

**University of Asia Pacific (UAP)**  
**Department of Computer Science and Engineering (CSE)**  
**BSc in CSE Program**

**Course Outline – Bioinformatics Engineering**

**Part A – Introduction**

- 1. Course No. / Course Code:** BIE 301
- 2. Course Title:** Bioinformatics Engineering
- 3. Course Type:** Core Course
- 4. Level/Term and Section:** 3<sup>rd</sup> Year 1<sup>st</sup> Semester
- 5. Academic Session:** Spring 2025
- 6. Course Instructor:** Atia Rahman Orthi, Md. Shafayatul Haque
- 7. Pre-requisite (If any):**
- 8. Credit Value:** 3.00
- 9. Contact Hours:** 3.00
- 10. Total Marks:** 100
- 11. Course Objectives and Course Summary:** Introduction; Molecular biology basics: DNA, RNA, genes, and proteins; Restriction mapping algorithm; Motif in DNA sequences, motif finding algorithms; Genome rearrangements, sorting by reversals and breakpoints; DNA sequence alignments; Gene prediction; Space-efficient sequence alignments, sub-quadratic alignment; DNA sequencing, genome sequencing, protein sequencing, spectrum graphs; Combinatorial pattern matching: Exact pattern matching, heuristic similarity search algorithms, approximate string matching, BLAST, FASTA; Clustering: Microarrays, hierarchical clustering, K-means clustering, corrupted cliques problem, CAST clustering algorithm; Evolutionary trees.
- 12. Course Learning Outcomes: at the end of the Course, the Student will be able to –**

<b>CLO1</b>	<b>Define</b> molecular biology basics such as DNA, RNA, genes, and proteins; motifs in DNA; phylogeny
<b>CLO 2</b>	<b>Explain</b> algorithms such as DNA sequencing, DNA fragment assembly, spectrum graphs; sequence similarity; genome alignments and rearrangements; suffix tree, and evolutionary tree
<b>CLO3</b>	<b>Apply</b> combinatorial pattern matching such as FASTA, and BLAST to search databases; sequencing, and alignment algorithms; genome rearranging; clustering algorithms
<b>CLO4</b>	<b>Analyze</b> genome through alignments, phylogeny through comparison, motifs, and RNA and protein secondary structures

### 13. Mapping / Alignment of CLOs with Program Learning Outcomes (PLO) (Optional):

<b>CLO No.</b>	<b>Corresponding PLOs (Appendix-1)</b>	<b>Bloom's taxonomy domain/level (Appendix-2)</b>	<b>Delivery methods and activities</b>	<b>Assessment Tools</b>
CLO1	PLO-a	Understand	Lectures, Group Discussions	Written Exam
CLO2	PLO-c	Understand	Lectures, Group Discussions	Written Exam
CLO3	PLO-c	Apply	Lectures, Problem Solving	Written Exam
CLO4	PLO-e	Analyze	Lectures, Problem Solving	Written Exam

## **Part B – Content of the Course**

**14. Course Content:** Molecular biology basics, graph algorithms, sequence similarities, genome alignment, motifs in DNA, database search, BLAST, FASTA, phylogenetic reconstruction, protein and RNA secondary structure prediction, clustering, genome rearrangement.

### 15. Alignment of topics of the courses with CLOs:

<b>SL. No</b>	<b>Topics / Content</b>	<b>Course Learning Outcome (CLO)</b>
<b>1</b>	Molecular biology basics: DNA, RNA, genes, and proteins	CLO1
<b>2</b>	Graph algorithms: DNA sequencing, DNA fragment assembly, Spectrum graphs	CLO3
<b>3</b>	Sequence similarity, Suffix Tree and variants with applications, Evolutionary Tree	CLO2
<b>4</b>	Genome Alignment: maximum unique match, LCS, mutation sensitive alignments, multiple sequence alignment	CLO3, CLO4

<b>5</b>	Motif in DNA sequences, motif finding algorithms	CLO1, CLO3, CLO4
<b>6</b>	Database search: Smith-Waterman algorithm, FASTA, BLAST and its variations, Locality-sensitive hashing	CLO3
<b>7</b>	Phylogeny reconstruction; Phylogeny comparison: similarity and dissimilarity measurements, consensus tree problem	CLO1, CLO4
<b>8</b>	RNA and protein secondary structure prediction	CLO4
<b>9</b>	Clustering: Microarrays, hierarchical clustering, K-means clustering, corrupted cliques problem, CAST clustering algorithm	CLO3
<b>10</b>	Genome rearrangement: types of genome rearrangements, sorting by reversal and other operations	CLO2

#### **16. Class Schedule/Lesson Plan/Weekly Plan:**

Topics	Specific Outcome(s)	Time Frame	Suggested Activities	Teaching Strategy(s)	Alignment with CLO
Molecular biology basics: DNA, RNA, genes, and proteins, Graph algorithms: DNA sequencing, DNA fragment assembly, Spectrum graphs	Molecular biology basics, graph algorithms	Week 1	Practice, Assignment, Quiz	Lecture, Multimedia	CLO1, CLO3
		Week 2			
		Week 3			
Sequence similarity, Suffix Tree and variants with applications, Evolutionary Tree, Genome Alignment: maximum unique match, LCS, mutation sensitive alignments, multiple sequence alignment	Sequence similarity and alignment	Week 4	Practice, Assignment, Quiz	Lecture, Multimedia	CLO2, CLO3, CLO4
		Week 5			

Motif in DNA sequences, motif finding algorithms	Motifs	Week 6	Practice, Assignment, Quiz	Lecture, Multimedia	CLO1, CLO3, CLO4
		Week 7			
MID-TERM EXAMINATION					
Database search: Smith-Waterman algorithm, FASTA, BLAST and its variations, Locality-sensitive hashing	Use of advanced tools for searching databases	Week 8	Practice, Assignment, Quiz	Lecture, Multimedia	CLO3
Phylogeny reconstruction; Phylogeny comparison: similarity and dissimilarity measurements, consensus tree problem	Phylogeny	Week 9			
RNA and protein secondary structure prediction	Secondary structure prediction	Week 10	Practice, Assignment, Quiz	Lecture, Multimedia	CLO1, CLO4
RNA and protein secondary structure prediction	Secondary structure prediction	Week 11			
RNA and protein secondary structure prediction	Secondary structure prediction	Week 12	Practice, Assignment, Quiz	Lecture, Multimedia	CLO4
Clustering: Microarrays, hierarchical clustering, K-means clustering, corrupted cliques problem, CAST clustering algorithm	Clustering	Week 13	Practice, Assignment, Quiz	Lecture, Multimedia	CLO3
Genome rearrangement: types of genome rearrangements, sorting by reversal and other operations	Genome rearrangement	Week 14	Practice, Assignment, Quiz	Lecture, Multimedia	CLO2
FINAL EXAMINATION					

### 17. Teaching-Learning Strategies:

- Active Learning and Discussions
- Problem-Based Learning
- Case-Based Learning

- Simulations and Role-Playing

#### 18. Assessment Techniques of each topic of the course:

SL. No	Topics / Content	Assessment Techniques
1	Molecular biology basics: DNA, RNA, genes, and proteins	Quiz, Midterm
2	Graph algorithms: DNA sequencing, DNA fragment assembly, Spectrum graphs	Quiz, Midterm
3	Sequence similarity, Suffix Tree and variants with applications, Evolutionary Tree	Quiz, Midterm
4	Genome Alignment: maximum unique match, LCS, mutation sensitive alignments, multiple sequence alignment	Quiz, Midterm, Assignment
5	Motif in DNA sequences, motif finding algorithms	Quiz, Midterm, Final Exam
6	Database search: Smith-Waterman algorithm, FASTA, BLAST and its variations, Locality-sensitive hashing	Quiz, Final Exam, Assignment
7	Phylogeny reconstruction; Phylogeny comparison: similarity and dissimilarity measurements, consensus tree problem	Quiz, Final Exam
8	RNA and protein secondary structure prediction	Quiz, Assignment
9	Clustering: Microarrays, hierarchical clustering, K-means clustering, corrupted cliques problem, CAST clustering algorithm	Assignment
10	Genome rearrangement: types of genome rearrangements, sorting by reversal, and other operations	Quiz, Final Exam

#### Part C – Assessment and Evaluation

##### 19. Assessment Strategy

**Class Tests:** Altogether 4 class tests may be taken during the semester, 2 class tests will be taken for midterm and 2 class tests will be taken for final term. No makeup class tests will be taken. Students are strongly recommended not to miss any class tests.

**Assignment:** The students will have to form a group of a maximum of 4 members. The topic or case studies will be given as assignments in groups during the class which they have to prepare at home and will submit on or before the due date. No late submission of assignments will be accepted. Students will have to do a presentation on the given topic as an assignment.

### CIE- Continuous Internal Evaluation (30 Marks)

Bloom's Category Marks (out of 30)	Class Tests (20)	Assignments (10)
Remember		
Understand	<b>5</b>	
Apply	<b>5</b>	
Analyze	<b>5</b>	<b>5</b>
Evaluate	<b>5</b>	<b>5</b>
Create		

### SMEB- Semester Mid & End Examination (70 Marks)

Bloom's Category	Mid	Final
Remember	<b>4</b>	<b>5</b>
Understand	<b>4</b>	<b>5</b>
Apply	<b>12</b>	<b>10</b>
Analyze		<b>20</b>
Evaluate		<b>10</b>
Create		<b>5</b>

### 20. Evaluation Policy

Grades will be calculated as per the university grading structure and individual students will be evaluated based on the following criteria with respective weights.

1. Class Tests and Assignments 30%
2. Term Examination 50%
3. Mid-Term Examination 20%

### UAP Grading Policy

Numeric Grade	Letter Grade	Grade Point
80% and above	A+	4.00
75% to less than 80%	A	3.75
70% to less than 75%	A-	3.50
65% to less than 70%	B+	3.25

60% to less than 65%	B	3.00
55% to less than 60%	B-	2.75
50% to less than 55%	C+	2.50
45% to less than 50%	C	2.25
40% to less than 45%	D	2.00
Less than 40%	F	0.00

## **Part D – Learning Resources**

### **21. Text Book**

1. Bioinformatics Computing, Bryan Bergeron, Prentice Hall, 1st Edition, 2002
2. An Introduction to Bioinformatics Algorithms, By Neil C. Jones, Pavel Pevzner, The MIT Press, 1st Edition, 2004.