Comprehensive Exam 2018
Biomath 202: Structure, Function, and Evolution of Biological Systems

Consider a mutation that makes a vascular network terminate three levels earlier than a normal wild-type network for an individual of that species.

a. By what fraction is the number of terminal units reduced? By what fraction would the mass of an organism be reduced if you apply standard biological scaling—metabolic rate $\propto$ (body mass)$^{3/4}$?

b. If we want to analyze how selection and drift will direct the establishment or elimination of this mutation, what stochastic differential equation from population genetics should we use? Write down the exact equation and identify the term representing selection and the term representing drift and explain why they have the form they do.

c. Derive the equilibrium probability distribution, $P(p)$, as a function of allele frequency, p, for the equation in part b. and apply appropriate boundary conditions to find forms for integration constants.

d. Let the percent reduction in body mass you found in part a. serve as an estimate for the percent reduction in fitness and thus be the value for the selection coefficient. Substitute this value for the selection coefficient into your solution for part c. If the mutation is introduced with an initial frequency of $p = 0.05$, estimate how big a population needs to be before selection will dominate and eliminate the mutations. Show how your solutions leads to $P(p)\rightarrow 0$ for this case.

e. What if a scientist intervenes in the laboratory and artificially selects for this mutation with a selection coefficient of $s = 0.33 = 1/3$, but the mutation is still introduced at $p = 1/20$. Estimate the population size at which selection dominates and the mutation will go to fixation. Show that $P(p)\rightarrow 1$ for this case.

f. Based on a knowledge of selection and drift along with your answers to d. and e., if the scientist wants to use smaller populations in the laboratory to achieve fixation of the mutation, should they increase or decrease the selection coefficient?

g. Now consider another type of mutation that creates cross-linking between vessels within the same hierarchical branching level and thus results in loop-like structures instead of just tree-like structures. If an individual has this mutation, these cross-linkings and loops occur in about 10% of vessels. Draw

examples of the kinds of network motifs (e.g., squares) that you would expect to observe in this network.

h. Choose the three simplest types of motifs from part g. and calculate how many of each type of motif you would expect to see in a random Erdös-Renyi graph corresponding to a vascular network with 31 bifurcating branching levels before loops are added. Can you estimate how many of the motifs would occur if you know cross-linkings occur with a frequency of 10% as in part g.? How does these estimates for motif numbers compare with the Erdös-Renyi predictions? Which motifs will be identified as nonrandom? What about in comparison to the estimates for motif numbers based on the geometric network predictions as in the paper by Itzkovitz et al. that was covered in class?