

**Practical Bioinformatics**  
**Quiz 1 (TOTAL OF 20 POINTS)**  
**Duration: 1 hour (12.30 am - 1.30 pm)**

**February 18, 2021**

**Instructions:**

- Please turn on the camera.
- Do your Quiz questions individually.
- Submit your R Script files saved with .R extension
- ***Do not zip your submissions.***
- If the solution requires you to use paper, paste a good quality image of the solution in the document that you are submitting.
- All the Queries, if any will be cleared by your respective TA.

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1. 6 boys and 9 girls are present in a class. Write the set of R commands which will (i) sample 3 boys and 2 girls from each group respectively, and (ii) concatenate them into a team of 5 members.

[1]

2. Which among the following is true?

- A. Type I error is when the null hypothesis is true and  $H_0$  is accepted. This is also called False positive.
- B. Type I error is when the null hypothesis is true and  $H_0$  is rejected. This is also called False positive.
- C. Type I error is when the null hypothesis is true and  $H_0$  is accepted. This is also called True positive.
- D. Type II error is when the null hypothesis is true and  $H_0$  is accepted. This is also called True positive.

[1]

3. Tabulate at least four similarities and four differences between Microarray and RNAseq technologies.

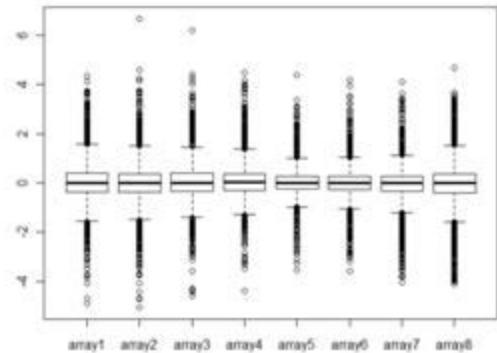
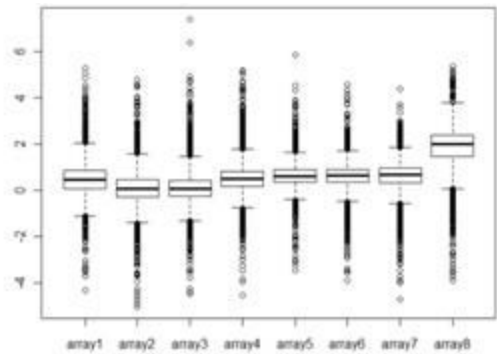
[2+2=4]

4. Which among the following is true?

- a. Microarray is reverse southern blot
- b. Probes are radioactive labelled in microarray slides
- c. Signal intensity depends upon the amount of hybridisation in Microarrays

[1]

5. The following transition represents



- a. Quantile Normalisation
- b. Background correction
- c. Log Transformation
- d. Median Normalization

[1]

6. Which of the following facts about RNA is true?

- a. The most abundant RNA is hnRNA
- b. Thymine in DNA is replaced by Uracil in RNA
- c. The sugar in RNA is hexose
- d. The sugar in RNA is deoxyribose

[1]

7. (i) What is the central dogma of molecular biology? (ii) Write an R code to transcribe the DNA sequence GTATCTTGAAATTAGCAG into RNA that it will transcribe. (iii) Assuming that the first base of this sequence is the start site for transcription, write an R code to translate the sequence into the corresponding amino acid sequence.

[3]

8. What is reverse transcription and cDNA? Where is reverse transcription used in Microarray?

[1+1=2]

9. In a microarray experiment, (i) what is the range of gene expression values in log2 transformed data? (ii) What is the range of log2 fold change?

[1+1=2]

10. Briefly explain the need for normalization in microarray datasets. Mention the specific issues that are addressed during normalization.

[1.5]

11. Intake of a certain amount of sugar by a set of 12 patients resulted in an increased blood pressure by following values:

5, 2, 8, -1, 3, 0, -2, 1, 5, 0, 4, 6.

Can it be concluded that the intake of sugar will, in general, be accompanied by an increase in blood pressure?

[2.5]