

NAME.....

ROLL NO.....

JAWAHARLAL NEHRU TECHNOLOGICAL UNIVERSITY-2008

**III B.TECH SUPPLEMENTARY EXAMINATIONS
BIO INFORMATICS
(BIO-TECHNOLOGY)**

AUG/SEP -2008

TIME-3 HOUR
MARK-80

ANSWER ANY FIVE QUESTIONS. ALL QUESTIONS CARRY EQUAL MARKS.

1. Write short notes on:
 - (a) Shannons formula
 - (b) Channel capacity
2. Explain in detail about Dynamic: Programming method for sequence alignment?
3. What is a multiple alignment and why we do it?
4. Define Secondary databases? Give an overview of secondary databases?
5. What is Block Substitution Matrices (BLOSUM)? Describe them in detail?
6. Describe the following:
 - (a) Perfect phylogeny
 - (b) The relationship of Phylogenetic analysis and sequence alignment.
7. Describe the steps involved in sequence assembly?
8. Write short notes on:
 - (a) GRAIL II
 - (b) ORF