	Universitas Negeri Surabaya Faculty of Mathematics and Natural Sciences Chemistry Masters Study Program	Document Code

SEMESTER LEARNING PLAN

Courses	CODE	Course Family	Credit Weight			SEMESTER	Compilation Date
Bioinformatics	4710202029	Study Program Elective Courses	T=2	P=0	ECTS=4.48	3	July 19, 2023

AUTHORIZATION	SP Developer	Course Cluster Coordinator	Study Program Coordinator
	Muhammad Nurrohman Sidiq, Ph.D.	Prof. Dr. Nuniek Herdyastuti, M.Si.	Prof. Dr. Nuniek Herdyastuti, M.Si.

Learning model	**Case Studies**

Program Learning Outcomes (PLO)

PLO study program that is charged to the course	
PLO-2	Demonstrate the character of being tough, collaborative, adaptive, innovative, inclusive, lifelong learning and entrepreneurial spirit
PLO-3	Develop logical, critical, systematic and creative thinking in carrying out specific work in their field of expertise and in accordance with work competency standards in the field concerned
PLO-4	Develop yourself continuously and collaborate.
PLO-8	Compile and communicate ideas, thoughts and scientific arguments responsibly and based on academic ethics.
PLO-9	Make decisions in the context of solving scientific and technological development problems based on analytical or experimental studies of information and data.
PLO-14	Master theoretical concepts about the function of advanced chemical instruments and how to operate them, and master
Program Objectives (PO)	
PO - 1	Able to demonstrate basic knowledge of Bioinformatics to analyze contemporary biochemical problems
PO - 2	Able to master the use of bioinformatics tools to manage, analyze, interpret, document and store research data
PO - 3	Able to communicate scientific ideas, both verbally and in writing using targeted communication media, as a means of lifelong learning for academic self-development

PLO-PO Matrix

P.O	PLO-2	PLO-3	PLO-4	PLO-8	PLO-9	PLO-14
PO-1						
PO-2						
PO-3						

PO Matrix at the end of each learning stage (Sub-PO)

P.O	Week															
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
PO-1																
PO-2																
PO-3																

Short Course Description	This course discusses the basics of bioinformatics and its development as well as its relationship to discussions of biochemistry, BLAST analysis, DNA primer and tracer design, synthetic gene construction, nucleic acids both DNA and RNA, protein analysis related to the shape and arrangement of amino acids, protein topology analysis and molecular docking. which is delivered through guided discussions and practice by carrying out computational analysis.

References

Main :

1. Pervsner, J., 2015. , Bioinformatics and Functional Genomic, third edition, USA, Willey Blackwel.
2. Selzer, P.M., Marhover, R.J. dan Koch, O. 2018, Applied Bioinformatics, Germany, Springer International Publishing
3. Taguchi, 2020, Unsupervised Feature Extraction Applied to Bioinformatics: A PCA Based and TD Based Approach, Tokyo, Springer
4. Bedel, J. Korf, I, dan Yandell, M, BLAST, USA, OReilly

Supporters:

Supporting lecturer	Prof. Dr. Nuniek Herdyastuti, M.Si. Muhammad Nurrohman Sidiq, S.Si., M.Sc., Ph.D.

Week-	Final abilities of each learning stage (Sub-PO)	Evaluation		Help Learning, Learning methods, Student Assignments, [Estimated time]		Learning materials [References]	Assessment Weight (%)
		Indicator	Criteria & Form	Offline (*offline*)	Online (*online*)		
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
1	Understand the basics of bioinformatics, its development and role	1. Explain the definition of Bioinformatics 2. Explain the history and development of Bioinformatics 3. Explain how to find scientific articles and data on a gene or topic of interest 4. Explain the genomic basics of Bioinformatics 5. Use common genomic tools 6 . Identify the gene of interest	**Form of Assessment** : Participatory Activities	Discussion, Guided discovery		**Material:** Introduction to bioinformatics **References:** *Pervsner, J., 2015. , Bioinformatics and Functional Genomics, third edition, USA, Willey Blackwel.*	5%
2	Understand the basics of biochemical science from bioinformatics	1. Explain the basic structure of DNA and RNA 2. Explain the storage of genetic information at the molecular level 3. Understand the structure of nucleic acids (DNA and RNA) further 4. Explain how genetic information is stored 5. Explain the primary, tertiary, secondary and quaternary structures of proteins 6. Explain the differences between Genomics, Transcriptomics and Proteomics, Metabolomics and Multi-omics	**Form of Assessment** : Participatory Activities			**Material:** Introduction to bioinformatics and multiomics **References:** *Pervsner, J., 2015. , Bioinformatics and Functional Genomics, third edition, USA, Willey Blackwel.*	5%
3	Understanding primary databases	1. Explain the global storage database of Biological information. 2. Explain the differences between primary and secondary databases 3. Explain genotype-phenotype databases 4. Explain molecular structure databases	**Form of Assessment** : Participatory Activities, Practice/Performance	Discussion, Guided discovery		**Material:** primary database **References:** *Pervsner, J., 2015. , Bioinformatics and Functional Genomics, third edition, USA, Willey Blackwel.*	5%
4	Understand secondary databases and genotype-phenotype databases	1. Prosite 2. PRINTS 3. Pfam 4. Interpo 5. PhenomicDB	**Form of Assessment** : Participatory Activities, Practice/Performance	Discussion, Guided discovery		**Material:** Practice of using databases **Bibliography:** *Selzer, PM, Marhover, RJ and Koch, O. 2018, Applied Bioinformatics, Germany, Springer International Publishing*	6%
5	Understand how to use molecular structure databases	1. Protein Data Bank 2. SCOP 3. CATH 4. PubChem	**Form of Assessment** : Participatory Activities	Discussion, Guided discovery		**Material:** Practice of using databases **References:** *Taguchi, 2020, Unsupervised Feature Extraction Applied to Bioinformatics: A PCA Based and TD Based Approach, Tokyo, Springer*	5%

6	Understand sequence comparison and sequence-based database searching	1. Know pairwise and multiple sequence comparisons 2. Search for nucleotide and protein sequences from databases 3. Understand the use of software for sequence analysis	**Form of Assessment** : Participatory Activities	Discussion , Guided discovery		**Material:** Practice of using databases **References:** *Taguchi, 2020, Unsupervised Feature Extraction Applied to Bioinformatics: A PCA Based and TD Based Approach, Tokyo, Springer*	5%
7	Understand how eukaryotic genomes are broken down	1. Understand how to sequence a whole genome 2. Be able to perform characterization using STS and EST sequences 3. Implement an EST project 4. Identify unknown genes 5. Find splice variants	**Form of Assessment** : Participatory Activities	Discussion		**Material:** BLAST Practice **Bibliography:** *Pervsner, J., 2015. , Bioinformatics and Functional Genomics, third edition, USA, Willey Blackwel.*	5%
8	UTS		**Form of Assessment** : Test				10%
9	Understanding the genetic causes of individual diversity	1. Knowing Pharmacogenetics 2. Personalized medicine and biomarkers 3. Next-generation Sequencing (NGS) 4. Proteogenomics	**Form of Assessment** : Participatory Activities, Practice/Performance	Discussion		**Material:** Pharmacogenomics and Precision Medicine **Bibliography:** *Selzer, PM, Marhover, RJ and Koch, O. 2018, Applied Bioinformatics, Germany, Springer International Publishing*	5%
10	Understanding rational drug design based on drug structure and protein structure	1. Explain the structure of proteins 2. Explain transmembrane proteins 3. Analyze protein structures with Alphafold (AI) 4. Design drug designs based on structure	**Form of Assessment** : Participatory Activities	Discussion		**Material:** rational drug design **Bibliography:** *Selzer, PM, Marhover, RJ and Koch, O. 2018, Applied Bioinformatics, Germany, Springer International Publishing*	5%
11	Understand functional genomic analysis		**Form of Assessment** : Participatory Activities	Discussion, guided discovery		**Material:** Multiomic analysis **References:** *Bedel, J. Korf, I, and Yandell, M, BLAST, USA, OReilly*	5%
12		1. Explain genomic sequencing 2. Explain drug research from the perspective of target proteins 3. Explain comparative genomic analysis related to organisms 4. Carry out comparative analysis of metabolites	**Form of Assessment** : Participatory Activities	Discussion, Guided discovery		**Material:** comparative genomic analysis **References:** *Pervsner, J., 2015. , Bioinformatics and Functional Genomics, third edition, USA, Willey Blackwel.*	5%
13	Analyze genomics with database-linked demonstrations	Carry out database-related demonstrations according to the topic at meetings 1-4	**Forms of Assessment** : Participatory Activities, Project Results Assessment / Product Assessment, Practices / Performance	Guided discussion and discovery		**Material:** demonstration **Bibliography:** *Selzer, PM, Marhover, RJ and Koch, O. 2018, Applied Bioinformatics, Germany, Springer International Publishing*	8%
14	Analyzing transcriptomics and proteomics with demonstrations related to protein databases	Carry out a demonstration of the protein database according to meeting material 5-7	**Form of Assessment** : Participatory Activities	Guided Discussion and Discovery		**Material:** demonstration **Bibliography:** *Selzer, PM, Marhover, RJ and Koch, O. 2018, Applied Bioinformatics, Germany, Springer International Publishing*	8%

15	Perform a demonstration of multiomics analysis	Carry out demonstrations related to multiomics analysis according to the material provided at meetings 9-12	**Form of Assessment** : Participatory Activities			**Material:** demonstration **References:** *Taguchi, 2020, Unsupervised Feature Extraction Applied to Bioinformatics: A PCA Based and TD Based Approach, Tokyo, Springer*	8%
16	UAS		**Form of Assessment** : Test				10%

Evaluation Percentage Recap: Case Study

No	Evaluation	Percentage
1.	Participatory Activities	66.67%
2.	Project Results Assessment / Product Assessment	2.67%
3.	Practice / Performance	10.67%
4.	Test	20%
		100%

Notes

1. **Learning Outcomes of Study Program Graduates (PLO - Study Program)** are the abilities possessed by each Study Program graduate which are the internalization of attitudes, mastery of knowledge and skills according to the level of their study program obtained through the learning process.
2. **The PLO imposed on courses** are several learning outcomes of study program graduates (CPL-Study Program) which are used for the formation/development of a course consisting of aspects of attitude, general skills, special skills and knowledge.
3. **Program Objectives (PO)** are abilities that are specifically described from the PLO assigned to a course, and are specific to the study material or learning materials for that course.
4. **Subject Sub-PO (Sub-PO)** is a capability that is specifically described from the PO that can be measured or observed and is the final ability that is planned at each learning stage, and is specific to the learning material of the course.
5. **Indicators for assessing** ability in the process and student learning outcomes are specific and measurable statements that identify the ability or performance of student learning outcomes accompanied by evidence.
6. **Assessment Criteria** are benchmarks used as a measure or measure of learning achievement in assessments based on predetermined indicators. Assessment criteria are guidelines for assessors so that assessments are consistent and unbiased. Criteria can be quantitative or qualitative.
7. **Forms of assessment:** test and non-test.
8. **Forms of learning:** Lecture, Response, Tutorial, Seminar or equivalent, Practicum, Studio Practice, Workshop Practice, Field Practice, Research, Community Service and/or other equivalent forms of learning.
9. **Learning Methods:** Small Group Discussion, Role-Play & Simulation, Discovery Learning, Self-Directed Learning, Cooperative Learning, Collaborative Learning, Contextual Learning, Project Based Learning, and other equivalent methods.
10. **Learning materials** are details or descriptions of study materials which can be presented in the form of several main points and sub-topics.
11. **The assessment weight** is the percentage of assessment of each sub-PO achievement whose size is proportional to the level of difficulty of achieving that sub-PO, and the total is 100%.
12. TM=Face to face, PT=Structured assignments, BM=Independent study.