Structural equation models with a binary outcome using STATA and Mplus

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Motivation

- Structural equation modelling (SEM) provides a framework for assessing likely causal pathways
- Specific research question: Is Homocysteine (HCY) an independent risk factor for **CAD** or is it merely a marker of increased risk?
- Which software offers most flexibility for SEM analysis with **binary outcomes**?

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Study dataset

- Elderly Chinese population (76±7 years age)
- Case-control data: 460 individuals with (50%) and without (50%) hypertension
- Cross-sectional data: Individuals with (53%) and without (47%) CAD
- 1 binary variable
  - Coronary artery disease (CAD) status
- 9 continuous variables
  - Lipids (LDL, HDL-cholesterol, Triglycerides (TG))
  - Body mass index (BMI)
  - Systolic Blood pressure (SBP)
  - Homocysteine (HCY)
  - Kidney function (Blood urea nitrogen: BUN)
  - Inflammation (C-reactive protein (CRP))
  - Oxidative stress (Uric acid (UA))

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Structural Equation Modelling (SEM)

- Allows estimation of
  - Underlying “latent” factors
  - Multiple regression models
  - Direction of causal pathways
  - Strength of causal pathways
  - Direct and indirect effects
  - Tests of Mediation
- Traditionally used by the Social Sciences
- Gaining acceptance within the Health Sciences

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Research objectives

- **Obtain parameter estimates**
  - Determine the **direct effect** of HCY on CAD
  - Determine **explained variance** (R^2) of each variable
  - Determine the **indirect effects** of HCY on CAD
- **Mediation**
  - Through which variables are the indirect effects mediated?
    - Blood pressure
  - Are there indirect effects of other factors via HCY?
    - Insulin sensitivity
    - Inflammation
    - Oxidative stress
- **Model fit**
  - Does the proposed causal pathway model fit?
  - Is the model the same across genders?

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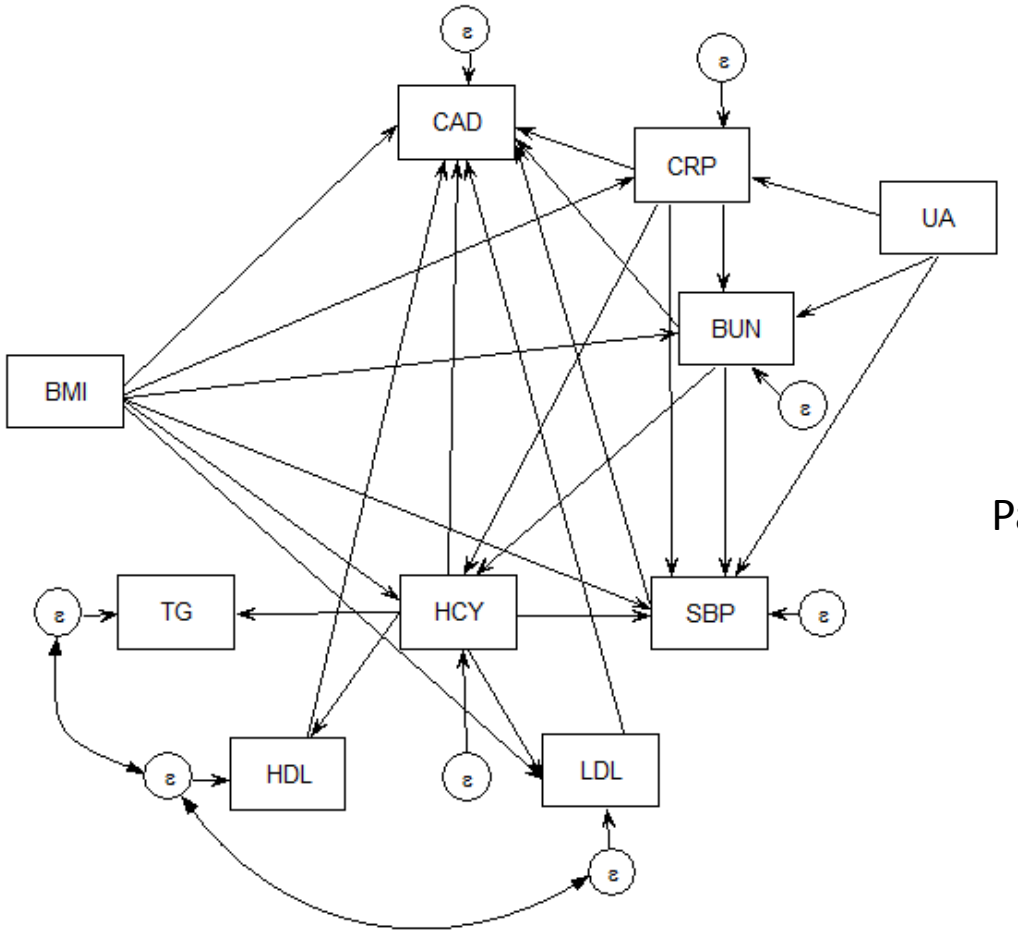
Hypothesised causal pathway for CAD and risk factors



Path diagram for analysis

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Software for SEM

- Software packages
  - STATA
  - Mplus
  - LISREL (Joreskog, 1986)
  - EQS (Bender, 1985)
  - AMOS (SPSS add-on)
  - R (libraries: sem and semPlot)
  - SmartPLS
- Analysis of binary outcomes available in
  - STATA (since version 13; 2013)
  - Mplus (since version 2; 2001)

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SEM estimation with categorical outcomes

- ML estimation requires numerical integration for combination of
  - Categorical outcomes and
    - Continuous latent variables
    - Missing data
- Numerical integration available in
  - STATA
  - Mplus
- Mplus has 2 additional estimation options
  - Weighted least squares (WLS)
  - Bayesian

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Mplus estimation methods with categorical outcomes

- Default method for categorical outcomes is means and variance adjusted weighted least squares
  - (Estimator=WLSMV)
  - Uses probit regression (CDF for CAD treated as a latent variable)
  - Computationally demanding
- ML estimation
  - (Estimator=ML)
  - Rectangular, Gauss-Hermite or Monte Carlo integration
  - With or without adaptive quadrature
- Bayes estimation

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STATA estimation methods with categorical outcomes

- GSEM
  - ML with numerical integration is default for GSEM
  - The **only** estimator option for categorical outcomes
- Integration methods
  - Mean-variance adaptive gauss hermite (mvaghermite) (the default)
  - Mcaghermite (computationally intensive but better convergence)
  - Ghermite
  - Laplace (less accurate but less computationally intensive)
- Technique (for VCE)
  - Observed information matrix (OIM)

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STATA code

```
gsem (CAD <- HCY CRP SBP LDL HDL BUN BMI, family(binomial) link(logit)) ///
     (BUN <- BMI CRP UA) ///
     (CRP <- BMI UA) ///
     (SBP <- BUN HCY BMI UA CRP) ///
     (HCY <- BMI BUN CRP) ///
     (LDL <- BMI HCY) ///
     (TG <- HCY) ///
     (HDL <- HCY) ///
     if sex==0, cov(e.TG*e.HDL e.HDL*e.LDL) nocapslatent ///

     method(ml) ///
     vce(oim) ///
     intmethod(mvaghermite) ///
     iterate(1001)
```

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Mplus code (for ML)

```
VARIABLE:
  Names are
   sex age HCY TG HDL LDL BUN CR UA CRP BS SBP DBP CAD BMI group;
   Missing are all (-9999);
   Usevariables are HCY TG HDL LDL BUN SBP  CAD BMI CRP UA;
   Categorical is CAD;
   Useobservations are sex==0;

ANALYSIS:
estimator=ml;
iter=200000;
Algorithm=int;
integration=GAUSSHERMITE;
Adaptive=on;

MODEL:
  CAD on BUN SBP HCY HDL LDL CRP BMI;
  BUN on BMI CRP UA;
  CRP on BMI UA;
  SBP on BUN HCY BMI UA CRP;
  HCY on BMI BUN CRP;
  LDL on BMI HCY;
  TG on HCY;
  HDL on HCY;
  TG with HDL; LDL with HDL;

OUTPUT:stdyx;tech1 tech2;modindices(3)

Model indirect:
          CAD ind HCY;
          CAD ind BUN;
          CAD ind BMI;
          CAD ind SBP;
          CAD ind LDL;
          CAD ind HDL;
          CAD ind CRP;
          CAD ind UA;
```

To obtain indirect effects on CAD with 95% CI's

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Typical SEM research questions

- Parameter estimates
  - Non-standardised
  - Standardised
- Model fit
  - Absolute fit (χ^2 for proposed model versus saturated model)
  - Relative fit (AIC/BIC)
- Test for group invariance of parameter estimates
  - i.e. can the same parameter estimates be used for different groups?
  - E.g. Males versus females, race
  - Typically uses
    - χ^2 difference testing of constrained and unconstrained models
    - Difference in -2 LL
- Estimate indirect effects

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Non-standardised β's

	β STATA GSEM (Logit coefficient)	β Mplus ML (Logit coefficient)	β Mplus WLSMV (Probit coefficient)	β Mplus Bayes (Probit coefficient)
Males				
CAD				
HCY	**0.311±0.046**	**0.311±0.046**	**0.108±0.019**	**0.187±0.024**
CRP	0.119±0.131	0.119±0.132	0.047±0.050	0.059±0.069
SBP	**0.034±0.014**	**0.034±0.014**	**0.013±0.004**	**0.014±0.007**
LDL	-0.28±0.299	-0.28±0.299	-0.048±0.094	-0.202±0.158
HDL	0.527±00.681	0.527±0.681	0.158±0.226	0.119±0.353
BUN	0.114±0.122	0.114±0.122	**0.089±0.045**	0.049±0.064
BMI	0.037±0.057	0.037±0.057	0.020±0.019	-0.001±0.029

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Standardised β's

	β STATA GSEM	β Mplus ML	β Mplus WLSMV	β Mplus Bayes
Males				
CAD				
HCY	N/A	**0.62±0.08**	**0.58±0.08**	**0.68±0.07**
CRP	N/A	0.07±0.07	0.07±0.08	0.06±0.07
SBP	N/A	**0.20±0.07**	**0.21±0.07**	**0.15±0.07**
LDL	N/A	-0.06±0.07	0.030±0.058	-0.08±0.06
HDL	N/A	0.05±0.06	0.04±0.06	0.02±0.06
BUN	N/A	0.07±0.07	**0.15±0.08**	0.05±0.07
BMI	N/A	0.04±0.07	0.07±0.06	-0.001±0.06

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CAD as continuous - standardised β's

Males	β STATA SEM	β Mplus ML	β Mplus Bayes
CAD			
HCY	**0.65±0.06**	**0.64±0.05**	**0.63±0.05**
CRP	0.07±0.05	0.07±0.05	0.07±0.05
SBP	**0.11±0.04**	**0.11±0.05**	**0.11±0.05**
LDL	-0.037±0.039	-0.032±0.04	-0.032±0.04
HDL	0.038±0.041	0.038±0.04	0.39±0.04
BUN	0.026±0.04	0.024±0.04	0.02±0.04
BMI	0.02±0.04	0.02±0.04	0.022±0.04
χ^2	49.2 (38df); p=0.11	48.8 (37df); p=0.09	
Satorra-Bentler χ^2	46.3 (38df); p=0.17	47.9 (37df); p=0.11	

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Model fit - Mplus

Absolute fit (χ^2 test of model fit) with WLSMV

```
Value                              32.717*
Degrees of Freedom                 36
P-Value                            0.6255
χ² Contribution From Each Group
MALES                              12.877
FEMALES                            19.839
```

Relative Fit (AIC/BIC) with ML (single groups only)

```
Loglikelihood    H0 Value    -2567.236
Akaike (AIC)                  5216.472
Bayesian (BIC)                5348.727
Sample-Size Adjusted BIC      5218.866
```

Nested model comparisons

WLSMV: Use **difftest** option

```
SAVEDATA:
difftest is mydiff.dat;
ANALYSIS:
difftest is mydiff.dat;

Chi-Square Test for Difference Testing
          Value                28.409
          Degrees of Freedom   22
          P-Value              0.1625
```

ML: Apply with and without **model constraint** option and compare -2LL e.g:

```
MODEL CONSTRAINT:
0 = b1;

Loglikelihood  H0 Value  -2567.854
Loglikelihood  H0 Value  -2567.236
```

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Testing group invariance - Mplus

WLSMVχ^2 test of model fit

Unconstrained model

```
VARIABLE:
Grouping is sex (0=males, 1=females)
SAVEDATA:
difftest is mydiff.dat;

Value                    32.717*
Degrees of Freedom       36
P-Value                  0.6255
χ² Contribution From Each Group
MALES                    12.877
FEMALES                  19.839
```

Constrained model

```
ANALYSIS:
estimator=wlsmv;
iter=20000;
difftest is mydiff.dat;
MODEL:
BUN on BMI(b1); etc.

Chi-Square Test for Difference Testing
Value                    28.409
Degrees of Freedom       22
P-Value                  0.1625
```

ML: Mixture models

```
VARIABLE:
  Categorical is CAD;
  classes=sex(2);
  knownclass= sex (sex=0, sex=1);
ANALYSIS:
 type=mixture;
 estimator=ml;
 iter=20000;
 algorithm=integration;
```

Unconstrained model

```
MODEL:
%overall%
Model code
%sex#1%
Model code
%sex#2%
Model code
```

Constrained Model

```
MODEL:
%OVERALL%
Model code

Number of Free Parameters   76
Loglikelihood H0 Value      -6589.617
Number of Free Parameters   50
Loglikelihood H0 Value      -6572.265

di chi2(34.7, 26)
.14339388
```

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Mplus versus STATA for categorical outcomes

	Mplus (WLSMV)	Mplus (ML)	STATA (GSEM)
Estimates			
Non-standardised	✓		✓
Standardised	✓		×
Model fit			
Absolute fit (χ^2 test of model fit)	✓		×
Relative fit (AIC/BIC)	✓		✓
Nested models (χ^2 diff testing with LL)		✓	✓
Test for group invariance			
with χ^2 difference testing	✓		×
with -2 x Log Likelihood difference testing		✓ (ML Mixture model)	×
Test of indirect effects	✓		×
R^2 for CAD	✓	✓	×

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Summary of results

- Treating binary variables as continuous can produce quite biased results although substantive conclusions remain
- Mplus allows 3 estimation options versus 1 for STATA
  - WLSMV more accurate? (Psychological Methods, 17(3): 354-373)
- Mplus provides
  - tests of absolute fit
  - tests of indirect effects for ML
  - testing for group invariance using WLSMV (`difftest`)
  - Testing for group invariance using ML (mixture model)
  - standardised estimates for ML
  - R^2 estimates

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Diagrammer – Mplus: From syntax to diagram

Step 1: Run from syntax file

Mplus - [hcy_wlsmv_M&Funconstrained.inp]

File Edit View Mplus Plot Diagram Window Help

```
TITLE:
   Hcy_ml_Males
DATA:
  File is hcy.dat;
  LISTWISE=ON;
VARIABLE:
  Names are
      sex age HCY TG HDL LDL BUN CR UA CRP BS SBP DBP CAD BMI group;
  Missing are all (-9999);
  Usevariables are HCY TG HDL LDL BUN SBP  CAD BMI CRP UA;
  Categorical is CAD;
   grouping is sex (0=males, 1=females);
 !   USEOBSERVATIONS ARE SEX==0;

ANALYSIS:
! estimator=wls;
 iter=30000;
MODEL:
  BUN on BMI CRP UA;
  CRP on BMI UA;
  SBP on BUN HCY BMI UA CRP;

  CAD on BUN SBP HCY HDL LDL CRP BMI;

  HCY on BMI BUN CRP;
  LDL on BMI HCY;
  TG on HCY;
  HDL on HCY;

  TG with HDL; LDL with HDL;
  CAD with TG@0;
savedata:
 ! difftest is mydiff2.dat;
OUTPUT:stdyx;tech1 tech2;modindices(3)

Model indirect:
          CAD ind HCY;
          CAD ind BUN;
          CAD ind BMI;
          CAD ind SBP;
          CAD ind LDL;
          CAD ind HDL;
          CAD ind CRP;
          CAD ind UA;
```

Ready Ln 32, Col 1 NUM

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Diagrammer – Mplus: From syntax to diagram

Step 2: In the output file, click: Diagram - View diagram

Mplus - [hcy_wlsmv_m&funconstrained.out]

File Edit View Mplus Plot Diagram Window Help

```
Mplus VERSION 7.31
MUTHEN & MUTHEN
08/12/2015  12:48 PM

INPUT INSTRUCTIONS

  TITLE:
     Hcy_ml_Males
  DATA:
    File is hcy.dat;
    LISTWISE=ON;
  VARIABLE:
    Names are
       sex age HCY TG HDL LDL BUN CR UA CRP BS SBP DBP CAD BMI group;
    Missing are all (-9999);
    Usevariables are HCY TG HDL LDL BUN SBP  CAD BMI CRP UA;
    Categorical is CAD;
     grouping is sex (0=males, 1=females);
   !   USEOBSERVATIONS ARE SEX==0;

  ANALYSIS:
  ! estimator=wls;
   iter=30000;
  MODEL:
    BUN on BMI CRP UA;
    CRP on BMI UA;
    SBP on BUN HCY BMI UA CRP;

    CAD on BUN SBP HCY HDL LDL CRP BMI;

    HCY on BMI BUN CRP;
    LDL on BMI HCY;
    TG on HCY;
    HDL on HCY;

    TG with HDL; LDL with HDL;
    CAD with TG@0;
  savedata:
   ! difftest is mydiff2.dat;
  OUTPUT:stdyx;tech1 tech2;modindices(3)

  Model indirect:
            CAD ind HCY;
            CAD ind BUN;
            CAD ind BMI;
            CAD ind SBP;
            CAD ind LDL;
            CAD ind HDL;
            CAD ind CRP;
            CAD ind UA;


INPUT READING TERMINATED NORMALLY
```

Ready Ln 1, Col 1 NUM

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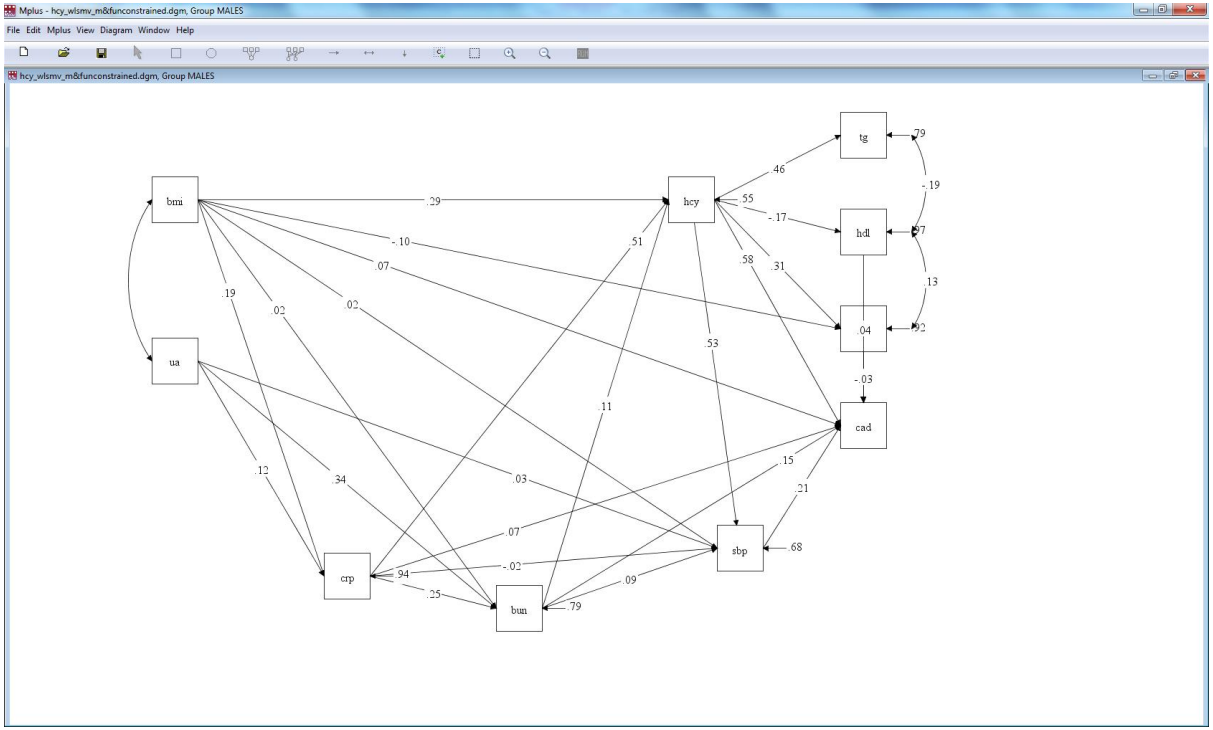
Diagrammer – Mplus: From syntax to diagram

Step 3: This brings up the model with the estimates (.dgm file)



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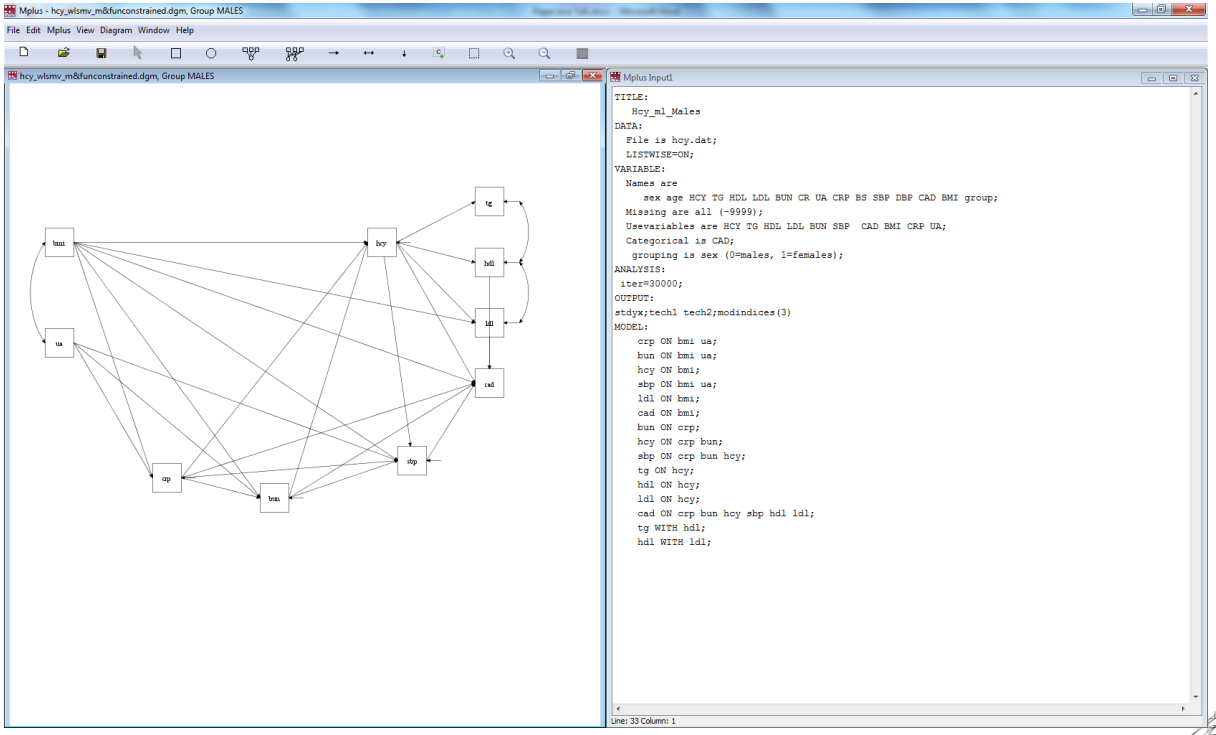
Diagrammer – Mplus: From syntax to diagram

Step 4: Go to Input mode (click on Diagram-Input), and either alter the syntax in the newly written Input file, or alter the path diagram (.mdg file) (this will automatically alter the syntax). Save input file and click "Run"



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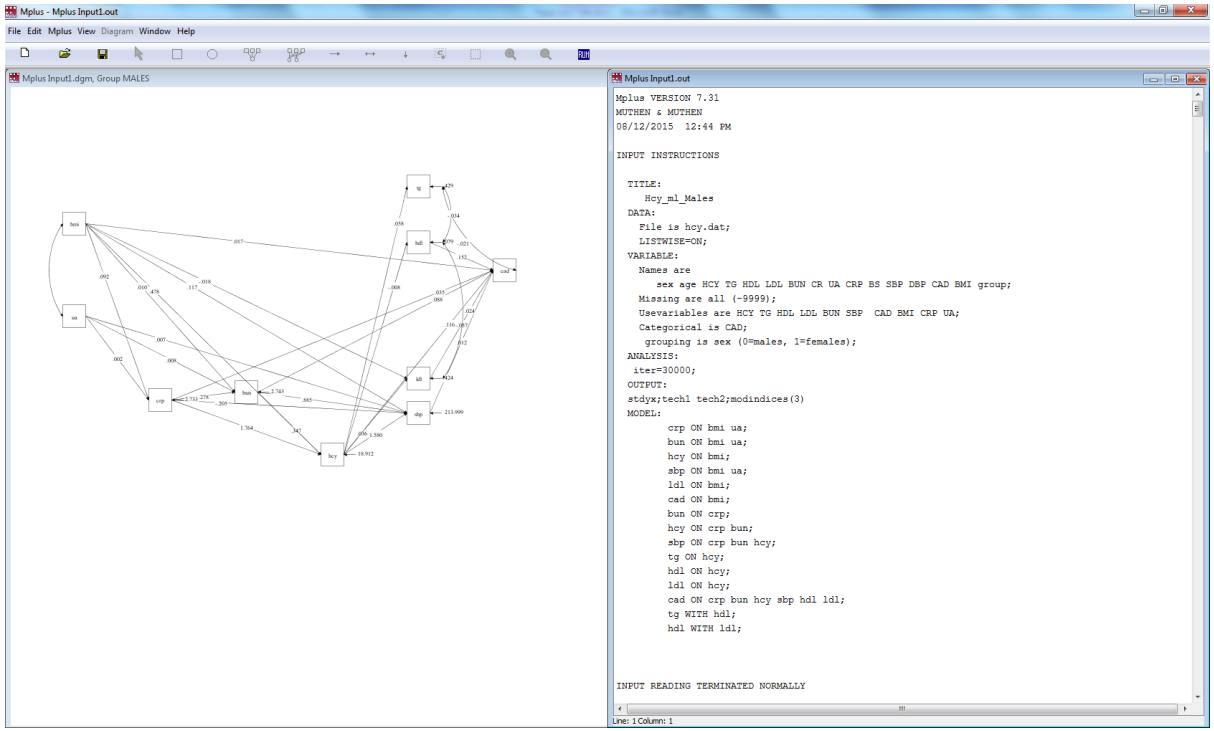
Diagrammer – Mplus: From syntax to diagram

Step 5: View output and new path diagram



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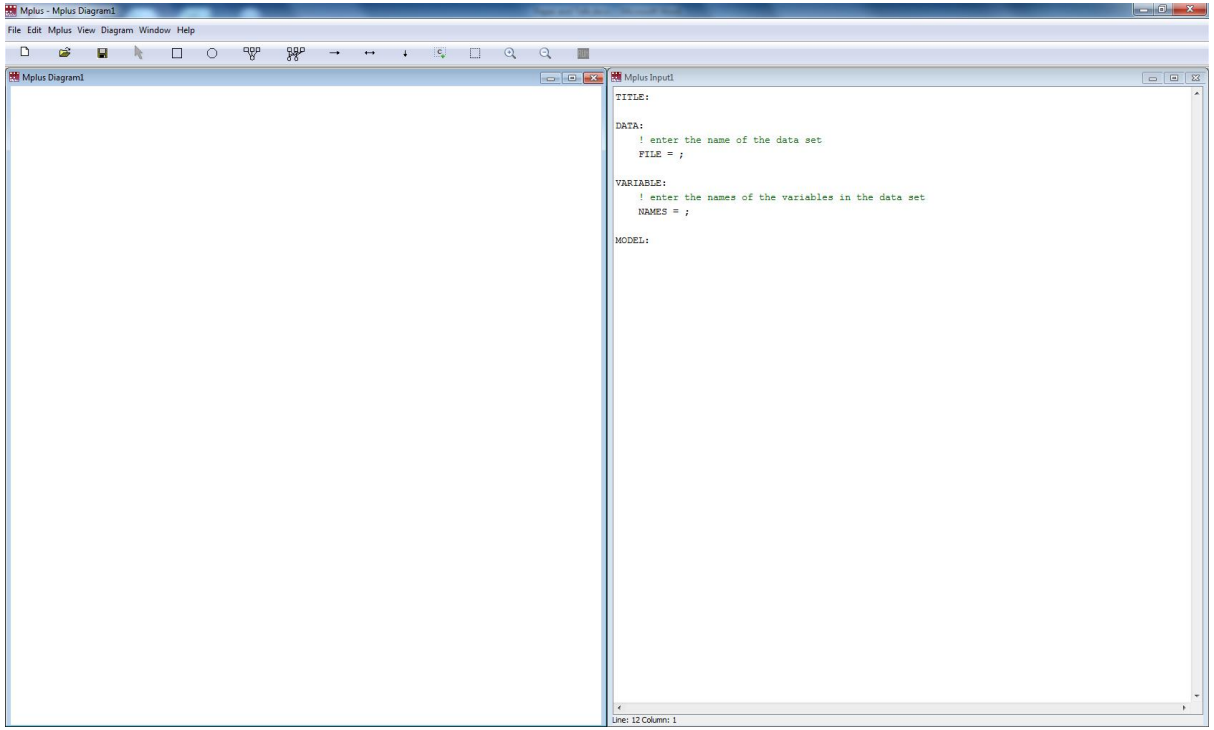
Diagrammer – Mplus: From diagram to syntax

Step 1: Open up Diagrammer from within Mplus Editor (Diagram – Open Diagrammer)



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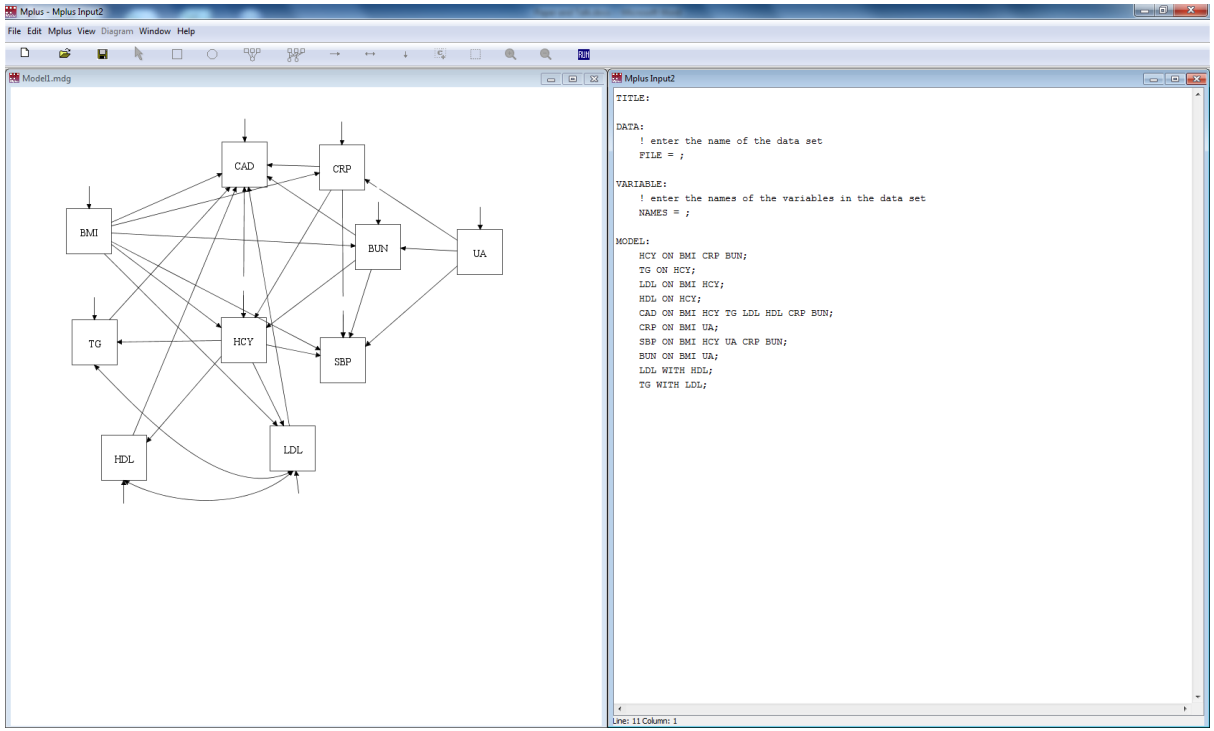
Diagrammer – Mplus: From diagram to syntax

Step 2: Create path diagram. The model part of the syntax will appear on the RH side but not other aspects of the syntax. The path diagram is a .mdg file.
The syntax file is a .inp file.



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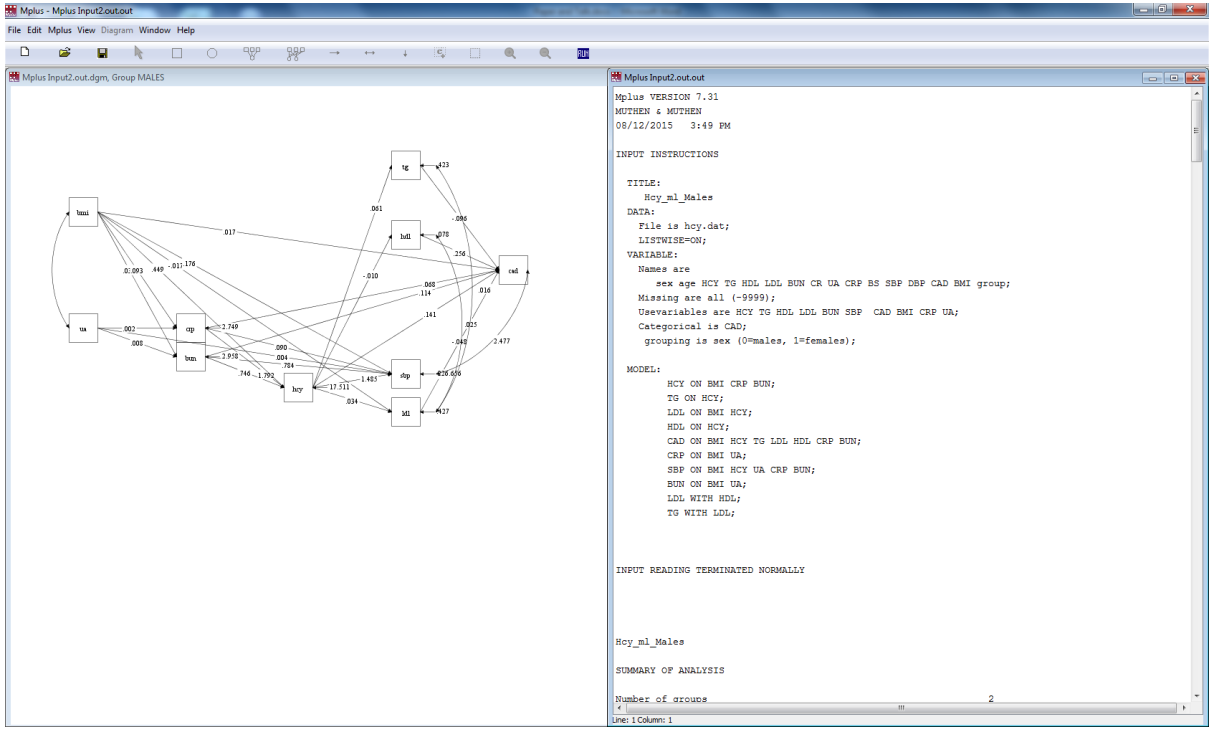
Diagrammer – Mplus: From diagram to syntax

Step 3: Save the Input file and click Run. This will produce a path diagram (.dgm file) with estimates and some output. This is the equivalent of step 5 for option 1



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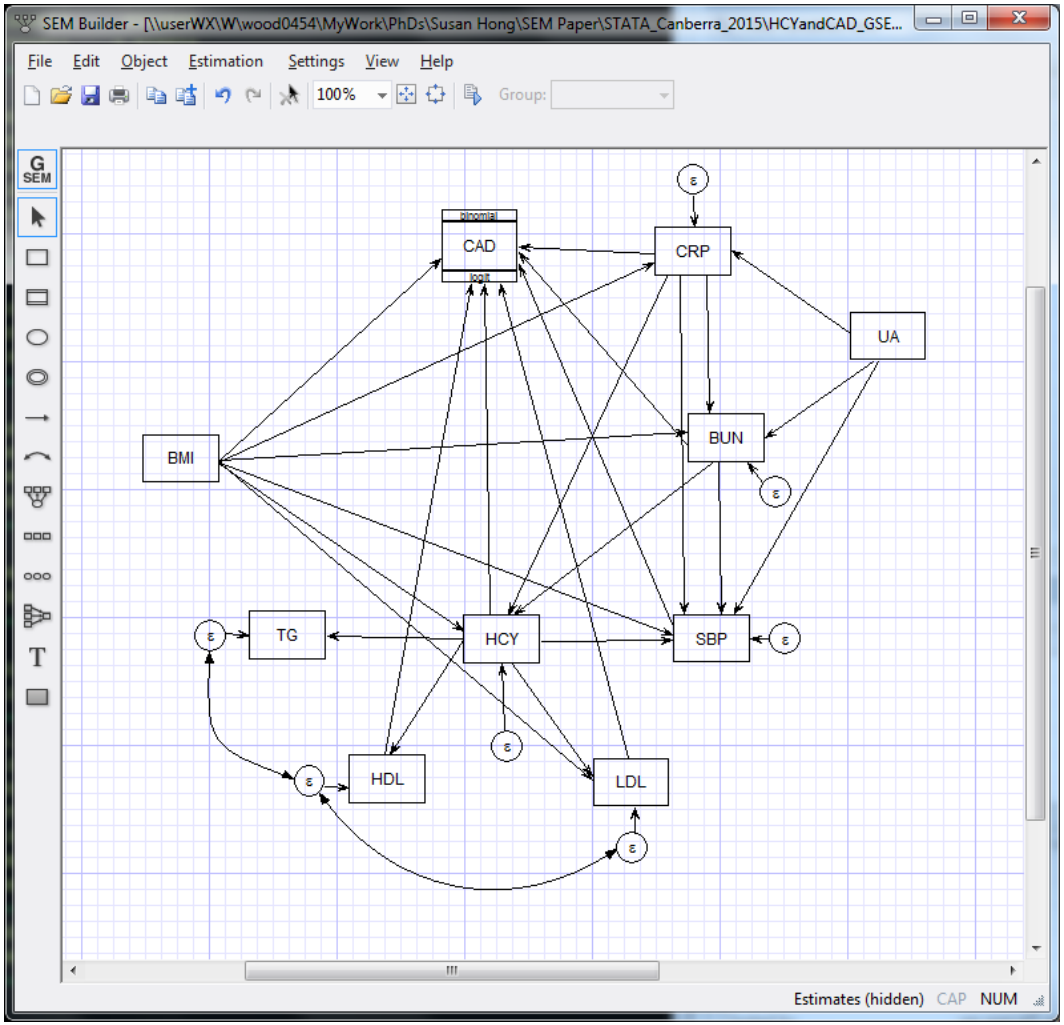
Diagrammer – STATA

Step 1: Draw diagram



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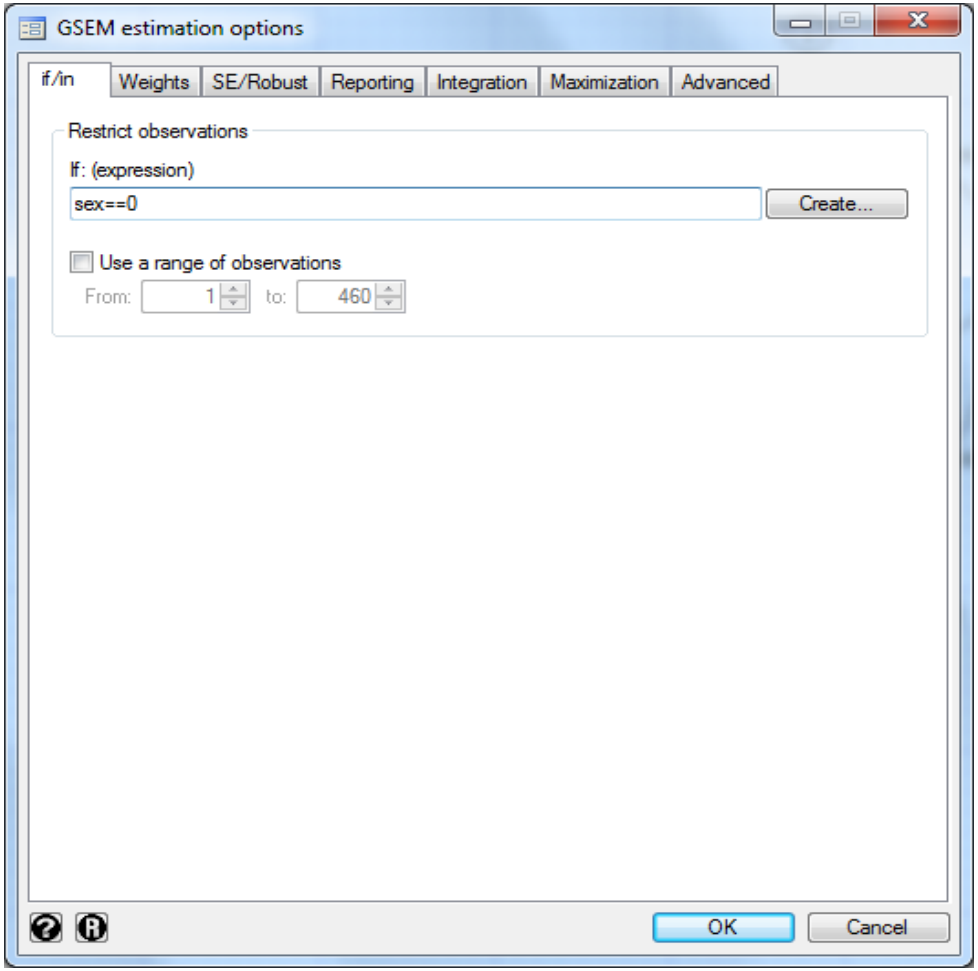
Diagrammer – STATA

Step 2: Select options and click OK



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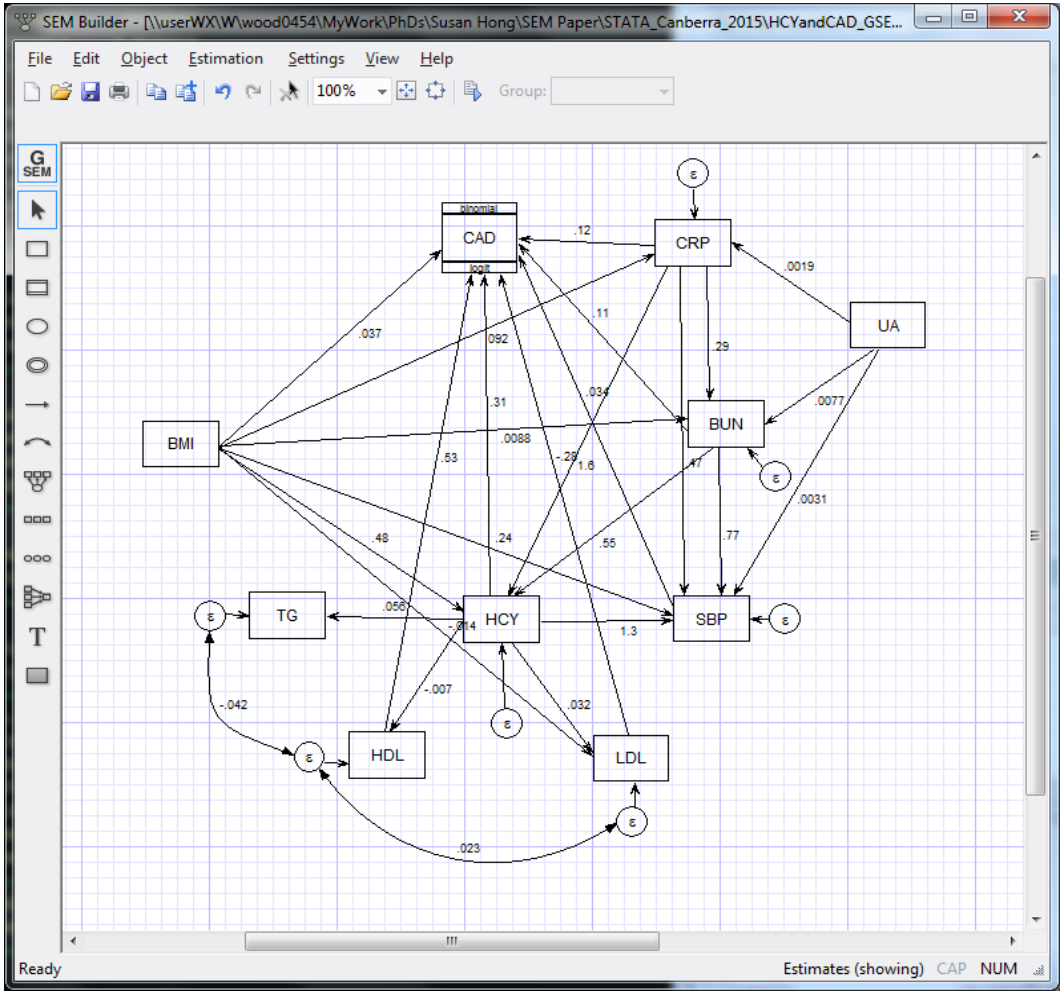
Diagrammer – STATA

Step 3: View results and Output



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Diagrammer – STATA

Step 4: Copy syntax from Output window

```
. gsem (BMI -> HCY, ) (BMI -> CAD, family(binomial) link(logit))
(BMI -> CRP, ) (BMI -> SBP, ) (BMI -> LDL, ) (BMI -> BUN, )
> (HCY -> TG, ) (HCY -> CAD, family(binomial) link(logit)) (HCY ->
SBP, ) (HCY -> LDL, ) (HCY -> HDL, ) (CRP -> HCY, ) (CRP -
> > CAD, family(binomial) link(logit)) (CRP -> SBP, ) (CRP -> BUN,
) (SBP -> CAD, family(binomial) link(logit)) (LDL -> CAD,
> family(binomial) link(logit)) (HDL -> CAD, family(binomial)
link(logit)) (UA -> CRP, ) (UA -> SBP, ) (UA -> BUN, ) (BUN ->
> HCY, ) (BUN -> CAD, family(binomial) link(logit)) (BUN -> SBP, )
if sex==0, cov( e.TG*e.HDL e.HDL*e.LDL) nocapslatent
```

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Diagrammer - STATA

- PROS
  - Simple to create
    - observed variables, factors, paths, variable names
  - Path diagram (.stem) files can be
    - saved and modified
    - converted to other file forms (.pdf, .tiff etc.)
  - Additional estimation options easy to apply via a GUI
  - Writes out the corresponding syntax when run
- CONS
  - Some aspects of drawing are a bit tricky
    - Resizing
    - Variances and co-variance arrows are hard work to get just right
  - Cannot produce a diagram from syntax

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Diagrammer - Mplus

- PROS
  - Writes syntax as a diagram is drawn
  - Provides a diagram from syntax
- CONS
  - Automatic xxx.dmg output files often ugly
  - Dealing with 2 rather than 1 file type
    - .mdg (the hand drawn diagram file from scratch)
    - .dmg (the automatically produced diagram from syntax estimation)

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Diagrammer comparison

	Mplus	STATA
Run a diagram to produce syntax	✓	✓✓
Run syntax to produce a diagram	✓	×
Run syntax to produce a **nice** diagram	×	×
Diagrams simple to create	✓	✓✓
Diagrams convert to .pdf, .tiff	✓	✓
Wizard option to improve appearance (available in some packages e.g. AMOS)	×	×

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Overall Summary of results

- PRO's for Mplus
  - 3 estimation options (ML, WLS, Bayes)
  - Provides
    - Tests of model fit (WLS estimator)
    - Indirect effects (ML and WLS)
    - Standardised estimates (ML and WLS)
    - Testing for group invariance (ML and WLS)
    - R^2 estimate

- PRO's for STATA
  - Only one estimation option to choose from!
  - Better path diagrammer
    - Diagrams easier to draw
    - For saving diagrams - pdf's **and** tiff's
    - For obtaining the syntax from the diagram
    - HELP menu

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