Computational Biology
Genomes - Networks - Evolution

Learn about:
- Comparative genomics
- Epigenomics
- Regulatory motifs and networks
- Functional genomics
- Phylogenomics

Prof. Manolis Kellis - MIT / CSAIL / Broad Institute

Covers the algorithmic and machine learning foundations of computational biology combining theory with practice. We cover both foundational topics in computational biology, and current research frontiers. We study fundamental techniques, recent advances in the field, and work directly with current large-scale biological datasets.

- **Genomes:** Biological sequence analysis, hidden Markov models, gene finding, comparative genomics, RNA structure, sequence alignment, hashing
- **Networks:** Gene expression, clustering/classification, EM/Gibbs sampling, motifs, Bayesian networks, microRNAs, regulatory genomics, epigenomics
- **Evolution:** Gene/species trees, phylogenomics, coalescent, genome duplication, population genomics, human ancestry, recent selection, disease mapping

In addition to the technical material in the course, the term project provides practical experience (1) writing an NIH-style research proposal, (2) reviewing peer proposals, (3) planning and carrying out independent research, (4) presenting research results orally in a conference setting, and (5) writing results in a journal-style scientific paper.

**Satisfies TQE requirement in AI (6.878)**
**Serves as EC elective in Theory (6.047)**
**Final project can lead to papers/thesis**

First class: Thu Sept 9 at 9:30am in 4-159