جامعة الكويت
KUWAIT UNIVERSITY

نموذج توصيف مقرر
Course Description Form

Name of College\Faculty: Faculty of Science **اسم الكلية:**

Name of Department: Department of Biological Science - Mol. Bio. Program **اسم القسم العلمي:**

Course Name	**Introduction to Genomics**	**اسم المقرر**
Course No.	**0497485**	**رقم المقرر**
No. of Credits	**3**	**عدد الوحدات**
Theoretical Hours	**3**	**عدد الساعات النظرية**
Practical Hours	**0**	**عدد الساعات العملية**

Course topics **مواضيع المقرر**

1. Introduction
2. The genome: the word and beyond
3. Exploring the genome: workable pieces
4. Exploring the genome: DNA extraction
5. Exploring the genome: quality and quantity
6. DNA sequencing: the thing to the information
7. The sequence: reading the reads
8. Genome assembly: stitching the sequences
9. Genome annotation: the meaning
10. Coding sequence: meaningful parts
11. Non-coding sequence: not very meaningful parts
12. Functional annotation: the sequence with certainty
13. Polymorphisms
14. Population genetics
15. Reading a genomics paper

See attached details.
Text book: (Name, Author , Year , Publisher) **عنوان الكتاب : (الاسم ، المؤلف ، سنة الطبع ، دار النشر)**
Introduction to Genomics 2nd edition, by Arthur M. Lesk, 2012, Oxford University Press
References: (Name , Author , Year . Publisher) **عنوان المرجع : (الاسم ، المؤلف ، سنة الطبع ، دار النشر)**

Prerequisites						**متطلبات المقرر**
Grading	**Exams**	**40**	**%**		**الاختبارات**	**آلية رصد المقرر**
	Quizzes		**%**		**امتحانات قصيرة**	
	H.W.	**10**	**%**		**واجبات**	
	Project (field study)	**10**	**%**		**مشاريع (دراسة ميدانية)**	
	Final	**40**	**%**		**الاختبار النهائي**	
	100%					

Course objectives					
No.	**Course Objectives (Learning Outcomes)**	**Example(s) of relevant (Topics and activities)**	**Recommended Level to satisfy the objectives**		
			High	**Medium**	**Low**
1	To understand the field of genomics in relation to other biological fields	**Exploring the genome**	**X**		
2	To understand the process and methods involved in sequencing a genome.	**DNA sequencing**	**X**		
3	To know in details the old and current sequencing technologies.	**DNA sequencing**	**X**		
4	To understand general biological outcome of sequencing a given genome.	**Function annotation**	**X**		
5	To read a genome-sequencing scientific article and understand its components and objectives.	**Reading genomics**	**X**		
Fields	**Genetics, Molecular Biology, Biology**				

Skills	**Extracting DNA, DNA amplification, DNA sequencing, Reading scientific papers**
Coordinator (Name and Rank) :	Hasan Alhaddad (Assoc. Prof.)
Signature and stamp :	
Date:	\ \ 5/11/2025

Catalogue Brief Description:

The course is an introduction to the study of the genome, which is arguably considered the most recent field of biology. The genome is the collection of all genetic material of a species and genomics is the field that takes the genetic material out of the cell and through a molecular biology journey to end up as information in a computer. Genomics then looks at the biological meaning of the genome, which is stored as information and apply the findings to understand the biology or use it for practical applications such as agriculture and medicine.

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Course Content

	Hours
1. Introduction: general review of genetics and molecular biology topics and concepts with an emphasis on their significance to the study of genomics. **Topics include:** Mendelian genetics, linkage maps, genetic maps, identification of the genetic material and its experiments, chromosome theory, the chemistry of DNA, DNA structure, genome organization, the central dogma of molecular biology, the genetic code.	4 hours
2. The genome-the word and beyond: introduction to the origins of the words: "genome" and "genomics, the uses and misuses of OME and OMIC terms, the general characteristics of viral, prokaryotic, eukaryotic genomes. **Topics include:** genome chemical identity, genome size, genome physical architecture, number of genome units, genome copy number, the genome and evolutionary history.	2 hours
3. Exploring the genome-workable pieces: introduction to the requirements for studying the genome and highlight the chemistry limitations necessitate studying the genome in fragments rather than as a whole. **Topics include:** restriction enzymes, cloning vectors, molecular cloning, polymerase chain reaction (PCR), cloning vs. PCR.	2 hours
4. Exploring the genome-DNA extraction: introduce the sources from which the DNA will be isolated for genomic applications. **Topics include:** DNA sources of viruses, DNA sources of bacteria, DNA sources of animal and plant cells, cell and tissue disruption, lysis of the cell membrane, DNA extraction, DNA storage.	1 hour
5. Exploring the genome-quality and quantity: introduce the concepts DNA quality and quantity analysis and their importance for genomic studies. **Topics include:** gel electrophoresis, DNA staining, spectrophotometry.	1 hour
6. DNA sequencing-the thing to the information: introduce what DNA sequencing is. Introduce the sequencing technologies that are used to transform DNA from a chemical to information with an emphasis on the method of sequencing and the method of nucleotide identity detection. **Topics include:** Maxam-Gilbert sequencing, Sanger sequencing, Next-generation sequencing (NGS), pyrosequencing, Illumina sequencing, SOLiD sequencing, Ion Torrent sequencing, Nanopore sequencing, and PacBio sequencing.	4 hours
7. The sequence-reading the reads: introduce the genome sequencing strategies and topics and ideas related to raw DNA sequences. **Topics include:** BAC sequencing, hierarchical sequencing, whole-genome shotgun sequencing (WGS), single-end sequencing, paired-end sequencing, sequence reads, sequence-read quality, error detection and assessment, short-reads vs. long-reads, sequence coverage, sequence depth.	2 hours
8. Genome assembly-stitching the sequences: introduce the concepts, topics, and calculations that are related to genome assembly. **Topics include:** sequence alignment, methods of sequence alignment, test of alignments, contiguous sequence (contig), scaffold, N50 contig, N50 scaffold, evaluation of genome assembly.	3 hours
9. Genome annotation-the meaning: introduce the topics related to identifying the meaning of the DNA sequences. **Topics include:** structural annotation vs. functional annotation, in-silico annotation, computational annotation, biochemical annotation, nucleotide composition, genome-wide nucleotide content, overlapping and non-overlapping sliding windows and genomic measures, GC content.	2 hours

10. Coding sequence-meaningful parts: introduce the structural annotation methods of coding sequences via sequence-pattern identification and classification. **Topics include:** prokaryotic coding-gene structure, operons, eukaryotic coding-gene structure, open read frame (ORF), rDNA, tRNA, gene number, average exon and intron sizes, UTR sizes, proportion of genome made of genes, gene density, predicted genes.	2 hours
11. Non-coding sequence-not very meaningful parts: introduce the structural annotation of non-coding sequences via sequence-pattern identification and classification. **Topics include:** Pseudogenes, DNA pseudogenes, retro-pseudogenes, repeat elements, tandem repeats, interspersed repeats, dispersed repeats, simple sequence repeats (SSR), short-tandem repeats (STR), DNA satellites, DNA mini-satellites, DNA micro-satellites, di-nucleotide repeat, tri-nucleotide repeats, tetra-nucleotide repeats, transposons, transposable elements, retro-transposons, proportion of genome made of repeats.	2 hours
12. Functional annotation-the sequence function with certainty: introduce the methods and genomic applications that are associated with biochemically identifying the function of genomic elements with increased certainty. **Topics include:** forward genetics, reverse genetics, RNA interference (RNAi), gene knockout, expression arrays, RNA sequencing (RNA-seq).	2 hours
13. Polymorphisms: introduce the methods and topics that are related to sequence variation. **Topics include:** reference genome sequencing, single genome sequencing, genome resequencing, population sequencing, sequence variation, single nucleotide polymorphisms (SNPs), SNP abbreviations, alignment of multiple genomes.	2 hours
14. Population genetics: introduce methods and calculations that utilizes sequence variation towards understanding the genetics of a population. **Topics include:** major allele, minor allele, allele frequency, genotype, genotype frequency, haplotype, haplotype frequency, Hardy-Weinberg equilibrium, genome-wide association	3 hours
15. Reading a genomics paper: As part of a project and a presentation assignment, introduce how to read a genome sequencing scientific paper and relate the topics learned to the contents of the paper. **Topics include:** objectives of genome sequencing papers, components of a genome paper, findings of a genome paper.	2 hours
Lecture hours	**34 hours**
Midterm exams	**2 hours**
Presentations	**2 hours**
Total	**38 hours**