

Bioinformatics Math 3994

(crosslisted as BIOL 4620, CHEM 3994, CS3994)

TR 9-10AM Room 403

Team taught by: Colette Calmelet, Todd Amon, Bruce Howard,
and Charlotte Pedersen.

Colette Calmelet (Coordinator)

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Office Hours: (every other week)

T: 5-6PM, W: 10-12PM,

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Course description:

Mathematical Modeling, introduction to sequence analysis including genomics/proteomics, database searches, pairwise and multiple sequence alignments, phylogenetic trees, with a supportive framework of mathematical, statistical, and computer concepts and applications, including graph theory, Markov models, computational complexity, decision and search trees, Perl scripting, BLAST, PyMOL.

Prerequisites:

Besides a familiarity with basic biology, chemistry, probability, statistics, Mathematica Programming, the specific courses CS 1100 and MATH 3210 are required.

Recommended background: BIOL 2150, CHEM 2320

Required textbook:

Modeling Nature by Richard Gaylord. We will also use a variety of texts, handouts, and internet resources.

Homework:

Each instructor will assign (and grade) homework problems.

Attendance:

Regular attendance is required at all class meetings.

Grading:

Homework Assignments: 60%

Research Project: 40%

Grading policy:

A = 93-100 B⁻ = 79-83 D⁺ = 66-69

A⁻ = 89-93 C⁺ = 76-79 D = 63-66

B⁺ = 86-89 C = 73-76 D⁻ = 60-63

B = 83-86 C⁻ = 69-73 F = < 60

There will be no curving of the grades. A straight percentage scale will be used.

Academic integrity policy:

Read it [here](#).

Students with disabilities:

Please read [this](#).

Follow this link for more information on [Mathematics and the Genome](#)

Here are some more links:

[Mathematica Applications to Bioinformatics](#)

[National Center for Biotechnology Information](#)

[TIGR](#)

[A microarray presentation](#) (requires Flash player)

[DNA Databank of Japan](#)

[EMBL Database](#)

[ExPASy Molecular Biology Server](#)

[Protein Data Bank](#)

[DOE Internship information](#)

[Amon's links for bioinformatics](#)

[DNA and RNA folding](#)

[Science Magazine's Functional Genomics](#)

Lecture Schedule

Lecture Material (and links!)	Lecturer
Introduction to Mathematica Programming, H/W Cellular Automata Simulations and Mathematica Programming, H/W Applications to Bioinformatics, HW Graph & matrix theory, metabolic pathways, HMMs, READ: newly found function of RNA , graph theory and RNA , graph theory and proteins . Research Project in Biomathematics.	Professor Calmelet
Introduction and programming in Perl, HW Trees, more programming, HW Computational complexity	Professor Amon
Basic DNA science, transcription/translation, DNA sequencing, PCR cDNA libraries. Functional genomics, shotgun sequencing, proteomics and microarrays. H/W Functional genomics NCBI resources, Entrez, PubMed, GenBank flatfile and FASTA annotation formats, H/W ORFS, Pairwise sequence alignment, Smith-Waterman , BLAST , PSI-BLAST , H/W	Professor Rosendahl
Crystallography, PDB database, motifs, PyMOL, O, Cn3D, and some H/W (TBA)	Professor Howard

Disclaimer:

Information contained in this syllabus, other than the grading, late assignments, makeup work, and attendance policies, may be subject to change with advance notice, as deemed appropriate to the class or instructor.