

BIOINFORMATICS AND GENE SEQUENCE ANALYSIS
PABIO/MEBI/PHG 536

Course Information: Spring Quarter 2013

HOME PAGE: <http://courses.washington.edu/bioinfo/>
EMAIL: bioinfo@u.washington.edu

LECTURE/COMPUTER LAB: Mondays and Wednesday 10:00-11:20 HSL Learning Commons Classroom C

INSTRUCTOR:

Timothy Rose, Ph.D.

Professor, Dept. Pediatrics, School of Medicine

Public Health Genetics Institute, School of Public Health

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Adjunct – Epidemiology, School of Public Health, Oral Biology, School of Dentistry, Microbiology, School of Medicine

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Lab Web Site: <http://courses.washington.edu/bioinfo/roselab>

Email: trose@u.washington.edu

TEACHING ASSISTANT:

Emilia Gan

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Phone: 206-884-8232

OFFICE HOURS: The instructor and teaching assistant can be contacted by phone or email.

COURSE FORMAT: The course will be given as a series of lectures and lecture/computer labs, as indicated in the [Course Schedule](#).

COURSE MATERIALS: Although there is no required text-book, "Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Baxevanis AD and Ouellette BF 2nd ed. (2001), Wiley Interscience, New York", available at the University Bookstore, South Campus Center for \$65, may be helpful. On-line access to most other reading material is available on the class Web site ([Reading List](#)). Computers for student use are available in the Health Sciences Library Learning Commons.

COURSE WORK:

1). Weekly homework assignments will consist of sequence analysis problems. Assignments will be due by email to bioinfo@u.washington.edu by 5pm the Friday of each week. Grades for each assignment will drop 1.0 unit for each week late. If extra credit problems are given, the extra points can raise the homework grade to the maximum 4.0.

2) A take-home final will be given. This final is to be done individually with no collaboration with others.

3). This is a graded class with an option for Credit/No-Credit; Grades will be determined from the homework (2/3) and final (1/3). Grading will be on the 4.0 scale and you must obtain a 2.7 to get

credit. Collaborating on the homework is encouraged but the work must be done individually. The take-home final is not collaborative and must be done individually.

Lectures and computer labs will be held in the Health Sciences Library Learning Commons Classroom C from 10:00-11:20 AM. These will be part lecture, part hands-on exercises. We will be using PCs running Windows.

LEARNING OBJECTIVES – PABIO/MEBI/PHG 536 “Bioinformatics and Gene Sequence Analysis”

This course is a joint offering of the Department of Pathobiology, Department of Medical Education and Biomedical Informatics and the Institute of Public Health Genetics. It forms part of the curriculum for the Ph.D. program in Pathobiology and the M.S. program in Genetic Epidemiology, Institute of Public Health Genetics, and is open to students and postgraduate trainees in the biomedical, computer, and information sciences. Students are expected to learn key concepts and skills in the accumulation, analysis, and retrieval of biological sequence information in the context of computer-based informatics, the Internet, and world-wide databases. At the end of this course, the student should be able to:

1. Describe the basic nucleotide building blocks of DNA and how to detect the presence of important features such as stem-loop structures and complementary DNA.
2. Describe the basic amino acid building blocks of protein sequences and how these building blocks contribute to structure and function
3. Demonstrate a working knowledge of the relevant protein, DNA and genomic databases at the National Center for Biotechnology Information and other centers, including record analysis, data archiving and search strategies.
4. Demonstrate a working knowledge of basic DNA sequence analysis tools and their applications, including restriction site analysis, DNA translation, open reading frame analysis, primer prediction, pair-wise alignments, sequence assembly, nucleotide frequencies, multiple sequence alignment, pattern matching, and dot-matrix analysis.
5. Demonstrate a working knowledge of basic protein sequence analysis tools and their applications, including motif searching, pattern matching, amino acid frequencies, molecular weight and isoelectric point determinations, hydrophobicity, hydrophilicity, amphipathicity and secondary structure prediction.
6. Describe the basics of amino acid substitution in proteins with regard to structural and functional outcomes in both mutational and evolutionary studies.
7. Demonstrate the use of available tools and databases to identify the important structural elements of a complex gene, including sequence motifs, exons, introns, coding, non-coding and regulatory regions.
8. Demonstrate the use of available tools and databases to decipher the structural elements of a complex protein, including conserved motifs, maturation sites, signal peptides, transmembrane domains, secondary structural domains and tertiary protein structure.
9. Demonstrate a working knowledge of the basics of BLAST similarity searches, multiple sequence alignment, and phylogenetic analysis and their use in DNA and protein sequence comparisons.
10. Describe the basics of gene and protein evolution and how available bioinformatic tools can be used to ascertain gene relationships, including similarity, homology, orthology and paralogy.

If you would like to request academic accommodations due to a disability, please contact Disabled Student Services, 448 Schmitz, 543-8924 (V/TDD). If you have a letter from Disabled Student

Services indicating that you have a disability that requires academic accommodations, please present the letter to me so we can discuss the accommodations you might need for the class.

BioInformatics and Gene Sequence Analysis

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Web -- <http://courses.washington.edu/bioinfo/>

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