

Functional Genomics

Room 3351 MSB on Wednesdays, from 1:00-3:00pm

1. (Jan 7): **Introduction to Genomics, Informatics, and Functional Genomics.** Melanie T. Cushion, Ph.D. (Dept. Medicine)
2. (Jan 14): **Genomics Strategies and Techniques.** A. George Smulian, M.D. (Dept. Medicine)
3. (Jan 21): **Informatics of Assembly.** Bradley E. Slaven, M.S. (Dept. Medicine)
- 3.a (Jan 26) **Assembly Lab.** Bradley Slaven
4. (Jan 28) **Annotation Strategies.** Jarek Meller, Ph.D. (CHMCC, Informatics)
- 4.a (Feb 2) **Annotation Lab.** Jarek Meller and Bradley Slaven
5. (Feb 4) **Structural Bioinformatics.** Jarek Meller, Ph.D. (CHMCC, Informatics)
- 5.a (Feb 9) **Structural Bioinformatics Lab.** Jarek Meller
6. (Feb 11) **Microarray Analysis Fundamentals and Data analysis.** Craig R. Tomlinson, UC Genomics and Microarray Lab
7. (Feb 18) **Medical Applications of Genomics.** Bruce Aronow, Ph.D. CHMCC Informatics
- 7.a (Feb 23) **Microarray Data Analysis Lab.** Bruce Aronow
8. (Feb 25) **Proteomics Techniques.** Pat Limbach, Ph.D. UC Dept. of Chemistry
9. (Mar 3): **Proteomics Informatics.** Michael Wagner, Ph.D., CHMCC, Dept. Informatics
- 9.a (Mar 8) **In silico Protein Identification Lab.** Michael Wagner
10. (Mar 10): **Research Application of Proteomics/genomics techniques.** To be announce

MARCH 17 EXAM

Seminar 1 (Jan 7): Introduction to Genomics, Informatics, and Functional

Genomics. This lecture will cover the basic outline and goals of the seminar series and provide a broad overview of the general terms and concepts used in the different disciplines contributing to the field of Genomics. An overview of genomics and the projects completed since 1995 and currently ongoing will be discussed.

- a. Gain an understanding of the goals of the series
- b. Become familiar with terms used in the field
- c. Understand basic concepts fundamental to the disciplines
- d. Method of course evaluation- test

Speaker: Dr. Cushion

Reading assignment: A Primer of Genome Sequence, Chapter 1.

Seminar 2 (Jan 14): Genomics Strategies and Techniques. This lecture will describe the biological side of the techniques used to generate sequence for whole genome assemblies. Strategies for large genomes (e.g. human, mouse) as well as for smaller genomes (C. elegans, fungi) will be discussed.

- e. Understand the differences in library construction strategies for large vs small genome projects; learn the fundamentals of vectors which contain different size DNA inserts (e.g. BAC, cosmid, pUC)
- f. Gain an understanding of genomic sequencing methods, depth of coverage, creation of an EST database

Speaker: George Smulian, M.D., UC Department of Internal Medicine

Reading Assignment: A Primer of Genome Sequence, Chapter 1.

Seminar 3 (Jan 21,26): Informatics of Assembly. Lecture and lab session. This lecture will describe the fundamentals of high throughput sequencing technology and the theory and concept behind the methods used. Standard assembly software tools will be highlighted and the algorithms supporting these approaches will be presented. Practical applications will be considered during the following computer lab “hands-on” class (3.a).

- g. Understand the form of the output from a sequencing project (sequence formats) and the basic tools to evaluate the integrity of the sequence reads
- h. Learn the basic algorithms used to underpin standard programs, e.g. PHRED, PHRAP and understand the differences

Speaker: Bradley E. Slaven, M.S., UC Department of Internal Medicine

Reading assignment: A Primer of Genome Sequence, Chapter 2; pp 63-90.

Seminar 4 (Jan 28, Feb2): Informatics of Annotation. Lecture and lab session. The term "annotation" comprises everything that can be known about a gene: where it works, what it does and how it interacts with other genes. Currently, the term usually applies to the initial step of genome examination immediately after assembly: gene finding. There are several approaches to gene finding and predicting function available in current software. These programs and the differences in approaches along with the problems in this area will be discussed in this lecture and then presented during computer lab “hands-on” class (4.a).

- i. Understand the multiple tasks of “annotation” and the current approaches used to identify genes in complex genomes.
- j. Learn the other functions of annotation and their associated programs.
- k. Understand the problems with all the current approaches.

Speaker: Jarek Meller, Ph.D. CHMCC

Reading assignment: A Primer of Genome Sequence, Chapter 2; pp 91-120.

Seminar 5 (Feb 4,9): Structural Bioinformatics. Lecture and lab session. The goal of initial genomic annotations is to identify genes. However their subsequent

functional annotations require characterization of structure and interactions of proteins encoded by the genes. Since experimental methods for protein structure and function are costly and lengthy there is a growing gap between the number of known protein sequences and known protein structures. Various computational methods are used in order facilitate experimental efforts in that regard, starting from sequence based methods and “guilt by association” rule to *de novo* protein folding simulations. Different approaches to protein structure and protein-protein interactions prediction will be discussed in this lecture. Practically oriented case studies and structural annotations of unknown proteins will presented in the following “hands-on” class (5.a).

Speaker: Jarek Meller, Ph.D. CHMCC

Reading assignment: A Primer of Genome Sequence, Chapter 4; pp 183-212.

Seminar 6 (Feb 11) Microarray Analysis Fundamentals and Data analysis.

Microarray analysis has a variety of applications. One of its primary applications is the use of the sequences created by a genome project to understand the differences in gene expression during different perturbation events. In the first section of this lecture, the fundamentals of the various microarray matrices will be discussed as well as their biological preparations and supportive hardware/software. The data produced from microarray analyses are complex and numerous. In the second part of the lecture, the fundamentals of analyzing the output from the arrays will be discussed as well as the currently available software programs that are used for this purpose.

- l. Learn the components of microarray analysis and the advantages/disadvantages of the various systems
- m. Learn the methods for hybridization and analysis
- n. Understand the proper design for microarray experiments
- o. Become familiar with the multitude of applications that can be used to analyze the data

Speakers: Craig R. Tomlinson, Ph.D., UC Genomics and Microarray Lab

Reading assignment: A Primer of Genome Sequence, Chapter 3; pp123-141 and Chapter 3; pp 141-178

Seminar 7. (Feb 18,23) Medical Applications of Genomics. Lecture and lab session.

Speaker: Bruce Aronow, CHMCC Informatics.

Reading Assignment: A Primer of Genome Sequence, Chapter 6

Seminar 8 (Feb 25): Proteomics Techniques. Proteomics is the study of the expression of proteins and their modifications at a total cellular level under varying or specific conditions. The instrumentation and the procedure are

dramatically different than those used in structural and functional genomics. In this lecture, the field of proteomics will be introduced.

- p. Understand basic concepts in proteomics
- q. Become familiar with the procedures and instrumentation used for proteomic analysis
- r. Learn how the data is interpreted in this field
- s. Learn how proteomics can be applied to understanding pathogenesis and disease

Speaker: Pat Limbach, UC Dept. of Chemistry

Reading assignment: A Primer of Genome Sequence, Chapter 4; pp. 188-198

Seminar 9 (Mar 3,8): Proteomics Informatics. Lecture and lab session.

Speaker: Michael Wagner, Ph.D. Dept. Informatics

Reading assignment: A Primer of Genome Sequence, Chapter4; pp 184-188; 210-212

Seminar 10 (Mar 10): Medical Application of Proteomics Techniques

Speaker: To be announced. A Primer of Genome Sequence, Chapter 4 ; 198-204.

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