

Phenotypes Endophenotypes and Comorbidity

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Table of Contents

- Phenotype Measurement
- Definition of Endophenotype
- Models for Endophenotypes
- Models for Comorbidity

Measurement

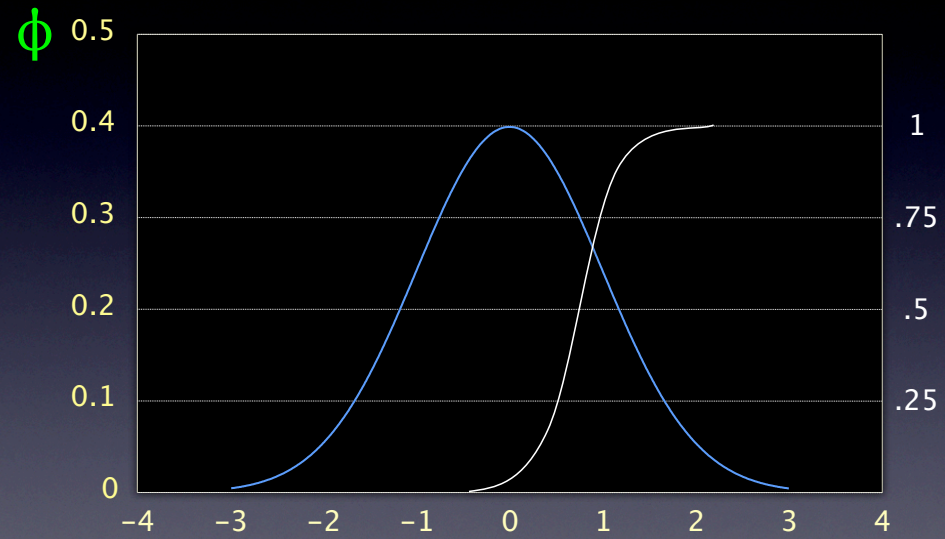
- Reduction of error variance
 - Increase external validity
 - Longitudinal (test-retest & prognostic)
 - Risk factors
 - Familial resemblance
 - Ability to find genes
- Efficiency of measurement
 - Fewer items to achieve same end
 - Equal assessment across range of (li)ability

Mathematical models for measurement

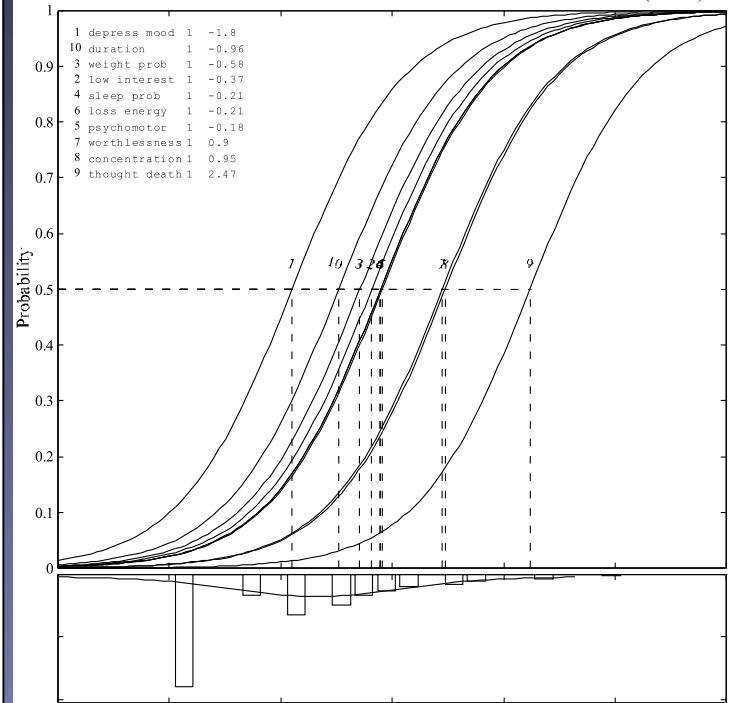
- Item response theory
 - Sigmoidal function describing $p(\text{response}=Y)$
 - Logistic
 - Cumulative normal
 - Steep is better than flat
 - More precise delineation of where subject is in the distribution
 - Equality of slopes important
 - Order of item response probabilities is same at all places
 - Position of mid-point of slopes = 'difficulty'
 - Ideal scale should have range of difficulties

Normal liability distribution ϕ

Example item response probability shown in white



IRC & Person Distribution for FF1 DSM MD 9 Criteria + Duration (Rasch)

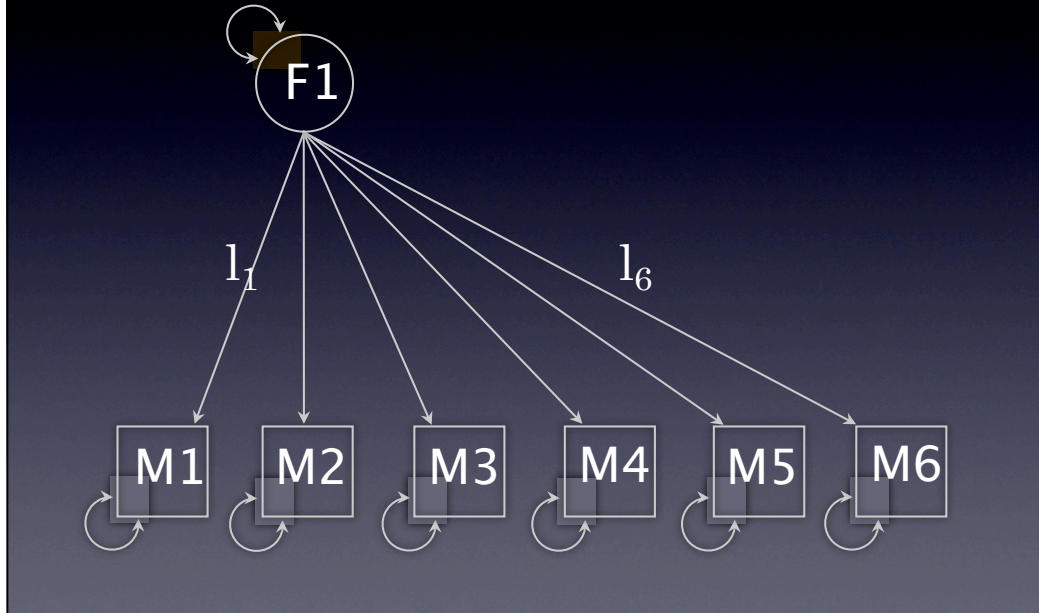


Example
results for
MD
symptoms
FF1

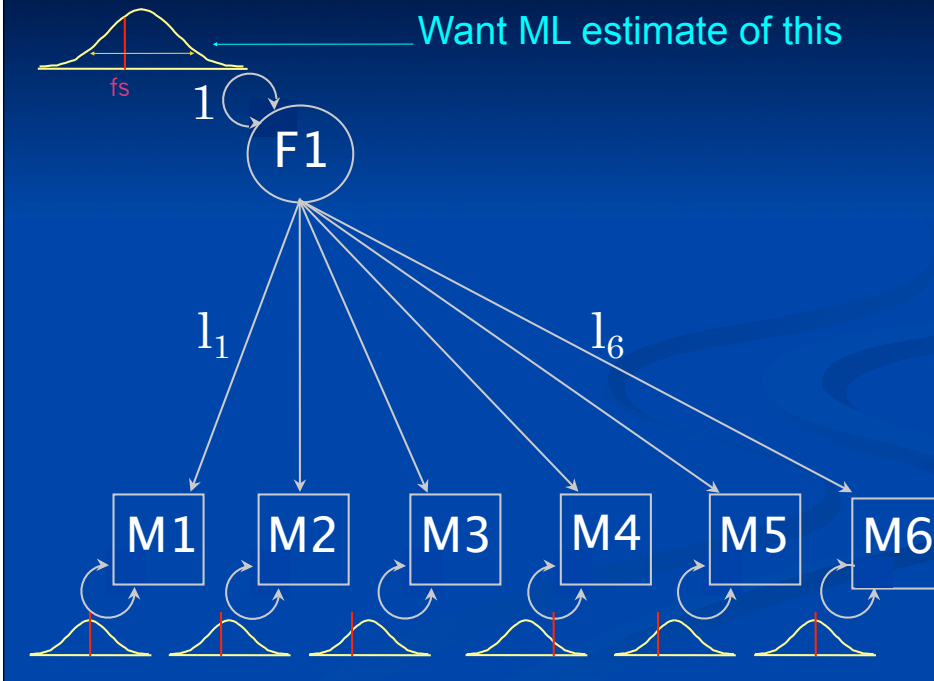
Structural Equation Model

- Two kinds of relationships
 - Linear regression $X \rightarrow Y$ single-headed
 - Unspecified Covariance $X \leftrightarrow Y$ double-headed
- Four kinds of variable
 - Squares – observed variables
 - Circles – latent, not observed variables
 - Triangles – constant (zero variance) for specifying means
 - Diamonds -- observed variables used as moderators (on paths)

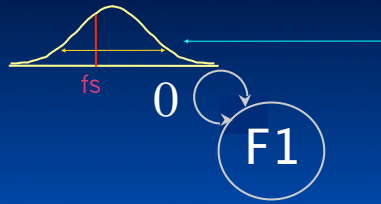
Latent Trait (Factor) Model



Estimate factor score



Estimate factor score



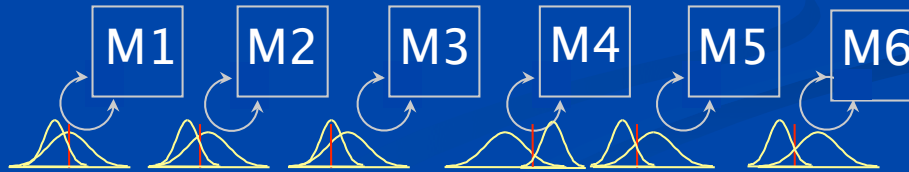
Conditional on this factor score

Factor mean = f_s

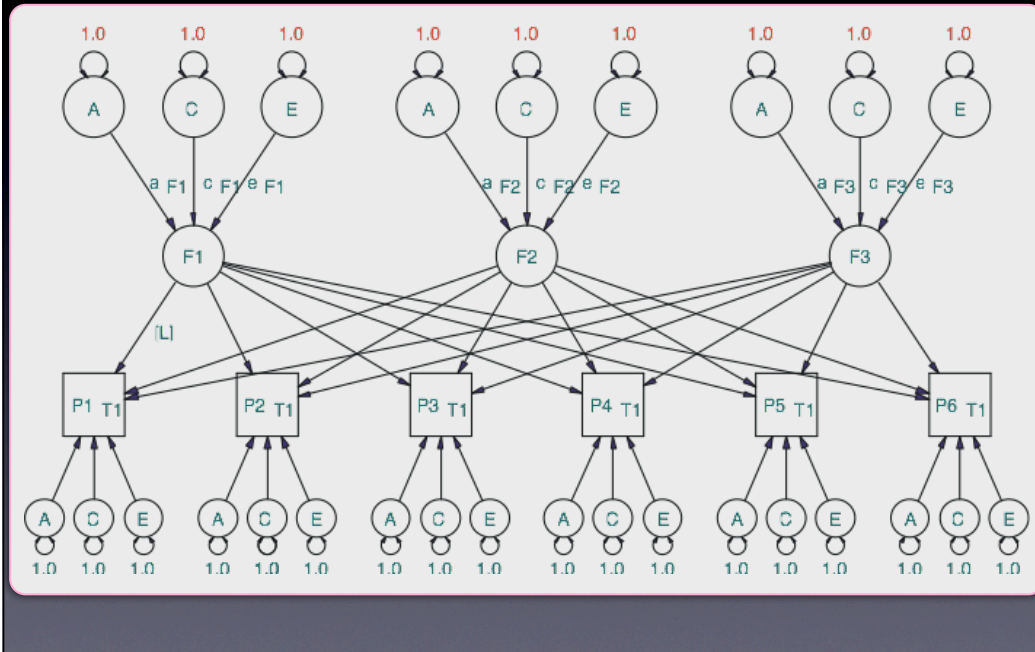
Factor variance = 0

Item means move

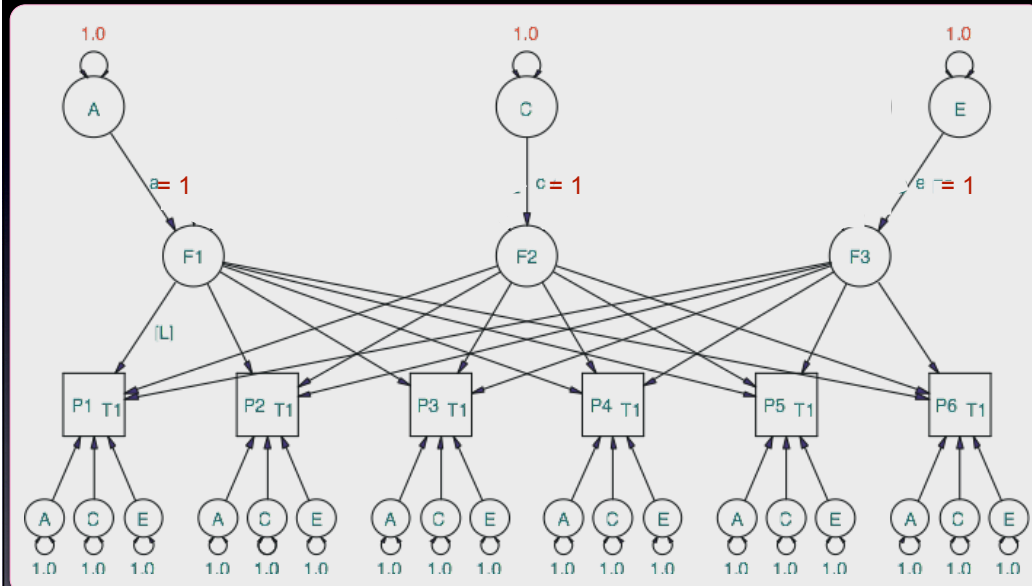
Item variances shrink



Common Pathway Model



Independent Pathway Model

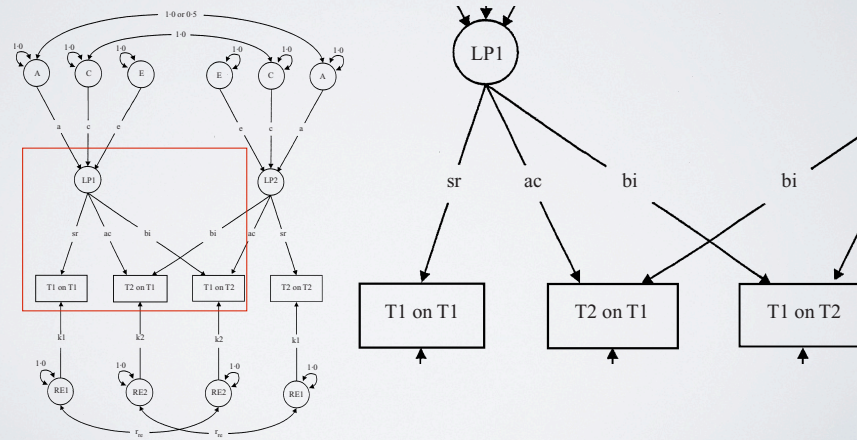


Independent pathway model is submodel of 3 factor common pathway model

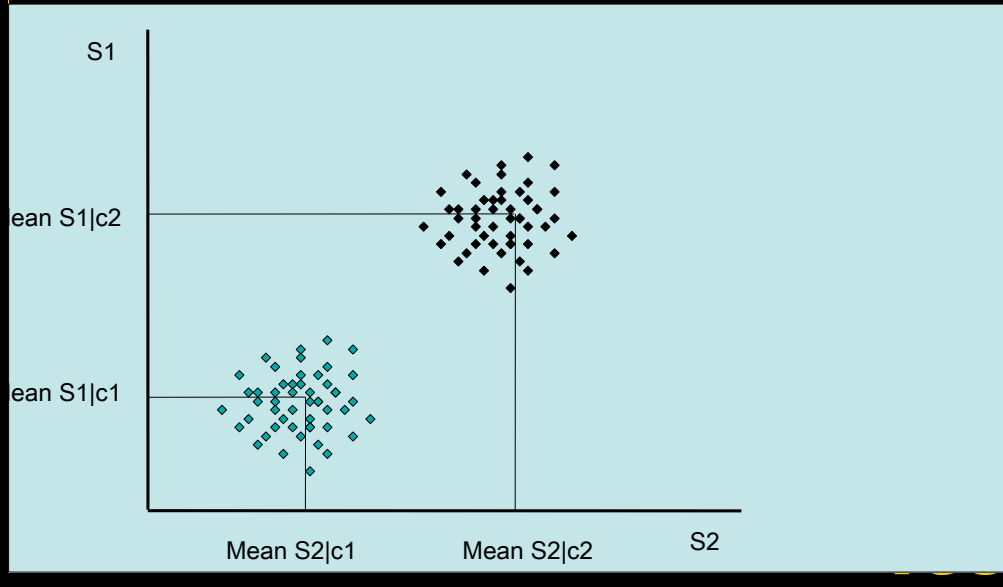
The joint analysis of personal interview and family history diagnoses: evidence for validity of diagnosis and increased heritability estimates

K. S. KENDLER,¹ C. A. PRESCOTT, K. JACOBSON, J. MYERS AND M. C. NEALE

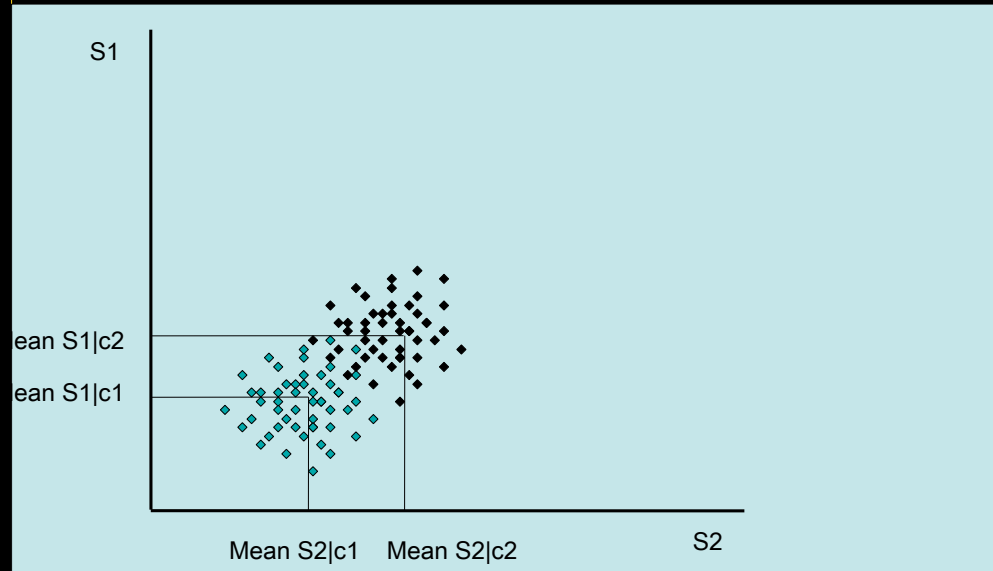
From the Virginia Institute for Psychiatric and Behavioral Genetics and Departments of Psychiatry and Human Genetics, Medical College of Virginia of Virginia Commonwealth University, Richmond, VA, USA



Latent Class Analysis (& FMM)

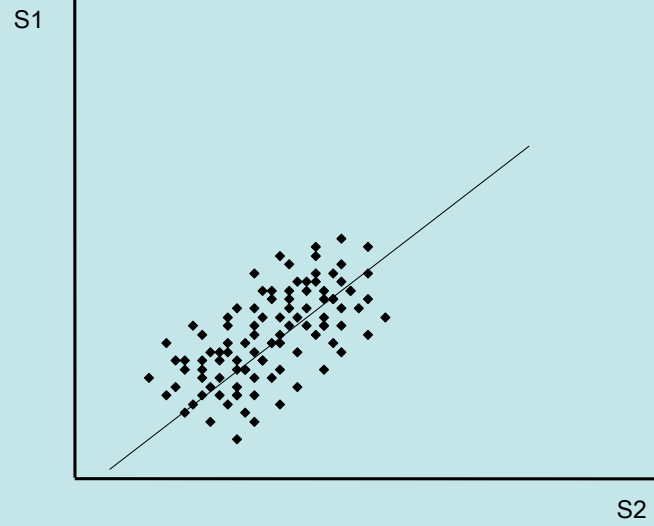


Scatterplot of 2 classes Closer means



Scatterplot of 2 classes

Latent heterogeneity: Factors or classes?



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...”

Endophenotype Definitions

Gottesman and Gould (AJP 2003)

- Associated with illness in the population
- Heritable
- Primarily state independent (manifests in an individual whether or not illness is active)
- Co-segregates with illness within families
- Found in unaffected family members at a higher rate than in the general population.

Endophenotype Concept

- “Intermediate phenotypes that form causal links between genes and overt expression of disorders” (Cannon and Keller, 2005)
- “Intermediate trait that sits closer to the genotype in the developmental scheme” (Gottesman and Hanson, 2005)

Endophenotype Defined

- Moderate heritability
- Endophenotype and illness co-segregate within families
- Found in affected family members at higher rate than in population
- Association with illness in the population
- State-independent

Endophenotype Defined

- Association with causes rather than effects of disorders
- Endophenotype should affect a disorder
- Should have continuous variation in a population
- Should be measured across several levels of analysis

Endophenotypes Take 2

Preston & Weinberger (2005)

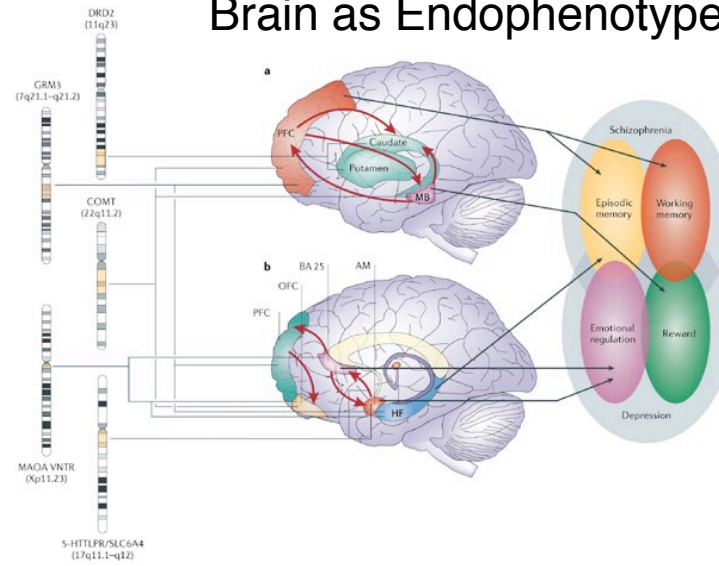
- A quantitative biological trait that is reliable and reasonably heritable, i.e., shows greater prevalence in unaffected relatives of patients than in the general population
- Should be associated with variant alleles that distinguish patients and their unaffected siblings from healthy controls on quantitative measures
- Based in part on (the) ... assumption that intermediate phenotypes in schizophrenia (reflect) ... a less complex genetic architecture than the disorder as a whole.

Endophenotypes Take 3

Cannon & Keller (2006)

- Endophenotypes should be:
 - Heritable
 - Associated with causes rather than effects of disorders
 - Affect a given complex disorder
 - Vary continuously in the general population
 - (optimally) measured across several levels of analysis
 - Found for genetically related disorders if they affect multiple disorders

Brain as Endophenotype



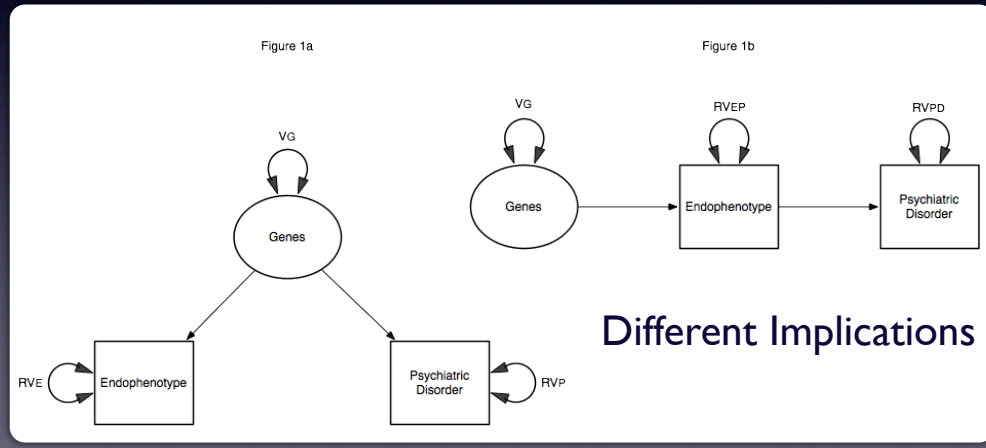
3,300,000,000 40,000 - 300,000_{Copys} Several

Meyer-Lindenberg and Weinberger *Nature Reviews Neuroscience* 7, 818–827 (October 2006) | doi:10.1038/nrn1993

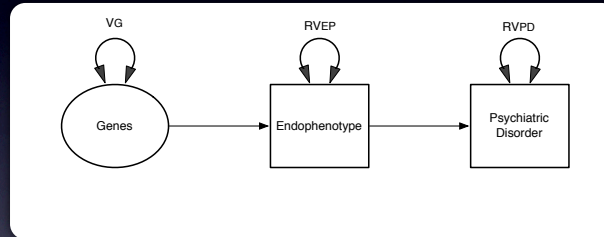
EP Conceptual Analysis

Kendler & Neale (Mol Psych 2010)

- Walters & Owen (2007): Distinction between 'Liability Index' and 'Mediatorial' models not explicit

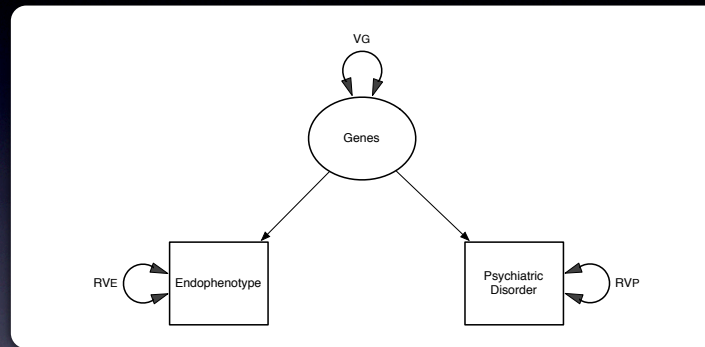


Traditional Endophenotype Model



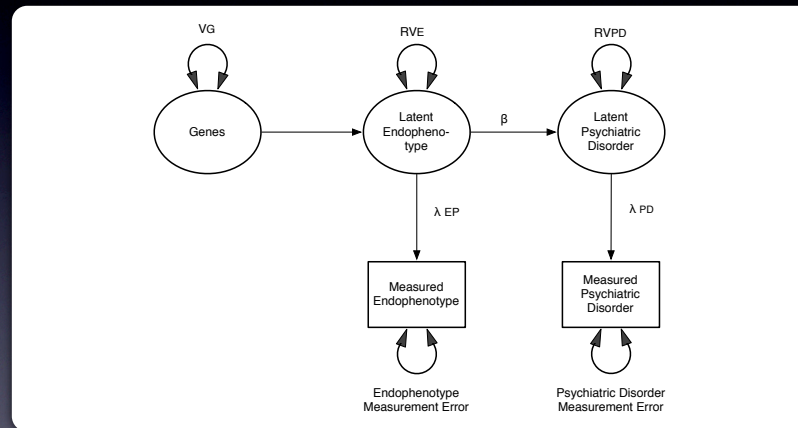
- Endophenotype is intermediate
- Ideally more heritable than PD

Common Factor Model



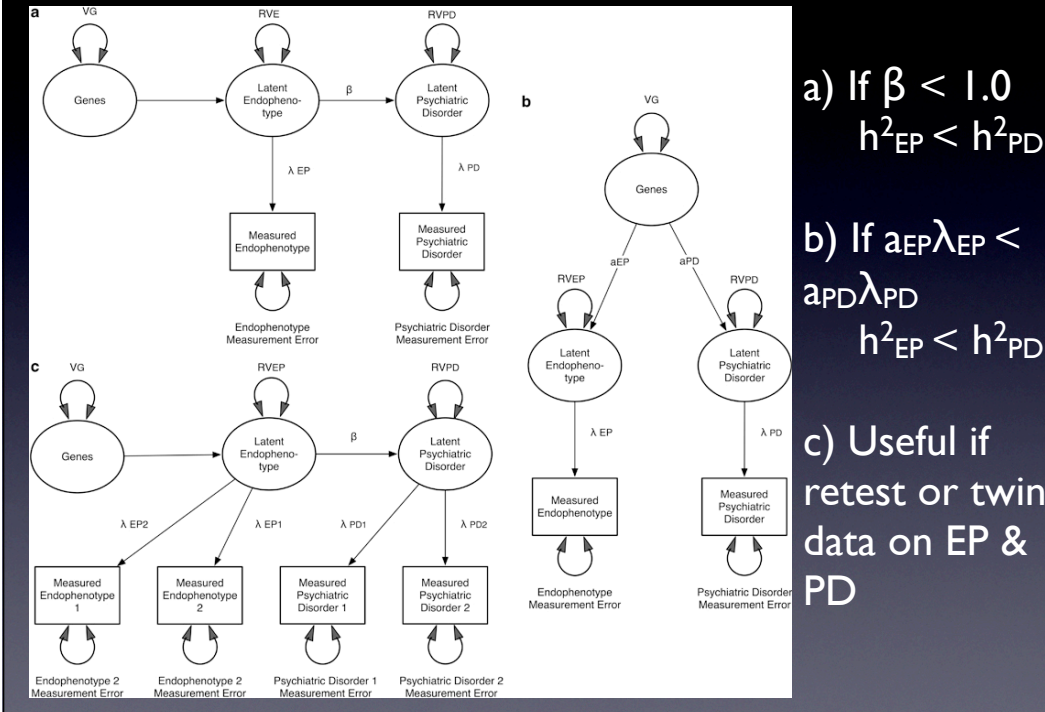
- Endophenotype is intermediate??
- Ideally more heritable than PD?

Endophenotype Error Model



- Error variances λ can change relative h^2
- Does it matter if more heritable than PD?

Include Measurement Error

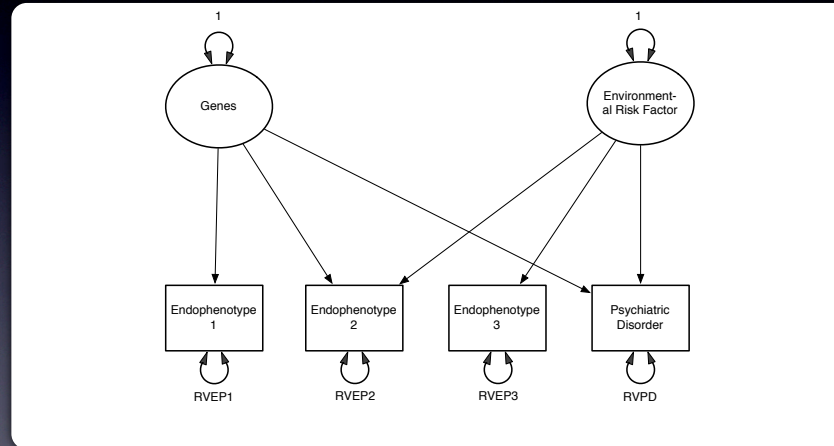


a) If $\beta < 1.0$
 $h^2_{EP} < h^2_{PD}$

b) If $a_{EP}\lambda_{EP} < a_{PD}\lambda_{PD}$
 $h^2_{EP} < h^2_{PD}$

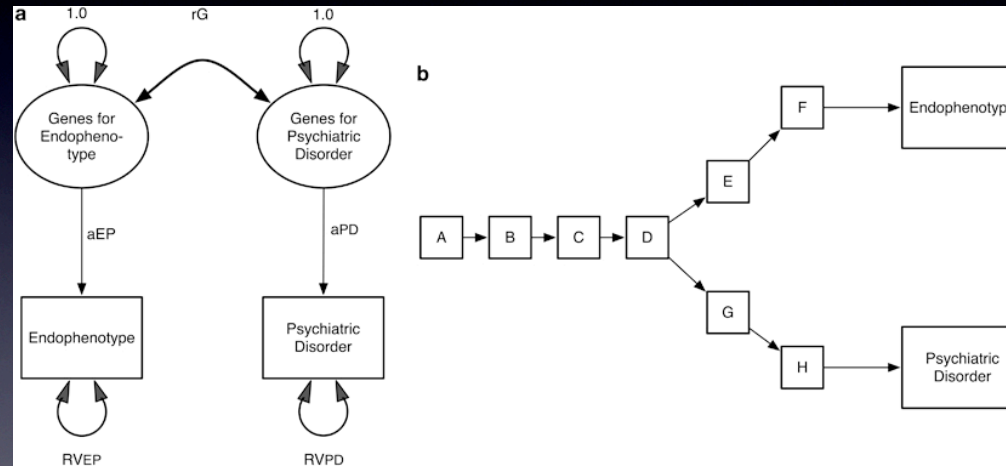
c) Useful if
 retest or twin
 data on EP &
 PD

Environmental Endophenotypes



- Establishing an endophenotype is a job for comorbidity modeling

Bivariate Model



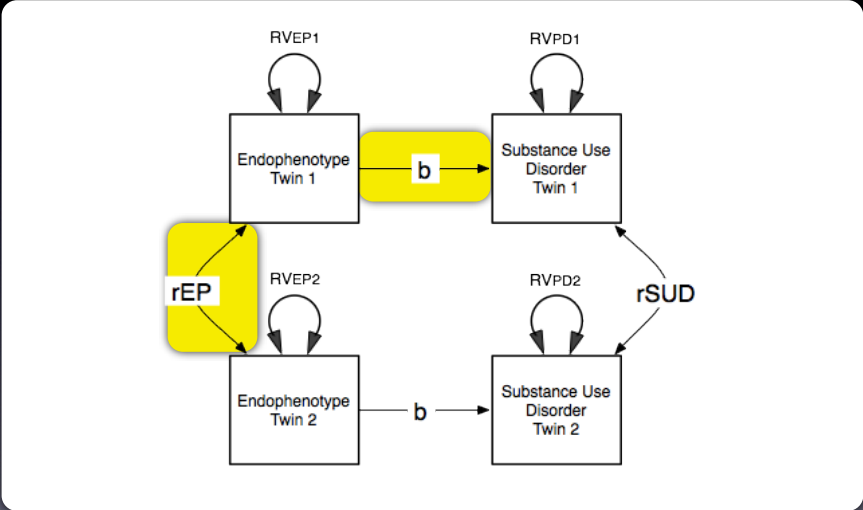
Gottesman Response

- Thank you for your in depth exegesis of EP. The nomological network you construct for the construct is in the finest tradition of Meehl's "straight thinking".
- A few scholars and deep thinkers (rare mutations in our field) may actually take the time to digest your ideas and make our field better.

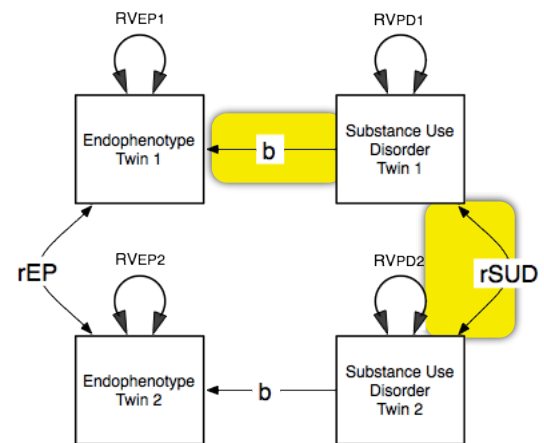
Direction of Causation

- Longitudinal Data
 - Reasonable assumption that Time 2 does not affect Time 1
 - Includes experimental designs
- Twin/Family Data
 - Contemporaneous assessment

EP causes SUD



SUD causes EP

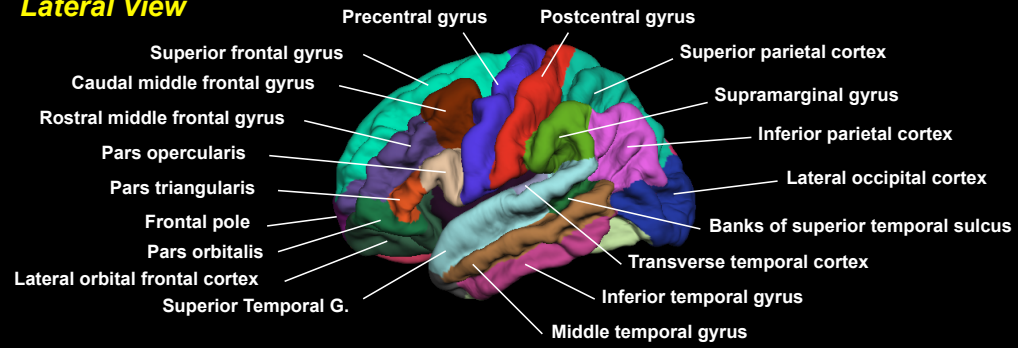


Makes different prediction about $cov(EPI, SUAD2)$

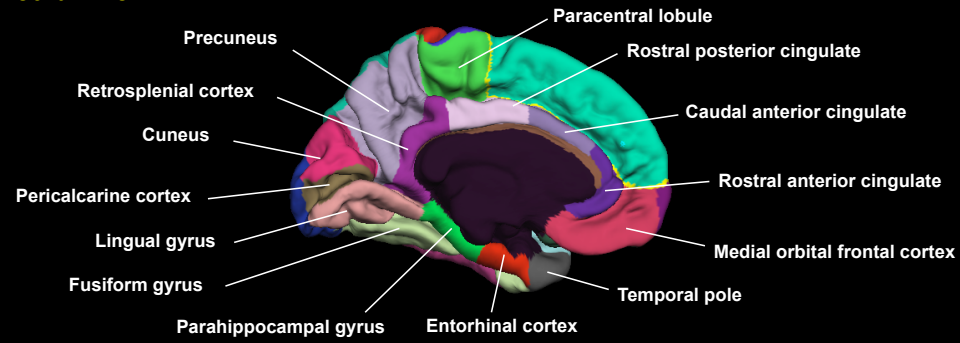
Rationale

- Brain: candidate endophenotype
 - Psychopathology
 - Substance abuse
 - Obesity
 - Personality
 - Cognition

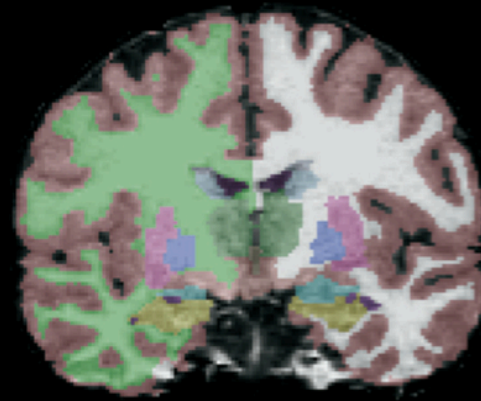
Lateral View



Medial View



Subcortical Regions

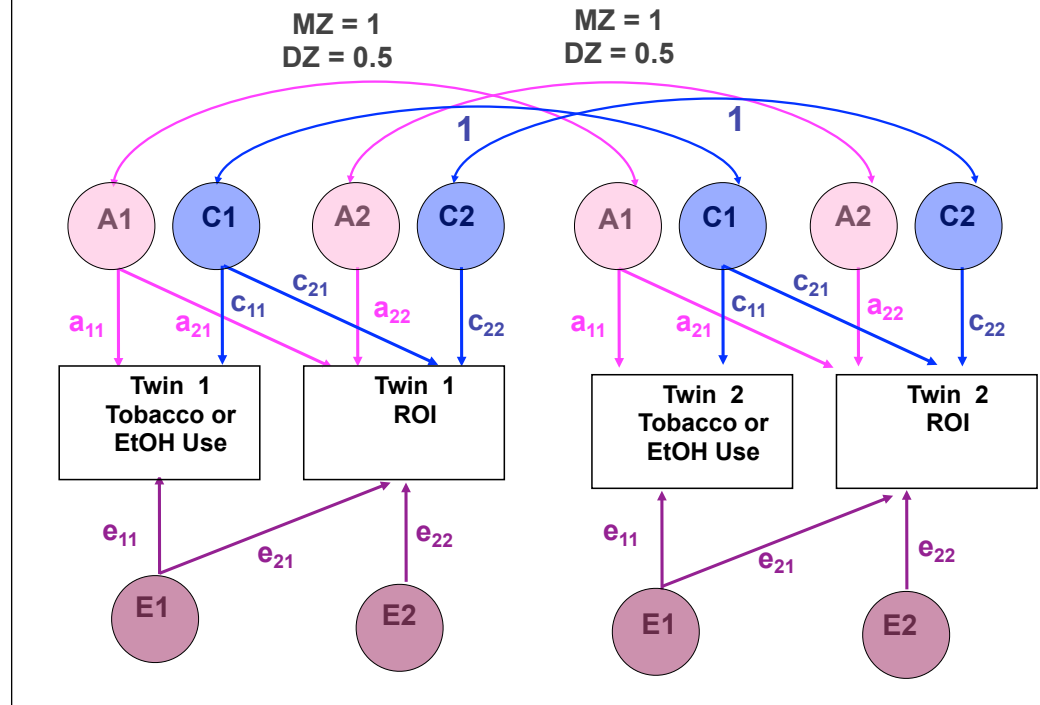


- Hippocampus
- Amygdala
- Caudate
- Pallidum
- Putamen
- Thalamus
- Inferior Lateral Ventricle
- Cortical Gray Matter
- Right Cerebral White Matter
- Left Cerebral White Matter

(Possible) Functional Significance of Morphometric Measures

- Volume (cortical and subcortical)
 - Overall size, implied neuronal connectivity and function
 - Associations between poor outcomes and decreased volume or increased ventricles
- Cortical structure
 - Neurons are organized into columns perpendicular to brain surface
- Radial Unit Hypothesis of Cortical Development (Rakic)
 - Cells within a column share a common origin and migrate to their location within the cortex during development
 - Cortical surface area driven by the number of columns
 - Cortical thickness is influenced by the number of cells within a column
 - Different genetic architecture for cortical thickness and surface area

Bivariate Cholesky



Significant Bivariate Results Nicotine Abuse/Dependence

ROI	rA	rC	rE	covA	covC	covE	rP
LCerebellumWM	-0.271	-0.397	-0.054	-0.208	0.000	-0.035	-0.197
RCerebellumWM	-0.245	0.107	0.027	-0.188	0.000	0.018	-0.159
RCTXbankssts1	1.000	-1.000	-0.238	0.727	0.277	-0.150	-0.029
RCTXprecuneus1	-0.127	0.747	0.147	-0.098	0.000	0.094	-0.026
RCTXSUPtemporal1	-0.033	0.474	0.315	-0.026	0.000	0.202	0.086
RCTXtransversetemporal1	0.424	-0.999	-0.262	0.326	0.000	-0.168	0.059
RCTXbankssts2	1.000	-1.000	-0.242	0.759	0.162	-0.152	-0.075
LCTXLAToccipital2	-0.740	1.000	0.265	-0.554	0.081	0.174	-0.016
RCTXrostralMIDfrontal2	0.594	1.000	-0.369	0.449	0.013	-0.242	-0.040
RCTXSUPtemporal2	0.056	0.826	0.263	0.043	0.000	0.168	0.169
RCTXtransversetemporal2	0.699	-0.621	-0.220	0.541	0.000	-0.139	0.106
RCTXTotalSurfaceArea2	0.528	-0.228	-0.256	0.397	0.000	-0.169	0.103
LCTXcaudalANTCING3	1.000	1.000	-0.252	0.753	0.134	-0.162	0.029
RCTXcorpuscallosum3	-0.636	1.000	0.273	-0.477	0.159	0.176	0.011
LCTXINFparietal3	-0.128	1.000	0.354	-0.100	0.029	0.222	0.121
LCTXpostcentral3	0.390	-0.842	-0.336	0.297	0.000	-0.218	-0.009
RCTXrostralANTCING3	-1.000	1.000	0.254	-0.744	0.202	0.162	0.100

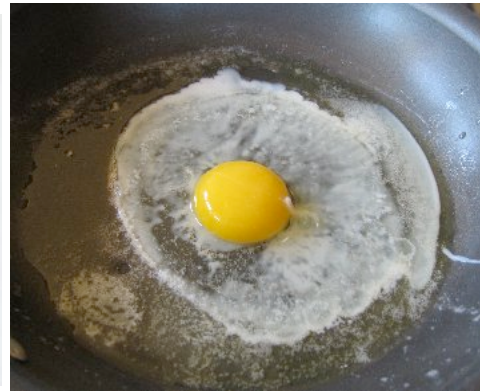
Is Brain Morphometry an Appropriate Endophenotype of Alcohol/Tobacco Use?

Satisfied?	Requirement
Y	Moderate heritability
	Endophenotype and illness co-segregate within families
	Found in affected family members at higher rate than in population
Y (kinda)	Association with illness in the population
	State-independent
	Association with causes rather than effects of disorders
	Endophenotype should affect a disorder
Y	Should have continuous variation in a population
Y	Should be measured across several levels of analysis

This is your brain...



This is your brain on
drugs...



This is your brain...



This is your brain on
drugs...



Modeling Comorbidity

- 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)

Comorbidity is High

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

Comorbidity due to symptom sharing

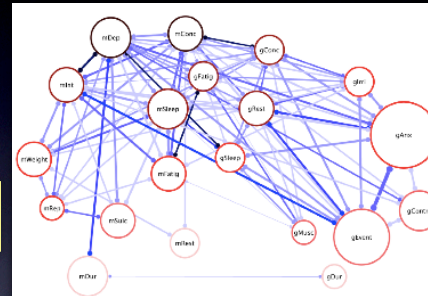
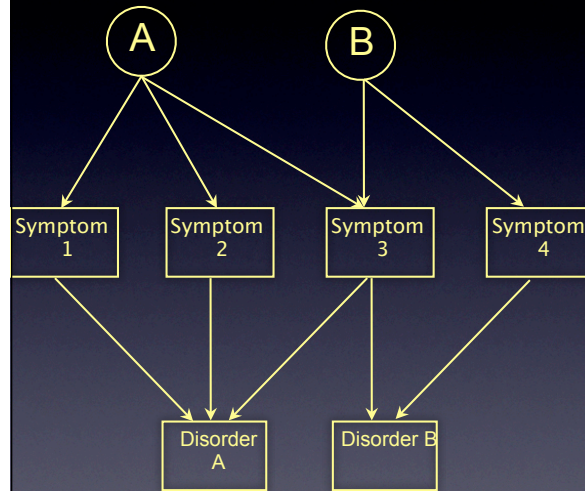
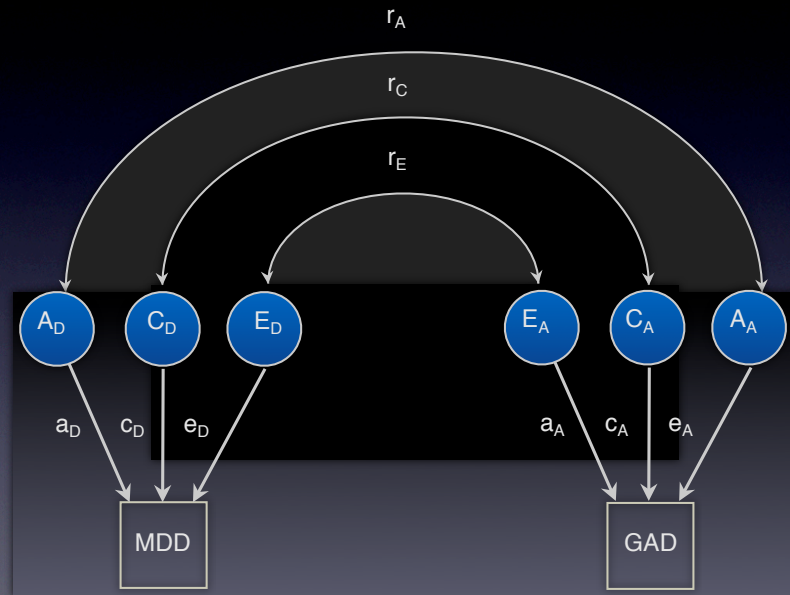


Figure 4. A comorbidity network for MDD and GAD. Larger nodes represent more frequent symptoms; darker circumference, higher centrality; thicker edges, higher frequency of co-occurrence; darker edges, stronger associations. Only edges with log odds ratio higher than (-) 0.50 are represented. Centrally positioned nodes (mConc, gConc, mSleep, gSleep, mFatig, gFatig, mRest and gRest) represent overlapping symptoms. Non-overlapping MDD symptoms are displayed on the left the figure, non-overlapping GAD symptoms on the right.

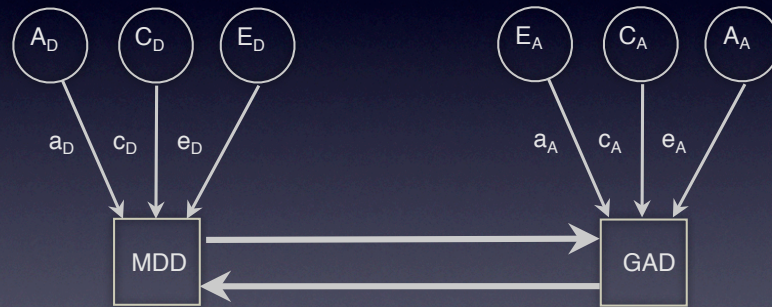
Not today!

Partitioning Comorbidity



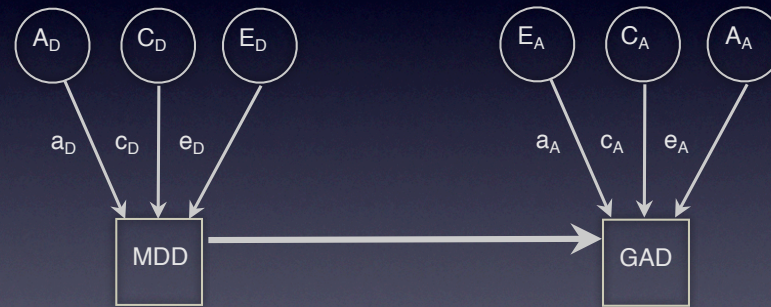
Modeling Comorbidity

Reciprocal Causation



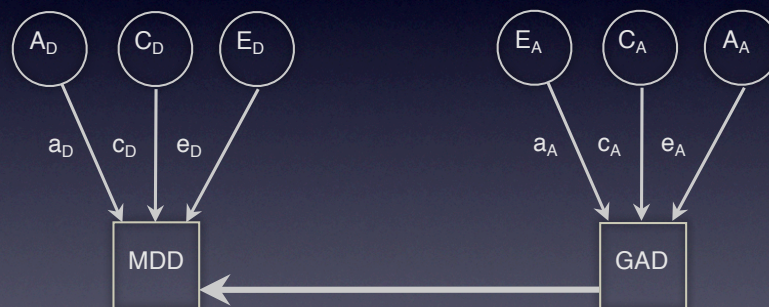
Modeling Comorbidity

Major Depression Causes Generalized Anxiety Disorder



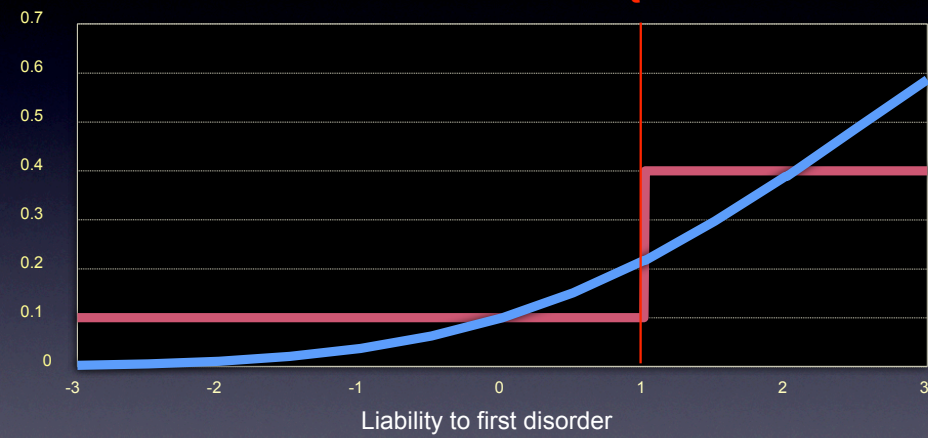
Modeling Comorbidity

Generalized Anxiety Disorder causes Major Depression



Alternative models of increasing risk to a second disorder

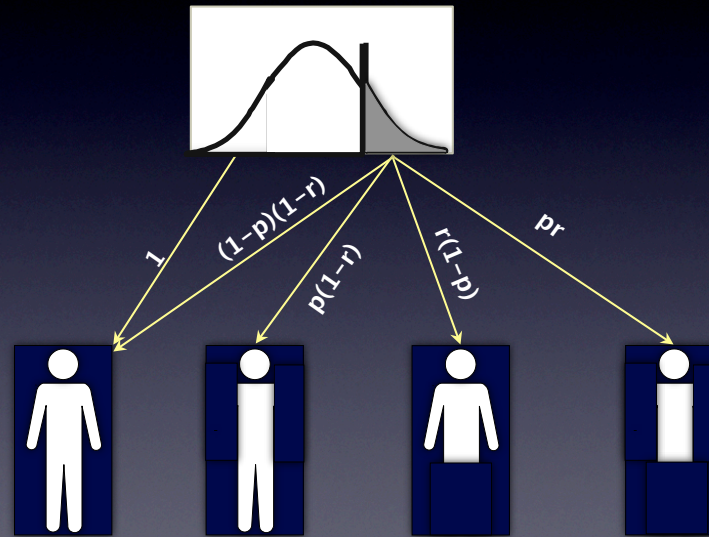
$p(\text{comorbid}) = \text{chance of getting second disorder}$



— Causal/Correlational Model — Jump Model

Threshold Model $t=1.5$

Alternate forms: One underlying continuum



Alternate forms: Detail of pairs

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

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

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

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

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

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

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

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

$$LL_A = \int_{-\infty}^{a_1} \int_{-\infty}^{a_2} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (24)$$

$$LM_A = \int_{-\infty}^{a_1} \int_{r_1}^{a_2} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (25)$$

$$LU_A = \int_{-\infty}^{a_1} \int_{a_2}^{\infty} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (26)$$

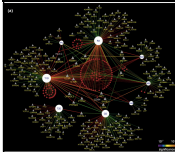
$$MM_A = \int_{r_1}^{a_1} \int_{r_2}^{a_2} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (27)$$

$$MU_A = \int_{r_1}^{a_1} \int_{r_2}^{\infty} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (28)$$

$$UU_A = \int_{a_1}^{\infty} \int_{a_2}^{\infty} \phi(R_{A1}, R_{A2}) dR_{A2} dR_{A1} \quad (29)$$

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

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



Large Database Studies

Top genetic associations in seven autoimmune diseases and T2D.

Most significant SNP per gene

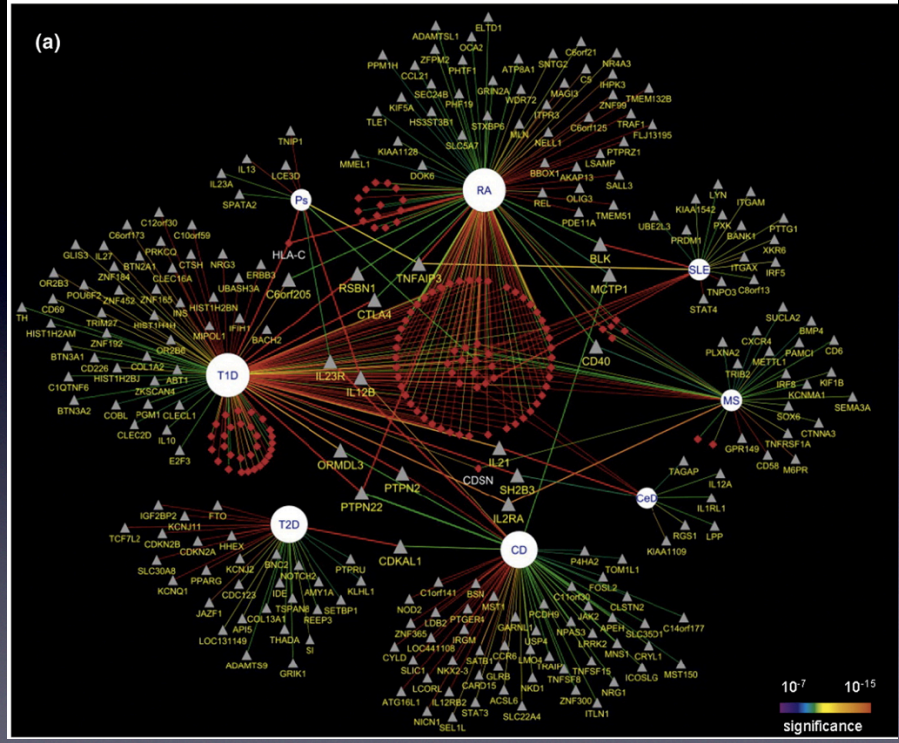
Only associations with the significance of at least $P < 10^{-7}$ are visualized.

If a given gene was identified in more than one disease, multiple lines connecting it with each disease were drawn.

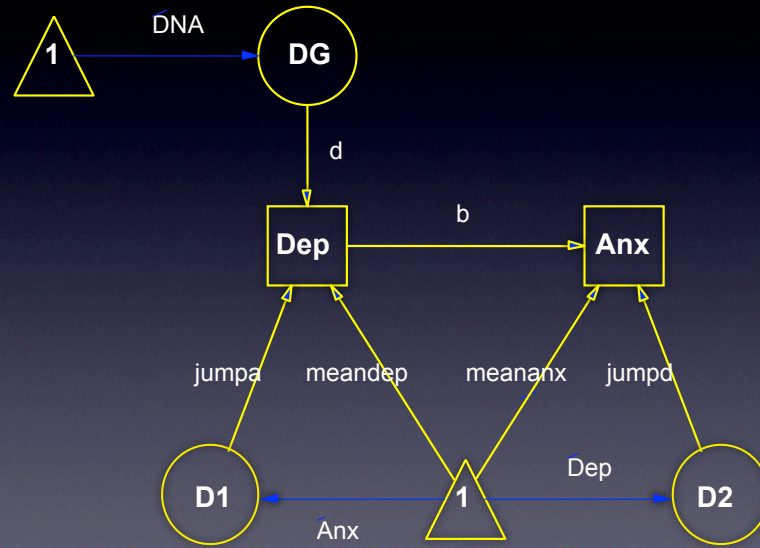
Lines are colored using a “heat” scheme according to the evidence for association. Thus “hot” edges (e.g. red, orange) represent more significant associations than “cold” edges (e.g. purple, blue).

Diseases are depicted by circles of size proportional to the number of associated genes, non-MHC genes by grey triangles, and genes in the MHC region are shown as red diamonds.

(a)



Unified Genetic Comorbidity Model?



Conclusion

- Endophenotypes have potential
 - Gene-finding
 - Environment-finding
 - Understanding etiology
 - Are intrinsically comorbid with outcomes
- Have Prevention & Treatment implications

