Interdepartmental Computational Biology and Bioinformatics

The Interdepartmental Ph.D. Program in Computational Biology and Bioinformatics provides opportunities for research and training in this rapidly growing multi-disciplinary field. The systematic acquisition of data made possible by genomics and proteomics technologies has created a tremendous gap between available data and their biological interpretation. Given the rate of data generation, it is well recognized that this gap will not be closed with direct individual experimentation. Computational and theoretical approaches to understanding biological systems provide an essential vehicle to help close this gap. These activities include computational modeling of biological processes, computational management of large-scale projects, database development and data-mining, algorithm development and high-performance computing, as well as statistical and mathematical analyses.

Faculty Research Interests [http://cbb.yale.edu/faculty.html]
- Murat Acar, Adaptive Gene Network Evolution and Cellular Aging
- Julien Berro, My lab aims to uncover the mechanisms of force transduction at the molecular level using quantitative microscopy and computational approaches
- Joseph Chang, Probability, stochastic processes, sequential analysis, quality control, genetics, evolution, and bioinformatics
- Kei-Hoi Cheung, Bioinformatics; interoperation of genomic databases
- Damon Clark, The Clark lab uses behavior, physiology, and mathematical modeling to investigate how circuits of neurons perform fundamental computations
- Ronald Coifman, Analysis tools for spectrometric diagnostics and hyperspectral imaging
- Chris Costapas, Arthritis, Rheumatoid; Autoimmune Diseases; Diabetes Mellitus, Type I; Genetics; Genetics, Medical; Genetics, Population; Graves Disease; Immune System Diseases; Lupus Erythematosus, Systemic; Multiple Sclerosis; Thyroiditis, Autoimmune; Inflammatory Bowel Diseases; Human Genome Project; Computational Biology; Autoimmune Diseases of the Nervous System; Demyelinating Autoimmune Diseases, CNS; Genomics; Genetic Research; Systems Biology
- Forrest Crawford, Mathematical and statistical problems related to stochastic processes in biomedical and evolutionary science
- Thierry Emonet, Modeling of biological systems
- Donald Engelman, Developing a chemical understanding of membrane protein folding and oligomerization to use in interpreting evolution and function
- Richard Flavell, Biology; Diabetes Mellitus; DNA, Recombinant; Immune System; Immunity; Lyme Disease; Autoimmunity; Gene Expression; Gene Transfer Techniques; Mice, Knockout; Cell Lineage; Lyme Neuroborreliosis
- Alison Galvani, Integrating epidemiology, evolutionary ecology and economics
- Mark Gerstein, Bioinformatics, large-scale analysis of genome sequences, macromolecular structures, and gene expression data
- Antonio Giraldez, The Giraldez lab investigates how gene expression regulates vertebrate development and the molecular mechanisms of Autism, using Zebrafish as a model system
- Murat Günel, My lab focuses on gene discovery in diseases of the human brain, specifically on abnormalities of its development, vasculature and tumors. We use next generation genomic technologies to identify disease causing mutations followed by in vitro and in vivo functional
studies to understand underlying molecular mechanisms with the goal to help design better/novel diagnostics, therapeutics and non-invasive treatments

**William Jorgensen**, Computational chemistry

**Douglas Kankel**, Genetic and molecular analysis of visual system development in Drosophila

**Steven Kleinstein**, Disease/tissue/pathway/process modeling and simulation

**Yuval Kluger**, Computational analysis of high-throughput datasets generated from experiments involving cancer, hematopoiesis, and cell cycle genomics.

**Michael Krauthammer**, Bioinformatics of molecular interaction networks; text mining

Smita Krishnaswamy, Computational modeling and analysis of high throughput single-cell data in developmental systems, immunology and cancer

**Haifan Lin**, RNA-mediated epigenetic programming and post-transcriptional regulation of stem cells

**Elias Lolis**, Structural biology of proteins involved in inflammation and cancer

**Jun Lu**, Using genomics to understand the role of non-coding RNAs in mammalian development and disease.

**Steven (Shuangge) Ma**, Bioinformatics and statistical analysis of survival data

**Andrew Miranker**, Molecular mechanisms of protein folding, misfolding and pathological assembly into amyloid fibers

**James Noonan**, Evolutionary dynamics of gene regulation; synthetic biology

**Corey O’Hern**, Statistical mechanics and molecular dynamics simulation applied to biology

**Anna Pyle**, Computational biology on RNA

**Lynne Regan**, Protein structure, function and design

**Valerie Reinke**, Stem Cell Self-Renewal and Cell Symmetry

**Gordon Shepherd**, Experimental and computational studies of sensory transduction, synapses, dendrites, and microcircuits using the olfactory pathway as a model system

**Avi Silberschatz**, Bioscience database systems

**Dieter Söll**, Biochemical and genomic studies of the evolution of protein synthesis

**Jeffrey Townsend**, Functional genomics and evolutionary biology

**Gunter Wagner**, Developmental evolution of morphological characters; conceptual and mathematical work on the theory of evolution

**Anita (Zuoheng) Wang**, Development of statistical and computational methods to address problems in genetics

**Heping Zhang**, Statistical genetics and neuroimaging analysis

**Hongyu Zhao**, Statistical genomics and proteomics

**Steven Zucker**, Computational vision, biological perception, artificial intelligence, and robotics