## JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST -1 EXAMINATION- 2023

## M.Tech-1 Semester (BT)

COURSE CODE(CREDITS): 13M11BT112 (3)	MAX. MARKS: 15
COURSE NAME: Advanced Bioinformatics	
COURSE INSTRUCTORS: Dr. Raj Kumar	MAX. TIME: 1 Hour
Note: (a) All questions are compulsory.	
(b) Marks are indicated against each question in square brackets.	
(c) The candidate is allowed to make Suitable numeric assumptions wi	herever required for
solving problems	
Q1. Provide a concise elucidation of how the central dogma of mole the primary reservoir of data in the field of bioinformatics.  Q2. Write a small description of the following R-functions with an example of the following R-functions with a following R-function with a f	[2]
a) rep() b) dim() c) length()	. ,
<ul> <li>Q3. Write a R-program to:</li> <li>a) Create a vector of a specified type and length. Create vector of and character types of length 4.</li> <li>b) Add two vectors of integers type and length 3.</li> <li>c) Sort a Vector in ascending and descending order.</li> </ul>	[2 × 3] numeric, complex, logical
Q4. Write the output of the given R-code:	[2]
sequence <-matrix(c("apple", "banana", "cherry", "orange", "grape", "pineapp print(sequence) sequence [c(1,2),]	le"), nrow = 3, ncol = 2)
Q5. Give the general expression to create an array in R-programmming	g. [2]