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M.Sc. Examination, 2019
Semester-IV
Biotechnology
Course : XVI
(Genomics, Proteomics and Bioinformatics)

Time : 3 Hours **Full Marks : 40**

Questions are of value as indicated in the margin.

Answer **any four** questions

1. a) Discuss any four characteristics considered when choosing markers for DNA fingerprinting.
   b) Why are molecular marker systems better than "classical" markers in detecting variation?
   c) Compare the relative advantages and disadvantages of the following molecular markers. 2+2+(3+3)=10
   i)SNPs ii) SSRs
2. Discuss briefly about different gel-based and non-gel based proteomic techniques. 5+5=10
3. a) What is meant by sequence format? Explain three frequently used sequence formats.
   b) Define homology modeling. Write different steps of homology modeling including the assumptions.
   c) Define BLAST and FASTA. 3+(1+4)+2=10
4. a) Describe the main features of human genome project along with its ethical issues.
   b) Why SNP consortium has been built and what are its aims?
   c) What are degenerate primers? What are the critical parameters of primer designing? 4+3(1+2)=10
5. a) Describe DNA barcoding along with its merits and demerits.
   b) Describe briefly a next generation DNA sequencing technique. 5+5=10
6. Write short notes on **any four** : 2.5×4=10
   a) International HapMap Project
   b) Needleman-Wunsch algorithm
   c) Pyrosequencing
   d) AELP
   e) cDNA microarray
   f) Global alignment versus local alignment

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M.Sc. Examination, 2019
Semester-IV
Biotechnology
Course : XVII
(Bioethics, Intellectual Property Rights, Biosafety and Research Methodologies)

Time : 3 Hours **Full Marks : 40**

Questions are of value as indicated in the margin.

Answer **any four** questions

1. a) What is the difference between research methods and research methodology?
   b) Describe briefly on writing a research article. 4+6=10
2. a) What are the socio-economic and ethical issues regarding releasing GMOs.
   b) Write down the role of Institutional Biosafety Committee. 4+6=10
3. What are the environment concerns regarding genetically modified food crops? How can these issues be addressed?
4. a) What are the different elements of writing research proposal for funding?
   b) What is a PCT application? What are the advantages of a PCT application? 4+6=10
5. a) Briefly describe the role of FSSAI.
   b) Comment briefly on the medical ethics in euthanasia.
6. Describe briefly the Protection of Plant Varieties and Farmers' Right Act, 2001. What are the provisions which protect the interest of Indian farmers' in the Act. 6+4=10

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Department of Biotechnology

M.Sc. 4th Semester, 2019

Paper XVIII - Practical Examination

Time 7 hrs (10.00 AM to 5.00 PM) **Total marks 40**

1 Download the following gene sequence from NCBI
Accession number: **XM_003614410.3**

a. BLAST it & identify the 5 best homologs. Do the multiple alignments with default parameters.
b. Translate this gene sequence to corresponding protein sequence using any freely available bioinformatic software.
c. BLAST the protein sequence & identify the best 5 homologs. Do the multiple alignments with default parameters.
d. Find whether this protein has any crystal structure submitted in the PDB. (4+1+4+1)

2a. Write the principle of cDNA synthesis from RNA. What is RT-qPCR? Write its principle. (2+1+2)

2b. You are given a plant cDNA sample. Perform RT-qPCR to quantitate the housekeeping gene Actin. Take primer cons- 3µM and cDNA concentration- 200 ng/µl using following RT-qPCR conditions:

Step 1. 95°C for 2 mins.

Step 2. 95°C for 15s

Step 3. 50°C for 20s (10)

Step 4. 72°C for 1min

Step 5. 40 cycles from step 2 to step 4

Melt curve analysis from 45°C- 55°C.

3. Viva voice (10)

4. Practical copy (5)

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M.Sc. Examination, 2020

Semester –IV

Biotechnology

Course: XVIII

(Laboratory IV - Genomics, Proteomics & Bioinformatics)

Time: 3 hrs **Full marks: 40**

1 Download the following gene sequence from NCBI
Accession number: **AY297425**

a. BLAST it & identify the five best homologs. Do the multiple alignments with default parameters. Write the name of the 5 best gene homologs. (5)

b. Translate this gene sequence to corresponding protein sequence using any freely available bioinformatic software. BLAST the protein sequence & identify the best five homologs. Do the multiple alignments with default parameters. Write the name of the 5 best homologous proteins. (5)

c. Design a pair of primers to amplify this partial gene. Write the sequence of the primer pair along with all the necessary parameters. (5)

2. a) Write the principle of cDNA synthesis from RNA. b) What is RT-qPCR? c) Write its principle. (2+1+2 = 5)

3. Viva voce (20)

Tolly Basak 29/09/2020

Sandip Das 29/09/2020

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M.Sc. Examination, 2020
Semester - IV
Biotechnology
Course XX
Project Works and Presentation (Elective)

Time: 6 hours | Full Marks: 80

Questions are of value as indicated in the margin

1. Deliver an online PowerPoint presentation on the project works you have carried out. Defend your presentation giving appropriate answers to the questions raised by the examiners. 25 + 15 = 40

2. Submit a report on the project work you have carried out. 40

26/9/2020

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26/09/2020

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26/09/2020

Basak
26/9/2020

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M.Sc. Examination, 2022
Semester –IV
Biotechnology
Course/Paper: XVI
(Genomics, Proteomics and Bioinformatics)

Time: 3 hrs **Full marks: 40**

Questions are of value as indicated in the margin

Answer any four questions

1a. Discuss the principle and applications of DNA barcoding.
b. Why we should not consider DNA barcoding as a taxonomic technique?
c. What is BOLD?

6+2+2=10

2a. Define Homology Modeling.
b. What are the assumptions in homology modeling methods?
c. Write down the different steps in homology modeling.
d. Describe Dynamic Programming.
e. Differentiate local and global alignment in terms of algorithm.

1+2+2+2+3=10

3a. Discuss four characteristics of DNA markers.
b. Why molecular marker systems are better than classical markers in detecting variation?
c. Compare the relative advantages and disadvantages of the following molecular markers.
i) SNPs ii) SSRs

2+2+(3+3)=10

4.a. What are degenerate primers?
b. Describe the steps of primer designing using any primer designing software.
c. What are the critical parameters of primer designing?
d. Describe any one technique of next generation sequencing. 1+2+2+5=10

5a. Discuss one non-gel based proteomic technique.
b. Describe the main features of human genome project along with its ethical issues.

5+5=10

6. Write notes on any four of the following. 4x2.5 = 10

(i) MSAP
(ii) PDB
(iii) Pyrosequencing
(iv) cDNA microarray
(v) Needleman-Wunsch algorithm.
(vi) BLAST

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M. Sc. Examination 2022
Semester IV
Biotechnology
Course/Paper XVII
(Bioethics, Intellectual property rights, Biosafety and Research Methodologies)

Time: 3 hours **Full Marks: 40**

Questions are of value as indicated in the margin

Answer any four questions

1. What do you understand by assisted reproductive technologies? Briefly describe the reservations regarding these technologies.

4+6=10

2. (a) What are the advantages and concerns regarding gene therapy?
   (b) Describe briefly the controversy regarding ownership of Basmati.

(3+3)+4=10

3. Describe briefly the different sections of a patent application.

10

4. Describe briefly:
   (a) Field trials of GM crops
   (b) Biosafety guidelines for working on GMOs at the laboratories.

4+6=10

5. Write short notes on:
   (a) Euthanasia
   (b) Role of FSSAI

2.5+7.5=10

6. Explain 'raw data' and 'processed data' in experimental research with a suitable example. What is the significance of statistical analysis of experimental results? When writing a research project proposal to some central government funding agency in India, what are the major sections to be covered and discussed?

3+3+4=10

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M.Sc. Examination, 2022

Semester –IV

Biotechnology

Course: XVIII

(Laboratory IV - Genomics, Proteomics & Bioinformatics)

Time: 6 hrs **Full marks: 40**

1. Download the following gene sequence with accession number: HQ711937 from NCBI and answer the questions from A, B and C using this gene sequence.

A. i. Design a pair of primers to amplify this gene using any free primer designing software.

ii. Discuss all the necessary parameters.

iii. Mention the name of the software that you used. (2 + 2 +1 =5)

B. i. Mention the name of the gene and its type.

ii. Apply BLAST and identify the five best homologs of this gene. Write the name of the 5 best gene homologs.

iii. Do the multiple alignments of all of them including the given gene with default parameters.

(1 + 2 +2 = 5)

C. i. Translate the given gene sequence to corresponding protein sequence using any freely available bioinformatic software. Apply BLAST with the protein sequence & identify the best five protein homologs. Write the name of the 5 best homologous proteins.

ii. Is the 3D structure of this protein present in PDB? Mention how you can check it? If yes, mention the name of that protein. If not, find the closest structural homolog of this protein in PDB and mention its name.

(3+2=5)

2 a) Write the principle of RT-qPCR.

b). Discuss its application with special reference to Covid-19

c) Measure the expression of Actin gene from the given cDNA sample of *Phaseolus vulgaris*

(2+2 +6 = 10)

3. Submission of practical copy and Viva-Voce. (5 + 10 = 15)

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M.Sc. Examination, 2022
Semester - IV
Biotechnology
Course XIX
(Classical Papers & Seminar)

Time: 10 am onwards | Full Marks: 40

Questions are of value as indicated in the margin

1. Deliver an online PowerPoint presentation on the final classical paper that was assigned to you. Defend your presentation giving appropriate answers to the questions raised by the examiners. [Presentation: 10 mins; Discussion & defence: 5 mins.] 20 + 10 = 30

2. Submit seminar presentation reports. 10

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M.Sc. Examination, 2022
Semester - IV
Biotechnology
Course XX
Project Works and Presentation (Elective)

Time: 10 am onwards

Full Marks: 80

Questions are of value as indicated in the margin

1. Deliver a PowerPoint presentation on the project works you have carried out. Defend your presentation by giving appropriate answers to the questions raised by the examiners. [Presentation 15 mins. Discussion & Defence 5 mins.] 25 + 15 = 40

2. Submit a report on the project work you have carried out. 40

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M.Sc. Examination, 2023
Semester –IV
Biotechnology
Course XVI: Genomics, Proteomics and Bioinformatics

Time: 3 hrs **Full marks: 40**

Questions are of value as indicated in the margin

Answer any four questions

1a. Describe DNA barcoding along with its merits and demerits..
b. Explain BOLD
c. Discuss one non-gel based proteomic technique. 4+2+4=10

2a. Discuss any four characteristics considered when choosing markers for DNA fingerprinting.
b. Why are molecular marker systems better than classical markers in detecting variation?
c. Compare the relative advantages and disadvantages of the following molecular markers.
i) SNPs
ii) SSRs
2+2+(3+3)=10

3a. What are degenerate primers?
3b. Describe the steps of primer designing using any primer designing software.
3c. What are the critical parameters of primer designing?
3d. Describe Dynamic Programming. Differentiate local and global alignment in terms of algorithm.
1+3+2+4=10

4a. What is meant by sequence format? Explain three frequently used sequence formats.
b. What is NGS. Explain one NGS technique. 4+6=10

5a. What is meant by Needleman-Wunsch algorithm?
b. Calculate the best alignments from the following pair of DNA sequences assuming +2 for math, -2 for mismatch and -1 for gap penalty.
ATGCG
ATGG
2+8=10

6. Write notes on any four of the following.

(i) BLAST
(ii) Pyrosequencing
(iii) cDNA microarray
(iv) AFLP
(v) Human genome project
4x2.5 = 10

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M. Sc. Examination 2023
Semester IV
Biotechnology
Paper XVII: Bioethics, Intellectual property rights, Biosafety and Research Methodologies

Time: 3 hours **Full Marks: 40**

Questions are of value as indicated in the margin.

Answer any four questions

1. (a) Why are there so many regulatory issues regarding biotechnology research? Describe briefly the relevant national and international regulations.
(b) What is PCT? Describe briefly the advantages of PCT.

(3+2)+(2.5+2.5)=10

2. What do you understand by patient confidentiality? What is the necessity of patient confidentiality? How can an organization working with patient data maintain the confidentiality of data?

2+4+4=10

3. Describe briefly the procedure for field trials of genetically modified food crops. What are the precautions that need to be taken in this regard.

10

4. Write short notes
(a) Budapest treaty.
(b) Bioprospecting.
(c) Ethics in assisted reproductive technologies.
(d) Cartagena protocol.

2.5x4=10

5. (a) What are the concerns regarding euthanasia?
(b) Briefly describe the role of FSSAI. How is FSSAI involved with the biotechnology industry?

4+(3+3)=10

6. (a) Describe the provision for protection of new varieties of plants in India.
(b) Describe briefly the different sections of writing a project proposal for funding.

5+5=10

Department of Biotechnology

M.Sc. 4th Semester, 2023

Paper XVIII - Practical Examination

Time 7 hrs (10.00 AM to 5.00 PM) **Total marks 40**

1 Download the following gene sequence from NCBI
Accession number: **XM_003614410.3**

a. Using BLAST identify the 5 best homologs. Do the multiple alignments with default parameters.

b. Translate this gene sequence to corresponding protein sequence using any freely available bioinformatic software.

c. Using appropriate BLAST, identify the 5 best protein homologs. Do the multiple alignments with default parameters.

a. Find whether this protein has any crystal structure submitted in the PDB.

6+2+6+1=15

2. a. Design a pair of primers for the amplification of the given gene sequence using any free primer designing software.

b. Discuss the important parameters that you should consider while designing the primer pair.

7+3=10

3. Viva voice (10)

4. Practical copy (5)

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M. Sc. Examination 2023
Semester IV
Biotechnology
Paper XIX: Classical Papers & Seminars)

Time: 10 A.M. onwards **Full Marks: 40**

Questions are of value as indicated in the margin.

1. Deliver a PowerPoint presentation on the final classical paper that was assigned to you. Defend your presentation with appropriate answers to the questions raised by the examiners.
   [Presentation 10 mins. Discussion and defence: 5 mins] 20+10=30

2. Submit seminar presentation reports. 10

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M. Sc. Examination 2023
Semester IV
Biotechnology
Paper XX: Project Works and Presentation (Elective)

Time: 10 A.M. onwards **Full Marks: 80**

Questions are of value as indicated in the margin.

3. Deliver a PowerPoint presentation on the project works that you have carried out. Defend your presentation with appropriate answers to the questions raised by the examiners.
   [Presentation 15 mins. Discussion and defence: 5 mins] 25+15=40

4. Submit a report on the project work you have carried out. 40

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M.Sc. Examination, 2024

Semester –IV

Biotechnology

Paper: XVI

(Genomics, Proteomics and Bioinformatics)

Time: 3 hrs **Full marks: 40**

Questions are of value as indicated in the margin

Answer any four questions

1a. What is NGS?
b. Describe one NGS technique with schematic diagrams.
c. Discuss the advantages of NGS technique over Sanger sequencing technique. 1+7+2=10

2a. What is Needleman-Wunsch algorithm?
b. What are the assumptions of this algorithm?
c. What are degenerate primers?
d. What parameters should be followed during primer designing?
e. Name one free software for primer designing.
f. What do you understand by dynamic programming? 2+2+1+3+1+1=10

3a. What is AFLP?
b. Discuss this fingerprinting technique elaborately with schematic diagrams.
c. Compare the relative advantages and disadvantages of the following molecular markers.
i) SNPs ii) RAPDs 1+5+(2+2) =10

4a. What is BLAST?
b. How many types of BLAST are available in NCBI and what are their applications?
c. What are the need of different types of sequence formats?
d. Explain three frequently used sequence formats. 1+5+1+3 = 10

5a. Name three non-gel based proteomic techniques and elaborately discuss any one of them with schematic diagrams.
b. What are the advantages of a non-gel based technique over a gel-based technique?
c. What is DNA bar-coding?
d. Discuss its advantages and disadvantages. 5+2+1+2 = 10

6. Write notes on any four of the following. 4x2.5 = 10
(i) Human genome project
(ii) SCAR marker
(iii) Pyrosequencing
(iv) BOLD
(v) Homology modeling
(vi) Dot-plot

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M. Sc. Examination 2024
Semester IV
Biotechnology
Paper XVI: Genomics, Proteomics and Bioinformatics

Time: 3 hours **Full Marks: 40**

Questions are of value as indicated in the margin.

Answer *any four* questions

1 (a). Discuss the advantages of non-gel based techniques over gel-based techniques.
(b). Briefly describe one non-gel based technique,
(c). Explain DNA barcoding. What are its merits and demerits?
2+4+3+1=10

2 (a). Discuss about the ethical issues of human genome project. What do you mean by HAPMAP?
(b). Describe one NGS technique. Discuss its advantage over Sanger sequencing.
2+2+5+1=10

3 (a). What is AFLP? Discuss this fingerprinting technique elaborately with schematic diagrams.
(b). What is meant by a primer for PCR? Name one free software for primer designing. What parameters should be considered during primer designing?
1+4+1+1+3=10

4 (a). Define BLAST. Discuss about the different types of BLAST available in NCBI.
(b). Discuss the three different types of sequence formats.
(4). What is the difference between local alignment and global alignment?
1+4+3+2=10

5 (a). Discuss the Needleman-Wunsch algorithm with its assumptions.
(b). Calculate the best alignments from the following pair of DNA sequences assuming +2 for match, -2 for mismatch and -1 for gap penalty.
ATGCG
ATGG
3+7=10

6. Write short notes on any four 2.5 x4
a. Dot Matrix Analysis.
b. Significance of E value in BLAST
c. Pyrosequencing
d. MSAP
e. BOLD
f. 2D-DIGE

M. Sc. Examination 2024
Semester IV
Biotechnology
Paper XVII: Bioethics, Intellectual property rights, Biosafety and Research Methodologies

Time: 3 hours **Full Marks: 40**

Questions are of value as indicated in the margin.

Answer *any four* questions

1. What do you understand by "Patents"? Why is this important for commercial activity?

4+6=10

2. Name the different forms of IPR. Briefly explain any two (besides patents).

2+4+4=10

3. What are the concerns relating to the environment with regard to growth/use of genetically modified crops? Are those concerns valid?

7+3-10

4. What is FSSAI? What are its main roles and how does it operate? What is the proposed criteria regarding genetic modifications?

2+(3+3)+2=10

5. How do the information from thorough literature survey help in research? Distinguish between standardization and validation for methods and data. Mention the salient features of preparing a list of references.

4+3+3=10

6. Write short notes on:
   (a) Geographical indications
   (b) Patent cooperation treaty
   (c) Convention of Biological Diversity
   (d) Controversy regarding stem cell therapy

2.5x4=10

M. Sc. Examination 2024
Semester IV
Biotechnology
Paper XVII:
(Bioethics, Intellectual property rights, Biosafety and Research Methodologies)

Time: 3 hours **Full Marks: 40**

Questions are of value as indicated in the margin.

Answer *any four* questions

1. (a) What is the difference between ethics and morals? Give an example which is ethical but immoral.
   (b) What are the ethical concerns regarding gene therapy?

   (2.5+2.5)+5

2. What do you understand by intellectual property rights? What are the different types of intellectual property rights? Briefly describe two types of intellectual property rights.

   3+2+(2.5+2.5)

3. Briefly describe the steps for applying for a patent from an invention..

   10

4. What are the ethical concerns regarding use of animals in scientific research? How can they be addressed?

   5+5=10

5. Write short notes on
   (a) Concerns regarding use of AI in the healthcare sector.
   (b) Role of FSSAI in Biotechnology
   (c) Biopiracy
   (d) TRIPS

   2.5x4=10

6. (a) What are the steps and considerations for a 'problem identification' in research? What do you mean by 'Objectives'?
   (b) During project proposal preparation for funding, under which headings the technical information are commonly sought? What are the different sectors of budget for a project proposal?

   (2+2)+(3+3)=10

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Department of Biotechnology

M.Sc. 4th Semester, 2024

Paper XVIII - Practical Examination

Time 6 hrs (10.00 AM to 4.00 PM) **Total marks 40**

1 Download the following gene sequence from NCBI
Accession number: XM_003614410.3

a. BLAST it & identify the 5 best homologs. Do the multiple alignments using all six sequences with default parameters.

b. Translate this gene sequence to corresponding protein sequence using any freely available bioinformatic software.

c. BLAST the protein sequence & identify the best 5 homologs. Do the multiple alignments using all six sequences with default parameters.

d. Find whether this protein has any crystal structure submitted in the PDB.

(4+1+4+1=10)

2. Write the principle of cDNA synthesis from RNA. What is RT-qPCR? Write its principle. (2+1+2=5)

3a. Set up and run the first dimension rod gel of the 2- gel electrophoresis with the given apparatus and reagents. Enlist the materials and reagents required for your experiment.

3b. Write down the principle of IEF. (7+3=10)

4. Viva voice (10)

5. Practical copy (5)

M.Sc. Examination, 2025

Semester –IV

Biotechnology

Course: XVIII

(Laboratory IV - Genomics, Proteomics & Bioinformatics)

Time: 4 hrs **Full marks: 40**

1. Download the following gene sequence with accession number: HQ711937 from NCBI and answer the questions from A, B and C using this gene sequence.

A. i. Design a pair of primers to amplify this gene using any free primer designing software.

ii. Discuss all the necessary parameters.

iii. Mention the name of the software that you used. (2 + 2 +1 =5)

B. i. Mention the name of the gene and its type.

ii. Apply BLAST and identify the five best homologs of this gene. Write the name of the 5 best gene homologs.

iii. Do the multiple alignments of all of them including the given gene with default parameters.

(1 + 2 +2 = 5)

C. i. Translate the given gene sequence to corresponding protein sequence using any freely available bioinformatic software. Apply BLAST with the protein sequence & identify the best five protein homologs. Write the name of the 5 best homologous proteins.

ii. Is the 3D structure of this protein present in PDB? Mention how you can check it? If yes, mention the name of that protein. If not, find the closest structural homolog of this protein in PDB and mention its name.

(3+2=5)

2 A) Write the principle of Needlemann Wunch algorith.

B) Deduce the best alignment for the following pair of sequences using this algorithm assuming match score =2, mismatch score = -2 and GAP penalty = -1

Seq 1: AGTCT

Seq 2: AGCT

(3+7 = 10)

3. Submission of practical copy and Viva-Voce. (5 + 10 = 15)