Instructors: Eric Johannsen, M.D., WIMR 6531, Phone: 262-9952
Mitch Hayes, WIMR 6559, Phone: 262-6697

Office Hours: By appointment.

Description: Course goal is threefold: First, to familiarize students with bioinformatics theory and principles; second, to provide students with real-world experience that they can apply to their own work; and third, to use the first two goals to provide a foundation of knowledge that the students can use critically to evaluate existing bioinformatics tools that they can use in their work - and in the absence of an appropriate tool, identify the analyses that demand the development of novel tools.

Format: This course will meet on T/TH for 75 minutes from 1:00-2:15 PM. Class sessions involve traditional lecture interspersed with class discussion. Students will be assess on the following: class participation (20 points), homework (140 points), and their final project (40 points).

Lecture Topics: Introduction to Bioinformatics, Statistics, Algorithms; Nucleic Acid Alignment; NextGen Sequencing Analysis; Proteomic Analysis; and Motif Search.


Prerequisites: 2nd (+) Year Graduate Student and enrollment in the Biophysics Graduate Program; Cancer Biology Graduate Program; the Cellular & Molecular Biology Graduate Program; Cellular Molecular Pathology Graduate Program; Integrated Program in Biochemistry; Molecular & Cellular Pharmacology Graduate Program; Molecular & Environmental Toxicology MD Graduate Program; or the Physiology Graduate Program.

*Available online: https://ebookcentral.proquest.com/lib/wisc/detail.action?docID=3338847
Course Outline (Tentative):

Introductory Lecture .......................................................... 1/23
  Review Syllabus; Introduction to algorithms
Lab 01 .................................................................................. 1/25
  Setup of local environments; Introduction to data structures
Alignment Lecture 1 ............................................................... 1/30
  Global Alignment (Needleman-Wunsch); Mismatch penalties; Introduction to
  Dynamic Programming
Lab 02 .................................................................................. 2/1
  Global Alignment Exercises; Computer tools to solve alignments
Alignment Lecture 2 ............................................................... 2/6
  Local Alignment (Smith-Waterman); BLAST
Lab 03 .................................................................................. 2/8
  Local Alignment Exercises; BLAST; Sanger Sequencing
NGS Intro Lecture ................................................................. 2/13
  Review of Next-Generation Sequencing Platforms; Libraries; Quality Scores
Lab 04 .................................................................................. 2/15
  NGS Workflow; File Formats; Galaxy; FASTQC
NGS Alignment Lecture ........................................................ 2/20
  Short Read Alignment; Suffix Trees; STAR
Lab 05 .................................................................................. 2/22
  BWA; IGV; STAR Genome Indexes (local)
Lab 06 .................................................................................. 2/27
  STAR 2-pass RNAseq (local); STAR (Galaxy); Handling unmapped reads; UCSC
  Genome Browser
Differential Expression Analysis Lecture ................................ 3/1
  Statistics for differential expression analysis; DESeq2
Labs 07A&B ........................................................................... 3/6, 3/8
  Processing STAR output; DESeq2 (local and Galaxy); R Intro; DESeq2; GSEA
ChIP-Seq Lecture ................................................................. 3/13
  Principles of ChIP-Seq; Peak calling; Normalization
Lab 08 .................................................................................. 3/15
  MACS; Visualization of ChIP-Seq tracks on UCSC Genome Browser
Protein Alignment Lecture .................................................... 3/20
  BLOSUM50; BLASTP; synonymous/nonsynonymous mutations
Lab 09 .................................................................................. 3/22
  BLOSUM exercises; BLASTP
Spring Break 3/24-4/1
Multiple Alignment Lecture .................................................... 4/3
  Neighbor-Joining; ClustalW; PSI-BLAST
Lab 10 .................................................................................. 4/5
  Multiple Alignment Exercises; Plasmid annotation
Motif Finding; Special Topics ................................................. 4/10, 4/12, 4/17, 4/19
Student Project Presentations ................................................. 4/24, 4/27, 5/1
**Grade Policy:** The final grade will be determined by the percentage earned of total points available for the course.

The final grade scale is:

**Graduate Students**
- A 186-200 points
- AB 176-185 points
- B 166-175 points
- BC 156-165 points
- C 146-155 points
- D 130-145 points
- F 0-129 points

**Learning Outcomes:** Upon successful completion of this course, students will have sufficient knowledge to select the appropriate analysis tools for common bioinformatics problems, appropriately format their data, execute the analysis, adjust different parameters, and interpret their results.

**Grading:** Component breakdowns are as follows:

- 10% Participation
- 70% Problem Sets
- 20% Final Project

**Problem Sets:** Problem Sets will be distributed to students throughout the semester. These are intended to provide hands-on experience in the evaluation and application of bioinformatics algorithms and tools. Some problems will require the use of bioinformatics software (both locally installed on students’ computers and cloud-based tools) to solve real-world problems.

**Guidelines for Evaluating Participation:**

1. **Outstanding Contributor:** Contributions in class reflect exceptional preparation. Ideas offered are always substantive; provide one or more major insights as well as direction for the class. Challenges are well substantiated and persuasively presented. If this person were not a member of the class, the quality of discussion would be diminished markedly. (Outstanding contributors will receive full credit = 20 points.)

2. **Good Contributor:** Contributions in class reflect thorough preparation. Ideas offered are usually substantive; provide good insights and sometimes direction for the class. Challenges are well substantiated and often persuasive. If this person were not a member of the class, the quality of discussion would be diminished. (Good contributors will receive 15 out 20 points.)

3. **Adequate Contributor:** Contributions in class reflect satisfactory preparation. Ideas offered are sometimes substantive, provide generally useful insights but seldom offer a new direction for the discussion. Challenges are sometimes presented, fairly well substantiated, and are sometimes persuasive. If this person were not a member of the class, the quality of discussion would be diminished somewhat. (Adequate contributors will receive 10-14.5 out of 20 points.)
4. Non-Participant: This person says little or nothing in class. Hence, there is not an adequate basis for evaluation. If this person were not a member of the class, the quality of discussion would not be changed. (Non-participants will receive 5.5-9.5 out of 20 points.)

5. Unsatisfactory Contributor: Contributions in class reflect inadequate preparation. Ideas offered are seldom substantive; provide few if any insights and never a constructive direction for the class. Integrative comments and effective challenges are absent. If this person were not a member of the class, valuable air-time would be saved. (Unsatisfactory contributors will receive 0-5.0 out of 20 points.)

Important Dates:

- First Session .................................................. Jan 23
- Add Deadline .................................................... Feb 2
- Last Session ..................................................... May 3