



## BMS656: FUNCTIONAL GENOMICS

Course Name (English)	FUNCTIONAL GENOMICS APPROVED
Course Code	BMS656
MQF Credit	2
Course Description	This course surveys the basic findings and approaches in the field of genomics. The life sciences are being transformed by massive infusions of molecular sequence data together with new computational advances and database technologies. We will cover conceptual aspects as well as methodology and technical advances that are central to obtaining and exploring genome sequences. The course is design to equip student with new information on the latest technology in the genomic area. The topics covered are the basic knowledge on Next Generation Sequencing; determination of complete genome sequences and the exploitation of genome sequences to answer biological questions.
Transferable Skills	At the end of the course, student should be able to describe and understand the structure of eukaryotes and prokaryotes genome, regulation of gene expression, various method and technology platform used in genomics and its exploitation in solving real problems.
Teaching Methodologies	Lectures, Case Study, Presentation
CLO	<p>CLO1 Describe the architecture and components of the general genome structure of eukaryote and bacteria.</p> <p>CLO2 Describe the technology platforms and methods available for genome sequencing projects , and the objectives and challenges of the different genome projects</p> <p>CLO3 Explain how comparative genomics can be used in the characterization of genomes and how comparative genomics can be used to transfer genomic information from one species to another, and understand the regulation of gene expression on different levels.</p> <p>CLO4 For a given scientific question or case study, retrieve and collate genomics data from various resources and analyse the data to provide new insights or understanding to the problem</p> <p>CLO5 Prepare and present a properly researched report on the case study and response appropriately to questions raised.</p>
Pre-Requisite Courses	No course recommendations
Topics	<p><b>1. Introduction to course</b></p> <p>1.1) 1.0 Introduction to course</p> <p>1.2) 1.1 Genome structure and organization</p> <p>1.3) 1.2 The Human Genome Project</p> <p>1.4) 1.3 Other genome projects</p> <p>1.5) 1.4 Why genome sequencing?</p> <p><b>2. Genomic Data: Technologies and strategies</b></p> <p>2.1) 2.1 Computational biology</p> <p>2.2) 2.2 Strategies for genome sequencing</p> <p>2.3) 2.3 NGS vs WGS</p> <p>2.4) 2.4 Next-generation sequencing platforms</p> <p>2.5) a) Sequencing-by-synthesis (e.g. Illumina)</p> <p>2.6) b) Pyrosequencing (e.g. Roche 454)</p> <p>2.7) c) Single molecule sequencing (e.g PacBio)</p> <p>2.8) d) Nanopore sequencing (e.g. Oxford Nanopore)</p> <p>2.9) e) other emerging platforms</p> <p>2.10) 2.3 Genome Databases</p> <p><b>3. Assembly</b></p> <p>3.1) 3.1 Genome Assembly</p> <p>3.2) 3.2 Transcriptome Assembly</p> <p>3.3) 3.3 De Novo Assembly</p> <p>3.4) 3.4 Reference Mapping Assembly</p> <p><b>4. Annotations</b></p> <p>4.1) 4.1 Gene prediction</p> <p>4.2) 4.2 Gene profiling</p> <p>4.3) 4.3 Genome Annotation</p> <p><b>5. Functional Genomics- Transcriptomics and Pharmacogenomics</b></p> <p>5.1) 5.1 Comparative genomics</p> <p>5.2) 5.2 Drug Discovery</p> <p>5.3) 5.3 Gene Mutation</p> <p><b>6. Functional Genomics- Molecular Evolution</b></p> <p>6.1) 6.1 Phylogenomics</p> <p>6.2) 6.2 Metagenomics</p> <p>6.3) 6.3 Population Study</p>

Assessment Breakdown		%	
Continuous Assessment		60.00%	
Final Assessment		40.00%	
Details of Continuous Assessment			
Assessment Type	Assessment Description	% of Total Mark	CLO
Case Study	case study/assignment- duration 1 week	20%	CLO4
Presentation	Via presentation (10 minutes) /assignment (1 week)	10%	CLO5
Test	test 1/quiz	15%	CLO1 , CLO2
Test	test 2/quiz	15%	CLO2 , CLO3
Reading List			
Recommended Text	<ul style="list-style-type: none"> <li>Jonathan Pevsner 2015, <i>Bioinformatics and Functional Genomics</i>, 3rd Ed., 1,2,3, Wiley-Blackwell [ISBN: 9781118581]</li> <li>Caroline St. Clair,Jonathan E. Visick 2013, <i>Exploring Bioinformatics</i>, 2nd Ed., Jones &amp; Bartlett Publishers [ISBN: 9781284034240]</li> </ul>		
Article/Paper List	Reference Article/Paper Resources	<ul style="list-style-type: none"> <li>Goodwin, S., McPherson, J.D., &amp; Mc Combie, W.R. 2016, Coming of age: ten years of next-generation sequencing technologies, <i>Nature Review Genetic</i>, 17(6), 33335 [ISSN: doi: 10.1] <a href="http://cbm.msos.edu/markMyweb/ggpmResources/documents/sequencingNextGen.pdf">http://cbm.msos.edu/markMyweb/ggpmResources/documents/sequencingNextGen.pdf</a></li> <li>Escalona, M., Rocha, S., &amp; Posada, D. 2016, A comparison of tools for the simulation of genomic next-generation sequencing data., <i>Nature Reviews Genetic</i>, 17(8), 45946 [ISSN: oi: 10.10]</li> <li>Hall, B.G. 2013, Building Phylogenetic Trees from Molecular Data with MEGA., <i>Molecular Biology and Evolution</i>, 30(5), 1229 [ISSN: mst012]</li> </ul>	
Other References	This Course does not have any other resources		