

SHIVAJI UNIVERSITY, KOLHAPUR - 416004, MAHARASHTRA

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शिवाजी विद्यापीठ, कोल्हापूर - ४१६००४,महाराष्ट्र

दूरध्वनी - ईपीएबीएक्स - २६०९०००, अभ्यासमंडळे विभाग दुरध्वनी विभाग २३१—२६०९०९३/९४



SU/BOS/Science/

Date:

19 JUL 2022 No 0 0 4 7 1

To,

The Head, Department of Zoology. Shivaji University, Kolhapur.

Subject : Regarding syllabi of Value Added programme under The Science and Technology.

Sir/Madam,

With reference to the subject mentioned above, I am directed to inform you that the University authorities have accepted and granted approval to the syllabi Value Added Course under the Faculty of Science and Technology.

Value	Added Course
ALUE ADDED COUR	SE IN BIOINFORMATIC

This syllabi and equivalence shall be implemented from the academic year 2022-2023 onwards. A soft copy containing the syllabus is attached herewith and it is also available on university website **www.unishivaji.ac.in**)

You are, therefore, requested to bring this to the notice of all students and teachers concerned.

Thanking you,

Yours faithfully

Dy Registrar

Copy to:

1	The Dean, Faculty of Commerce and Management	7	1200
2	Director Board of Commerce and Wallagement	/	P.G.Seminar Section
2	Director, Board of Examinations and Evaluation	8	Computer Centre
3	The Chairman, Respective Board of Studies	0	
4	B Com Exam	10	Affiliation Section (U.G.)
5		10	Affiliation Section (P.G.)
J	Eligibility Section	11	P.G.Admission Section
6	Appointment Section		1.6.7 Idillission Section

DEPARTMENT OF ZOOLOGY SHIVAJI UNIVERSITY, KOLHAPUR

"VALUE ADDED COURSE IN BIOINFORMATICS"

SYLLABUS

UNIT- I: Introductory Bioinformatics and Phylogenetics:

- 1. Data Resources in Bioinformatics:
 - a. Introduction of various biological databases.
 - b. Submissions and retrieval of sequences.
 - c. Importance and utilization of databases.

2. Sequence alignments:

- a. Concept of sequence similarity, identity and homology and its importance.
- b. Alignment types-local, global, pairwise and multiple.
- c. Tools in sequence alignment.

3. Phylogenetic analysis:

- a. Types of trees their construction and interpretation.
- b. Methods in Construction of phylogeny and their usage.
- c. Tools in construction of phylogenetic trees.

UNIT-II: Genomics and proteomics:

1. Protein Bioinformatics:

- a. Tools in primary structure analysis.
- b. Protein structure secondary and tertiary structure prediction methods (Homology modeling).
- 2. Molecular Docking: Data Requirements, docking tools and their usage.
- 3. Genome annotation: Nucleic acid and protein level, Annotation tools.

