

Roll. No.

Question Booklet Number

O.M.R. Serial No.

--	--	--	--	--	--	--	--

B.Sc. (SEM.-VI) (NEP) (SUPPLE.) EXAMINATION, 2024-25

BIOTECHNOLOGY

(Bioinformatics)

(Elective)

(BBT6004)

Paper Code

Z	0	1	0	1	1	9	T
---	---	---	---	---	---	---	---

Question Booklet
Series

A

Time : 1 : 30 Hours

Max. Marks : 75

Instructions to the Examinee :

1. Do not open the booklet unless you are asked to do so.
2. The booklet contains 100 questions. Examinee is required to answer 75 questions in the OMR Answer-Sheet provided and not in the question booklet. All questions carry equal marks.
3. Examine the Booklet and the OMR Answer-Sheet very carefully before you proceed. Faulty question booklet due to missing or duplicate pages/questions or having any other discrepancy should be got immediately replaced.
4. Four alternative answers are mentioned for each question as - A, B, C & D in the booklet. The candidate has to choose the correct / answer and mark the same in the OMR Answer-Sheet as per the direction :

(Remaining instructions on last page)

परीक्षार्थियों के लिए निर्देश :

1. प्रश्न-पुस्तिका को तब तक न खोलें जब तक आपसे कहा न जाए।
2. प्रश्न-पुस्तिका में 100 प्रश्न हैं। परीक्षार्थी को 75 प्रश्नों को केवल दी गई OMR आन्सर-शीट पर ही हल करना है, प्रश्न-पुस्तिका पर नहीं। सभी प्रश्नों के अंक समान हैं।
3. प्रश्नों के उत्तर अंकित करने से पूर्व प्रश्न-पुस्तिका तथा OMR आन्सर-शीट को सावधानीपूर्वक देख लें। दोषपूर्ण प्रश्न-पुस्तिका जिसमें कुछ भाग छपने से छूट गए हों या प्रश्न एक से अधिक बार छप गए हों या उसमें किसी अन्य प्रकार की कमी हो, उसे तुरन्त बदल लें।
4. प्रश्न-पुस्तिका में प्रत्येक प्रश्न के चार सम्भावित उत्तर- A, B, C एवं D हैं। परीक्षार्थी को उन चारों विकल्पों में से सही उत्तर छानना है। उत्तर को OMR उत्तर-पत्रक में सम्बन्धित प्रश्न संख्या में निम्न प्रकार भरना है :

(शेष निर्देश अन्तिम पृष्ठ पर)

1. Who is considered the father of Bioinformatics?
 - (A) Gregor Mendel
 - (B) Watson
 - (C) Sanger
 - (D) Margaret Dayhoff
2. The notion of homology primarily refers to:
 - (A) Chemical similarity
 - (B) Shared ancestry
 - (C) Shared function only
 - (D) Sequence length
3. Which is a major nucleotide sequence database?
 - (A) PDB
 - (B) SWISSPROT
 - (C) GENBANK
 - (D) BRENDA
4. EMBL is a database for:
 - (A) Protein sequences
 - (B) Nucleotide sequences
 - (C) Metabolite profiles
 - (D) Species taxonomy
5. Entrez is best described as:
 - (A) Sequence searching algorithm
 - (B) Visualization software
 - (C) Spectroscopy instrument
 - (D) Integrated database retrieval system
6. Which source is well known for protein sequence data?
 - (A) GENBANK
 - (B) SWISSPROT
 - (C) EMBL
 - (D) Unigene
7. Unigene database clusters:
 - (A) Protein families
 - (B) Chemical structures
 - (C) Chromosomes
 - (D) EST sequences by gene
8. Which one is a feature of GENBANK?
 - (A) Only protein data
 - (B) Not web accessible
 - (C) Gene expression data only
 - (D) Flatfile format

9. The term homology implies:
 - (A) 100% sequence identity
 - (B) Evolutionary relatedness
 - (C) Only structural similarity
 - (D) Randomness
10. A web portal for accessing multiple NCBI databases is:
 - (A) FASTA
 - (B) Entrez
 - (C) PDB
 - (D) UNIPROT
11. Sequence Annotation means:
 - (A) Deleting genes
 - (B) Only sequencing
 - (C) Protein folding
 - (D) Predicting the biological function of sequences
12. Which database is a primary source of nucleotide information in Europe?
 - (A) GENBANK
 - (B) EMBL
 - (C) SWISSPROT
 - (D) PDB
13. Which of these would you use to find gene sequences in Humans?
 - (A) GENBANK
 - (B) KEGG
 - (C) PDB
 - (D) SCOP
14. History of Bioinformatics traces back to the compilation of:
 - (A) Sequence data
 - (B) Protein structures only
 - (C) Literature only
 - (D) Plasmid maps
15. Sequence information sources are important for:
 - (A) Text mining
 - (B) Mass spectrometry
 - (C) Chemical structure elucidation
 - (D) Designing PCR primers
16. What does NCBI stand for?
 - (A) National Center for Big Informatics
 - (B) National Center for Biotechnology Information
 - (C) New Computational Biology Institute
 - (D) None of these

17. What is meant by curated database?
- (A) Automatically generated only
 - (B) Checked and annotated by experts
 - (C) Only for clinical trials
 - (D) Contains only raw data
18. Searchable sequence databases are necessary to:
- (A) Identify homologs
 - (B) Detect plagiarism
 - (C) Synthesize DNA
 - (D) Purify proteins
19. The primary bioinformatics tool for sequence similarity is:
- (A) BLAST
 - (B) PCR
 - (C) ELISA
 - (D) Microarray
20. Unigene primarily helps in:
- (A) Genome assembly
 - (B) Identifying unique expressed genes
 - (C) Protein structure prediction
 - (D) Taxonomy only
21. Which of the following does EMBL focus on?
- (A) Europe
 - (B) North America
 - (C) Asia
 - (D) Africa
22. The main purpose of sequence information sources is to:
- (A) Store recipes
 - (B) Run PCR only
 - (C) Determine pH
 - (D) Help understand DNA, RNA, protein sequences
23. Which is not a nucleotide sequence database?
- (A) EMBL
 - (B) SWISSPROT
 - (C) GENBANK
 - (D) DDBJ
24. GenBank updates:
- (A) Annually
 - (B) Monthly
 - (C) Daily
 - (D) Never

25. EST stands for:
- (A) Expressed Sequence Tags
 - (B) Experimental Synthesis Theory
 - (C) Electronic Supplementary Table
 - (D) Extended Sequence Transcription
26. Which database focuses on protein sequences?
- (A) EMBL
 - (B) GENBANK
 - (C) SWISSPROT
 - (D) DDBJ
27. PDB primarily contains
- (A) DNA sequences
 - (B) Carbohydrate pathways
 - (C) Egg shell proteins
 - (D) Protein 3D structures
28. SWISSPROT's main feature is:
- (A) Raw unannotated data
 - (B) High quality, curated protein sequences
 - (C) Only RNA data
 - (D) Only nucleotides
29. The technique used to detect DNA fragments by size:
- (A) PCR
 - (B) ELISA
 - (C) HPLC
 - (D) Southern blotting
30. Mass spectrometry is used for:
- (A) DNA sequencing
 - (B) Protein identification
 - (C) Blotting
 - (D) PCR
31. Restriction digestion helps in:
- (A) Amplifying DNA
 - (B) Sequencing RNA
 - (C) Modifying proteins
 - (D) Cutting DNA at specific sites
32. Chromatograms result from:
- (A) Sequence alignment
 - (B) Chromatography
 - (C) PCR only
 - (D) Mass spectrometry

33. TREMBL is a supplement to:
- (A) GenBank
 - (B) PDB
 - (C) SWISSPROT
 - (D) KEGG
34. Microarrays are commonly used for:
- (A) Protein folding
 - (B) DNA sequencing
 - (C) Restriction digestion
 - (D) Gene expression profiling
35. PCR is essential for:
- (A) Protein purification
 - (B) Amplifying DNA
 - (C) RNA stability
 - (D) Sequence alignment
36. Which is not a protein database?
- (A) SWISSPROT
 - (B) PDB
 - (C) GENBANK
 - (D) TREMBL
37. Which method can be used to measure mRNA abundance?
- (A) Southern blot
 - (B) Microarray
 - (C) Restriction digestion
 - (D) HPLC
38. SWISSPROT provides:
- (A) Protein structures
 - (B) Protein-coding genes information
 - (C) Annotated protein sequence data
 - (D) DNA microarray results
39. PDB entries are described by:
- (A) Atomic coordinates
 - (B) Nucleotide sequences
 - (C) Only chemical formulas
 - (D) Band sizes
40. The protein data bank (PDB) is updated:
- (A) Once a year
 - (B) Never
 - (C) By request only
 - (D) Regularly

41. Digestion by restriction enzymes produces:
- (A) Amino acids
 - (B) DNA fragments
 - (C) Sugars
 - (D) Fats
42. The first step in most proteomics workflows:
- (A) Mass spectrometry
 - (B) Bioinformatics
 - (C) PCR
 - (D) Protein separation
43. Microarrays use:
- (A) Labeled probes
 - (B) Proteases
 - (C) Restriction enzymes
 - (D) All of the above
44. Mass spectrometry is not used for:
- (A) Protein identification
 - (B) Quantifying proteins
 - (C) Finding DNA sequences
 - (D) Protein modification analysis
45. PDB provides information about:
- (A) DNA
 - (B) RNA
 - (C) Protein and Nucleic Acid structures
 - (D) Lipids
46. Biospectrometry databases are mainly for:
- (A) Protein sequences
 - (B) Spectral analysis
 - (C) Chromatography
 - (D) Plasmid mapping
47. Data generation techniques commonly used in bioinformatics include:
- (A) Restriction digestion
 - (B) PCR
 - (C) Mass spectrometry
 - (D) All of the above
48. What is primary source in Bioinformatics?
- (A) Textbooks
 - (B) Direct experimental data
 - (C) Review articles
 - (D) Wikipedia

49. Which is true about PROSITE?
- (A) Protein families and domains database
 - (B) Nucleotide sequences
 - (C) Carbohydrates database
 - (D) mRNA only
50. The output of mass spec can be:
- (A) Chromatograms
 - (B) Blot images
 - (C) DNA sequences
 - (D) pH values
51. What does the acronym BLAST stand for?
- (A) Bioinformatics Language Analysis Search Tool
 - (B) Biological Layout Algorithm Search Tool
 - (C) Basic Local Alignment Search Tool
 - (D) Biochemical Local Array System Tool
52. Open Reading Frames (ORFs) are used to:
- (A) Detect possible protein-coding regions
 - (B) Sequence DNA
 - (C) Calculate molecular weight
 - (D) Align protein sequences
53. Multiple sequence alignment helps in:
- (A) Determining gene expression
 - (B) Protein folding
 - (C) PCR efficiency
 - (D) Finding conserved regions
54. A mutation matrix is used to:
- (A) Count PCR cycles
 - (B) Sequence mapping only
 - (C) Cloning vectors
 - (D) Score residue substitutions in alignments
55. Phylogenetic trees represent:
- (A) Protein folding
 - (B) Evolutionary relationships
 - (C) Mass spectrometry data
 - (D) Chromatograms
56. The matrix commonly used in protein alignments:
- (A) FASTA
 - (B) GenBank
 - (C) PAM
 - (D) Microarray

57. Pairwise alignment compares:
- (A) Two sequences
 - (B) Multiple sequences
 - (C) Only proteins
 - (D) Images
58. The FASTA program is used for:
- (A) DNA synthesis
 - (B) Protein folding
 - (C) Database curation
 - (D) Sequence alignment searching
59. In sequence assembly, contigs are:
- (A) Completed chromosomes
 - (B) Overlapping DNA sequence fragments
 - (C) Protein motifs
 - (D) Restriction enzymes
60. What is a substitution matrix used in?
- (A) PCR
 - (B) DNA extraction
 - (C) ELISA
 - (D) Sequence alignment
61. Pairwise sequence alignment can be done using:
- (A) ClustalW
 - (B) BLAST
 - (C) Both (A) and (B)
 - (D) None of these
62. The result of BLAST search with a small E-value indicates:
- (A) Unreliable match
 - (B) Statistically significant similarity
 - (C) Mismatched primer
 - (D) DNA degradation
63. The initial step in phylogenetic analysis:
- (A) Sequence retrieval
 - (B) Protein purification
 - (C) Electrophoresis
 - (D) PCR only
64. Multiple sequence alignments are made using:
- (A) BLAST
 - (B) FASTA
 - (C) CLUSTAL Omega
 - (D) Gel electrophoresis

65. Sequence assembly is required in:
- (A) Genomics projects
 - (B) PCR
 - (C) Western blot
 - (D) Mass spec
66. Tree building algorithms include:
- (A) UPGMA
 - (B) Neighbor joining
 - (C) Both (A) and (B)
 - (D) None of these
67. NCBI BLAST can align:
- (A) Nucleotide only
 - (B) Protein only
 - (C) Both (A) and (B)
 - (D) RNA only
68. Interpreting BLAST result includes:
- (A) Looking at E-value
 - (B) Checking alignment score
 - (C) Both (A) and (B)
 - (D) None of these
69. Detecting open reading frames is key for:
- (A) Gene prediction
 - (B) RNA editing
 - (C) Chromosome painting
 - (D) Mass analysis
70. Substitution matrices are used for:
- (A) Cloning
 - (B) Evaluating alignments
 - (C) Chemical synthesis
 - (D) Microarray design
71. Phylogenetic analysis helps to:
- (A) Amplify DNA
 - (B) Separate proteins
 - (C) Understand gene evolution
 - (D) None of these
72. Which is a global alignment tool?
- (A) Needleman-Wunsch
 - (B) Smith-Waterman
 - (C) BLAST
 - (D) PCR

73. Assembly of sequences results in:
- (A) Exons
 - (B) Restriction sites
 - (C) Contigs
 - (D) Domain families
74. PAM and BLOSUM matrices are examples of:
- (A) Substitution matrices
 - (B) Restriction enzymes
 - (C) Sequencing primers
 - (D) None of these
75. Which program finds sequence similarity against protein databases?
- (A) BLASTp
 - (B) BLASTn
 - (C) BLASTx
 - (D) All of these
76. SRS in bioinformatics stands for:
- (A) Sequence Retrieval System
 - (B) Sequence Reading Software
 - (C) Standardized Resource System
 - (D) Sample Reference Software
77. FASTA is:
- (A) Only a file format
 - (B) An algorithm and file format
 - (C) Imaging technique
 - (D) Genome cloning method
78. BLAST is used for:
- (A) Finding sequence similarities
 - (B) DNA sequencing only
 - (C) PCR only
 - (D) Protein synthesis
79. Data submission in genomics is necessary for:
- (A) Publication of research
 - (B) Increasing public access to data
 - (C) Both (A) and (B)
 - (D) None of these
80. Genome annotation is:
- (A) Identifying genomic features and functions
 - (B) RNA synthesis
 - (C) Protein folding
 - (D) Only gene expression

81. The main sequence similarity searching method:
- (A) Microarray
 - (B) FASTA/BLAST
 - (C) PCR
 - (D) Southern blot
82. Gene identification tools can include:
- (A) GENSCAN
 - (B) Augustus
 - (C) Both (A) and (B)
 - (D) PCR primer designer
83. Which database would you use for protein domain annotation?
- (A) PROSITE
 - (B) GenBank
 - (C) ENA
 - (D) ArrayExpress
84. Pattern and repeat finding in genomes helps to:
- (A) Identify microsatellites
 - (B) Annotate gene families
 - (C) Both (A) and (B)
 - (D) None of these
85. Submission format for GenBank is:
- (A) XML only
 - (B) Flatfile
 - (C) FASTA
 - (D) Both (B) and (C)
86. A recognized tool for genome browsing:
- (A) UCSC Genome Browser
 - (B) Microarray
 - (C) PCR
 - (D) PDB
87. Entrez can access:
- (A) Protein data
 - (B) DNA sequence
 - (C) Structure data
 - (D) All of the above
88. Data submission to NCBI is called:
- (A) Depositing
 - (B) Data warehousing
 - (C) PCR
 - (D) Dry-lab
89. Similarity search with BLAST provides:
- (A) E-value
 - (B) Alignment score
 - (C) Both (A) and (B)
 - (D) Laboratory protocol
90. Which file format is commonly used for sequence data?
- (A) JPEG
 - (B) FASTA
 - (C) PNG
 - (D) HTML

91. Genome annotation helps to:
- (A) Identify new genes
 - (B) Predict gene function
 - (C) Both (A) and (B)
 - (D) None of these
92. What is the major aim of data submission?
- (A) Sharing data with the community
 - (B) Reducing computer memory
 - (C) Destroying old data
 - (D) Only storage
93. Which tool predicts exons and introns in eukaryotic genomes?
- (A) GENSCAN
 - (B) BLAST
 - (C) PCR
 - (D) BLAT
94. FASTA format begins with:
- (A) A letter A
 - (B) > symbol
 - (C) # symbol
 - (D) ; semicolon
95. Sequence similarity search can detect:
- (A) Homology
 - (B) Function
 - (C) Conserved domains
 - (D) All of these
96. Data submission can be rejected if:
- (A) Format errors
 - (B) No annotation
 - (C) Partial sequence
 - (D) Any of these
97. BLAST report does not provide:
- (A) E-value
 - (B) Percent identity
 - (C) Protein size
 - (D) Alignment region
98. Sequence annotation pipelines use:
- (A) Gene prediction software
 - (B) Manual curation
 - (C) Both (A) and (B)
 - (D) None of these
99. What does genome pattern finding help with?
- (A) Short sequence motifs
 - (B) Repeat regions
 - (C) Both (A) and (B)
 - (D) Microarrays
100. New gene identification commonly involves:
- (A) Similarity searching
 - (B) Experimental validation
 - (C) Genome annotation
 - (D) All of the above

Rough Work / रफ कार्य

Example :

Question :

Q.1 (A) ● (C) (D)

Q.2 (A) (B) ● (D)

Q.3 (A) ● (C) (D)

5. Each question carries equal marks. Marks will be awarded according to the number of correct answers you have.
6. All answers are to be given on OMR Answer Sheet only. Answers given anywhere other than the place specified in the answer sheet will not be considered valid.
7. Before writing anything on the OMR Answer Sheet, all the instructions given in it should be read carefully.
8. After the completion of the examination, candidates should leave the examination hall only after providing their OMR Answer Sheet to the invigilator. Candidate can carry their Question Booklet.
9. There will be no negative marking.
10. Rough work, if any, should be done on the blank pages provided for the purpose in the booklet.
11. To bring and use of log-book, calculator, pager & cellular phone in examination hall is prohibited.
12. In case of any difference found in English and Hindi version of the question, the English version of the question will be held authentic.

Impt. On opening the question booklet, first check that all the pages of the question booklet are printed properly. If there is any discrepancy in the question Booklet, then after showing it to the invigilator, get another question Booklet of the same series.

उदाहरण :

प्रश्न :

प्रश्न 1 (A) ● (C) (D)

प्रश्न 2 (A) (B) ● (D)

प्रश्न 3 (A) ● (C) (D)

5. प्रत्येक प्रश्न के अंक समान हैं। आपके जितने उत्तर सही होंगे, उन्हीं के अनुसार अंक प्रदान किये जायेंगे।
6. सभी उत्तर केवल ओ०एम०आर० उत्तर-पत्रक (OMR Answer Sheet) पर ही दिये जाने हैं। उत्तर-पत्रक में निर्धारित स्थान के अलावा अन्यत्र कहीं पर दिया गया उत्तर मान्य नहीं होगा।
7. ओ०एम०आर० उत्तर-पत्रक (OMR Answer Sheet) पर कुछ भी लिखने से पूर्व उसमें दिये गये सभी अनुदेशों को सावधानीपूर्वक पढ़ लिया जाये।
8. परीक्षा समाप्ति के उपरान्त परीक्षार्थी कक्ष निरीक्षक को अपनी OMR Answer Sheet उपलब्ध कराने के बाद ही परीक्षा कक्ष से प्रस्थान करें। परीक्षार्थी अपने साथ प्रश्न-पुस्तिका ले जा सकते हैं।
9. निगेटिव मार्किंग नहीं है।
10. कोई भी रफ कार्य, प्रश्न-पुस्तिका में, रफ-कार्य के लिए दिए खाली पेज पर ही किया जाना चाहिए।
11. परीक्षा-कक्ष में लॉग-बुक, कैल्कुलेटर, पेजर तथा सेल्युलर फोन ले जाना तथा उसका उपयोग करना वर्जित है।
12. प्रश्न के हिन्दी एवं अंग्रेजी रूपान्तरण में भिन्नता होने की दशा में प्रश्न का अंग्रेजी रूपान्तरण ही मान्य होगा।

महत्वपूर्ण: प्रश्नपुस्तिका खोलने पर प्रथमतः जाँच कर देख लें कि प्रश्नपुस्तिका के सभी पृष्ठ भलीभाँति छपे हुए हैं। यदि प्रश्नपुस्तिका में कोई कमी हो, तो कक्षनिरीक्षक को दिखाकर उसी सिरिज की दूसरी प्रश्नपुस्तिका प्राप्त कर लें।