PURDUE
UNIVERSITY

DEPARTMENTS OF BIOCHEMISTRY &
COMPUTER SCIENCE

CS 490-001 (with Hands-on experience) (Computational Genomics) Syllabus Fall, 2020

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LECTURE TIME AND PLACE

WF, 3:30pm-5:20pm, LILY G428

COURSE DESCRIPTION

This course introduces you to basics of modern genomics and computational tools that will be used for understanding diseases such as cancer. We will review the notion of gene, genome, transcriptome, and epigenome, and show how next generation sequencing technologies are utilized to measure these within cells.

LEARNING OUTCOMES

- Evaluate features of a genome (e.g. conservation, GC content, gene coding potential)
- Understand how data from next-generation sequencing experiments (e.g. RNA-seq) are generated and processed
- Analyze next-generation sequencing data (e.g. RNA-seq, ChIP-seq) from various experiments
- Integrate various genomics data to answer specific biological question related to genomics and gene regulation

Prerequisites

Some knowledge or experience with programing and basic molecular biology is welcomed. Necessary concepts from biology, statistics, and computational algorithms will be provided during the course.

TENTATIVE LECTURE SCHEDULE

Week	**Topics (Lecture)**	**Hands-on Lab**	NOTES
1	Introduction	Unix commands and shell programs	
2	Genomes and features	UCSC genome browser	
3	Gene prediction tools and methods	Identifying new genes (e.g. from a plasmid)	
4	Sequence alignment and mapping techniques	BLAST	
5	Genome sequencing technologies	File formats (FASTQ, BED) and Quality Control	
6	Genome assembly techniques	De-novo assembly (e.g. wide-seq data)	
7	Mid-term		
8	Transcriptome and cells	RNA-seq data analysis	
9	Transcriptomic data analysis	Finding differentially expressed genes (DEGs)	
10	Biological Networks and Pathway	Pathway analysis of DEGs	
11	Epigenetics: techniques and applications	ChIP-seq data analysis and visualization	
12	Gene Regulatory networks	Motif finding using meme suite	
13	Genetic variation and diseases	SNP calling	
14	Genomic structural variations	Structural variation identification	
15	Biological databases	information integration from SRA	