

COURSE SYLLABUS

(Revised 07/20/2022)

COURSE NAME: **Genome Data Analysis**
 CLASS DATES: August 24, 2022 – November 16, 2022 (**Wednesdays**)
 LOCATION: **Online (Zoom)**
 CLASS HOURS: **3:00 PM – 4:00 PM**

BACKGROUND	Technologies to probe genomes and their products have exploded in the past decade. Bioinformatics and computational biology play a role in cancer research and familiarity with concepts in these areas becomes important for hypothesis generation, target validation and discovery. This course provides an overview of genomic data analysis, specifically analytical techniques involving DNA and gene sequences, gene mutations, gene expression and protein measurements. The lectures provide an overview of the topics and introduce key issues in experimental design and analytical strategies for these molecular types. This lecture series is intended for individuals with limited exposure to specific areas of bioinformatics.		
COURSE DESCRIPTION	Bioinformatics analysis techniques, including derivation of analytical variables from raw signal, descriptive methods and hypothesis testing in large dimensional studies will be presented. The basic concepts, issues and applications of these analysis techniques will be introduced. Examples using website tools and R will be used.		
COURSE GOAL	The goal of this class is to introduce the basic bioinformatics concepts and methods in genomic analysis for cancer research.		
WHO WILL TAKE THIS COURSE?	Clinicians, Fellows, Cancer Researchers, and Cancer Biology Students. *Note: Only Moffitt/PHSU Members are eligible, and exceptional cases should be discussed with the Administrative Coordinator prior to August 24.		
COURSE PREREQUISITES	Bios101 or previous statistical experience is recommended for the statistical issues in high-dimensional data that will be discussed. Knowledge of basic molecular biology and cancer care concepts are assumed.		
REGISTRATION POLICY	There is <i>not</i> a fee for this lecture series. However, attendees must self-register at http://bio2.moffitt.org/lms . Please email bio2admin@moffitt.org if you have registration questions. *Note: Some students may attend only selective lectures as long as they are registered.		
COURSE FORMAT	The course will consist of lectures and online questions to assess understanding of content. The lecture materials (slides) will be posted before each class.		
HOMEWORK	Every week there will be a homework assignment (3 question quiz) for each lecture, and this will be considered a test that engages if the student understood the material. Pass: A Score of 66 or higher (2 out of 3).		
CLASS CERTIFICATION	Class certification requires successfully passing 9 or more quizzes.		
COURSE LOCATIONS	Remote course attendance unless otherwise determined by Cancer Center Leadership; please contact Bio2 Admin (bio2admin@moffitt.org) for details.		
COURSE EVALUATION	At the end of <u>each</u> class, students are recommended to complete an online evaluation form for the lecture.		
COURSE ORGANIZER	Xiaoqing Yu, PhD Assistant Member Steven Eschrich, PhD Senior Member Dept. of Biostatistics & Bioinformatics	COURSE ADMINISTRATIVE COORDINATOR	Keona McDonald, MHA Executive Assistant, Dept. of Biostatistics & Bioinformatics Keona.McDonald@moffitt.org Tel: (813) 745-0198

FACULTY PROFILE

Name	Academic Rank	Primary Research Focus
Anders Berglund, Ph.D.	Associate Member	Gene Expression, Methylation, Principal Components Analysis
Ling Cen, Ph.D.	Bioinformatics Supervisor	RNASeq
Julie Dutil, Ph.D.	Associate Professor	Bioinformatics, Ancestry Markers
Steven Eschrich, Ph.D.	Senior Member	Gene Expression, Proteomics
Quincy Mo, Ph.D.	Associate Member	Cancer genomics, Statistical analysis, multi-omics integrative analysis
Timothy Shaw, Ph.D.	Assistant Member	Alternative splicing, Regulatory network
Sophia Song, Ph.D.	Assistant Member	Single-Cell Sequencing
Paul Stewart, Ph.D.	Assistant Member	Proteomics, Metabolomics, Multi-omics Integration
Jamie Teer, Ph.D.	Associate Member	Massively Parallel Sequencing, DNA Sequencing
Mingxiang Teng, Ph.D.	Assistant Member	ChIP-seq, RNASeq
Eric Welsh, Ph.D.	Sr. Bioinformatics Staff Scientist	Gene Expression, QC, Proteomics
Xiaoqing Yu, Ph.D.	Assistant Member	Computational immunology, Single-Cell Sequencing

COURSE SCHEDULE/DESCRIPTION (Revised 07/20/2022)

Day/Date	Instructor	Contents	Goals
Lecture #1 August 24	Steven Eschrich, Ph.D.	Introduction and Overview to Bioinformatics	<ul style="list-style-type: none"> - Overview - Discussion of bioinformatics collaborative resources - Basic bioinformatics techniques
Lecture #2 August 31	Jamie Teer, Ph.D.	Next Generation Sequencing	<ul style="list-style-type: none"> - Next-gen overview - Alignments - Capture approaches - Interpreting mutations in the context of cancer
Lecture #3 September 7	Julie Dutil, Ph.D.	Genetic Ancestry	<ul style="list-style-type: none"> - ADMIXTURE, PCA, tSNE
Lecture #4 September 14	Mingxiang Teng, Ph.D.	Expanded sequencing approaches: ChipSeq	<ul style="list-style-type: none"> - Quality control - Peak calling - Super enhancers & Differential peak calling
Lecture #5 September 21	Anders Berglund, Ph.D.	DNA Methylation	<ul style="list-style-type: none"> - Methylation Arrays - Visualization - Gene expression regulation
Lecture #6 September 28	Eric Welsh, Ph.D.	Gene Expression	<ul style="list-style-type: none"> - Overview of gene expression - Normalization techniques - PCA/MDS/Clustering visualizations - QC, Batch corrections (Combat)
Lecture #7 October 5	Ling Cen, Ph.D.	RNASeq	<ul style="list-style-type: none"> - Overview of the workflow - Experimental design - Data analytics - Advanced applications
Lecture #8 October 12	Timothy Shaw, Ph.D.	Alternative Splicing	<ul style="list-style-type: none"> - Transcript-level RNASeq - Detecting alternate splicing - Outlier splicing analysis
Lecture #9 October 19	Sophia Song, Ph.D.	Single-Cell Sequencing	<ul style="list-style-type: none"> - Description of technology - Analytical approaches - Experimental design
Lecture #10 October 26	Paul Stewart, Ph.D.	Proteomics & Metabolomics	<ul style="list-style-type: none"> - Introduction to mass spectrometry-based omics - Analysis techniques (Labeled vs. Label-free) - Metabolomics
Lecture #11 November 2	Anders Berglund, Ph.D.	Public Data Sources, Visualization	<ul style="list-style-type: none"> - GEO, ArrayExpress, TCGA, TCGA tools, cBioPortal, GTEx and PanCancer Analysis
Lecture #12 November 9	Quincy Mo, Ph.D.	Multi-omics Integrative Analysis	<ul style="list-style-type: none"> - Multi-Omics integration
Lecture #13 November 16	Xiaoqing Yu, PhD	Computational Immunology	<ul style="list-style-type: none"> - BCR/TCR sequencing - Neoantigen prediction - HLA typing