MAHISHADAL RAJ COLLEGE

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NAAC Accredited 'A' Grade College
DST (FIST) Govt. Of India approved College, NSDC Training Partner
Estd. : 1946

Mahishadal : Purba Medinipur   **Phone STD 03224**   No. 240220

===

Ref. No........................   **Date:**

ADD ON COURSE 2019-20

Organised by Department Zoology & Computer Science

Topic: Basic Bioinformatics

Add on course summary:

REPORT:

Name of the course- Basic Bioinformatics

Course coordinator: *Dr. Shubhamoy Das*, (Associate Professor, HOD, Department of Zoology , Mahishadal Raj College)

Date of commencement: 14.08.2019

Date of completion: - 31.08.2019

Number of participant enrolled: 30

Total duration day: 15

Total duration hour: 30

Evaluation method:- Paper pen MCQ and practical work

RESULT DETAILS:-

Number of student participate in this program: 30

Number of student completes this program: 27

Number of student got certificate in this program: 27

Name of the course: Basic Bioinformatics

Course coordinator: *Dr. Shubhamoy Das*, (Associate Professor, HOD, Department of Zoology , Mahishadal Raj College)

Basic Bioinformatics

About the course:

Bioinformatics course is an interdisciplinary field of Science that deals with Biological information. The two main Sciences that find applications in bioinformatics are Molecular Biology and Genetics. Bioinformatics course is a fusion of many fields such as Computer Science, Mathematics, Engineering, and Statistics. These fields combine to examine and exemplify Biological data. In other words, a Bioinformatics course is a study of information on Biological data. The Bioinformatics course is among the fastest growing fields in the field of Science, which helps in advancements of Biology as well as the processing and storing of related data. These tools are used in Bioinformatics courses to advance Biology research and to handle and store data linked to Biology. In a Bioinformatics course, candidates can study a variety of areas holistically while earning their degree.

Learning outcomes:

Completing a bioinformatics course opens up various job opportunities in diverse sectors where biological data analysis and computational biology skills are in demand. Job opportunities in bioinformatics continue to grow as advancements in genomics, personalized medicine, and data-driven research become increasingly important in various industries. Completion of this course, you have job opportunities in the fields of computational biologist, genomic data analyst, clinical bioinformatician, biotech research scientist, data scientist in life science, agricultural bioinformatics specialist, and environmental bioinformatician. Along with the booming Bioinformatics career scope, it has also become one of the highest-paid sectors and is continually rising.

Target audience:

Any interested students (UG & PG), research scholars, faculty members and, Industrial personals. Persons who have very much interest in Software based work.

Course content overview:

Bioinformatics is an interdisciplinary field of science that develops methods and software tools for understanding biological data, especially when the data sets are large and complex. Bioinformatics uses biology, chemistry, physics, computer science, computer programming, information engineering, mathematics and statistics to analyze and interpret biological data. The subsequent process of analyzing and interpreting data is referred to as computational biology. Computational, statistical, and computer programming techniques have been used for computer simulation analyses of biological queries. They include reused specific analysis "pipelines", particularly in the field of genomics, such as by the identification of genes and single nucleotide polymorphisms (SNPs). These pipelines are used to better understand the genetic basis of disease, unique adaptations, desirable properties (esp. in agricultural species), or differences between populations. Bioinformatics also includes proteomics, which tries to understand the organizational principles within nucleic acid and protein sequences.

Schedule: Total 30 hours

DAY	SCHEDULE
Day 1	Introduction to Bioinformatics (T) (2 hours)
Day 2	Nucleic acid databases and sequence retrieval (T+P) (2 hours)
Day 3	Sequence alignment- BLAST, pair wise sequence alignment, multiple sequence alignment. (T+P) (2 hours)
Day 4	Phylogenetic analysis and interpretation (T+P) (2 hours)
Day 5	Protein databases and protein structure analysis (T+P) (2 hours)
Day 6	Protein interaction study (T+P) (2 hours)
Day 7	Protein Tertiary structure and Visualization tools(T+P)(2 hours)
Day 8	Enzyme database. (T+P) (2 hours)
Day 9	Bioinformatics in Agriculture – Challenges and Opportunities (T) (2 hours)
Day 10	Basics of molecular interactions in medicinal chemistry and Drug design (P) (2 hours)
Day 11	Artificial Intelligence for Bioinformatics. (T) (2 hours)
Day 12	Introduction to functional genomics data analysis (T). (2 hours)
Day 13	Hands-on training session on "Genomics data analysis in R 1 (P). (2 hours)
Day 14	Hands-on training session on "Genomics data analysis in R 2 (P)
Day 15	Hands-on training session on "Genomics data analysis in R 3 (P)

Detail Work Schedule

Date	Day	Contents	Time	Duration	Experts	Designation
14.08.19	1	Introduction to Bioinformatics (T)	12 to 2pm	2	Dr. Subhamoy Das	HOD DEP. of ZOOLOGY
16.08.19	2	Nucleic acid databases and sequence retrieval (T+P)	1 to 3 pm	2	Dr. Subhamoy Das	HOD DEP. of ZOOLOGY
17.08.19	3	Sequence alignment- BLAST, pairwise sequence alignment, multiple sequence alignment. (T+P)	3 to 5pm	2	Prof. Saheli Maiti	SACT Mahishadal Raj College
19.08.19	4	Phylogenetic analysis and interpretation (T+P)	03 to 05pm	2	Prof. Saheli Maiti	SACT Mahishadal Raj College
20.08.19	5	Protein databases and protein structure analysis (T+P)	02 to 04pm	2	Dr. Subhamoy Das	HOD DEP. of ZOOLOGY
21.08.19	6	Protein interaction study (T+P)	01 to 03pm	2	Dr. Subhamoy Das	HOD DEP. of ZOOLOGY
22.08.19	7	Protein Tertiary structure and Visualization tools(T+P)preparation (T+P)	03 to 05pm	2	Dr. Subhamoy Das	HOD DEP. of ZOOLOGY

23.08.19	8	Enzyme database	02 to 05pm	2	Prof. Sagnik Mandal	SACT Mahishadal Raj College
24.08.19	9	Bioinformatics in Agriculture – Challenges and Opportunities (T)	02 to 04pm	2	Prof. Manik Das	SACT Mahishadal Raj College
25.08.19	10	Basics of molecular interactions in medicinal chemistry and Drug design (P)	01 to 03pm	2	Prof. Manik Das	SACT Mahishadal Raj College
27.08.19	11	Artificial Intelligence for Bioinformatics. (T)	02 to 04pm	2	Prof. Moumita Jana	SACT Mahishadal Raj College
28.08.19	12	Introduction to functional genomics data analysis (T)	02 to 04pm	2	Dr. Rajkumar Guchhait	SACT Mahishadal Raj College
29.08.19	13	Hands-on training session on "Genomics data analysis in R 1 (P)	01 to 03pm	2	Dr. Rajkumar Guchhait	SACT Mahishadal Raj College
30.08.19	14	Hands-on training session on "Genomics data analysis in R 2 (P)	02 to 04pm	2	Dr. Rajkumar Guchhait	SACT Mahishadal Raj College
31.08.19	15	Hands-on training session on "Genomics data analysis in R 3 (P) Evaluation, valediction, feedback	02 to 04pm	2	Dr. Subhamoy Day, Dr. Rajkumar Guchhait, Prof. Sagnik Manadal, Prof. Manik Das and Prof. Moumita Jana. DR.Asim Kr Bera	HOD & SACT., Zoology; Principal, MRC
				30 hours		

Course structure and examination scheme:

Course name	Theory classes (hr.)	Practical classes (hr.)	Continuous assessment		Total marks
			Theory	Practical	
Basic bioinformatics	15	15	50	50	100

Participant's Details and attendance:

Enrolment Details of Students

Sl. No.	Student ID	Roll No.	Name
1.	B.Sc/18/0002	2180002	MONIKA DAS
2.	B.Sc/18/0006	2180006	KRISHNENDU MAITI
3.	B.Sc/18/0007	2180007	SOMNATH GUCHHAIT
4.	B.Sc/18/0009	2180009	MRIDUL KANTI BERA
5.	B.Sc/18/0010	2180010	JAYANTA PAIK
6.	B.Sc/18/0011	2180011	SAHEB JANA
7.	B.Sc/18/0013	2180013	BAISAKHI MAITY
8.	B.Sc/18/0017	2180017	JYOTSNA MAITI
9.	B.Sc/18/0018	2180018	RIYA MAL
10.	B.Sc/18/0019	2180019	SHILARCHANA MAITI
11.	B.Sc/18/0020	2180020	SOUHARDYA DE
12.	B.Sc/18/0025	2180025	SWARUP DAS
13.	B.Sc/18/0026	2180026	ARJUN KUMAR JANA
14.	B.Sc/18/0028	2180028	BANDITA MANNA
15.	B.Sc/18/0029	2180029	SOUMILI SAHOO
16.	B.Sc/18/0031	2180031	SOMA CHITRAKAR
17.	B.Sc/18/0034	2180034	SOURAV DAS
18.	B.Sc/18/0035	2180035	SOUMYADIP MONDAL
19.	B.Sc/18/0036	2180036	DISHANTO DASGUPTA
20.	B.Sc/18/0037	2180037	PRITAM HAIT
21.	B.Sc/18/0044	2180044	SOURAV PATTANAYAK
22.	B.Sc/18/0046	2180046	DEBASISH HAZRA
23.	B.Sc/18/0047	2180047	SANATAN MANNA
24.	B.Sc/18/0048	2180048	BIKRAM DINDA
25.	B.Sc/18/0049	2180049	ARITRA AYAN MANNA
26.	B.Sc/18/0050	2180050	ATRI SUKUL
27.	B.Sc/18/0051	2180051	SREEDIP SAMANTA
28.	B.Sc/18/0052	2180052	ARPAN KOTAL
29.	B.Sc/18/0053	2180053	RIBHU PRAMANIK
30.	B.Sc/18/0054	2180054	JIBESH SINHA

Sample Question of Examination

1. Who is the initiator of the PIR database and collection of Protein sequences
   - a) Madam Curie
   - b) David Lipman
   - c) Stephen Altchul
   - d) Margaret Dayhoff

2. Find the one primary database of INSDC among the following
   - a) MIPS
   - b) PDB
   - c) NCBI
   - d) UniProt

3. There are two types of sequence alignments, find the right among the following
   - a) Pairwise and Multiple
   - b) Three to three and Multiple
   - c) Single and Multiple
   - d) Four to Nine and Multiple

4. Find the best example tool for Pairwise Alignment from the following
   - a) CLUSTAL W
   - b) CLUSTAL X
   - c) BLAST
   - d) PHYLIP

5. Sequence similarity between the matched sequences was observed in
   - a) Decimals
   - b) Percentage
   - c) Simple numbers
   - f) Factorial

6. The memory that access and process the speed of CPU is
   - a) ROM
   - b) HDD
   - c) RAM
   - d) Modem

7. The symbol used for the FASTA format is
   - a) :
   - b) #
   - c) <
   - d) >

8. The line used for the description of the sequence information after FASTA symbol is called
   - a) Description line
   - b) Definition line
   - c) Forward line
   - d) Keyword Line

9. Find the right symbol for ending the GenBank Format in NCBI database
   - a) >
   - b)]
   - c) //

10. Find out the correct too...
    - a) BLAST
    - c) Pfam

11. Primers will be designed by which of the following web tool
    - a) PrimePlex
    - b) Primer 3
    - c) Oligo 4.0
    - d) Prime tool

12. Boolean Operators are
    - a) A machine operator
    - b) The words used in Key words
    - c) A software
    - d) A Server

13. The search engine of NCBI
    - a) Entres
    - b) Entreg
    - c) Entrez
    - d) Entrance

14. A centre that governs all the nucleotide databases
    - a) ICGEB
    - b) INSDA
    - c) ISNDC
    - d) INSDC

15. UniProt is abbreviated as
    - a) Unified Protein resource
    - b) Union Protein resource
    - c) Universal Protein resource
    - d) United Protein resource

16. The database that accepts only protein crystallographic and NMR structures
    - a) Protein Families
    - b) Protein Data Bank
    - c) Protein Data Resource
    - d) Protein Param

17. Match the following
    - A) pBLAST
    - B) nBLAST
    - C) BLASTx
    - D) tBLASTx
    - E) tBLASTn
    - i) Search Protein database ► Translated Nucleotide query
    - ii) Search Translated Nucleotide ► Protein query
    - iii) Search Nucleotide database ► Nucleotide query
    - iv) Search Protein database ► Protein query
    - v) Search Translated Nucleotide ► Translated Nucleotide query
    - a) A-iii, B-v, C-ii, D-i, E-iv
    - b) A-iv, B-iii, C-i, D-v, E-ii
    - c) A-ii, B-iv, C-i, D-v, E-iii
    - c) A-v, B-iii, C-ii, D-iv, E-i

18. EST refers to
    - a) Expressed Sequence Tongs
    - b) Expressed Sequence Tails
    - c) Expressed S... ...ce Tags
    - d) Expressed Sequence Traits

    ...t aligned
    b) Same characters aligned
    ...th gaps
    d) Different characters aligned

20. The process...
21. The biologica...
22. The translate...
23. Among the f...
24. Find the corr... analysis
25. What is Liga...
26. EMBL refers...
27. The data sto...
28. The term us...
29. What are An...
30. Find the cor...

...System
b) Search and Save
...l and Literature
d) Prediction and Analysis
...sed protein database is
b) PDB
d) PIR
...rching protein structures in BLAST programme is
b) nr/nt
...base
d) Protein Ref-Sequence database
...ST to search the protein sequences Patented
b) Patented protein sequences
...uences
d) Protein databank sequences
...d the protein structures from PDB database is
b) .doc
d) .pdb
...Interface
b) Great User Interaction
...Interfaced) Graph User Interface
...ELLER tool is
b) Andrez Sali lab
d) Amberson lab
...sion that is used for Protein modelling
...0
b) MODELLER 9.0
...R 4.0
d) Easy MODELLER 7.0
...site prediction from the following
...ction server
b) SFC-Bio server
...erver
d) Epitope prediction server
...docking server among the following
...rver
b) PETCH DOCK server
...erver
d) PACH DOCK server
...odelling methods are available in bioinformatics
b) 2
d) 1
...e sequence to sequence similarity is called as
...ng
b) Match based modelling

    c) Comparative modelling
    d) Homology modelling

42. What is Python programme?
    - a) Script Command Prompt
    - b) Database programme
    - c) Modelling tool
    - d) Docking server

43. Find the right web-based protein modelling server
    - a) Easy MODELLER
    - b) PATCH MODELLER
    - c) Swiss MODELLER
    - d) Script MODELLER

44. What is PyMol stands for?
    - a) Pyrate Molecular viewer
    - b) Pyrol Molecular viewer
    - c) Pyton molecular viewer
    - d) Python based Molecular vierwer

45. PyMol has the following five uniform editing options, find the correct series.
    - a) A, H, C, L, S
    - b) A, S, H, L, C
    - c) S, A, H, C, L
    - c) H, A, S, L, C

46. CADD stands for
    - a) Command Altered Drug Design
    - b) Common Aided Drug Design
    - c) Computer Aided Drug Design
    - d) Computer Act Drug Design

47. The protein docking based drug targets or amino acids are termed as
    - a) Amino acid residues
    - b) Interact residues
    - c) contact residues
    - d) Interface residues

48. To alter the protein structures in PyMol, the symbol for sequence selection is
    - a) A
    - b) L
    - c) S
    - d) H

49. What type of interface residues are said to be highly covalent in nature
    - a) Distant interface residues
    - b) Moderate interface residues
    - c) Intact interface residues
    - d) Weak interface residues

50. For successful protein modelling, choose the correct series of events required
    - a) Template structure, Alignment, Query sequence, Generate Model
    - b) Query Sequence, Template structure, Alignment, Generate Model
    - c) Generate Model, Alignment, Query sequence, Template structure
    - d) Alignment, Generate Model, Template Structure, Query sequence

SAMPLE CERTIFICATE OF COURSE COMPLETION

CERTIFICATE
OF COURSE COMPLETION

THIS IS TO CERTIFY THAT

Monika Das

has successfully completed the **Add-on Course** on Basic Bioinformatics held during 2019-2020 academic year at Mahishadal Raj College.

Course Co-ordinator	IQAC Co-ordinator	Principal

CERTIFICATE
OF COURSE COMPLETION

THIS IS TO CERTIFY THAT

JAYANTA PAIK

has successfully completed the **Add-on Course** on Basic Bioinformatics held during 2019-2020 academic year at Mahishadal Raj College.

Course Co-ordinator	IQAC Co-ordinator	Principal