CURRICULUM IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY (GRAD)

Contact Information
Curriculum in Bioinformatics and Computational Biology
http://bcb.unc.edu

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Modern biology, in this postgenome age, is being greatly enriched by an infusion of ideas from a variety of computational fields, including computer science, information science, mathematics, operations research, and statistics. In turn, biological problems are motivating innovations in these computational sciences. There is a high demand for scientists who can bridge these disciplines. The goal of the Curriculum in Bioinformatics and Computational Biology (BCB) is to train such scientists through a rigorous and balanced curriculum that transcends traditional departmental boundaries.

Incoming students are expected to matriculate from a broad range of disciplines; thus, it is important to ensure that all students have a common foundation on which to build their BCB training. The first year is dedicated to establishing this foundation and training all students with a common set of core BCB courses. BCB students will also participate in three laboratory research rotations their first year and ultimately join a laboratory at the end of those rotations. Research work is done in the laboratory facilities of the individual faculty member and is supported primarily by faculty research grants.

Curriculum faculty have appointments in 18 departments in the School of Medicine, School of Dentistry, Gillings School of Global Public Health, Eshelman School of Pharmacy, School of Information and Library Science, and the College of Arts and Sciences. This level of diversity allows students a broad range of research opportunities.

Requirements for Admission for Graduate Work

Ideal BCB candidates should have an undergraduate degree in a biological, physical, mathematical, or computational science. They must apply to the program through a unified application program known as the Biological and Biomedical Sciences Program (BBSP). Students apply for graduate study in the biological or biomedical sciences at UNC-Chapel Hill. Students interested in any of the BBSP research areas apply to BBSP, and those whose application portfolio places them highest on the admission list are asked to visit Chapel Hill for interviews. Students who are ultimately admitted to UNC-Chapel Hill make no formal commitment to a Ph.D. program. After completing their first year of study students leave BBSP, join a thesis laboratory, and matriculate into one of 14 participating Ph.D. programs. During their first year BBSP students are part of small, interest-based groups led by several faculty members. These groups meet frequently and provide a research community for students until they join a degree-granting program. Students are encouraged to apply as early as possible, preferably before December 1. (Applicants seeking a master's degree are not considered for admission.)

Financial Aid

Stipends for predoctoral students are available from an NIH predoctoral training grant and from the University. Tuition, student fees, and graduate student health insurance are also covered by the training grant and the University.

In addition to the dissertation requirements of The Graduate School (four full semesters of credit including at least six hours of doctoral dissertation, a written preliminary examination, an oral examination and a dissertation), students in the Curriculum in Bioinformatics and Computational Biology must meet the following requirements:

- complete all six of the BCB core courses,
- complete four elective courses (as determined by thesis advisor),
- participate in the BCB Colloquium as attendees during the first and second years and as presenters in later years,
- act as teaching assistants for one of the BCB modules,
- attend BCB sponsored seminars,
- attend the BCB annual retreat, and
- participate in the yearly BCB mini-symposium.

Students are required to rotate through at least three laboratories before choosing a thesis advisor. The advisor or co-advisor must be from BCB Core Faculty list. It is strongly recommended that students attend national meetings in order to better understand how their research fits with progress in their field.

Professors

Max Berkowitz, Theoretical and Computational Chemistry
Kerry Bloom, Mechanisms of Chromosome Segregation in Yeast; Chromosome and Spindle Dynamics
Charles Carter, Protein Crystallography, Structural Polymorphism and Function
Jeff Dangl, Plant Genetics and Cellular Biology, Plant Disease Resistance and Cell Death Control
Henrik Dohlman, Regulators of G Protein Signaling
Nikolay Dokholyan, Protein Folding, Design, and Evolution
Timothy Elston, Mathematical Modeling of Biological Networks
Gregory Forest, Mathematical Modeling of Mucociliary Transport Processes
Klaus Hahn, Spatio-Temporal Dynamics of Signaling in Living Cells
Brian Kuhlman, Protein Design/Modeling, Protein Interactions
Yufeng Liu, Statistical Learning and Genomic Analysis
Terry Magnuson, Mammalian Genetics/Genomics/Development/Mouse Models of Human Disease
Steve Marron, Analyzing Data That Lie in Nonstandard Spaces
William Marzluff, Regulation of RNA Metabolism in Animal Cells
Karen Mohlke, Complex Traits, Genetics of Type 2 Diabetes
Peter Mucha, Networks, Complex Systems, Interacting Particle Systems, Computational Social Science
Fernando Pardo-Manuel de Villena, Evolution, Mouse Genetics, Epigenetics, Female Meiosis, Chromosome Segregation, Meiotic Drive
Charles Perou, Genomic and Molecular Classification of Human Tumors to Guide Therapy
Jan Prins, High-Performance Computing, Algorithms, Programming Languages, Scientific Computing
Maria Servedio, Mathematical Models Integrating Evolutionary Theories with Behavioral and Ecological Phenomena
Jack Snoeyink, Discrete and Computational Geometry Applications to Molecular Biology
John Sondek, Structural Biology of Signal Transduction
Alex Tropsha, Computational Analysis of Protein Structure and Drug Design
Kevin Weeks, Structural and Chemical Biology of the Transcriptome
Kirk Wilhelmson, Genetic Mapping of Susceptibility Loci for Complex Neurological Diseases

Associate Professors
Terry Furey, Chromatin and Gene Regulation, Cancer Genomics, High-Throughput Sequencing
Shawn Gomez, Systems Biology, Mathematical Modeling of Protein Interaction Networks
Bradley Hemminger, Bioinformatics, Medical Informatics, User Interface Design
Corbin Jones, Evolution and Underlying Genetics of Species-Specific Adaptations
Ethan Lange, Statistical Genetics of Human Disease
Yun Li, The Development of Statistical Methods and Their Application to the Genetic Dissection of Complex Diseases and Traits
Laura Miller, Mathematical Biology, Computational Fluid Dynamics, Biomechanics
William Valdar, Mapping of Complex Disease Loci in Animal Models, Statistical Genetics
Todd Vision, Evolution of Genome Organization, Architecture of Complex Traits
Zefeng Wang, Splicing Regulation and Modulation
Mark Zylka, Use of Genome-Wide Approaches to Study Transcriptional Regulators Linked to Autism, Use of RNA Sequencing and Targeted Sequencing to Identify Chemical Risk Factors for Brain Disorders (Autism, Brain Aging, Neurodegeneration, ADHD), Transcriptional Mechanisms Associated with Long Genes

Assistant Professors
Brian Bennett, Genetic and Dietary Factors Leading to Increased Susceptibility for Atherosclerosis
J. Mauro Calabrese, Sequence Rules to Predict Long Noncoding RNA Function, Mechanisms of Transcriptional Regulation by Long Noncoding RNAs
Mengjie Chen, Bioinformatics, Statistical and Populational Genetics
Flavio Frohlich, Cortical Neurophysiology, Computational Neuroscience, Brain Stimulation, Epilepsy
Boyce Griffith, Mathematical Modeling and Computer Simulation in Physiology, Especially Cardiovascular Mechanics, Fluid Dynamics, and Fluid-Structure Interaction and Cardiac Electrophysiology
Samir Kelada, The Identification of Gene-Environment Interaction in Allergic Asthma
Alain Laederach, RNA Folding Bioinformatics
Leslie Lange, Genetics of Complex Diseases, Genetics of Chronic Inflammation, Cardiovascular Disease and Asthma
Amy Shaub Maddox, The Mechanisms of Cell Shape Change
Ben Major, Computational Proteomics and Mass Spectrometry, Network Structure and Dynamics of Protein-Protein Interactions, Multi-OMIC Integrations Focused on Signal Transduction in Cancer Initiation and Evolution
Adrian Marchetti, Ecophysiology, Biogeochecmy and Genomics of Marine Phytoplankton
Dan McKay, Developmental Genomics, Regulation of Gene Expression

Jeremy Purvis, Signal Transduction in Cancer and Stem Cells
Praveen Sethupathy, Genomics of Gene Regulation, MicroRNAs, Epigenomics, Computational Biology, Metabolic Disease
Jason Stein, Finding and Modeling Genetic Variants Influencing Human Brain Structure and Function
Benjamin Vincent, How Immunogenomics Features including T-Cell Receptor and B-Cell Receptor Repertoire Characteristics Predict Survival and Response to Immunotherapy in Breast Cancer, Bladder Cancer, and Acute Myeloid Leukemia

BCB
Graduate-level Courses
BCB 701. Genome Sciences Seminar Series. 1 Credit.
Open to bioinformatics students only. Diverse but current topics in all aspects of bioinformatics. Relates new techniques and current research of notables in the field of bioinformatics and computational biology.
Repeat rules: May be repeated for credit.

BCB 702. Genome Sciences Seminar Series. 1 Credit.
Open to bioinformatics students only. Diverse but current topics in all aspects of bioinformatics. Relates new techniques and current research of notables in the field of bioinformatics.
Repeat rules: May be repeated for credit.

BCB 710. Bioinformatics Colloquium. 1 Credit.
The goal of this course is to expose students to the research interests of BCB faculty and to provide an opportunity for students to present their own work and receive input from their peers and faculty.

BCB 712. Databases, Metadata, Ontologies, and Digital Libraries for Biological Sciences. 1 Credit.
Course introduces the basic information-science methods for storage and retrieval of biological information.

BCB 715. Mathematical and Computational Approaches to Modeling Signaling and Regulatory Pathways. 1 Credit.
The course provides an introduction to the basic mathematical techniques used to develop and analyze models of biochemical networks. Both deterministic and stochastic models are discussed.

BCB 716. Sequence Analysis. 1 Credit.
Course designed to introduce students to the computational analysis of nucleic acids sequences, including sequence comparison, alignment, and assembly.

BCB 717. Structural Bioinformatics. 1 Credit.
Course introduces methods and techniques for protein modeling.

BCB 718. Computational Modeling Laboratory. 1 Credit.
This course provides a practical introduction to computational modeling of cellular systems. We will focus on how to choose and implement different modeling techniques—deterministic, stochastic, and inferred—to describe the same biological phenomenon. Although no formal mathematical or computational background is required, the course will involve a fair amount of programming in MATLAB.

BCB 720. Introduction to Statistical Modeling. 3 Credits.
This course introduces foundational statistical concepts and models that motivate a wide range of analytic methods in bioinformatics, statistical genetics, statistical genomics, and related fields. Students are expected to know single-variable calculus, be familiar with matrix algebra, and have some programming experience.
This short course will cover methods of inferring/estimating natural selection, including the Dn/Ds ratio, the McDonald-Kreitman test, and the Poisson Random Field model. The course will feature discussions of high-profile publications that describe the application of these methods to yield insights into the forces that have shaped organismal evolution.

BCB 725. Introduction to Statistical Genetics. 3 Credits.
Covers statistical methods for the analysis of family and population-based genetic data. Topics include classical linkage analysis, population-based and family-based association analysis, haplotype analysis, genome-wide association studies, basic principles in population genetics, imputation-based analysis, pathway-based analysis, admixture mapping, analysis of copy number variations, and analysis of massively parallel sequencing data.

BCB 850. Training in Bioinformatics and Computational Biology Teaching. 3 Credits.
Principles of bioinformatic and computational biology pedagogy. Students are responsible for assistance in teaching BCB and work under the supervision of the faculty, with whom they have regular discussion of methods, content, and evaluation of performance.
Repeat rules: May be repeated for credit.

BCB 899. Special Topics in Bioinformatics and Computational Biology. 1-6 Credits.
Special topics course in the Bioinformatics and Computational Biology Curriculum. Topics will vary.
Repeat rules: May be repeated for credit. 9 total credits. 9 total completions.

BCB 905. Research in Bioinformatics and Computational Biology. 1-8 Credits.
Credit awarded to students for research in bioinformatics and computational biology.
Repeat rules: May be repeated for credit.

BCB 993. Master's Research and Thesis. 3 Credits.
Students are not accepted for master's program.
Repeat rules: May be repeated for credit.

BCB 994. Doctoral Research and Dissertation. 3 Credits.
Credit for work done towards doctorate.
Repeat rules: May be repeated for credit.