Multivariate Questions I

- Bivariate Analysis: What are the contributions of genetic and environmental factors to the covariance between two traits?
- Multivariate Analysis: What are the contributions of genetic and environmental factors to the covariance between more than two traits?
Phenotypic Cholesky F1

Phenotypic Cholesky F2
Phenotypic Cholesky

\[
\begin{align*}
F_1 & \rightarrow P_{11} \\
F_2 & \rightarrow P_{21} \\
F_3 & \rightarrow P_{31} \\
F_4 & \rightarrow P_{41} \\
F_1 & \rightarrow F_2 \\
F_2 & \rightarrow F_3 \\
F_3 & \rightarrow F_4
\end{align*}
\]

\[
\begin{bmatrix}
f_{11} & 0 & 0 \\
f_{21} & f_{22} & 0 \\
f_{31} & f_{32} & f_{33} \\
f_{41} & f_{42} & f_{43} & f_{44}
\end{bmatrix}
\]
Saturated Model

- Use Cholesky decomposition to estimate covariance matrix
- Fully saturated
- Model: \( \text{Cov } P = FF' \)

\( F: \text{Full nvar nvar} \)
Factor Analysis

- Explain covariance by limited number of factors
- Exploratory / Confirmatory
- Model: \( \text{Cov } P = F*F' + E*E' \)
  - \( F \): Full \( nvar \) \( nfac \)
  - \( E \): Diag \( nvar \) \( nvar \)

Twin Data
Genetic Single Factor

1.0 / 0.5

Single [Common] Factor

- **X**: genetic
  - Full 4 x 1
  - Full nvar x nfac

- **A1**
  - \(a_{11}\)
  - \(a_{21}\)
  - \(a_{31}\)
  - \(a_{41}\)

- **Y**: shared environmental
- **Z**: specific environmental

\[
\begin{bmatrix}
A1 \\
P1 \\
P2 \\
P3 \\
P4
\end{bmatrix}
= \begin{bmatrix}
a_{11} & a_{21} & a_{31} & a_{41}
\end{bmatrix}
\]

\[
X \times X'
\]
Common Environmental Single Factor

Specific Environmental Single Factor
Residuals partitioned in ACE

Residual Factors

- **T**: genetic
- **U**: shared environmental
- **V**: specific environmental

- Diag 4 x 4
- Diag nvar x nvar

\[
V = \begin{bmatrix}
    e_{11} & 0 & 0 & e_{11} \\
    0 & e_{22} & 0 & 0 \\
    0 & 0 & e_{33} & 0 \\
    0 & 0 & 0 & e_{44}
\end{bmatrix} * V'
\]
Independent Pathway Model

Path Diagram to Matrices

<table>
<thead>
<tr>
<th>Variance Component</th>
<th>a^2</th>
<th>c^2</th>
<th>e^2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common Factors</td>
<td>[X] 6 x 1</td>
<td>[Y] 6 x 1</td>
<td>[Z] 6 x 1</td>
</tr>
<tr>
<td>Residual Factors</td>
<td>[T] 6 x 6</td>
<td>[U] 6 x 6</td>
<td>[V] 6 x 6</td>
</tr>
</tbody>
</table>

#define nvar 6
#define nfac 1
Independent Pathway I

G1: Define matrices
Calculation
Begin Matrices;
X full nvar nfac Free ! common factor genetic path coefficients
Y full nvar nfac Free ! common factor shared environment paths
Z full nvar nfac Free ! common factor unique environment paths
T diag nvar nvar Free ! variable specific genetic paths
U diag nvar nvar Free ! variable specific shared env paths
V diag nvar nvar Free ! variable specific residual paths
M full 1 nvar Free ! means
End Matrices;
Start
Begin Algebra;
A = X*X' + T*T' ; ! additive genetic variance components
C = Y*Y' + U*U' ; ! shared environment variance components
E = Z*Z' + V*V' ; ! nonshared environment variance components
End Algebra;
End

Independent Pathway II

G2: MZ twins
#include iqmlmz.dat
Begin Matrices = Group 1;
Means M | M ;
Covariance A+C+E | A+C _
A+C | A+C+E ;
Option Residuals
End

G3: DZ twins
#include iqnlqdz.dat
Begin Matrices = Group 1;
H full 1 1
End Matrices;
Matrix H .5
Means M | M ;
Covariance A+C+E | HSA+C _
HSA+C | A+C+E ;
Option Residuals
End
Independent Pathway III

- G4: Calculate Standardised Solution
  - Calculation
  - Matrices = Group 1
  - I Iden nvar nvar
  - End Matrices;
  - Begin Algebra;
  - R=A+C+E;                   ! total variance
  - S=(\sqrt(I.R))~;          ! diagonal matrix of standard deviations
  - P=S*X_ S*Y_ S*Z;          ! standardized estimates for common factors
  - Q=S*T_ S*U_ S*V;          ! standardized estimates for spec factors
  - End Algebra;
  - Labels Row P a1 a2 a3 a4 a5 a6 c1 c2 c3 c4 c5 c6 e1 e2 e3 e4 e5 e6
  - Labels Col P var1 var2 var3 var4 var5 var6
  - Labels Row Q as1 as2 as3 as4 as5 as6 cs1 cs2 cs3 cs4 cs5 cs6 es1 es2 es3 es4 es5 es6
  - Labels Col Q var1 var2 var3 var4 var5 var6
  - Options NDecimals=4
  - End

IP

- Independent pathways
  - Biometric model
  - Different covariance structure for A, C and E
Phenotypic Single Factor

Latent Phenotype
Twin Data

Factor on Latent Phenotype

\[
\begin{align*}
\text{P1} & \begin{bmatrix} f_{11} \end{bmatrix} \\
\text{P2} & \begin{bmatrix} f_{21} \end{bmatrix} \\
\text{P3} & \begin{bmatrix} f_{31} \end{bmatrix} \\
\text{P4} & \begin{bmatrix} f_{41} \end{bmatrix} \\
\end{align*}
\]

\[
\begin{bmatrix} a \end{bmatrix} \begin{bmatrix} a \end{bmatrix} \begin{bmatrix} f_{11} f_{21} f_{31} f_{41} \end{bmatrix}
\]

\[
\mathbf{F} \times \mathbf{X} \times \mathbf{X}' \times \mathbf{F}'
\]

\[
= \mathbf{F} \& \left( \mathbf{X} \times \mathbf{X}' \right)
\]
Common Pathway Model

Path Diagram to Matrices

<table>
<thead>
<tr>
<th>Variance Component</th>
<th>$a^2$</th>
<th>$c^2$</th>
<th>$e^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common Factor</td>
<td>$[X]$ 1 x 1</td>
<td>$[Y]$ 1 x 1</td>
<td>$[Z]$ 1 x 1</td>
</tr>
<tr>
<td>Residual Factors</td>
<td>$[T]$ 6 x 6</td>
<td>$[U]$ 6 x 6</td>
<td>$[V]$ 6 x 6</td>
</tr>
</tbody>
</table>

#define nvar 6
#define nfac 1
Common Pathway Model I

- G1: Define matrices
  - Calculation
  - Begin Matrices;
    - X full nfac nfac Free ! latent factor genetic path coefficient
    - Y full nfac nfac Free ! latent factor shared environment path
    - Z full nfac nfac Free ! latent factor unique environment path
    - T diag nvar nvar Free ! variable specific genetic paths
    - U diag nvar nvar Free ! variable specific shared env paths
    - V diag nvar nvar Free ! variable specific residual paths
    - F full nvar nfac Free ! loadings of variables on latent factor
  - I Idem 2 2
  - M full 1 nvar Free ! means
  - End Matrices;
  - Start ..
  - Begin Algebra;
    - A= F&(X*X') + T*T';       ! genetic variance components
    - C= F&(Y*Y') + U*U';       ! shared environment variance components
    - E= F&(Z*Z') + V*V';       ! nonshared environment variance components
    - L= X*X' + Y*Y' + Z*Z';    ! variance of latent factor
  - End Algebra;
- Options NDecimals=4
- End

Common Pathway II

- G4: Constrain variance of latent factor to 1
  - Constraint
  - Begin Matrices;
    - L computed =L1
    - I unit 1 1
  - End Matrices;
  - Constraint L = I ;
- End

- G5: Calculate Standardised Solution
  - Calculation
  - Matrices = Group 1
  - D Idem nvar nvar
  - End Matrices;
  - Begin Algebra;
    - R=A+C+E;               ! total variance
    - S=(\sqrt(D.R))^~;      ! diagonal matrix of standard deviations
    - P=S*F;                ! standardized estimates for loadings on F
    - Q=S*T_ S*U_ S*V;      ! standardized estimates for specific factors
  - End Algebra;
  - Options NDecimals=4
- End
Common pathway
- Psychometric model
- Same covariance structure for A, C and E

Practical Example
- Dataset: NL-IQ Study
- 6 WAIS-III IQ subtests
  - var1 = onvolledige tekeningen / picture completion
  - var2 = woordenschat / vocabulary
  - var3 = paren associeren / digit span
  - var4 = incidenteel leren / incidental learning
  - var5 = overeenkomsten / similarities
  - var6 = blokpatronen / block design
- N MZF: 27, DZF: 70
Summary

- Independent Pathway Model
  - Biometric Factor Model
  - Loadings differ for genetic and environmental common factors
- Common Pathway Model
  - Psychometric Factor Model
  - Loadings equal for genetic and environmental common factor

WAIS-III IQ

- Verbal IQ
  - var2 = woordenschat / vocabulary
  - var3 = paren associeren / digit span
  - var5 = overeenkomsten / similarities
- Performance IQ
  - var1 = onvolledige tekeningen / picture completion
  - var4 = incidenteel leren / incidental learning
  - var6 = blokpatronen / block design
Pathway Model

Two Common Pathway Model
Two Independent CP Model

Two Reduced Indep CP Model
Common Pathway Model

Independent Pathway Model