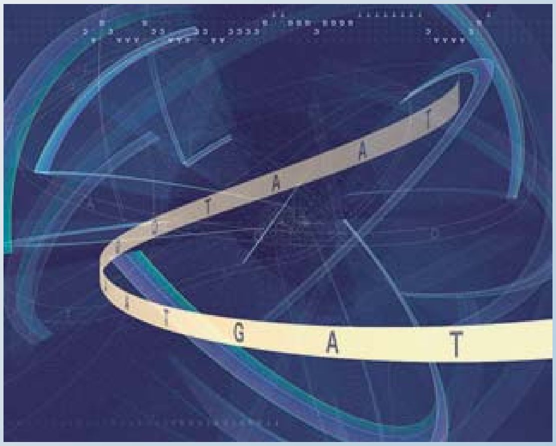
6.096 - Algorithms for Computational Biology

Spring 2005



Valence visualization of the BLAST algorithm by Ben Fry

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This new course covers the algorithmic foundations of computational biology, combining theory with practice. We study the principles of algorithm design for biological datasets, analyze existing algorithms, and apply these to real datasets.

Strings: biological sequence analysis, gene finding, motif discovery, RNA folding, global and local sequence alignment

Genomes: genome assembly, comparative genomics, genome duplication, genome rearrangements, evolutionary theory

Networks: gene expression, clustering algorithms, scale-free networks, machine learning applications to genomics

Lectures: F9:30-11
Units: 2-0-4
Prereq: 6.001, 7.01
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Lectures and homeworks are coordinated with 6.046, the quintessential introductory algorithms course taught by Charles Leiserson and Ron Rivest.

How to enroll:

With 6.046: The best of both worlds! Enroll simultaneously in 6.046 and 6.096. 6.046 meets on MW 9^{30}-11. Grading is separate in the two courses.

After 6.046: If you're already taken algorithms, you can enroll for 6.096 only, as a separate course, with permission of instructors.

Enrollment may be limited. Preregister at http://student.mit.edu/