

OMICS

Semester: available on demand

Course Time and Location: available on demand

Course Instructor: Ka-Lok Ng

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Office Hour: By appointment

Course description: This course is designed for students who major in engineering and science. Omics is a new area of study in molecular biology that examine the feature of a large family of biological molecules, such as DNA, mRNA, proteins, metabolites, lipids and carbohydrates (saccharides).

This course is designed to give students a general understanding of the genomes, transcriptomes, proteomes and their integration, i.e. omic. Genomes, transcriptomes, proteomes are the large-scale study of genes, transcripts and proteins. In addition, this course will also cover the following topics: regulatory elements, epigenetic mechanism (DNA methylation, chromatin modeling), and non-coding RNA biology.

Networks of interactions are fundamental to all biological processes. In the last ten years, we began to see much progress in analyzing biological networks using the random graph approach. Network motifs are patterns that occur more often than their randomized parts. A complex network can be characterized by certain topological measurements. Students will learn those techniques in the course.

Pre-requisite:

Students are expected to have basic knowledge in probability, statistics, linear algebra, and molecular biology.

Required Textbook: Not required

References:

- A. Brown TA, Genomes, Wiley
- B. Gibson & Muse, A primer of genome science, Sineuer
- C. Draghici, Data Analysis tools for DNA microarray, Chapman & Hall/CRC
- D. Liebler DC , Introduction to proteomics, Humana Press

E. Klipp, Liebermeister, Wierling, Kowald, Lehrach, Herwig – Systems biology, Wiley Blackwell

Required Equipment: A laptop computer (either Mac or PC with wireless internet capability)

Topics and Schedules:

Week	Topic	Type	Assignments
1	The Structures of DNA and RNA Chromatin and the Nucleosome. Mechanisms of Transcription	Lecture	Homework 1
2	Mechanisms of Transcription.		
2	The Processing of RNA. The Genetic Code. And Translation. Gene Regulation in Prokaryotes and Eukaryotes.	Lecture	Homework 2
3	Genomic databases (NCBI, UCSC, Ensembl)	Lecture	
4	Regulatory element databases (EPD, dbTSS)	Lecture	Homework 3
5	Epigenetic databases (MethHC, Methyl-cancer)	Lecture	
6	Non-coding RNA sequence, microRNA, lncRNA databases & target prediction tools (Targetscan, miRanda, RNAHybride)	Lecture	Homework 4
7	Gene Expression Analysis & Clustering	Lecture	Homework 5
8	Protein-protein interaction, domain-domain interaction databases	Lecture	Homework 6
9	Mid-term	Lecture	
10	Biological pathway databases (KEGG, PANTHER)	Lecture	
11	Network motif analysis I (Random graph, entropy, machine learning classifiers)	Lecture	
12	Network motif analysis II (Random graph, entropy, machine learning classifiers)	Lecture	Homework 7
13	Functional genomics (Gene set enrichment analysis, DAVID, CPdb)	Lecture	Homework 8
14	Plant omics, human cancer atlas database (TCGA)	Lecture	
15	Integrative analysis using Meta-analysis	Lecture	Homework 9
16	Network visualization tool, Cytoscape and plugins (MCODE, MCL)	Lecture	Homework 10
17	Kinomics, Metabolomics and drug repositioning	Lecture	
18	Final exam. or paper presentation		

Workload: There will be 10 homework assignment (4% each), mid-term and final exam or paper presentation (30% each).

Grading: Passing score for graduate course is 70. In general, score is allocated between class attendance, homework, mid-term written exam, final written exam and student oral presentation. Course instructor reserves the right to adjust the grading scheme.

Late Assignments: All homework assignments are due within one week. Late assignment submissions will be penalized 25%. Assignments more than 3 days late will not be accepted.