23.320    3.986    5.851    0.000
  Lbmi ~~
    Lfat     (ph23)  20.976    1.584   13.244    0.000
 .Lcholest ~~
   .Ldiastl (ps12)  -45.861   24.968   -1.837    0.066
 .age1 ~~
   .bmi1    (w112)   3.998    0.945    4.231    0.000
   .fat1    (w113)   2.389    1.505    1.587    0.112
   .cholst1 (w114)   2.702    9.091    0.297    0.766
   .diastl1 (w115)  10.562    3.824    2.762    0.006
```

```
 .bmi1 ~~
   .fat1     (w123)    8.969    0.956    9.382    0.000
   .cholst1  (w124)   -0.884    4.178   -0.212    0.832
   .diastl1  (w125)   10.060    2.274    4.424    0.000
 .fat1 ~~
   .cholst1  (w134)    7.923    6.741    1.175    0.240
   .diastl1  (w135)   -2.927    3.409   -0.859    0.390
 .cholest1 ~~
   .diastl1  (w145)   -0.098   16.907   -0.006    0.995
 .age2 ~~
   .bmi2     (w212)   -0.661    0.735   -0.899    0.369
   .fat2     (w213)   -2.703    1.369   -1.974    0.048
   .cholst2  (w214)   -1.962    8.962   -0.219    0.827
   .diastl2  (w215)    2.273    2.710    0.839    0.402
 .bmi2 ~~
   .fat2     (w223)   -1.849    0.705   -2.624    0.009
   .cholst2  (w224)   -2.653    3.476   -0.763    0.445
   .diastl2  (w225)    2.652    1.487    1.784    0.074
 .fat2 ~~
   .cholst2  (w234)  -11.376    6.546   -1.738    0.082
   .diastl2  (w235)   -4.839    2.536   -1.908    0.056
 .cholest2 ~~
   .diastl2  (w245)   -8.972   12.605   -0.712    0.477

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)
    Lage      (ph11)  147.330    9.699   15.190    0.000
    Lbmi      (ph22)   13.341    0.986   13.528    0.000
    Lfat      (ph33)   44.485    3.101   14.345    0.000
   .Lcholst   (ps11) 2534.505  171.258   14.799    0.000
   .Ldiastl   (ps22)   56.169    9.221    6.092    0.000
   .age1      (w111)   18.584    2.914    6.378    0.000
   .bmi1      (w122)    8.665    0.708   12.239    0.000
   .fat1      (w133)   16.125    1.659    9.717    0.000
   .cholst1   (w144)  200.109   57.422    3.485    0.000
   .diastl1   (w155)  195.040   14.323   13.617    0.000
   .age2      (w211)    6.861    2.701    2.540    0.011
   .bmi2      (w222)    1.089    0.491    2.220    0.026
   .fat2      (w233)    9.332    1.539    6.064    0.000
   .cholst2   (w244)  344.449   60.290    5.713    0.000
   .diastl2   (w255)   48.349    8.246    5.864    0.000

>
> parTable(fit2)

   id      lhs op      rhs user block group free ustart exo  label plabel    start      est
1   1 Lcholest  ~     Lage    1     1     1    1     NA   0 beta11   .p1.   -0.385   -0.320
2   2 Lcholest  ~     Lbmi    1     1     1    2     NA   0 beta12   .p2.   -0.189    0.393
3   3 Lcholest  ~     Lfat    1     1     1    3     NA   0 beta13   .p3.    2.968    2.774
4   4 Ldiastol  ~     Lage    1     1     1    4     NA   0 beta21   .p4.    0.022    0.020
5   5 Ldiastol  ~     Lbmi    1     1     1    5     NA   0 beta22   .p5.   -0.356   -0.480
6   6 Ldiastol  ~     Lfat    1     1     1    6     NA   0 beta23   .p6.    1.407    1.480
7   7     Lage =~     age1    1     1     1    0      1   0          .p7.    1.000    1.000
8   8     Lage =~     age2    1     1     1    0      1   0          .p8.    1.000    1.000
9   9     Lbmi =~     bmi1    1     1     1    0      1   0          .p9.    1.000    1.000
10 10     Lbmi =~     bmi2    1     1     1    0      1   0         .p10.    1.000    1.000
11 11     Lfat =~     fat1    1     1     1    0      1   0         .p11.    1.000    1.000
12 12     Lfat =~     fat2    1     1     1    0      1   0         .p12.    1.000    1.000
13 13 Lcholest =~ cholest1    1     1     1    0      1   0         .p13.    1.000    1.000
14 14 Lcholest =~ cholest2    1     1     1    0      1   0         .p14.    1.000    1.000
15 15 Ldiastol =~ diastol1    1     1     1    0      1   0         .p15.    1.000    1.000
16 16 Ldiastol =~ diastol2    1     1     1    0      1   0         .p16.    1.000    1.000
17 17     Lage ~~     Lage    1     1     1    7     NA   0  phi11  .p17.  148.221  147.330
18 18     Lage ~~     Lbmi    1     1     1    8     NA   0  phi12  .p18.    4.329    4.160
19 19     Lage ~~     Lfat    1     1     1    9     NA   0  phi13  .p19.   24.420   23.320
20 20     Lbmi ~~     Lbmi    1     1     1   10     NA   0  phi22  .p20.   13.194   13.341
21 21     Lbmi ~~     Lfat    1     1     1   11     NA   0  phi23  .p21.   21.018   20.976
```

```
22 22     Lfat ~~     Lfat    1     1     1   12     NA   0  phi33  .p22.   45.133   44.485
23 23 Lcholest ~~ Lcholest    1     1     1   13     NA   0  psi11  .p23. 2548.173 2534.505
24 24 Lcholest ~~ Ldiastol    1     1     1   14     NA   0  psi12  .p24.  -36.631  -45.861
25 25 Ldiastol ~~ Ldiastol    1     1     1   15     NA   0  psi22  .p25.   57.642   56.169
26 26     age1 ~~     age1    1     1     1   16     NA   0   w111  .p26.   19.640   18.584
27 27     age1 ~~     bmi1    1     1     1   17     NA   0   w112  .p27.    4.611    3.998
28 28     age1 ~~     fat1    1     1     1   18     NA   0   w113  .p28.    1.634    2.389
29 29     age1 ~~ cholest1    1     1     1   19     NA   0   w114  .p29.    4.499    2.702
30 30     age1 ~~ diastol1    1     1     1   20     NA   0   w115  .p30.   12.164   10.562
31 31     bmi1 ~~     bmi1    1     1     1   21     NA   0   w122  .p31.    8.700    8.665
32 32     bmi1 ~~     fat1    1     1     1   22     NA   0   w123  .p32.    8.754    8.969
33 33     bmi1 ~~ cholest1    1     1     1   23     NA   0   w124  .p33.   -1.518   -0.884
34 34     bmi1 ~~ diastol1    1     1     1   24     NA   0   w125  .p34.   10.671   10.060
35 35     fat1 ~~     fat1    1     1     1   25     NA   0   w133  .p35.   15.034   16.125
36 36     fat1 ~~ cholest1    1     1     1   26     NA   0   w134  .p36.    3.889    7.923
37 37     fat1 ~~ diastol1    1     1     1   27     NA   0   w135  .p37.   -2.197   -2.927
38 38 cholest1 ~~ cholest1    1     1     1   28     NA   0   w144  .p38.  213.761  200.109
39 39 cholest1 ~~ diastol1    1     1     1   29     NA   0   w145  .p39.   11.250   -0.098
40 40 diastol1 ~~ diastol1    1     1     1   30     NA   0   w155  .p40.  196.445  195.040
41 41     age2 ~~     age2    1     1     1   31     NA   0   w211  .p41.    5.863    6.861
42 42     age2 ~~     bmi2    1     1     1   32     NA   0   w212  .p42.   -1.220   -0.661
43 43     age2 ~~     fat2    1     1     1   33     NA   0   w213  .p43.   -2.156   -2.703
44 44     age2 ~~ cholest2    1     1     1   34     NA   0   w214  .p44.   -2.978   -1.962
45 45     age2 ~~ diastol2    1     1     1   35     NA   0   w215  .p45.    0.780    2.273
46 46     bmi2 ~~     bmi2    1     1     1   36     NA   0   w222  .p46.    1.147    1.089
47 47     bmi2 ~~     fat2    1     1     1   37     NA   0   w223  .p47.   -1.715   -1.849
48 48     bmi2 ~~ cholest2    1     1     1   38     NA   0   w224  .p48.   -1.206   -2.653
49 49     bmi2 ~~ diastol2    1     1     1   39     NA   0   w225  .p49.    2.108    2.652
50 50     fat2 ~~     fat2    1     1     1   40     NA   0   w233  .p50.   10.034    9.332
51 51     fat2 ~~ cholest2    1     1     1   41     NA   0   w234  .p51.   -6.423  -11.376
52 52     fat2 ~~ diastol2    1     1     1   42     NA   0   w235  .p52.   -4.913   -4.839
53 53 cholest2 ~~ cholest2    1     1     1   43     NA   0   w244  .p53.  333.453  344.449
54 54 cholest2 ~~ diastol2    1     1     1   44     NA   0   w245  .p54.  -21.659   -8.972
55 55 diastol2 ~~ diastol2    1     1     1   45     NA   0   w255  .p55.   47.231   48.349
```

```
> # Now a LR test of BMI, H0: beta12 = beta22 = 0
> # Will the constraint conflict with the starting values?
>
> nobmi = lavaan(bmimodel1, data=bmidata, start = p1mom,
+             constraints = 'beta12 == 0
+                            beta22 == 0')
>
> anova(nobmi,fit2)
Chi-Squared Difference Test

      Df   AIC   BIC  Chisq Chisq diff Df diff Pr(>Chisq)
fit2  10 35758 35947 4.6537
nobmi 12 35755 35936 6.1457      1.492       2     0.4743
```

```
> # Two follow-up issues
>     # Shorter syntax
>     # Bootstrap
```

```
> cat(bmimodel1)
#########################################################
    # Latent variable model
    # ---------------------
    Lcholest ~ beta11*Lage + beta12*Lbmi + beta13*Lfat
    Ldiastol ~ beta21*Lage + beta22*Lbmi + beta23*Lfat
    #
    # Measurement model
    # -----------------
    Lage =~ 1*age1 + 1*age2
    Lbmi =~ 1*bmi1 + 1*bmi2
    Lfat =~ 1*fat1 +1*fat2
    Lcholest =~ 1*cholest1 + 1*cholest2
    Ldiastol =~ 1*diastol1 + 1*diastol2
    #
    # Variances and covariances
    # -------------------------
    # Of latent explanatory variables
    Lage ~~ phi11*Lage; Lage ~~ phi12*Lbmi; Lage ~~ phi13*Lfat
                        Lbmi ~~ phi22*Lbmi; Lbmi ~~ phi23*Lfat
                                            Lfat ~~ phi33*Lfat
    # Of error terms in latent the regression (epsilon_ij)
    Lcholest ~~ psi11*Lcholest; Lcholest ~~ psi12*Ldiastol
                                Ldiastol ~~ psi22*Ldiastol
    # Of measurement errors (e_ijk) for measurement set 1
    age1 ~~ w111*age1; age1 ~~ w112*bmi1; age1 ~~ w113*fat1;
    age1 ~~ w114*cholest1; age1 ~~ w115*diastol1
            bmi1 ~~ w122*bmi1; bmi1 ~~ w123*fat1; bmi1 ~~ w124*cholest1; bmi1 ~~ w125*diastol1
                    fat1 ~~ w133*fat1; fat1 ~~ w134*cholest1; fat1 ~~ w135*diastol1
                            cholest1 ~~ w144*cholest1; cholest1 ~~ w145*diastol1
                                                       diastol1 ~~ w155*diastol1
    # Of measurement errors (e_ijk) for measurement set 2
    age2 ~~ w211*age2; age2 ~~ w212*bmi2; age2 ~~ w213*fat2;
    age2 ~~ w214*cholest2; age2 ~~ w215*diastol2
            bmi2 ~~ w222*bmi2; bmi2 ~~ w223*fat2; bmi2 ~~ w224*cholest2; bmi2 ~~ w225*diastol2
                    fat2 ~~ w233*fat2; fat2 ~~ w234*cholest2; fat2 ~~ w235*diastol2
                            cholest2 ~~ w244*cholest2; cholest2 ~~ w245*diastol2
                                                       diastol2 ~~ w255*diastol2
> bmimodel2 =
+    '#########################################################
+     # Latent variable model
+     # ---------------------
+     Lcholest ~ beta11*Lage + beta12*Lbmi + beta13*Lfat
+     Ldiastol ~ beta21*Lage + beta22*Lbmi + beta23*Lfat
+     #
+     # Measurement model
+     # -----------------
+     Lage =~ 1*age1 + 1*age2; Lbmi =~ 1*bmi1 + 1*bmi2;  Lfat =~ 1*fat1 +1*fat2
+     Lcholest =~ 1*cholest1 + 1*cholest2; Ldiastol =~ 1*diastol1 + 1*diastol2
+     #
+     # Variances and covariances DO NOT NEED NAMES!
+     # -------------------------
+     # Of latent explanatory variables
+     Lage ~~ Lage +  Lbmi +  Lfat
+             Lbmi ~~ Lbmi +  Lfat
+                     Lfat ~~ Lfat
+     # Of error terms in the latent regression
+     Lcholest ~~ Lcholest +  Ldiastol
+                  Ldiastol ~~ Ldiastol
+     # Of measurement errors for measurement set 1
+     age1 ~~ age1 +  bmi1 +  fat1 + cholest1 + diastol1
+             bmi1 ~~ bmi1 +  fat1 + cholest1 + diastol1
+                     fat1 ~~ fat1 + cholest1 + diastol1
+                             cholest1 ~~ cholest1 + diastol1
+                                         diastol1 ~~ diastol1
+     # Of measurement errors for measurement set 2
+     age2 ~~ age2 +  bmi2 +  fat2 + cholest2 + diastol2
+             bmi2 ~~ bmi2 +  fat2 + cholest2 + diastol2
+                     fat2 ~~ fat2 + cholest2 + diastol2
+                             cholest2 ~~ cholest2 + diastol2
+                                         diastol2 ~~ diastol2
+    ' ################## End of bmimodel2 ##################
```

```
> fit3 = lavaan(bmimodel2, data=bmidata, start = fit2); fit3
lavaan 0.6-11 ended normally after 2 iterations

  Estimator                                         ML
  Optimization method                           NLMINB
  Number of model parameters                        45

  Number of observations                           500

Model Test User Model:

  Test statistic                                 4.654
  Degrees of freedom                                10
  P-value (Chi-square)                           0.913
> summary(fit3)
lavaan 0.6-11 ended normally after 2 iterations

  Estimator                                         ML
  Optimization method                           NLMINB
  Number of model parameters                        45

  Number of observations                           500

Model Test User Model:

  Test statistic                                 4.654
  Degrees of freedom                                10
  P-value (Chi-square)                           0.913

Parameter Estimates:

  Standard errors                             Standard
  Information                                 Expected
  Information saturated (h1) model          Structured

Latent Variables:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lage =~
    age1              1.000
    age2              1.000
  Lbmi =~
    bmi1              1.000
    bmi2              1.000
  Lfat =~
    fat1              1.000
    fat2              1.000
  Lcholest =~
    cholest1          1.000
    cholest2          1.000
  Ldiastol =~
    diastol1          1.000
    diastol2          1.000

Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lcholest ~
    Lage     (bt11)   -0.320    0.228   -1.404    0.160
    Lbmi     (bt12)    0.393    1.708    0.230    0.818
    Lfat     (bt13)    2.774    0.980    2.829    0.005
  Ldiastol ~
    Lage     (bt21)    0.020    0.050    0.407    0.684
    Lbmi     (bt22)   -0.480    0.419   -1.145    0.252
    Lfat     (bt23)    1.480    0.235    6.312    0.000
```

```
Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lage ~~
    Lbmi              4.160    2.141    1.944    0.052
    Lfat             23.320    3.986    5.851    0.000
  Lbmi ~~
    Lfat             20.976    1.584   13.244    0.000
 .Lcholest ~~
   .Ldiastol        -45.861   24.968   -1.837    0.066
 .age1 ~~
   .bmi1              3.998    0.945    4.231    0.000
   .fat1              2.389    1.505    1.587    0.112
   .cholest1          2.702    9.091    0.297    0.766
   .diastol1         10.562    3.824    2.762    0.006
 .bmi1 ~~
   .fat1              8.969    0.956    9.382    0.000
   .cholest1         -0.884    4.178   -0.212    0.832
   .diastol1         10.060    2.274    4.424    0.000
 .fat1 ~~
   .cholest1          7.923    6.741    1.175    0.240
   .diastol1         -2.927    3.409   -0.859    0.390
 .cholest1 ~~
   .diastol1         -0.098   16.907   -0.006    0.995
 .age2 ~~
   .bmi2             -0.661    0.735   -0.899    0.369
   .fat2             -2.703    1.369   -1.974    0.048
   .cholest2         -1.962    8.962   -0.219    0.827
   .diastol2          2.273    2.710    0.839    0.402
 .bmi2 ~~
   .fat2             -1.849    0.705   -2.624    0.009
   .cholest2         -2.653    3.476   -0.763    0.445
   .diastol2          2.652    1.487    1.784    0.074
 .fat2 ~~
   .cholest2        -11.376    6.546   -1.738    0.082
   .diastol2         -4.839    2.536   -1.908    0.056
 .cholest2 ~~
   .diastol2         -8.972   12.605   -0.712    0.477

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)
    Lage            147.330    9.699   15.190    0.000
    Lbmi             13.341    0.986   13.528    0.000
    Lfat             44.485    3.101   14.345    0.000
   .Lcholest       2534.505  171.258   14.799    0.000
   .Ldiastol         56.169    9.221    6.092    0.000
   .age1             18.584    2.914    6.378    0.000
   .bmi1              8.665    0.708   12.239    0.000
   .fat1             16.125    1.659    9.717    0.000
   .cholest1        200.109   57.422    3.485    0.000
   .diastol1        195.040   14.323   13.617    0.000
   .age2              6.861    2.701    2.540    0.011
   .bmi2              1.089    0.491    2.220    0.026
   .fat2              9.332    1.539    6.064    0.000
   .cholest2        344.449   60.290    5.713    0.000
   .diastol2         48.349    8.246    5.864    0.000
```

```
> # Even shorter syntax: Do we really need the beta symbols?
>
> bmimodel3 =
+     '#### Regressions ####
+      Lcholest ~ Lage + Lbmi + Lfat
+      Ldiastol ~ Lage + Lbmi + Lfat
+      #### Measurement model ####
+      Lage =~ 1*age1 + 1*age2; Lbmi =~ 1*bmi1 + 1*bmi2;  Lfat =~ 1*fat1 +1*fat2
+      Lcholest =~ 1*cholest1 + 1*cholest2; Ldiastol =~ 1*diastol1 + 1*diastol2
+      #### Variances and covariances ####
+      Lage ~~ Lage +  Lbmi +  Lfat
+              Lbmi ~~ Lbmi +  Lfat
+                      Lfat ~~ Lfat
+      Lcholest ~~ Lcholest +  Ldiastol
+                  Ldiastol ~~ Ldiastol
+      age1 ~~ age1 +  bmi1 +  fat1 + cholest1 + diastol1
+              bmi1 ~~ bmi1 +  fat1 + cholest1 + diastol1
+                      fat1 ~~ fat1 + cholest1 + diastol1
+                              cholest1 ~~ cholest1 + diastol1
+                                          diastol1 ~~ diastol1
+      age2 ~~ age2 +  bmi2 +  fat2 + cholest2 + diastol2
+              bmi2 ~~ bmi2 +  fat2 + cholest2 + diastol2
+                      fat2 ~~ fat2 + cholest2 + diastol2
+                              cholest2 ~~ cholest2 + diastol2
+                                          diastol2 ~~ diastol2
+     ' ################## End of bmimodel3 ##################
>
> fit4 = lavaan(bmimodel3, data=bmidata, start = fit2); fit4
lavaan 0.6-11 ended normally after 2 iterations

  Estimator                                         ML
  Optimization method                           NLMINB
  Number of model parameters                        45

  Number of observations                           500

Model Test User Model:

  Test statistic                                 4.654
  Degrees of freedom                                10
  P-value (Chi-square)                           0.913
>
> summary(fit4)
```

Some output omitted.

```
Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lcholest ~
    Lage             -0.320    0.228   -1.404    0.160
    Lbmi              0.393    1.708    0.230    0.818
    Lfat              2.774    0.980    2.829    0.005
  Ldiastol ~
    Lage              0.020    0.050    0.407    0.684
    Lbmi             -0.480    0.419   -1.145    0.252
    Lfat              1.480    0.235    6.312    0.000
```

More output omitted.

```
> # Bootstrap
> fit3B = lavaan(bmimodel2, data=bmidata, start = fit2, se = "bootstrap")
> # Waited between 2 and 3 minutes
> summary(fit3B)
lavaan 0.6-11 ended normally after 2 iterations

  Estimator                                         ML
  Optimization method                           NLMINB
  Number of model parameters                        45

  Number of observations                           500

Model Test User Model:

  Test statistic                                 4.654
  Degrees of freedom                                10
  P-value (Chi-square)                           0.913

Parameter Estimates:

  Standard errors                            Bootstrap
  Number of requested bootstrap draws             1000
  Number of successful bootstrap draws            1000

Latent Variables:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lage =~
    age1              1.000
    age2              1.000
  Lbmi =~
    bmi1              1.000
    bmi2              1.000
  Lfat =~
    fat1              1.000
    fat2              1.000
  Lcholest =~
    cholest1          1.000
    cholest2          1.000
  Ldiastol =~
    diastol1          1.000
    diastol2          1.000

Regressions:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lcholest ~
    Lage    (bt11)   -0.320    0.232   -1.381    0.167
    Lbmi    (bt12)    0.393    1.732    0.227    0.820
    Lfat    (bt13)    2.774    1.026    2.705    0.007
  Ldiastol ~
    Lage    (bt21)    0.020    0.053    0.383    0.702
    Lbmi    (bt22)   -0.480    0.456   -1.051    0.293
    Lfat    (bt23)    1.480    0.257    5.754    0.000

Covariances:
                   Estimate  Std.Err  z-value  P(>|z|)
  Lage ~~
    Lbmi              4.160    2.027    2.053    0.040
    Lfat             23.320    3.918    5.952    0.000
  Lbmi ~~
    Lfat             20.976    1.687   12.435    0.000
 .Lcholest ~~
   .Ldiastol        -45.861   26.501   -1.731    0.084
 .age1 ~~
   .bmi1              3.998    0.924    4.328    0.000
   .fat1              2.389    1.438    1.661    0.097
```

```
   .cholest1          2.702    9.090    0.297    0.766
   .diastol1         10.562    3.997    2.643    0.008
 .bmi1 ~~
   .fat1              8.969    0.883   10.154    0.000
   .cholest1         -0.884    4.057   -0.218    0.828
   .diastol1         10.060    2.068    4.865    0.000
 .fat1 ~~
   .cholest1          7.923    6.450    1.228    0.219
   .diastol1         -2.927    3.298   -0.888    0.375
 .cholest1 ~~
   .diastol1         -0.098   17.721   -0.006    0.996
 .age2 ~~
   .bmi2             -0.661    0.723   -0.913    0.361
   .fat2             -2.703    1.295   -2.088    0.037
   .cholest2         -1.962    8.650   -0.227    0.821
   .diastol2          2.273    2.873    0.791    0.429
 .bmi2 ~~
   .fat2             -1.849    0.656   -2.819    0.005
   .cholest2         -2.653    3.537   -0.750    0.453
   .diastol2          2.652    1.353    1.961    0.050
 .fat2 ~~
   .cholest2        -11.376    6.829   -1.666    0.096
   .diastol2         -4.839    2.410   -2.008    0.045
 .cholest2 ~~
   .diastol2         -8.972   12.716   -0.706    0.480

Variances:
                   Estimate  Std.Err  z-value  P(>|z|)
    Lage            147.330    9.419   15.642    0.000
    Lbmi             13.341    0.987   13.518    0.000
    Lfat             44.485    3.411   13.041    0.000
   .Lcholest       2534.505  176.818   14.334    0.000
   .Ldiastol         56.169    9.689    5.797    0.000
   .age1             18.584    2.770    6.708    0.000
   .bmi1              8.665    0.679   12.756    0.000
   .fat1             16.125    1.491   10.815    0.000
   .cholest1        200.109   53.771    3.722    0.000
   .diastol1        195.040   14.805   13.174    0.000
   .age2              6.861    2.833    2.422    0.015
   .bmi2              1.089    0.436    2.498    0.012
   .fat2              9.332    1.373    6.799    0.000
   .cholest2        344.449   59.165    5.822    0.000
   .diastol2         48.349    8.194    5.901    0.000
```

Normal model for comparison

```
Variances:
                   Estimate  Std.Err  z-value  P(>|z|)
    Lage    (ph11)  147.330    9.699   15.190    0.000
    Lbmi    (ph22)   13.341    0.986   13.528    0.000
    Lfat    (ph33)   44.485    3.101   14.345    0.000
   .Lcholst (ps11) 2534.505  171.258   14.799    0.000
   .Ldiastl (ps22)   56.169    9.221    6.092    0.000
   .age1    (w111)   18.584    2.914    6.378    0.000
   .bmi1    (w122)    8.665    0.708   12.239    0.000
   .fat1    (w133)   16.125    1.659    9.717    0.000
   .cholst1 (w144)  200.109   57.422    3.485    0.000
   .diastl1 (w155)  195.040   14.323   13.617    0.000
   .age2    (w211)    6.861    2.701    2.540    0.011
   .bmi2    (w222)    1.089    0.491    2.220    0.026
   .fat2    (w233)    9.332    1.539    6.064    0.000
   .cholst2 (w244)  344.449   60.290    5.713    0.000
   .diastl2 (w255)   48.349    8.246    5.864    0.000
```