Week 1 Assignment 1

Due date for submitting the assignment is passed.

1. You are designing a miRNA microarray study to understand changes in expression of genes in various organs. What will be the focus of the study to find the patient a major hurdle towards generating statistically reliable data?

   - Availability of clinical samples
   - Availability of a statistical
   - Issues during sample processing
   - Availability of statistical

   *For the question 1, select the answer:
   1. Accepted Answer

2. For the SDP gene, one sample RNAseq is:

   - Most reactive in single chronic sample
   - Least reactive in single chronic sample
   - Most reactive in all chronic samples
   - Least reactive in all chronic samples

   *For the question 2, select the answer:
   1. Accepted Answer

3. Two students (Rita and Shree) are working on a case-studied parasite which is not sequenced at genome or transcriptome level. Rani extracted DNA from the parasites and Shree extracted RNA from the same sample. Answer the following questions Q3, Q4 and Q6 on the basis of the conditions provided below:

   a) Which of the following sequence is the correct strategy to study the organism?

   - 3' RACE
   - 5' RACE
   - RT-qPCR
   - 5' RACE

   *For the question 3, select the answer:
   1. Accepted Answer

4. Which of the following tools can be used for RNA-seq processing?

   - STAR
   - BWA
   - DEXseq
   - MEDUSA

   *For the question 4, select the answer:
   1. Accepted Answer

5. Among the following normalizing methods, which method is best suited for the normalization of RNAseq data?

   - KINSHIP
   - FBA
   - Minc-mard
   - LIMMA

   *For the question 5, select the answer:
   1. Accepted Answer

6. Which is not an example of single nucleotide polymorphism (SNP) for "TACCTC AACGCGT"

   - TCTCTAC
   - TTTCGCGAT
   - TCTCCTAC
   - TTTCGCGAT

   *For the question 6, select the answer:
   1. Accepted Answer

7. What are the three components of CpG islands?

   - Pre-LTR characterisation, Genome Characterisation and Methylation Characterisation
   - Pre-LTR characterisation, Genome Characterisation and Pre-LTR characterisation
   - Pre-LTR characterisation, Genome Characterisation and Pre-LTR characterisation
   - Genome Characterisation, Pre-LTR characterisation and Methylation characterisation

   *For the question 7, select the answer:
   1. Accepted Answer

8. Use basic tool alignment search tool like: https://blast.ncbi.nlm.nih.gov/Blast.cgi search for the nearest homologue protein to a parasite ID. Find: RIBOSOME to the following questions Q8, Q9 and Q10.

   - How many homologues are found with identity percentage greater than 70% for the query protein?

     - 3
     - 5
     - 10

   *For the question 8, select the answer:
   1. Accepted Answer

9. How many gaps are present in the sequence alignment when target query is aligned with P protein (home sapiens) protein?

   - 3
   - 5
   - 10

   *For the question 9, select the answer:
   1. Accepted Answer

10. As SLCAT7 is the target parasite protein with Reboumis tacanum protein database. How many paralogs are found with percentage identity greater than 70% in the database?

    - 3
    - 5
    - 10

   *For the question 10, select the answer:
   1. Accepted Answer