

**COURSE SYLLABUS**

(Revised 08/01/2023)

COURSE NAME: **Genome Data Analysis**  
 CLASS DATES: August 23, 2023 – November 15, 2023 (**Wednesdays**)  
 LOCATION: **Online (Zoom)**  
 CLASS HOURS: **3:00 PM – 4:00 PM**

<b>BACKGROUND</b>	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.		
<b>COURSE DESCRIPTION</b>	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.		
<b>COURSE GOAL</b>	The goal of this class is to introduce the basic bioinformatics concepts and methods in genomic analysis for cancer research.		
<b>WHO WILL TAKE THIS COURSE?</b>	Clinicians, Fellows, Cancer Researchers, and Cancer Biology Students. <b>*Note:</b> Only Moffitt/PHSU Members are eligible, and exceptional cases should be discussed with the Administrative Coordinator <b>prior</b> to August 23.		
<b>COURSE PREREQUISITES</b>	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.		
<b>REGISTRATION POLICY</b>	There is <i>not</i> a fee for this lecture series. However, attendees must self-register at <a href="http://bio2.moffitt.org/lms">http://bio2.moffitt.org/lms</a> . Please email <a href="mailto:bio2admin@moffitt.org">bio2admin@moffitt.org</a> if you have registration questions. <b>*Note:</b> Some students may attend only selective lectures as long as they are registered.		
<b>COURSE FORMAT</b>	The course will consist of lectures and online questions to assess understanding of content. The lecture materials (slides) will be posted before each class.		
<b>HOMEWORK</b>	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. <b>Pass: A Score of 66 or higher (2 out of 3).</b>		
<b>CLASS CERTIFICATION</b>	Class certification requires successfully passing 9 or more quizzes.		
<b>COURSE LOCATIONS</b>	Remote course attendance unless otherwise determined by Cancer Center Leadership; please contact Bio2 Admin ( <a href="mailto:bio2admin@moffitt.org">bio2admin@moffitt.org</a> ) for details.		
<b>COURSE EVALUATION</b>	At the end of <u>each</u> class, students are recommended to complete an online evaluation form for the lecture.		
<b>COURSE ORGANIZER</b>	Xiaoqing Yu, PhD Associate Member  Steven Eschrich, PhD Senior Member  Dept. of Biostatistics & Bioinformatics	<b>COURSE ADMINISTRATIVE COORDINATOR</b>	Keona McDonald, MHA Executive Assistant, Dept. of Biostatistics & Bioinformatics <a href="mailto:Keona.McDonald@moffitt.org">Keona.McDonald@moffitt.org</a> Tel: (813) 745-0198

## FACULTY PROFILE

<b>Name</b>	<b>Academic Rank</b>	<b>Primary Research Focus</b>
Anders Berglund, Ph.D.	Associate Member	Gene Expression, Methylation, Principal Components Analysis
Ling Cen, Ph.D.	Bioinformatics Supervisor	RNASeq
Julie Dutil, Ph.D.	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.	Associate Member	Computational immunology, Single-Cell Sequencing

**COURSE SCHEDULE/DESCRIPTION** (Revised 08/01/2023)

Day/Date	Instructor	Contents	Goals
<b>Lecture #1</b> August 23	Steven Eschrich, Ph.D.	Introduction and Overview to Bioinformatics	<ul style="list-style-type: none"> <li>- Overview</li> <li>- Discussion of bioinformatics collaborative resources</li> <li>- Basic bioinformatics techniques</li> </ul>
<b>Lecture #2</b> August 30	Jamie Teer, Ph.D.	Next Generation Sequencing	<ul style="list-style-type: none"> <li>- Next-gen overview</li> <li>- Alignments</li> <li>- Capture approaches</li> <li>- Interpreting mutations in the context of cancer</li> </ul>
<b>Lecture #3</b> September 6	Julie Dutil, Ph.D.	Genetic Ancestry	<ul style="list-style-type: none"> <li>- ADMIXTURE, PCA, tSNE</li> </ul>
<b>Lecture #4</b> September 13	Mingxiang Teng, Ph.D.	Expanded sequencing approaches: ChipSeq	<ul style="list-style-type: none"> <li>- Quality control</li> <li>- Peak calling</li> <li>- Super enhancers &amp; Differential peak calling</li> </ul>
<b>Lecture #5</b> September 20	Anders Berglund, Ph.D.	DNA Methylation	<ul style="list-style-type: none"> <li>- Methylation Arrays</li> <li>- Visualization</li> <li>- Gene expression regulation</li> </ul>
<b>Lecture #6</b> September 27	Eric Welsh, Ph.D.	Gene Expression	<ul style="list-style-type: none"> <li>- Overview of gene expression</li> <li>- Normalization techniques</li> <li>- PCA/MDS/Clustering visualizations</li> <li>- QC, Batch corrections (Combat)</li> </ul>
<b>Lecture #7</b> October 4	Ling Cen, Ph.D.	RNASeq	<ul style="list-style-type: none"> <li>- Overview of the workflow</li> <li>- Experimental design</li> <li>- Data analytics</li> <li>- Advanced applications</li> </ul>
<b>Lecture #8</b> October 11	Timothy Shaw, Ph.D.	Alternative Splicing	<ul style="list-style-type: none"> <li>- Transcript-level RNASeq</li> <li>- Detecting alternate splicing</li> <li>- Outlier splicing analysis</li> </ul>
<b>Lecture #9</b> October 18	Sophia Song, Ph.D.	Single-Cell Sequencing	<ul style="list-style-type: none"> <li>- Description of technology</li> <li>- Analytical approaches</li> <li>- Experimental design</li> </ul>
<b>Lecture #10</b> October 25	Paul Stewart, Ph.D.	Proteomics & Metabolomics	<ul style="list-style-type: none"> <li>- Introduction to mass spectrometry-based omics</li> <li>- Analysis techniques (Labeled vs. Label-free)</li> <li>- Metabolomics</li> </ul>
<b>Lecture #11</b> November 1	Anders Berglund, Ph.D.	Public Data Sources, Visualization	<ul style="list-style-type: none"> <li>- GEO, ArrayExpress, TCGA, TCGA tools, cBioPortal, GTEx and PanCancer Analysis</li> </ul>
<b>Lecture #12</b> November 8	Quincy Mo, Ph.D.	Multi-omics Integrative Analysis	<ul style="list-style-type: none"> <li>- Multi-Omics integration</li> </ul>
<b>Lecture #13</b> November 15	Xiaoqing Yu, PhD	Computational Immunology	<ul style="list-style-type: none"> <li>- BCR/TCR sequencing</li> <li>- Neoantigen prediction</li> <li>- HLA typing</li> </ul>