

BIOST 551/STAT 551: Autumn Quarter 2014

Homework 5

Due Thursday, December 4, 2014

Show All Work

1. [50 points] In homework 4, the Pedstats software was used to analyze the data files “BMI_BIOST551.ped” and “BMI_BIOST551.dat” for heritability estimation of BMI in European pedigrees for different classes of relative pairs. You will now estimate heritability of BMI considering all pedigree individuals together in a joint analysis using mixed linear models with the QTDT software. The two data files for the European pedigrees previously used for the homework 4 BMI heritability analysis with Pedstats (available on the course website) are also in the required format for the QTDT software.
 - (a) Provide variance component estimates for BMI using a mixed linear model (MLM) with the following two random effects: additive polygenic and unique (or non-shared) environmental effects. Provide an estimate of the narrow sense heritability of BMI from the variance component estimates from this mixed linear model.
 - (b) Now provide variance components estimates for BMI assuming the following three random effects: additive polygenic, shared household, and unique environmental effects. Provide an estimate for narrow sense heritability of BMI with the variance component estimates from this mixed linear model.
 - (c) Is the shared household effect for BMI significant for the mixed linear model in 1(b) above? Provide evidence to support your answer.
 - (d) Now compare your BMI heritability estimates from the mixed linear models with variance components in 1(a) and 1(b) above to the BMI estimates obtained in homework 4 based on different relative pair types. Discuss and provide plausible explanations for any differences and/or similarities that you find in the heritability estimates.
2. [50 points] A quantitative trait Y is influenced by a single autosomal locus, family effects, and unique environmental effects in a population. The autosomal locus that influences the trait is bi-allelic with alleles A and a , and the frequency of allele A is 0.15. Assume that the population is in Hardy-Weinberg equilibrium (HWE) at the locus. For an individual j from family i in the population, the trait has the following model:

$$Y_{ij} = 1.5 + 0.4G_{ij} + c_i + \epsilon_{ij}$$

where G_{ij} is the number of copies of the A allele that individual j from family i has, c_i is the family effect on the trait for family i , and ϵ_{ij} is the unique environmental effect for individual j in family i . Assume that G_{ij} , c_i , and ϵ_{ij} are independent with $c_i \sim N(0, \sigma_c^2 = 0.02)$ (i.e., c_i has a normal distribution with mean 0 and variance $\sigma_c^2 = 0.02$), and $\epsilon \sim N(0, \sigma_e^2 = 0.09)$

- (a) Calculate the expected value and variance of the phenotype Y in the population.
- (b) What is the broad sense heritability (H^2) of the phenotype in the population? What is the narrow sense heritability (h^2) of this phenotype in the population?
- (c) Consider two individuals j and k from family i . Calculate $Cov(Y_{ij}, Y_{ik})$ (i.e., the covariance of Y_{ij} and Y_{ik}) for the following relationship types for j and k :
- j and k are mono-zygotic (MZ) twins reared in the same household.
 - j and k are full-siblings reared in the same household.
 - j and k are half-siblings reared in the same household.
 - j and k are half-siblings reared in different households.
 - j and k are first-cousins reared in different households.
 - j and k are unrelated but reared in the same household (e.g., one of the individuals is adopted).
- (d) Now consider two individuals j and k who are from two different (unrelated) families i and l , respectively, where individual j is from family i and individual k is from family l . Calculate $Cov(Y_{ij}, Y_{lk})$.