

Name \_\_\_\_\_

*Integrative Biology 200A*

Spring 2008

"PRINCIPLES OF PHYLOGENETICS: SYSTEMATICS"

**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 and pictures are fine. Word-processed answers are OK, as long as they are the equivalent length. **The Quiz is due at 3:30 sharp**, either in room 3083 VLSB, or by email to: BMishler@berkeley.edu. Relative point value is given -- 85 points total.

1. (10 points) Morphological and molecular characters are often treated as being akin to ‘apples and oranges’ and have generated debates over whether they should be treated separately or in combined analyses. However, molecular characters also have morphology – e.g. secondary structure in proteins or synteny in genomes. Give an argument either for or against the use of molecular structural characters in phylogenetic analysis. How should they be used/combined with other data sources?

2. (10 points) Discuss and contrast the role that the established nomenclatural codes (ICZN & ICBN) and Phylocode have, or would have, in establishing and validating taxonomic names. What do you think the implications (in terms of basic science and practical application) of using one or the other would be for conservation of endangered evolutionary and biologically significant units?

3. (10 points) “DNA Barcoding” has been proposed as a means to address the biodiversity crisis and remove the taxonomic impediment. By a series of chance events you are now in control of the barcoding project, its infrastructure, manpower and \$30 million. How would you proceed to use these to address biodiversity and taxonomic problems? Specifically, what would you keep or continue to do and what would you change or eliminate?

4. (10 points) We have discussed 3 views regarding the incorporation of fossil stratigraphy into phylogenetic analysis - a strict cladistic approach, a limited use of stratigraphic data, and the full incorporation. Chose one and discuss the pros and cons of its implementation for phylogenetic analyses.

5. (10 points) Imagine that you submitted sequences to ClustalW and got back the following alignment. If you would make changes to the alignment, describe them. Explain why you would or would not make changes to the alignment, what effects on phylogenetic analysis your choice would have, and any parameters you would change if you were to submit the sequences to to ClustalW again.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<i>Bandersnatch</i>	A	C	G	-	A	A	T	A	C	-	A	A	T	A
<i>Borogove</i>	A	C	C	A	-	A	C	A	T	G	-	-	T	A
<i>Jabberwocky</i>	A	C	C	A	-	A	C	G	C	G	-	-	T	A
<i>Jubjub</i>	G	C	C	A	-	A	C	A	C	G	-	-	T	G
<i>Rath</i>	A	C	C	-	C	A	T	A	C	G	-	C	T	A
<i>Snark</i>	A	C	G	-	A	A	T	A	C	-	A	A	T	A
<i>Tove</i>	A	C	C	C	-	A	T	A	C	G	-	-	T	A
<i>Tumtum</i>	A	C	G	-	A	A	T	A	C	-	A	A	T	A

6. (35 points: 5 points each) Briefly contrast the following pairs of terms (Use diagrams if they help)

character-state polarity vs. character-state ordering

progressive alignment vs. direct optimization

ontology vs. epistemology

orthology vs. paralogy

Manhattan vs. Euclidian distance

Biological species concept vs. phylogenetic species concept

heuristic search vs. an exact (or exhaustive) tree search