

MODULE HANDBOOK

INTRODUCTION TO STATISTICAL BIOINFORMATICS



**STATISTICS UNDERGRADUATE PROGRAM
DEPARTMENT OF STATISTICS
FACULTY OF SCIENCE AND DATA ANALYTICS
INSTITUT TEKNOLOGI SEPULUH NOPEMBER
SURABAYA**

ENDORSEMENT PAGE



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INTRODUCTION TO STATISTICAL
BIOINFORMATICS
STATISTICS UNDERGRADUATE PROGRAM
DEPARTMENT OF STATISTICS
INSTITUT TEKNOLOGI SEPULUH NOPEMBER**

Proses <i>Process</i>	Penanggung Jawab <i>Person in Charge</i>			Tanggal <i>Date</i>
	Nama <i>Name</i>	Jabatan <i>Position</i>	Tanda tangan <i>Signature</i>	
Perumus <i>Preparation</i>	Shofi Andari, Ph.D	Dosen Lecturer		
Pemeriksa dan Pengendalian <i>Review and Control</i>	Shofi Andari, Ph.D.; Santi W. Purnami, Ph.D.	Tim kurikulum Curriculum team		
Persetujuan <i>Approval</i>	Dr. Bambang Widjanarko Otok, M.Si	Koordinator RMK Course Cluster Coordinator		
Penetapan <i>Determination</i>	Dr. Kartika Fithriasari, M.Si	Kepala Departemen Head of Department		

MODULE HANDBOOK

INTRODUCTION TO STATISTICAL BIOINFORMATICS

Module name	INTRODUCTION TO STATISTICAL BIOINFORMATICS	
Module level	Undergraduate	
Code	SS234755	
Course (if applicable)	INTRODUCTION TO STATISTICAL BIOINFORMATICS	
Semester	7	
Person responsible for the module	Shofi Andari, Ph.D	
Lecturer	Shofi Andari, Ph.D.; Santi W. Purnami, Ph.D.	
Language	Bahasa Indonesia and English	
Relation to curriculum	Undergraduate degree program, elective, 7th semester.	
Type of teaching, contact hours		
Workload	1. Lectures [L] : 3 x 50 = 150 minutes per week. 2. Exercises and Assignments [EA] : 3 x 60 = 180 minutes (3 hours) per week. 3. Independent learning [IL]: 3 x 60 = 180 minutes (3 hours)perweek.	
Credit points	3 credit points (SKS) Equivalent to 4.8 ECTS	
Requirements according to the examination regulations	A student must have attended at least 80% of the lectures to sit in the exams.	
Mandatory prerequisites	Computational Statistics; Stochastics Process; Applied Multivariate Analysis	
Learning outcomes and their corresponding PLOs	CLO – 1 Mastering the general concept of central dogma in biology, biological data, and being able to determine the necessary database sources for different types of biological problems. CLO – 2 Able to formulate biological problems in the context of probability and its distributions. CLO – 3 Be able to determine statistical methods that can be applied in the context of biological problems. CLO – 4 Able to apply statistical software to solve bioinformatics problems.	PLO-4 PLO-5 PLO-7 PLO-10
Content	This course introduces bioinformatics in the context of statistical methods that are commonly used in biological research. The emphasis in this course is bioinformatics understanding biological data and databases, and using statistical methods in the context of microarray and omics data so that students can appropriately analyze a high-throughput study. The first half of this course reviews basic	

	genetics, the concept of central dogma in biology, biological databases and how data are collected. Next, students will learn the principle behind statistical methods they have learned and how they can be applied to analyze biological sequences and data.
Assessment and its weight	Assignment & Test I – 20% Midterm Exam – 30% Assignment & Test II – 20% Final Exam– 30%
Media employed	LCD, whiteboard, websites (myITS Classroom), zoom
Reading list	<ol style="list-style-type: none"> 1. Ewens, WJ & Grant, GR. 2005. Statistical Methods in Bioinformatics: An Introduction, 2nd Ed. <i>Springer</i>. 2. Nettleton, D & Datta, S. 2014. Statistical Analysis of Next Generation Sequencing Data. Springer. 3. Krijnen, WP. 2009. Applied Statistics for Bioinformatics using R. 4. Mathur, SK. 2010. Statistical Bioinformatics with R. Elsevier. 5. Zvelebil, M & Baum, JO. 2008. Understanding Bioinformatics. Garland Science, Taylor & Francis Group, LLC. 6. Neapolitan, RE. 2009. Probabilistic Methods for Bioinformatics. Elsevier.



INSTITUT TEKNOLOGI SEPULUH NOPEMBER
FAKULTAS SAINS DAN ANALITIKA DATA
PROGRAM STUDI SARJANA STATISTIKA
DEPARTEMEN STATISTIKA

Kode Dokumen

RENCANA PEMBELAJARAN SEMESTER/
SEMESTER LEARNING PLAN

MATA KULIAH (MK)/ <i>Course</i>	KODE/ <i>Code</i>	Rumpun MK/ <i>Course Group</i>	BOBOT (sks)/ <i>Weight (credit)</i>		SEMESTER/ <i>Semester</i>	Tgl Penyusunan/ <i>Drafting Date</i>
PENGANTAR STATISTIKA BIOINFORMATIK / <i>INTRODUCTION TO STATISTICAL BIOINFORMATICS</i>	SS234755	LINGKES	T=3	P=0	III	18 Januari 2022
OTORISASI/ <i>AUTHORIZATION</i>	Pengembang RPS/ <i>RPS Developer</i>		Koordinator RMK/ <i>Course Group Coordinator</i>		Ketua PRODI/ <i>Head of Department</i>	
	Shofi Andari, Ph.D.; Santi W. Purnami, Ph.D.		Santi W. Purnami, Ph.D.		Dr. Kartika Fithriasari, M.Si	
Capaian Pembelajaran (CP)/ <i>Learning Achievement</i>	CPL-PRODI yang dibebankan pada MK/ <i>PLO</i>					
	CPL-4	Mampu menerapkan Sains dan Matematika untuk mendukung pemahaman metode statistika				
	CPL-5	Mampu menerapkan teori statistika pada metode statistika				
	CPL-7	Mampu menggunakan perangkat komputasi modern untuk menyelesaikan permasalahan statistik				
	CPL-10	Mampu menerapkan metode statistika Bisnis, Industri, Ekonomi, Sosial, Kesehatan, atau Lingkungan pada permasalahan riil				
	<i>PLO-4</i>	<i>Able to apply Science and Mathematics to support the understanding of statistical methods.</i>				
	<i>PLO-5</i>	<i>Able to apply statistical theory to statistical methods.</i>				
	<i>PLO-7</i>	<i>Able to use modern computing devices to solve statistical problems.</i>				
	<i>PLO-10</i>	<i>Able to apply business, industrial, economic, social, health or environmental statistical methods to real problems</i>				
	Capaian Pembelajaran Mata Kuliah (CPMK)/ <i>CLO</i>					
	CPMK-1 Menguasai konsep umum <i>central dogma</i> dalam biologi, data biologi, dan mampu menentukan sumber database yang diperlukan					

	<p>untuk jenis-jenis permasalahan biologi yang berbeda.</p> <p>CPMK-2 Mampu merumuskan permasalahan biologi dalam konteks probabilitas dan distribusi-distribusinya.</p> <p>CPMK-3 Mampu menentukan metode statistika yang dapat diaplikasikan dalam konteks permasalahan biologi.</p> <p>CPMK-4 Mampu mengaplikasikan perangkat lunak statistika untuk menyelesaikan problem bioinformatika.</p> <p><i>CLO – 1 Mastering the general concept of central dogma in biology, biological data, and being able to determine the necessary database sources for different types of biological problems.</i></p> <p><i>CLO – 2 Able to formulate biological problems in the context of probability and its distributions.</i></p> <p><i>CLO – 3 Be able to determine statistical methods that can be applied in the context of biological problems.</i></p> <p><i>CLO – 4 Able to apply statistical software to solve bioinformatics problems.</i></p>																									
	<p>Matrik CPL – CPMK <i>PLO-CLO Matrix</i></p> <table border="1"> <thead> <tr> <th></th> <th>CPL-4</th> <th>CPL-5</th> <th>CPL-7</th> <th>CPL-10</th> </tr> </thead> <tbody> <tr> <td>CPMK-1</td> <td>v</td> <td></td> <td></td> <td></td> </tr> <tr> <td>CPMK-2</td> <td>v</td> <td>v</td> <td></td> <td>v</td> </tr> <tr> <td>CPMK-3</td> <td></td> <td>v</td> <td>v</td> <td>v</td> </tr> <tr> <td>CPMK-4</td> <td></td> <td></td> <td>v</td> <td>v</td> </tr> </tbody> </table>		CPL-4	CPL-5	CPL-7	CPL-10	CPMK-1	v				CPMK-2	v	v		v	CPMK-3		v	v	v	CPMK-4			v	v
	CPL-4	CPL-5	CPL-7	CPL-10																						
CPMK-1	v																									
CPMK-2	v	v		v																						
CPMK-3		v	v	v																						
CPMK-4			v	v																						
<p>Deskripsi Singkat MK/ <i>Course Description</i></p>	<p>Mata kuliah ini memperkenalkan bioinformatika dalam konteks metode statistik yang umum digunakan dalam penelitian biologi. Penekanan dalam kursus ini adalah bioinformatika dalam memahami data biologis, basis data, dan bagaimana penggunaan metode statistik dalam konteks microarray dan data omics sehingga mahasiswa dapat menganalisis throughput studi yang tinggi dengan tepat. Paruh pertama mata kuliah ini mengulas mengenai genetika dasar, konsep dogma sentral dalam biologi, basis data biologis, dan bagaimana data dikumpulkan. Selanjutnya, mahasiswa akan mempelajari prinsip di balik metode statistik yang telah mereka pelajari dan bagaimana penerapannya untuk menganalisis sekuens dan data biologis</p> <p><i>This course introduces bioinformatics in the context of statistical methods that are commonly used in biological research. The emphasis in this course is bioinformatics understanding biological data and databases, and using statistical methods in the context of microarray and omics data so that students can appropriately analyze a high-throughput study. The first half of this course reviews basic genetics, the concept of central dogma in biology, biological databases and how data are collected. Next, students will learn the principle behind statistical methods they have learned and how they can be applied to analyze biological sequences and data.</i></p>																									
<p>Bahan Kajian: Materi</p>	<p>Dasar Sains, Teori Statistika, Deskripsi dan Eksplorasi, Komputasi dan Data Processing, dan Pemodelan <i>Basic Science, Statistical Theory, Description and Exploration, Computation and Data Processing, and Modeling</i></p>																									

Pembelajaran/ Course Material							
Pustaka/ References		Utama/Primary:					
		1. Ewens, WJ & Grant, GR. 2005. <i>Statistical Methods in Bioinformatics: An Introduction</i> , 2 nd Ed. <i>Springer</i> .					
		Pendukung/Secondary :					
		1. Nettleton, D & Datta, S. 2014. <i>Statistical Analysis of Next Generation Sequencing Data</i> . <i>Springer</i> . 2. Krijnen, WP. 2009. <i>Applied Statistics for Bioinformatics using R</i> . 3. Mathur, SK. 2010. <i>Statistical Bioinformatics with R</i> . <i>Elsevier</i> . 4. Zvelebil, M & Baum, JO. 2008. <i>Understanding Bioinformatics</i> . <i>Garland Science, Taylor & Francis Group, LLC</i> . 5. Neapolitan, RE. 2009. <i>Probabilistic Methods for Bioinformatics</i> . <i>Elsevier</i> .					
Dosen Pengampu/ Lecturers		Shofi Andari, Ph.D.; Santi W. Purnami, Ph.D.					
Matakuliah syarat/ Pre-requisite Course		Komputasi statistika; Proses Stokastik; Analisis Multivariat Terapan <i>Computational Statistics; Stochastics Process; Applied Multivariate Analysis</i>					
Mg Ke- Week	Kemampuan akhir tiap tahapan belajar (Sub-CPMK) <i>Final capability for each learning step</i>	Penilaian <i>Evaluation</i>		Bantuk Pembelajaran, Metode Pembelajaran, Penugasan Mahasiswa, [Estimasi Waktu] <i>Learning Format Learning Methods Assignment for Student [Estimated Time]</i>		Materi Pembelajaran [Pustaka] <i>Learning Material [References]</i>	Bobot Penilaian (%) <i>Evaluation Weight (%)</i>
		Indikator <i>Indicator</i>	Kriteria & Bentuk <i>Criteria and Format</i>	Luring <i>Offline</i>	Daring <i>Online</i>		
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
1 dan 2	Mampu menjelaskan	a. Dapat menjelaskan	Tugas 1, tes	Ceramah, diskusi		- Bioinformatika dan	5%

	<p>peran statistika dalam bioinformatika dan prinsip dasar genetika, khususnya <i>central dogma</i></p> <p><i>Be able to explain the role of statistics in bioinformatics and the basic principles of genetics, especially the central dogma</i></p>	<p>mengapa dan bagaimana statistika berperan penting dalam bioinformatika</p> <p>b. Dapat menjelaskan mengenai konsep central dogma dalam biologi</p> <p><i>a. Can explain why and how statistics play an important role in bioinformatics</i></p> <p><i>b. Can explain the concept of central dogma in biology</i></p>	<p>tulis, observasi di kelas</p> <p><i>Task 1, written test, observation in class</i></p>	<p>dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p> <p>TM: 2 x 3 x 50" LT: 2 x 3 x 60" BM: 2 x 3 x 60"</p>		<p>peranan statistika dalam di dalamnya (Xiong2006, Chapter 1; Neapolitan2009, Chapter 1; Lee2010, Chapter1; Mathur2010, Chapter 1)</p> <ul style="list-style-type: none"> - Terminologi dalam biologi yang perlu diketahui (Can2013) + central dogma dalam biologi - Sekilas mengenai dasar genetika (Neapolitan2009, Chapter 4) - Dunia asam nukleik (Xvelebil2008, Chapter 1) - Dunia asam amino/protein (Zvelebil2008, Chapter 2) - <i>Bioinformatics and the role of statistics within it</i> (Xiong2006, Chapter 1; Neapolitan2009, Chapter 1; Lee2010, Chapter1; Mathur2010, Chapter 1) - <i>Terminology in biology that you need to know</i> (Can2013) + central dogma in biology - <i>Overview of the genetic basis</i> (Neapolitan2009, Chapter 4) - <i>The world of nucleic acids</i> (Xvelebil2008, Chapter 1) - <i>The world of amino acids/proteins</i> (Zvelebil2008, Chapter 2) 	
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3	<p>Dapat mengaplikasikan paket-paket dan fungsi-fungsi R yang relevan dengan problem bioinformatika sederhana</p> <p><i>Able to apply R packages and functions that are relevant to simple bioinformatics problems</i></p>	<p>a. Dapat menerangkan penggunaan uji chi-square dalam tabulasi data biologi.</p> <p><i>a. Can explain the use of the chi-square test in the tabulation of biological data.</i></p>	<p>Tugas 2, tes tulis, observasi di kelas</p> <p><i>Task 2, written test, observation in class</i></p>	<p>Ceramah, diskusi dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p> <p>TM: 3 x 50" LT: 3 x 60" BM: 3 x 60"</p>	<ul style="list-style-type: none"> - Tabulasi data dalam genetika (contoh: menggunakan chi-square test), replikasi DNA dan DNA rearrangements, transcription dan translations, kode genetic, sintesis protein (Ewens2005, hal. 132; Mathur2010, Chapter 1) - R-Bioconductor (Lee2010, Chapter 13) - <i>Tabulation of data in genetics (e.g. using chi-square test), DNA replication and DNA rearrangements, transcription and translations, genetic code, protein synthesis (Ewens2005, p. 132; Mathur2010, Chapter 1)</i> - <i>R -Bioconductor (Lee2010, Chapter 13)</i> 	5%
4 dan 5	<p>Mampu menjelaskan mengenai teknologi <i>microarray</i> dan <i>gene expression</i></p> <p><i>Able to explain about microarray technology and gene expression</i></p>	<p>a. Dapat menjelaskan bagaimana data diperoleh</p> <p>b. Dapat mengeksplorasi data <i>microarray</i></p> <p>c. Dapat menjelaskan masalah <i>differential expression</i> dan metode statistika yang relevan untuk</p>	<p>Tugas 3, tes tulis, observasi di kelas</p> <p><i>Task 3, written test, observation in class</i></p>	<p>Ceramah, diskusi dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p> <p>TM: 2 x 3 x 50" LT: 2 x 3 x 60" BM: 2 x 3 x 60"</p>	<ul style="list-style-type: none"> - Bagaimana data diperoleh, apa masalah-masalah yang biasanya diangkat dalam teknologi <i>microarray</i>, <i>gene expression</i>, dan <i>proteomics</i> (Lee2010, Chapter3.3; Mathur 2010, Chapter 2; Ewens2004, Chapter 2013; Zvelebil2008, Chapter 15) - Eksplorasi data <i>microarray</i> (Krijnen2009, Chapter 6) 	5%

		<p>menentukan solusinya</p> <p>a. <i>Can explain how the data was obtained</i></p> <p>b. <i>Can explore micro - array data</i></p> <p>c. <i>Can explain differential expression problems and relevant statistical methods to determine the solution</i></p>				<p>- <i>How the data was obtained, what are the issues usually raised in microarray technology, gene expression, and proteomics (Lee2010, Chapter 3.3; Mathur 2010, Chapter 2; Ewens 2004, Chapter 2013; Zvelebil 2008, Chapter 15)</i></p> <p>- <i>Exploration of microarray data (Krijnen2009, Chapter 6)</i></p>	
6	<p>Mampu mengakses, mengeksplorasi dan menjelaskan data yang dihasilkan dari teknologi <i>next generation sequencing</i> (NGS)</p> <p><i>Able to access, explore and explain data generated from next generation sequencing (NGS) technology</i></p>	<p>a. Dapat menjelaskan proses <i>sequencing</i> DNA secara umum</p> <p>b. Dapat mengidentifikasi beberapa macam problem dan analisis statistika dalam data yang dihasilkan NGS</p> <p>a. <i>Can explain the process of DNA sequencing in general</i></p> <p>b. <i>Can identify various kinds of problems and statistical analysis in the data generated by NGS</i></p>	<p>Tugas 4, tes tulis, observasi di kelas</p> <p><i>Task 4, written test, observation in class</i></p>	<p>Ceramah, diskusi dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p> <p>TM: 3 x 50" LT: 3 x 60" BM: 3 x 60"</p>		<p>- Sejarah teknologi DNA sekuens, apa yang terjadi saat DNA fragment disekuens dalam mesin Illumina, <i>long</i> dan <i>short read technologies</i></p> <p>- <i>History of DNA sequencing technology, what happens when DNA fragments are sequenced in the Illumina machine, long and short read technologies</i></p>	5%
7	<p>Mampu menjelaskan macam-macam database dan format data</p>	<p>a. Dapat menerangkan proses dari menguduh data lewat <i>bash</i></p>	<p>Tugas 4, tes tulis, observasi di kelas</p>	<p>Ceramah, diskusi dan latihan soal</p>		<p>- Preprocessing data dengan R, quality reporting dengan FastQC</p>	10%

	<i>Able to explain the various databases and data formats</i>	<p>command dan/atau R.</p> <p>b. Dapat melakukan preprocessing, reporting dan visualisasi data</p> <p>a. <i>Can explain the process of downloading data via bash command and/or R.</i></p> <p>b. <i>Able to do preprocessing, reporting and data visualization</i></p>	<i>Task 4, written test, observation in class</i>	<p><i>Lectures, discussions, and exercise</i></p> <p>TM: 3 x 50" LT: 3 x 60" BM: 3 x 60"</p>		<p>(Zvelebil2008, Chapter 3; Xiong2006, Chapter 2)</p> <p>- <i>Data preprocessing with R, quality reporting with FastQC (Zvelebil 2008, Chapter 3; Xiong2006, Chapter 2)</i></p>	
8	ETS/Midterm						
9	<p>Mampu menjelaskan mengenai probabilitas dan distribusi-distribusi probabilitas penting dalam kaitannya dengan model pada data-data biologi</p> <p><i>Be able to explain probability and important probability distributions in relation to models on biological data</i></p>	<p>a. Dapat mengidentifikasi model data biologi berdasarkan distribusi-distribusi penting</p> <p>a. <i>Can identify biological data models based on important distributions</i></p>	<p>Tugas 5, tes tulis, observasi di kelas</p> <p><i>Task 5, written test, observation in class</i></p>	<p>Ceramah, diskusi dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p> <p>TM: 3 x 50" LT: 3 x 60" BM: 3 x 60"</p>		<p>- Model-model biologi dalam distribusi peluang diskret dan kontinu (Mathur2010, Chapter 4; Krijnen2009, Chapter 3)</p> <p>- <i>Biological models of discrete and continuous probability distributions (Mathur2010, Chapter 4; Krijnen2009, Chapter 3)</i></p>	7.5%
10	<p>Mampu menjelaskan aplikasi statistika inferensi parametrik dan nonparametrik dalam beberapa kasus bioinformatika</p>	<p>a. Dapat mengidentifikasi permasalahan biologi dan metode statistika inferensi yang sesuai untuk menyelesaikannya</p>	<p>Tugas 6, tes tulis, observasi di kelas</p> <p><i>Task 6, written test, observation in</i></p>	<p>Ceramah, diskusi dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p>		<p>- Uji-uji hipotesis untuk masalah-masalah biologi (Zvelebil2008, Chapter 3)</p> <p>- Pendekatan statistika nonparametrik dalam permasalahan biologi (Xiong2006, Chapter 2)</p>	7.5%

	<i>Able to explain the application of parametric and nonparametric inference statistics in several cases of bioinformatics</i>	<i>a. Can identify biological problems and inference statistical methods that are appropriate to solve them</i>	<i>class</i>	TM: 3 x 50" LT: 3 x 60" BM: 3 x 60"		<ul style="list-style-type: none"> - <i>Hypothesis tests for biological problems (Zvelebil 2008, Chapter 3)</i> - <i>Nonparametric statistical approach to biological problems (Xiong 2006, Chapter 2)</i> 	
11	<p>Mampu menjelaskan bagaimana teknik <i>clustering</i> diaplikasikan dalam beberapa analisis bioinformatika</p> <p><i>Be able to explain how clustering techniques are applied in several bioinformatics analyses</i></p>	<p>a. Dapat menjelaskan dan menerapkan pengukuran jarak, normalisasi data, dan <i>principal component analysis</i> (PCA) pada analisis ekspresi gen</p> <p>b. Dapat menjelaskan dan menerapkan metode clustering yang sesuai untuk membangun pohon filogeni</p> <p><i>a. Can explain and apply distance measurement, data normalization, and principal component analysis (PCA) in gene expression analysis</i></p> <p><i>b. Be able to explain and apply appropriate clustering methods to construct phylogenetic trees</i></p>	<p>Tugas 7, tes tulis, observasi di kelas</p> <p><i>Task 7, written test, observation in class</i></p>	<p>Ceramah, diskusi dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p> <p>TM: 3 x 50" LT: 3 x 60" BM: 3 x 60"</p>		<ul style="list-style-type: none"> - <i>Eksplorasi data: data normalisasi, menganalisis level-level ekspresi gen, PCA (Zvelebil2008, Chapter 16; Krijnen2009, Chapter 7)</i> - <i>Menentukan validitas hasil clustering (Lee2010, Chapter 7)</i> - <i>Data exploration: data normalization, analyzing gene expression levels, PCA (Zvelebil 2008, Chapter 16; Krijnen 2009, Chapter 7)</i> - <i>Determining the validity of clustering results (Lee2010, Chapter 7)</i> 	7%
12	Mampu menjelaskan	a. Dapat menerapkan	Tugas 8, tes	Ceramah, diskusi		- Metode-metode	7%

	<p>bagaimana teknik klasifikasi berguna dalam analisis bioinformatika</p> <p><i>Be able to explain how classification techniques are useful in bioinformatics analysis</i></p>	<p>metode-metode klasifikasi, <i>feature selection</i> dalam studi <i>expression profiles</i> pada teknologi DNA <i>microarray</i>, <i>cross validation</i></p> <p>a. <i>Able to apply classification methods, feature selection in the study of expression profiles on DNA microarray technology, cross validation</i></p>	<p>tulis, observasi di kelas</p> <p><i>Task 8, written test, observation in class</i></p>	<p>dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p> <p>TM: 3 x 50" LT: 3 x 60" BM: 3 x 60"</p>		<p>klasifikasi, <i>feature selection</i> dalam studi <i>expression profiles</i> pada teknologi DNA <i>microarray</i>, <i>cross validation</i> (Lee2010, Chapter 6; Krijnen2009, Chapter 8)</p> <p>- <i>Classification methods, feature selection in studies of expression profiles on DNA microarray technology, cross validation (Lee2010, Chapter 6; Krijnen2009, Chapter 8)</i></p>	
13	<p>Mampu menjelaskan dan menentukan desain eksperimen yang sesuai untuk permasalahan biologi</p> <p><i>Able to explain and Determine appropriate experimental designs for biological problems</i></p>	<p>a. Dapat mengidentifikasi desain eksperimen yang diterapkan dalam teknologi <i>microarray</i> dan NGS</p> <p>b. Dapat menentukan desain, menganalisis data yang dikumpulkan lewat eksperimen, dan mengambil kesimpulan dari hasilnya</p> <p>a. <i>Can identify experimental designs applied in microarray and NGS technology</i></p>	<p>Tugas 9, tes tulis, observasi di kelas</p> <p><i>Task 9, written test, observation in class</i></p>	<p>Ceramah, diskusi dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p> <p>TM: 3 x 50" LT: 3 x 60" BM: 3 x 60"</p>		<p>- Desain faktorial untuk dua platform pengumpulan data biologi (Nettleton2014)</p> <p>- <i>Factorial design for two biological data collection platforms (Nettleton2014)</i></p>	6%

		<i>b. Can determine designs, analyze data collected through experiments, and draw conclusions from the results</i>					
14 - 15	Mampu menjelaskan aplikasi <i>hidden Markov models</i> (HMMs) pada masalah <i>sequence alignments</i> <i>Be able to explain the application of hidden Markov models (HMMs) on sequence alignments problems</i>	<p>a. Dapat menjelaskan konsep dasar pemrograman dinamis dalam pairwise/multiple sequence alignment dan menerapkannya untuk kasus sederhana</p> <p>b. Dapat mengidentifikasi <i>unknown states</i> dalam <i>sequence alignment</i></p> <p>c. Dapat menjelaskan dan menerapkan HMMs dalam <i>sequence alignments</i></p> <p><i>a. Can explain the basic concepts of dynamic programming in pairwise/multiple sequence alignment and apply them to simple cases</i></p> <p><i>b. Can identify unknown states in sequence alignment</i></p> <p><i>c. Can explain and</i></p>	<p>Tugas 10 (bonus), tes tulis, observasi di kelas</p> <p><i>Task 10, written test, observation in class</i></p>	<p>Ceramah, diskusi dan latihan soal</p> <p><i>Lectures, discussions, and exercise</i></p> <p>TM: 2 x 3 x 50" LT: 2 x 3 x 60" BM: 2 x 3 x 60"</p>		<p>- <i>Pairwise dan multiple sequence alignment</i></p> <p>- Algoritma <i>forward, backward, Viterbi, Expectation Maximization</i> (Ewens2004, Chapter 13)</p> <p>- <i>Pairwise and multiple sequence alignment</i></p> <p>- Algorithms <i>forward, backward, Viterbi, Expectation Maximization</i> (Ewens2004, Chapter 13)</p>	7.5%

		<i>apply HMMs in sequence alignments</i>					
16	Evaluasi Akhir Semester / Ujian Akhir Semester/ <i>final exam</i>						

