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 and H0 is accepted. This is also called False positive.
   B. Type I error is when the null hypothesis is true and and H0 is rejected. This is also called False positive.
   C. Type I error is when the null hypothesis is true and and H0 is accepted. This is also called True positive.
   D. Type II error is when the null hypothesis is true and and H0 is accepted. This is also called True positive.

[1]

3. Tabulate at least four similarities and four differences between Microarray and RNAseq technologies.
   Similarities : For expression analysis, both have high run to run reproducibility, hypothesis testing, exploratory statistics etc.
   Differences : hybridisation in microarray, probe binding in microarray, only predefined sequences could be analysed in microarray, RNA seq is sequencing based method, low sensitivity of microarray etc.

   (other similarities and differences are also considered for evaluation)

[2+2=4]
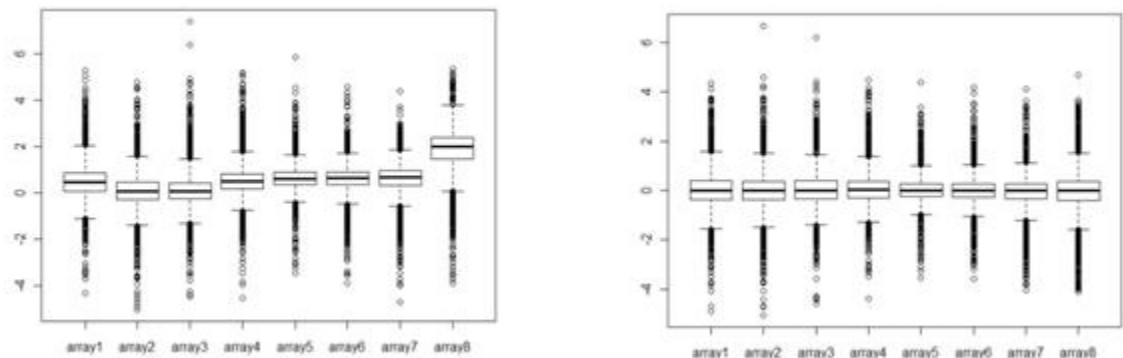
4. Which among the following is true?

   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.

[1+1+1]

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

[1+1=2]

Reverse transcription - conversion of RNA to DNA
cDNA - The DNA formed after the reverse transcription of RNA [1]

Reverse transcription in Microarray - For labelled target generation and for probe generation [1]

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?
   i) -infinity to +infinity
   ii) 0 to infinity

   [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]

    To test whether the mean increase in blood pressure of all patients with an intake if blood sugar will be positive, we have to assume that this population is normal with mean µ and standard deviation σ which are unknown.

    H_0: µ = 0; H_1: µ1 > 0
    The test statistic under H_0 is 2.897

    The tabulated value of $t_{0.05}$ at 11 difference is 2.2.

    ∵ | t | > $t_{0.05}$, H_0 is rejected.
    i.e., The intake of sugar in general will be accompanied by an increase in blood pressure.