Ex/M.Sc/M/B1.7/37/2017

# MASTER OF SCIENCE EXAMINATION, 2017

## (2nd Year, 1st Semester)

## MATHEMATICS

## Unit - 3.5 (B1.7)

## (Computational Biology - I)

Full Marks : 50 Time : Two Hours

*The figures in the margin indicate full marks.*

Answer question number 1 and any *two* from the rest.

1. (a) What is sequence alignment and how is genetic sequence related to Evolution ?

(b) What are "Longest Common Substring" and "Longest Common Subsequence" ?

(c) Describe an appropriate scoring scheme for optical alignment with justification.

(d) Explain how "Needleman-Wunsch" algorithm describes the matrix $F$ and its construction. 2+2+4+6

[*Turn over*]

2. (a) With suitable assumptions through schematic diagram formulate a mathematical model of pathogenic bacteria using antibiotic.

   (b) Give the stochastic approach and find the expected time to extinction of your formulated model.

   (c) Describe the results based on the computational approach with the help of numerical graphs. 6+8+4

3. (a) Formulate a mathematical model of HIV disease progression with basic assumptions, considering the effect of Interleukin-2 (IL-2) and Reverse Transcriptase Inhibitors (RTI) treatment.

   (b) Explain the formulated model with perfect drug adherence in explicit form.

   (c) How Reverse Transcriptase Inhibitors (RTI) and Interleukin-2 (IL-2) therapy will help to reduce the HIV infection based on your computational technique. 5+7+6

4. (a) With suitable assumptions, formulate a mathematical model for the control of the mosaic virus disease in Jatropha Curcas plantation.

(b) Find out the different equilibria and discuss the stability based on your formulated mathematical model.

(c) Describe how different bifurcation parameter affects the population variation with time and discuss the results based on computational study. 5+6+7