Uva Wellassa University, Sri Lanka

1st Semester Examination March 2011

SCT 411-1 Bioinformatics

Time: One (01) hour

Answer all questions
Each of the questions carries equal marks

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1. Briefly discuss **three (03)** of the following giving examples wherever possible
   - i. Sequence-structure deficit
   - ii. Primer design using bioinformatics tools
   - iii. Gap penalty
   - iv. DNA sequence (25 marks)

2. 'Prediction of three dimensional structure of protein is a difficult task'.
   - i. Explain why prediction of protein folding is difficult
   - ii. Name two protein folding methods currently employed
   - iii. Briefly outline the basis of one of the methods you stated in above (ii.)

   (25 marks)

3.
   - i. What is meant by homologous proteins?
   - ii. Name a tool that can be used in phylogeentic analysis.
   - iii. If the sequences of a homologous protein are given, explain how you would determine the phylogenetic relationships between species.

   (25 marks)

4.
   - i. Name **two** applications of bioinformatics in the field of medicine.
   - ii. Describe briefly the approach in **one** of the applications you mentioned in above (i).

   (25 marks)