2-11-03

• Review normal distributions
• Review correlation on web site
• Discuss how data from identical and fraternal twins can be used to assess the average influence of genes, shared environment, and non shared environment
Correlation, Genes, and Environment

- Distinguishing between genetic effects in individuals (i.e., Oskar and Jack), and average genetic effects across populations
- The normal distribution of measured traits
- Correlation: [www.seeingstatistics.com](http://www.seeingstatistics.com)
- What identical and fraternal twin correlations can tell us about average genetic, shared environment, and non-shared environment influences.
Why do individual cases or single twin pairs tell us almost nothing about genetic and environmental influences on their behavior?

- Where MZ (monozygotic) twins differ, it must be non shared “environment”
- Where MZ twins the same, genes and/or shared env.
- We can’t separate genetic and environmental influences for individuals, such as family members reared together
- We can only estimate the average proportional influence of genes and environment across the population from looking at many twin pairs (or many adopting families)
The Basis for Correlation

- Measured traits (weight, height, IQ) that have many causal influences follow a normal distribution (bell curve), with most people in the middle, fewer in the tails. Why?
- We can mathematically assess the average similarity for two normally distributed variables within individuals as for height and weight, or for a single variable across pairs of individuals (i.e., twins), where 0 = no correlation, and 1 = a perfect correlation.
Correlations can be...

- Statistically significant but small, with little influence or importance, in large samples (i.e., $r = .10$ with 400 cases is “significant” but very small)
- Large and statistically significant (i.e., $r=.75$ with 20 cases), but still allowing for a minority of large differences in individual cases (see demonstrations in [www.seeingstatistics.com](http://www.seeingstatistics.com) Chapter 12)
How twin correlations allow us to separate average genetic and environmental influences in the population (but not in individuals)

- Identical (MZ) twins reared apart share only their genes, so their correlation directly estimates the average percent of genetic influence (an r of \( .75 = 75\% \))
- Non-shared environmental influences cause the difference between 1 and the MZ correlation (1 - .75 = 25%)
Twin correlations continued…

- For twins reared together, similarity can be caused by shared genes and shared environment.
- But we can separate the influences of genes, shared environment, and non-shared environment by comparing MZ and DZ correlations for twins reared together.
Some extreme examples from twins reared together

- If MZ $r = 1$, DZ $r = .5$, heritability = 1 (DZs share half their genes, so their $r$ must = .5 if heritability = 1)
- If MZ $r = 1$ and DZ $r = 1$, twin similarity must be completely due to shared environment
- Same conclusion for MZ $r = .5$ and DZ $r = .5$, but now there is also evidence for 50% non-shared environment ($1 – MZ r .5 = 50\%$)
- If MZ $r = .5$, DZ $r = .25$, heritability is .5 (twice the MZ-DZ difference), non shared environment is .5 ($1 – MZ r$), and nothing left for shared environment.
A further example, including genetic, shared environment, and non-shared environment

- MZ r = .6, DZ r = .4: heritability is .4 or 40% (twice the MZ-DZ difference), non-shared environment is .4 or 40% (1 - MZ.6), and shared environment accounts for the rest (20%)
Assumptions for twin analyses:

- There are multiple genes with **additive** effects on the trait: there is no **dominance**, or **epistasis** (interaction between genes that would falsely inflate genetic estimates).
- There is no **assortative mating** (this would make DZ twins genetically more similar, and falsely reduce genetic estimates).
- There is equal shared-environment influence for MZ and DZ pairs (violation would falsely increase heritability).