Genetics of common complex psychiatric disorders

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Genetics and Environmental Influences on Behaviour and Mental Health

Topics:

- **Quantitative genetics and heritability**
- **Candidate gene studies**
- **Genome-wide studies**
- **Prediction**
- **Causality**

What is a *"common"*, *"complex"* psychiatric disorder?

Common: Affects 1% or more of the population
Complex: Inheritance cannot be explained by a single gene

Psychiatric disorders are defined by disruption to higher-order brain functions of moods, perceptions, thoughts, beliefs, and behaviours but usually in the absence of major neurological impairments (consciousness, senses, memory). Psychiatric disorders include depressive and anxiety disorders (major depressive disorder, panic disorder), manic and psychotic disorders (bipolar disorder, schizophrenia), obsessive-compulsive disorders, eating disorders (anorexia nervosa, bulimia nervosa), substance-use disorders and personality disorders. Childhood conditions like attention-deficit/hyperactivity and autism can also be included, but only when they lead to clinically-salient impairment or distress. There are also many shades of sadness, hallucinations, eccentricities, mood swings, body-image preoccupations, recreational substances

use, personalities, etc that are not psychiatric disorders but may still be informative to study from an aetiological and genetic standpoint.

- Sullivan PF and Geschwind DH (2019) Defining the Genetic, Genomic, Cellular, and Diagnostic Architectures of Psychiatric Disorders. *Cell* doi:10.1016/j.cell.2019.01.015

- Depression: 3% in a week
- Schizophrenia: 1% in lifetime
- Bipolar disorder: 2% in lifetime
- Anxiety disorder: 6% in a week

Psychiatric disorders have many causes, correlates, and consequences (genetics, environment, family life, substance use, relationships)

Incidence of psychiatric disorders range from the common (depression, anxiety) to the rare (bipolar disorder, schizophrenia).

Why genetics?

Why use genetics to study mental health and psychiatric disorders?

- Biological understanding of genes, pathways
- Shared aetiology with other disorders
- Risk prediction
- Drug retargeting
- Causal analysis of environmental risk factors

Genetics of categorical traits

Seed		Flower	Pod		Stem	
Form	Cotyledons	Color	Form	Color	Place	Size
Grey & Round	Yellow	White	Full	Yellow	Axial pods, Flowers along	Long (6-7ft)
White & Wrinkled	Green	Violet	Constricted	Green	Terminal pods, Flowers top	Short (¾ -1ft)
1	2	3	4	5	6	7

Figure 1: Diagram showing the seven "characters" observed by Mendel

Gregor Mendel (1822–1884), working in what is now Czechia, discovered the transmission of traits from parents to offspring could be explained by the inheritance of two "elements", which we now call alleles. Mendel was concerned with discrete or categorical phenotypes.

Mendel pea plant figure by Mariana Ruiz (LadyofHats) [public domain]

Genetics of continuous traits

RATE OF REGRESSION IN HEREDITARY STATURE.
Fig. (a)

The Deviates of the Children are to those of their Mid-Parents as 2 to 3.

When Mid-Parents are taller than mediocrity, their Children tend to be shorter than they.

When Mid Parents are shorter than mediocrity, their Children tend to be taller than they.
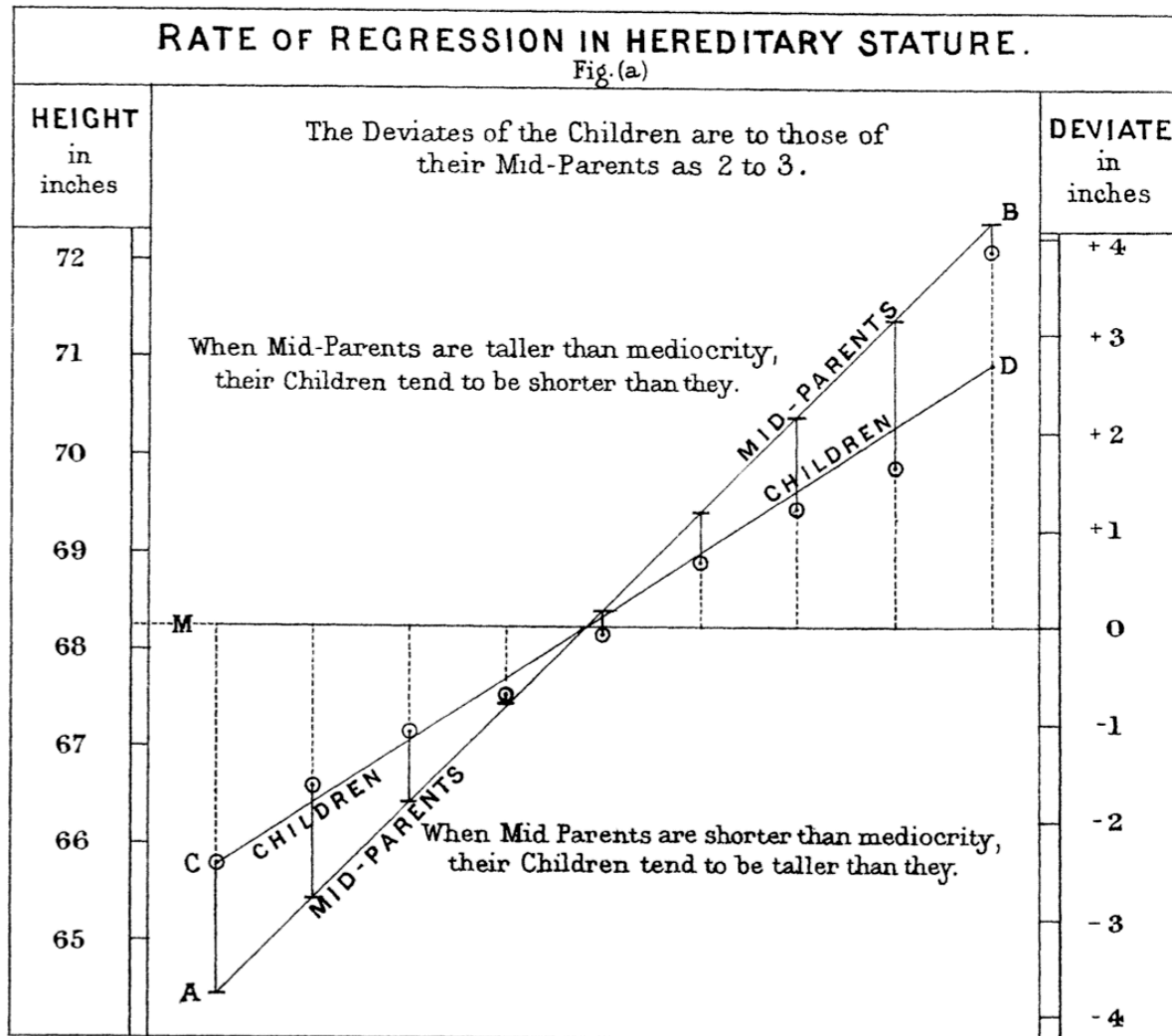
Separately, Francis Galton (1822–1911), was studying the inheritance of continuous or metric phenotypes. He noticed the parents who were tall tended to have children that were slightly shorter than themselves (and vice versa). This was termed "regression to the mean" from which the name of the statistical method "regression" is derived.

> "In their search for universal hereditary laws, Galton and Pearson were driven by the linear model and the normal distribution because the associated parameters had scientific meaning for them that went beyond mere description." - Wachsmuth, A., Wilkinson, L., & Dallal, G. E. (2003). Galton's Bend. The American Statistician, 57(3), 190–192. doi:10.1198/0003130031874

For more on Galton's legacy, see https://adelphigenetics.org/history/

Reconciling categorical + continuous genetics = quantitative genetics
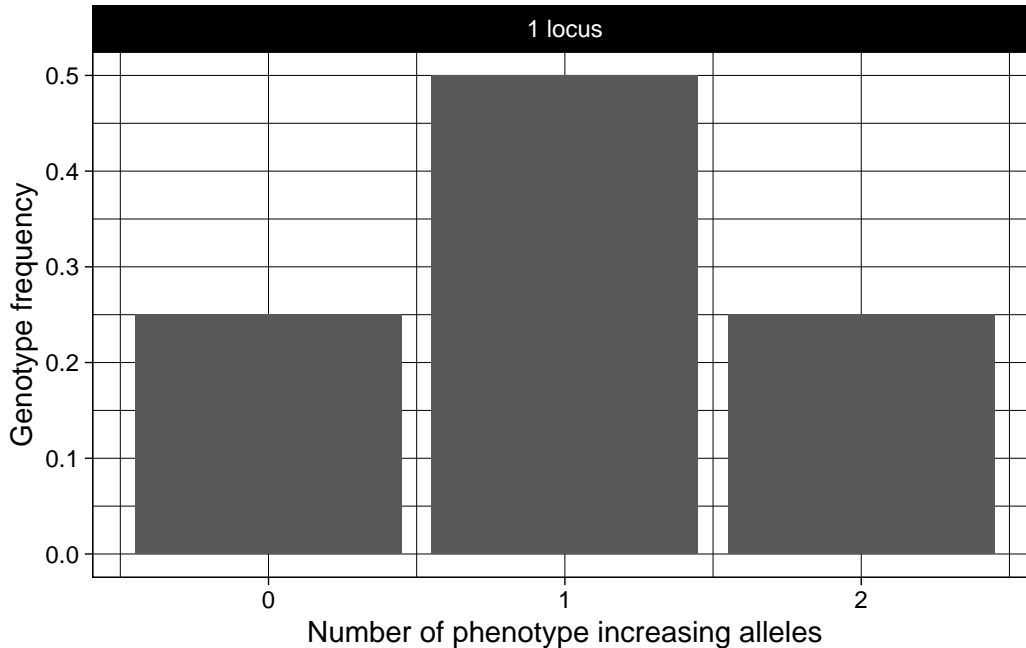
Ronald Fisher reconciled the inheritance of continuous and categorical phenotypes by showing that a continuous phenotype could be made from the inheritance of a large number (dozens, hundreds, or thousands) categorical genes. The term "variance" comes from Fisher's discoveries.

- Fisher, R. A. (1918). XV.—The correlation between relatives on the supposition of Mendelian inheritance. *Transactions of the Royal Society of Edinburgh.* doi:10.1017/S0080456800012163
- Charlesworth and Edwards (2018). A century of variance. *Significance* 15(4). doi:10.1111/j.1740-9713.2018.01170.x
- Bodmer et al (2021) The outstanding scientist, R.A. Fisher: his views on eugenics and race. *Heredity* doi:10.1038/s41437-020-00394-6

Polygenic traits are quantitative traits

Adding up effects from a large number of genetic effects to make a continuous phenotype is related to the Central Limit Theorem.
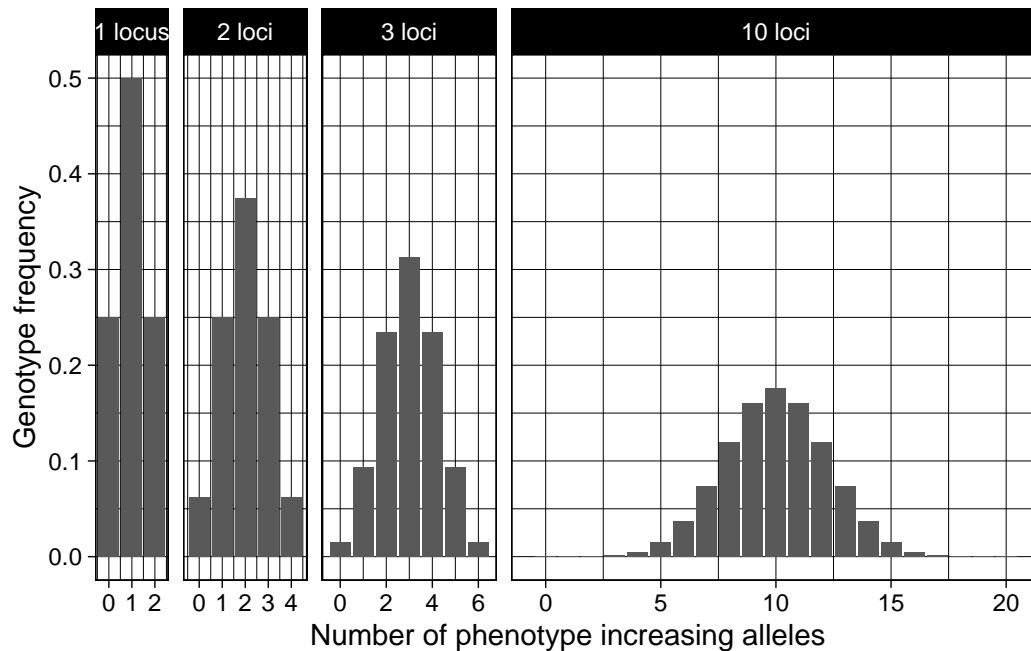
"R. A. Fisher's 1918 paper, 'The correlation between relatives on the supposition of Mendelian inheritance', resolved the often bitter conflict between biometricians and Mendelians, which raged for a decade following the rediscovery of Mendel's work. Fisher showed that a complex quantitative trait could be explained by Mendelian inheritance if several genes affect the trait."Because he crossed true-breeding plants, Mendel's experiments showed that a single locus with two alleles of equal frequency results in three genotypes (see the figure, part a). If the allelic effects are additive, the three genotypes produce three phenotypes; in the case of Mendel's qualitative traits, the allelic effects showed complete dominance, so only two phenotypes were observed. However, assuming equal and additive effects, 2 genes yield 9 genotypes and 5 phenotypes (part b) and 3 genes yield 27 genotypes and 7 phenotypes (part c). With unequal and non-additive allelic effects and some environmental influence, three genes would result in a normal bell-shaped curve of continuous variation (part d). This logic assumes common alleles; rare alleles will skew the distribution. Genome-wide association research suggests that many more than three genes affect most traits, which underscores the expectation that polygenic traits are quantitative traits."

- Plomin, R., Haworth, C. & Davis, O. Common disorders are quantitative traits. *Nat Rev Genet* **10**, 872-878 (2009). doi:10.1038/nrg2670

Biometrics

What are the sources of family resemblance? How do we quantify them numerically?

Heritability

Proportion of similarity in phenotypes that can be attributed to similarity in genotypes.

Model: Phenotype (P) = Genotype (G) + Environment (E)
Variance decomposition

$$\text{var}(P) = \text{var}(G) + \text{var}(E)$$

Proportion of variance

$$h^2 = \frac{\text{var}(G)}{\text{var}(P)}$$

- Tenesa, A., Haley, C. The heritability of human disease: estimation, uses and abuses. *Nat Rev Genet* **14**, 139–149 (2013). doi:10.1038/nrg3377
- Visscher, P., Hill, W. & Wray, N. Heritability in the genomics era — concepts and misconceptions. *Nat Rev Genet* **9**, 255–266 (2008). doi:10.1038/nrg2322

How to estimate heritability from data
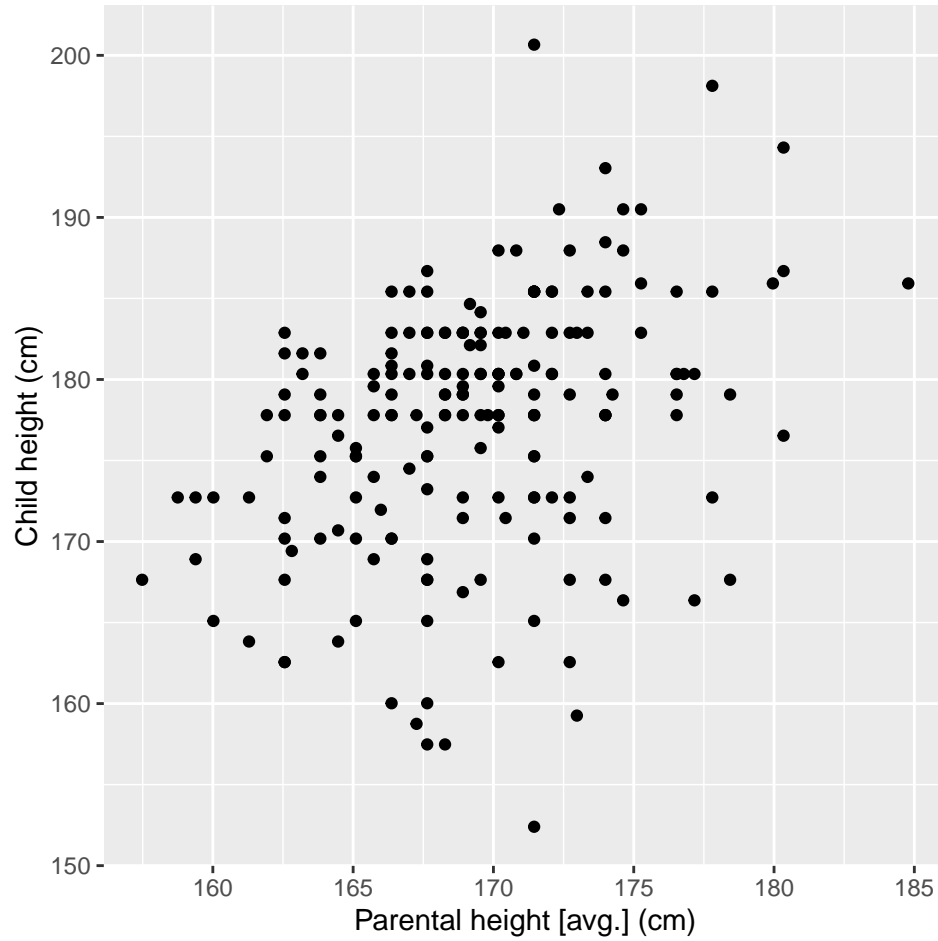
Plot of child (offspring) height versus the average of their parents' heights. What is a statistic that can be used to summarise the relationship between these two variables?

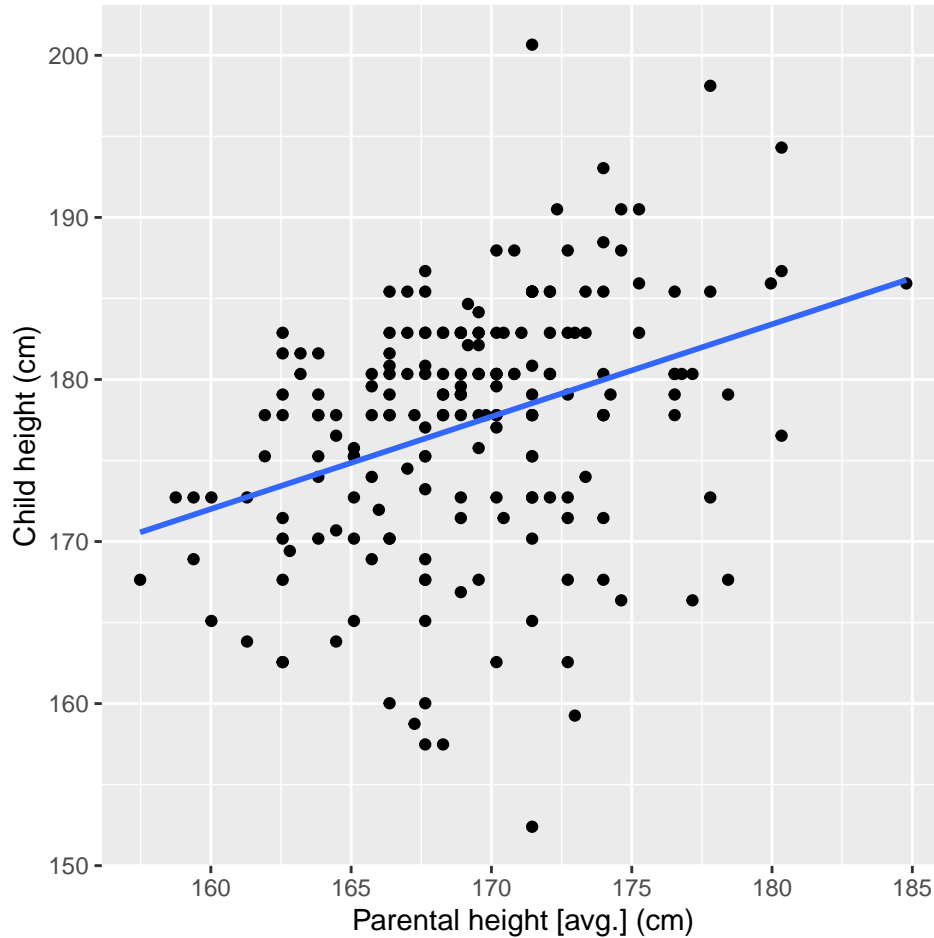**How to estimate heritability from data**

$\beta = \frac{\text{cov}(A,B)}{\text{var}(A)}$

Estimate the beta coefficient (slope) for a simple regression from the covariance between predictor (A) and outcome (B) variable divided by the variance of the predictor (A).

Simple model of genetic and environmental effects

$$P = G + E$$

The phenotype value P is influenced by a genetic effect G and and environmental effect E.

For simplicity assume that P is an individual's deviation from the average phenotype in the population.
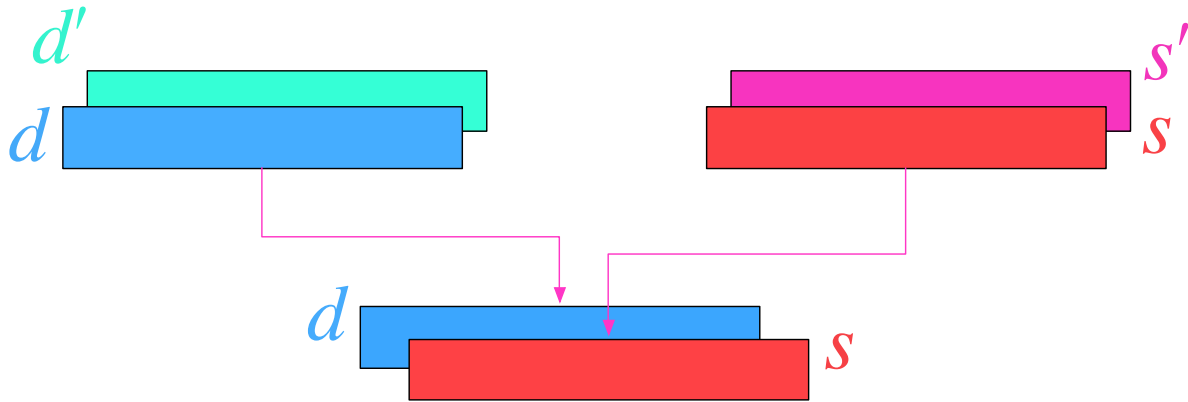
Simple model of genomics

$$G = d + s$$

Each individual has two copies of the genome, one inherited from each parent.

Here we label the genome from the mother d and the genome from the father s. These are the transmitted genetic effects.

Simple model of inheritance

Each parent also has a copy of the genome which they do not pass on to their child, labelled d' for the mother and s' for the father. These are the non-transmitted genetic effects.

Simple model of genetics, environment, and inheritance

Phenotype (P) value is the sum of the two genetic values plus an environmental value (e).

- Mother's phenotype: $P_d = d + d' + e_d$
- Father's phenotype: $P_s = s + s' + e_s$
- Child's phenotype: $P_o = d + s + e_o$

Regression equation

$\beta = \frac{\text{cov}(A,B)}{\text{var}(A)}$

- A = average of parents' phenotypes
- B = offspring phenotype

Therefore, $\beta = \frac{\text{cov}(\frac{P_d+P_s}{2}, P_o)}{\text{var}(\frac{P_d+P_s}{2})}$

Parent–offspring covariance

$$\text{cov}(\frac{P_d + P_s}{2}, P_o)$$

$$= \text{cov}(\frac{d + d' + e_d + s + s' + e_s}{2}, d + s + e_o)$$

Parent-offspring covariance

Expand the terms. Recall that:

$$\text{cov}(A + X, B + Y) = \text{cov}(A, B) + \text{cov}(A, Y) + \text{cov}(X, B) + \text{cov}(X, Y)$$

Thus we can do a pairwise expansion to:

$$= \text{cov}(\frac{d}{2} + \frac{d'}{2} + \frac{e_d}{2} + \frac{s}{2} + \frac{s'}{2} + \frac{e_s}{2}, d + s + e_o)$$

$$= \text{cov}(\frac{d}{2}, d) + \text{cov}(\frac{d'}{2}, d) + \cdots + \text{cov}(\frac{e_s}{2}, e_o)$$

$$

Simplifications

Some terms can be simplified.

Covariance between a genetic effect and itself

$$\text{cov}(\frac{d}{2}, d), \text{cov}(\frac{s}{2}, s)$$

Simplifies to:

$$\text{cov}(\frac{d}{2}, d) = \frac{1}{2}\text{cov}(d, d) = \frac{1}{2}\text{var}(d)$$

$$\text{cov}(\frac{s}{2}, s) = \frac{1}{2}\text{cov}(s, s) = \frac{1}{2}\text{var}(s)$$

Assumptions

For some terms we might make an assumption that they are equal to 0.

Covariance between genetic effects from the same parent

$$\text{cov}(\frac{d'}{2}, d), \text{cov}(\frac{s'}{2}, s)$$

If there is inbreeding (individual does not have ancestors that are closely related) or assortative mating in the grandparental generation, then genetic effects from the same parent would be expected to have a non-zero covariance.

Covariance between genetic effects from different parents

$$\text{cov}(\frac{d'}{2}, s), \text{cov}(\frac{s'}{2}, d)$$

If there is assortative mating between the parents, then these effects would be expected to covary

Covariance between parent and offspring environment effects

$$\text{cov}(\frac{e_d}{2}, e_o), \text{cov}(\frac{e_s}{2}, e_o)$$

If aspects of the parental environment are transmitted as well or if parents and offspring tend to encounter similar environments, then these effects are expected to covary.

Covariance between parental genetic and offspring environmental effects

$$\text{cov}(\frac{d}{2}, e_o), \text{cov}(\frac{s}{2}, e_o)$$

If parental genetic effects shape the environment of the offspring (referred to as indirect genetic effects), then these effects are expected to covary as well.

Using those assumptions the parent–offspring covariance simplifies to

$$\text{cov}(\frac{P_d + P_s}{2}, P_o) = \frac{\text{var}(d) + \text{var}(s)}{2}$$

Parent variance

The denominator in the regression equation was

$$\text{var}(\frac{P_d + P_s}{2})$$

Using the identity

$$\text{var}(aX + bY) = a^2\text{var}(X) + b^2\text{var}(Y) + 2ab\text{cov}(X,Y)$$

the variance of the average parental phenotypes is:

$$\text{var}(\frac{P_d + P_s}{2}) = \text{var}(\frac{1}{2}P_d + \frac{1}{2}P_s)$$

$$= \left(\frac{1}{2}\right)^2 \text{var}(P_d) + \left(\frac{1}{2}\right)^2 \text{var}(P_s) + 2 \cdot \frac{1}{2} \cdot \frac{1}{2}\text{cov}(P_d, P_s)$$

$$= \frac{1}{4}\text{var}(P_d) + \frac{1}{4}\text{var}(P_s) + \frac{1}{2}\text{cov}(P_d, P_s)$$

If we assume as above that there is no covariation between parental effects $(\text{cov}(P_d, P_s) = 0)$, this simplifies to

$$= \frac{\text{var}(P_d) + \text{var}(P_s)}{4}$$

Thus the regression equation is:

$$\beta = \frac{\text{cov}(\frac{P_d+P_s}{2}, P_o)}{\text{var}(\frac{P_d+P_s}{2})} = \frac{\frac{\text{var}(d)+\text{var}(s)}{2}}{\frac{\text{var}(P_d)+\text{var}(P_s)}{4}} = 2\frac{\text{var}(d) + \text{var}(s)}{\text{var}(P_d) + \text{var}(P_s)}$$

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Previously we defined

$$G = d + s$$

thus

$$\text{var}(G) = \text{var}(d) + \text{var}(s)$$

and assume variances in parental phenotypes are equal

$$\text{var}(P_d) = \text{var}(P_s) = \text{var}(P)$$

Then substitute into the regression equation

$$\beta = 2\frac{\text{var}(d) + \text{var}(s)}{\text{var}(P_d) + \text{var}(P_s)} = 2\frac{\text{var}(G)}{\text{var}(P) + \text{var}(P)} = 2\frac{\text{var}(G)}{2\text{var}(P)} = \frac{\text{var}(G)}{\text{var}(P)} = h^2$$
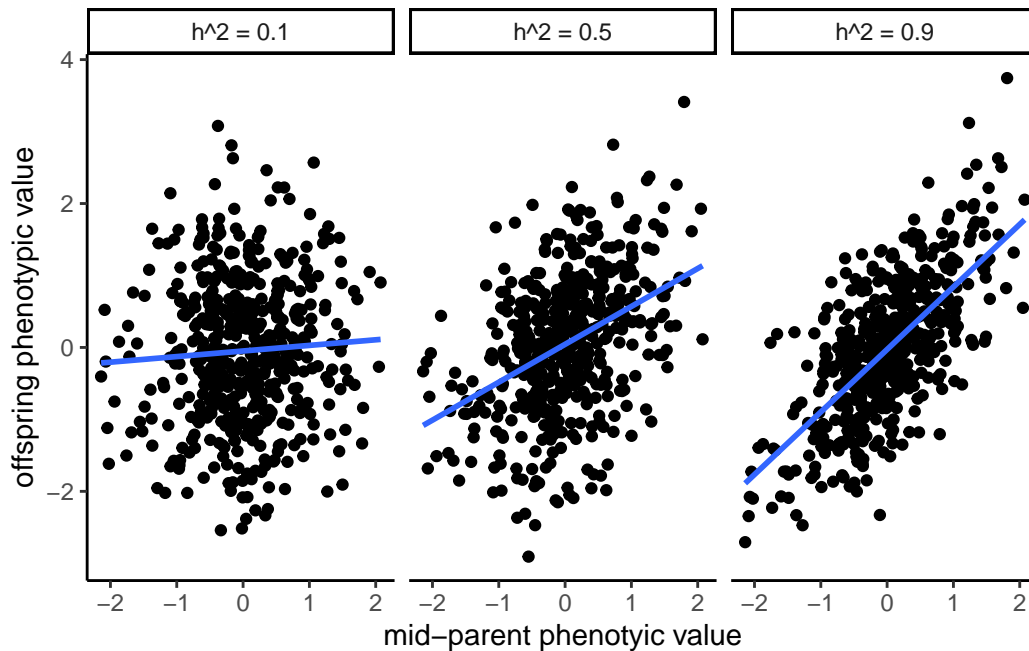
In other words, the beta coefficient from the regression of offspring phenotype on average parent phenotype yields an estimate of the heritability!

Height data

Using the height data, we can calculate the mid-parent–offspring covariance and mid-parent variance and then use that as an estimate for the heritability.

- $\text{cov}(\frac{P_d + P_s}{2}, P_o) = 12.57$
- $\text{var}(\frac{P_d + P_s}{2}) = 22.04$
- $\hat{h}^2 = 12.57 \ / \ 22.04 = 0.57$

Parent and offspring phenotypes become more highly correlated as heritability increases.

Wray, N. & Visscher, P. (2008) Estimating trait heritability. Nature Education 1(1):29

Mini review: What assumptions have we made when estimating h^2?

- Parents' environments are not similar: $\mathrm{cov}(e_d, e_s) = 0$
- No assortative mating: $\mathrm{cov}(d, s) = 0$
- Parents do not transmit their environments: $\mathrm{cov}(e_o, e_d) = 0$, $\mathrm{cov}(e_o, e_s) = 0$
- No gene-environment correlation: $\mathrm{cov}(d, e_d) = 0$, $\mathrm{cov}(s, e_s) = 0$
- No genetic nature: $\mathrm{cov}(d, e_o) = 0$, $\mathrm{cov}(s, e_o) = 0$
- No inbreeding: $\mathrm{cov}(d, d') = 0$, $\mathrm{cov}(s, s') = 0$
- Genetic effects are additive: $Y = a + a' + e$
- Genetic influence is the same for both sexes: $\mathrm{var}(d + d') = var(s + s')$
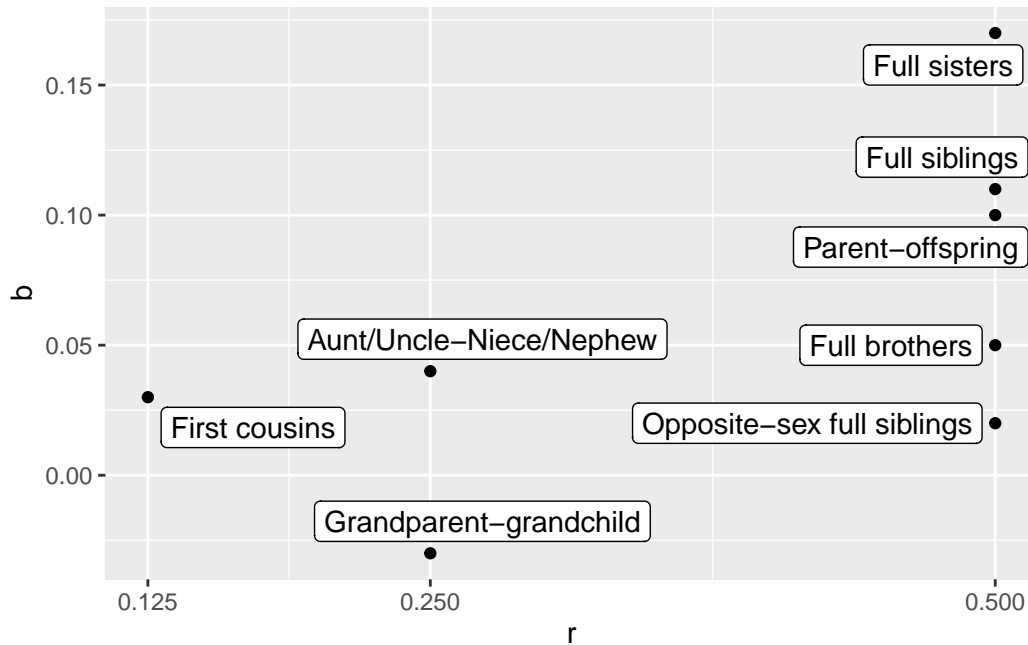
Generalising to other relatives

Heritability can also be estimated from resemblance between different types of related pairs. The general equation is:

$$h^2 = \frac{b}{r}$$

- b = regression coefficient
- r = coefficient of additive variance ("relatedness")

Example data: depression scores

Correlation of depression scores for different pairs of relatives

Fernandez-Pujals AM et al. (2015) Epidemiology and Heritability of Major Depressive Disorder, Stratified by Age of Onset, Sex, and Illness Course in Generation Scotland: Scottish Family Health Study (GS:SFHS). *PLOS ONE* 10(11): e0142197. doi:10.1371/journal.pone.0142197

Recurrance risk to relatives

$$\lambda_{\mathrm{R}} = \frac{P(\text{affected}|\text{relativeaffected})}{P(\text{affectedinpopulation})} = \frac{K_{\mathrm{R}}}{K}$$
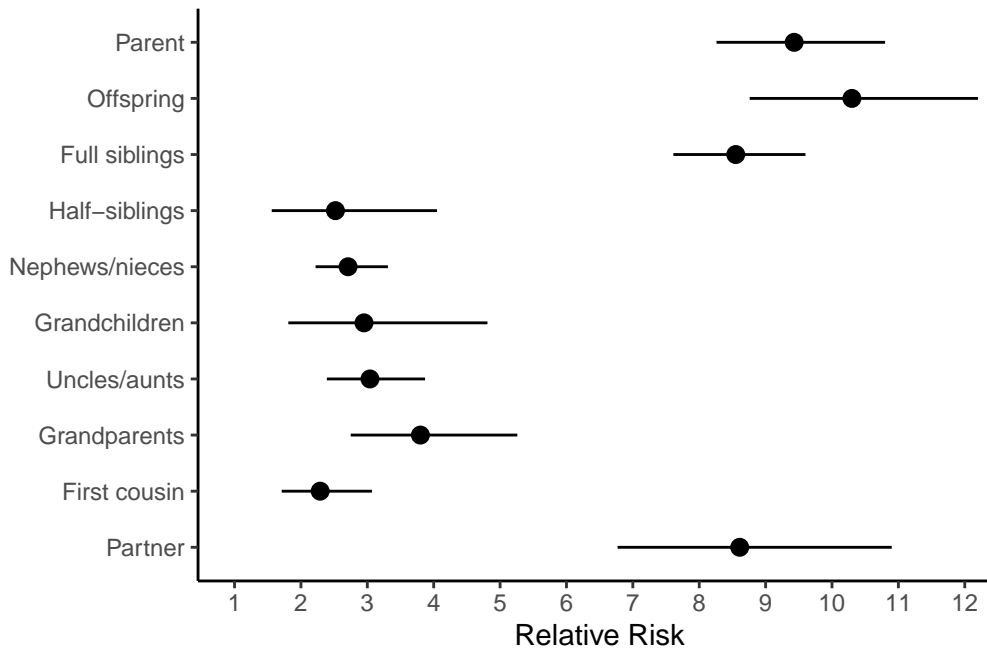
Represents how much more likely to are to be affected by a disorder given that a relative is affected, compared to someone from the general population.

Example:

- $K_{\mathrm{sib}} = P(\text{affected}|\text{siblingaffected}) = 0.09$
- $K = P(\text{affectedinpopulation}) = 0.02$
- $\frac{K_{\mathrm{sib}}}{K} = \frac{0.09}{0.02} = 4.5$

Recurrance risk for schizophrenia

Recurrance risk to relatives for schizophrenia in Sweden, which has a baseline risk of $K = 0.047\%$.

Lichtenstein, P. et al. Recurrence risks for schizophrenia in a Swedish National Cohort. Psychol. Med. 36, 1417–1425 (2006). doi:10.1017/s0033291706008385

Recurrance risk and heritability

- Code $\text{unaffected} = 0, \text{unaffected} = 1$
- If population prevalence is K, then phenotypic variance is $K(1-K)$ (Bernoulli distribution)

- Y = score of individual (proband)
- Y_{R} = score of relative of proband
- Expectation: $E[Y] = E[Y_{\mathrm{R}}] = K$
- $K_{\mathrm{R}} = E[Y_{\mathrm{R}}|Y = 1]$
- Probability that both Y and $Y_{\mathrm{R}} = 1$: $E[YY_{\mathrm{R}}] = K \times K_{\mathrm{R}}$

$$\mathrm{cov}(Y, Y_{\mathrm{R}}) = E[YY_{\mathrm{R}}] - E[Y]E[Y_{\mathrm{R}}] = K \times K_{\mathrm{R}} - K^2$$

- James, J. W. Frequency in relatives for an all-or-none trait. Ann. Hum. Genet. 35, 47–49 (1971). doi:10.1111/j.1469-1809.1956.tb01377.x
- Risch N. Linkage strategies for genetically complex traits. I. Multilocus models. Am J Hum Genet. 1990 Feb;46(2):222-8. PMID: 2301392
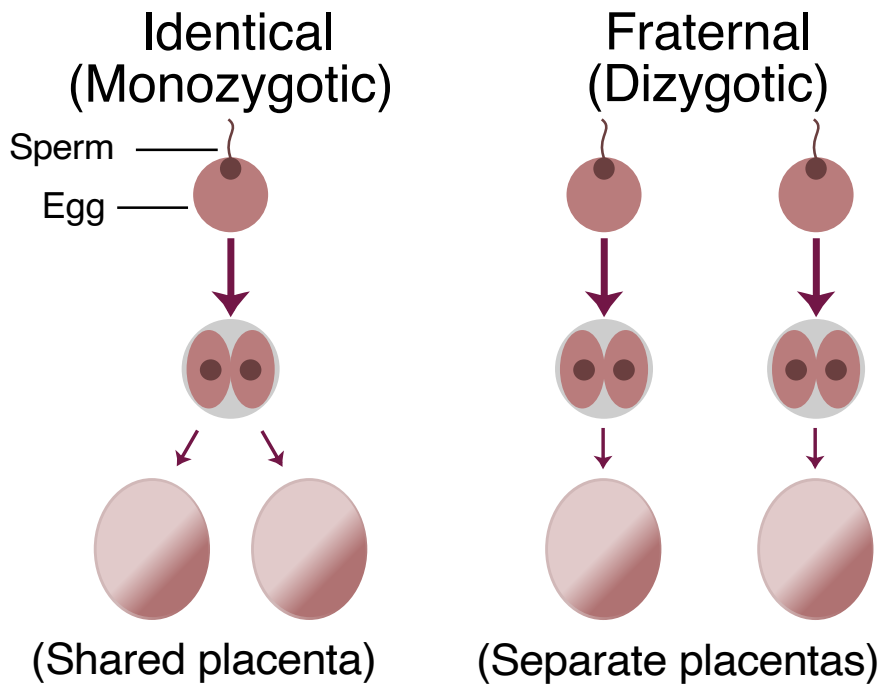
$$= K \times K_{\mathrm{R}} - K^2 = K(K_{\mathrm{R}} - K) = K^2(\frac{K_{\mathrm{R}}}{K} - 1) = K^2(\lambda_{\mathrm{R}} - 1)$$

Heritability estimate

$$h^2 = \frac{\mathrm{cov}_{\mathrm{R}}}{rV_{\mathrm{P}}} = \frac{K^2(\lambda_{\mathrm{R}} - 1)}{rK(1 - K)} = \frac{K(\lambda_{\mathrm{R}} - 1)}{r(1 - K)}$$

Estimating environmental effects

Contrast pairs of relatives that have comparable environmental similarity but different genetic similarity.

Identical (Monozygotic) — Sperm, Egg — (Shared placenta)

Fraternal (Dizygotic) — (Separate placentas)

- Monozygotic (MZ) twins $r = 1.0$
- Dizygotic (DZ) twins $r = 0.5$

Zygote development figure CC-BY-SA Trikly.

Twin correlations

MZ twins: $t(\text{MZ}) = h^2 + c^2$

DZ twins: $t(\text{DZ}) = \frac{1}{2}h^2 + c^2$

Solve for genetic similarity (h^2)

Start with the MZ twin equation:

$$t(\text{MZ}) = h^2 + c^2$$

Take the DZ twin correlation and solve for c^2

$$t(\text{DZ}) = \frac{1}{2}h^2 + c^2 c^2 = t(\text{DZ}) - \frac{1}{2}h^2$$

Substitute c^2 into the MZ equation

$$t(\text{MZ}) = h^2 + c^2\, t(\text{MZ}) = h^2 + [t(\text{DZ}) - \frac{1}{2}h^2]$$
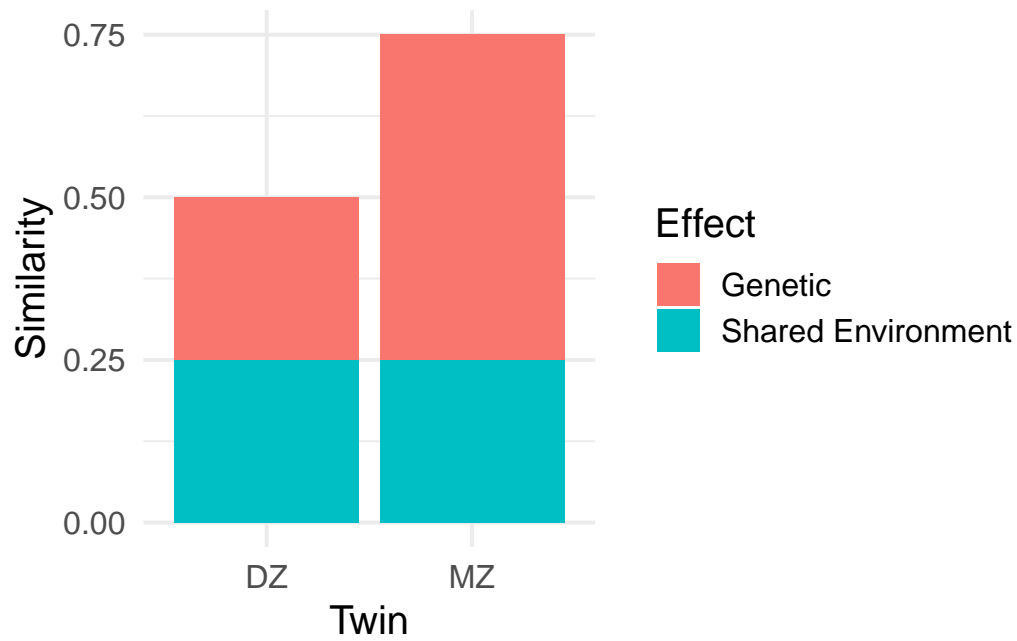
Solve for h^2

$$t(\text{MZ}) = h^2 + t(\text{DZ}) - \frac{1}{2}h^2\, t(\text{MZ}) = t(\text{DZ}) + h^2 - \frac{1}{2}h^2\, t(\text{MZ}) = t(\text{DZ}) + \frac{1}{2}h^2\, \frac{1}{2}h^2 = t(\text{MZ}) - t(\text{DZ})\, h^2 = 2[t(\text{MZ}) - t(\text{DZ}$$

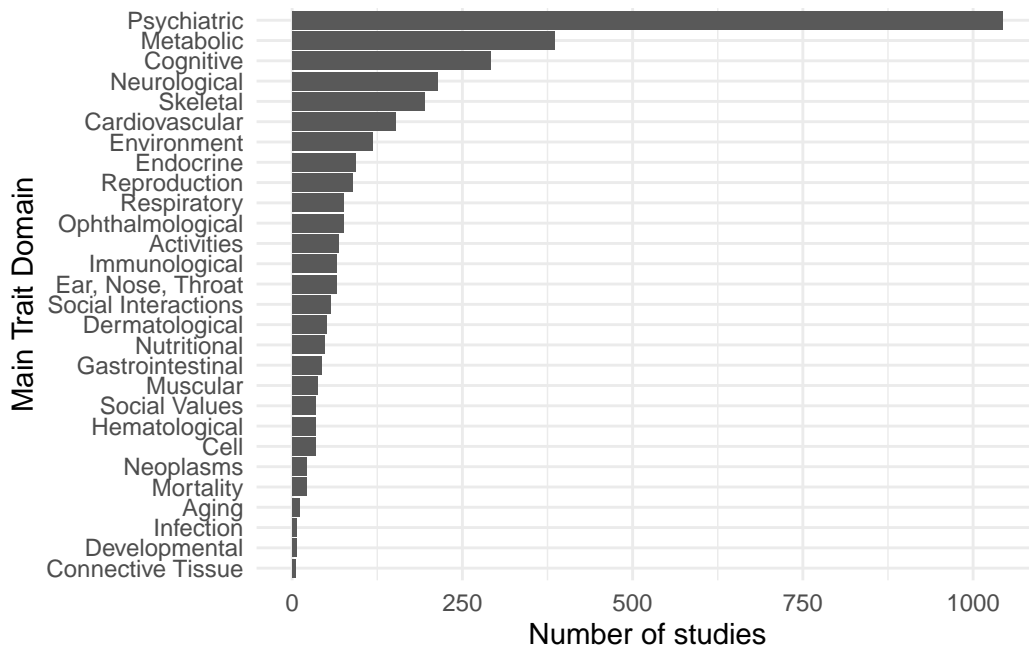Substitute h^2 into MZ equation and solve for shared environment similarity (c^2)

$$t(\text{MZ}) = h^2 + c^2\, t(\text{MZ}) = 2[t(\text{MZ}) - t(\text{DZ})] + c^2\, t(\text{MZ}) - 2[t(\text{MZ}) - t(\text{DZ})] = c^2 c^2 = t(\text{MZ}) - 2t(\text{MZ}) + 2t(\text{DZ})\, c^2 = 2t($$

Therefore from MZ and DZ twin correlations we can estimate:

$$h^2 = 2[t(\text{MZ}) - t(\text{DZ})]\, c^2 = 2t(\text{DZ}) - t(\text{MZ})\, e^2 = 1 - h^2 - c^2$$

What do we know about psychiatric genetics from twins studies

Meta-analysis of twin heritability

match.ctglab.nl