



Genomic Structural Equation Modeling: A Brief Introduction

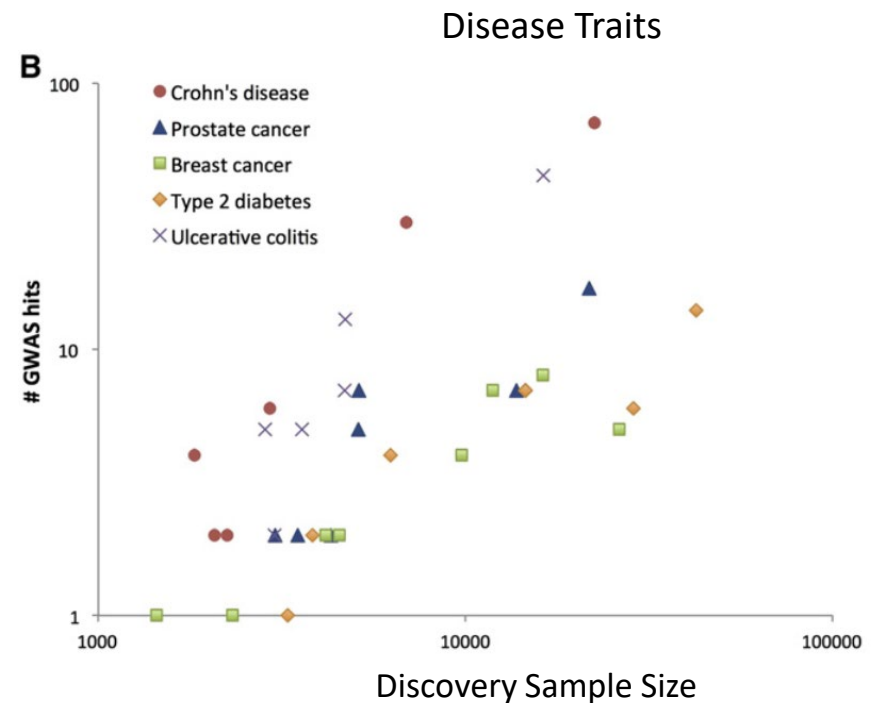
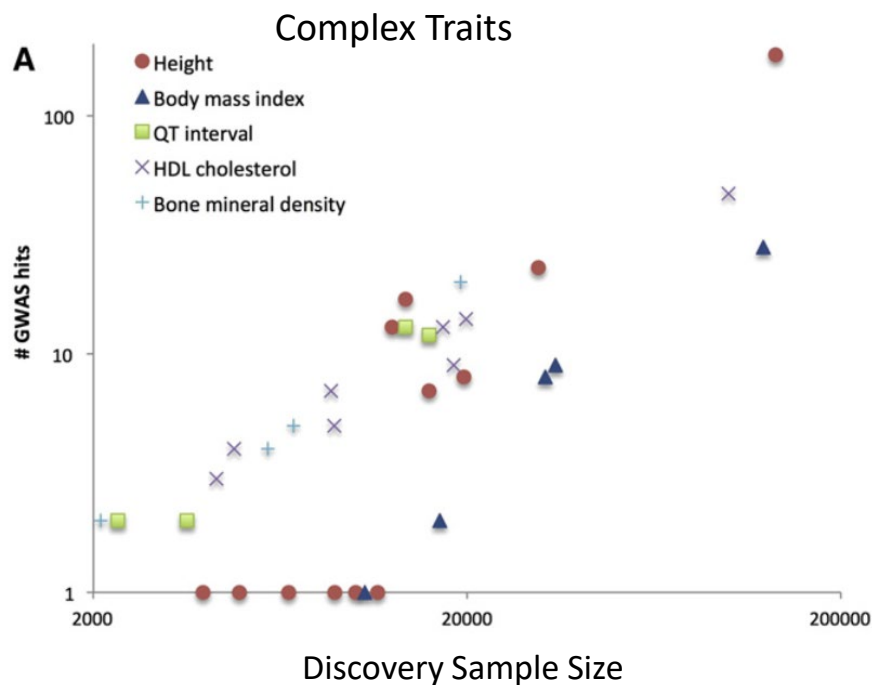
Andrew Grotzinger

IBG Workshop 2021

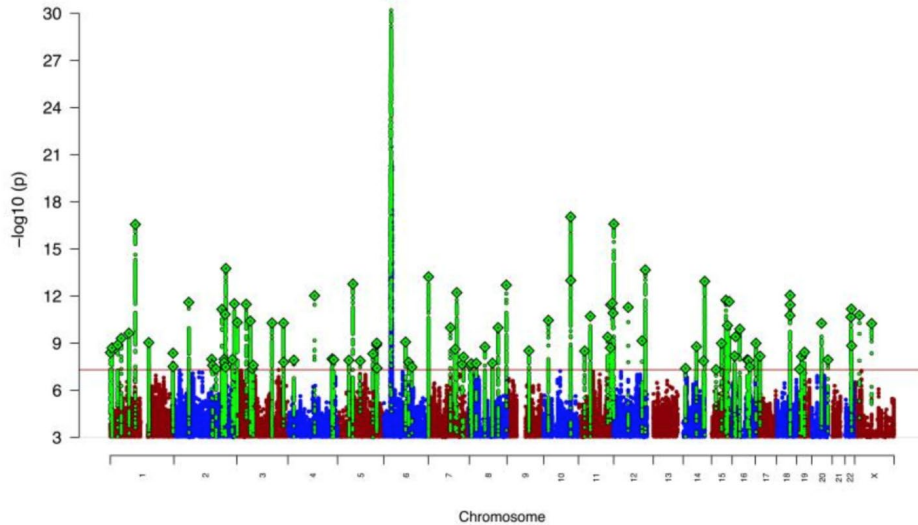
Paper: Grotzinger, A. D., Rhemtulla, M., de Vlaming, R., Ritchie, S. J., Mallard, T. T., Hill, W. D, Ip, H. F., McIntosh, A. M., Deary, I. J., Koellinger, P. D., Harden, K. P., **Nivard, M. G., & Tucker-Drob, E. M.** (in press). **Genomic SEM provides insights into the multivariate genetic architecture of complex traits.** *Nature Human Behaviour*.

Link to paper: rdcu.be/bvn7t

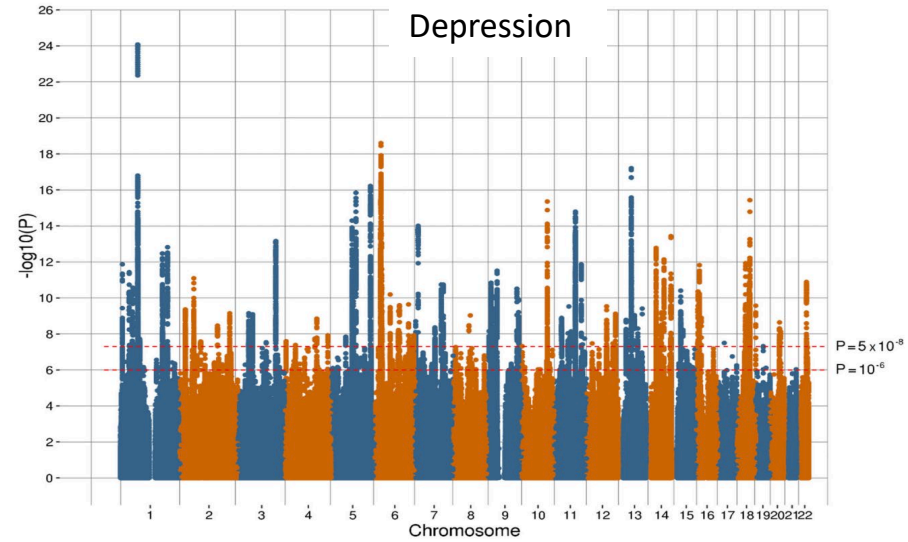
The gradual realization that human complex traits are associated with *many* genes



Schizophrenia



Depression



Traits are highly polygenic,
so not simply a matter of
identifying ~5 overlapping
genes

An atlas of genetic correlations across human diseases and traits

Brendan Bulik-Sullivan [✉](#), Hilary K Finucane [✉](#), Verner Anttila, Alexander Gusev, Felix R Day, Po-Ru Loh, ReproGen Consortium, Psychiatric Genomics Consortium, Genetic Consortium for Anorexia Nervosa of the Wellcome Trust Case Control Consortium 3, Laramie Duncan, John R B Perry, Nick Patterson, Elise B Robinson, Mark J Daly, Alkes L Price [✉](#) & Benjamin M Neale [✉](#)

Nature Genetics **47**, 1236–1241 (2015) | [Download Citation](#) [↓](#)

Estimates genetic correlations between samples with varying degrees of sample overlap using publicly available data

Pervasive (Statistical) Pleiotropy Necessitates Methods for Analyzing Joint Genetic Architecture

Analysis of shared heritability in common disorders of the brain

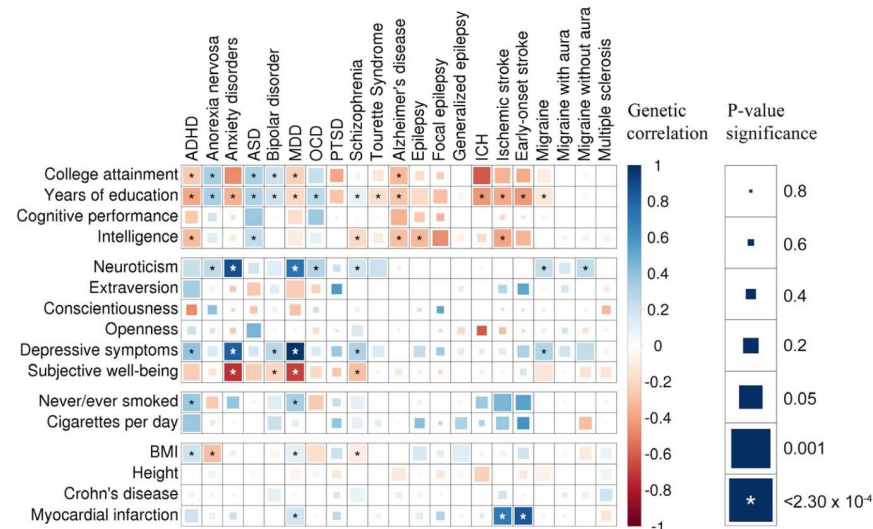
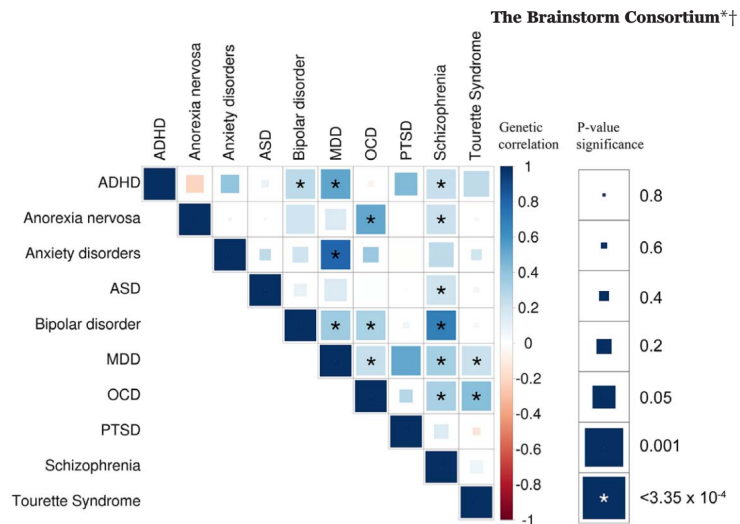


Fig. 1. Genetic correlations across psychiatric phenotypes. The color of each box indicates the magnitude of the correlation, and the size of the box indicates its significance (LDSC), with significant correlations filling each square completely. Asterisks indicate genetic correlations that are significantly different from zero after Bonferroni correction.

Fig. 4. Genetic correlations across brain disorders and behavioral-cognitive phenotypes. The color of each box indicates the magnitude of the correlation, and the size of the box indicates its significance (LDSC), with significant correlations filling each square completely. Asterisks indicate genetic correlations that are significantly different from zero after Bonferroni correction.

Background

- Genome-wide methods are clearly suggestive of both high polygenicity and pervasive pleiotropy
- **Genetic correlations as data to be modeled, not simply results by themselves**
 - What data-generating process gave rise to the correlations?






Genomic SEM

nature
human behaviour

ARTICLES

<https://doi.org/10.1038/s41562-019-0566-x>

Genomic structural equation modelling provides insights into the multivariate genetic architecture of complex traits

Andrew D. Grotzinger ^{1*}, Mijke Rhemtulla², Ronald de Vlaming ^{3,4}, Stuart J. Ritchie^{5,6},
Travis T. Mallard¹, W. David Hill^{5,6}, Hill F. Ip ⁷, Riccardo E. Marioni^{5,8}, Andrew M. McIntosh ^{5,9},
Ian J. Deary^{5,6}, Philipp D. Koellinger^{3,4}, K. Paige Harden^{1,10}, Michel G. Nivard ^{7,11} and
Elliot M. Tucker-Drob^{1,10,11}

Nivard

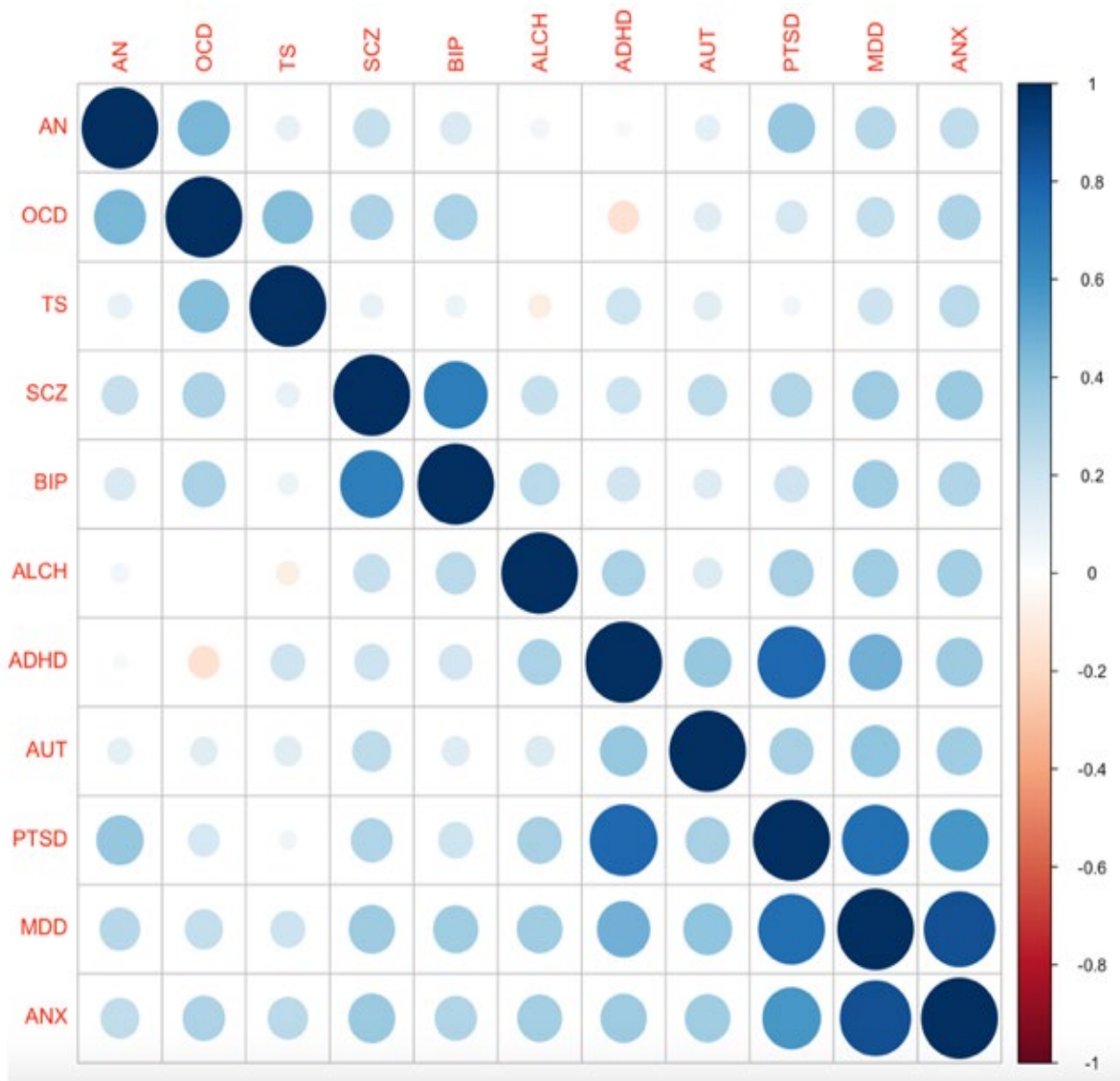


Tucker-Drob



Our solution: GenomicSEM

- Apply structural equation model to estimated genetic covariance matrices
 - Allows user to examine traits that could not be measured in the same sample
- Genomic SEM provides flexible framework for estimating limitless models using GWAS summary statistics
 - Can be applied to GWAS “sumstats” with varying and unknown degrees of overlap

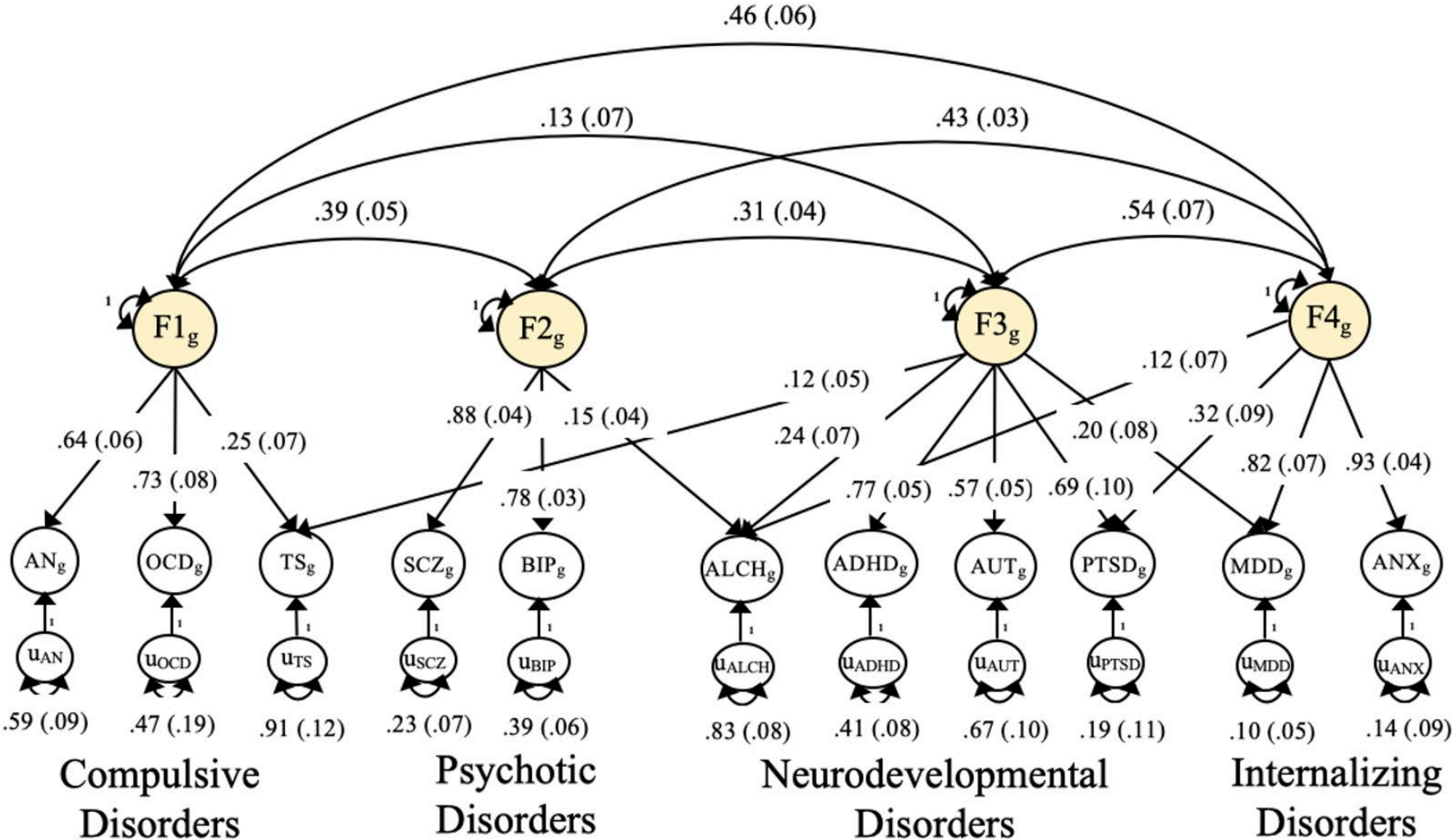


Genetic “heatmap”
across 11 Major
Psychiatric Disorders

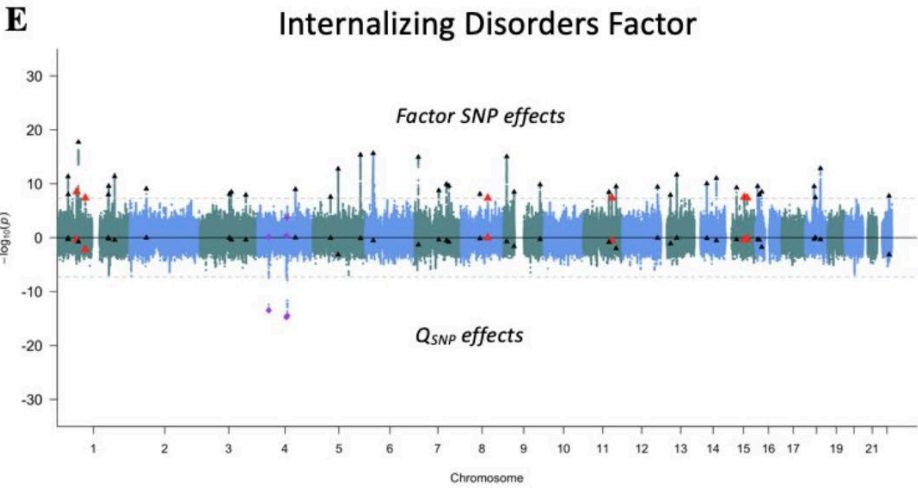
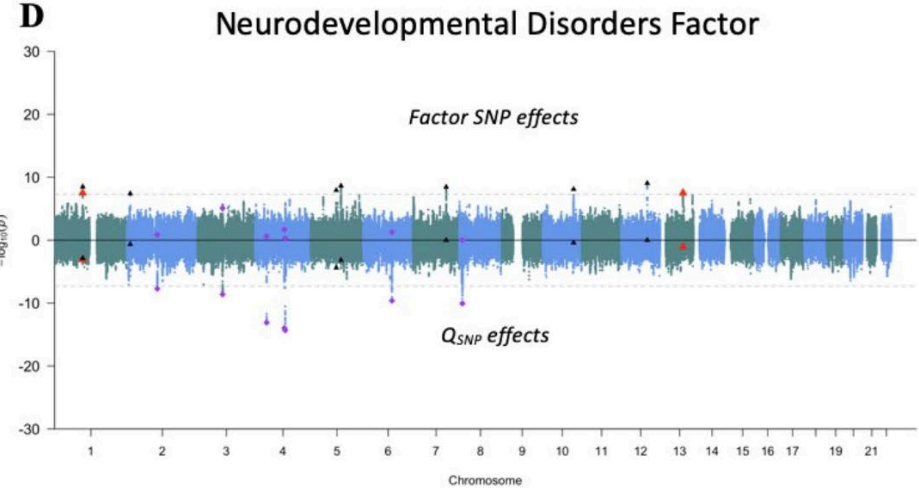
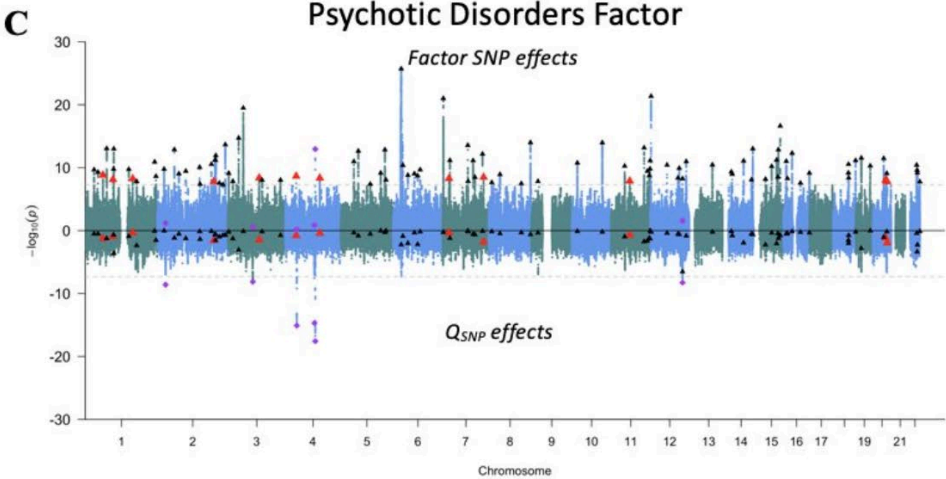
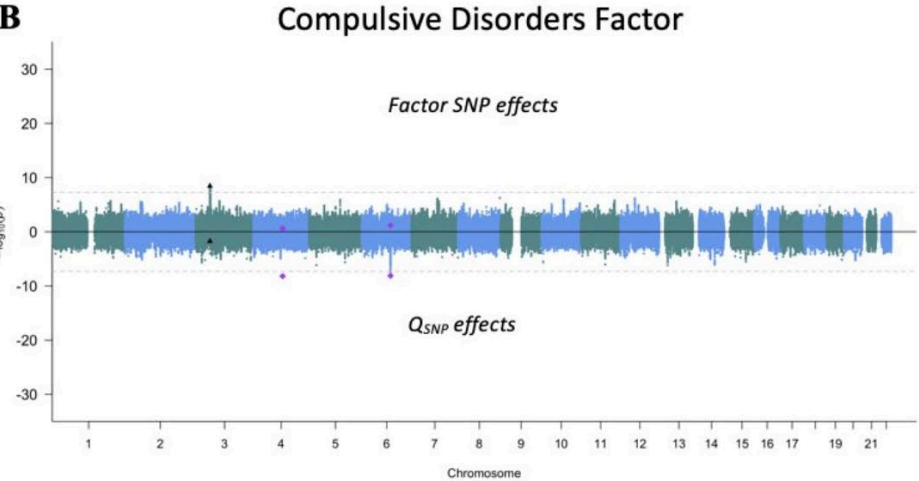
Many of these
disorders could not
be measured in the
same sample

Genomic SEM offers
unique opportunity
to model system of
relationships across
rare and mutually
exclusive clinical
presentations

Genetic Relationships Across Eleven Major Psychiatric disorders



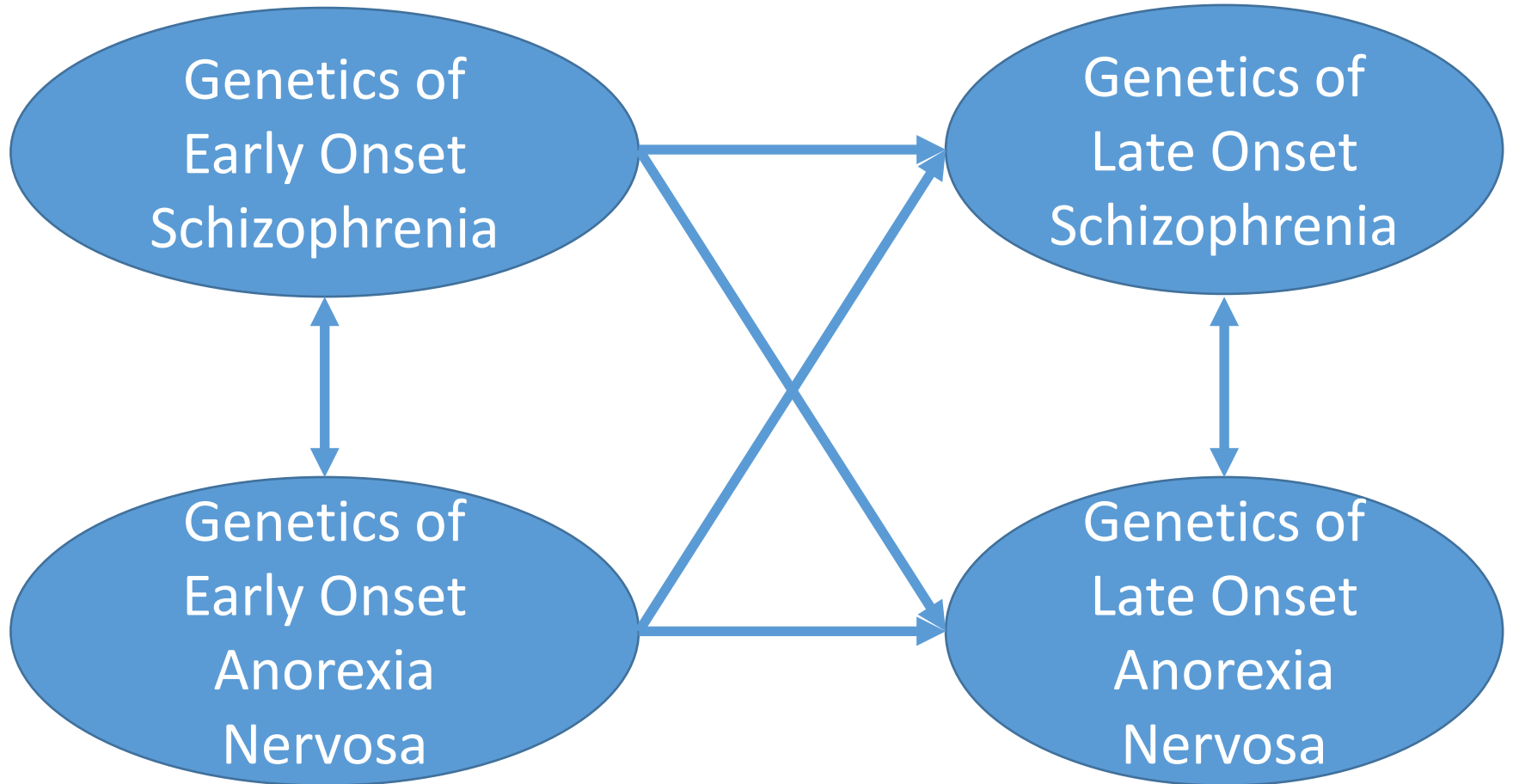
Genetic Relationships Across Eleven Major Psychiatric disorders



***Even if you are not
interested in genetics:***

Can now examine systems of
relationships between a wide array of
(rare) traits

***that could not be measured in the
same sample***



Genetics of
Early Onset
Schizophrenia

This diagram consists of two blue ovals connected by a vertical double-headed arrow. The top oval contains the text 'Genetics of Early Onset Schizophrenia' and the bottom oval contains 'Genetics of Early Onset Anorexia Nervosa'. The entire diagram is set against a light gray background.

Genetics of
Early Onset
Anorexia
Nervosa

Genetics of
Late Onset
Schizophrenia

This diagram consists of two blue ovals connected by a vertical double-headed arrow. The top oval contains the text 'Genetics of Late Onset Schizophrenia' and the bottom oval contains 'Genetics of Late Onset Anorexia Nervosa'. The entire diagram is set against a light gray background.

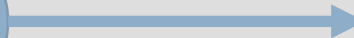
Genetics of
Late Onset
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Genetics of
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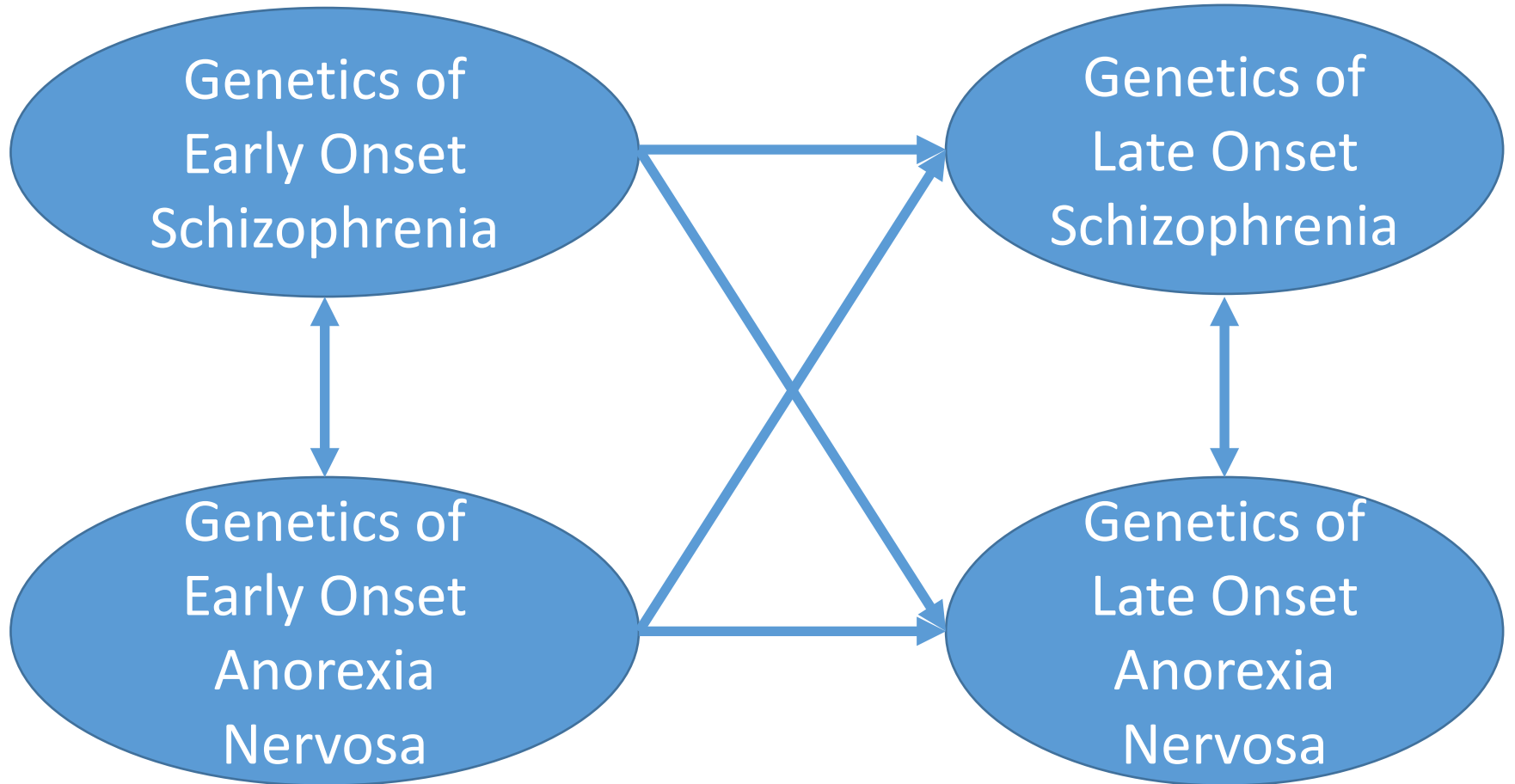


Genetics of
Late Onset
Schizophrenia

Genetics of
Early Onset
Anorexia
Nervosa





Genetics of
Late Onset
Anorexia
Nervosa



Psychological Medicine

Genetic heterogeneity in self-reported depressive symptoms identified through genetic analyses of the PHQ-9


Jackson G. Thorp  (a1), Andries T. Marees (a1) (a2), Jue-Sheng Ong (a3), Jiyuan An (a3) ... 


DOI: <https://doi.org/10.1017/S0033291719002526>

Published online by Cambridge University Press: 18 September 2019

Molecular
Psychiatry

Genomic prediction of cognitive traits in childhood and adolescence

A. G. Allegrini , S. Selzam, K. Rimfeld, S. von Stumm, J. B. Pingault & R. Plomin

Molecular Psychiatry **24**, 819–827 (2019) | [Download Citation](#) 

nature
genetics

ARTICLES
<https://doi.org/10.1038/s41588-020-00754-2>

 Check for updates

Investigating the genetic architecture of noncognitive skills using GWAS-by-subtraction

Perline A. Demange ^{1,2,3,20}, Margherita Malanchini^{4,5,6,20}, Travis T. Mallard ⁶, Pietro Biroli ⁷, Simon R. Cox ⁸, Andrew D. Grotzinger ⁹, Elliot M. Tucker-Drob ^{6,9}, Abdel Abdellaoui ^{1,10}, Louise Arseneault ⁵, Elsie van Bergen ^{1,3}, Dorret I. Boomsma ¹, Avshalom Caspi ^{5,11,12,13}, David L. Corcoran ¹², Benjamin W. Domingue ¹⁴, Kathleen Mullan Harris ¹⁵, Hill F. Ip¹, Colter Mitchell¹⁶, Terrie E. Moffitt^{5,11,12,13}, Richie Poulton ¹⁷, Joseph A. Prinz¹², Karen Sugden¹¹, Jasmin Wertz¹¹, Benjamin S. Williams¹¹, Eveline L. de Zeeuw^{1,3}, Daniel W. Belsky ^{18,19,21,22}, K. Paige Harden ^{6,21}  and Michel G. Nivard ^{1,21} 

Cell

Volume 179, Issue 7, 12 December 2019, Pages 1469–1482.e11










Article

Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders

Cross-Disorder Group of the Psychiatric Genomics Consortium¹ 



Genetic stratification of depression by neuroticism: revisiting a diagnostic tradition

Mark J. Adams¹ , David M. Howard^{1,2} , Michelle Luciano^{3,4} , Toni-Kim Clarke¹ , Gail Davies^{3,4}, W. David Hill^{3,4}, 23andMe Research Team⁵, Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium†, Daniel Smith⁶, Ian J. Deary^{3,4} , David J. Porteous⁷  and Andrew M. McIntosh^{1,3} 

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Article | Published: 07 September 2020

A general dimension of genetic sharing across diverse cognitive traits inferred from molecular data

Javier de la Fuente, Gail Davies, Andrew D. Grotzinger, Elliot M. Tucker-Drob  & Ian J. Deary 

Nature Human Behaviour **5**, 49–58(2021) | [Cite this article](#)

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