

Question 1.

- a) Explain the basic mechanisms of genetic evolution
- b) Consider a diploid population and a gene with two alleles (A,a), with allele frequencies $p = \text{Freq}(A) = 0.4$ and $q = \text{Freq}(a) = 0.6$. Assume Hardy-Weinberg equilibrium with respect to other factors, but the relative fitness of the genotypes are $W_{AA} = 1$, $W_{Aa} = 0.3$ and $W_{aa} = 0.1$. Calculate the genotype and allele frequencies for the next two generations.

Question 2.

- a) Explain briefly the main characteristics and differences of linkage analysis and association analysis in gene mapping
- b) Give detailed description of **either** of the following tests
 - TDT-test (Transmission-Disequilibrium Test)
 - ASP-test (Affected sib pair)

Question 3.

- a) Explain the principle of Bayesian networks very briefly
- b) Sketch the Bayesian network that describes the joint distribution $P(A,B,C,D,E)$ of variables A,B,C,D,E, when we know that $P(A,B,C,D,E) = P(A) P(B) P(C|A,B) P(D|B) P(E|C,D)$
- c) Assume the variables A,B,C,D,E have only values TRUE/FALSE and the conditional probabilities are modeled by multinomial distribution. Add parameter tables to the Bayesian network, that contain all the parameters required to evaluate the joint probability of the variables A,B,C,D,E. Compare the size of the tables to tabulating the probabilities of the joint distribution $P(A,B,C,D,E)$ directly.

Question 4.

- a) Explain what is Bonferroni-correction and derive the correction for N tests with the probability of false positive of p in one test.
- b) Draw the 50% majority tree for the following cladograms

