MODULE DESCRIPTION FORM

نموذج وصف المادة الدراسية

| **Module Information**  **معلومات المادة الدراسية** | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Module Title** | Bioinformatics Algorithms | | | | **Module Delivery** | | |
| **Module Type** | Core | | | | * **☒ Theory** * **☐ Lecture** * **☒ Lab** * **☐ Tutorial** * **☐ Practical** * **☐ Seminar** | | |
| **Module Code** | BID311 | | | |
| **ECTS Credits** | 5.00 | | | |
| **SWL (hr/sem)** | 125 | | | |
| **Module Level** | | UGx1 3 | **Semester of Delivery** | | | | 5 |
| **Administering Department** | | BID | **College** | BMIC | | | |
| **Module Leader** | Ahmed Oday | | **e-mail** | ahmed.oday@uoitc.edu.iq | | | |
| **Module Leader’s Acad. Title** | |  | **Module Leader’s Qualification** | | | |  |
| **Module Tutor** | Name (if available) | | **e-mail** | E-mail | | | |
| **Peer Reviewer Name** | | Omar A. M | **e-mail** | omara.m@uoitc.edu.iq | | | |
| **Scientific Committee Approval Date** | | 18/06/2023 | **Version Number** | | | 1.0 | |

| **Relation with other Modules**  **العلاقة مع المواد الدراسية الأخرى** | | | |
| --- | --- | --- | --- |
| **Prerequisite module** | Bioinformatics Programming / BID221 | **Semester** | 4 |
| **Co-requisites module** | None | **Semester** |  |

| **Module Aims, Learning Outcomes and Indicative Contents**  **أهداف المادة الدراسية ونتائج التعلم والمحتويات الإرشادية** | |
| --- | --- |
| **Module Objectives**  **أهداف المادة الدراسية** | Module objectives in Bioinformatics Algorithms may include the following:  Understanding Bioinformatics: Develop an understanding of the field of bioinformatics and its significance in analyzing biological data. Algorithms in Bioinformatics: Learn about the fundamental algorithms used in bioinformatics for sequence analysis, genome assembly, gene expression analysis, protein structure prediction, and other relevant tasks. Sequence Alignment: Gain knowledge of sequence alignment algorithms such as pairwise alignment (global and local), multiple sequence alignment, and their applications in identifying similarities and differences in DNA, RNA, and protein sequences. Genome Assembly: Understand the challenges and algorithms involved in genome assembly from short reads obtained through next-generation sequencing technologies. selection, classification, and clustering methods. |
| **Module Learning Outcomes**  **مخرجات التعلم للمادة الدراسية** | The outcomes of studying Bioinformatics Algorithms can vary depending on the level and depth of the course. However, here are some general outcomes that students can expect to achieve:  1. Knowledge of Bioinformatics Algorithms: Acquire a solid understanding of the fundamental algorithms used in bioinformatics, such as sequence alignment, gene expression analysis, protein structure prediction, and genome assembly.  2. Algorithm Application: Apply bioinformatics algorithms to solve practical problems in analyzing biological data, including DNA, RNA, and protein sequences, as well as high-throughput sequencing data.  3. Computational Skills: Develop proficiency in using computational tools, software packages, and programming languages commonly used in bioinformatics for data analysis and algorithm implementation.  4. Data Analysis and Interpretation: Gain the ability to analyze and interpret biological data generated from various sources, including next-generation sequencing technologies, microarrays, and other high-throughput experiments.  5. Problem-Solving: Enhance problem-solving skills by employing critical thinking and analytical reasoning to address complex bioinformatics challenges, such as data integration, algorithm selection, and parameter optimization.  6. Algorithm Evaluation and Comparison: Evaluate and compare the performance of bioinformatics algorithms based on metrics like accuracy, sensitivity, specificity, and computational efficiency.  7. Machine Learning and Data Mining: Understand and apply machine learning and data mining techniques in bioinformatics to extract meaningful patterns and insights from large-scale biological data sets.  8. Practical Implementation: Gain hands-on experience in implementing bioinformatics algorithms and methodologies using appropriate software tools and programming languages.  9. Scientific Communication: Develop effective communication skills to present bioinformatics analysis results, both in written reports and oral presentations, to diverse audiences, including researchers and non-experts.  10. Ethical and Professional Conduct: Understand and adhere to ethical guidelines and best practices in bioinformatics research, including data privacy, integrity, responsible data sharing, and ethical considerations in handling sensitive biological information.  These outcomes reflect the knowledge, skills, and competencies that students can expect to acquire upon completion of a course or program in Bioinformatics Algorithms. The specific outcomes may vary depending on the curriculum, learning objectives, and intended level of the course. |
| **Indicative Contents**  **المحتويات الإرشادية** | The indicative contents in a course on Bioinformatics Algorithms can cover a wide range of topics. Here are some common content areas that may be included:  1. Introduction to Bioinformatics:  - Overview of bioinformatics and its applications in biological research  - Introduction to biological data types (DNA, RNA, protein sequences) and their characteristics  2. Sequence Alignment Algorithms:  - Pairwise sequence alignment (global and local alignment)  - Multiple sequence alignment (progressive and iterative methods)  - Scoring matrices (e.g., BLOSUM, PAM) and substitution models  3. Genome Assembly Algorithms:  - De novo genome assembly methods  - Overlapping, layout, and consensus stages in genome assembly  - Challenges in genome assembly (repeats, sequencing errors) and corresponding algorithms  4. Gene Expression Analysis:  - Preprocessing and normalization of gene expression data  - Differential expression analysis using statistical tests and fold change methods  - Clustering and visualization of gene expression profiles  5. Phylogenetic Analysis Algorithms:  - Phylogenetic tree construction using distance-based, parsimony, and maximum likelihood methods  - Evaluation of phylogenetic trees and bootstrapping techniques  - Molecular clock estimation and molecular phylogenetic  6. Protein Structure Prediction Algorithms:  - Homology modeling and comparative protein structure prediction  - Ab initio methods for protein structure prediction  - Protein structure alignment and comparison |

| **Learning and Teaching Strategies**  **استراتيجيات التعلم والتعليم** | |
| --- | --- |
| **Strategies** | Strategies in Bioinformatics Algorithms involve various approaches and techniques to effectively analyze biological data and apply algorithms. Here are some common strategies used in the field of bioinformatics:  1. Data Preprocessing and Quality Control:  - Perform data preprocessing steps to clean and normalize biological data, such as removing noise, correcting errors, and handling missing values.  - Apply quality control measures to ensure the reliability and accuracy of the data, including filtering out low-quality sequences or samples.  2. Algorithm Selection and Optimization:  - Evaluate and select appropriate algorithms based on the specific task and type of biological data being analyzed.  - Optimize algorithm parameters to achieve better performance and accuracy, such as adjusting alignment scoring parameters or optimization thresholds.  3. Parallel and Distributed Computing:  - Utilize parallel and distributed computing techniques to handle large-scale biological data sets and computationally intensive algorithms.  - Implement algorithms that can take advantage of multi-core processors, distributed computing clusters, or cloud computing resources for faster analysis. |

| **Student Workload (SWL)**  **الحمل الدراسي للطالب محسوب لـ ١٥ أسبوعا** | | | |
| --- | --- | --- | --- |
| **Structured SWL (h/sem)**  **الحمل الدراسي المنتظم للطالب خلال الفصل** | 64 | **Structured SWL (h/w)**  **الحمل الدراسي المنتظم للطالب أسبوعيا** | 4 |
| **Unstructured SWL (h/sem)**  **الحمل الدراسي غير المنتظم للطالب خلال الفصل** | 61 | **Unstructured SWL (h/w)**  **الحمل الدراسي غير المنتظم للطالب أسبوعيا** | 4 |
| **Total SWL (h/sem)**  **الحمل الدراسي الكلي للطالب خلال الفصل** | **125** | | |

| **Module Evaluation**  **تقييم المادة الدراسية** | | | | | |
| --- | --- | --- | --- | --- | --- |
|  | | **Time/Number** | **Weight (Marks)** | **Week Due** | **Relevant Learning Outcome** |
| **Formative assessment** | **Quizzes** | 2 | 10% (10) | 5 and 10 | LO #1, #2 and #10, #11 |
| **Assignments** | 2 | 10% (10) | 2 and 12 | LO #3, #4 and #6, #7 |
| **Projects / Lab.** | 1 | 10% (10) | Continuous | All |
| **Report** | 1 | 10% (10) | 13 | LO #5, #8 and #10 |
| **Summative assessment** | **Midterm Exam** | 2hr | 10% (10) | 7 | LO #1 - #5 |
| **Final Exam** | 3hr | 50% (50) | 16 | All |
| **Total assessment** | | | 100% (100 Marks) |  |  |

| **Delivery Plan (Weekly Syllabus)**  **المنهاج الاسبوعي النظري** | |
| --- | --- |
| **Week** | **Material Covered** |
| **Week 1** | Introduction to Bioinformatics |
| **Week 2** | Sequence Alignment Algorithms |
| **Week 3** | Genome Assembly Algorithms |
| **Week 4** | Gene Expression Analysis |
| **Week 5** | Phylogenetic Analysis Algorithms |
| **Week 6** | Protein Structure Prediction Algorithms |
| **Week 7** | Mid-term Exam |
| **Week 8** | Next-Generation Sequencing (NGS) Data Analysis |
| **Week 9** | Network Analysis in Bioinformatics |
| **Week 10** | Ethical Considerations in Bioinformatics |
| **Week 11** | Case Studies and Practical Applications |
| **Week 12** | Emerging Trends and Future Directions |
| **Week 13** | Exploration of emerging trends and advancements in bioinformatics algorithms |
| **Week 14** | Hands-on exercises and practical assignments using bioinformatics software and tools |
| **Week 15** | Review and discuss |

| **Delivery Plan (Weekly Lab. Syllabus)**  **المنهاج الاسبوعي للمختبر** | |
| --- | --- |
| **Week** | **Material Covered** |
| **Week 1** | Part 1: Sequence Alignment Algorithms |
| **Week 2** | Part 2: Sequence Alignment Algorithms |
| **Week 3** | Part 1: Genome Assembly Algorithms |
| **Week 4** | Part 2: Genome Assembly Algorithms |
| **Week 5** | Part 1: Protein Structure Prediction Algorithms |
| **Week 6** | Part 2: Protein Structure Prediction Algorithms |
| **Week 7** | Part 1: Next-Generation Sequencing (NGS) Data Analysis |
| **Week 8** | Part 2: Next-Generation Sequencing (NGS) Data Analysis |
| **Week 9** | Part 1: Network Analysis in Bioinformatics |
| **Week 10** | Part 2: Network Analysis in Bioinformatics |
| **Week 11** | Part 1: Ethical Considerations in Bioinformatics |
| **Week 12** | Part 2: Ethical Considerations in Bioinformatics |
| **Week 13** | Part 1: Case Studies and Practical Applications |
| **Week 14** | Part 2: Case Studies and Practical Applications |
| **Week 15** | Review and discuss |

| **Learning and Teaching Resources**  **مصادر التعلم والتدريس** | | |
| --- | --- | --- |
|  | **Text** | **Available in the Library?** |
| **Required Texts** | Salzberg, S. L. (2019). Bioinformatics: Introduction and Methods. CRC Press | No |
| **Recommended Texts** | Compeau, P., & Pevzner, P. (2018). Bioinformatics Algorithms: An Active Learning Approach. | No |

| **Grading Scheme**  **مخطط الدرجات** | | | | |
| --- | --- | --- | --- | --- |
| **Group** | **Grade** | **التقدير** | **Marks %** | **Definition** |
| **Success Group**  **(50 - 100)** | **A –** Excellent | **امتياز** | 90 - 100 | Outstanding Performance |
| **B -** Very Good | **جيد جدا** | 80 - 89 | Above average with some errors |
| **C –** Good | **جيد** | 70 - 79 | Sound work with notable errors |
| **D –** Satisfactory | **متوسط** | 60 - 69 | Fair but with major shortcomings |
| **E –** Sufficient | **مقبول** | 50 - 59 | Work meets minimum criteria |
| **Fail Group**  **(0 – 49)** | **FX –** Fail | **راسب (قيد المعالجة)** | (45-49) | More work required but credit awarded |
| **F –** Fail | **راسب** | (0-44) | Considerable amount of work required |
|  |  |  |  |  |
| **Note:** Marks Decimal places above or below 0.5 will be rounded to the higher or lower full mark (for example a mark of 54.5 will be rounded to 55, whereas a mark of 54.4 will be rounded to 54. The University has a policy NOT to condone "near-pass fails" so the only adjustment to marks awarded by the original marker(s) will be the automatic rounding outlined above. | | | | |