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CS 790: Evolutionary Computation in Bioinformatics

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Instructor: Dr. Michael Raymer  
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Room and Time: Tue/Thu, 6:05 – 7:20 pm, 302 Russ Center  
Office Hours: Tue/Thu: 3:30 – 6:00 pm, or by appointment.


Overview: This course will provide a guided investigation into advanced computational techniques in bioinformatics, especially techniques involving evolutionary computation. The first few weeks will consist of guided in-class discussions reviewing the basic principles of bioinformatics and evolutionary computation. During weeks 3 – 6 students will present tutorials on advanced computational topics (see the list of suggested topic areas below). During weeks 7 – 10, the students will present papers from the literature in which topics covered in the tutorials have been applied to specific problems in bioinformatics. The class will discuss the quality and findings of these papers.

Course Organization:

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<th>Weeks</th>
<th>Topics</th>
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<td>1 - 2</td>
<td>Guided Discussions: Molecular Biology, Bioinformatics, Genetic Algorithms, Pattern Recognition</td>
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<td>Tutorials on advanced techniques</td>
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Web Page: We will be using the WSU WINGS course web page for distribution of files, course announcements, links, etc. Please check the announcements section of this page often.

Tutorials: Each student will present one or more tutorial on an advanced computational technique that is employed in bioinformatics investigations. The tutorials are expected to be presented at such a level that the rest of the class will be able to successfully apply the technique in question to a small sample data set. At the end of each tutorial, the presenter will provide a small take-home homework problem for the rest of the class. The presenter will correct the completed homework assignments. The presenter's performance will be evaluated by the rest of
the class (20% of the presentation grade) and the instructor (80% of the grade). Some possible tutorial topics include:

- Evolution strategies
- Hidden Markov models
- Bayesian classification
- Random forest classification
- Support vector machines
- Principal component analysis
- Linear discriminant analysis
- Wavelet representations
- Clustering or biclustering techniques
- Kernel-based density estimation and parametric classification
- Messy genetic algorithms and fast messy GA’s
- Evolutionary programming
- Genetic learning techniques
- Feature selection and extraction techniques
- Gene expression microarrays
- Metabolic and regulatory network inference
- Radial basis functions
- Decision tree classification
- Protein folding algorithms
- Threading
- Gene finding
- Drug lead screening and/or docking
- QSAR
- Genetic symbolic and numeric regression
- Multiple sequence alignments
- Protein secondary structure prediction

**Literature Presentations:**

After the tutorials have been completed, each student will present one or more papers from the literature for presentation to the class. The papers will be selected and distributed to the class at least one week prior to the presentation. Students will be expected to come to class having read the paper and prepared to discuss its contents. The class session will then consist of a 45 - 55 minute presentation of the paper contents followed by (or perhaps punctuated by) a class discussion of the techniques, results, and quality of the presentation. Literature presentations will be evaluated by the instructor for completeness and quality.
Proposal: The take-home final exam will consist of a proposal, written in a format that would be presentable to the National Science Foundation (NSF) for application of an advanced computational technique to a current problem in bioinformatics. Further details will be provided later in the class.

Grading: The course grade will be based on participation in class discussions, and student and instructor evaluations of the quality of your in-class presentations. There will also be a take-home final paper in which you will write an NSF-style proposal for funding based on a hypothetical application of one of the techniques covered in this course to an open problem in bioinformatics.

Grade Scale: Discussion participation & homework = 10%
Tutorial presentation(s) = 30%
Paper presentation(s) = 30%
Take-home final exam = 30%

Academic Integrity:
Discussion of course contents with other students is an important part of the academic process and is encouraged. However, it is expected that course assignments will be completed on an individual basis. Students may discuss general concepts with one another, but may not, under any circumstances, work together on the actual implementation of any course assignment. If you work with other students on "general concepts" be certain to acknowledge the collaboration and its extent in the assignment. Unacknowledged collaboration will be considered dishonest.

Plagiarism: Plagiarism is defined as the use of another’s ideas or words without appropriate acknowledgment. Examples of plagiarism include the use of someone else’s ideas without properly citing the source, and the use of another’s writings without placing the text in quotes and providing an appropriate citation. Plagiarism on course assignments is a violation of the University’s academic integrity policy. For more details see: http://www.wright.edu/students/judicial/integrity.html

NOTE: Failure to attend the first day of class, during which time I will explain these academic honesty policies in detail, does not excuse you from following these policies. If you have any questions about collaboration or any other issues related to academic integrity, please see me immediately for clarification.