
SYLLABUS FOR BOARD OF STUDIES ADOPTION — generated from the live catalogue record

Bioinformatics and Computational Biology

X-S2 · 5 days (configurable 1–5 days) · Science & Food Technology · Applied Science · Years: 2nd, 3rd, PG

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OVERVIEW

Students analyse biological sequence data and interpret results with bioinformatics tools.

Life-sciences research and biotech increasingly run on computation; graduates who can handle sequence data hold a differentiated, research-ready skill.

HOURS AND CREDIT POSITION

Contact hours: 40 Guided project: 20 Self-study: 0 Notional total: 60

Credit claim: 2

60 notional hours ÷ 30 hours per credit (NSQF track, UGC Micro-credentials Guidelines §5.3.3) = 2 credits.

COURSE OUTCOMES

CO1. Describe the major biological databases and data formats (K2)

CO2. Perform pairwise and multiple sequence alignment (K3)

CO3. Search databases for homology using BLAST (K3)

CO4. Construct a phylogenetic tree from sequence data (K3)

CO5. Interpret a sequence analysis in a written report (K5)

COURSE CONTENT — MODULES

Hours shown are the recommended format; module time scales proportionally when the engagement runs 1–5 days.

Module 1 — Bioinformatics foundations (5h recommended)

Theory: Biological data, databases

Lab: Explore biological databases

Output: Database exercise

Module 2 — Sequences (5h recommended)

Theory: DNA and protein sequences, formats

Lab: Handle sequence files

Output: Sequence exercise

Module 3 — Sequence alignment (5h recommended)

Theory: Pairwise and multiple alignment

Lab: Align sequences

Output: Alignment output

Module 4 — Database searching (5h recommended)

Theory: BLAST, homology

Lab: Search for homology with BLAST

Output: BLAST results

Module 5 — Phylogenetics (5h recommended)

Theory: Trees, evolutionary analysis

Lab: Build a phylogenetic tree

Output: Phylogenetic tree

Module 6 — Genomics basics (5h recommended)

Theory: Genome data, annotation

Lab: Inspect an annotated genome

Output: Annotation notes

Module 7 — Tools and scripting (5h recommended)

Theory: Bioinformatics tools, basic scripting

Lab: Automate a small analysis

Output: Analysis script

Module 8 — Capstone (5h recommended)

Theory: A sequence analysis with a written interpretation

Lab: Analyse and interpret a sequence set

Output: Sequence analysis report

ASSESSMENT SCHEME (100 MARKS)

Continuous exercises — 40 marks

Analytical report — 40 marks

Viva voce — 20 marks

CO-PO MAPPING

CO1 !' PO1 (strength 2)

Databases are foundational domain knowledge.

CO2 !' PO5 (strength 2)

Alignment tools are modern-tool usage.

CO3 !' PO5 (strength 2)

BLAST is a modern tool.

CO4 !' PO3 (strength 2)

Building a tree is a developed analysis.

CO5 !' PO10 (strength 2)

The interpretation report is professional communication.

EVERY PARTICIPANT RECEIVES

- Certificate of completion
- Course material
- LMS access
- Interview question bank
- Mock interview & viva practice

FEE

13,200 per student, incl. GST

Excludes the optional nasscom assessment where offered. Final pricing on your college's quotation.

DESIGNED BY

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