



Multivariate Analysis

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TC19

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Files to Copy to your Computer

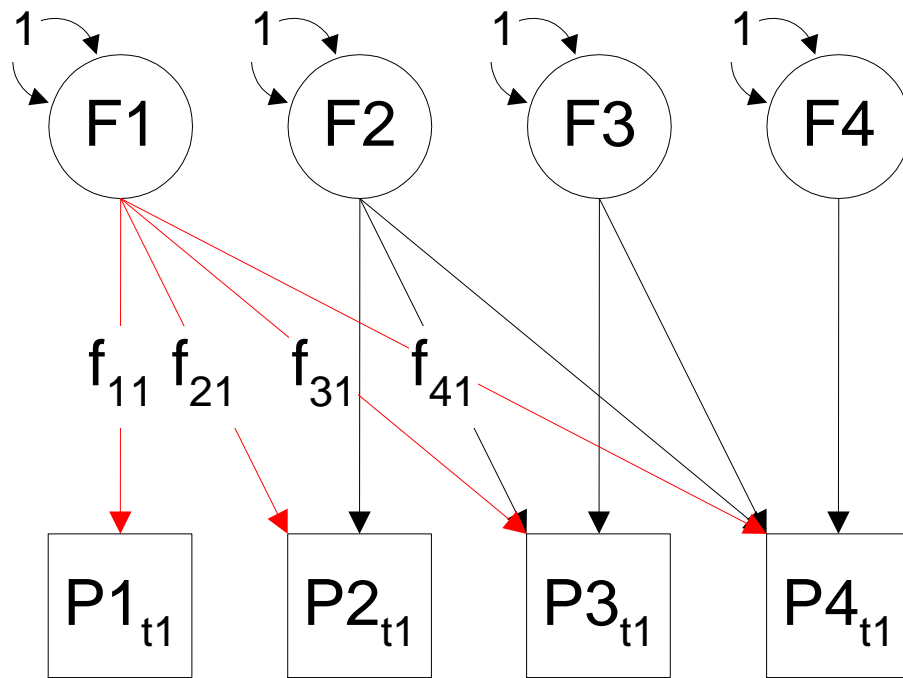
- Faculty/hmaes/tc19/maes/multivariate
 - *.rec
 - *.dat
 - *.mx
 - Multivariate.ppt



Multivariate Questions I

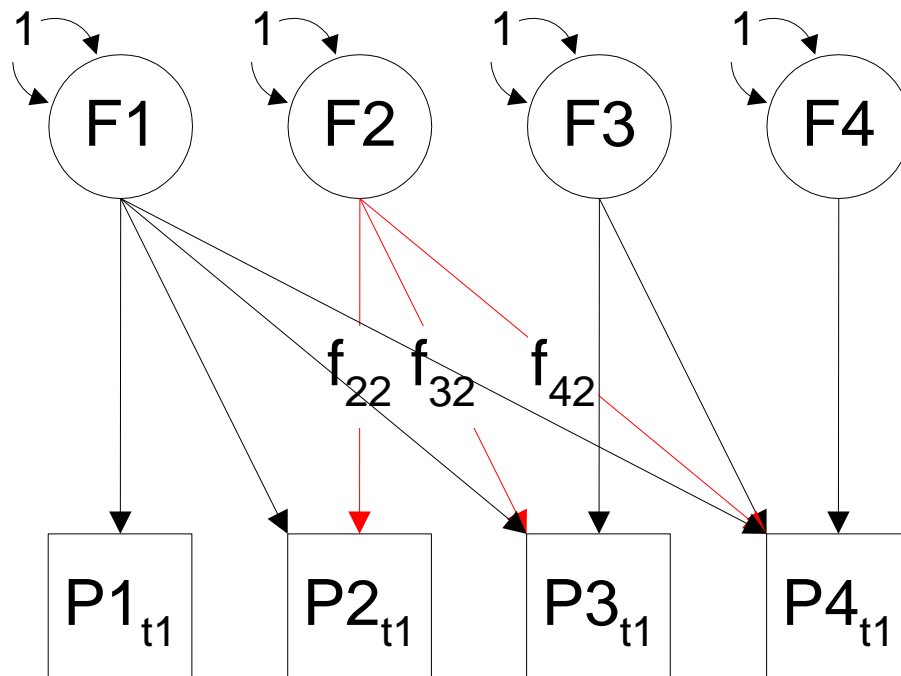
- Bivariate Analysis: What are the contributions of genetic and environmental factors to the covariance between two traits?
- Multivariate Analysis: What are the contributions of genetic and environmental factors to the covariance between more than two traits?

Phenotypic Cholesky F1



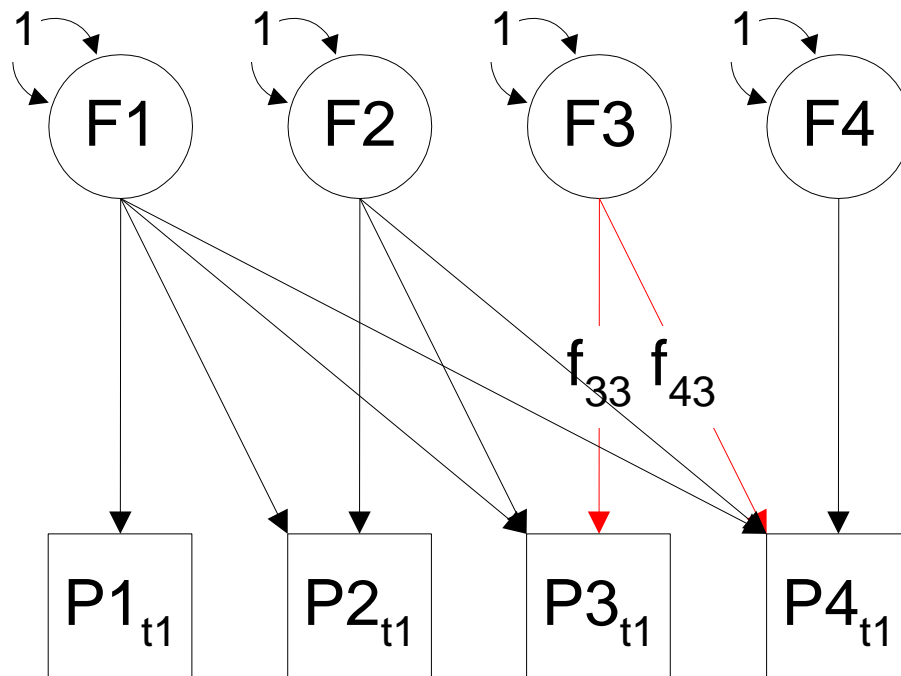
$$\begin{matrix} & F1 & F2 & F3 & F4 \\ \begin{matrix} P1 \\ P2 \\ P3 \\ P4 \end{matrix} & \begin{bmatrix} f_{11} \\ f_{21} \\ f_{31} \\ f_{41} \end{bmatrix} & & & \end{matrix}$$

Phenotypic Cholesky F2



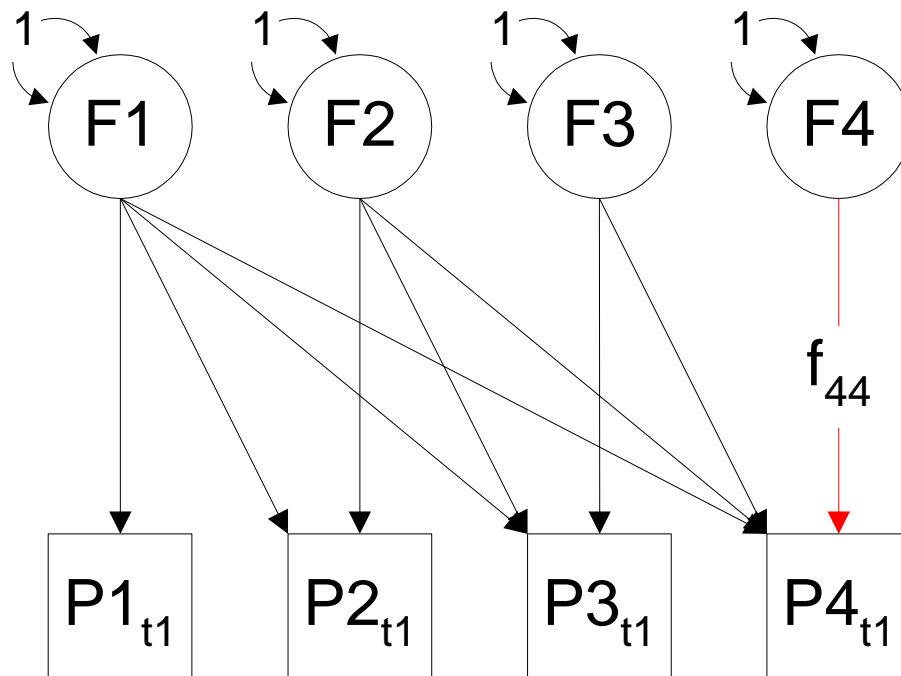
$$\begin{array}{c} P1 \\ P2 \\ P3 \\ P4 \end{array} \begin{bmatrix} F1 & F2 & F3 & F4 \\ f_{11} & 0 & & \\ f_{21} & f_{22} & & \\ f_{31} & f_{32} & & \\ f_{41} & f_{42} & & \end{bmatrix}$$

Phenotypic Cholesky



$$\begin{array}{c} P1 \\ P2 \\ P3 \\ P4 \end{array} \begin{bmatrix} F1 & F2 & F3 & F4 \\ f_{11} & 0 & 0 & \\ f_{21} & f_{22} & 0 & \\ f_{31} & f_{32} & f_{33} & \\ f_{41} & f_{42} & f_{43} & \end{bmatrix}$$

Phenotypic Cholesky



$$\begin{array}{c} P1 \\ P2 \\ P3 \\ P4 \end{array} \begin{array}{c} F1 \\ F2 \\ F3 \\ F4 \end{array} \begin{bmatrix} f_{11} & 0 & 0 & 0 \\ f_{21} & f_{22} & 0 & 0 \\ f_{31} & f_{32} & f_{33} & 0 \\ f_{41} & f_{42} & f_{43} & f_{44} \end{bmatrix}$$

Cholesky Decomposition

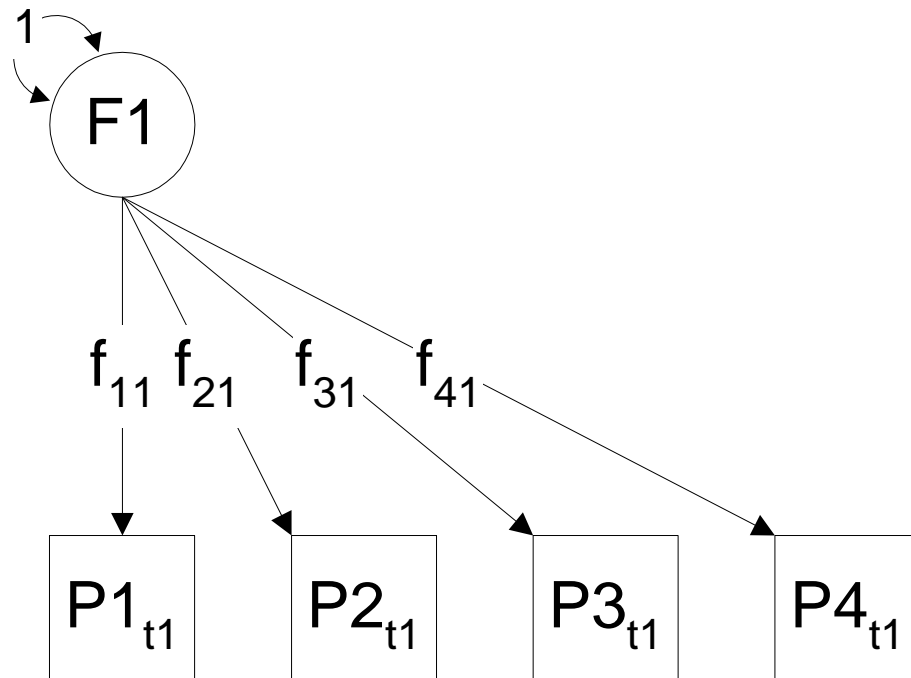
$$\begin{array}{c} \text{P1} \\ \text{P2} \\ \text{P3} \\ \text{P4} \end{array} \begin{array}{c} \text{F1} \text{ F2} \text{ F3} \text{ F4} \\ \left[\begin{array}{cccc} f_{11} & 0 & 0 & 0 \\ f_{21} & f_{22} & 0 & 0 \\ f_{31} & f_{32} & f_{33} & 0 \\ f_{41} & f_{42} & f_{43} & f_{44} \end{array} \right] \\ \mathbf{F} \end{array} * \begin{array}{c} \left[\begin{array}{cccc} f_{11} & f_{21} & f_{31} & f_{41} \\ 0 & f_{22} & f_{32} & f_{42} \\ 0 & 0 & f_{33} & f_{43} \\ 0 & 0 & 0 & f_{44} \end{array} \right] \\ \mathbf{F}' \end{array}$$



Saturated Model

- Use Cholesky decomposition to estimate covariance matrix
- Fully saturated
- Model: $\text{Cov } P = F * F'$
 - F: Lower nvar nvar

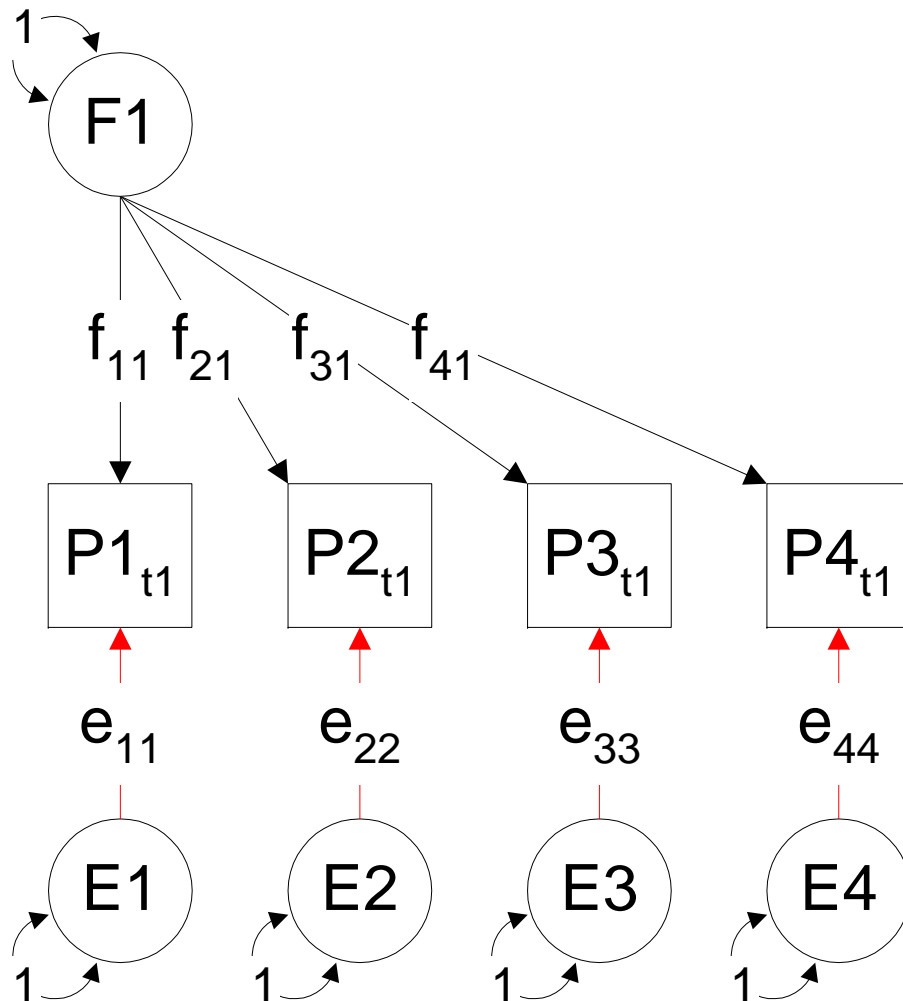
Phenotypic Single Factor



$$\begin{matrix} & F1 \\ P1 & \begin{bmatrix} f_{11} \\ f_{21} \\ f_{31} \\ f_{41} \end{bmatrix} \\ P2 & \\ P3 & \\ P4 & \end{matrix} * \begin{bmatrix} f_{11} & f_{21} & f_{31} & f_{41} \end{bmatrix}$$

F * **F'**

Residual Variances



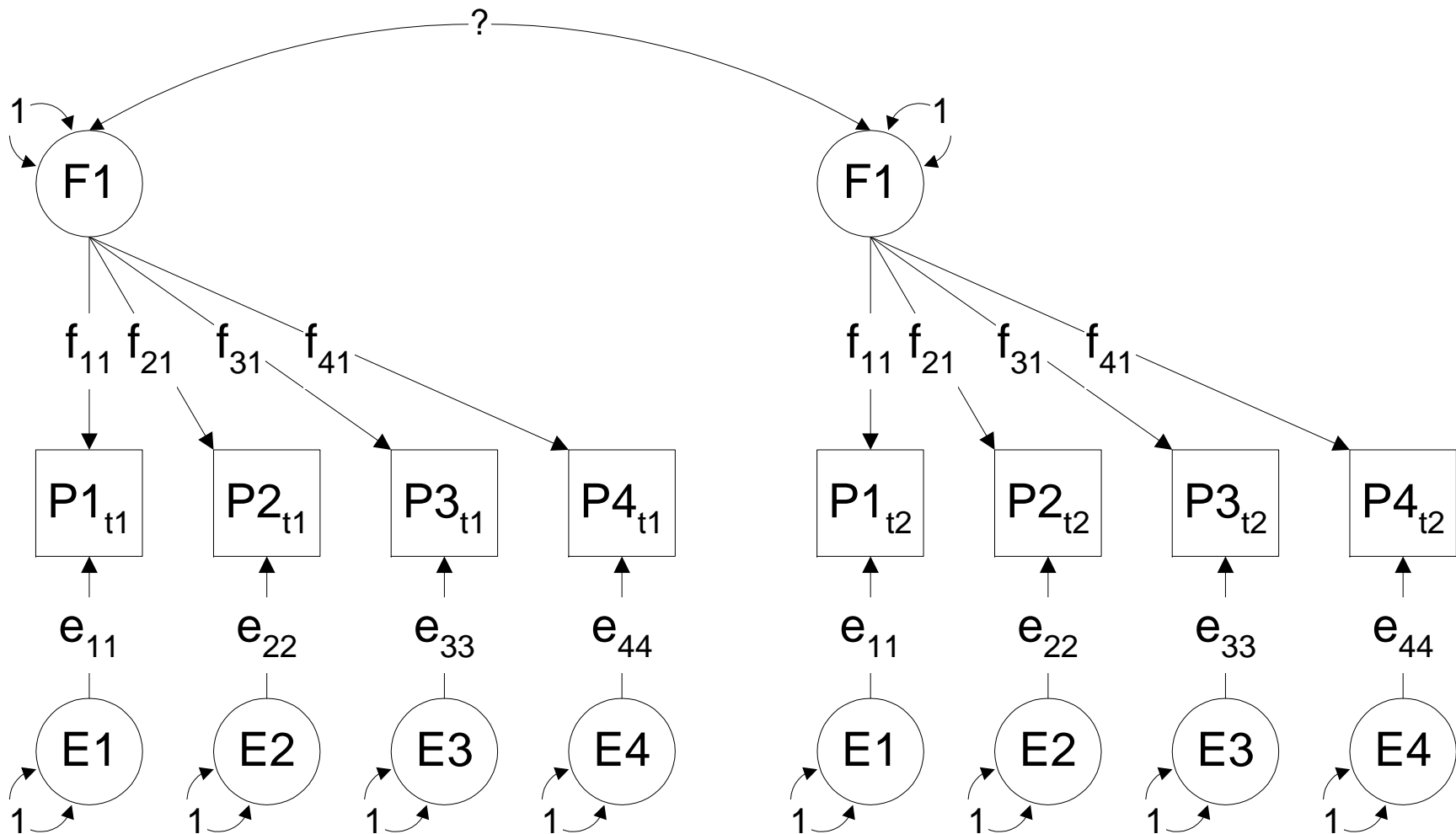
$$\begin{array}{c}
 \text{E1 E2 E3 E4} \\
 \text{P1} \begin{bmatrix} e_{11} & 0 & 0 & 0 \\ 0 & e_{22} & 0 & 0 \\ 0 & 0 & e_{33} & 0 \\ 0 & 0 & 0 & e_{44} \end{bmatrix} * \begin{bmatrix} e_{11} & 0 & 0 & 0 \\ 0 & e_{22} & 0 & 0 \\ 0 & 0 & e_{33} & 0 \\ 0 & 0 & 0 & e_{44} \end{bmatrix} \\
 \text{P2} \\
 \text{P3} \\
 \text{P4} \\
 \mathbf{E} \quad * \quad \mathbf{E}'
 \end{array}$$



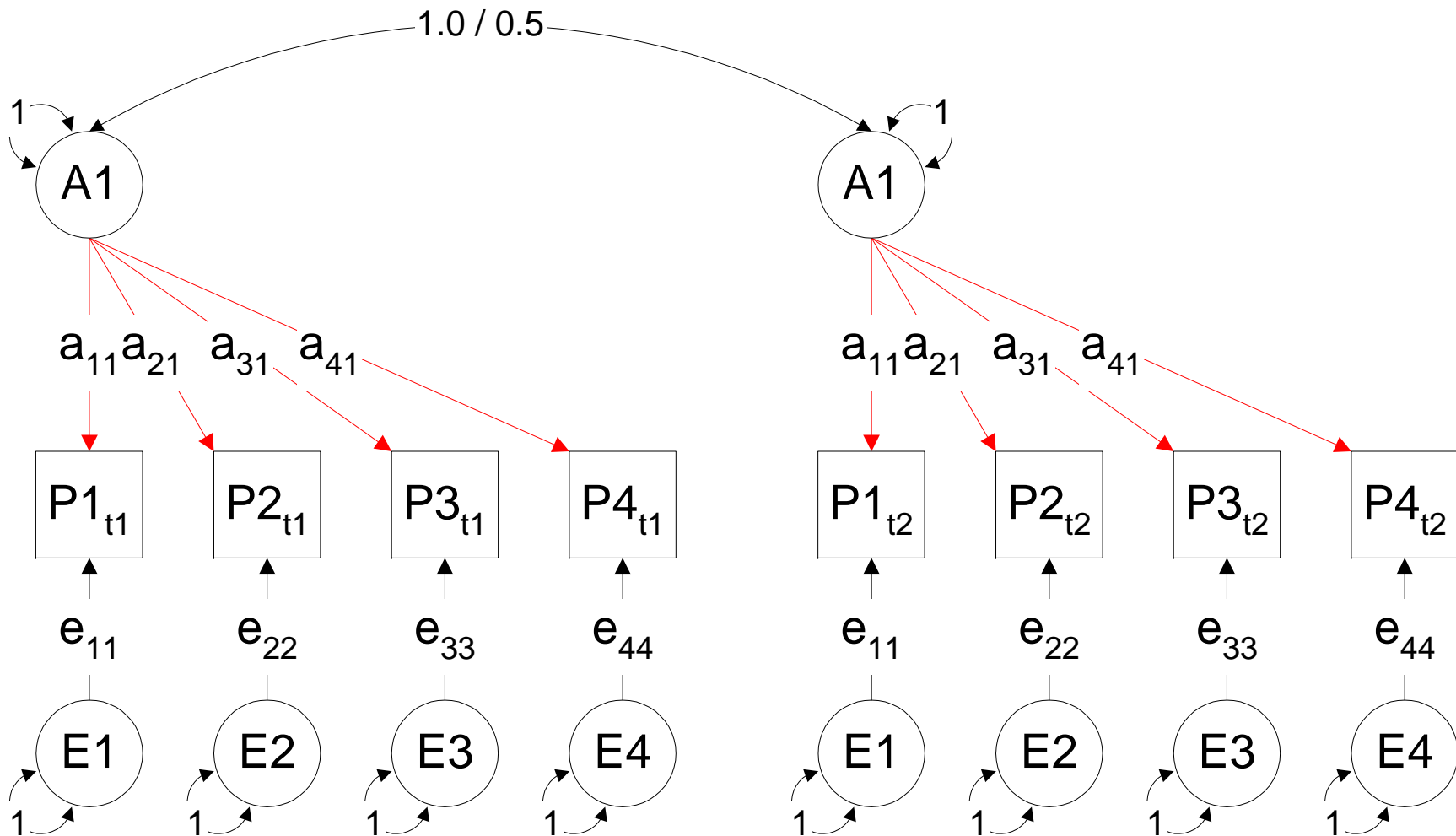
Factor Analysis

- 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
- Model: $\text{Cov } P = F * I * F' + E * E'$

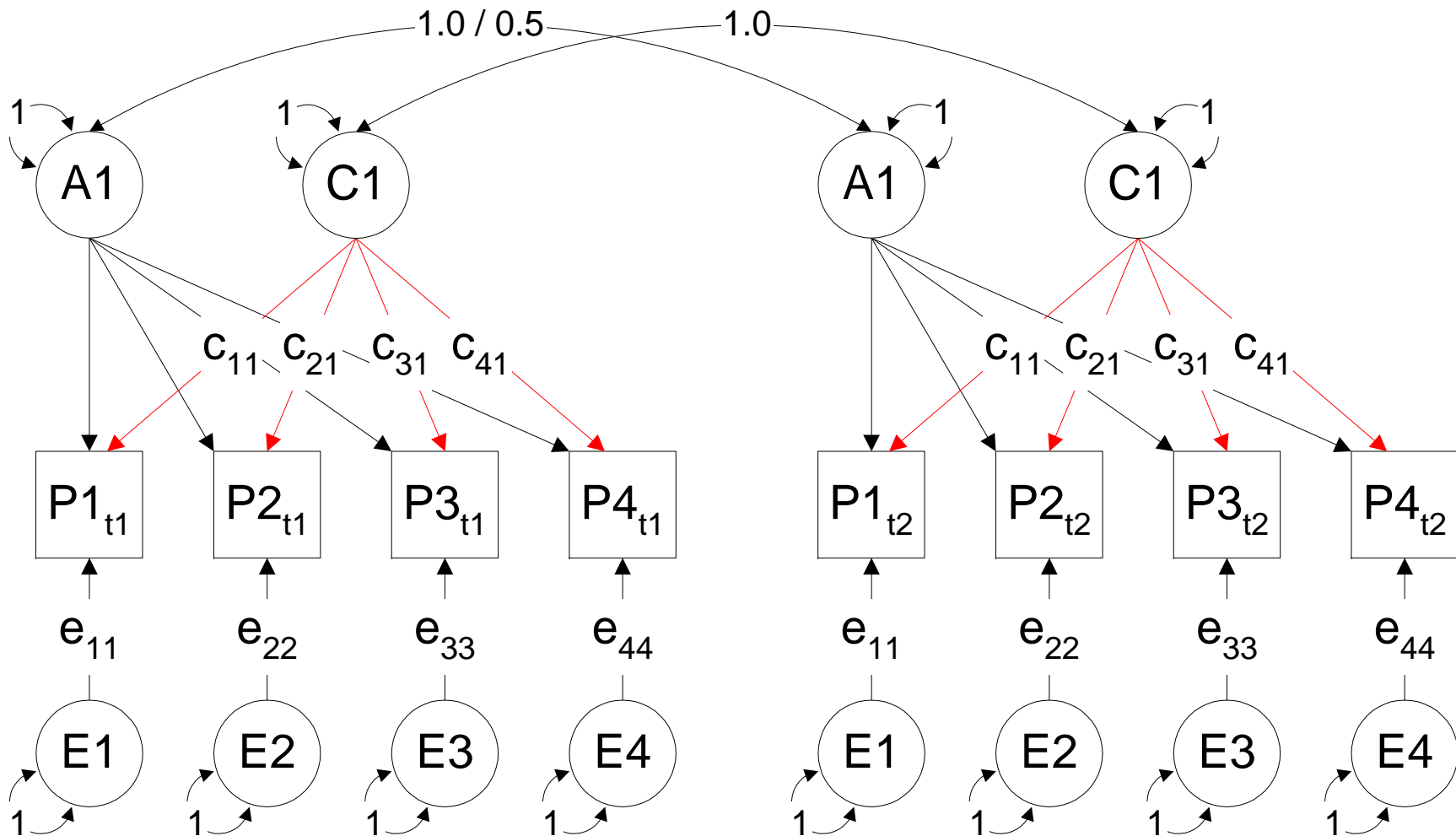
Twin Data



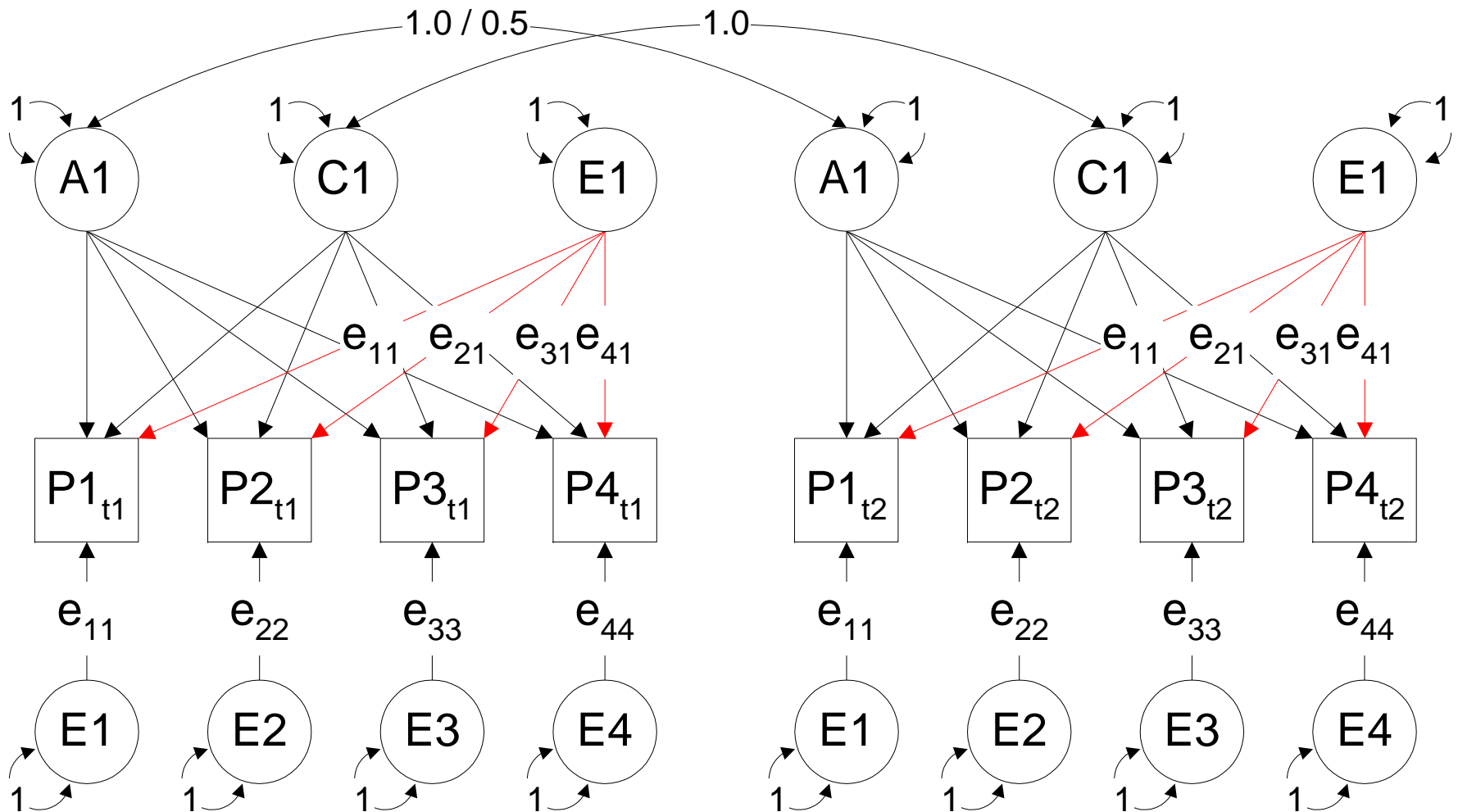
Genetic Single Factor



Common Environmental Single Factor



Specific Environmental Single Factor



Single [Common] Factor

- X: genetic

- Full 4 x 1

- Full nvar x nfac

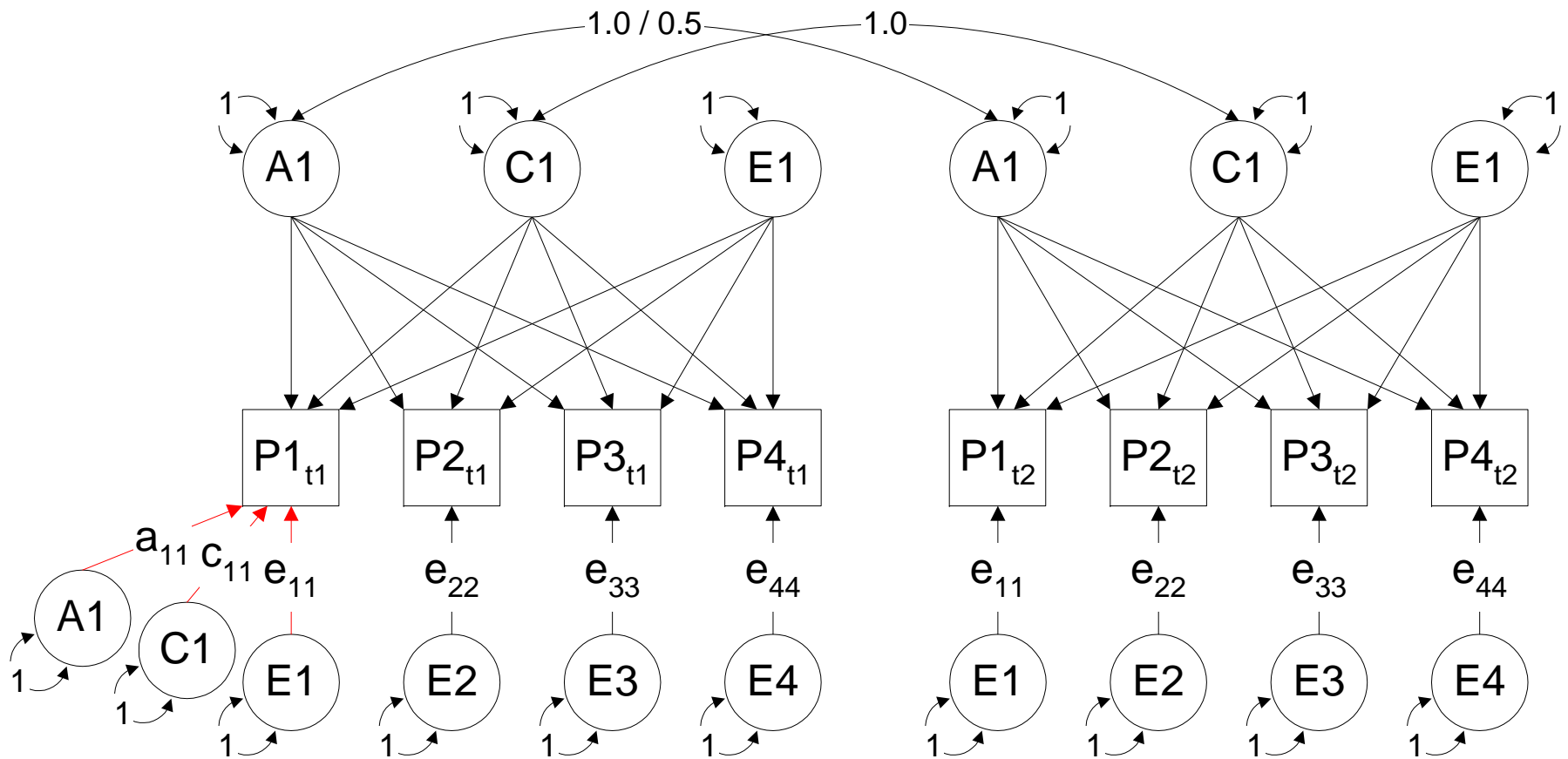
$$\begin{array}{c} \text{P1} \\ \text{P2} \\ \text{P3} \\ \text{P4} \end{array} \begin{array}{c} \text{A1} \\ \left[\begin{array}{c} a_{11} \\ a_{21} \\ a_{31} \\ a_{41} \end{array} \right] \end{array} * \begin{array}{c} \left[a_{11} \ a_{21} \ a_{31} \ a_{41} \right] \\ \\ \\ \end{array}$$

X * **X'**

- Y: shared environmental

- Z: specific environmental

Residuals partitioned in ACE

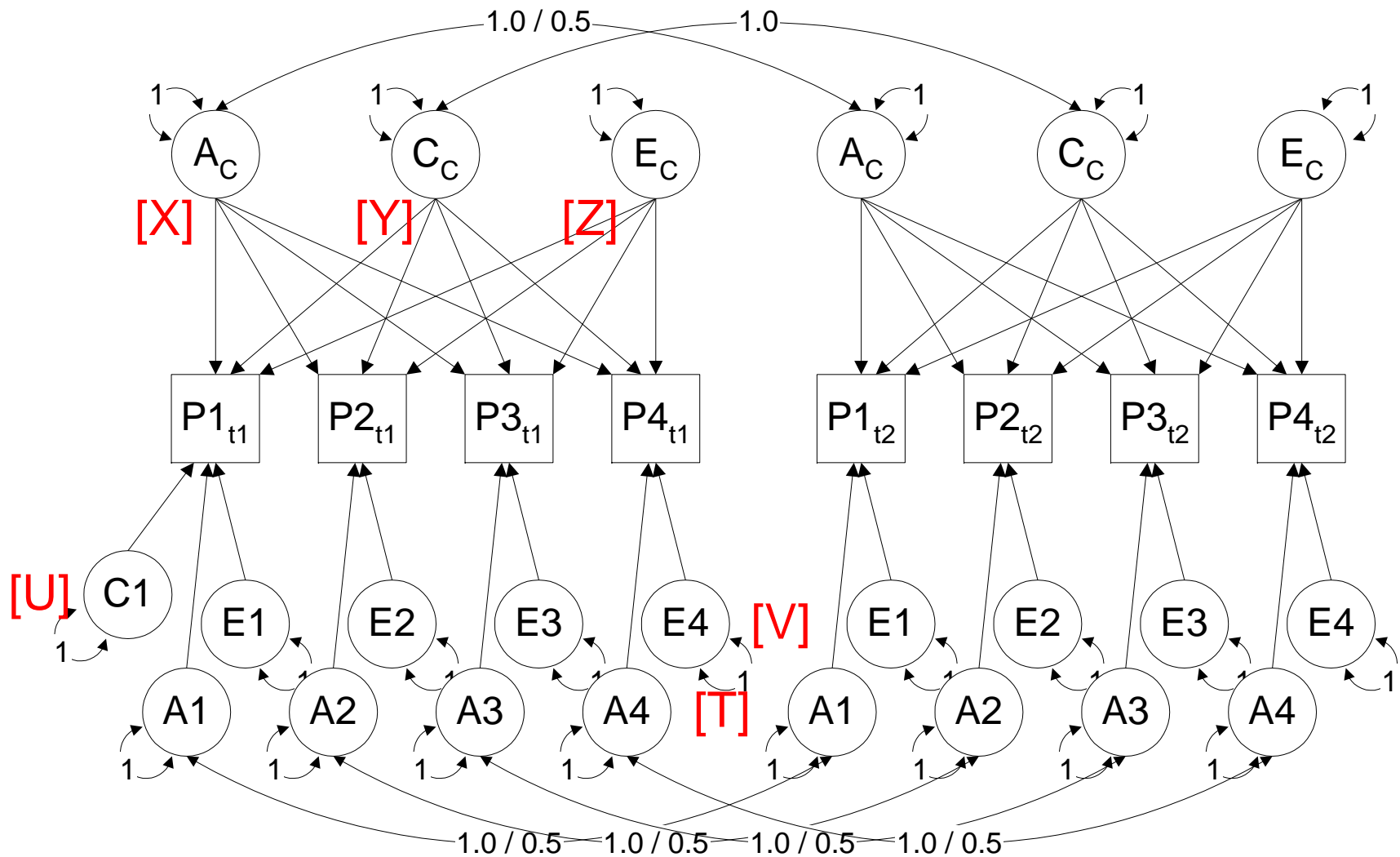


Residual Factors

- T: genetic
- U: shared environmental
- V: specific environmental
 - Diag 4 x 4
 - Diag nvar x nvar

$$\begin{array}{c} \text{P1} \\ \text{P2} \\ \text{P3} \\ \text{P4} \end{array} \begin{array}{c} \text{E1} \text{ E2} \text{ E3} \text{ E4} \\ \left[\begin{array}{cccc} e_{11} & 0 & 0 & 0 \\ 0 & e_{22} & 0 & 0 \\ 0 & 0 & e_{33} & 0 \\ 0 & 0 & 0 & e_{44} \end{array} \right] \\ \mathbf{V} \end{array} * \begin{array}{c} \left[\begin{array}{cccc} e_{11} & 0 & 0 & 0 \\ 0 & e_{22} & 0 & 0 \\ 0 & 0 & e_{33} & 0 \\ 0 & 0 & 0 & e_{44} \end{array} \right] \\ \mathbf{V}' \end{array}$$

Independent Pathway Model





IP

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

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

indpath.mx

Independent Pathway II

- G2: MZ twins
- `#include iqnlmz.dat`
- `Begin Matrices = Group 1;`
- `Means M | M ;`
- `Covariance`

$A+C+E$	$A+C$	$—$
$A+C$	$A+C+E$	$;$
- `Option Rsiduals`
- `End`

- G3: DZ twins
- `#include iqnldz.dat`
- `Begin Matrices= Group 1;`
- `H full 1 1`
- `End Matrices;`
- `Matrix H .5`
- `Means M | M ;`
- `Covariance`

$A+C+E$	$H@A+C$	$—$
$H@A+C$	$A+C+E$	$;$
- `Option Rsiduals`
- `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




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

Dat Files

- **iqnlmz.dat**
- Data NInputvars=18
- Missing=-1.00
- Rectangular File=iqnl.rec
- Labels famid zygos
- age_t1 sex_t1 var1_t1 var2_t1 var3_t1 var4_t1 var5_t1 var6_t1
- age_t2 sex_t2 var1_t2 var2_t2 var3_t2 var4_t2 var5_t2 var6_t2
- `Select if zygos < 3 ; !select mz's`
- Select
- var1_t1 var2_t1 var3_t1 var4_t1 var5_t1 var6_t1
- var1_t2 var2_t2 var3_t2 var4_t2 var5_t2 var6_t2 ;

- **iqnldz.dat**
-
- `Select if zygos > 2 ; !select dz's`
-



MATRIX M

This is a FULL matrix of order 1 by 6

1 2 3 4 5 6
1 64 65 66 67 68 69

MATRIX X

This is a LOWER TRIANGULAR matrix of order 6 by 6

1 2 3 4 5 6
1 1
2 2 3
3 4 5 6
4 7 8 9 10
5 11 12 13 14 15
6 16 17 18 19 20 21

MATRIX Y

This is a LOWER TRIANGULAR matrix of order 6 by 6

1 2 3 4 5 6
1 22
2 23 24
3 25 26 27
4 28 29 30 31
5 32 33 34 35 36
6 37 38 39 40 41 42

MATRIX Z

This is a LOWER TRIANGULAR matrix of order 6 by 6

1 2 3 4 5 6
1 43
2 44 45
3 46 47 48
4 49 50 51 52
5 53 54 55 56 57
6 58 59 60 61 62 63

MATRIX M

This is a FULL matrix of order 1 by 6

	1	2	3	4	5	6
1	8.6579	6.5193	8.1509	8.8697	6.9670	7.9140

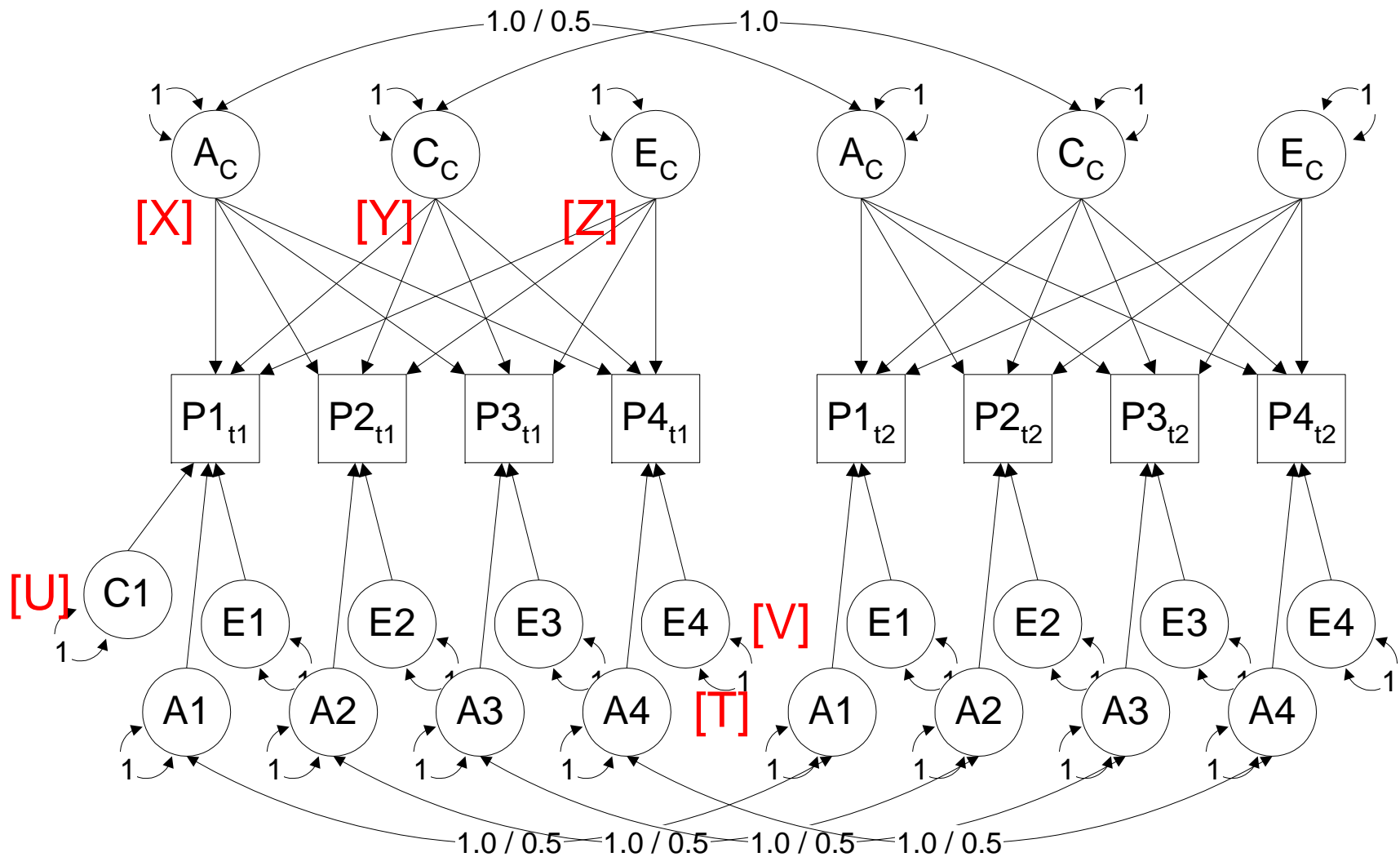
MATRIX P

This is a computed FULL matrix of order 18 by 6

[=S*X_S*Y_S*Z]

	VAR1	VAR2	VAR3	VAR4	VAR5	VAR6
A1	0.8373	0.0000	0.0000	0.0000	0.0000	0.0000
A2	-0.0194	0.8774	0.0000	0.0000	0.0000	0.0000
A3	0.1209	0.1590	-0.6408	0.0000	0.0000	0.0000
A4	0.3281	0.1001	-0.6566	0.0235	0.0000	0.0000
A5	0.1680	0.4917	0.0297	-0.1399	-0.0002	0.0000
A6	0.3087	0.3156	-0.2956	-0.7862	-0.0009	-0.0003
C1	-0.2040	0.0000	0.0000	0.0000	0.0000	0.0000
C2	-0.2692	0.0045	0.0000	0.0000	0.0000	0.0000
C3	0.0586	0.0608	-0.0234	0.0000	0.0000	0.0000
C4	0.0552	0.0126	-0.0043	0.0000	0.0000	0.0000
C5	-0.5321	-0.1865	0.0724	-0.0001	0.0002	0.0000
C6	-0.0294	0.0463	-0.0198	0.0000	0.0000	0.0000
E1	-0.5072	0.0000	0.0000	0.0000	0.0000	0.0000
E2	-0.1656	-0.3604	0.0000	0.0000	0.0000	0.0000
E3	-0.0630	-0.1009	0.7264	0.0000	0.0000	0.0000
E4	0.1751	-0.0590	0.3896	-0.5114	0.0000	0.0000
E5	-0.0941	-0.0660	-0.0411	-0.0367	-0.6084	0.0000
E6	-0.0978	0.0803	0.0224	-0.0449	-0.0393	-0.2761

Independent Pathway Model





Path Diagram to Matrices

Variance Component	a^2	c^2	e^2	
Common Factors	[X] 6 x 1	[Y] 6 x 1	[Z] 6 x 1	
Residual Factors	[T] 6 x 6	[U] 6 x 6	[V] 6 x 6	
<pre>#define nvar 6 #define nfac 1</pre>				

MATRIX M

This is a FULL matrix of order 1 by 6

```
  1  2  3  4  5  6
1  37 38 39 40 41 42
```

MATRIX T

This is a DIAGONAL matrix of order 6 by 6

```
  1  2  3  4  5  6
1  19
2  0 20
3  0  0 21
4  0  0  0 22
5  0  0  0  0 23
6  0  0  0  0  0 24
```

MATRIX U

This is a DIAGONAL matrix of order 6 by 6

```
  1  2  3  4  5  6
1  25
2  0 26
3  0  0 27
4  0  0  0 28
5  0  0  0  0 29
6  0  0  0  0  0 30
```

MATRIX V

This is a DIAGONAL matrix of order 6 by 6

```
  1  2  3  4  5  6
1  31
2  0 32
3  0  0 33
4  0  0  0 34
5  0  0  0  0 35
6  0  0  0  0  0 36
```

MATRIX X

This is a FULL matrix of order 6 by 1

```
  1
1  1
2  2
3  3
4  4
5  5
6  6
```

MATRIX Y

This is a FULL matrix of order 6 by 1

```
  1
1  7
2  8
3  9
4 10
5 11
6 12
```

MATRIX Z

This is a FULL matrix of order 6 by 1

```
  1
1 13
2 14
3 15
4 16
5 17
6 18
```


MATRIX M

This is a FULL matrix of order 1 by 6

	1	2	3	4	5	6
1	8.6602	6.5252	8.1571	8.8747	6.9730	7.9133

MATRIX P

18 by 1

[=S*X_S*Y_S*Z]

	VAR1
A1	-0.4395
A2	-0.5741
A3	-0.3603
A4	-0.3932
A5	-0.6905
A6	-0.5802
C1	0.0120
C2	-0.4167
C3	0.3551
C4	0.4341
C5	-0.4406
C6	0.1435
E1	0.0341
E2	-0.0857
E3	-0.8626
E4	-0.5373
E5	0.1131
E6	-0.0313

MATRIX Q

This is a computed FULL matrix of order 18 by 6

[=S*T_S*U_S*V]

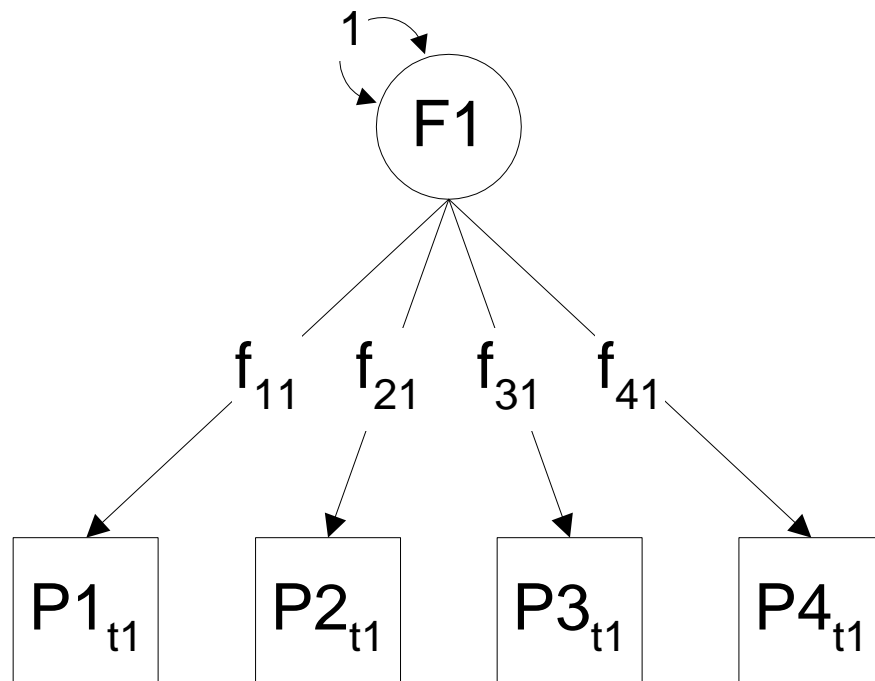
	VAR1	VAR2	VAR3	VAR4	VAR5	VAR6
AS1	0.6384	0.0000	0.0000	0.0000	0.0000	0.0000
AS2	0.0000	0.5342	0.0000	0.0000	0.0000	0.0000
AS3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
AS4	0.0000	0.0000	0.0000	0.0001	0.0000	0.0000
AS5	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
AS6	0.0000	0.0000	0.0000	0.0000	0.0000	0.7382
CS1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CS2	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CS3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CS4	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CS5	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CS6	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
ES1	0.6309	0.0000	0.0000	0.0000	0.0000	0.0000
ES2	0.0000	-0.4517	0.0000	0.0000	0.0000	0.0000
ES3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
ES4	0.0000	0.0000	0.0000	-0.6068	0.0000	0.0000
ES5	0.0000	0.0000	0.0000	0.0000	-0.5625	0.0000
ES6	0.0000	0.0000	0.0000	0.0000	0.0000	-0.3112



Exercise I

- 1. Drop common factor for shared environment
- 2. Drop common factor for specific environment
- 3. Add second genetic common factor

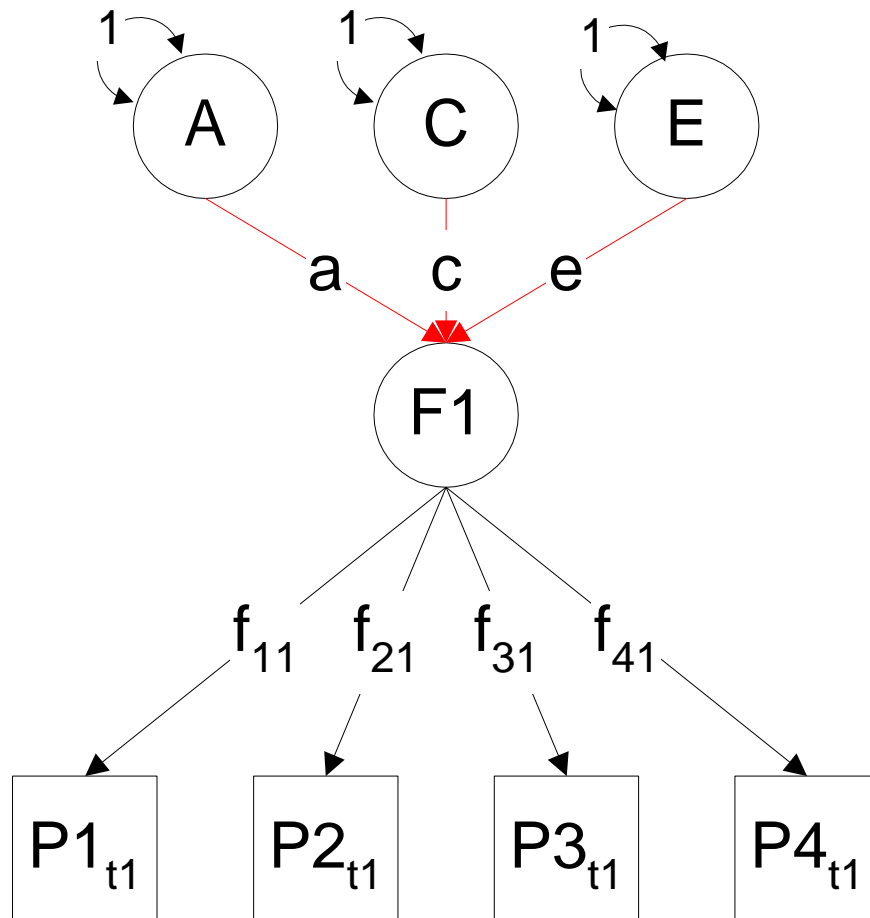
Phenotypic Single Factor



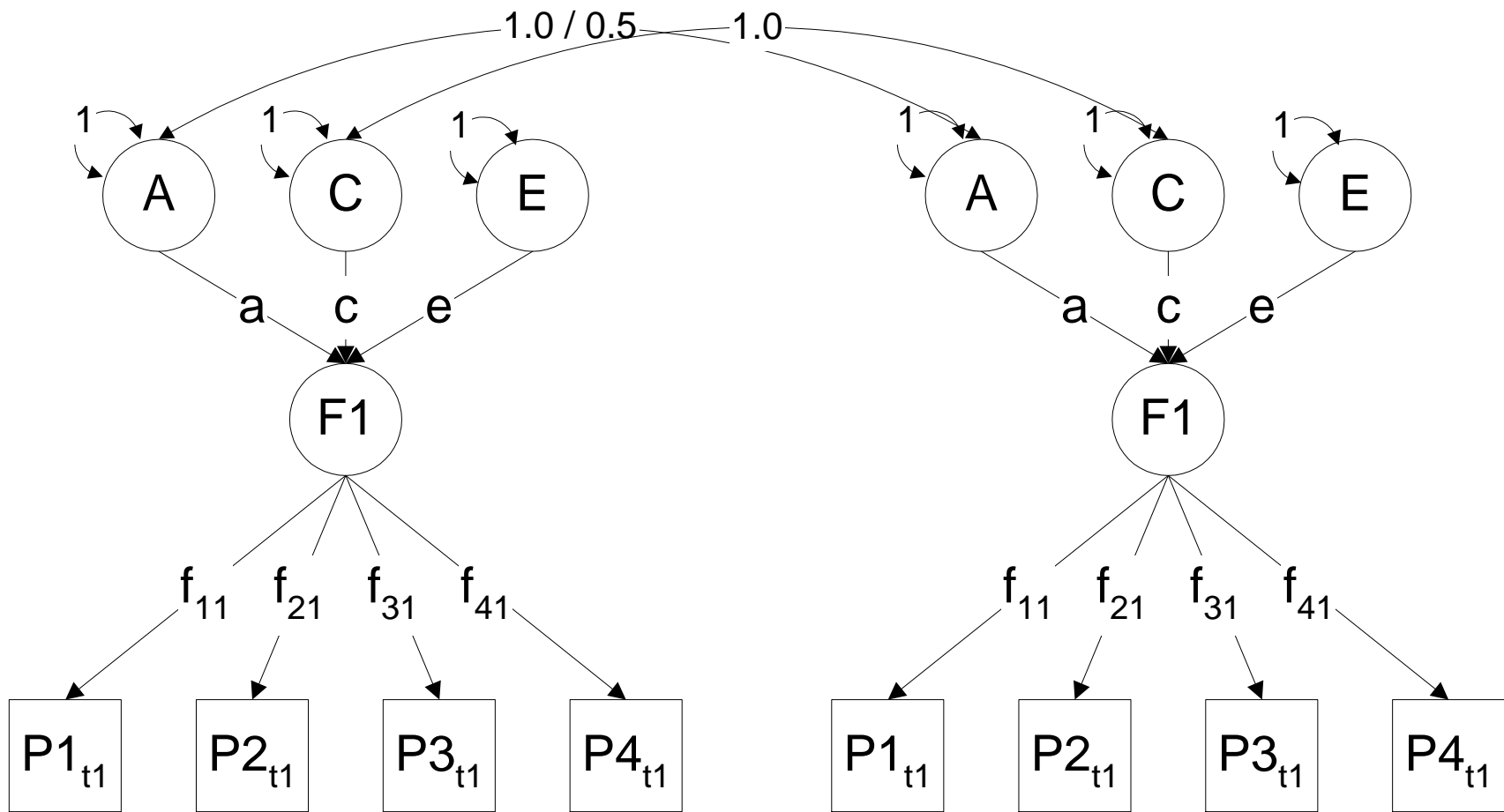
$$\begin{array}{l} F1 \\ P1 \\ P2 \\ P3 \\ P4 \end{array} \begin{bmatrix} f_{11} \\ f_{21} \\ f_{31} \\ f_{41} \end{bmatrix} * \begin{bmatrix} f_{11} & f_{21} & f_{31} & f_{41} \end{bmatrix}$$

F * **F'**

Latent Phenotype



Twin Data

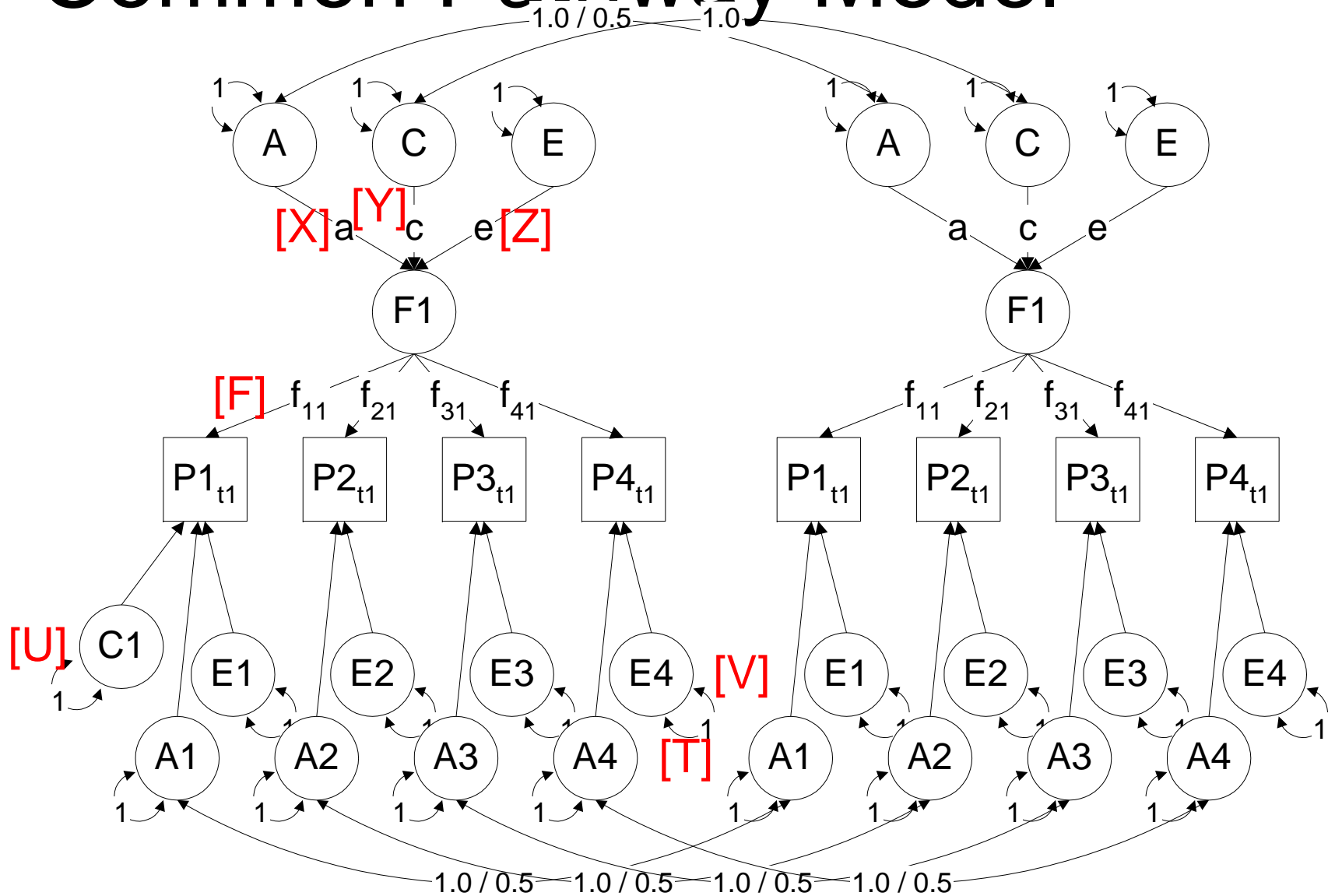


Factor on Latent Phenotype

$$\begin{array}{l} \text{P1} \\ \text{P2} \\ \text{P3} \\ \text{P4} \end{array} \begin{array}{c} \text{F1} \\ \left[\begin{array}{c} f_{11} \\ f_{21} \\ f_{31} \\ f_{41} \end{array} \right] \end{array} * \begin{array}{c} [a] \\ [a] \end{array} * \begin{array}{c} [a] \\ [a] \end{array} * \begin{array}{c} [f_{11} \ f_{21} \ f_{31} \ f_{41}] \end{array}$$

$$\begin{aligned} & \mathbf{F} * \mathbf{X} * \mathbf{X}' * \mathbf{F}' \\ = & \mathbf{F} \& (\mathbf{X} * \mathbf{X}') \end{aligned}$$

Common Pathway Model



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 Iden 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;
- 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

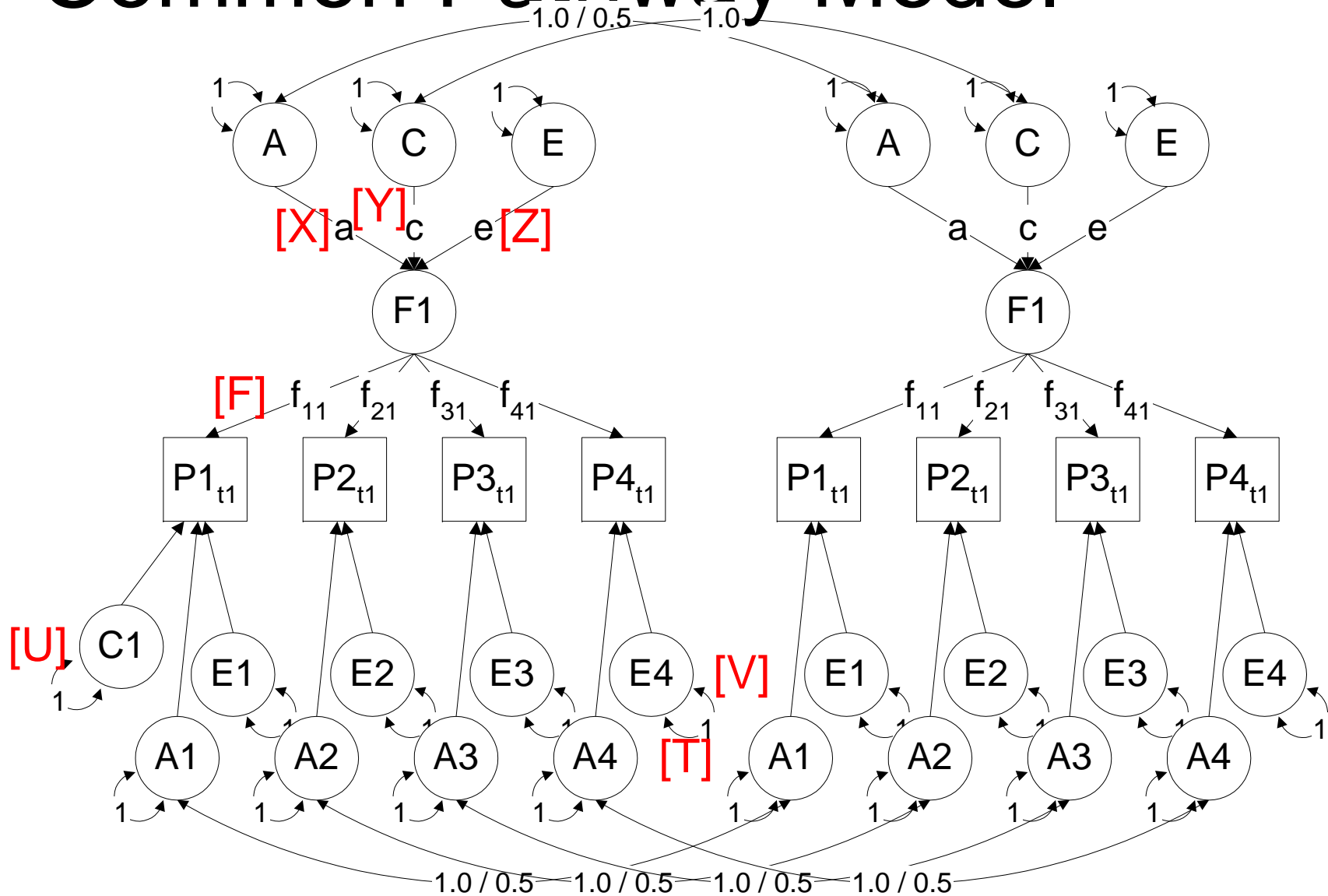
- G5: Calculate Standardised Solution
- Calculation
- Matrices = Group 1
- D Iden nvar nvar
- End Matrices;
- Begin Algebra;
- `R=A+C+E;` ! total variance
- `S=(\sqrt(D.R))~;` ! diagonal matrix of standard deviations
- `P=S*F;` ! standardized estimates for loadings on F
- `Q=S*T_ S*U_ S*V;` ! standardized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



CP

- Common pathway
 - Psychometric model
 - Same covariance structure for A, C and E

Common Pathway Model



Path Diagram to Matrices

Variance Component	a^2	c^2	e^2	
Common Factor	[X] 1 x 1	[Y] 1 x 1	[Z] 1 x 1	[F] 6 x 1
Residual Factors	[T] 6 x 6	[U] 6 x 6	[V] 6 x 6	
<code>#define nvar 6</code> <code>#define nfac 1</code>				

MATRIX M

This is a FULL matrix of order 1 by 6

```
  1  2  3  4  5  6
1 28 29 30 31 32 33
```

MATRIX T

This is a DIAGONAL matrix of order 6 by 6

```
  1  2  3  4  5  6
1  4
2  0  5
3  0  0  6
4  0  0  0  7
5  0  0  0  0  8
6  0  0  0  0  0  9
```

MATRIX U

This is a DIAGONAL matrix of order 6 by 6

```
  1  2  3  4  5  6
1 10
2  0 11
3  0  0 12
4  0  0  0 13
5  0  0  0  0 14
6  0  0  0  0  0 15
```

MATRIX V

This is a DIAGONAL matrix of order 6 by 6

```
  1  2  3  4  5  6
1 16
2  0 17
3  0  0 18
4  0  0  0 19
5  0  0  0  0 20
6  0  0  0  0  0 21
```

MATRIX X

This is a FULL matrix of order 1 by 1

```
  1
1  1
```

MATRIX Y

This is a FULL matrix of order 1 by 1

```
  1
1  2
```

MATRIX Z

This is a FULL matrix of order 1 by 1

```
  1
1  3
```

Goodness-of-Fit Statistics

-2LL	df	R^2	df	p	AIC	ΔR^2	df	p
Saturated								
2656.32	780							
Cholesky								
2878.97	891	222.65	111	.00	0.65			
Independent Pathway								
2909.65	918	253.33	138	.00	-22.7	30.68	27	.28
Common Pathway								
3005.87	928	349.55	148	.00	53.5	126.89	37	.00

MATRIX M

This is a FULL matrix of order 1 by 6

	1	2	3	4	5	6
1	8.6632	6.5259	8.1482	8.8711	6.9694	7.9199

MATRIX P

6 by 1

[=S*F]

	1
F1	-0.1703
F2	-0.1453
F3	-0.8555
F4	-0.8788
F5	-0.0761
F6	-0.3144

MATRIX Q

This is a computed FULL matrix of order 18 by 6

[=S*T_S*U_S*V]

	1	2	3	4	5	6
AS1	0.8247	0.0000	0.0000	0.0000	0.0000	0.0000
AS2	0.0000	0.8981	0.0000	0.0000	0.0000	0.0000
AS3	0.0000	0.0000	0.0001	0.0000	0.0000	0.0000
AS4	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
AS5	0.0000	0.0000	0.0000	0.0000	-0.3939	0.0000
AS6	0.0000	0.0000	0.0000	0.0000	0.0000	0.8929
CS1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CS2	0.0000	-0.0001	0.0000	0.0000	0.0000	0.0000
CS3	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CS4	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CS5	0.0000	0.0000	0.0000	0.0000	0.6309	0.0000
CS6	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
ES1	0.5393	0.0000	0.0000	0.0000	0.0000	0.0000
ES2	0.0000	0.4150	0.0000	0.0000	0.0000	0.0000
ES3	0.0000	0.0000	0.5178	0.0000	0.0000	0.0000
ES4	0.0000	0.0000	0.0000	0.4773	0.0000	0.0000
ES5	0.0000	0.0000	0.0000	0.0000	-0.6640	0.0000
ES6	0.0000	0.0000	0.0000	0.0000	0.0000	-0.3222



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



Exercise II

- 1. Change to 2 Latent Phenotypes corresponding to Verbal IQ and Performance IQ



Summary

- Independent Pathway Model

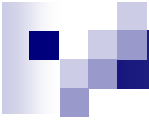
- Biometric Factor Model

- Loadings differ for genetic and environmental common factors

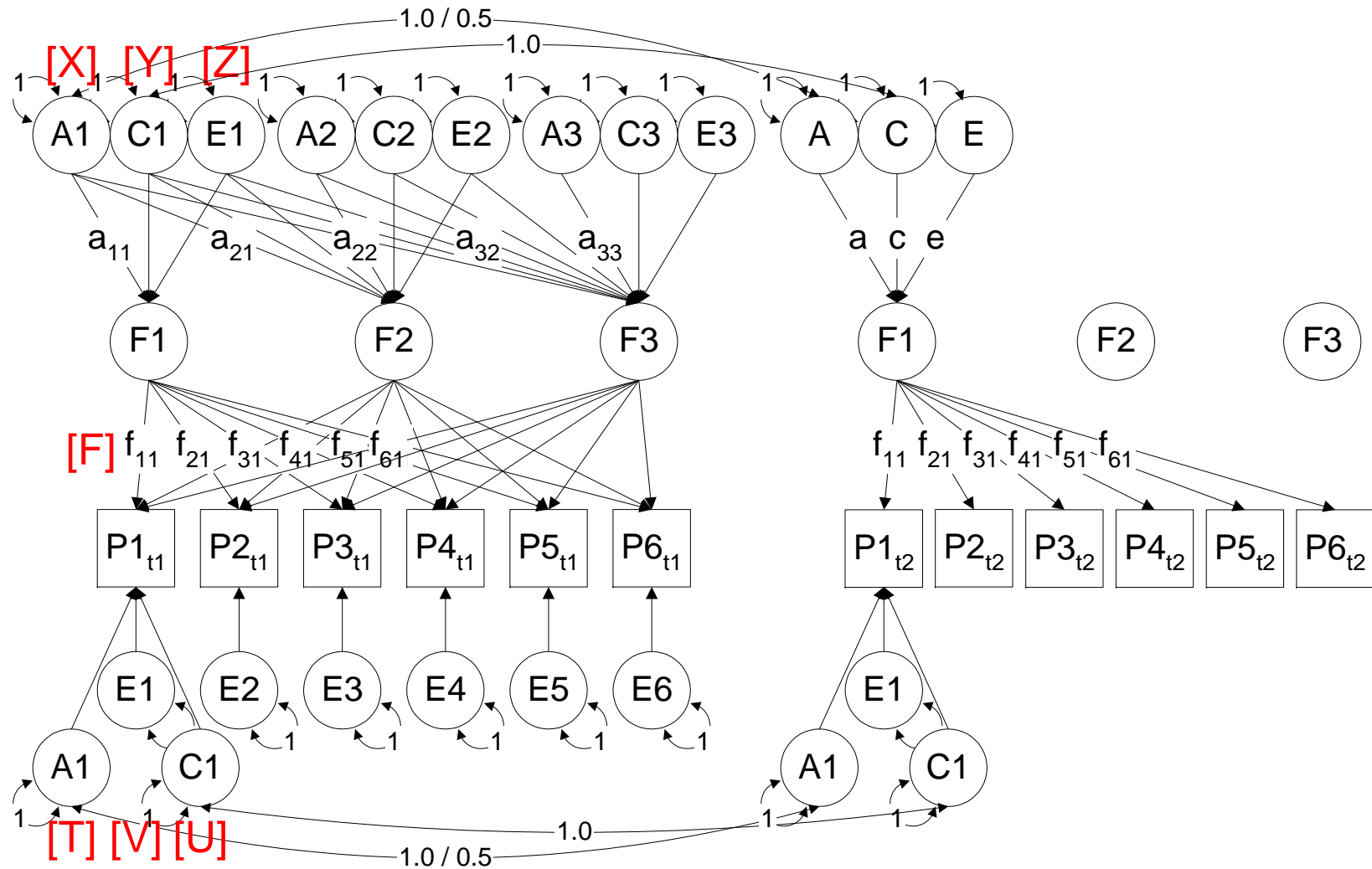
- Common Pathway Model

- Psychometric Factor Model

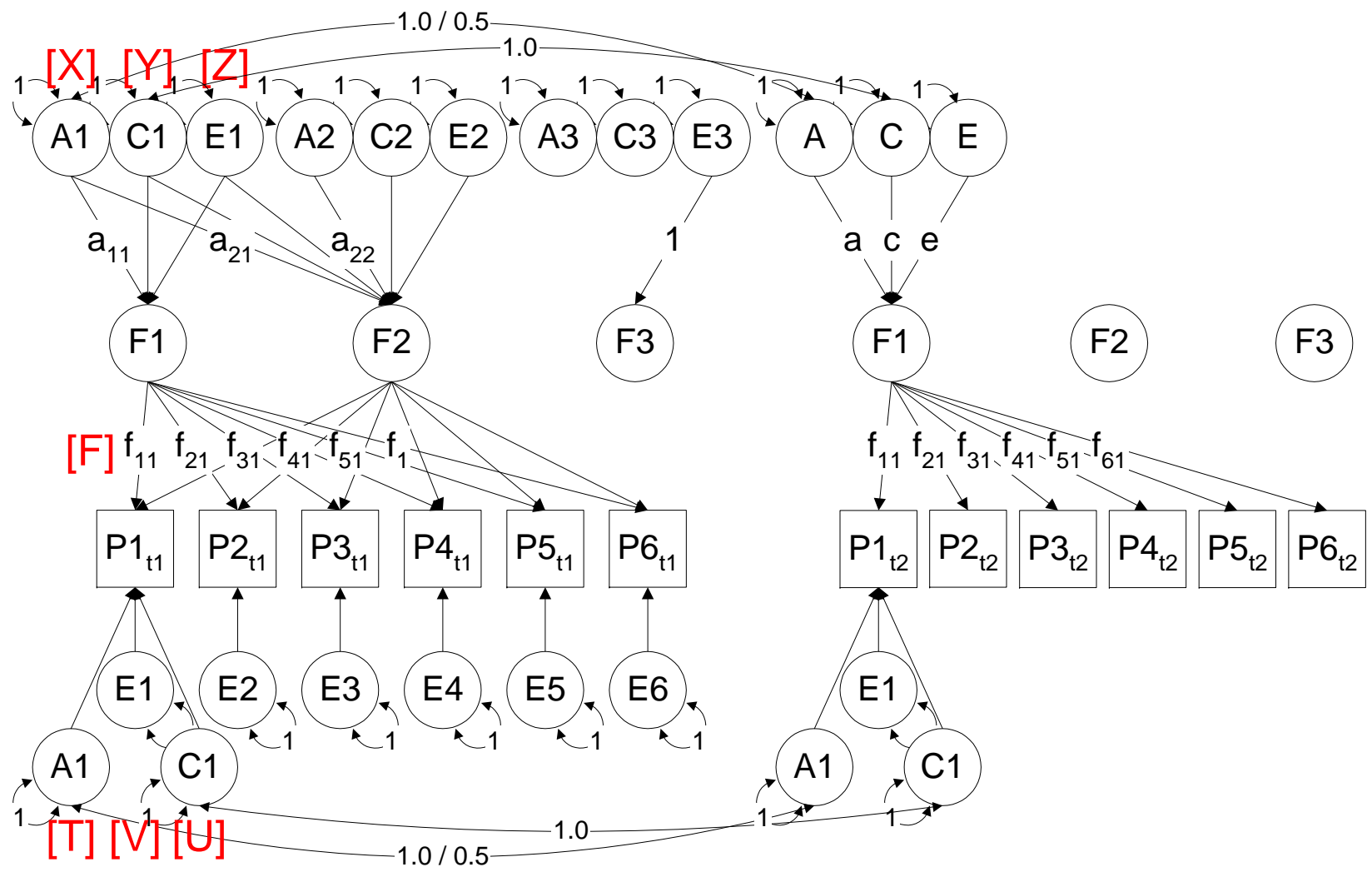
- Loadings equal for genetic and environmental common factor



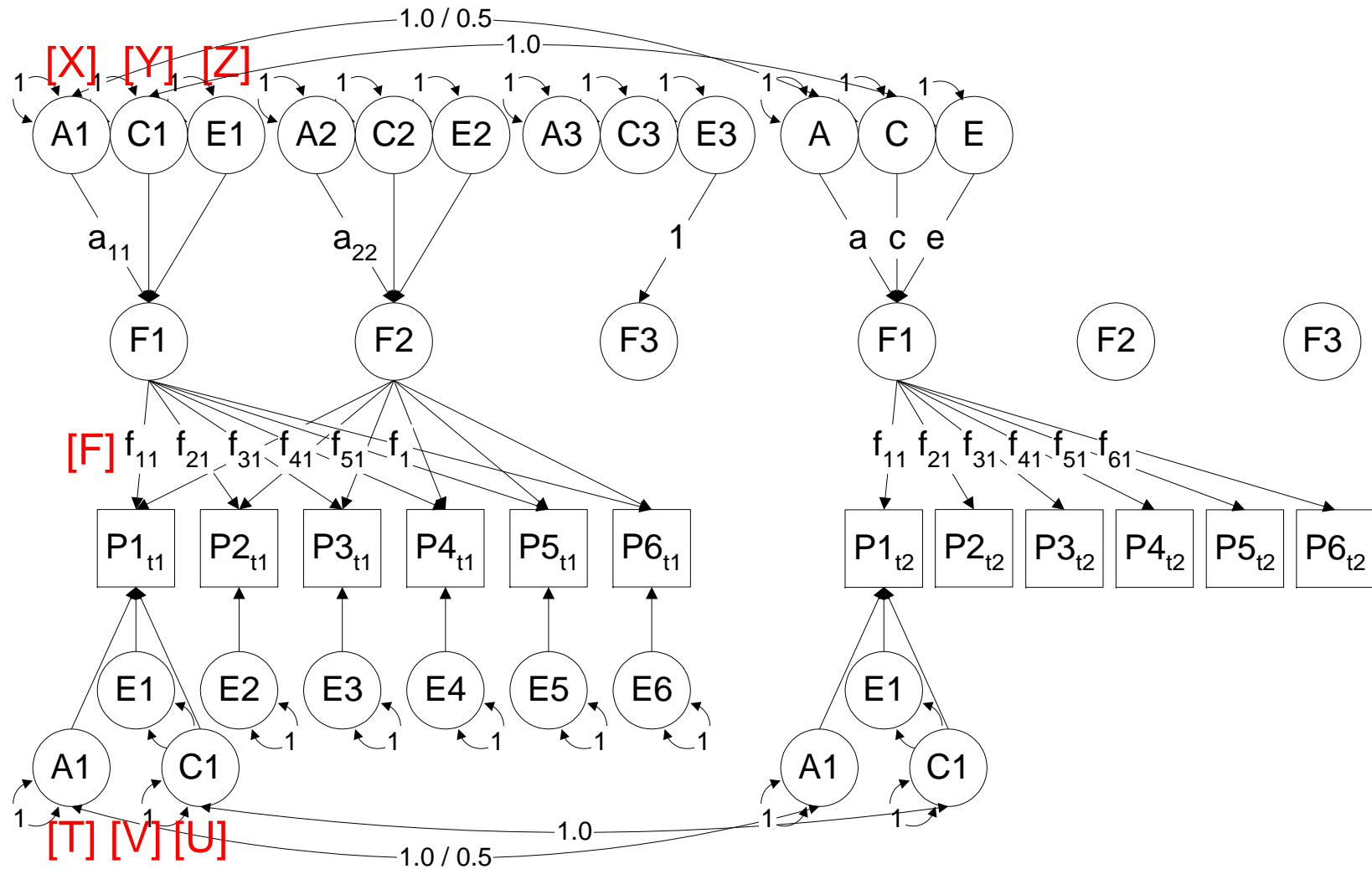
Pathway Model



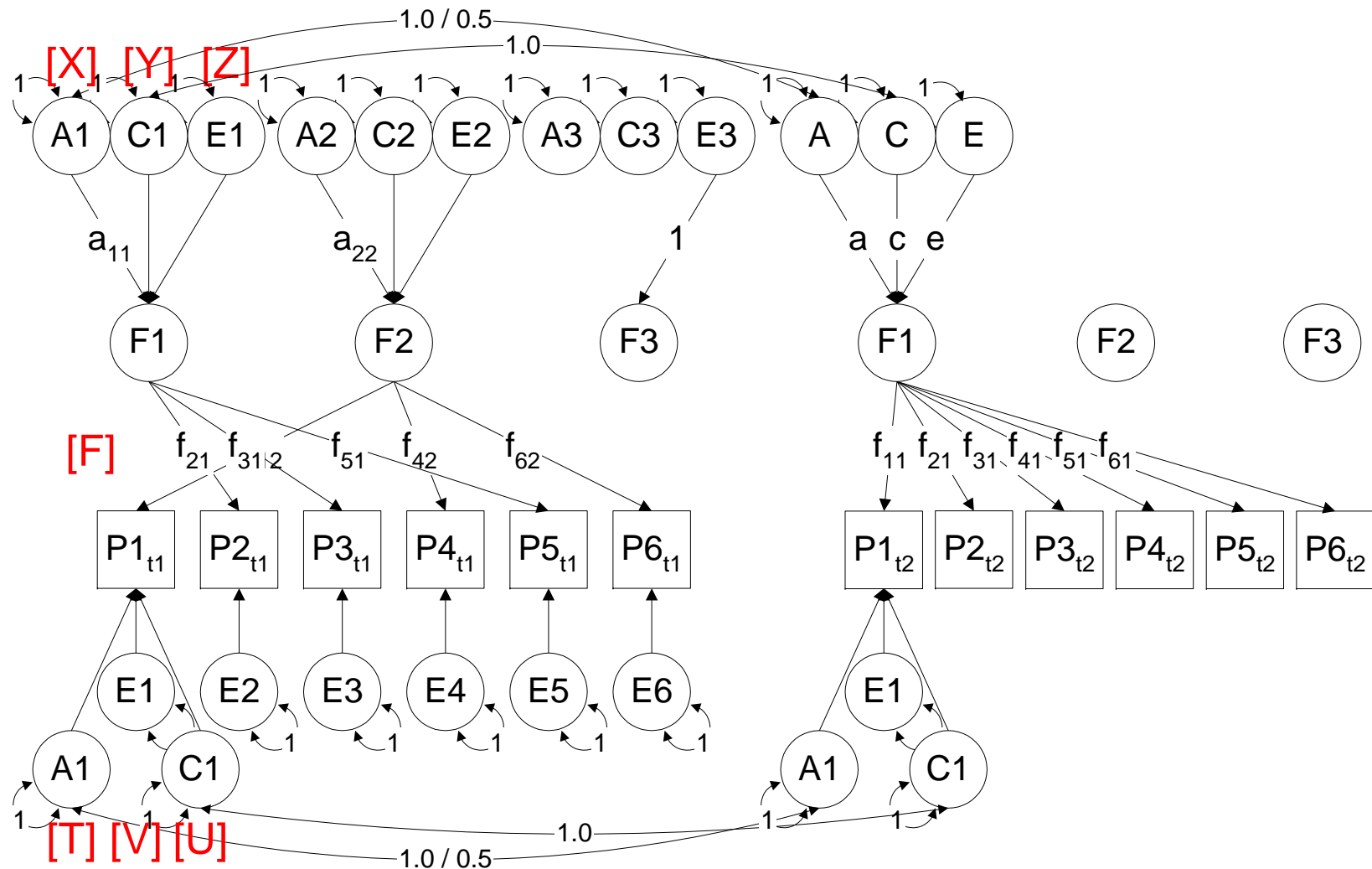
Two Common Pathway Model



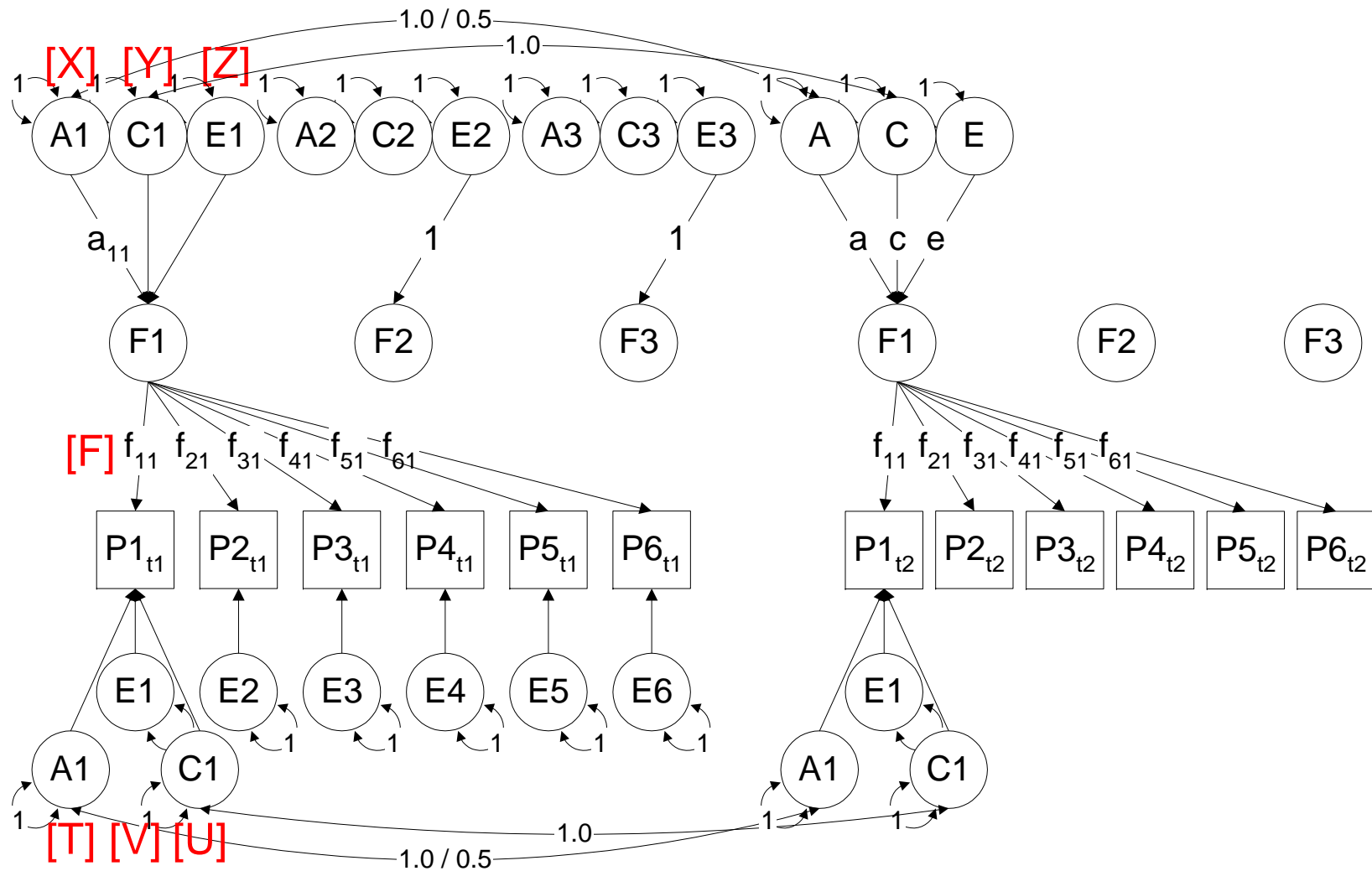
Two Independent CP Model



Two Reduced Indep CP Model



Common Pathway Model



Independent Pathway Model

