

Course Syllabus
STM 3900E – Special Topics: Bioinformatics Algorithms (1.5 credits)
Winter Term AY25–26

Instructor information

Prof. Eliah Overbey, coverbey@uaustin.org

Office hours: 1:00-2:00 Fri

Course meeting schedule

2:00-3:15pm Fridays in Scarbrough Building (Room TBD)

Required Text

None

Course description

A first course in bioinformatics algorithms. Topics include algorithmic approaches to identifying origins of replication through genome skew analysis and frequent pattern discovery; motif discovery and regulatory pattern identification as molecular clocks; graph-based genome assembly using overlap graphs and de Bruijn graphs; sequence alignment and dynamic programming for comparing DNA sequences; string matching and clump finding algorithms in large genomes; probabilistic scoring models for motifs and alignments; and computational reconstruction of genomes from high-throughput sequencing reads.

This course is an experiment in AI-native instruction at UATX. Artificial intelligence functions as the primary engine of instruction and feedback, while human educators serve as coaches, evaluators, and architects of accountability. Students will follow lecture signposts provided by the instructor while using a large language model for concept understanding, guided exploration, and mastery.

Course learning outcomes

Upon successful completion of this course, a student will be able to:

- Formulate biological questions (e.g., replication origin detection, motif discovery, genome assembly, sequence comparison) as precise computational problems.
- Implement and analyze string algorithms for pattern matching, frequent word discovery, clump finding, and skew analysis in genomic sequences.
- Design and evaluate motif-finding approaches, including deterministic and randomized strategies, and interpret their biological significance.

- Construct and analyze graph-based models (overlap graphs and de Bruijn graphs) for genome assembly and solve the string reconstruction problem.
- Apply dynamic programming techniques to compute global and local sequence alignments and interpret alignment scores biologically.
- Compare DNA sequences using scoring matrices and gap penalties, and evaluate evolutionary or functional similarity.
- Assess algorithmic complexity and tradeoffs between exact, heuristic, and randomized methods in computational genomics.
- Translate raw sequencing reads into reconstructed genomic structures and articulate the limitations imposed by repeats, coverage, and sequencing error.

Course Policies/Requirements

- Your instructor will specify all homework assignments, quizzes, and examinations, along with required completion dates.
- AI-native lecture guides and corresponding assignments will be posted in Populi.
- Late assignments will not be accepted. The final course examination will be held during the university-wide exam week after Week 10.
- No makeup exams will be given unless you have a prior excusal or are sick in quarters. It is your responsibility to arrange for a makeup exam if required.
- Course grades are on a 100-point scale. All professors are required to target a course average of 85/100. See the [UATX Academic Catalog](#) for complete grading policy details.
- Grade weighting will be:

Homework 30% In-Class Quizzes 40% Final Exam 30%

- Collaboration on homework is encouraged. Document any such collaboration.
- You may refer to outside sources to assist with homework. Document any such assistance.
- Cheating will not be tolerated. In particular, exchanging electronic files containing work you have done for a graded assignment is prohibited unless stated otherwise. Cheating also includes but is not limited to looking at another student's quiz or exam, copying someone else's homework, and using unauthorized material during a quiz or exam.
- You must have a laptop available for use outside of class. The use of computing technology is encouraged in support of all work outside of class unless otherwise stated.
- Please see the Student Handbook for policies regarding support for special needs or disabilities.

Attendance and Tardiness Policy

- Attendance is mandatory.
- Each student may miss 10% of classes for any reason, with no excuse needed, and without penalty, i.e., 1, 2, or 3 classes, respectively, in a 1.5, 3, or 4.5 credit course.
- After that, each additional absence (for any reason) will result in a 4% or 6% or 12% final grade penalty for a 4.5 or 3.0 or 1.5 credit course, respectively.
- Missing more than 25% of the classes in a course (without medical excuse), including "free" absences, will result in failing the course.
- Being more than 20 minutes late to a class counts as an unapproved absence.

Accessibility Statement

Please review the University Accessibility Statement in the student catalog. Students having special needs should contact the Polaris Center or email Accommodations@uaustin.org.

Disability Support Services: The university will make reasonable accommodations for students with disabilities in compliance with Section 504 of the Rehabilitation Act and the Americans with Disabilities Act. The purpose of accommodations is to provide equal access to educational opportunities for eligible students with academic and/or physical disabilities.

Academic Misconduct

Instructors at UATX have the authority to assess possible plagiarism, unauthorized use of artificial intelligence, and other forms of cheating in their courses. Normally, cheating will result in failing the assignment.

Course outline (subject to change)

Week	Dates	Agenda	Attendance Required?
1	3-Apr	Course Introduction	Yes
2	10-Apr	In-Class Office Hours Students should be working on Topic Area 1: Algorithmic Detection of DNA Replication Origins	No
3	17-Apr	Topic 1 Quiz Covers core themes from Topic Area 1, including pattern matching in genomes, frequency analysis, skew diagrams, clump finding, replication origin detection.	Yes
4	24-Apr	In-Class Office Hours Students should be working on Topic Area 2: Motif Discovery and Molecular Pattern Recognition	No
5	1-May	Topic 2 Quiz Covers core themes from Topic Area 2, including conserved sequence motifs, regulatory elements, consensus strings, probabilistic scoring, randomized motif search.	Yes
6	8-May	In-Class Office Hours Students should be working on Topic Area 3: Graph Algorithms for Genome Assembly	No
7	15-May	Topic 3 Quiz Covers core themes from Topic Area 3, including overlap graphs, de Bruijn graphs, Eulerian paths, string reconstruction, repeat resolution.	Yes
8	22-May	In-Class Office Hours Students should be working on Topic Area 4: Sequence Alignment and Comparative Genomics	No
9	29-May	Topic 4 Quiz Covers core themes from Topic Area 4, including global and local alignment, dynamic programming, scoring systems, evolutionary interpretation.	Yes
10	5-June	In-Class Office Hours Students should be studying Topic Areas 1-4 for the Final Exam.	No