**Course Description Form**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 1. Course Name: | | | | | | | | |
| Bioinformatics | | | | | | | | |
| 1. Course Code: | | | | | | | | |
|  | | | | | | | | |
| 1. Semester / Year: | | | | | | | | |
| 2023-2024 | | | | | | | | |
| 1. Description Preparation Date: | | | | | | | | |
|  | | | | | | | | |
| 1. Available Attendance Forms: | | | | | | | | |
|  | | | | | | | | |
| 1. Number of Credit Hours (Total) / Number of Units (Total) **2** | | | | | | | | |
|  | | | | | | | | |
| 1. Course administrator's name (mention all, if more than one name) | | | | | | | | |
| Name: Dr.Bashar Talib AL-Nuaimi  Email: alnuaimi\_bashar@uodiyala.edu.iq | | | | | | | | |
| 1. Course Objectives | | | | | | | | |
| **Course Objectives** | | | | * The goal of studying Bioinformatics is to apply knowledge and understanding of fundamental principles and concepts in biology, computer science, and mathematics. Effectively utilizing existing software to extract information from large databases and utilizing it in computer modeling. Identifying basic sequence and structural Bioinformatics, introduction to Bioinformatics algorithms, pairwise and multiple sequence alignment, methods for phylogenetic analysis and pattern recognition, Bioinformatics databases and servers, classification and comparison of protein structures, prediction of secondary and tertiary structure from sequence. Identifying genes and proteins, determining their functions, establishing evolutionary relationships, and predicting their conformation. Applied to the analysis of sequences of biological molecules, bioinformatics is a field of computational science that typically focuses on genes, DNA, RNA, or proteins. It is particularly valuable for comparing gene sequences in proteins and other sequences within an organism, as well as comparing evolutionary relationships between organisms. | | | | |
| 1. Teaching and Learning Strategies | | | | | | | | |
| **Strategy** | | Biological data is stored, analyzed, and disseminated via bioinformatics, a interdisciplinary field consisting of both biology and computer science. An application of bioinformatics is to determine the function of genes and proteins, to establish evolutionary relationships, and to calculate the three-dimensional shape of proteins by using computer programs. | | | | | | |
| 1. Course Structure | | | | | | | | |
| **Week** | **Hours** | | **Required Learning Outcomes** | | | **Unit or subject name** | **Learning method** | **Evaluation method** | |
| **1** | **3** | | **Fundamentals of Bioinformatics** | | | **The meaning of computational technology and bioinformatics, along with their scope, are explained in this subject.** | **Lecture Base** |  |
| **2** | **3** | | **Data Structure and Algorithms** | | | **Introduction to Computing Applications** | **Lecture Base** |  |
| **3** | **3** | | **Genomics and Proteomics** | | | **Genome, Chromosome, Gene, (DNA, RNA, Protein)** | **Lecture Base** |  |
| **4** | **3** | | **Mathematical & Statistical applications in bioinformatics** | | | **Random Variables, Markov Chains, Metropolis–Hastings Algorithm, Maximum Likelihood. Monte Carlo, Genetic Algorithms, ,Genomic Segmentation Algorithm** | **Lecture Base** |  |
| **5** | **3** | | **Lecture Base** |  |
| **6** | **3** | | **Genome Alignment**  **Pair wise sequence alignment** | | | ***Sequence Similarity, Suffix Tree***  **Dot plots, Sequence alignment, Local alignment, Global alignment,** | **Lecture Base** |  |
|  |
| **7** | **3** | | **Genome Alignment** | | | **Multiple alignments** | **Lecture Base** |  |
| **8** | **3** | | **Bioinformatics Databases** | | | **Practically appreciate the utility of resources like NCBI / Entrez, the UCSC genome browser, EBI / EMBL, Uniprot, BLAST,** | **Lecture Base** |  |
| **9** | **3** | | **Phylogenetic tree construction** | | | **Distance based phylogenies (The neighbor-joining method)** | **Lecture Base** |  |
| **10** | **3** | | **Phylogenetic tree construction** | | | **Character based phylogenies(Maximum parsimony method, The maximum likelihood** | **Lecture Base** |  |
| **11** | **3** | | **Phylogeny Reconstruction** | | | ***Phylogeny Comparison*** | **Lecture Base** |  |
| **12** | **3** | | **Gene Prediction** | | | **Determination of consensus sequences, locating genes (gene prediction) and open reading frames in DNA sequences** | **Lecture Base** |  |
| **13** | **3** | | **Protein Classification and Structure Prediction** | | | **Prediction of protein structure and function** | **Lecture Base** |  |
| **14** | **3** | | **Bioinformatics Applications to Protein Structure Analysis** | | | **Protein structure related databases, motifs and folds, molecular docking, protein fold classification, etc., are explained in this subject.** | **Lecture Base** |  |
| **15** | **2** | | **EXAM** | | |  | **Lecture Base** |  |
| 1. Course Evaluation | | | | | | | | |
| The course serves as an introduction to how Bioinformatics is used in Biomedical research. The aim is that students should understand how Bioinformatics can be applied and evaluated and provide tools for practical approaches to Bioinformatics | | | | | | | | |
| 1. Learning and Teaching Resources | | | | | | | | |
| Required textbooks (curricular books, if any) | | | | |  | | | |
| Main references (sources) | | | | | * **Algorithms in Bioinformatics A Practical Introduction. Basics\_of\_Bioinformatics** * **bioinformatics-sequence-and-genome-analysis** * **Bioinformatics - Computational Molecular Biology. Basics\_of\_Bioinformatics** * **bioinformatics-sequence-and-genome-analysis. Basics\_of\_Bioinformatics** | | | |
| Electronic References, Websites | | | | | **NCBI** | | | |