

QUANTITATIVE GENETICS PROBLEMS- EVOLUTIONARY BIOLOGY FALL 2016
(20 points total)(due November 4th 2016)

1) Suppose that in a population of Peacocks the phenotypic variance for tail length is 2.5 and the slope of the father – offspring regression for this trait is 0.2. From a long-term captive population you also have data from a line of completely inbred individuals. In this line the phenotypic variance among individuals is 0.50. Assume that there are no shared environmental effects (V_{es}) and no epistatic variance (V_i) for this trait. (Note that these questions are not given in the order that you need to solve them)(6 points)

- What is the total genetic variance for tail length?
- What is the additive genetic variance?
- What is the dominance genetic variance?
- What is the environmental variance?
- What is the narrow-sense heritability (h^2)?
- What is the expected phenotypic covariance among full-sibs?

2) While Peacocks are great animals, they are large, noisy and difficult to work with. So, you switch to studying Barn Swallows. Suppose that you have estimates of tail length (**T in cm**) in Barn Swallows from a set of ten pairs of **paternal half-sibs** (denoted by the subscripts **x** and **y**) that share the same father, but have different mothers. For the first sib (denoted by **x** below), the number of offspring they produce over their lifetime (R_x) is known as well. The number of offspring produced (R_x) is a measure of absolute fitness. For each sib, first calculate the relative fitness value (W_x). To estimate relative fitness, divide each R_x value by the mean absolute fitness value. (6 points)

Sibship	T_x	T_y	R_x
1	17.00	18.00	23.00
2	16.00	25.00	29.00
3	23.00	15.00	43.00
4	13.00	13.00	19.00
5	15.00	16.00	29.00
6	11.00	19.00	37.00
7	24.00	23.00	31.00
8	19.00	12.00	49.00
9	17.00	18.00	35.00
10	21.00	15.00	53.00

Then using these data:

- Compute the phenotypic mean and variance of tail length (use all the available data, i.e., both of the half-sibs).
- Compute the phenotypic covariance between paternal half-sibs, and estimate the heritability of tail length (remember that the denominator in a covariance equation is the number of pairs of observations).
- Assuming that progeny production is the only way in which these individuals differ in fitness, use Price's Rule to estimate the directional selection differential on tail length.
- What is the variance in relative fitness?
- Will relative fitness increase or decrease in the next generation? By how much?

3) A striking feature of phenotypic change in the human lineage is a dramatic increase in brain size. This trait has increased from an average of approximately 500 cm^3 to 1200 cm^3 over the past 3 million years. Assume humans have an average generation time of 20 years and that the slope of a single parent-offspring regression for brain size is 0.20. (3 points)

- If this evolutionary change is a consequence of natural selection (and only natural selection) operating directly on brain size, what average **directional selection differential** per generation (**S**) is necessary to account for the observed change?
- If directional selection of this magnitude were to continue, what is the expected response to selection one generation from now?
- How many additional years would be required for the average brain size of humans to reach 1500 cm^3 ? (Assume the heritability remains constant).

4) On a recent trip to the Galapagos Islands some of your classmates were able to collect data on Darwin's finches. They measured data on beak size in a set of related individuals. Consider the following data on beak size. These quantitative trait values (in mm) are given for the mother, father and one of their offspring. (5 points)

Mother	Father	Offspring
8	11	10
7	13	11
14	9	10
9	11	10
11	10	13
14	15	14
8	12	11
9	10	8
11	6	10
13	7	12
8	9	11

- Calculate the **midparent** values for each parent pair and use a midparent-offspring regression approach to calculate the **heritability (h^2)** of this trait. There is more than one way to do this, but it will be easiest if you use Microsoft Excel. You can use the **VARP** function to calculate the necessary variances and the **COVAR** function to calculate the covariance. Remember that the slope of the regression line is the $\text{Cov}(x,y)/\text{Var}(x)$. You can also calculate these value by hand given the formulas from lecture.
- Now calculate the heritability (h^2) for the trait using a **mother-offspring regression** and a **father-offspring regression**. Are they the same?
- Maternal effects are nongenetic effects of the mother on the phenotype of the offspring, caused by things like the brooding environment, cytoplasmic factors and nutritional state of the mother. Do you see any evidence for maternal effects with respect to this trait? Explain your reasoning.
- If the only individuals that could get sufficient resources to breed successfully are the five males and five females with the largest beak sizes what is the selection differential (**S**) on beak size? Assume the mean of the sample of the parents above represents the mean of the whole population of finches.
- How much of an increase in beak size would expect to see in the next generation?