



KEMENTERIAN RISET, TEKNOLOGI, DAN PENDIDIKAN TINGGI
UNIVERSITAS BRAWIJAYA
FAKULTAS KEDOKTERAN
PROGRAM MAGISTER ILMU BIOMEDIK

Jalan Veteran, Malang 65145, Jawa Timur – Indonesia
 Telp. (62)(341) 569117; 567192 Pes. 134, 135 – Fax. (62)(341) 564755
 E-mail: sekr.fk@ub.ac.id Website: <http://biomedical.fk.ub.ac.id>

Teaching Plan

Course Title : Bioinformatics in Biomedical Fields
Course Code : DKF6216
Credits : 2
Course Coordinator : Widodo, M.Si., Ph.D.Med.Sc. (Phone no. 081230017307)

Course Description

This course was designed with overall goal is to introduce students to the comprehensive knowledge of bioinformatics in the biomedical field. Topics previously covered in the earlier biomedical field will be expanded and placed in the context of analyzing big data and information of the living organism *in silico*. The key objective is to understand and be able to apply concepts rather than merely memorize information. Subject areas covered include bioinformatics and its clinical implication, bioinformatics workflow, protein structure, 2D and 3D of protein structure prediction, interaction between two molecule, vaccine design and antigenicity prediction, Immunogenicity and peotope mapping, molecular docking software utilization, binding affinity, ligand-receptor analysis with DS and ligplot, genome database, identification of polymorphism (SNPs and haplotype), primer designing, finding gene and gene function, sequence alignment, sequence similarity prediction, DNA Barcoding, microarray data analysis, gene pathways analysis, RNA database, RNA structure prediction, siRNA design, protein database, protein function prediction, protein classification, and the implementation of bioinformatics for drug discovery and development.

Course Learning Outcomes

On successful completion of this course students will (be):		Bloom's Taxonomy
CLO1	Demonstrate a comprehensive understanding of bioinformatics and its clinical implications, also bioinformatic workflow.	Level 2. Understanding
CLO2	Demonstrate a comprehensive understanding of protein structure; genome database; sequence alignment; DNA barcoding; RNA database; and the use of bioinformatics for drug discovery and development.	Level 2. Understanding
CLO3	Able to apply bioinformatics to predict 2D and 3D of protein structure; analyse interaction between two molecules, its energy and stability; predict antigenicity, immunogenicity and peotope mapping; analyse binding affinity of two molecules; analyse ligand-receptor; analyse the database for identifying polymorphisms (SNPs and haplotype) and designing primer; analyse microarray data; analyse gene pathways; predict RNA structure and design siRNA; predict protein function and classification; and perform sequence alignment to predict sequence similarity and apply it in biomedical field.	Level 3. Applying

Alignment between CLOs and PLOs

	PLO1.1	PLO1.2	PLO2.1	PLO2.2	PLO2.3	PLO3.1	PLO3.2	PLO3.3	PLO3.4	PLO4
CLO1	√	√								
CLO2	√	√								
CLO3					√					

Topics and Schedule

Week	Topics	Competencies	Lecturers
1.	Introduction 1. From data to knowledge: the aim of bioinformatics 2. Information flows in bioinformatics 3. Curation, annotation and quality control 4. Clinical implications	Able to explain: bioinformatics and its clinical implications, also bioinformatic workflow.	WI
2.	Protein structure 1. Protein folding and stability 2. Protein properties	Able to explain: protein structure and proficient in predicting 2D and 3D of protein structure by using	WI



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	<ol style="list-style-type: none"> 3. Predict structure 2d 4. Predict structure 3d 5. Superposition structure 6. Structure alignments 7. Classification of protein structures 8. Predict protein function 	bioinformatic tools.	
3.	Molecule interaction and molecular dynamic	Able to analyse interaction between two molecules; its energy and stability	WI
4.	Vaccine design <ol style="list-style-type: none"> 1. Antigenicity analysis 2. Immunogenicity analysis 3. Epitope mapping 	Able to explain: how to use bioinformatic to design vaccine and proficient to predict antigenicity, immunogenicity and peotope mapping.	WI
5.	Molecular docking and analysis of ligand-receptor	Able to use molecular docking software to analyse binding affinity of two molecules; able to use DS and ligplot to analyse ligand-receptor.	WI
6.	Genome Database and information retrieval <ol style="list-style-type: none"> 1. Genome on the web 2. Genome of Prokaryotes 3. Genome of eukaryote 4. The Human Genome 5. SNPs and Haplotypes 6. Genetic diversity and personal identification 7. Evolution of Genome 8. Comparative Genomics of Eukaryote (ENCODE) 	Able to explain: genome database and proficient in analysing the database for identifying polymorphysm (SNPs and haplotype)	EW
7.	Genome Database and information retrieval <ol style="list-style-type: none"> 1. Metagenomics analysis 2. Gene finding and structure 3. Polymorphism identification 4. Primer design 	Able to explain: genome database and proficient to design primer and to find gene structure & function	EW
8.	Mid-term Exam		TEAM
9.	Sequence alignments <ol style="list-style-type: none"> 1. Measures of sequence similarity 2. Computing the alignment of two sequences 3. Multiple sequence alignment 4. Application of multiple sequence alignments to database searching 	Able to explain: sequence alignment and proficient in performing sequence alignment to predict sequence similarity and apply it in biomodical field.	EW
10.	DNA Barcoding	Able to explain: DNA Barcoding	EW
11.	Proteomic and system biology <ol style="list-style-type: none"> 1. Analysis DNA microarray data 2. Protein interaction networks 3. Networks and pathways analysis 4. Biomarker analysis 	Able to explain: how to use bioinformatics to analyse microarray data and proficient to analyse gene pathways	DL
12.	RNA Database and Retrieval <ol style="list-style-type: none"> 1. Predicting and modeling RNA structure 2D 2. Finding RNAs in genome: mRNA, miRNA, and siRNA 3. Designing siRNA 	Able to explain: RNA database and proficient in predicting RNA structure and designing siRNA	DL
13.	Protein Database and Information Retrieval <ol style="list-style-type: none"> 1. Database of protein family 2. Database of protein structure 3. Classification of protein structure 4. Accuracy and precision of protein structure determinations 5. Classification and assignment of protein 	Able to explain: protein database and proficient in predicting protein function, protein clasification, protein function from the database	DL



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	function 6. The Protein Identification Resource 7. Expert Protein Analysis System 8. Protein motif and function		
14.	Drug discovery and development 1. The lead compound 2. Identification molecule target 3. Interaction between ligand and receptor	Able to explain: how to use bioinformatics for drug discovery and development	DL
15.	Final Examination		TEAM

Lecturers:

WI : Widodo, M.Si., Ph.D.Med.Sc. (0341-3140691)
EW : Edwin Widodo, S.Si., M.Sc. (082234608052)
DL : Diana Lyrawati, Dra., Apt., MS., Ph.D. (08179640968)

Teaching and Learning Strategy

Core material will be delivered through lectures and/or online delivery systems.

Assessment Methods

Type	Weighting	CLO Assessed	Description
Written exam (mid)	50%	1, 2	The examination will be a 2-hour unseen paper with questions on theoretical aspects of bioinformatics.
Written exam (final)	50%	1, 2, 3	

Learning Sources

Essential reading/resources	Bioinformatics: Sequence and Genome Analysis, 2nd edition, by David W. Mount. Publisher: Cold Spring Harbor Press
Further reading/resources	1. An Introduction to Bioinformatics Algorithms by Neil C Jones and Pavel Pevzner. Publisher: The MIT Press. 2. Introduction to Bioinformatics by Arthur M Lesk. Publisher: Oxford University Press. 3. Scientific Journals (Nature Bioinformatics, Nature Protocols)

Course Coordinator,

Widodo, M.Si., Ph.D.Med.Sc.