

# Syllabus for BB485/585 Applied Bioinformatics

**Course Name:** Applied Bioinformatics

**Course Number:** BB485/585

**Course Credits:** 3

**Pre-requisites and Co-requisites:** BB314 or equivalent, or by instructor approval.

**Course Description:** Fundamental concepts needed to understand the software and methods used in bioinformatics. Includes contemporary techniques such as databases, gene and genome annotations, functional annotations, sequence alignment, motif finding, secondary structure prediction, phylogenetic tree construction, high-throughput sequence data, ChIP-Seq peak identification, transcriptome profiling by RNA-Seq, microRNA discovery and target prediction.

## **Course Content:**

Week 1: Introduction

Reading: Chapter 1: Introduction to Biological Sequences

Objectives: In week 1 you will learn how to

- Represent biological sequences in python, biopython, and more generally
- Navigate the GNU/Linux command line environment
- Represent sequences with the Bio.Seq module
- Read and write sequence files with SeqIO module
- Retrieve and print sequences with the Entrez module.

Week 2: Sequence Motifs

Reading: Chapter 2: Sequence Motifs

Objectives: In week 2 you will learn how to:

- Represent sequence motifs as consensus sequences and weight matrices
- Search for sequences patterns
- Discover motifs with MEME
- Search for motif instances with FIMO
- Represent sequence motifs with the Bio.motifs module

Week 3: Sequence Alignment

Reading: Chapter 3: Sequence Alignment

Objectives: In week 3 you will learn how to:

- Compute sequence alignments with Smith-Waterman and Needleman-Wunsch
- Search for sequences alignments using BLAST
- Understand BLAST statistics

Week 4: Molecular Evolution and Phylogenetics

Reading: Chapter 4: Molecular Evolution and Phylogenetics

Objectives: In week 4 you will learn how to:

- Understand the concept of phylogentic trees
- Understand how to computer a multiple sequence alignment with Clustalw and Phylip
- Understand how to use the python module Phylo
- Represent multiple sequence alignments in various file formats

## Week 5: Genomics

Reading: Chapter 5: Genomics

Objectives: In week 5 you will learn how to:

- Understand how to represent genomic annotations
- Interpret genome annotation files: GFF, BED, BedGraph
- Navigate with a genome browser

## Week 6: Transcriptomics

Reading: Chapter 6: Transcriptomics

Objectives: In week 6 you will learn how to:

- Perform an RNA-seq analysis including alignment, transcriptome assembly, expression quantification
- Understand paired-end vs single-end sequencing
- Understand high-throughput methods for determining transcription start sites, RNA polymerase stalling, small RNA expression

## Week 7: Noncoding RNAs

Reading: Chapter 7: Noncoding RNAs

Objectives: In week 7 you will learn how to:

- Understand thermodynamic parameters in RNA structure formation
- Understand thermodynamic parameters in triplex formation
- How to computer RNA structures using RNAfold

## Week 8: Proteins

Reading Chapter 8: Proteins

Objectives: In week 8 you will learn how to:

- Identify protein domains with HMMer
- Predict protein secondary structure with jnet
- How to retrieve substitution matrices using Bio.SubsMat module
- Understand substitution matrices

## Week 9: Gene Regulation

Reading: Chapter 9: Gene Regulation

Objectives: In week 9 you will learn how to:

- Understand how genes are regulated by transcription factors
- Perform a data-analysis workflow for ChIP-Seq with bowtie, MACS and MEME
- Understand how microRNAs regulate gene expression
- Predict microRNA targets with TargetScan

## Week 10: Catch-up and Review

**Course Specific Measurable Student Learning Outcomes:** As a result of taking BB485 the students will:

- Correctly utilize the specialized language of bioinformatics and computational biology.
- Analyze data using bioinformatics to understand eukaryotic gene regulation.
- Choose appropriate methods and research questions for bioinformatics investigations.
- Appropriately use command-line software in a GNU/Linux environment to answer specific bioinformatics questions.
- Appropriately use modules and methods from Biopython to answer specific bioinformatics questions.
- Apply modern methods of bioinformatics to medicine and biology.

In addition to these learner outcomes, students taking BB585 will also:

- Correctly synthesize different ideas from the course to use Biopython to carry out more complex tasks
- Correctly implement algorithms presented in the class including Smith-Waterman and Nussinov Algorithms
- Correctly integrate different concepts from the course into a research proposal using bioinformatics, genomics, transcriptomics, or other methods.

### **Evaluation of Student Performance:**

#### **BB485:**

Homework, 5 problem sets (50%: 5 sets 10% each for weeks 2,4,6,8,10)

Project write-ups (10%, close to weekly)

Mid Term Exam 50pts (20%)

Final Exam 100pts (20%)

#### **BB585:**

Graduate students will have additional, more advanced homework and/or test questions, as well as a Term Project consisting of either a **research proposal** or **Biopython implementation** in which ideas from the course are further synthesized and learned at a deeper level.

Homework, 5 problem sets (40%: 5 sets 8% each for weeks 2,4,6,8,10)

Project write-ups (10%, close to weekly)

Mid Term Exam 50pts (20%)

Final Exam 100pts (20%)

Term Project (10%)

### **Learning Resources:**

We will use the text “Applied Bioinformatics of Nucleic Acid Sequences” here:

<http://hendrixlab.cgrb.oregonstate.edu/teaching/ab/AB.pdf>

We will also follow computer lab projects outlined here:

<http://hendrixlab.cgrb.oregonstate.edu/teaching/appliedBioinformatics.html>

Class Lecture slides provided by Professor on canvas.

**Statement Regarding Students with Disabilities:** Accommodations for students with disabilities are determined and approved by Disability Access Services (DAS). If you, as a student, believe you are eligible for accommodations but have not obtained approval please contact DAS immediately at 541-737-4098 or at <http://ds.oregonstate.edu>. DAS notifies students and faculty members of approved academic accommodations and coordinates implementation of those accommodations. While not required, students and faculty members are encouraged to discuss details of the implementation of individual accommodations.

**Statement of Expectations for Student conduct:** The Student Conduct & Community Standards office has generated a set of standards & expectations for student behavior. This information is at <http://studentlife.oregonstate.edu/code>.

Cheating or plagiarism by students is subject to the disciplinary process outlined in the Student Conduct Regulations. Students are expected to be honest and ethical in their academic work. Academic dishonesty is defined as an intentional act of deception in one of the following areas:

- cheating – use or attempted use of unauthorized materials, information or study aids
- fabrication – falsification or invention of any information

- assisting – helping another commit an act of academic dishonesty
- tampering – altering or interfering with evaluation instruments and documents
- plagiarism – representing the words or ideas of another person as one's own

Behaviors disruptive to the learning environment will not be tolerated and will be referred to the Office of Student Conduct for disciplinary action.

*“The goal of Oregon State University is to provide students with the knowledge, skill and wisdom they need to contribute to society. Our rules are formulated to guarantee each student’s freedom to learn and to protect the fundamental rights of others. People must treat each other with dignity and respect in order for scholarship to thrive. Behaviors that are disruptive to teaching and learning will not be tolerated, and will be referred to the Student Conduct Program for disciplinary action. Behaviors that create a hostile, offensive or intimidating environment based on gender, race, ethnicity, color, religion, age, disability, marital status or sexual orientation will be referred to the Affirmative Action Office.”*