JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST-1, EXAMINATION – 2016
B. TECH. BIOINFORMATICS (VI SEM)

COURSE CODE: 10B11BI612 MAX. MARKS: 15
COURSE NAME: MACHINE LEARNING FOR BIOINFORMATICS
COURSE CREDITS: 4 MAX TIME: 1 HR

Q1. Each question carries 1 mark. **(1x5=5)**

i. How does an expert system work and discuss the advantages of machine learning approach over expert system?

ii. How do you determine a machine learning system is robust?

iii. Suppose in a hidden Markov model (HMM), the sequence length is 10 and the states are C, M & E as provided in HMM model (Supplementary data). For calculation of best path, how many paths do you need to explore if you have to follow exhaustive method?

iv. What is posterior decoding which uses forward and backward algorithms to determine probability of a state emitting particular symbol w.r.t. a given sequence?

v. Draw equivalence between dynamic programming and Viterbi algorithm by taking suitable example?

Q2. Transition and emission probabilities of an initial HMM model will be provided (Supplementary data). Two sequences are given as "H L H" and "L H L" where H is hydrophilic and L is lipophilic amino acids. Implement the Baum-Welch iteration for 1 step to determine new transition and emission probabilities and also provide new HMM model. How the learning is done in HMM? (9+1)

10 Marks