

Quiz 1

You may use any books, notes, or references, but you must work independently of other people.

To keep the amount of writing under control, please confine the answers to the space provided (but write clearly and large enough to see!); outlines are fine.

1. (10 points) What are the major ontological and methodological issues regarding sequence alignment? Compare how manual alignment, automated multiple alignment and direct optimization deal with these.

2. (10 points) Discuss possible uses and benefits of DNA barcoding methodology and some of the major drawbacks. How do you think a broad application of this methodology will impact scientific research in systematics, biodiversity, and conservation?

3. (10 points) What are the arguments pro and con for rank-free phylogenetic classification versus the current Linnaean system?

4. (20 points) What are the general attributes of a "good" taxonomic character? Give: (a) a list with a one sentence explanation; b) An indication of any particular problems faced by morphological and DNA-sequence data for each.

5. (10 points) How is ontogeny important to phylogenetic inference? When and how would you use it?

6. (40 points) Briefly contrast the following pairs of terms (Use diagrams if they help)

transformational vs. taxic homology

ontogeny of vertebrates vs. ontogeny of mosses

semaphoront vs. OTU

apomorphy vs. symplesiomorphy

holotype vs. paratype

Manhattan vs. Euclidian distance

rooted vs. unrooted phylogenetic trees

ordering vs. polarity of character states

exhaustive vs. heuristic searches

local optimum vs. global optimum (as they apply to tree searches)