JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-3 EXAMINATION – MAY 2019

B.Tech VIth Semester (Bioinformatics)
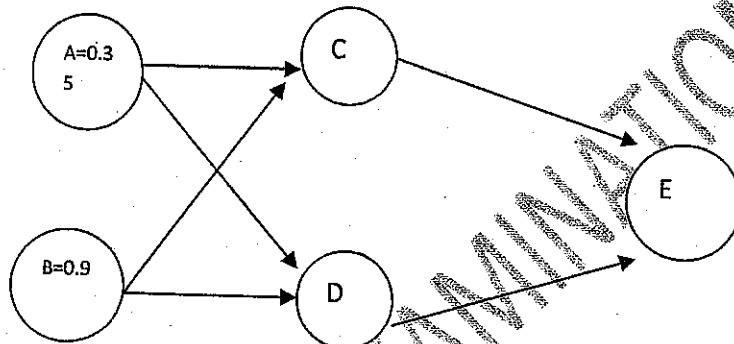
COURSE CODE: 10B11BI612

MAX. MARKS: 35

COURSE NAME: Machine Learning for Bioinformatics

COURSE CREDITS: 4

MAX. TIME: 2HRS

Note: All questions are compulsory. Carrying mobile phone during examinations will be treated as a case of unfair means.

1. (a) Perform one forward pass on the given neural network. $w_{AC} = 0.1$, $w_{AD} = 0.4$, $w_{BC} = 0.8$, $w_{BD} = 0.4$. $w_{CE} = 0.3$, $w_{DE} = 0.9$. (3)

(b) Perform a reverse pass on the network (target =0.5). (5)

(c) Perform a further reverse pass on this network. Comment on the results. (2)

2. Explain and illustrate the following concepts with respect to HMM and transformational grammars. (10)

   (a) Finite state automaton with example

   (b) Deterministic and non-deterministic automaton

   (c) Decoding and evaluation

   (d) Forward variable

   (e) Regular grammar

3. Real DNA sequences are inhomogeneous and can be described by a HMM with hidden states representing different types of nucleotide composition. Consider and HMM that includes two hidden states H and L for higher and lower C+G content respectively. Initial probabilities for both H and L are equal to 0.5., while transition probabilities are as follows: a_{HH}=0.5, a_{HL}=0.5, a_{LL}=0.6, a_{LH}=0.4. Nucleotides T, C, A and G are emitted from states H and L with probabilities 0.2, 0.3, 0.3 and 0.3, and 0.3, 0.2, 0.3, 0.2, respectively. For the sequence x= GGCAC, predict the most likely state at position 3 using posterior decoding. (10)

4. Describe how will you use HMM to identify CpG islands from the given set of sequences. (5)