

Avinashilingam Institute for Home Science and Higher Education for Women,  
(Deemed to be University) Coimbatore- 641 043

Master's Degree Examination-November,2018  
Semester - III

Class : II PG  
Major: Bioinformatics

Time: 3 Hrs  
Max. Marks: 60

17MBIC17 NEXT GENERATION SEQUENCING AND DATA ANALYSIS

PART A

Choose the correct answer

10x1/2=5

- Big data platform generally consists of
  - Big data storage
  - servers
  - database
  - a and b
- Probability distribution of all possible values the statistic may assume
  - sampling distribution
  - distribution
  - probability
  - Poisson distribution
- Expand NGS
  - Next Generation Source
  - Next Structure Generation
  - Next Generation Sequencing
  - Next Genomic Structure
- Expand SAM and BAM
  - Sequence Alignment Map and Binary Alignment Map
  - Sequence Adjacent Map and Binary Adjacent Map
  - Sequence Alignment Mode and Binary Alignment Mode
  - Sequence Adjacent Mode and Binary Adjacent Mode
- Phred Quality Score of 30 indicates base call accuracy of
  - 99.9 %
  - 99.99%
  - 99%
  - 90%
- You can check to see whether an R object is NULL with the \_\_\_\_\_ function.
  - is.null()
  - is.nullobj()
  - null()
  - all of the above
- Point out the correct statement
  - In R, a function is an object which has the mode function
  - R interpreter is able to pass control to the function, along with arguments that may be necessary for the function to accomplish the actions that are desired
  - Functions are also often written when code must be shared with others or the public
  - All of the above
- Which of these projects would be best suited for NGS?
  - To determine if a tumor sample contains a common missense mutation
  - To find the transcriptome of a tumor sample
  - To genotype ten genomic DNA samples for a known single nucleotide polymorphism
  - All of the above.
- Once the sequences are obtained from your NGS experiment what is the first thing you should do?
  - Perform a bioinformatics analysis of your data
  - Check your data using a different method
  - Publish your results
  - Further investigate the sequences of interest
- \_\_\_\_\_ is the synthesis of unnatural DNA segments encoding protein or RNA molecules that control each other's levels
  - Genetic circuits engineering
  - Genetic engineering
  - Gene chip
  - Molecular Biology

**PART-B****Answer the following****Answer should not exceed 200 words or one page**

11 a. Write short notes on statistical inference.

Or

b. Give a detailed account on challenges of conventional system of data analysis.

12 a. Discuss in detail about transcriptome sequencing.

Or

b. Write short notes on pyrosequencing.

13 a. Give an account on quality score.

Or

b. Write short notes on de Bruijn approach.

14 a. Discuss in detail about Data structures.

Or

b. How will you read RNA-seq data? Explain.

15 a. Brief about telemedicine.

Or

b. Discuss in detail about electronic health records.

**PART-C****Answer the following****5x7=35****Answer should not exceed 600 words or three pages**

16 a. Explain in detail about Big data platforms

Or

b. Discuss in detail about modern data analytical tools.

17 a. Give a detailed account on applications of sequencing NGS.

Or

b. Discuss about NGS platform.

18 a. How will you align short reads to reference genome? Explain in detail.

Or

b. Elaborate on *De novo* assembly.

19 a. Explain in detail about RNA-seq analysis.

Or

b. Give a detailed account on ChiSeq analysis.

20 a. Explain in detail about acquisition, storage and use of biomedical data.

Or

b. Mention the importance of telehealth in detail.