



**UNIVERSITAS INDONESIA**  
Faculty of Mathematics and Natural Sciences  
Department of Mathematics  
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### MODULE HANDBOOK

Module designation	<i>Bioinformatics</i>
Semester(s) in which the module is taught	6
Person responsible for the module	<i>Module Coordinator</i>
Language	<i>Indonesian</i>
Relation to curriculum	<i>Compulsory</i>
Teaching methods	<i>lecture, lab works</i>
Workload (incl. contact hours, self-study hours)	<i>(Estimated) Total workload: 8.5 hours x 14 weeks + 3 hours x 2 weeks Contact hours: 150 minutes lectures, 180 minutes structured activities, and 180 minutes individual study per week Private study including examination preparation, specified in hours<sup>1</sup>:</i>
Credit points	<i>3 sks (4, 77 ECTS)</i>
Required and recommended prerequisites for joining the module	<i>Parallel Computing, Machine Learning</i>
Module objectives/intended learning outcomes	<i>After completing the course, students have the ability</i> <ol style="list-style-type: none"><li><i>1. to express biological sequences (DNA and protein) as string information</i></li><li><i>2. to explain methods for determining patterns in biological sequences</i></li><li><i>3. to describe with basic concepts and terminology in computational science</i></li><li><i>4. to apply methods to determine patterns in biological sequences</i></li><li><i>5. to apply bioinformatics methods for sequence and structure analysis</i></li><li><i>6. to use the program as a tool to solve basic scientific problems</i></li><li><i>7. to analyze different biological sequences from generic string analysis</i></li></ol>

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<sup>1</sup> When calculating contact time, each contact hour is counted as a full hour because the organisation of the schedule, moving from room to room, and individual questions to lecturers after the class, all mean that about 60 minutes should be counted.

<p>Content</p>	<ol style="list-style-type: none"> <li>1. <i>Introduction of Bioinformatics</i></li> <li>2. <i>Pair-wise sequence alignments and database search</i></li> <li>3. <i>Phylogenic tree and multiple sequence alignments</i></li> <li>4. <i>Protein Structure Alignments</i></li> <li>5. <i>Modelling of Protein-protein interactions</i></li> <li>6. <i>Biological Data Modeling</i></li> <li>7. <i>Analyzing Data From High Throughput Experiments</i></li> </ol>																				
<p>Examination forms</p>	<ol style="list-style-type: none"> <li>1. <i>Class activities : homework, mini project</i></li> <li>2. <i>Mid-term examination</i></li> <li>3. <i>Final examinations</i></li> </ol>																				
<p>Study and examination requirements</p>	<p><i>The final mark will be weighted as follows:</i></p> <ol style="list-style-type: none"> <li>1. <i>Homework (10%).</i></li> <li>2. <i>Mini Project (30%)</i></li> <li>3. <i>Mid-term examination (30%)</i></li> <li>4. <i>Final examinations (30%)</i></li> </ol> <p><i>To succesfully pass the module it requires minimum 55% of the total mark.</i></p> <table data-bbox="619 1003 880 1458"> <thead> <tr> <th><i>Mark</i></th> <th><i>Grade</i></th> </tr> </thead> <tbody> <tr> <td><i>85 – 100</i></td> <td><i>A</i></td> </tr> <tr> <td><i>80 – &lt;85</i></td> <td><i>A-</i></td> </tr> <tr> <td><i>75 – &lt;80</i></td> <td><i>B+</i></td> </tr> <tr> <td><i>70 – &lt;75</i></td> <td><i>B</i></td> </tr> <tr> <td><i>65 – &lt;70</i></td> <td><i>B-</i></td> </tr> <tr> <td><i>60 – &lt;65</i></td> <td><i>C+</i></td> </tr> <tr> <td><i>55 – &lt;60</i></td> <td><i>C</i></td> </tr> <tr> <td><i>40 – &lt;55</i></td> <td><i>D</i></td> </tr> <tr> <td><i>&lt;40</i></td> <td><i>E</i></td> </tr> </tbody> </table>	<i>Mark</i>	<i>Grade</i>	<i>85 – 100</i>	<i>A</i>	<i>80 – &lt;85</i>	<i>A-</i>	<i>75 – &lt;80</i>	<i>B+</i>	<i>70 – &lt;75</i>	<i>B</i>	<i>65 – &lt;70</i>	<i>B-</i>	<i>60 – &lt;65</i>	<i>C+</i>	<i>55 – &lt;60</i>	<i>C</i>	<i>40 – &lt;55</i>	<i>D</i>	<i>&lt;40</i>	<i>E</i>
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Reading list

1. *Supratim Choudhuri, Bioinformatics for Beginners: Genes, Genomes, Molecular Evolution, Databases and Analytical Tools 1st Edition, Elsevier and AP, 2014*
2. *Elloumi M., and Zomaya A.Y., Biological Knowledge Discovery Handbook, Wiley Series on Bioinformatics Computational Techniques and Engineering, 2012.*
3. *Dress, A., Linial, M., Troyanskaya, O., Vingron, M. Computational Biology, Springer, 2015.*
4. *Röbbe Wünschiers, Computational Biology: A Practical Introduction to BioData Processing and Analysis with Linux, MySQL, and R 2nd ed, Springer, 2013.*
5. *Lecturer's Handout (powerpoint)*