

FEDERAL UNIVERSITY OF TECHNOLOGY, OWERRI
SCHOOL OF HEALTH TECHNOLOGY
DEPARTMENT OF BIOMEDICAL TECHNOLOGY
2010/2011 HARMATTAN SEMESTER EXAMINATION
COURSE: BIOMEDICAL INFORMATICS COURSE CODE: BMT 561

Instruction: Answer any four questions

Time: 2hours; Unit: 2

- 1(a) What do you understand by the term biomedical informatics?
(b) What are the roles of biomedical informaticians in the health care delivery system?
(c) State eight areas with related examples where biomedical informatics can be employed in the health care delivery.
- (Total: 20marks)
- 2(a) Explain two approximation algorithms commonly used by biomedical informaticians.
(b) What are the uses of approximation algorithms in biomedical disciplines?
(c) What are the tools employed in the field of biomedical informatics?
(d) Briefly explain four random walk MCMC (Markov Chain Monte Carlo) methods in the approximation algorithms.
- (Total: 20marks)
- 3(a) Discuss two methods employed by biomedical informaticians for modeling biological system.
(b) Discuss any three software algorithms used in the structure classification.
(c) State four criteria used in the class level classification of CATH.
(d) What do you understand by the term homologous in the sequence alignment?
- (Total: 20marks)
- 4(a) State the importance of decodes sequence information on database.
(b) What do you understand by the term sequence alignment?
(c) What is the difference in the nucleotide base of RNA and DNA?
(d) Briefly discuss the two types of computational methods in sequence alignment.
- (Total: 20marks)
- 5(a) What are the differences between pairwise alignment and multiple alignments?
(b) Explain phylogenetic analysis.
(c) Explain three methods of sequence alignment.
- (Total: 20marks)
- 6(a) Briefly explain three techniques of pairwise alignments.
(b) Briefly explain four techniques of multiple alignments.
(c) Explain Structural alignments.
- (Total: 20marks)