

**BINDURA UNIVERSITY OF SCIENCE EDUCATION
BIOLOGICAL SCIENCES DEPARTMENT
MOLECULAR SYSTEMATICS (BZH401/BTEC BTEC419)**

EXAMINATION

2 HOURS (100 MARKS)

INSTRUCTIONS

Answer **FOUR** questions. You **MUST** answer **QUESTION 1** (Section A) and any **THREE** questions from Section B. Each question carries **25 MARKS**. Where a question contains subdivisions, the mark value of each subdivision is given in brackets. Illustrate your answers where appropriate with large, clearly labelled diagrams. You should not spend more than thirty minutes on each question.

SECTION A (COMPULSORY)

1. Given the following basic data matrix of ten taxa (T1-T10, a monophyletic group), plus an outgroup representing related taxa, and eighteen characters.

		Characters																	
		1 1 1 1 1 1 1 1 1 1																	
		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8
Outgroup		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
T1		1	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
T2		1	1	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
T3		1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
T4		1	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
T5		1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0
T6		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
T7		0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0
T8		0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	1	0	0
T9		0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	1	0
T10		0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	1

- (a) Draw the most parsimonious tree showing shared ancestry among the taxa T1-T10 and indicate where each character changes on the tree. (Clearly show all your calculations). (20 marks).
- (b) Identify the characters in the matrix above which are considered informative and which are considered non informative according to parsimony. (5 marks).

SECTION B

2. (a) How is bootstrap analysis performed? (7 marks)
- (b) How should the bootstrap values be interpreted, i.e., what do they mean and what useful information the analysis provide? (8 marks)
- (c) Explain the alternative(s) to bootstrapping. (5 marks)

3. (a) Describe each of maximum parsimony and maximum likelihood methods of phylogenetic construction as applied to DNA data. Be sure to identify the critical differences between these criteria. (15 marks)
- (b) Discuss the distance based methods of phylogenetic analysis of molecular data. (10 marks).
4. Describe any five molecular markers used in molecular taxonomy. (15 marks)
- (b) Discuss the advantages and disadvantages of Isozyme (or allozyme) analysis method. (10 marks).
5. (a) Discuss multiple sequence alignment methods and how they are important for modern phylogenetics. (10 marks).
- (b) Outline Steps for preparing the Phylogenetic Tree. (15 marks).
6. (a) Describe the features of a phylogenetic tree. (15 marks).
- (b) Outline Importance of Phylogenetic Tree. (10 marks).

END OF EXAMINATION QUESTION PAPER