

GOVERNMENT ZIRTIRI RESIDENTIAL SCIENCE COLLEGE

Subject: **Zoology**
Paper name: **Biotechnology and bioinformatics**
Paper No: **XXIII A**
Semester: **VI**

A. Multiple choice questions

1. DNA polymerase synthesizes new DNA strand complimentary to original DNA strand by adding dNTPs in
 - a) 3' to 5' direction
 - b) 5' to 3' direction
 - c) 3 to 5 direction
 - d) 5 to 3 direction
2. Each individual has a unique DNA fingerprint as individuals differ in
 - a) Size of minisatellites on chromosome
 - b) Location of minisatellites on chromosome
 - c) Number of minisatellites on chromosome
 - d) All of the above
3. Which of the following is a technique used for detecting specific RNA separated by Agarose gel electrophoresis?
 - a) Western blotting
 - b) Southern blotting
 - c) Northern blotting
 - d) Agarose gel electrophoresis
4. Separation of proteins in SDS-PAGE occur in
 - a) resolving gel
 - b) stacking gel
 - c) agarose gel electrophoresis
 - d) nitrocellulose membrane
5. Which of the following is a chemical nucleotide sequencing method?
 - a) Edmans method
 - b) Automated sequencing method
 - c) Sanger method
 - d) Maxam-Gilbert method
6. cDNA is synthesized from mRNA using which of the following enzyme
 - a) DNA polymerase
 - b) Reverse transcriptase
 - c) Helicase

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- d) RNase
7. Which of the following vector can be used to clone large DNA fragments?
- Cosmids
 - Plasmids
 - Bacterial Artificial Chromosome
 - Yeast Artificial Chromosome
8. Enzyme used for joining DNA fragments is
- Polymerase
 - DNase
 - Ligase
 - Topoisomerase I
9. The mechanism of intake of DNA fragments from the surrounding medium by a cell is called
- Transformation
 - Conjugation
 - Transduction
 - Transfection
10. Restriction enzymes are
- exonuclease
 - palindromic sequence
 - lyases
 - endonuclease
11. A technique for correcting defective genes responsible for disease development is called
- Genetic engineering
 - Gene cloning
 - Gene therapy
 - Gene editing
12. Which bacteria is used in the production of insulin by genetic engineering?
- Mycobacterium tuberculosis*
 - Saccharomyces cerevisiae*
 - Rhizobium*
 - Escherichia coli*
13. Gene library contain complete genomic sequences or complementary DNA sequences, the latter being formed from messenger RNA and lack
- intron sequences
 - exon sequences
 - mRNA

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- d) cDNA
14. The first step in the construction of genomic gene library is
- Fragmentation
 - Ligation
 - DNA isolation
 - Synthesis
15. Bt cotton is a genetically modified organism (GMO) which produces an insecticide to combat
- Hookworm
 - Bollworm
 - Fall armyworm
 - Silkworm
16. Software that manages the computer hardware, and provides common services for execution of various application software is
- resource management
 - operating system
 - information retrieval
 - job management
17. The most commonly used search engine that have about 1,600,000,000 monthly visitors is
- Yahoo
 - Ask.com
 - Google
 - Bing
18. The biological data that contain original biological data that is a raw sequence or structural data submitted by the authors directly is
- primary data e.g. GenBank, EMBL and DDBJ
 - secondary data e.g. SWISS-Prot and PIR
 - tertiary data e.g. NCBI
 - specialized data e.g. TADB, DrugBank
19. The term Bioinformatics was coined by _____ in the year _____
- Paul Berg, 1972
 - NCBI, 2001
 - Paulien Hogeweg, 1979
 - Watson and Crock, 1953
20. Which database provide information on the physiological role of gene products, e.g. enzyme activities, mutant phenotypes, or biological pathways?

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- a) functional database
 - b) nucleotide database
 - c) sequence database
 - d) structural database
21. You have protein sequence and you wish to know what other proteins look like it. Which of the five Basic Blast programs should you use?
- a) Blastn
 - b) Blastp
 - c) Blastpgp
 - d) Blastx
22. A free search engine accessing primarily the MEDLINE database of references and abstracts on life sciences and biomedical topics is
- a) Medpub
 - b) Pubmed
 - c) NCBI
 - d) askMEDLINE
23. Which of the following is a sequence alignment tool for nucleotide sequence provided by NCBI?
- a) BLAST(N)
 - b) FASTA
 - c) BLAST(P)
 - d) Clustal W
24. The most popular and frequently used methods of phylogentic tree building can be classified into two major categories:
- a) cladistic methods based on *distances* and phenetic methods based on *characters*.
 - b) phenetic methods based on *distances* and cladistic methods based on *characters*.
 - c) phenetic methods based on *characters* and cladistic methods based on *distances*.
 - d) Maximum methods based on *distances* and NJ method based on *characters*.
25. A _____ infers the existence of a common ancestors from which all the other species originate and indicate the direction on the evolutionary process
- a) binary tree
 - b) polytomy tree
 - c) unrooted tree
 - d) rooted tree

B. Fill up the blanks

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1. Annealing of primer to the single stranded DNA take place _____ degree Celsius below the melting temperature of the primer.
2. The labeled probe in Southern Blotting binds to the _____ sequences of the gene of interest.
3. _____ sequencing method is designed to analyze the sequences longer than 1000 base pair where the large genome is broken down into random fragments.
4. The production of exact copies of a particular gene or DNA sequence is known as _____.
5. 5'-G AATTC-3' is the specific recognition site for _____.
6. DNA ligase I ligates _____ strand.
7. The genomic DNA libraries can be prepared by the complete digestion of the total genomic DNA with _____ enzyme.
8. Bt gene is isolated from a bacterium called _____.
9. _____ transports DNA inside cells within an organism.

10. A _____ is a software program or script available through the Internet that searches documents and files for keywords and returns the results of any files containing those keywords
11. _____ is a molecular biology database and retrieval system developed by the NCBI, that provides integrated access to nucleotide and protein sequence data.
12. In 1977, Allan Maxam and Walter Gilbert (Harvard Univ.) and Frederick Sanger (U.K) discovered methods for _____
13. The European resource for the collection, organisation and dissemination of data on biological macromolecular structures is _____
14. The comprehensive database that contains publicly available nucleotide sequences for more than 300000 organisms, built and distributed by NCBI is _____
15. A DNA and protein sequence alignment software package, a format which is now ubiquitous in bioinformatics is _____

Key Answers

A. Multiple choice questions

1. b) 5' to 3' direction
2. d) All of the above

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3. c) Northern blotting
4. a) resolving gel
5. d) Maxam-Gilbert method
6. b) Reverse transcriptase
7. d) Yeast Artificial Chromosome
8. c) Ligase
9. a) Transformation
10. d) endonuclease
11. c) Gene therapy
12. d) *Escherichia coli*
13. a) intron sequences
14. c) DNA isolation
15. b) Bollworm
16. b) operating system
17. c) Google
18. a) primary data e.g. GenBank, EMBL and DDBJ
19. c) Paulien Hogeweg, 1979
20. a) functional database
21. b) Blastp
22. b) Pubmed
23. a) BLAST(N)
24. b) phenetic methods based on *distances* and cladistic methods based on *characters*.
25. d) rooted tree

B. Fill up the blanks

1. 3-5°C
2. complementary
3. Shotgun
4. Gene cloning
5. EcoRI
6. lagging
7. restriction
8. *Bacillus thuringiensis*
9. Vector
10. Search engine
11. Entrez
12. Sequencing DNA/DNA sequencing
13. PDBe
14. GenBank
15. FASTA