



# Comorbidity Models

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# Overview

- Psychiatric Disorders: binary phenotypes
  - Lots of comorbidity
  - Substance abuse similar
- ACE model is but one of many
- Two twins, two binary variables
  - 16 outcome combinations
- Fit models by maximum likelihood
  - (alternatives exist)

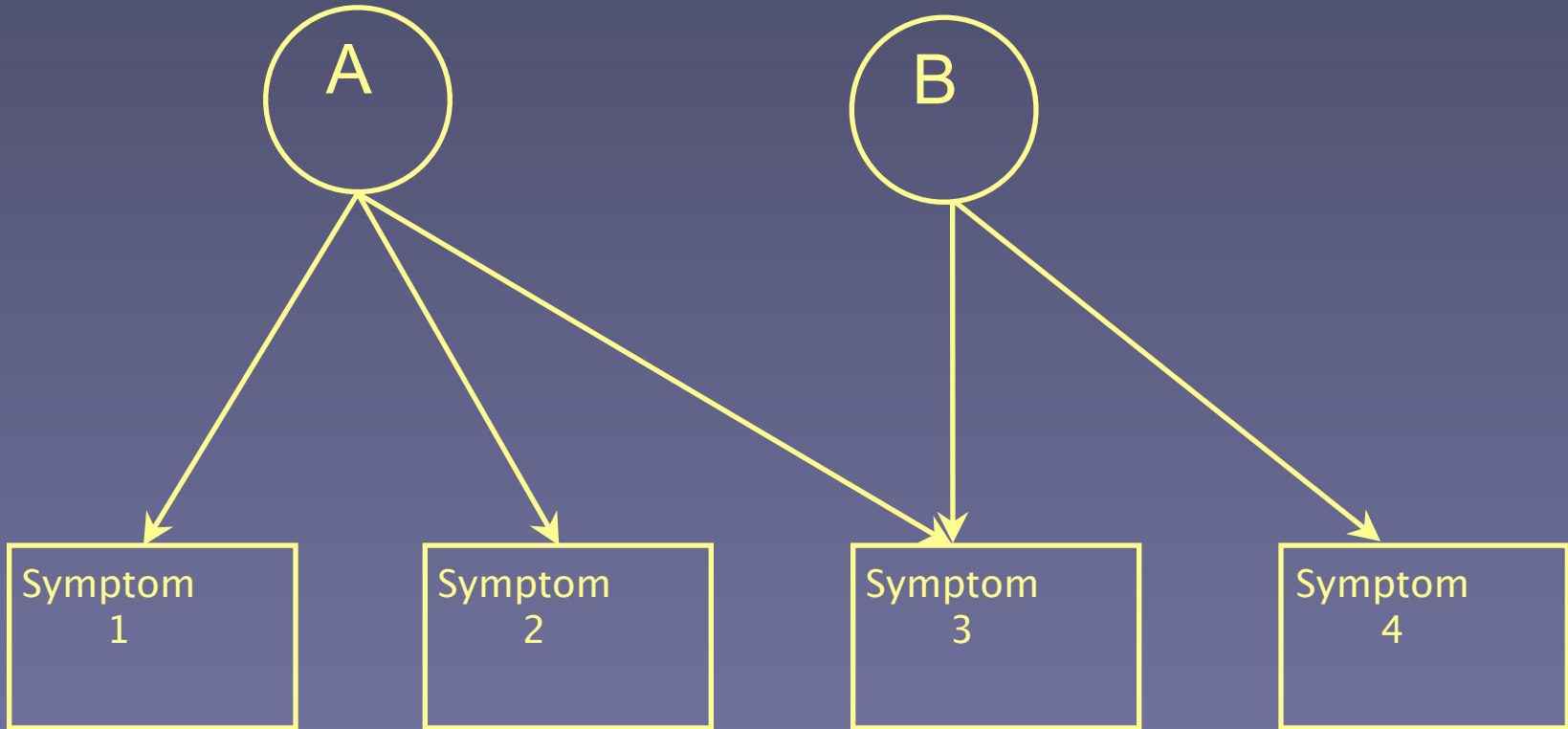
# Assessment of Psychiatric Disorders

- Psychiatrists can agree on symptoms better than on diagnoses (Kendell et al 1971)
- Diagnostic and Statistical Manual of Mental Disorders (DSM-III 1980; DSM-III-R 1987; DSM-IV 1994; DSM-IV 2012). Widespread use
- Little empirical basis for classification
- “If you believe...”

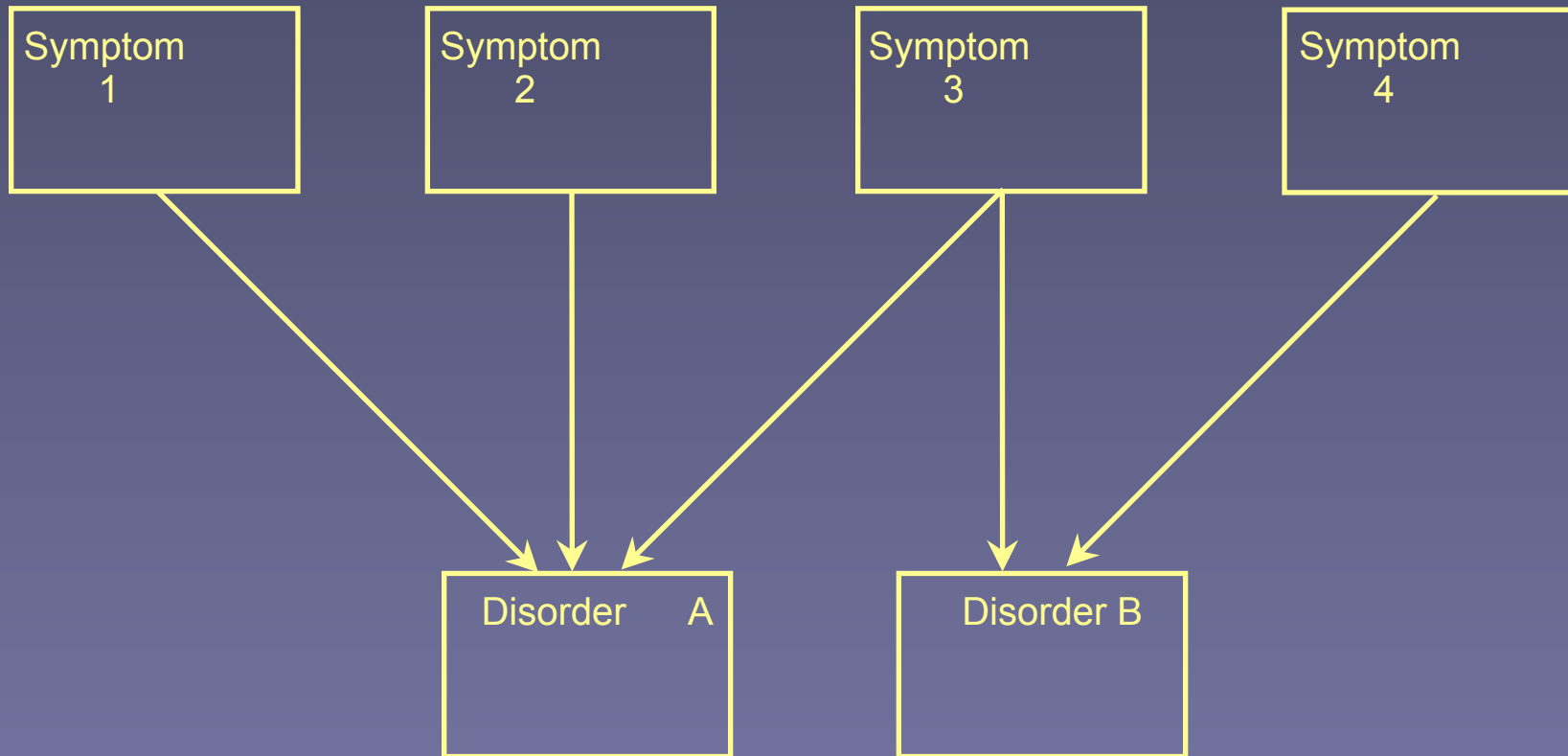
# Comorbidity is High

- High for Psychiatric Disorders
  - Anxiety
  - Depression
  - Phobias
  - Panic
  - Alcohol Abuse
- 70% of those with history of 1 have history of at least one other (Kessler 1993; N=18,000)
- Similar rates in 10,000+ Virginia twins

# Pure forms of two disorders A & B generate some of the same symptoms

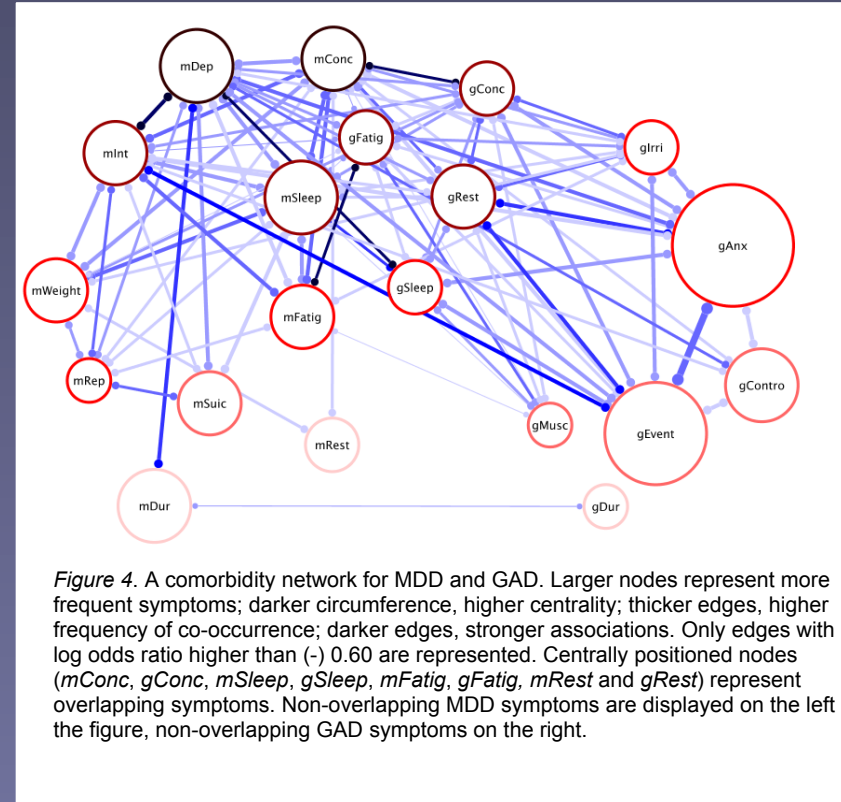
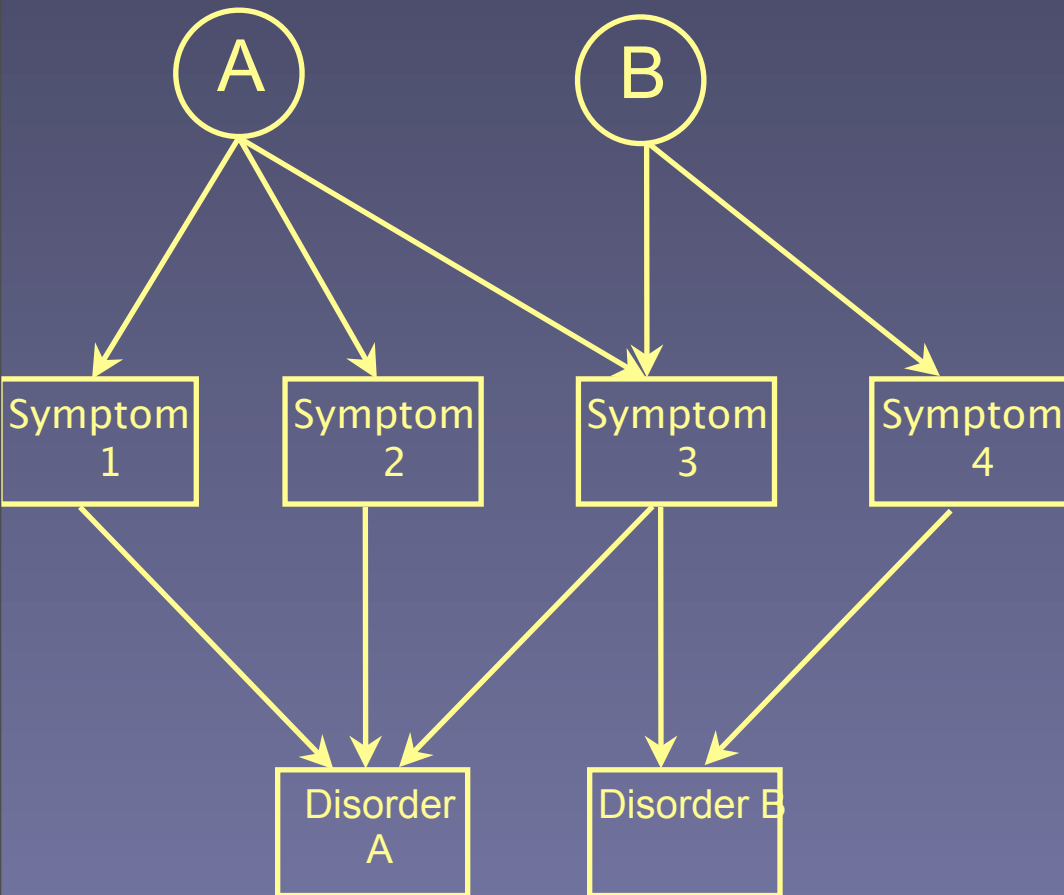


# Assessments of disorders A & B share some symptoms



Cramer, Waldrop, Van der Maas, Borsboom (In Press)  
Comorbidity: A network perspective. Brain Behavior Sciences

# Comorbidity due to symptom sharing



Not today!

# Why do people get a disorder?

Single factor of large effect?

Lots of little factors of cumulative effect?

Both?

How do we find out which?

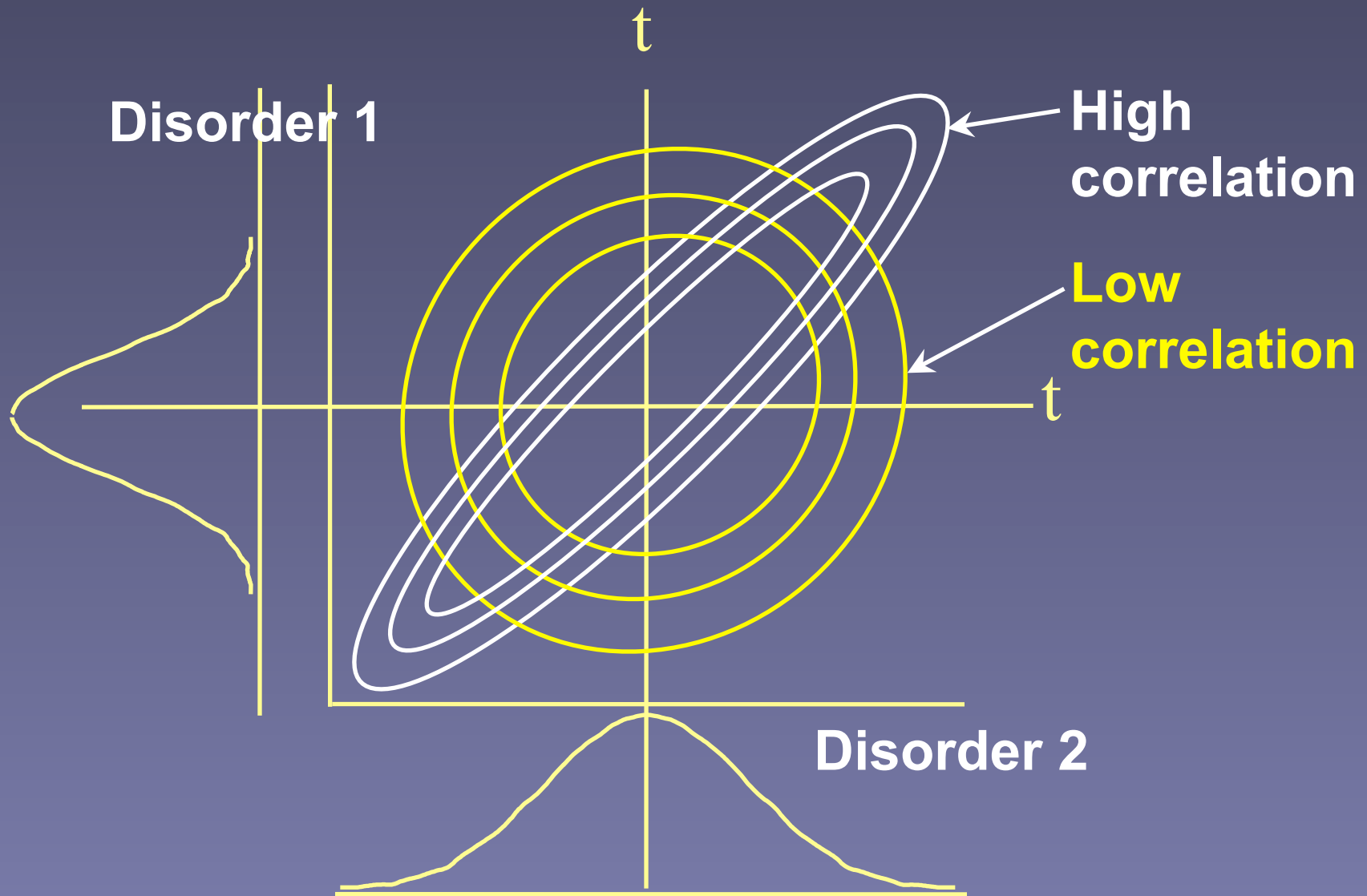
- Measure variation

- Measure covariation to understand it

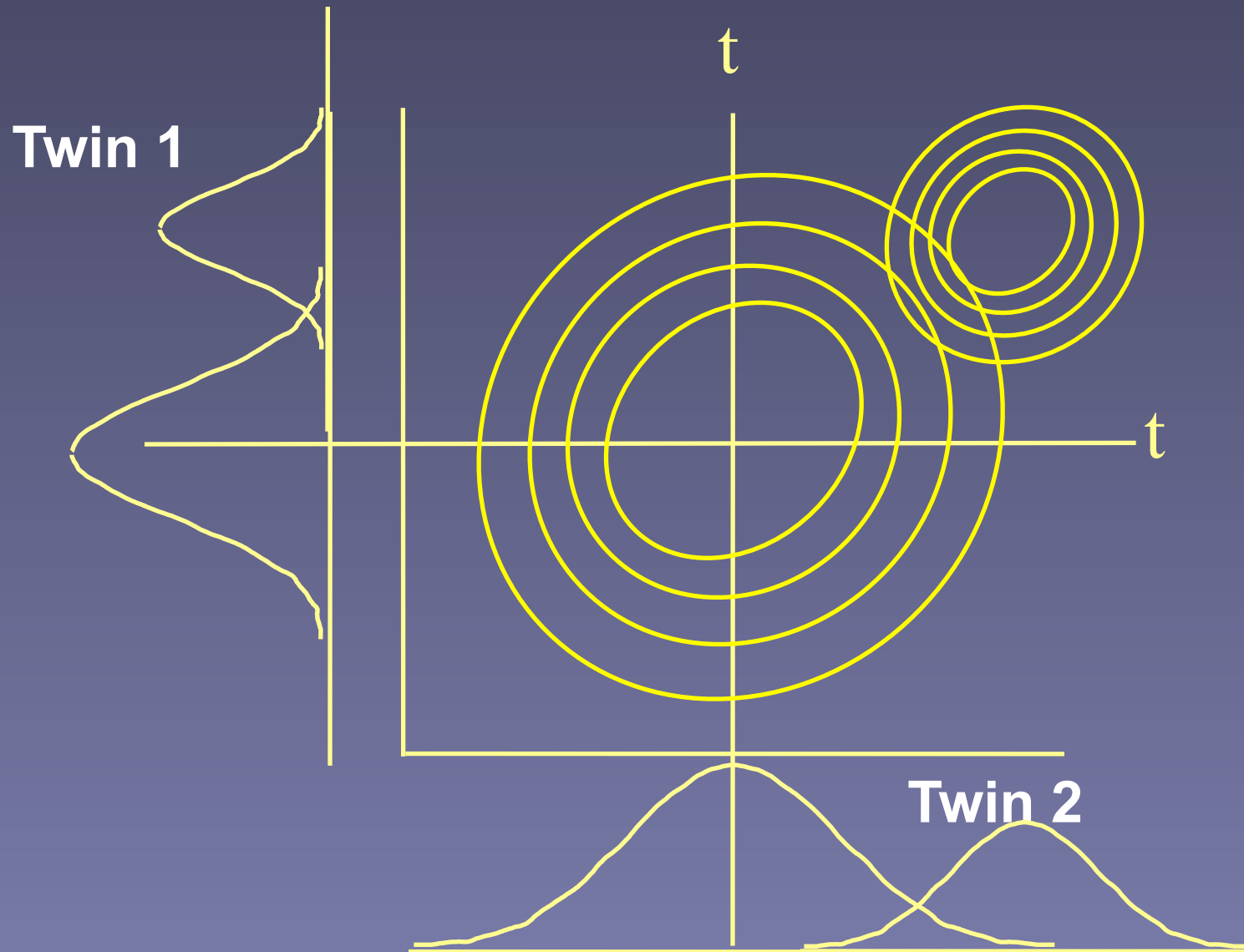
Basic statistical theory



# Two Dimensions: Contours



# Non-normal distribution: Contours



# Basic Theory

- Models for symptoms:
  - Latent class analysis
  - Factor analysis
  - Factor mixture model
  - Reprieved...

*Am. J. Hum. Genet.* 57:935–953, 1995

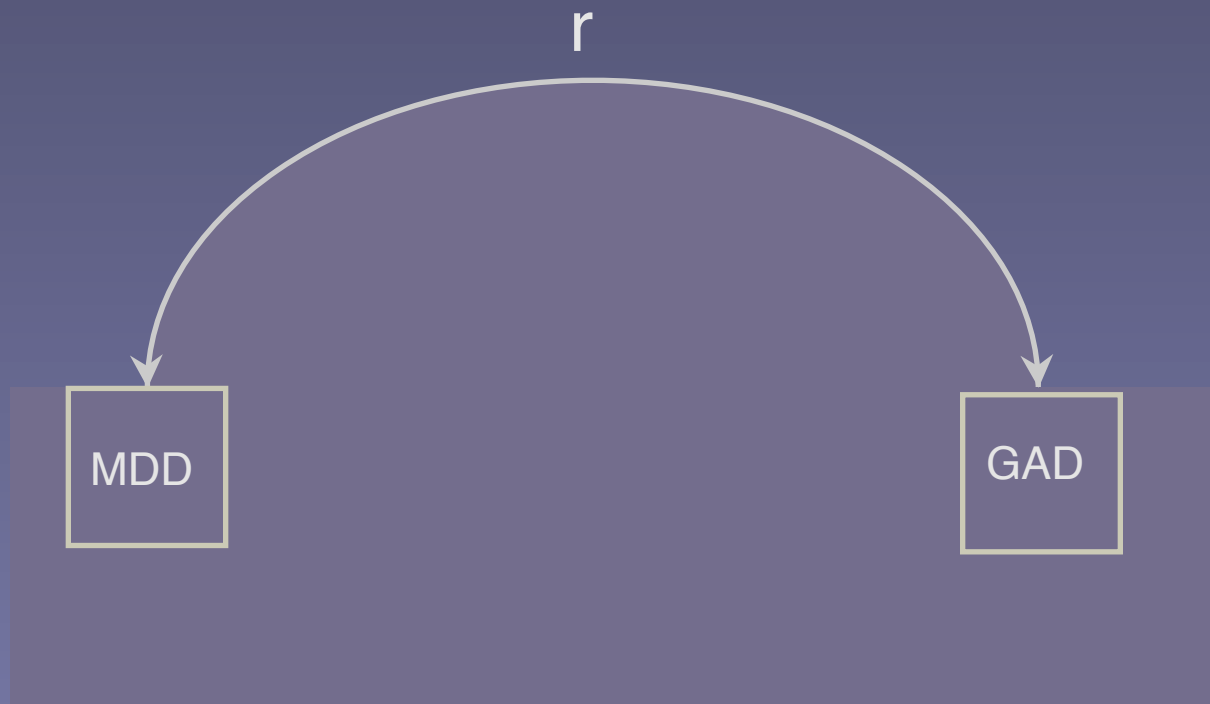
## **Models of Comorbidity for Multifactorial Disorders**

Michael C. Neale<sup>1</sup> and Kenneth S. Kendler<sup>1,2</sup>

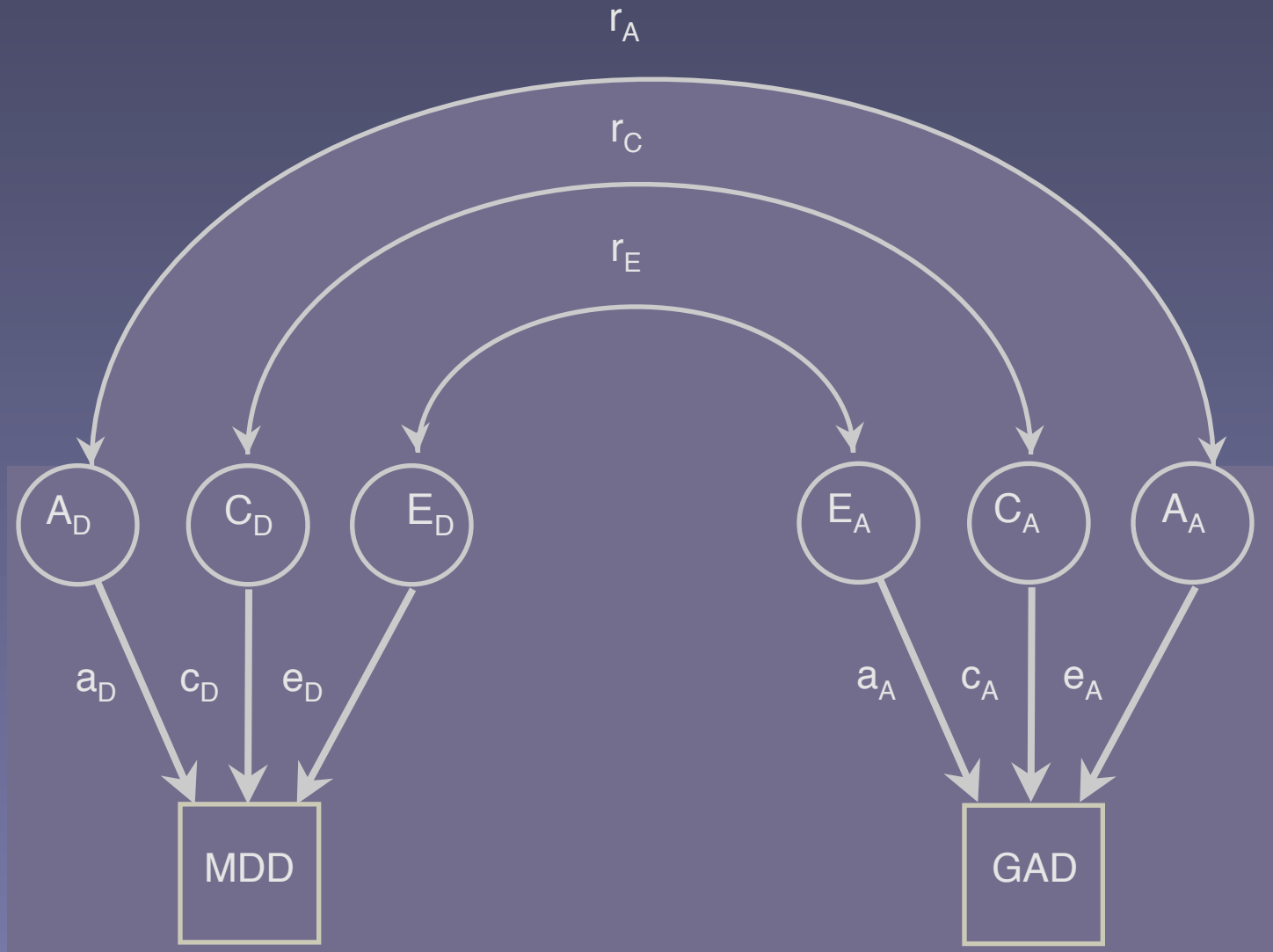
Departments of <sup>1</sup>Psychiatry and <sup>2</sup>Human Genetics, Medical College of Virginia, Richmond

# Comorbidity

A correlation between (binary) traits  
Neale & Kendler (1995) 13 Models  
Based on Klein & Riso (1994)

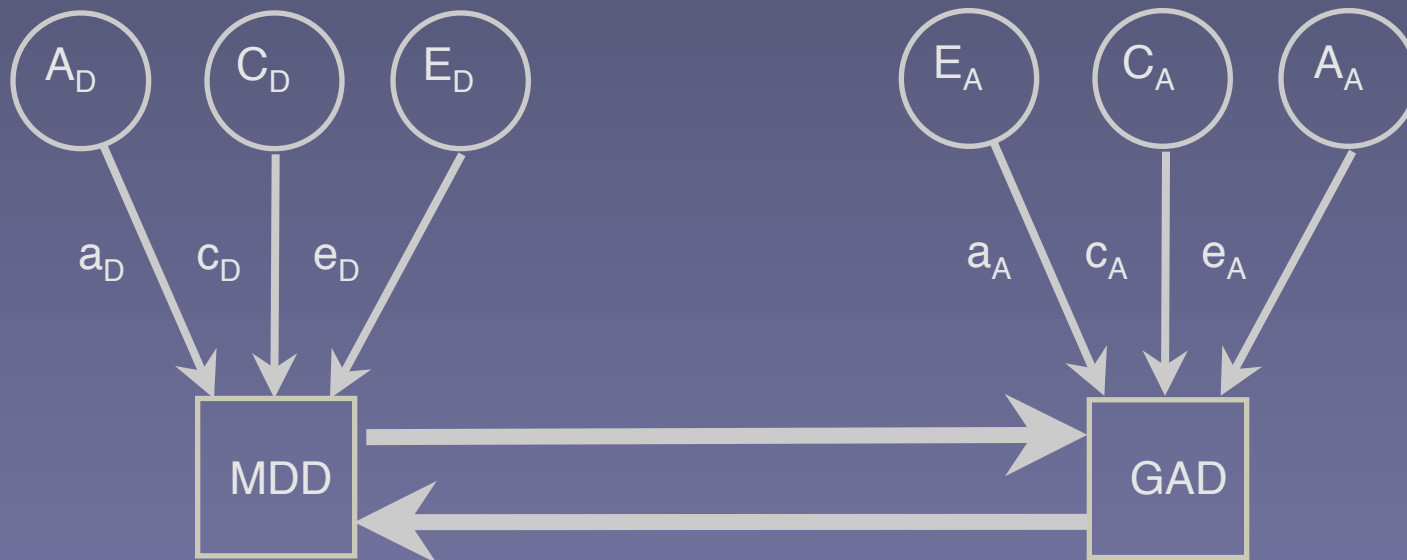


# Partitioning Comorbidity



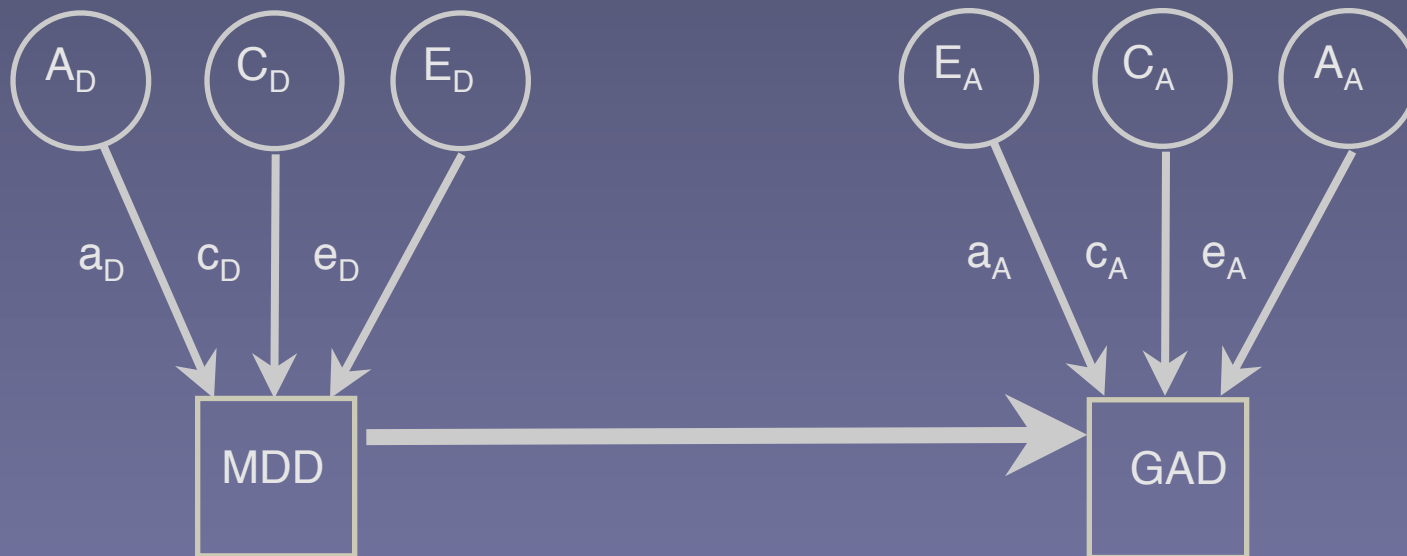
# Modeling Comorbidity

Reciprocal Causation



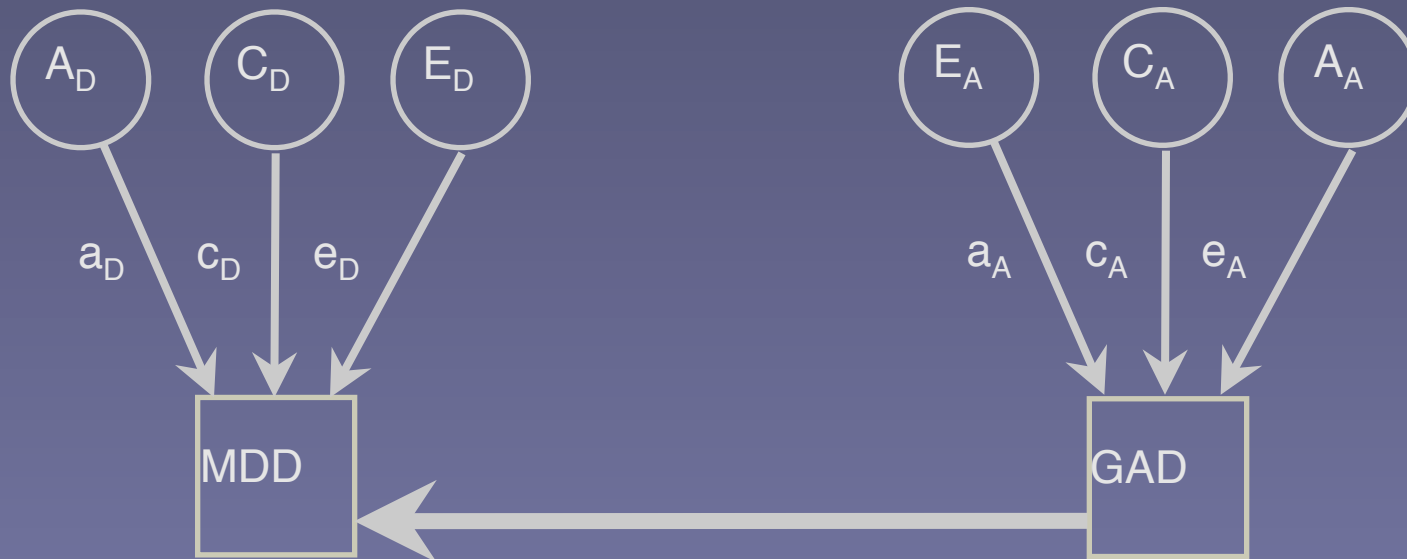
# Modeling Comorbidity

Major Depression Causes Generalized Anxiety Disorder



# Modeling Comorbidity

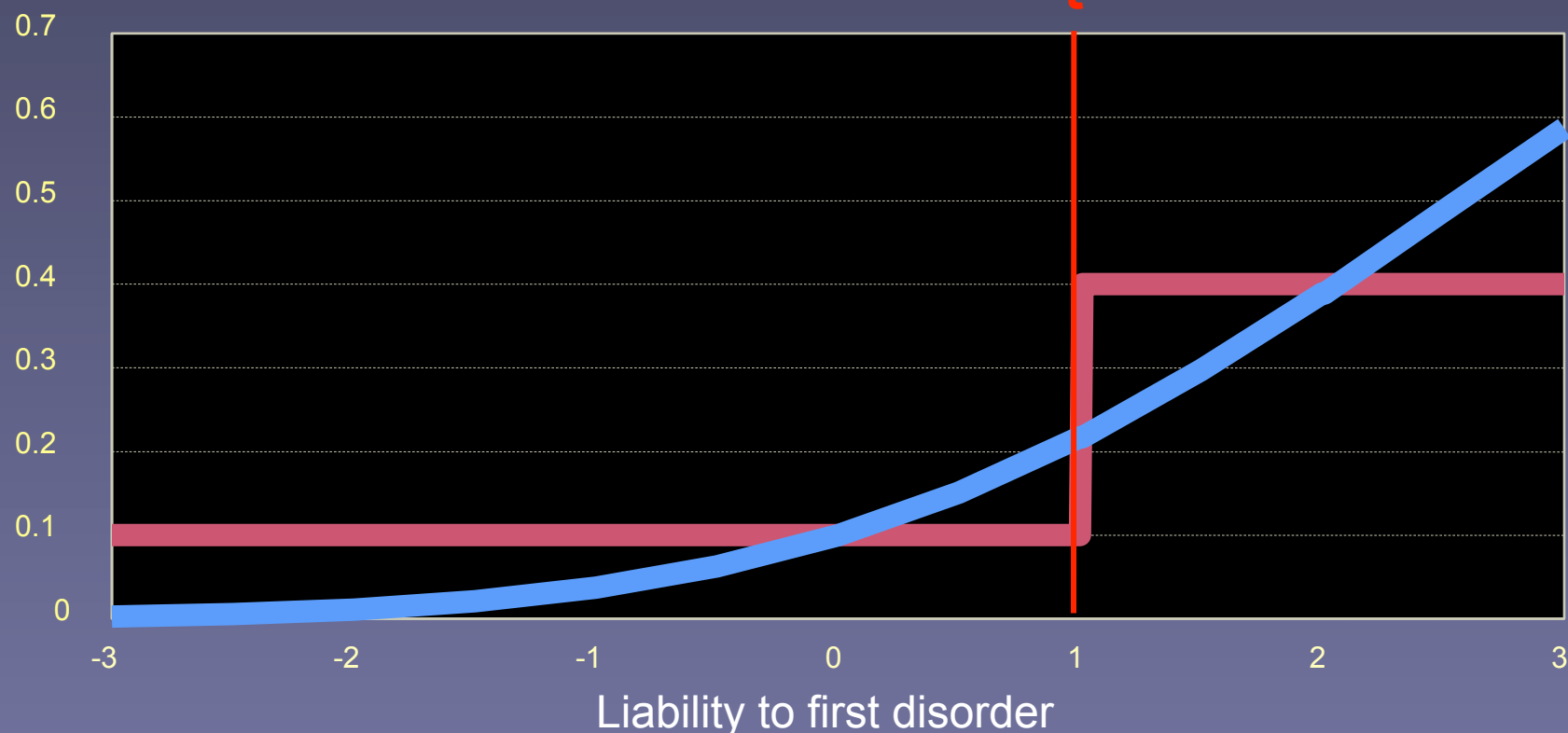
Generalized Anxiety Disorder causes Major Depression





# Alternative models of increasing risk to a second disorder

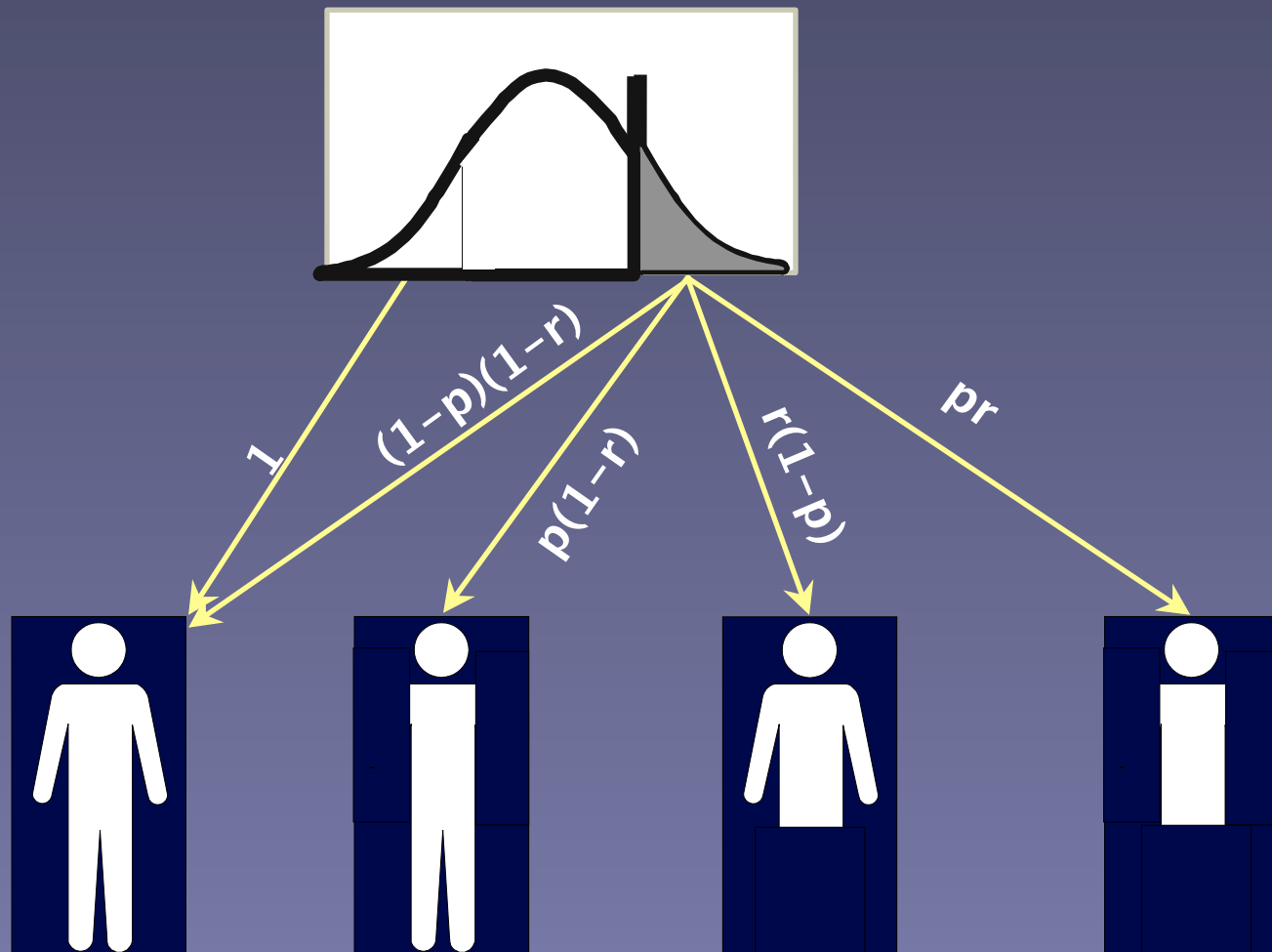
$p(\text{comorbid})$  = chance of getting second disorder



■ Causal/Correlational Model      ■ Jump Model

Threshold Model  $r=.5$

# Alternate forms: One underlying continuum



# Alternate forms: More detail

$$L = \int_{-\infty}^{t_1} \phi(R) dR \quad (1)$$

$$M = \int_{t_1}^{t_2} \phi(R) dR \quad (2)$$

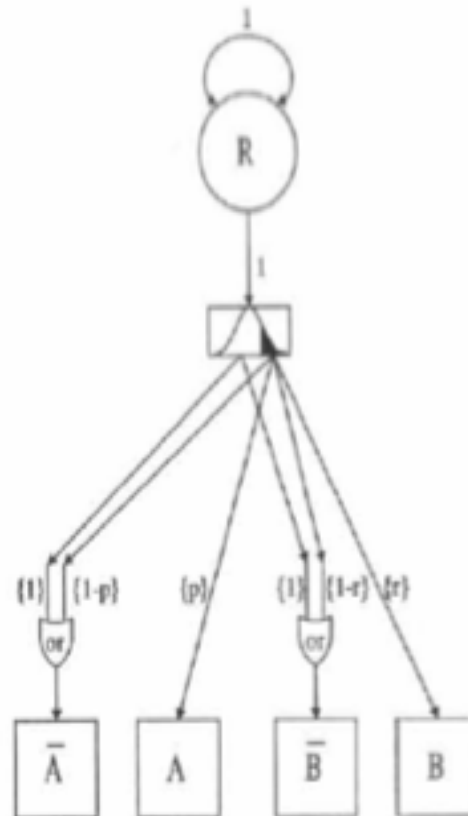
$$U = \int_{t_2}^{\infty} \phi(R) dR . \quad (3)$$

$$P(\bar{A}, \bar{B}) = L + (1 - p)(1 - r)U \quad (4)$$

$$P(\bar{A}, B) = p(1 - r)U \quad (5)$$

$$P(A, \bar{B}) = (1 - p)rU \quad (6)$$

$$P(A, B) = prU , \quad (7)$$



# Alternate forms: Detail of pairs

$$P(\bar{A}1, \bar{B}1, \bar{A}2, \bar{B}2) = LL + 2(1-p)(1-r)UL \\ + (1-p)^2(1-r)^2UU \quad (30)$$

$$P(\bar{A}1, \bar{B}1, \bar{A}2, B2) = r(1-p)LU \\ + (1-p)^2r(1-r)^2UU \quad (31)$$

$$P(\bar{A}1, \bar{B}1, A2, \bar{B}2) = p(1-r)LU \\ + p(1-p)(1-r)^2UU \quad (32)$$

$$P(\bar{A}1, \bar{B}1, A2, B2) = prLU \\ + p(1-p)r(1-r)UU \quad (33)$$

$$P(\bar{A}1, B1, \bar{A}2, B2) = (1-p)^2r^2UU \quad (34)$$

$$P(\bar{A}1, B1, A2, \bar{B}2) = p(1-p)r(1-r)UU \quad (35)$$

$$P(\bar{A}1, B1, A2, B2) = p(1-p)r^2UU \quad (36)$$

$$P(A1, \bar{B}1, A2, \bar{B}2) = p^2(1-r)^2UU \quad (37)$$

$$LL_A = \int_{-\infty}^{\epsilon_{1A}} \int_{-\infty}^{\epsilon_{1A}} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (24)$$

$$LM_A = \int_{-\infty}^{\epsilon_{1A}} \int_{\epsilon_{1A}}^{\epsilon_{2A}} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (25)$$

$$LU_A = \int_{-\infty}^{\epsilon_{1A}} \int_{\Omega_A}^{\infty} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (26)$$

$$MM_A = \int_{\epsilon_{1A}}^{\epsilon_{2A}} \int_{\epsilon_{1A}}^{\epsilon_{2A}} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (27)$$

$$MU_A = \int_{\epsilon_{1A}}^{\epsilon_{2A}} \int_{\epsilon_{1A}}^{\infty} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (28)$$

$$UU_A = \int_{\Omega_A}^{\infty} \int_{\Omega_A}^{\infty} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (29)$$

$$P(A1, \bar{B}1, A2, B2) = p^2r(1-r)UU \quad (38)$$

$$P(A1, B1, A2, B2) = p^2r^2UU \quad (39)$$

# OpenMx Script algebra for Alternate Forms

```
# Program: Alternate Forms

require(OpenMx)
nv<-1
# Fit Alternate Forms Model with Cell Frequencies Input, ACE.one overall Threshold
# -----
AltFormsModel <- mxModel("AlternateForms",
  mxModel("ACE",
    # Matrices a, c, and e to store a, c, and e path coefficients
    mxMatrix( type="Full", nrow=nv, ncol=nv, free=TRUE, values=.6, label="a11",
name="a" ),
    mxMatrix( type="Full", nrow=nv, ncol=nv, free=TRUE, values=.6, label="c11",
name="c" ),
    mxMatrix( type="Full", nrow=nv, ncol=nv, free=TRUE, values=sqrt(.28), label="e11",
name="e" ),
    # Matrices A, C, and E compute variance components
    mxAlgebra( expression=a %*% t(a), name="A" ),
    mxAlgebra( expression=c %*% t(c), name="C" ),
    mxAlgebra( expression=e %*% t(e), name="E" ),
    # Algebra to compute total variances and standard deviations (diagonal only)
    mxAlgebra( expression=A+C+E, name="V" ),
    mxMatrix( type="Iden", nrow=nv, ncol=nv, name="I"),
    mxAlgebra( expression=solve(sqrt(I*V)), name="sd"),
    # Constraint on variance of A+C+E latent variables
    mxConstraint( alg1="V", "=", alg2="I", name="Var1"),
```

# OpenMx Script algebra for Alternate Forms

```
# Algebra for expected variance/covariance matrix in MZ
mxAlgebra( expression= rbind ( cbind(A+C+E , A+C),
                                cbind(A+C , A+C+E)), name="expCovMZ" ),

# Algebra for expected variance/covariance matrix in DZ, note use of 0.5,
mxAlgebra( expression= rbind ( cbind(A+C+E , 0.5%x%A+C),
                                cbind(0.5%x%A+C , A+C+E)), name="expCovDZ"),

# Matrices for probabilities P Q R S of being affected given below/above threshold
mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE, values=.8, label="p", name="P" ),
mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE, values=.6, label="r", name="R" ),
mxMatrix( type="Iden", nrow=1, ncol=1, free=F, name="I" ),
mxAlgebra( expression= I-P, name="Q" ),
mxAlgebra( expression= I-R, name="S" ),

# Threshold parameter & matrices for (fixed at zero) means
mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE, values=1, label="tmz", name="T" ),
mxMatrix( type="Zero", nrow=1, ncol=nv, name="M" ),
mxAlgebra( expression= cbind(M,M), name="expMean" ),

# Integrals for computing the pairwise probabilities of being above/below threshold - MZ
mxAlgebra(expression=omxMnor(expCovMZ, expMean, cbind(-Inf,-Inf), cbind(T,T)),
name="bothBelow"),
mxAlgebra(expression=omxMnor(expCovMZ, expMean, cbind(-Inf,T), cbind(T,Inf)),
name="oneBelow"),
mxAlgebra(expression=omxMnor(expCovMZ, expMean, cbind(T,T), cbind(Inf,Inf)),
name="bothAbove"),
```

# OpenMx Script algebra for Alternate Forms

```
# Integrals for computing the pairwise probabilities of being above/below threshold - DZ
mxAlgebra(expression=omxMnor(expCovDZ, expMean, cbind(-Inf,-Inf), cbind(T,T)),
name="bothBelowDZ"),
mxAlgebra(expression=omxMnor(expCovDZ, expMean, cbind(-Inf,T), cbind(T,Inf)),
name="oneBelowDZ"),
mxAlgebra(expression=omxMnor(expCovDZ, expMean, cbind(T,T), cbind(Inf,Inf)),
name="bothAboveDZ"),

# Finally, predicted proportions in each of 10 cells for MZ
mxAlgebra(rbind(
bothBelow + 2*oneBelow*Q*S + bothAbove*Q*Q*S*S,
2*(oneBelow*R*Q + bothAbove*Q*Q*R*S),
2*(oneBelow*P*S + bothAbove*P*Q*S*S),
2*(oneBelow*P*R + bothAbove*P*R*Q*S),
bothAbove*Q*Q*R*R,
2*bothAbove*P*Q*R*S,
2*bothAbove*P*Q*R*R,
bothAbove*P*S*P*S,
2*bothAbove*P*S*P*R,
bothAbove*P*R*P*R
),name="MZExpectedFrequencies"),
```

# OpenMx Script algebra for Alternate Forms

```
# Finally, predicted proportions in each of 10 cells for DZ
mxAlgebra(rbind(
  bothBelowDZ + 2*oneBelowDZ*Q*S + bothAboveDZ*Q*Q*S*S,
  2*(oneBelowDZ*R*Q + bothAboveDZ*Q*Q*R*S),
  2*(oneBelowDZ*P*S + bothAboveDZ*P*Q*S*S),
  2*(oneBelowDZ*P*R + bothAboveDZ*P*R*Q*S),
  bothAboveDZ*Q*Q*R*R,
  2*bothAboveDZ*P*Q*R*S,
  2*bothAboveDZ*P*Q*R*R,
  bothAboveDZ*P*S*P*S,
  2*bothAboveDZ*P*S*P*R,
  bothAboveDZ*P*R*P*R), name="DZExpectedFrequencies")),

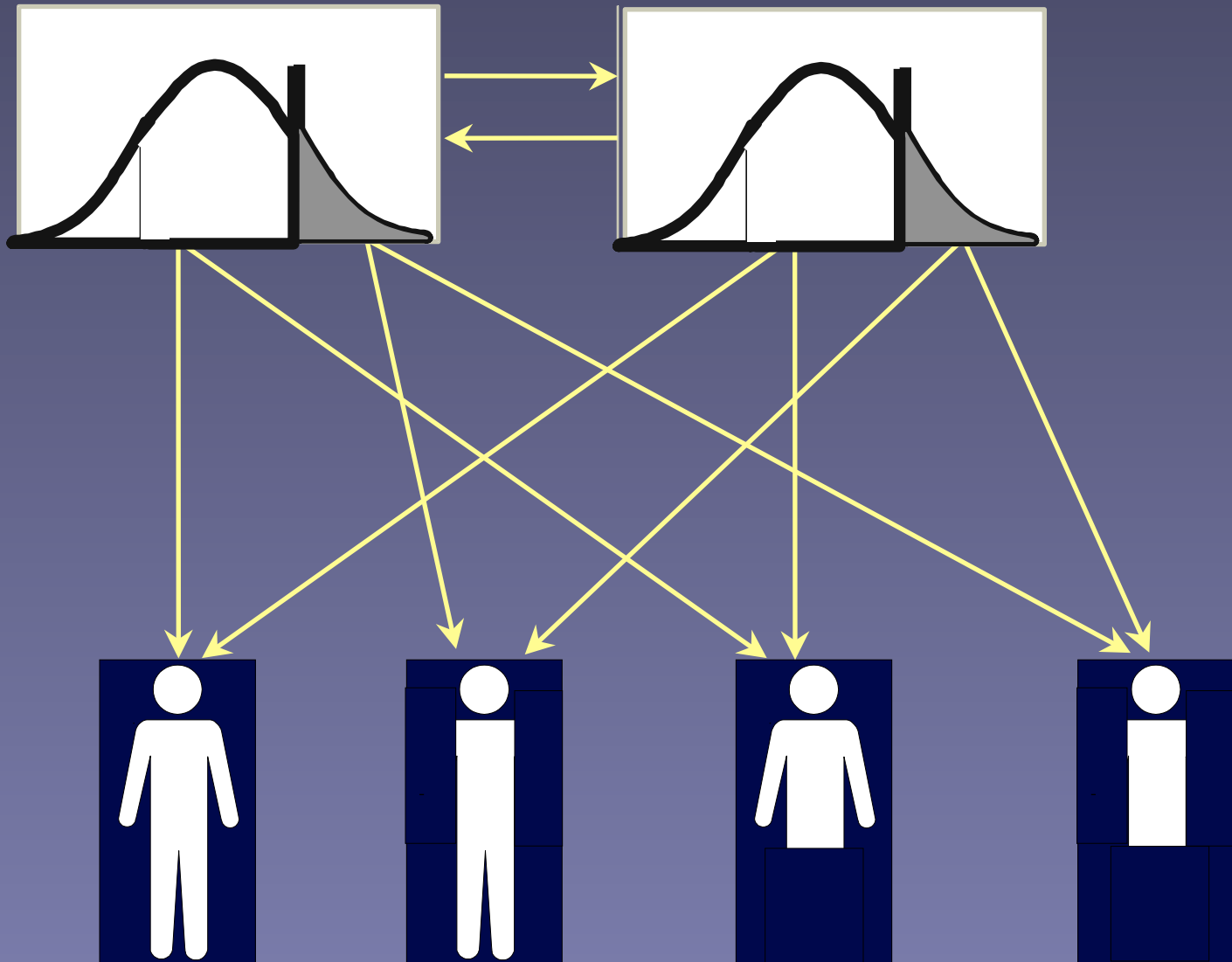
mxModel("MZ",
  mxMatrix(type="Full", nrow=10, ncol=1, free=FALSE,
    values=c(141,35,32,25,15,7,33,18,39,47), name="MZObservedFrequencies"),
  mxAlgebra( -2 * sum(MZObservedFrequencies * log
    (ACE.MZExpectedFrequencies)), name="MZalgebraobj"),
  mxAlgebraObjective("MZalgebraobj")),
```



# OpenMx Script algebra for Alternate Forms

```
mxModel("DZ",  
  mxMatrix(type="Full", nrow=10, ncol=1, free=F, values=c(58,18,27,44,7,6,33,15,38,81),  
    name="DZObservedFrequencies"),  
  mxAlgebra(  
    -2 * sum(DZObservedFrequencies *  
      log (ACE.DZExpectedFrequencies)),name="DZalobj"),  
  mxAlgebraObjective("DZalobj"),  
  mxAlgebra( MZ.objective + DZ.objective, name="-2sumll" ),  
  mxAlgebraObjective("-2sumll"))  
  
AltFormsRun<-mxRun(AltFormsModel)  
summary(AltFormsRun)
```

# Causal or correlated models

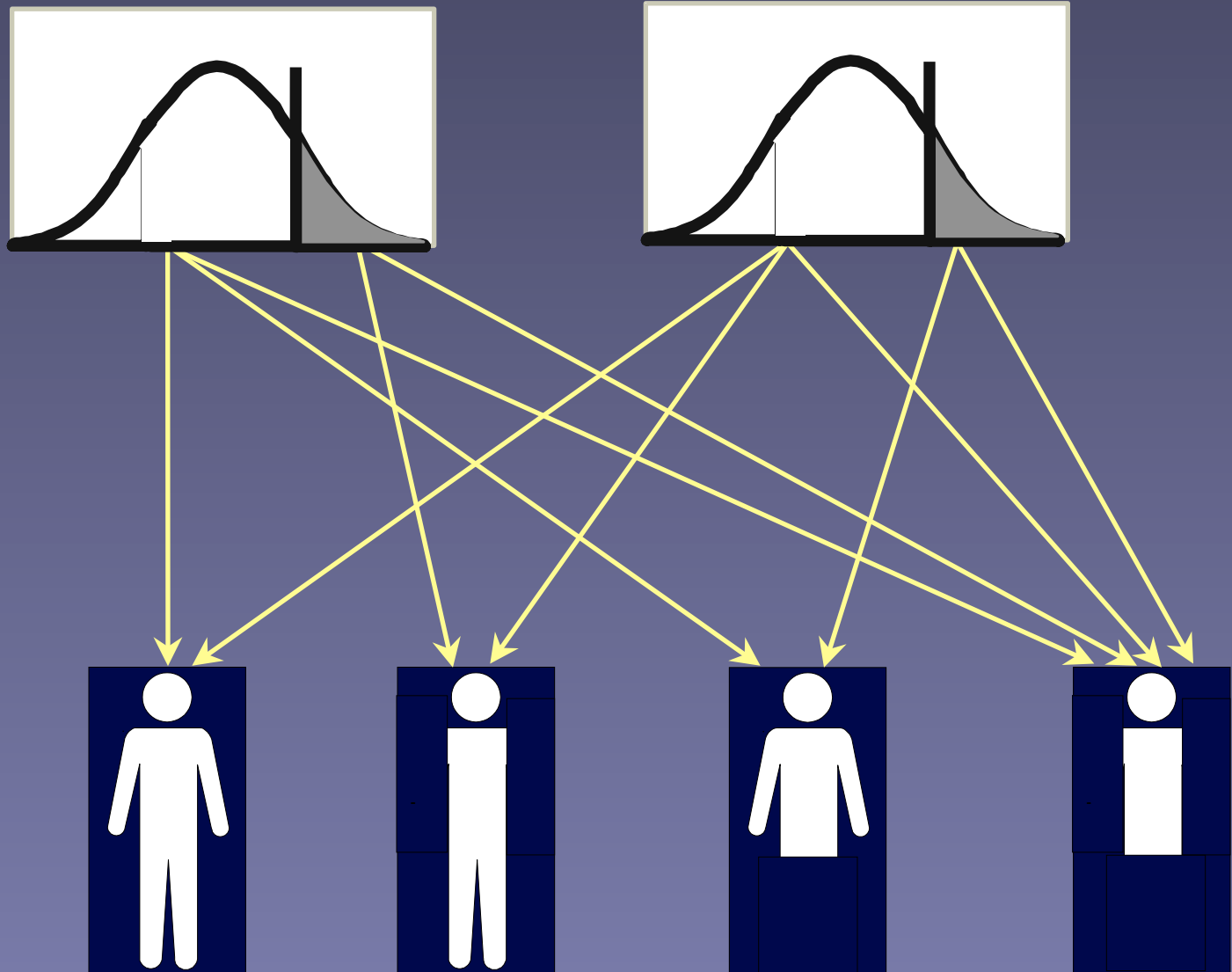


# Correlated Liabilities

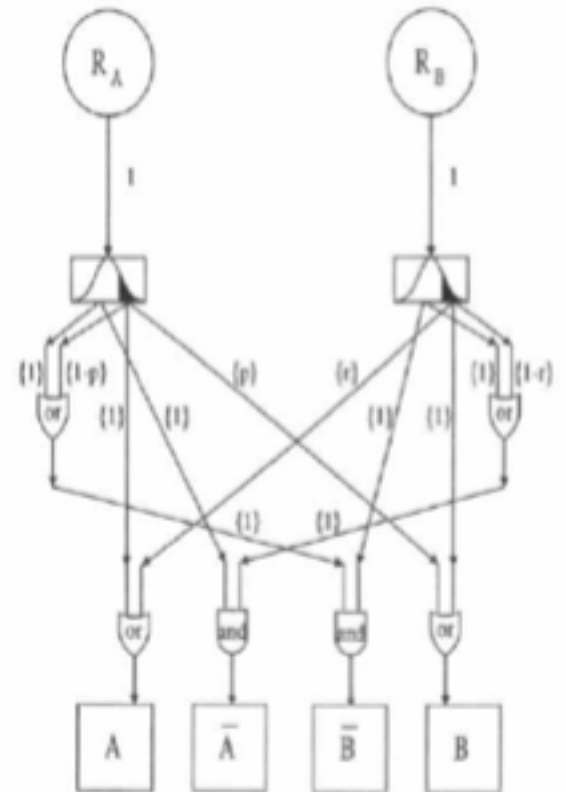
$$\begin{aligned} & P(A1, B1, A2, B2) \\ &= UUUU_{A1,B1,A2,B2} \\ &= \int_{t_A}^{\infty} \int_{t_B}^{\infty} \int_{t_A}^{\infty} \int_{t_B}^{\infty} \phi(R_{A1}, R_{B1}, R_{A2}, R_{B2}) \\ & \quad dR_{B2} dR_{A2} dR_{B1} dR_{A1} \end{aligned} \tag{70}$$

Inherent in OpenMx Ordinal Data Analysis  
We can do it by hand as well

# Jump Model: Actually having one disorder raises chance of getting second



# Random Multiformity: Detail



R = Risk factors

A = Distance A



- Threshold Filtration process

Or operation: A arises when LA or with probability r if LB is above threshold

And operation: not A arises when LA is below threshold and LB are above threshold

$$P(\bar{A}, \bar{B}) = L_A \cdot L_B \quad (8)$$

$$P(\bar{A}, B) = (1 - r)L_A \cdot U_B \quad (9)$$

$$P(A, \bar{B}) = U_A \cdot (1 - p)L_B \quad (10)$$

$$P(A, B) = U_A \cdot (U_B + pL_B) + rL_A \cdot U_B, \quad (11)$$

$$P(\bar{A}1, \bar{B}1, \bar{A}2, \bar{B}2) = LL_A \cdot LL_B \quad (40)$$

$$P(\bar{A}1, \bar{B}1, \bar{A}2, B2) = LL_A \cdot (1 - r)LU_B \quad (41)$$

$$P(\bar{A}1, \bar{B}1, A2, \bar{B}2) = (1 - p)LU_A \cdot LL_B \quad (42)$$

$$P(\bar{A}1, \bar{B}1, A2, B2) = LU_A \cdot (pLL_B + LU_B) + LL_A \cdot rLU_B \quad (43)$$

$$P(\bar{A}1, B1, \bar{A}2, B2) = LL_A \cdot (1 - r)^2UU_B \quad (44)$$

$$P(\bar{A}1, B1, A2, \bar{B}2) = (1 - p)LU_A \cdot (1 - r)LU_B \quad (45)$$

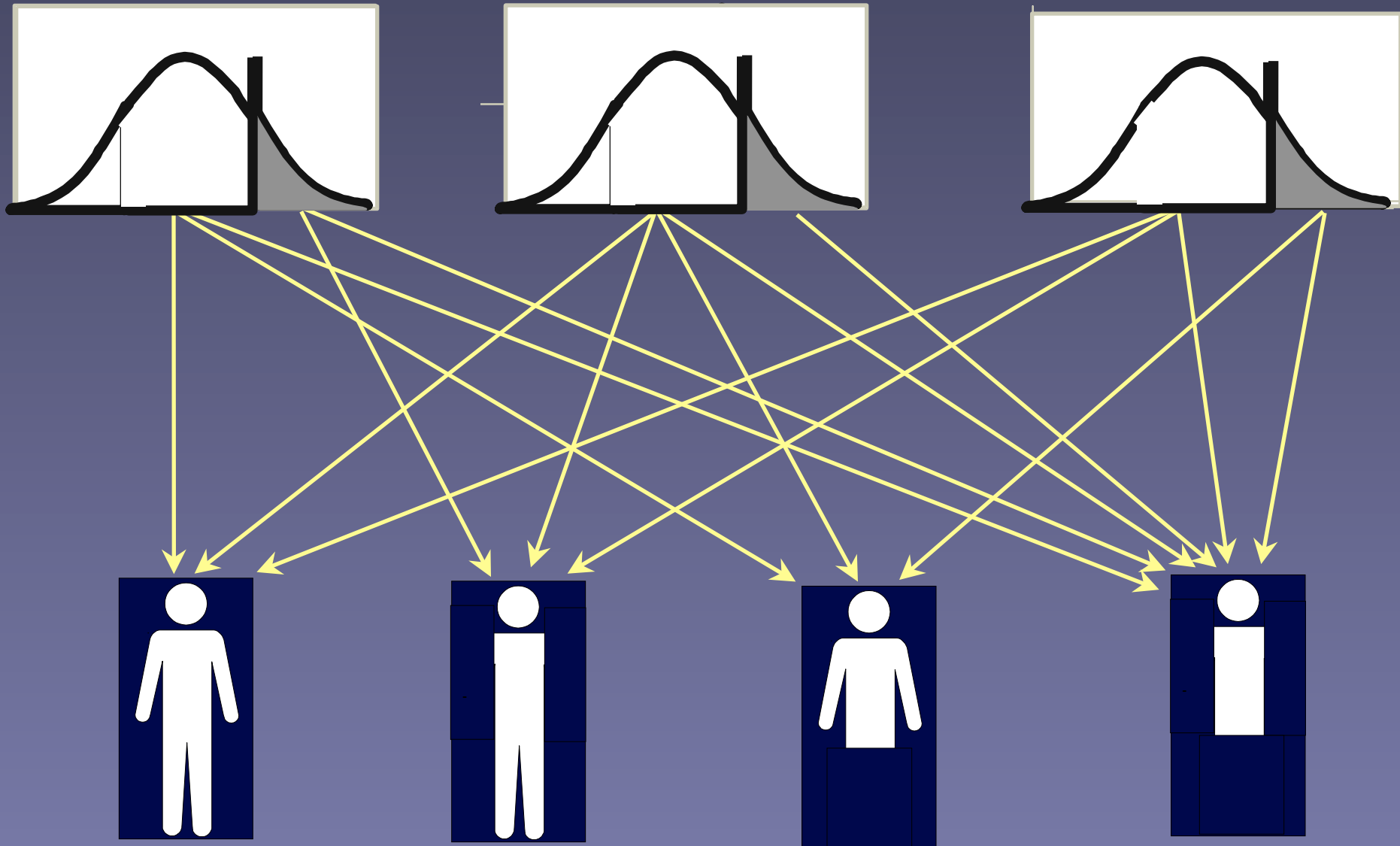
$$P(\bar{A}1, B1, A2, B2) = (1 - r)LU_A \cdot (pLU_B + UU_B) + LL_A \cdot rLU_B \quad (46)$$

$$P(A1, \bar{B}1, A2, \bar{B}2) = (1 - p)^2UU_A \cdot LL_B \quad (47)$$

$$P(A1, \bar{B}1, A2, B2) = UU_A \cdot (p(1 - p)LL_B + (1 - p)LU_B) + (1 - p)LU_A \cdot rLU_B \quad (48)$$

$$P(A1, B1, A2, B2) = p^2UU_A \cdot LL_B + 2pUU_A \cdot LU_B + UU_A \cdot UU_B + LU_A \cdot 2rLU_B + 2pLU_A \cdot rLU_B + LL_A \cdot r^2UU_B. \quad (49)$$

# Three separate disorders



# Three Independent Disorders

$$P(\bar{A}1, \bar{B}1, \bar{A}2, \bar{B}2) = LL_A \cdot LL_{AB} \cdot LL_B \quad (60)$$

$$P(\bar{A}1, \bar{B}1, \bar{A}2, B2) = LL_A \cdot LL_{AB} \cdot LU_B \quad (61)$$

$$P(\bar{A}1, \bar{B}1, A2, \bar{B}2) = LU_A \cdot LL_{AB} \cdot LL_B \quad (62)$$

$$P(\bar{A}1, \bar{B}1, A2, B2) = L_A \cdot LL_{AB} \cdot LL_B + LU_A \cdot LL_{AB} \cdot LU_B \quad (63)$$

$$P(\bar{A}1, B1, \bar{A}2, B2) = LL_A \cdot LL_{AB} \cdot UU_B \quad (64)$$

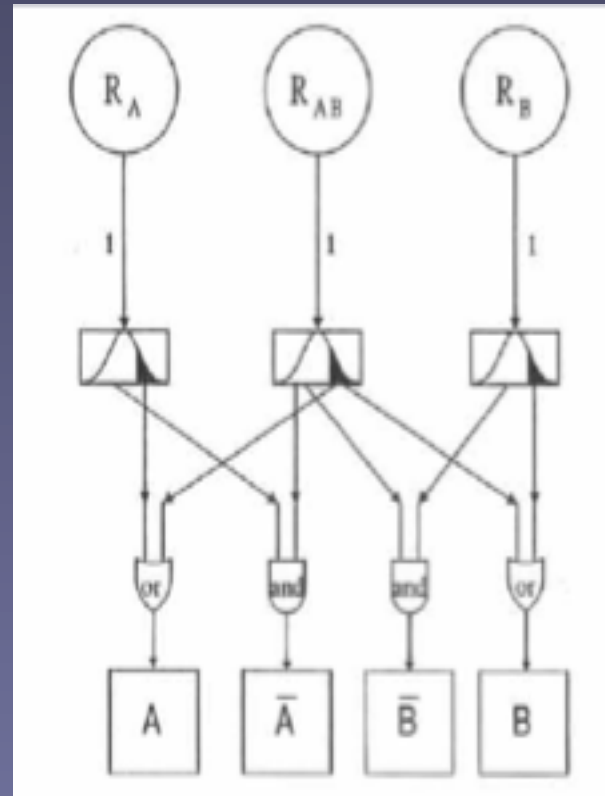
$$P(\bar{A}1, B1, A2, \bar{B}2) = LU_A \cdot LL_{AB} \cdot LU_B \quad (65)$$

$$P(\bar{A}1, B1, A2, B2) = L_A \cdot LU_{AB} \cdot U_B + LU_A \cdot LL_{AB} \cdot UU_B \quad (66)$$

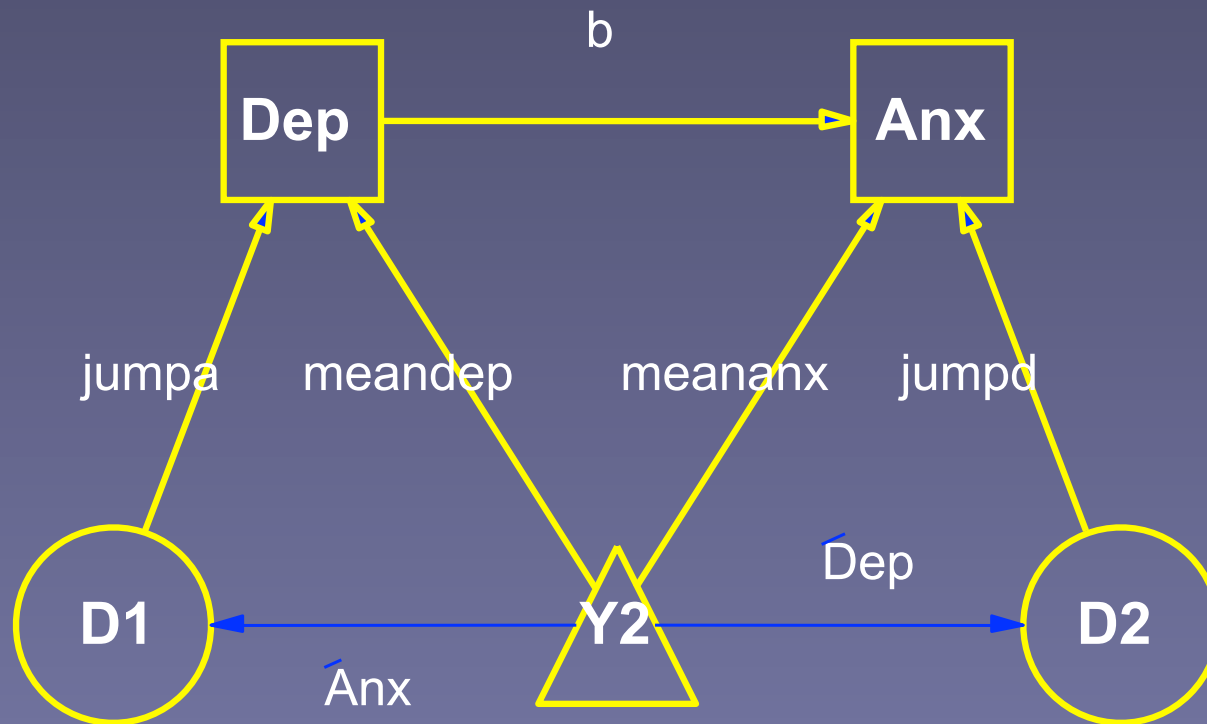
$$P(A1, \bar{B}1, A2, \bar{B}2) = UU_A \cdot LL_{AB} \cdot LL_B \quad (67)$$

$$P(A1, \bar{B}1, A2, B2) = L_A \cdot LU_{AB} \cdot L_B + UU_A \cdot LL_{AB} \cdot LU_B \quad (68)$$

$$P(A1, B1, A2, B2) = UU_{AB} + UU_A \cdot LL_{AB} \cdot UU_B + 2U_A \cdot LU_{AB} \cdot U_B \quad (69)$$

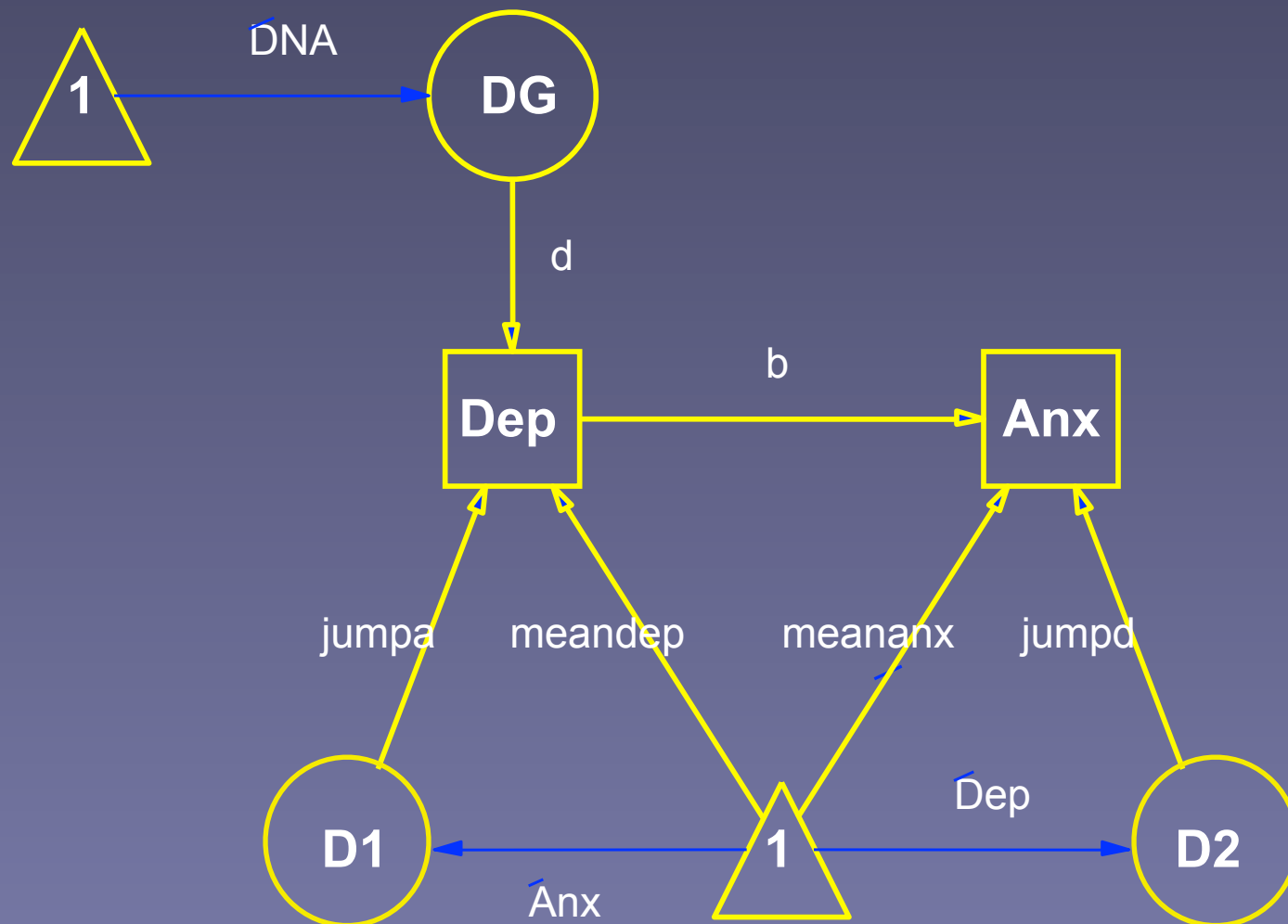


# Unified Comorbidity Model?





# Unified Genetic Comorbidity Model?



# Sources for comorbidity scripts

- <http://ibgwww.colorado.edu/cadd/software>
  - Soo Rhee's website! Excellent!
  - Includes covariates e.g., age (Rhee et al submitted)
  - Clinical selected samples as well
  - Exercise: download and fit the examples and decide on best fit model
- 
- <http://www.vcu.edu/mx/examples>
  - Mike Neale's script website.
  - More than a little bit dusty

# OpenMx User-defined Functions

- Can specify AlgebraObjective

```
mxAlgebra( MZ.objective + DZ.objective, name="-2sumll" ),  
mxAlgebraObjective("-2sumll"))
```

- Any mxAlgebra you like!
  - Woohoo!
- See, e.g., <http://openmx.psyc.virginia.edu/repoview/1/trunk/models/passing/oneLocusLikelihood.R>
- One & two locus ABO blood group examples

# Comorbidity with covariates

- Soo Rhee's website again
- <http://ibgwww.colorado.edu/cadd/software>
- These scripts are in classic Mx
- Look out for updates

# Possible Extensions

- More than two disorders
  - More than one point in time
  - More than pairs of twins
  - Covariates & GxE
- 
- Models for symptoms (IRT)
  - Dynamical systems models
  - Generalization to continuous liability

# Possible Exercises

- Modify `directionofCausation.R` to fit:
  - Anxiety (P2) causes depression (P1)
  - Bidirectional causation (tricky, may need bounds)
  - Test hypothesis that comorbidity in ACE bivariate is purely due to  $rG$
- Use `tableFitStatistics` function to compare results of ACE & other comorbidity models
- Find some other data, rinse & repeat...

# Comorbidity Depression & Anxiety Disorders

