CURRICULUM IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY (GRAD)

Contact Information
Curriculum in Bioinformatics and Computational Biology
Visit Program Website (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 five of the BCB core courses
- complete twelve hours of elective courses (as determined by student and thesis advisor); at least 9 hours must be computational
- participate in the BCB Colloquium as attendees during the first and second years and as presenters in later years
- act as teaching assistant for one of the BCB modules in Year 2
- attend BCB Student Seminars in Years 2 and 3; present in BCB Student Seminars beginning in Year 3 until graduation
- participate in BCB Grant Writing course in Year 2
- attend BCB sponsored special seminars and new student symposium
- attend the BCB annual retreat; present posters or talks

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

Jim Bear, Cell Biology and Physiology
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
Ian Davis, Epigenomic and Transcriptomic Consequences of Genetic Alterations in Cancer and Applications to Therapeutic Discovery
Henrik Dohlman, Regulators of G Protein Signaling
Timothy Elston, Mathematical Modeling of Biological Networks
Gregory Forest, Mathematical Modeling of Mucociliary Transport Processes
Terry Furey, Chromatin and Gene Regulation, Cancer Genomics, High-Throughput Sequencing
Amy Gladfelter, Cell Cycle Control, Cytokinesis, and Cell Shape Determination From Fungi to Mammals
Shawn Gomez, Systems Biology, Mathematical Modeling of Protein Interaction Networks
Klaus Hahn, Spatio-Temporal Dynamics of Signaling in Living Cells
Corbin Jones, Evolution and Underlying Genetics of Species-Specific Adaptations
Brian Kuhlman, Protein Design/Modeling, Protein Interactions
Alain Laederach, RNA Folding Bioinformatics
Yun Li, The Development of Statistical Methods and Their Application to the Genetic Dissection of Complex Diseases and Traits
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
Jack Snoeyink, Discrete and Computational Geometry Applications to Molecular Biology
John Sondek, Structural Biology of Signal Transduction
Brian Strahl, The Role That Histone Post-Translational Modifications Have in Chromatin Biology
Alex Tropsha, Computational Analysis of Protein Structure and Drug Design
William Valdar, Mapping of Complex Disease Loci in Animal Models, Statistical Genetics
Kevin Weeks, Structural and Chemical Biology of the Transcriptome
Kirk Wilhelmson, Genetic Mapping of Susceptibility Loci for Complex Neurological Diseases
Mark Zylika, 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

Associate Professors
J. Mauro Calabrese, Sequence Rules to Predict Long Noncoding RNA Function, Mechanisms of Transcriptional Regulation by Long Noncoding RNAs
Boyce Griffith, Mathematical Modeling and Computer Simulation in Physiology, Especially Cardiovascular Mechanics, Fluid Dynamics, and Fluid-Structure Interaction and Cardiac Electrophysiology
Erin Heinzen, The Genetic and Genomic Basis of Epilepsy Disorders
Bradley Hemminger, Bioinformatics, Medical Informatics, User Interface Design
Samir Kelada, The Identification of Gene-Environment Interaction in Allergic Asthma
Sam Lai
Amy Shaub Maddox, the Mechanisms of Cell Shape Change
Adrian Marchetti, Ecophysiology, Biogeochemistry and Genomics of Marine Phytoplankton
Dan Mckay, Developmental Genomics, Regulation of Gene Expression
Leonard McMillan, Computer Science
Joel Parker, The Methodological Development and Integrated Analysis of High-Throughput Genetic and Genomic Studies of Cancer
Jeremy Purvis, Signal Transduction in Cancer and Stem Cells
Shehzad Sheikh, How Information is Encoded and Dynamically Utilized in Immune Cells From Healthy and Disease-Prone Intestines (Crohn’s Disease and Ulcerative Colitis)
Todd Vision, Evolution of Genome Organization, Architecture of Complex Traits

Assistant Professors
Brad Dickerson, Timing Precision in Drosophil Flight
Daniel Dominguez, How Gene Expression is Controlled by Proteins That Bind RNA
Jill Down, Integrates the Areas of Transcriptional Regulation, Three-Dimensional Genome Organization and Functional Genomics to Understand How the Architecture of the Genome Influences Gene Expression During Development and Disease
Marty Ferris, Genetics
Hector Franco, Gene Regulation, Epigenetics, Chromatin and RNA Biology, Especially As It Pertains to Cancer
Flavio Frohlich, Cortical Neurophysiology, Computational Neuroscience, Brain Stimulation, Epilepsy
Katherine Hoadley, Genomic Characterization and Integrative Genomic Approaches to Better Understand Cancer
Yuchao Jiang, Statistical Modeling, Method Development and Data Analysis in Genetics and Genomics
Wesley Legant, Microscopy, 3d Image Analysis, Biomaterials, Cell Migration, Cancer Metastasis, Tissue Engineering
Mike Love, Statistical and Computational Methods For the Analysis of High-Throughput Sequencing Assays to Facilitate Biomedical and Biological Research
Ehsan Nazockdast, Applied Physical Science
Adam Palmer, Investigate and Develop Combinations of Cancer Therapies Using Experiments, Simulations, and Computational Analysis of Clinical Data
Doug Phanstiel, Experimental and Computational Approaches to Study the Mechanisms Through Which Enhancers and Three-Dimensional Chromatin Structure Regulate Gene Transcription During Cellular Differentiation
Jesse Raab, Regulation and Function of Altered Chromatin Remodeling Complex Activity
Christoph Rau, the transcriptomic and epigenomic landscape underlying cardiovascular disorders
Alexander Rubinstein, Machine Learning for Adaptive Immunity, Immunogenomics, and Rapid Vaccine Design
Daniel Schrider, Computational Tools to Make Inferences About Evolution From Population Genomic Datasets
Jeremy Simon, Gene Expression and Gene Regulation in Primarily Mouse and Human Models of Autism, Cancer, and Environmental Exposures, and Across Development
Natalie Stanley, Computational and Systems Immunology
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
Hyejung Won, We Try to Bridge the Gap Between Genetic Risk Factors for Psychiatric Illnesses and Neurobiological Mechanisms by Decoding the Regulatory Relationships in the Human Brain
Di Wu, Development of Statistical Methods for Multidimensional Genomic Data Integration to Understand the Biological Mechanism of Diseases
Anthony Zannas, The Epigenetic Mechanisms Linking Psychosocial Stress With Disease Risk
**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.

*Grading status:* Letter grade.

**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.

*Grading status:* Letter grade.

**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.

*Grading status:* Letter grade.

**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.

*Grading status:* Letter grade.

**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.

*Grading status:* Letter grade.

**BCB 716. Sequence Analysis. 1 Credit.**
This module is designed to introduce students to concepts and methods in the comparative analysis of nucleic acid sequences using state of the art sequencing platforms. Course topics will include sequence alignment, genome assembly, and computational details of contemporary protocols for DNA and RNA sequencing.

*Grading status:* Letter grade.

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

*Grading status:* Letter grade.

**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.

*Grading status:* Letter grade.

**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.

*Grading status:* Letter grade.

**BCB 722. Population Genetics. 1 Credit.**
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.

*Grading status:* Letter grade

*Same as:* BIOS 785.

**BCB 723. Topics in Statistical Genetics and Genomics. 1 Credit.**
This module introduces selected concepts and techniques in statistical genetics and genomics.

*Grading status:* Letter grade.

**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.

*Grading status:* Letter grade.

**BCB 730. Fundamentals of Quantitative Image Analysis for Light Microscopy. 1 Credit.**
This course is a practical introduction to quantitative analysis of light microscopy images. During the class students will follow tutorials that will guide them through common tasks in analysis of biological images. They will be introduced to basic concepts of image processing like image registration, filtering, object detection etc.

*Grading status:* Letter grade

*Same as:* BIOS 784.

**BCB 784. Introduction to Computational Biology. 3 Credits.**
Molecular biology, sequence alignment, sequence motifs identification by Monte Carlo Bayesian approaches, dynamic programming, hidden Markov models, computational algorithms, statistical software, high-throughput sequencing data and its application in computational biology.

*Requisites:* Prerequisites, BIOS 661 and 663; Permission of the instructor for students lacking the prerequisites.

*Grading status:* Letter grade

*Same as:* BIOS 785.

**BCB 785. Statistical Methods for Gene Expression Analysis. 3 Credits.**
Clustering algorithms, classification techniques, statistical techniques for analyzing multivariate data, analysis of high dimensional data, parametric and semiparametric models for DNA microarray data, measurement error models, Bayesian methods, statistical software, sample size determination in microarray studies, applications to cancer.

*Requisites:* Prerequisites, BIOS 661 or 673, and 663; Permission of the instructor for students lacking the prerequisites.

*Grading status:* Letter grade

*Same as:* BIOS 785.

**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.

*Grading status:* Letter grade.
BCB 870. Writing Fellowship Proposals. 1 Credit.
Provides practical experience to predoctoral students in writing fellowship proposals, using the NIH F31 as a template. Students will have weekly writing assignments, with feedback given by students and faculty. Open to 2nd and 3rd year students in the Curriculum or by permission of the instructor.
Grading status: Letter grade
Same as: GNET 870.

BCB 888. Responsible Conduct of Research. 1 Credit.
Classroom-based graduate level course covering critical topics for ethical and responsible conduct of experimental research. There are both classroom lecture, workshop-type discussion components, in addition to assigned outside of class readings. Case studies and hypothetical situations involving the most likely scenarios confronting graduate students will be covered, these topics include: mentor and mentee relationships, publication authorship, collaboration, peer review, conflicts of interest, intellectual property, plagiarism, data acquisition and data processing. Restricted to students in good standing as a graduate student at UNC; In the unlikely event that classroom space is limited, preference will be given to graduate students who have previously received external federal funding sources and may require a refresher course in RCR.
Repeat rules: May be repeated for credit. 2 total credits. 1 total completions.
Grading status: Letter grade
Same as: BIOC 888.

BCB 891. Special Topics. 1-3 Credits.
Advance topics in current research in statistics and operations research.
Repeat rules: May be repeated for credit; may be repeated in the same term for different topics.
Grading status: Letter grade
Same as: MATH 891, GNET 891.

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.
Grading status: Letter grade.

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.
Grading status: Letter grade.

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.