MODULE HANDBOOK
Biological Computing

MASTER DEGREE PROGRAM
DEPARTMENT OF MATHEMATICS
FACULTY OF SCIENCE AND DATA ANALYTICS
INSTITUT TEKNOLOGI SEPULUH NOPEMBER

MODULE HANDBOOK
BIOLOGICAL COMPUTING

Module name	**Biological Computing**	
Module level	Master	
Code	KM185374	
Course (if applicable)	Biological Computing	
Semester	Fall (Ganjil)	
Person responsible for the module	Prof. Dr. Mohammad Isa Irawan, M.T.	
Lecturer	Prof. Dr. Mohammad Isa Irawan, M.T.	
Language	Bahasa Indonesia and English	
Relation to curriculum	Master degree program, **mandatory**, 3rd semester.	
Type of teaching, contact hours	Lectures, <60 students	
Workload	1. Lectures : 2 x 50 = 100 minutes per week. 2. Exercises and Assignments : 2 x 60 = 120 minutes (2 hours) per week. 3. Private learning : 2 x 60 = 120 minutes (2 hours) per week.	
Credit points	3 credit points (sks)	
Requirements according to the examination regulations	A student must have attended at least 80% of the lectures to sit in the exams.	
Mandatory prerequisites	-	
Learning outcomes and their corresponding PLOs	Course Learning Outcome (CLO) after completing this module, [CLO-1] Students are able to explain the basic concepts of mutation and alignment and computational mathematical modeling approaches to solving problems therein. [CLO-2] Students are able to complete and compare the two-sequence alignment using an algorithmic approach based on dynamic programming [CLO-3] Students are able to recognize the weaknesses of the Needleman-Wunsch and Smith Waterman algorithms and explain alternative improvements for homologous sequences	

	[CLO-4] Students are able to compare several algorithms based on dynamic programming and stochastic models to solve multiple sequence alignment [CLO-5] Students are able to explain the mutation process modeling using a stochastic model approach [CLO-6] Students are able to explain the concept of modulus structure theory and relate it to sequence alignment [CLO-7] Students are able to explain the use of the Sequence Pairwise Alignment algorithm for the alignment of two sequences and compare it with the Dynamic Programming approach [CLO-8] Students are able to design phylogenetic tree structures to determine the closeness between sequences of several different species [CLO-9] Students are able to implement algorithms related to sequence analysis using opensource software and Matlab and are able to compare the results	
Content	Computer application issues are of growing importance in the field of bioinformatics and offer many challenges from a computational process point of view. In this course, students will gain the ability to formulate bioinformatics problems, especially sequence analysis into computational models and solve them with the help of software. In addition, students will learn several alternative solutions in sequence analysis. To deepen understanding, students will implement it with Matlab and use the concepts given to re-express and / or communicate ideas related to mathematics both in writing and orally with individual or group performance in teamwork. Topics discussed include solving the problem of sequence alignment, stochastic modeling for mutation analysis, super pairwise alignment and multiple alignment, and reconstruction of phylogenetic trees. The learning model is carried out through tutorials and discussions in the classroom / lab. Apart from being directed to learn independently through assignments, students are directed to work together in group work. Assessment of learning outcomes is done through written evaluation, independent assignments, and the ability to write and present the assignments given.	
Study and examination requirements and forms of examination	• In-class exercises • Assignment 1, 2, 3 • Mid-term examination • Final examination	
Media employed	LCD, whiteboard, websites (myITS Classroom), zoom.	
Reading list	Main :	

	1. Isaev, Alexander, “Introduction to Mathematical Methods in Bioinformatics”, Springer-Verlag, 2004 2. Shen, Shiyi Nankai, “Theory and Mathematical Methods for Bioinformatics”, Springer-Verlag, 2008 Supporting : 1. Ian Korf, Mark Yandell, Joseph Bedell, “Basic Local Alignment Search Tools” Oreilly, 2003