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Sardar Patel University
M.Sc. (BIOINFORMATICS) SEMESTER - III External Examination
PS03CMBI01: Genomics & Proteomics
Tuesday, 4th December 2012

Time: 02:30 p.m. to 05:30 p.m.

Max Marks: 70

Q1. Choose the most appropriate option for each question.

[8]

- a. In shotgun sequencing approach, problems will arise if there is _____ in sequence.
- A) Mutation
 - B) Tandem Repeat
 - C) Substitution
 - D) Insertion
 - E) None of above.
- b. In gel stretching method for restriction mapping once gel has solidified it is washed with solution containing _____.
- A) Magnesium Phenylindole
 - B) Sodium Chloride
 - C) Dihydrochloride
 - D) Magnesium Chloride
 - E) None of Above
- c. FISH mapping technique was originally used with _____ phase chromosomes.
- A) Ana
 - B) Telo
 - C) Pro
 - D) All of above
 - E) None of above
- d. Initial exons extend from.
- A) GT to AG
 - B) AG to TG
 - C) AG to GT
 - D) TG to GA
 - E) None of Above
- e. Ridges are genome domains that have a high:
- A) Gene density
 - B) GC content
 - C) SINE repeat density
 - D) All of Above
 - E) None of Above
- f. For non-covalent attachment of cDNA to primary aliphatic amine (NH₂) group in microarray, primary aliphatic amine (NH₂) group is attached to the _____.
- A) only at 5' end of DNA
 - B) only at 3' end of DNA
 - C) Surface of the glass
 - D) All of above
 - E) None of Above

g. With a $5\ \mu\text{m}$ laser size and $5\ \mu\text{m}$ pixel size, ____ of the emission are from the array, resulting from the laser is measured at that pixel and rest is from neighboring pixels?

- A) 90%
- B) 95%
- C) 91%
- D) 47%
- E) None of Above

h. In microarray normalisation process, subtracting the mean log ratio (or log intensity) of all of the data on the array from each log ratio (or log intensity) measurement on the array is called as

- A) Scaling
- B) Centering
- C) Distribution Normalisation
- D) all of above
- E) None of Above

Q2. Answer the following questions (Any seven):

[14]

- a. Discuss any one technique similar to RAPD.
- b. Which is the rare motif in the recognition sequences of restriction enzyme? Explain the reason with diagram.
- c. Explain ORF map produced by DNA STRIDER program for any segment of genome.
- d. Design and explain HMM model to detect a statistically significant frequency of the same base at interval of 10bp in sequences.
- e. Write short note on INFOGENE.
- f. Explain reasons why matrix methods do not achieve a better prediction of E.Coli promoters.
- g. Explain reverse-genetic analysis of gene function.
- h. Write short note Ancient Conserved Regions and its importance in Genome analysis.
- i. Discuss pattern discrimination method to predict eukaryotic genes.
- j. Discuss about the classical parametric statistic - t - tests for paired and unpaired microarray data.

Q3. "Genes that act sequentially in a biochemical pathway are frequently found to be adjacent to each other at one chromosome location" Explain the statement by [6]

- a. discussing tryptophan genes of *E.coli*.

- b. Discuss Hertz and Stormo method for locating common DNA binding site for regulatory proteins in unaligned sequences. [6]

OR

- b. Explain how Grail II system works for finding exons in eukaryotic genes. [6]

Q4.

- a. Enumerate physical and genetic mapping methods also give their full form. Discuss method for direct examination of DNA molecules for restriction sites in detail. [6]
- b. Explain maskless photodeprotection technology of oligonucleotide array synthesis. [6] Also discuss the Image Acquisition step with necessary details.

OR

- b. Lists commonly used methods for segmentation and explain any two in detail. [6]

Q5.

- a. Explain GFF/GTF a standard format for specifying features in a sequence.
- b. Define buoyant density. Discuss various factors responsible for the difference in buoyant density of DNA.

OR

- b. GCCATGGCGA
ACGATGCTGT
GACATGGTAC
AGGATGGGCT
GCGATGTGGC [6]

By using above MSA find out which one is more probable to be a translation start site from following sequences.

SEQ1. TCGAATGTT
SEQ2. CACCATGGC

Q6.

- a. Explain two-dimensional breakpoint graph that represents the rearrangements as closed loops.
- b. Describe output table of ImaGene tool.

OR

- b. Discuss various approaches used to classify genes according to their functions.

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