



## UNIVERSITI TEKNOLOGI MARA

### BMS651: BIOINFORMATICS

<b>Course Name (English)</b>	BIOINFORMATICS <b>APPROVED</b>
<b>Course Code</b>	BMS651
<b>MQF Credit</b>	2
<b>Course Description</b>	This course is designed to equip students with the necessary theoretical knowledge and practical skills in bioinformatics. Students will be introduced to 3 major concepts in bioinformatics namely the resources, databases and tools. In resources, students will learned type of biological resources and their level of studies, background, method in human genome project and its important result to mankind. In databases students will explored type and varieties of biological databases and their unique characteristics. In tools, students will have an opportunity in analysing biological data such as sequence alignment and phylogenetic tree reconstruction
<b>Transferable Skills</b>	computer skills self-learning skills
<b>Teaching Methodologies</b>	Lectures, Practical Classes, Tutorial, Web Based Learning, Problem Based Learning (PBL), Self-directed Learning, Directed Self-learning , Computer Aided Learning
<b>CLO</b>	CLO1 Describe principles of bioinformatics, genome organization, gene recognition and prediction, data formats and database repositories for biological data CLO2 Explain theory of bioinformatics tools such as basic alignments and phylogenetic tree reconstruction CLO3 Conduct experiment online on the sequence analysis, alignment and phylogenetic tree reconstruction
<b>Pre-Requisite Courses</b>	No course recommendations
<b>Topics</b>	
<b>1. Introduction to Bioinformatics and the –omics Technology</b> 1.1) Definition and relationship to other science discipline 1.2) Technology and application in bioinformatics 1.3) The omics technology and their research field 1.4) the human genome project-background & methodologies 1.5) Genome organisation in procaryotes & eucaryotes 1.6) gene structure, prediction & recognition	
<b>2. DNA Polymorphisms</b> 2.1) Defination of single nucleotide polymorphisms 2.2) Types and effect of DNA polymorphisms 2.3) Smoking and susceptability to lung cancer 2.4) SNP application	
<b>3. Biological database</b> 3.1) Characteristics of biological database 3.2) Categories of biological databases 3.3) Archives and information retrieval 3.4) Navigating database Information retrieval system	
<b>4. Sequence alignment</b> 4.1) Pairwise Vs. multiple sequence alignment 4.2) Matching Vs. Alignment 4.3) Alignment score 4.4) Algorithms of sequence alignment 4.5) Local Vs. Global alignment 4.6) Application of sequence alignment	

## **5. Phylogenetic Tree Reconstruction**

- 5.1) Introduction and terminologies
- 5.2) Modern Vs. traditional tree
- 5.3) Kind of Trees
- 5.4) Rooted Vs. unrooted tree
- 5.5) Distance based tree
- 5.6) Character based tree

Assessment Breakdown	%
Continuous Assessment	50.00%
Final Assessment	50.00%

Details of Continuous Assessment	Assessment Type	Assessment Description	% of Total Mark	CLO
	Case Study	active learning activities online	10%	CLO2
	Practical	LAB REPORT	20%	CLO3
	Test	TEST online	20%	CLO1

Reading List	Recommended Text	<ul style="list-style-type: none"> <li>Arthur Lesk 2014, <i>Introduction to Bioinformatics</i>, 4th. Ed., Oxford University Press [ISBN: 9780199651566]</li> </ul>
	Reference Book Resources	<ul style="list-style-type: none"> <li>Choudhuri, Supratim 2014, <i>Bioinformatics for Beginners: Genes, Genomes, Molecular Evolution, Databases and Analytical Tools</i> 1st. Ed., Elsevier Inc. USA [ISBN: 978-012410471]</li> <li>Arthur Lesk 2017, <i>Introduction to Genomics</i>, 2nd. Ed., Oxford University Press [ISBN: 9780199564354]</li> <li>Thomas Schmidt. 1999, <i>LINES, SINEs and repetitive DNA: non-LTR retrotransposons in plant genomes</i>, Kluwer Academic Publishers. the Netherlands</li> </ul>

Article/Paper List	Reference Article/Paper Resources	<ul style="list-style-type: none"> <li>Yue Xiong and Thomas H.Eickbush, 1990, Origin and evolution of retroelements based upon their reverse transcriptase sequences,, <i>EMBO J.</i>, vol.9, no 10, 3353</li> <li>Kambol, R., Kabat, P and Tristem, M., 2003, Complete nucleotide sequence of an endogenous retrovirus from the amphibian, <i>Xenopus laevis</i>,, <i>Virology</i>, 16, 311, 16</li> </ul>

Other References	<ul style="list-style-type: none"> <li>software Kumar S, Stecher G, and Tamura K, 2016, <i>MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets</i>, <i>Molecular Biology and Evolution</i> 33:1870-1874, , USA <a href="http://www.megastore.net">http://www.megastore.net</a></li> <li>software Chromas 2010, <i>DNA sequencing software, Chromas: DNA sequencing software</i>, , Technelysium Inc., Technelysium Inc., Australia <a href="https://technelysium.com.au/wp/">https://technelysium.com.au/wp/</a></li> <li>software NADNAstar Lasergene,, DNASTAR Inc.,USA, USA <a href="https://www.dnastar.com">https://www.dnastar.com</a></li> <li>software NA 2013, <i>DNA Sequence Assembler v4</i>,, Heracle BioSoft,, Romania, <a href="http://www.DnaBaser.com">http://www.DnaBaser.com</a></li> <li>Website NANational Center for Biotechnology Information and National Library of Medicine, , GENBANK, USA <a href="https://www.ncbi.nlm.nih.gov/genbank/">https://www.ncbi.nlm.nih.gov/genbank/</a></li> <li>Website Research Organization of Information and System National Institute of Genetics(NIG) in Mishima, Japan,<i>DNA Databank of Japan</i>,, Japan <a href="https://www.ddbj.nig.ac.jp/index-e.html">https://www.ddbj.nig.ac.jp/index-e.html</a></li> <li>Website NALThe European Molecular Biology Laboratory, <i>EMBL</i> <a href="https://www.embl.de/">https://www.embl.de/</a></li> <li>GENBANK record Razlan,N.F.A. and Kambol,R., 2015, <i>Cavia porcellus endogenous virus CpEB1409 protease and reverse transcriptase genes, partial cds</i>, GENBANK , GENBANK, USA <a href="https://www.ncbi.nlm.nih.gov/nucore/KP2_03851">https://www.ncbi.nlm.nih.gov/nucore/KP2_03851</a></li> </ul>
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