B. Sc. (Bioinformatics) (Sem. V) (CBCS) Examination
November / December - 2018
BI - 502 : Applied Genomics & Transcriptomics
(New Course)

Time : **2$\frac{1}{2}$** Hours]　　　　　　　　　　　　　[Total Marks : **70**

Instructions :
　(1)　All questions are compulsory.
　(2)　The right side figure indicates total marks
　　　　of the question.

1　Attempt the following :　　　　　　　　　　　　　　　　**14**
　(a)　Answer the followng short questions :　　　　　　　　**4**
　　　　(all compulsory)
　　　　(1)　Xenologues are homologues that are related by
　　　　　　_____ within a genome and have different functions.
　　　　(2)　Algorithm/tools used for polypharmacology.
　　　　(3)　_____ is an interaction repository with compiled
　　　　　　biological data and linked with software platform
　　　　　　for visualizing interaction network.
　　　　(4)　What are the biomarkers identified for Raspberries
　　　　　　and Citrus fruit using metabolomics approaches ?

　(b)　Answer any one of the following questions :　　　　　**2**
　　　　(1)　What are Orthologues, paralogues and
　　　　　　homologues ?
　　　　(2)　What is Horizontal gene transfer ?

　(c)　Answer any one of the following questions :　　　　　**3**
　　　　(1)　What are the applications of comparative genomics ?
　　　　(2)　What are the computational challenges of
　　　　　　pangenomics ?

　(d)　Answer any one of the following questions :　　　　　**5**
　　　　(1)　Explain polypharmacology and diffrent methods of
　　　　　　computational pharmacology.
　　　　(2)　Explain Agrigenomics, Nutrigenomics and Animal
　　　　　　genomics.

2   Attempt the following :   **14**
      (a)   Answer the following short questions :   **4**
             (all compulsory)
             (1)   What is HOT/ALOHA ?
             (2)   _____ aims to eliminate redundant reads region
                    of high depth coverage.
             (3)   Define Metabolomics.
             (4)   What is metagenomics ?

      (b)   Answer any one of the following questions.   **2**
             (1)   What are the problems of metagenomics
                    annotation ?
             (2)   Define FOSMID, COSMID and BAC.

      (c)   Answer any one of the following questions.   **3**
             (1)   What are the technical challenges of metagenomics
                    sequence analysis ?
             (2)   What are the metagenomics tools to improve
                    producer strains ?

      (d)   Answer any one of the following questions.   **5**
             (1)   Explain Metabolic engineering as a tool for
                    cell factories.
             (2)   Explain Algorithm of genome assembly.

3   Attempt the following :   **14**
      (a)   Answer the following short questions :   **4**
             (all compulsory)
             (1)   _____ Bacteria interact with foreign cells and
                    helps in exert influence innate and adaptive
                    immune cells and T-lymphocytes.
             (2)   TMA/TMAO is related to which diseases ?
             (3)   HOMD
             (4)   Colon cancer peptide of human _____.

      (b)   Answer any one of the following questions :   **2**
             (1)   What is 16s rRNA sequencing and analysis of skin
                    microbiome ?
             (2)   What is Metatrancriptomics, metaproteomics and
                    metabolomics ?

(c) Answer any one of the following questions : **3**

    (1) Explain oral microbiome in diagnosing and treating diseases.

    (2) What sequencing strategies are used in skin microbiome studies ?

(d) Answer any one of the following questions. **5**

    (1) What are the impacts of gut microbiota of human health ?

    (2) Explain human microbiome.

4 Attempt the following : **14**

(a) Answer the following short questions : **4**

(all compulsory)

    (1) Adenovirus is a useful model of studying gene expression because _____.

    (2) Presence of introns facilitates the formation of several different mRNAs, thus increasing protein yield of different types but from same gene. True/ False.

    (3) List out Small Non-Coding RNA.

    (4) _____ are a class of long transcribed but not translated RNAs that are longer than 200 nucleotides.

(b) Answer any one of the following questions : **2**

    (1) Short note on Non-Coding RNA.

    (2) Write a short note on circRNA.

(c) Answer any one of the following questions : **3**

    (1) Explain Pseudogenes.

    (2) Long Intergenic ncRNAs.

(d) Answer any one of the following questions : **5**

    (1) Clinical and therapeutic applications of noncoding RNAs.

    (2) Write an essay on Small RNA.

5 Attempt the following : 14

   (a) Answer the following questions : (all compulsory) 4

      (1) What is the first step of the bioinformatics pipeline of RNA-Seq ?

      (2) Name the method of choice for transcriptional profiling which were used until the late 2000s.

      (3) Two new developments in RNA-seq technologies are _____ and _____.

      (4) Mention one important limitation on the current RNA-seq-based approaches for studying sRNAs.

   (b) Answer any one of the following questions : 2

      (1) What are the challenges for direct sequencing of RNAs ?

      (2) Draw the flowchart that contains processes involved in transcriptome mapping.

   (c) Answer any one of the following questions : 3

      (1) What are the principles and advances in Microarray ?

      (2) There are various Quality-control checkpoints in RNA-Seq. Explain any three checkpoints in detail.

   (d) Answer any one of the following questions : 5

      (1) Explain the technique that uses high-throughput sequencing methodology used to capture and quantify transcripts present in an RNA extract.

      (2) The current limitations in RNA-seq technologies are eliminatd by two new developments. Justify this statement.

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