

INDIAN INSTITUTE OF INFORMATION TECHNOLOGY, ALLAHABAD

C1 Review test: 23rd February 2022

**Program Code & Semester: B.Tech. IT-VI Sem.
Paper Title: Eng. Biology, Paper Setter: Dr. Sintu Kumar Samanta**

Max Marks: 30

Duration: 50 min

Answer all the questions. Each question carries 2 marks

(1) Why genetic codon is considered as redundant but non-ambiguous? **(2)** How does 5' UTR and 3' UTR region of a gene help in its expression (protein synthesis)? **(3)** A diluted (5 times) sample was loaded in the Hemocytometer and cells were counted. If the total number of cells was found to be 500 in the 5 squares of the Hemocytometer, calculate the number of cells/ml in the original sample. **(4)** Consider that length of the coding region of a gene is 1500 base pairs. Calculate the number of codons in the corresponding mRNA molecule and molecular weight of the corresponding protein molecule (average molecular weight of an amino acid is 110 Da). **(5)** How active transport of molecules is differed from passive transport? **(6)** What is the logic behind the serial dilution method to isolate a pure culture? **(7)** What is the difference between batch culture and continuous culture? **(8)** Why the DNA synthesis in lagging strand of DNA double helix is not continuous? **(9)** Why the polarity of a DNA molecule is conventionally denoted by 5' to 3' ? **(10)** Why sterilization of media is necessary? **(11)** What functional groups attach to the 1st, 3rd and 5th carbon of the sugar in a nucleotide? **(12)** How does 'Phagocytosis' help in immuno-protection of human body? **(13)** The nucleotide sequence of the sense strand of a DNA molecule is 5' ATGCATACTTAA 3'. Write the nucleotide sequence of the corresponding antisense strand and the encoded mRNA molecule. **(14)** How tRNA and mRNA are involved in protein synthesis in cells? **(15)** A liquid sample was serially diluted with sterile water. 200 µl of sample from the 10⁻⁶ dilution was plated. It gave rise to 65 colonies on an agar plate. Determine the number of cells in the original sample in 'number of cells/liter'.