

Roll No.

Question Booklet Number

O. M. R. Serial No.

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Question Booklet Number

M. Sc. (Biochemistry) (Fourth Semester)

EXAMINATION, 2022-23

BIO-INFORMATICS

Paper Code						
B	C	H	4	0	0	2

Questions Booklet
Series

A

Time : 1:30 Hours]

[Maximum Marks : 75

Instructions to the Examinee :

परीक्षार्थियों के लिए निर्देश :

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.
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, तो उसे तुरन्त बदल लें।

(Remaining instructions on the last page)

(शेष निर्देश अन्तिम पृष्ठ पर)

(Only for Rough Work)

1. What is the source to retrieve gene sequences for downstream applications ?
 - (A) PubMed
 - (B) Google Scholar
 - (C) BLAST
 - (D) Wikipedia

2. Which of the following tools is used for identifying similarities between a query sequence and a database of known sequences :
 - (A) PubMed
 - (B) BLAST
 - (C) Google Scholar
 - (D) Ensemble

3. The software tool useful for performing multiple sequence alignments :
 - (A) NCBI
 - (B) BLAST
 - (C) PubMed
 - (D) Clustale

4. Which of the following internet resources is popularly used for searching research articles ?
 - (A) BLAST/FASTA
 - (B) Google Scholar
 - (C) Ensemble
 - (D) ClustalW

5. What does the acronym BLAST stand for ?
 - (A) Basic Local Alignment Search Tool
 - (B) Bioinformatics Link for Analysis of Sequence and Transcription
 - (C) Biological Laboratory for Advanced Sequence Techniques
 - (D) Base-Level Alignment and Sequence Tracker

6. The format in which DNA or protein sequences are represented ?
 - (A) FASTA
 - (B) UniProt
 - (C) NCBI
 - (D) GenBank

7. The database which provides comprehensive information of genomic resources of organisms ?
 - (A) GenBank
 - (B) NCBI
 - (C) EMBL
 - (D) Swiss-Prot

8. What is the primary purpose of constructing a virtual library for literature on MEDLINE and PubMed ?
- (A) To provide access to a wide range of scientific and medical literature.
 - (B) To reduce physical storage requirements for libraries.
 - (C) To enable remote access to research articles.
 - (D) All of the above
9. Which search engine is commonly used to access the MEDLINE and PubMed databases ?
- (A) Google Scholar
 - (B) Scopus
 - (C) Web of Science
 - (D) NCBI's search engine
10. How can you refine your search results in MEDLINE and PubMed to find more specific information ?
- (A) Using Boolean operators (AND, OR, NOT) to combine search terms.
 - (B) Applying filters based on publication date, study type or language.
 - (C) Utilizing MeSH terms (Medical Subject Headings) for precise topic-based searching.
 - (D) All of the above
11. Virtual library in the context of medical literature is useful :
- (A) To physically store and organize books and journals
 - (B) To provide a centralized platform for online access to medical literature
 - (C) To facilitate offline reading and research
 - (D) To enhance interlibrary loan services
12. Which of the following statements is true regarding the construction of a virtual library :
- (A) It requires physical space to store the digital content.
 - (B) It eliminates the need for remote access to scholarly resources.
 - (C) It enables users to access a vast collection of online medical literature.
 - (D) It restricts access to specific user groups only.
13. What is the purpose of searching for simple repeat sequences in DNA ?
- (A) To identify potential regulatory elements
 - (B) To locate transFactor binding sites
 - (C) To predict protein-coding regions
 - (D) To identify restriction enzyme recognition sites

14. Which tool is commonly used for restriction site analysis ?
- (A) BLAST
 - (B) MAR finder
 - (C) PCR
 - (D) Restriction enzyme database
15. What is the primary function of a MAR finder ?
- (A) To locate repetitive elements in a DNA sequence
 - (B) To predict protein-coding regions in a genome
 - (C) To identify transFactor binding sites
 - (D) To locate matrix attachment regions
16. What is proteomics ?
- (A) The study of proteins and their structures
 - (B) The study of genes and their functions
 - (C) The study of carbohydrates and their interactions
 - (D) The study of cell membranes and their components
17. What does GCG stand for in GCG sequence analysis ?
- (A) Genetic Code Generation
 - (B) Gene Cloning and Genomics
 - (C) Genome Composition Analysis
 - (D) Genetics Computer Group
18. What is the purpose of GCG sequence analysis software ?
- (A) To analyze and interpret protein sequences
 - (B) To study the structure of RNA molecules
 - (C) To determine the three-dimensional structure of proteins
 - (D) To identify specific DNA sequences in a genome
19. Which of the following techniques is commonly used in proteomics :
- (A) Polymerase Chain Reaction (PCR)
 - (B) Microarrays
 - (C) PAGE
 - (D) DNA sequencing
20. GCG sequence analysis refers to :
- (A) Analysis of DNA sequences only
 - (B) Analysis of protein sequences only
 - (C) Analysis of both DNA and protein sequences
 - (D) Analysis of RNA sequences only

21. What is SEQLAB in GCG sequence analysis ?
- (A) A software tool for DNA sequencing
 - (B) A database of protein sequences
 - (C) A graphical user interface for GCG software
 - (D) A protein structure prediction algorithm
22. The main purpose of the GCG interface is to :
- (A) Perform multiple sequence alignment
 - (B) Analyze gene expression data
 - (C) Predict protein structures
 - (D) Visualize and analyze DNA and protein sequences
23. Which of the following is an e-mail client commonly used for Linux systems ?
- (A) Pine
 - (B) Eudora
 - (C) Netscape
 - (D) Mail
24. The e-mail client which is not in use currently ?
- (A) Pine
 - (B) Eudora
 - (C) Netscape
 - (D) Mail
25. Which of the following is not an e-mail client ?
- (A) Pine
 - (B) Eudora
 - (C) Netscape
 - (D) FTP
26. Which file transfer protocol is commonly used for uploading and downloading files between a client and a server ?
- (A) Pine
 - (B) Eudora
 - (C) FTP
 - (D) Mail
27. Which e-mail client was popular among Unix users ?
- (A) Pine
 - (B) Eudora
 - (C) Netscape
 - (D) Mail
28. Which protocol is commonly used for transferring files over the Internet ?
- (A) FTP
 - (B) WSftp
 - (C) HTTP
 - (D) SMTP
29. Which of the following is a popular graphical FTP client ?
- (A) Pine
 - (B) Eudora
 - (C) Netscape
 - (D) WSftp

30. Which method is commonly used to identify simple repeat sequences in a DNA sequence ?
- (A) Polymerase Chain Reaction (PCR)
 - (B) Sanger sequencing
 - (C) Southern blotting
 - (D) Tandem repeat finder software
31. Restriction site analysis is used to identify :
- (A) DNA binding motifs
 - (B) Promoter regions
 - (C) Specific DNA sequences recognized by restriction enzymes
 - (D) Transcription factor binding sites
32. What is the purpose of MAR (matrix attachment region) finding in sequence analysis ?
- (A) To identify protein-coding genes in a genome
 - (B) To locate regulatory elements that control gene expression
 - (C) To predict protein-protein interactions
 - (D) To detect single nucleotide polymorphisms (SNPs)
33. Identification and characterization of repeated patterns within a DNA sequence involves :
- (A) Primary sequence analysis
 - (B) Higher-order sequence analysis
 - (C) Structural sequence analysis
 - (D) Comparative sequence analysis
34. What is the purpose of simple repeat sequence analysis ?
- (A) To identify and locate restriction sites within a DNA sequence.
 - (B) To analyze the presence of repetitive patterns in a DNA sequence.
 - (C) To predict the presence of mobile genetic elements in a genome.
 - (D) To study the secondary structure of a DNA molecule.
35. What does the term “restriction site” refer to in the context of DNA analysis ?
- (A) A DNA sequence where restriction enzymes can bind and cut the DNA
 - (B) A DNA sequence that is highly conserved across different species
 - (C) A region of the genome that is susceptible to genetic mutations
 - (D) A location on a chromosome where DNA replication initiates
36. What is the primary purpose of searching for simple repeat sequences in genomic analysis ?
- (A) To identify coding regions in a DNA sequence.
 - (B) To locate DNA segments that are prone to genetic mutations.
 - (C) To determine the presence of transposable elements in a genome.
 - (D) To predict potential microsatellite markers for genetic mapping studies.

37. What is the purpose of using MAR finders in higher order sequence analysis ?
- (A) To locate DNA regions that are involved in gene regulation and chromosome organization.
 - (B) To identify transposable elements in a genome.
 - (C) To predict the presence of simple repeat sequences.
 - (D) To analyze DNA sequences for the presence of restriction sites.
38. Which type of DNA sequence is commonly associated with matrix attachment regions (MARs) ?
- (A) Repetitive sequences
 - (B) Intron sequences
 - (C) Promoter sequences
 - (D) Exon sequences
39. What is the purpose of extracting the citation index from the ISI database ?
- (A) To identify influential research articles
 - (B) To access full-text versions of articles
 - (C) To gather statistical information about researchers
 - (D) To retrieve article abstracts and keywords
40. Which of the following databases provides the citation index for scientific literature ?
- (A) PubMed
 - (B) Scopus
 - (C) Web of Science
 - (D) IEEE Xplore
41. What does the citation index measure ?
- (A) The number of times an article has been cited by other articles
 - (B) The number of times an article has been downloaded
 - (C) The relevance of an article to a specific topic
 - (D) The publication impact factor of an article
42. Which of the following is not a benefit of constructing a virtual library for literature ?
- (A) Increased accessibility to a wider audience
 - (B) Reduction in physical storage space requirements
 - (C) Preservation of rare and fragile literary works
 - (D) Limited availability of literary resources

43. What is the primary purpose of metadata in a virtual library for literature ?
- (A) To provide a summary of each literary work
 - (B) To organize and categorize literary resources
 - (C) To authenticate the authorship of each work
 - (D) To restrict access to copyrighted materials
44. Which technology is commonly used for digitizing physical books in the construction of a virtual library ?
- (A) Optical Character Recognition (OCR)
 - (B) Augmented Reality (AR)
 - (C) Virtual Reality (VR)
 - (D) Artificial Intelligence (AI)
45. What is the purpose of extracting citation index information from the ISI database ?
- (A) To identify the most cited authors in a particular field
 - (B) To determine the impact and influence of research articles
 - (C) To track the development of scientific disciplines overtime
 - (D) All of the above
46. Which of the following is an example of system software ?
- (A) Microsoft Word
 - (B) Adobe Photoshop
 - (C) Windows Operating System
 - (D) Google Chrome Browser
47. Which of the following is a non-volatile memory storage device ?
- (A) Hard disk drive
 - (B) Solid-state drive
 - (C) Random Access Memory
 - (D) Cache Memory
48. Which component of a computer is responsible for executing instructions and performing calculations ?
- (A) CPU
 - (B) RAM
 - (C) GPU
 - (D) HDD
49. What is the primary function of an operating system ?
- (A) Managing hardware resources
 - (B) Creating documents and presentations
 - (C) Editing images and videos
 - (D) Browsing the internet

50. Which of the following is considered a high-level programming language ?
- (A) Assembly language
 - (B) C language
 - (C) Machine language
 - (D) Binary code
51. What is the role of a compiler in the programming process ?
- (A) It translates high-level code into low-level machine code
 - (B) It converts assembly language into machine code
 - (C) It executes the program line by line
 - (D) It debugs the program for errors
52. Proteome refers to :
- (A) Complete protein component of the cell
 - (B) Differentially expressed proteins
 - (C) Post-translationally modified proteins
 - (D) None of the above
53. The major database used in proteomics studies :
- (A) Swiss-Prot
 - (B) Uni-Prot
 - (C) Swiss-Model
 - (D) All of the above
54. Homology modeling is less accurate when :
- (A) The target and template proteins have low sequence similarity
 - (B) The target protein has a known structure
 - (C) The template protein has a different fold than the target protein
 - (D) The target protein has high expression levels
55. The evaluation of homology models involves :
- (A) Assessing stereochemistry
 - (B) Comparing with experimental data
 - (C) Checking energy profiles
 - (D) All of the above
56. Homology modeling can be used to predict :
- (A) Protein sequence
 - (B) Protein expression level
 - (C) Protein-protein interactions
 - (D) Protein function
57. h-index refers to :
- (A) n number of articles cited n number of times
 - (B) n - 1 number of articles cited n number of times
 - (C) n + 1 number of articles cited n number of times
 - (D) None of the above

58. The ideal way to search biological literature is by using :
- (A) Key words
 - (B) Author names
 - (C) Year of publication
 - (D) Country of publication
59. Predatory journal refers to :
- (A) Journals publishing high quality scientific content
 - (B) Journals following blind peer review process
 - (C) Journals that follow publishing ethics and guidelines
 - (D) None of the above
60. Which of the following is a scientific publisher ?
- (A) Elsevier
 - (B) Springer
 - (C) Wiley
 - (D) All of the above
61. What is the prerequisite to publish a research article ?
- (A) Funding
 - (B) Availability of experimental data
 - (C) Literature
 - (D) Scientific staff
62. Which of the following is NOT an ethical practice in publishing research articles ?
- (A) Plagiarism
 - (B) Cooked data
 - (C) Fabrication of data
 - (D) All of the above
63. Plagiarism indicates :
- (A) No similarity with existing literature
 - (B) Neat representation of experimental data
 - (C) High similarity with existing literature
 - (D) High quality scientific data
64. Proteomics is having application in :
- (A) Differential expression patterns of proteins in control and treated samples
 - (B) Identifying newly expressed proteins from experimental samples
 - (C) Both (A) and (B)
 - (D) Neither (A) nor (B)
65. Phylogenetic analysis can be performed by using the tool :
- (A) ORF finder
 - (B) MEGA7
 - (C) ClustalW
 - (D) BLAST
66. Bioinformatics deals with :
- (A) Computational analysis of biological data
 - (B) Simulations and modelling in biological research
 - (C) Prediction of gene and protein sequences
 - (D) All of the above

67. The authentic indexing database for extracting citation information :
- (A) Scopus
 - (B) Web of Science
 - (C) PubMed
 - (D) Google Scholar
68. What is the purpose of higher-order sequence analysis ?
- (A) To identify repetitive elements in a DNA sequence
 - (B) To search for simple repeat sequences in a DNA sequence
 - (C) To analyze transFactor binding sites in a DNA sequence
 - (D) To identify restriction sites in a DNA sequence
69. Which of the following scientists created the first bioinformatics database ?
- (A) Dayhoff
 - (B) Pearson
 - (C) Richard Durbin
 - (D) Michael J. Dunn
70. Homology modelling can be done using :
- (A) PDB
 - (B) Swiss-Prot
 - (C) Uni-Prot
 - (D) Swiss-Model
71. What is the purpose of reviewing the existing literature ?
- (A) To make sure you have a long list of references
 - (B) To reach the required word-count
 - (C) To find out what is already known about your area of interest
 - (D) To help in your general studying
72. What is self-plagiarism ?
- (A) When a person lifts material that they have previously written and pass it
 - (B) Talking about self too much
 - (C) Using somebody else's work and passing it off as your own work
 - (D) An epistemological stance
73. Protein annotation from transcriptome data can done using the database :
- (A) Uni-Prot
 - (B) Swiss-Prot
 - (C) Both (A) and (B)
 - (D) None of the above
74. The procedure of aligning many sequences simultaneously :
- (A) Multiple Sequence Alignment
 - (B) Pairwise alignment
 - (C) Global alignment
 - (D) Local alignment

75. SwissProt is :
- (A) Protein database
 - (B) Nucleotide database
 - (C) Uni-Prot consortium
 - (D) Both (A) and (C)
76. Which of the following tools is used to find repetitive sequences ?
- (A) Repbase
 - (B) CENSOR
 - (C) Dfam
 - (D) All of the above
77. Which of the following is NOT a protein database ?
- (A) EMBL
 - (B) Pfam
 - (C) Swiss-Prot
 - (D) Uni-Prot
78. Which of the following is NOT an example of protein structure database ?
- (A) PDB
 - (B) Swiss-Prot
 - (C) Uni-Prot
 - (D) EMBL
79. Ensemble is a tool useful to search :
- (A) Protein structures
 - (B) Human genome DNA sequences
 - (C) Epigenetic modifications
 - (D) None of the above
80. First line in a FASTA file begins with :
- (A) +
 - (B) >
 - (C) <
 - (D) =
81. GenBank is a database from :
- (A) NCBI
 - (B) Harvard
 - (C) EMBL
 - (D) HCU
82. Which of the following is an example for operating system ?
- (A) WINDOWS
 - (B) LINUX
 - (C) UNIX
 - (D) All of the above
83. Which of the following is the scientific database(s) ?
- (A) Science direct
 - (B) PubMed
 - (C) Web of Science
 - (D) All of the above

84. The software tool used for ORF analysis is :
- (A) ORF finder
 - (B) CLUSTALW
 - (C) Multalign
 - (D) BLAST
85. The software tool used for sequence alignment :
- (A) ORF finder
 - (B) CLUSTALW
 - (C) Multalign
 - (D) BLAST
86. Differential gene expression can be best measured using :
- (A) Gradient PCR
 - (B) Western blotting
 - (C) Next-generation sequencing
 - (D) Gel electrophoresis
87. Reverse transcription is applied :
- (A) To amplify DNA fragments
 - (B) To synthesize cDNA from RNA
 - (C) To isolate mRNA from a sample
 - (D) To visualize protein expression
88. Which statistical analysis method is often employed to identify differentially expressed genes ?
- (A) Student's *t*-test
 - (B) Chi-square test
 - (C) Standard deviation
 - (D) Median
89. What could be the role of control group in RT PCR experiment ?
- (A) To determine the optimal temperature for gene expression
 - (B) To establish a baseline for gene expression levels
 - (C) To assess the effect of different chemical treatments
 - (D) To compare different strains of microorganisms
90. Validating protein structures generated through computational modeling can be done by using :
- (A) X-ray crystallography
 - (B) Nuclear Magnetic Resonance (NMR)
 - (C) Electron microscopy
 - (D) Ramachandran plot analysis
91. The Ramachandran plot is a graphical representation of which protein structural feature ?
- (A) Secondary structure elements
 - (B) Tertiary structure elements
 - (C) Quaternary structure elements
 - (D) All of the above
92. The file format commonly used to store protein structures in the Protein Data Bank :
- (A) .doc
 - (B) .xls
 - (C) .pdb
 - (D) .txt

93. What is the purpose of NMR spectroscopy in protein structure determination ?
- (A) Generating high-resolution images of protein structures
 - (B) Studying protein-protein interactions
 - (C) Analyzing gene expression patterns
 - (D) Determining protein sequences
94. What is the main goal of proteomics analysis ?
- (A) Determining the structure of proteins
 - (B) Studying gene expression patterns
 - (C) Analyzing DNA sequences
 - (D) Identifying and characterizing proteins
95. Which method relies on the comparison of protein sequences to identify similar structures ?
- (A) Homology modelling
 - (B) Ab initio modelling
 - (C) Threading
 - (D) Structure validation
96. The tool to predict the structure of a target protein by comparing with similar sequence :
- (A) Homology modelling
 - (B) Threading
 - (C) Ab initio modelling
 - (D) Structure validation
97. Which method predicts protein structures from scratch, without relying on known templates or sequences ?
- (A) Homology modelling
 - (B) Threading
 - (C) Ab initio modelling
 - (D) Structure validation
98. Which method assesses the quality and correctness of a predicted protein structure ?
- (A) Homology modelling
 - (B) Threading
 - (C) Structure validation
 - (D) Ramachandran plot analysis
99. The database useful in storing protein structures with 3D coordinates ?
- (A) FASTA
 - (B) PDB
 - (C) BLAST
 - (D) CLUSTAL
100. What is the primary function of the CPU in a computer system ?
- (A) To execute instructions and perform calculations
 - (B) To store data for long-term storage
 - (C) To provide an interface for user interaction
 - (D) To connect various peripheral devices

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 :

Example :

Question :

Q. 1 (A) ● (C) (D)

Q. 2 (A) (B) ● (D)

Q. 3 (A) ● (C) (D)

Illegible answers with cutting and over-writing or half filled circle will be cancelled.

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 and 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.

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 छँटना है। उत्तर को OMR आन्सर-शीट में सम्बन्धित प्रश्न संख्या में निम्न प्रकार भरना है :

उदाहरण :

प्रश्न :

प्रश्न 1 (A) ● (C) (D)

प्रश्न 2 (A) (B) ● (D)

प्रश्न 3 (A) ● (C) (D)

अपठनीय उत्तर या ऐसे उत्तर जिन्हें काटा या बदला गया है, या गोले में आधा भरकर दिया गया, उन्हें निरस्त कर दिया जाएगा।

5. प्रत्येक प्रश्न के अंक समान हैं। आपके जितने उत्तर सही होंगे, उन्हीं के अनुसार अंक प्रदान किये जायेंगे।
6. सभी उत्तर केवल ओ. एम. आर. 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. ओ. एम. आर. 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 के अन्त में, रफ-कार्य के लिए दिए खाली पेज पर ही किया जाना चाहिए।
11. परीक्षा-कक्ष में लॉग-बुक, कैलकुलेटर, 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 प्रश्न-पुस्तिका के सभी पृष्ठ भलीभाँति छपे हुए हैं। यदि प्रश्नपुस्तिका में कोई कमी हो, तो कक्षनिरीक्षक को दिखाकर उसी सिरीज की दूसरी प्रश्न-पुस्तिका प्राप्त कर लें।