DEPARTMENT OF ELECTRICAL ENGINEERING AND COMPUTER SCIENCE
UNIVERSITY OF TENNESSEE - KNOXVILLE

# COSC 494/594 Special Topic: Bioinformatics Computing
# Fall 2018 Syllabus

**Time and Location**: Tuesday & Thursday 12:40 pm-1:55 pm, Min Kao 419

**Instructor:**


- Dr. Scott Emrich
  - Office: 608 Min Kao; 974-3891; **semrich@utk.edu**;
  - Tentative office hours: Mon 2:00pm-3:00pm, after class and by appointment
  - If my office door is open, you are welcome to come in and ask questions.


**Course Webpage:** http://web.eecs.utk.edu/~semrich/bcfall18/

**Short Course Description:**

- Broad overview of bioinformatics with a substantial problem-solving component. Topics include: generative models for sequences, pairwise sequence alignment, basic methods in molecular phylogeny and evolution, *ab initio* gene prediction, whole genome comparisons, genome assembly and analysis.

**Course Outcomes:** At the end of the course, you will be able to answer, "What is bioinformatics?" and "What does computer science really have to offer biologists?" Specifically, you will be able to:

1. Define computational genomics and phylogenetics concepts. Assessed in exams.
2. Apply common bioinformatics tools and techniques effectively. Assessed in exams and assignments.
3. Implement basic algorithms such as sequence alignment. Assessed in exams and programming assignments.
4. Perform independent genome comparisons and assemblies using gained knowledge. Assessed in assignments.
5. Evaluate on your own the promise and challenges for computing on biological datasets. Assessed in the final project.

**Ideal prerequisites:**
CS340 for CS students, at least one semester of programming for non-EECS students.

**Textbook:** Cristianini and Hahn, *Introduction to Computational Genomics*.

Additional material will be made available as needed throughout the semester.

**Schedule of Major Topics and Exams:**

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|---|---|---|
| 1. | DNA, genes and the genome | (8/23) |
| 2. | Sequence statistics | (8/28) |
| 3. | Sequence alignment | (8/30-9/6) |
| 4. | Variation and natural selection | (9/11) |
| 5. | Hidden Markov Models | (9/13-9/20) |
| 6. | *Ab initio* gene finding | (9/25) |
| 7. | Whole genome comparisons | (10/2-10/11) |
| 8. | Midterm exam | (10/9 *in class*) |
| 9. | Genome assembly and validation | (10/18-10/25) |
| 10. | Phylogenetic analysis | (10/30-11/13) |
| 11. | Special topics | (throughout) |
| 12. | Project presentations | (12/4 in *class*) |
| 13. | Final exam | (TBD) |

**Grading:** I will neither give an extension nor grade late work. You will have one of two alternatives. By default, the lowest homework grade greater than an 84% (B; see below) will be dropped before computing final grades. If the grade is below and/or by choice, students can alternatively submit one updated assignment for re-grading by 11/28. The revised grade will be used for final grading.

Final grades will be computed from a weighted sum of points as follows:

45%: homework (including programming and written answers submitted)
25%: final project
20%: midterm exam (Tuesday, October 9th)
10%: class participation

Course percentages will be translated into letter grades as follows: A: 94% and up; A-: 91-94$^{-}$%; B+: 88-91$^{-}$%; B: 84-88$^{-}$%; B-: 81-84$^{-}$%; C+: 78-81$^{-}$%; C: 74-78$^{-}$%; C-: 71-74$^{-}$%; D: 64-71$^{-}$%; F: 0-64$^{-}$%.

Absences will only be excused in accordance with University policy.

**Project:** A final project involving teams of students will be due at the end of the semester. Teams must consist of two to four students (solo projects won't be allowed).

**ADA statement:** If you need an accommodation based on a disability can contact Dr. Emrich privately. Full accommodation will be made once approved.

**Academic Code of Honor**: Any instance of academic dishonesty will not be tolerated. Because I want you to study and discuss course-related work with classmates, but will require you to submit independent assignments/programs, please refer to this document I co-wrote at ND for guidance: http://cse.nd.edu/undergraduates/courses/honor-code. I intend to use the "default" table listed this semester. In short, all graded work should go from your head to your fingers to submission; no copying of solutions (group or online).