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Fall 2007

### CS/BIO 471/671: Algorithms for Bioinformatics

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# CS/BIO 471/671 – ALGORITHMS FOR BIOINFORMATICS

Fall, 2007

## Course Description

Theory-oriented approach to the application of contemporary algorithms to bioinformatics. Graph theory, complexity theory, dynamic programming and optimization techniques are introduced in the context of application toward solving specific computational problems in molecular genetics. 4 credit hours.

## Meeting Time and Place

1:30 – 2:45      Monday and Wednesday      036 Rike Hall

## Textbooks

J. Setubal and J. Meidanis (1997), *Introduction to Molecular Biology*, Brooks/Cole Publishing, ISBN: 0-534-95262-3

D. Krane and M. Raymer (2003), *Fundamental Concepts of Bioinformatics*, Benjamin Cummings, ISBN: 0-8053-4633-3

## Instructors and Office Hours

Dr. Michael Raymer  
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<http://www.wright.edu/~michael.raymer>  
Office hours: Mon/Tue/Wed, 4:00 – 5:00 pm  
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Dr. Dan Krane  
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Office hours: Tues/Thurs, 1:30 – 2:45 pm  
*or by appointment.*

## Course Web Page

The course web page will be the primary method for distributing important announcements, course material, class notes, etc. Please check the page often. Login to the campus WebCT system using your CATS username and password. The URL is: <http://wisdom.wright.edu>

You can find an archive of the course materials at: <http://birg.cs.wright.edu/cs471>

## Grading

Course grades will be determined as follows:

30% Midterm Exam  
40% Final Exam  
30% Project/homework assignment(s)

*Final grades will be based on the standard university-wide score divisions (i.e. 90%, 80%, 70%, etc.). However, the instructors may choose to curve the final grades depending on the distribution of scores at the end of the term.*

## **Tentative Lecture Schedule**

### **Week 1 – Basic concepts of molecular biology** (Ch. 1, Krane & Raymer; Ch. 1 Setubal & Meidanis)

- The molecular mechanisms of transcription, translation and protein synthesis
- Junk DNA, reading frames and chromosomes, repeated DNA
- Is the genome like a computer program?
- How is the genome studied

### **Week 2 – Data structures and complexity** (Class notes only)

- The RAM model of computing, time and space complexity
- Design and analysis of simple algorithms, sorting
- Asymptotic notation
- Counting methods and Combinatorics
- Polynomial and non-polynomial growth, introduction to NP-completeness

### **Week 3 – Gene structure and regulation** (Chs. 1 & 6, Krane & Raymer)

- Prokaryotic and eukaryotic gene organization
- Regulation of gene activity, micro-RNAs
- DNA replication and error
- The process of molecular evolution

### **Week 4 – Sequence comparison and searching** (Ch. 3, Setubal & Meidanis)

- Global, local, and semi-global comparison
- General and affine gap-penalty functions
- Comparing multiple sequences
- BLAST and FASTA
- Sequence search statistics and significance

### **Week 5 – Introduction to graph theory and algorithms** (Section 2.2 of Setubal & Meidanis)

- Introduction to graph terminology and techniques
- Greedy strategies, exhaustive strategies, dynamic programming
- 0-1 knapsack problem

### **Week 6 – Fragment assembly of DNA** (Ch. 4, Setubal & Meidanis)

- Experimental methods for DNA sequencing
- Models for fragment assembly: shortest common superstring, reconstruction, Multicontig
- Experimental complications: base call errors, unknown orientation, repeats

### **Week 7 – Physical mapping of DNA** (Ch. 5, Setubal & Meidanis)

- Restriction site mapping, hybridization mapping
- Mathematical & computational models

### **Week 8 – Phylogenetic trees** (Chs. 4 & 5, Krane & Raymer)

- Trees and distances
- Distance-based approaches
- Character-based approaches
- Applications: PAM and BLOSSUM

### Week 9 – Gene expression and microarrays (Notes only)

- cDNA and oligonucleotide microarrays
- Computational challenges
- Clustering

### Week 10 – Forensic DNA & special topics (Notes only)

- Analysis of forensic DNA – computational and statistical issues

## Policies & Notes

**Homework assignments** are due by the end of the lecture period on the assigned due date. Late homework submissions cannot be accepted.

**Collaboration** is encouraged, as discussion of the course contents with other students is an important part of the learning process. However, it is expected that course assignments will be completed *on an individual basis* unless the assignment states otherwise.

Students may not, under any circumstances, work together in actual implementation of any course assignment. Do not allow other students to view or copy your code. Code sharing, including code from previous quarters, is strictly disallowed. Copying or significant collaboration on any graded assignment will be considered a violation of university guidelines for academic integrity and reported to the Office of Judicial Affairs. The Code of Student Conduct can be viewed at <http://www.wright.edu/students/judicial/conduct.html> or a hand copy can be obtained from the Office of Student Judicial Services in W035 Student Union. If you have any questions about these policies, it is your responsibility to discuss them with the instructor of the course or a representative of the Office of Judicial Affairs as soon as possible.

If the same work is turned in by two or more students, all parties will be held equally accountable for violation of academic integrity. In other words, *you are responsible for ensuring that other students do not have access to your work*. If you suspect that your work material has been compromised, notify an instructor immediately.