Practical

SCRIPT:

F:\meike\2010\Multi_prac\MultivariateTwinAnalysis_MatrixRaw.r

DATA:

DHBQ_bs.dat

DATA

- General Family Functioning, Subjective Happiness

- T1, T2, brother, sister

- missing -999

DATA

```
require(OpenMx)

source("GenEpiHelperFunctions.R")


FamData <- read.table ("DHBQ_bs.dat", header=T, na=-999)

require(psych)

summary (FamData)

describe(FamData)

names(FamData)

Famvars <- colnames (FamData)

Vars <- c('gff', 'hap')

nv <- 2

selVars <- paste(Vars,c(rep(1,nv),rep(2,nv)),sep="")   #c('gff1', 'hap1','gff2' 'hap2')

ntv <- nv*2

mzData <- subset(FamData, zyg2==1, selVars)

dzData <- subset(FamData, zyg2==2, selVars)
```

Observed Cross-twin Cross-trait Correlations

Print Descriptives

summary(mzData)

summary(dzData)

describe(mzData)

describe(dzData)

colMeans(mzData,na.rm=TRUE)

colMeans(dzData,na.rm=TRUE)

cov(mzData,use="complete")

cov(dzData,use="complete")

cor(mzData,use="complete")

cor(dzData,use="complete")

Observed Cross-twin Cross-trait Correlations

> cor(mzData,use="complete")

	gff1	hap1	gff2	hap2
gff1	1.00	0.40	0.50	0.27
hap1	0.40	1.0	0.26	0.31
gff2	0.50	0.26	1.00	0.31
hap2	0.27	0.31	0.31	1.00

> cor(dzData,use="complete")

	gff1	hap1	gff2	hap2
gff1	1.00	0.35	0.35	0.12
hap1	0.35	1.00	0.19	0.15
gff2	0.35	0.19	1.00	0.32
hap2	0.12	0.15	0.32	1.00

>

Estimated Cross-twin Cross-trait Correlations

```
# Fit Model to estimate Twin Correlations and Cross-twin Cross trait correlations by ML

multTwinCorModel <- mxModel(multTwinSatFit, name="multTwinSatCor",

   mxModel(multTwinSatFit$MZ,

      mxMatrix( type="Iden", nrow=ntv, ncol=ntv, name="I"),

      mxAlgebra( expression= solve(sqrt(I*expCovMZ)) %*% expCovMZ %*% solve(sqrt(I*expCovMZ)),
name="expCorMZ" )

   ),

   mxModel(multTwinSatFit$DZ,

      mxMatrix( type="Iden", nrow=ntv, ncol=ntv, name="I"),

      mxAlgebra( expression= solve(sqrt(I*expCovDZ)) %*% expCovDZ %*% solve(sqrt(I*expCovDZ)),
name="expCorDZ" )

   ) )

multTwinCorFit <- mxRun(multTwinCorModel)

multTwinCorFit$MZ$expCorMZ

multTwinCorFit$DZ$expCorDZ
```

PRAC I.
Estimated Cross-twin Cross-trait Correlations

1. Run Script

2. Compare Observed and Estimated Cross-Twin Cross-Trait Correlations

3. Based on these correlations what do you expect for A, C, and E (var and cov!)?

Cross-twin Cross-trait Correlations

> cor(mzData,use="complete")

	gff1	hap1	gff2	hap2
gff1	1.00	0.40	0.50	0.27
hap1	0.40	1.0	0.26	0.31
gff2	0.50	0.26	1.00	0.31
hap2	0.27	0.31	0.31	1.00

mxAlgebra '**expCorMZ**'

	[,1]	[,2]	[,3]	[,4]
[1,]	1.00	0.38	0.48	0.25
[2,]	0.38	1.00	0.24	0.29
[3,]	0.48	0.24	1.00	0.30
[4,]	0.25	0.29	0.30	1.00

> cor(dzData,use="complete")

	gff1	hap1	gff2	hap2
gff1	1.00	0.35	0.35	0.12
hap1	0.35	1.00	0.19	0.15
gff2	0.35	0.19	1.00	0.32
hap2	0.12	0.15	0.32	1.00

mxAlgebra '**expCorDZ**'

	[,1]	[,2]	[,3]	[,4]
[1,]	1.00	0.35	0.36	0.13
[2,]	0.35	1.00	0.20	0.16
[3,]	0.36	0.20	1.00	0.34
[4,]	0.13	0.16	0.34	1.00

>

Within individual cross trait correlation

Twin correlations

Cross-twin cross-trait correlations

ACE model

GFF -->   MZ > DZ, but not >2x -> ACE

HAP-->   MZ > DZ-> ACE, AE

GFF-HAP -->   MZ > DZ-> ACE, AE

Start with an ACE model

PRAC II.
The ACE model and its estimates

1. Run the ACE model

2. What is the heritability of GFF and HAP?

3. What is the genetic influence on the covariance?

4. What is the genetic correlation?

Standardized Variance and Covariance Components

[1] "Matrix ACE.A/ACE.V"

   stCovComp_A1 stCovComp_A2

gff	0.2491	0.4784
hap	0.4784	0.2673

[1] "Matrix ACE.C/ACE.V"

   stCovComp_C1 stCovComp_C2

gff	0.2441	0.2417
hap	0.2417	0.0292

[1] "Matrix ACE.E/ACE.V"

   stCovComp_E1 stCovComp_E2

gff	0.5069	0.2799
hap	0.2799	0.7035

GFF -->   MZ > DZ, but not >2x -> ACE

HAP-->   MZ > DZ-> ACE, AE

GFF-HAP -->   MZ > DZ-> ACE, AE

Genetic and Environmental Correlations

[1] "Matrix solve(sqrt(ACE.I*ACE.A)) %*% ACE.A %*% solve(sqrt(ACE.I*ACE.A))"

	corComp_A1	corComp_A2
gff	1.0000	0.6477
hap	0.6477	1.0000

[1] "Matrix solve(sqrt(ACE.I*ACE.C)) %*% ACE.C %*% solve(sqrt(ACE.I*ACE.C))"

	corComp_C1	corComp_C2
gff	1.0000	1.0000
hap	1.0000	1.0000

[1] "Matrix solve(sqrt(ACE.I*ACE.E)) %*% ACE.E %*% solve(sqrt(ACE.I*ACE.E))"

	corComp_E1	corComp_E2
gff	1.0000	0.1637
hap	0.1637	1.0000

>

ACE vs AE model

```
# Fit Multivariate AE model

# ------------------------------------------------------------------------

multAEModel <- mxModel(multACEFit, name="multAE",

  mxModel(multACEFit$ACE,

    mxMatrix( type="Lower", nrow=nv, ncol=nv, free=FALSE, values=0, name="c" ) # drop c at 0

  )

)
```

> tableFitStatistics(multACEFit, multAEFit)

Name	ep	-2LL	df	AIC	diffLL	diffdf	p
Model 1 : multACE	11	61033.46	10426	40181.46	-	-	-
Model 2 : multAE	8	61058.94	10429	40200.94	25.49	3	0

Standardized Variance and Covariance Components

[1] "Matrix ACE.A/ACE.V"

	stCovComp_A1	stCovComp_A2
gff	0.2491	0.4784
hap	0.4784	0.2673

[1] "Matrix ACE.C/ACE.V"

	stCovComp_C1	stCovComp_C2
gff	0.2441	0.2417
hap	0.2417	0.0292

[1] "Matrix ACE.E/ACE.V"

	stCovComp_E1	stCovComp_E2
gff	0.5069	0.2799
hap	0.2799	0.7035

ACE vs ACEAE model

Fit Multivariate GFF-ACE & HAP-AE model

--

multACE_ACEAEModel <- mxModel(multACEFit, name="multACE_ACEAE",

  mxModel(multACEFit$ACE,

    mxMatrix(type="Lower", nrow=nv, ncol=nv, free=c(T,F,F), values=0, name="c") # drop c21 &
c22 at 0

)

)

Name	ep	-2LL	df	AIC	diffLL	diffdf	p
Model 1 : multACE	11	61033.46	10426	40181.46	-	-	-
Model 2 : multAE	8	61058.94	10429	40200.94	25.49	3	0
Model 3 : multACE_ACEAE	9	61037.98	10428	40181.98	4.53	2	0.1

Genetic and Environmental Correlations

[1] "Matrix solve(sqrt(ACE.I*ACE.A)) %*% ACE.A %*% solve(sqrt(ACE.I*ACE.A))"

	corComp_A1	corComp_A2
gff	1.0000	0.6477
hap	0.6477	1.0000

Is the .65 significant different from 1 ?

[1] "Matrix solve(sqrt(ACE.I*ACE.C)) %*% ACE.C %*% solve(sqrt(ACE.I*ACE.C))"

	corComp_C1	corComp_C2
gff	1.0000	1.0000
hap	1.0000	1.0000

[1] "Matrix solve(sqrt(ACE.I*ACE.E)) %*% ACE.E %*% solve(sqrt(ACE.I*ACE.E))"

	corComp_E1	corComp_E2
gff	1.0000	0.1637
hap	0.1637	1.0000

>

rA=1

```
multACE_AcModel <- mxModel(multACEFit, name="multACE_Ac",
   mxModel(multACEFit$ACE,
      mxMatrix( type="Lower", nrow=nv, ncol=nv, free=c(T,T,F), values=0, name="a" ) # drop a22 at 0
   )
)
```

Name	ep	-2LL	df	AIC	diffLL	diffdf	p
Model 1 : multACE	11	61033.46	10426	40181.46	-	-	-
Model 2 : multAE	8	61058.94	10429	40200.94	25.49	3	0
Model 3 : multACE_ACEAE	9	61037.98	10428	40181.98	4.53	2	0.1
Model 4 : multACE_Ac	10	61036.73	10427	40182.73	3.27	1	0.07
Model 5 : multBest	8	61038.61	10429	40180.61	5.15	3	0.16

PRAC III.
Trivariate Model

1. Add a third variable (Satisfaction with Life) to the model

2. Run model and submodels

3. What is the best fitting model?

2. What are the parameter estimates?

3. What is the genetic correlation?

Changes that had to be made

```
FamData <- read.table ("DHBQ_bs.dat", header=T, na=-999)

require(psych)

summary (FamData)

describe(FamData)

names(FamData)

Famvars <- colnames (FamData)

Vars <- c('gff', 'hap', 'sat')

nv <- 3

selVars <- paste(Vars,c(rep(1,nv),rep(2,nv)),sep="")   #c('gff1', 'hap1', 'sat1','gff2' 'hap2', 'sat2')

ntv <- nv*2

mzData <- subset(FamData, zyg2==1, selVars)

dzData <- subset(FamData, zyg2==2, selVars)
```

Changes that had to be made

multACEModel <- mxModel("multACE",

  mxModel("ACE",

  # Matrices a, c, and e to store a, c, and e path coefficients

    mxMatrix(type="Lower", nrow=nv, ncol=nv, free=TRUE, values=.6,

        label=c("a11", "a21", "a31", "a22", "a32", "a33"), name="a"),

    mxMatrix(type="Lower", nrow=nv, ncol=nv, free=TRUE, values=.6,

        label=c("c11", "c21", "c31", "c22", "c32", "c33"), name="c"),

    mxMatrix(type="Lower", nrow=nv, ncol=nv, free=TRUE, values=.6,

        label=c("e11", "e21", "e31", "e22", "e32", "e33"), name="e"),

Changes that had to be made

```
 # Fit Multivariate ACE-AE-AE model
# ----------------------------------------------------------------------
multACEAEAEModel <- mxModel(multACEFit, name="multACEAEAE",
   mxModel(multACEFit$ACE,
      mxMatrix( type="Lower", nrow=nv, ncol=nv, free=c(T,F,F,F,F,F), values=c(.5,0,0,0,0,0),, name="c" )
   )
)
```

Changes that had to be made

```
 # Fit Multivariate ACE-AE-AE model

# ----------------------------------------------------------------------

multACEAEAEModel <- mxModel(multACEFit, name="multACEAEAE",

   mxModel(multACEFit$ACE,

      mxMatrix( type="Lower", nrow=nv, ncol=nv, free=c(T,F,F,F,F,F), values=c(.5,0,0,0,0,0),, name="c" )

   )

)
```

Genetic and Environmental Influences

[1] "Matrix ACE.A/ACE.V"

	stCovComp_A1	stCovComp_A2	stCovComp_A3
gff	0.2882	0.7759	0.8403
hap	0.7759	0.3027	0.3973
sat	0.8403	0.3973	0.3854

[1] "Matrix ACE.C/ACE.V"

	stCovComp_C1	stCovComp_C2	stCovComp_C3
gff	0.2066	0.0000	0.0000
hap	0.0000	0.0000	0.0000
sat	0.0000	0.0000	0.0000

[1] "Matrix ACE.E/ACE.V"

	stCovComp_E1	stCovComp_E2	stCovComp_E3
gff	0.5052	0.2241	0.1597
hap	0.2241	0.6973	0.6027
sat	0.1597	0.6027	0.6146

Genetic and Environmental Correlations

[1] "Matrix solve(sqrt(ACE.I*ACE.A)) %*% ACE.A %*% solve(sqrt(ACE.I*ACE.A))"

	corComp_A1	corComp_A2	corComp_A3
gff	1.0000	0.9014	0.9139
hap	0.9014	1.0000	0.8410
sat	0.9139	0.8410	1.0000

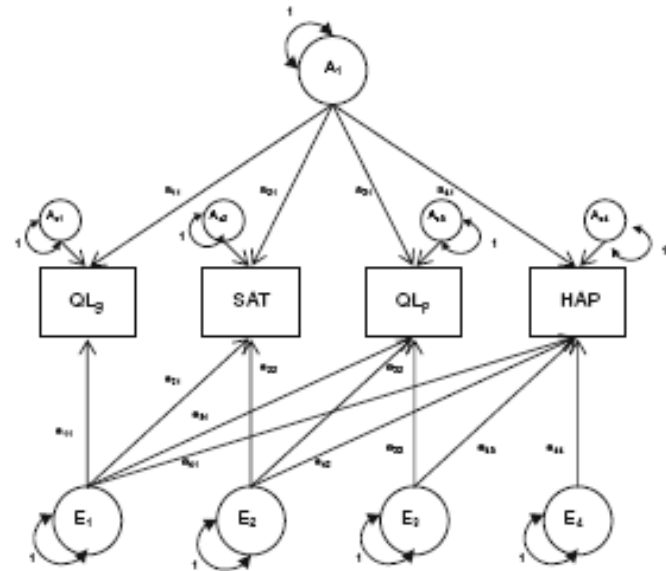[1] "Matrix solve(sqrt(ACE.I*ACE.E)) %*% ACE.E %*% solve(sqrt(ACE.I*ACE.E))"

	corComp_E1	corComp_E2	corComp_E3
gff	1.0000	0.1295	0.1039
hap	0.1295	1.0000	0.6654
sat	0.1039	0.6654	1.0000

After the Break

Genetic and environmental factor analysis examples
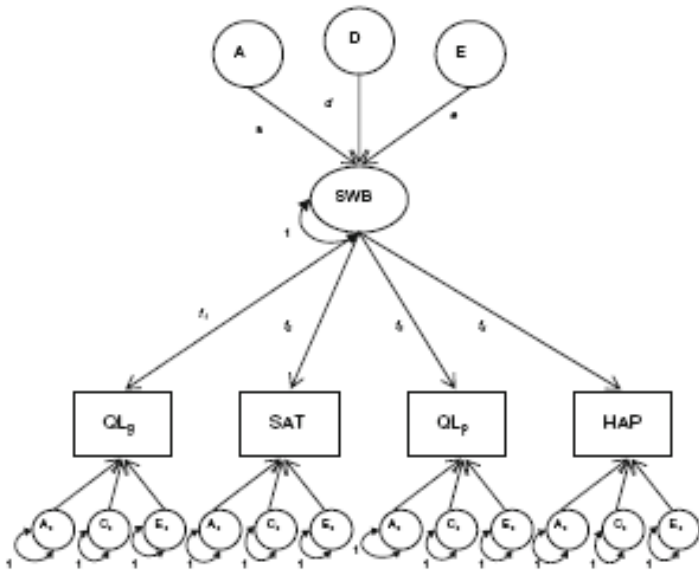
Common Pathway Model   Independent Pathway Model