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April 28, 2008

Dr. Harold L. Martin
Senior Vice President for Academic Affairs
General Administration
University of North Carolina
Post Office Box 2688
Chapel Hill, North Carolina 27515-2688

Dear Dr. Martin:

Enclosed is UNC Charlotte's request for authorization to plan a Ph.D. program in Bioinformatics and Computational Biology. The proposed Bioinformatics and Computational Biology program emerged from a feasibility study conducted by our College of Computing and Informatics and Graduate School. The program responds to an identified student demand and to the transformation and development of our region's economy.

Thank you for your consideration of this request. Provost Joan Lorden or I would be pleased to respond to any questions that you may have regarding this request.

Cordially,

Philip L. Dubois
Chancellor

PLD/cfh

Enclosure (5 copies of the proposal)

cc: Provost Joan F. Lorden
Dean Nancy Gutierrez
Dean Mirsad Hadzikadic
Dean Robert Johnson
Dean Karen Schmaling

The University of North Carolina at Charlotte

**Ph.D. in
Bioinformatics and Computational Biology**

Request for Authorization to Plan

APPENDIX B

THE UNIVERSITY OF NORTH CAROLINA
REQUEST FOR AUTHORIZATION TO PLAN A NEW DOCTORAL OR
FIRST PROFESSIONAL DEGREE PROGRAM

THE PURPOSE OF ACADEMIC PROGRAM PLANNING: Planning a new academic degree program provides an opportunity for an institution to make the case for need and demand and for its ability to offer a quality program. Authorization to plan, and the planning activity to follow, do not guarantee that authorization to establish will be granted. Requests (5 copies) may be submitted annually.

Date: April 30, 2008Constituent Institution: University of North Carolina at CharlotteCIP Discipline Specialty Title: BioinformaticsCIP Discipline Specialty Number: 26.1103 Level: D 1st Prof. Exact Title of the Proposed Degree: Bioinformatics and Computational BiologyExact Degree Abbreviation (e.g. Ph.D., Ed.D.): Ph.D.

Does the proposed program constitute a substantive change as defined by SACS?

Yes No a) Is it at a more advanced level than those previously authorized? Yes No b) Is the proposed program in a new discipline division? Yes No Approximate date for submitting the Request to Establish proposal (must be within two years of date of authorization to plan): April 30, 2009Proposed date to establish degree: month August year 2010 (Date should allow at least three months for review of the request to establish, once submitted.)

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1. Describe the proposed new degree program.

a. Brief description of the program and a statement of educational objectives

The University of North Carolina at Charlotte requests authorization to plan a Ph.D. program in *Bioinformatics and Computational Biology*. The program will be administered by a newly formed bioinformatics department but will also involve faculty from other departments who are members of the UNC Charlotte Bioinformatics Research Center.

The life sciences have changed dramatically in the last two decades. First, the widespread use of high-throughput technologies to generate massive databases caused biology to become, to a great extent, an information-driven science. Now, more generally, computation is at the heart of all leading edge biological science. *Bioinformatics and Computational Biology* are disciplines that have emerged in response to the need to utilize these new complex datasets to help solve difficult, important biological problems.

In 2000, the National Institutes of Health formed a committee to develop working definitions of these terms (<http://www.bisti.nih.gov/CompuBioDef.pdf>). The Committee offered the following definitions, recognizing that no definition could completely eliminate overlap with other activities:

Bioinformatics: *Research, development, or application of computational tools and approaches for expanding the use of biological, medical, behavioral or health data, including those to acquire, store, organize, archive, analyze, or visualize such data.*

Computational Biology: *The development and application of data-analytical and theoretical methods, mathematical modeling and computational simulation techniques to the study of biological, behavioral, and social systems.*

Their report noted that:

Bioinformatics and computational biology are rooted in life sciences as well as computer and information sciences and technologies. Both of these interdisciplinary approaches draw from specific disciplines such as mathematics, physics, computer science and engineering, biology, and behavioral science. Bioinformatics and computational biology each maintain close interactions with life sciences to realize their full potential. Bioinformatics applies principles of information sciences and technologies to make the vast, diverse, and complex life sciences data more understandable and useful. Computational biology uses mathematical and computational approaches to address theoretical and experimental questions in biology. Although bioinformatics and computational biology are distinct, there is also significant overlap and activity at their interface.

Background

Recognizing the critical importance of Bioinformatics and Computational Biology to 21st Century science and technology, UNC Charlotte requested and received \$35 million from the North Carolina General Assembly in the 2005 session to build a Bioinformatics building on campus. This building, which will be ready for occupancy in August 2009, has over 70,000 square feet for offices, wet labs, computational labs, and instructional space. Also in 2005, UNC Charlotte established a Bioinformatics Research Center (www.bioinformatics.uncc.edu) (BRC) that now has more than 30 faculty members from Computer Science, Biology, Physics, Kinesiology, Chemistry, and Mathematics and Statistics (see Appendix). At the same time, UNC Charlotte began hiring outstanding scientists for the Bioinformatics Division of the Department of Computer Science, within the College of Computing and Informatics. Currently, there are eight such faculty and four more are being recruited in the 2007-08 academic year. A new department will be formed within the College of Computing and Informatics around these faculty during 2008-09. Within five years, we expect this new department will grow to approximately 25, bringing the total number of faculty in the BRC to nearly 60.

Because of the strong growth in the Ph.D. program in Information Technology, the College of Computing and Informatics reorganized the program into distinct concentrations, to better serve the interests of students in major clusters. The Bioinformatics concentration now has 18 Ph.D. students enrolled and will add five additional students in the Fall of 2008. In developing the Bioinformatics concentration, we have established a comprehensive curriculum, including 15 new didactic courses in bioinformatics and computational biology. We have also instituted policies and procedures for student evaluation, advancement to doctoral candidacy, and thesis proposal and defense. Currently four students have passed their qualifying examinations, and three are completing the final work on their dissertations.

Educational Objectives of the Proposed Program

The development and use of new computational methods in biology generally stems from the interaction between biologists and computer or quantitative scientists with a substantial knowledge of biology. Computational scientists with little knowledge of biology are unlikely to be able to make a substantive contribution. The proposed Ph.D. program in Bioinformatics and Computational Biology has sought to avoid this pitfall. The educational objectives of this program are as follows:

- to provide students with a rigorous foundation in scientific computation
- to provide an understanding of the biological context for development and application of bioinformatics and computational biology methods
- to train students to develop and apply the appropriate methods to solve important problems in the biological sciences and
- to instill research, writing and critical thinking skills by teaching rigorous scholarly inquiry and research methods

This program has special appeal to students with undergraduate training in computing, life sciences, or physical science disciplines. Most current and future students entering the program have completed an undergraduate major in either a life science or a quantitative discipline, with substantial coursework or a minor in a complementary discipline. Nonetheless, the challenge of creating a single degree program that serves a diverse population of students is that some “catch-up” training in disciplines complementing the student’s undergraduate training is inevitably required. The curriculum has been designed to accommodate students entering with different backgrounds and to provide an accelerated introduction to either computing or life sciences as needed. The degree program includes additional training beyond introduction to the complementary discipline, and graduation from the program requires demonstrated competence in both life science concepts and scientific programming. The program is structured to provide students with the skills and knowledge to develop and evaluate bioinformatics and computational biology techniques, and apply them to important problems in biology. The first generation of bioinformatics and computational biology degree programs often focused strongly on application of common bioinformatics methods, especially for individuals who lacked a computing background, or neglected substantive biological training in favor of high-level abstractions of molecular data. While no program can be the same thing to all students, **we have made an effort to design the program so that all students will leave with strong programming, numerical and statistical analysis skills, as well as a substantive understanding of cellular and molecular biology, genomics, evolution and individual variation.**

Program Structure and Governance

The Program will be governed by a five-person Steering Committee of faculty from the new department. Initially, the Committee will be:

Dr. Dennis Livesay (Program Director) (Assoc Prof)
Dr. Anthony Fodor (Asst Prof)
Dr. Jennifer Weller (Assoc Prof)
Dr. Cynthia Gibas (Assoc Prof)
Dr. Ann Loraine (Assoc Prof)

Members will serve two-year, staggered terms and will be elected by the graduate faculty of the new Department. Members can be re-elected. The Program Director will be chosen by the Committee. The Graduate Coordinator (a position now held by Ms. Elise Marshall) will serve as an *ex-officio* member.

The Steering Committee will develop the curriculum and program requirements, serve as an admissions committee, arrange for the administration of the qualifying examination, and assign initial faculty advisors. The Steering Committee will also approve graduate faculty in other departments for inclusion in the degree program.

Participating Faculty

Brief biographical sketches of the participating faculty are provided in the Appendix. Eight of these faculty are members of the Bioinformatics Division and will teach the didactic courses. Additional faculty from other departments who currently participate in the graduate program are also listed.

Program Review Plan

The Steering Committee will meet at least once per semester and the entire program faculty will meet at least once per year. At the beginning of the program, it is anticipated that these meetings will occur more often. In addition, the Steering Committee will periodically review program direction and make recommendations to the entire faculty.

The Steering Committee will engage in regular, ongoing self-studies that address:

- its effectiveness in achieving program goals and objectives (i.e., its outcomes)
- how its goals and objectives are met through graduate education and
- its procedures to maintain current achievements or to make program changes as necessary.

The Steering Committee will also conduct periodic systematic reviews of its goals and objectives, the training model, and curriculum to ensure their appropriateness in relation to:

- the University's mission and goals
- local, regional, and national needs
- the evolving body of scientific and professional knowledge and
- its graduates' job placements and career paths.

b. Relationship of the proposed new program to the institutional mission and how the program fits into the institution's strategic plan

The proposed Ph.D. in Bioinformatics and Computational Biology is connected to a number of University goals, including those which a) increase the number of Ph.D. programs in high demand fields, b) extend the campus infrastructure supportive of research, c) expand extramurally supported research programs, and d) increase both faculty and student research that will address regional problems.

The proposed Ph.D. is also closely aligned with the recommendations of the UNC Tomorrow Commission. It is in an inherently interdisciplinary field that will help foster globally competitive collaborative research and educational efforts within a number of existing programs, and will help attract outstanding students and extramural funding. The development of a Ph.D. in Bioinformatics and Computational Biology is well aligned with the commitment to develop applied sciences and technologies in the Charlotte area. The region is well on its way to becoming a major biotechnology center in the state with

the development of the North Carolina Research Campus (NCRC) at Kannapolis. The expertise provided by this program is critical in a wide range of biotechnology research problems and applications, from genomics to health care and beyond.

c. relationship of the proposed new program to other existing programs at the institution

The Bioinformatics concentration of the IT Ph.D. program has a close working relationship with the Biology, Chemistry, Physics and Optical Science, Computer Science, and the Mathematics and Statistics Departments. Faculty in each of these departments serve as mentors, committee members, or provide laboratory rotations for our students. We expect these relationships to grow and for new relationships with faculty in other departments to develop. For example, we note that two of our students have dissertation advisors in the Physics and Optical Science Department working on computational biology problems. Other students work closely with Biology faculty on issues related to biomarkers for cancer. Still other students are, or will be, working with Chemistry faculty on analysis of mass spectrometry data.

d. special features or conditions that make the institution a desirable, unique, or appropriate place to initiate such a degree program.

The UNC Charlotte program is unique in several ways. First, it is *departmentally based*. The College of Computing and Informatics has given the Bioinformatics Division complete freedom in hiring faculty and assigning teaching responsibilities. This will continue, in a more formal way, when the Bioinformatics Division is given Departmental status in the 2008-09 academic year. This structure contrasts with that of North Carolina State University, Duke, and UNC Chapel Hill, which use faculty from various departments to teach courses and advise and mentor students. The departmentally based structure at UNC Charlotte ensures that the proper mix of faculty for the program can be hired, that the department can assign faculty to teach core courses as part of their primary teaching responsibilities, and that rigorous control over both student performance and course content and quality will be maintained. This later point is especially important for a Bioinformatics and Computational Biology curriculum, which involves a complex mix of topics from a variety of disciplines. By exercising precise control over our curriculum, we can ensure that our students will have the proper prerequisites, minimize gaps and overlap between courses, and schedule the courses appropriately.

UNC Charlotte is different from other North Carolina universities offering similar programs in that our program is *based in the College of Computing and Informatics*, as opposed to a Statistics or Genomics program or department. While these other programs are certainly comprehensive, and all programs, including UNC Charlotte's, will cover most of the same topics, UNC Charlotte will emphasize computational approaches. For example, our courses emphasize structured, object-oriented programming applications in bioinformatics. Students write data parsers, visualization tools, genome browsers, and alignment code. Our statistics course uses examples drawn from common problems in bioinformatics and incorporates assignments in the R language. Because we are based in

the College of Computing and Informatics, we are also able to offer, for example, a specialized database course with an emphasis on massive biological databases such as Genbank, rather than on the usual commercially oriented data structures. Students have ready access to two high performance computer clusters for bioinformatics as well as special purpose FPGA computers for bioinformatics applications.

Finally, UNC Charlotte is providing a cadre of six faculty and five service staff in bioinformatics to the *North Carolina Research Campus* (NCRC) at Kannapolis. We have already developed relationships with the UNC-CH Nutrition Research Institute (Dr. Zeisel), the NCSU plant genomics group (Dr. Lommel) and the Duke Translational Medicine group (Dr. Tennebaum) at the NCRC. When fully developed, the NCRC is expected to house over one hundred biotechnology companies and laboratories working in a variety of fields, including nutrigenomics, metabolomics, plant genomics and translational medicine. We expect that in 10 years, the Charlotte area will be the southwestern terminus of a biotechnology corridor reaching to the Triangle. UNC Charlotte has an important role to play in the extension of biotechnology across the State, and the proposed Ph.D. program will play a critical part in that role.

As noted above, the Bioinformatics concentration of the IT Ph.D. program has been very successful, having attracted 18 outstanding students in less than three years. However, it is clear that the curriculum, research interests, and philosophy of the Bioinformatics concentration have diverged from those of the other IT Ph.D. concentrations (i.e., Computer Science, Software Information Systems, Business Information Systems). Given the rapid developments in the computational aspects of the biological sciences, it seems likely that our program will continue to evolve and diverge from its origins. Our students have different backgrounds and aspirations, and they express a strong desire for a Ph.D. in Bioinformatics and Computational Biology instead of a Ph.D. in Information Technology. This is often a major issue when recruiting students, who want a program name that accurately describes their course of study. It is also an issue for graduates' potential employers, who are looking for people trained in Bioinformatics and Computational Biology, not Information Technology.

2. List all other public and private institutions of higher education in North Carolina currently operating programs similar to the proposed new degree program.

There are currently three other doctoral programs within North Carolina in Bioinformatics and Computational Biology. North Carolina State University (NCSU), located 160 miles from UNC Charlotte, established the first such program in 1999. This program was developed from their strength in the area of statistical genetics, and many of their faculty have appointments in either the Department of Statistics or Genetics. The NCSU program consists of courses in bioinformatics, molecular genetics, functional genomics, statistics, computational methods, a journal club, electives and dissertation research. Although there are a number of options within this curriculum, there is a strong emphasis on statistics and statistical/quantitative genetics.

Duke University, located 135 miles from UNC Charlotte, established a Ph.D. in Computational Biology and Bioinformatics in 2003. The Duke program offers over 15

courses, but only three are required (Genomic Tools and Technologies, Algorithms, and Statistics) in addition to a seminar. A Student Advisory Committee advises first and second year students with respect to courses, rotations, and advisor selection. The Duke program lists 40 faculty with appointments in several different departments.

The Ph.D. in Bioinformatics and Computational Biology at Chapel Hill (also 135 miles from UNC Charlotte) was recently approved. The Chapel Hill program requires two foundation courses, laboratory rotations, a colloquium, and seven one-credit “core modules” that cover most topics in bioinformatics and computational biology. A substantial number of electives are offered. Except for the short “core modules,” existing departments, such as Chemistry, Computer Science, Cell Biology, etc., currently offer all of the courses. Currently, 37 faculty are listed in the program, with primary appointments in 18 different departments.

- 3. Estimate the number of students that would be enrolled in the program during the first year of operation: Full-Time 24 Part-Time 0**
- 4. Estimate the current and projected demand for graduates of the proposed new degree program. Provide documentation about the sources of data used to estimate demand figures.**

The strongest indication of future student demand has been our success in attracting outstanding student to the existing Bioinformatics concentration. We currently have 18 Ph.D. students and will admit five more (including three U.S. students, two of whom are women, and one is an underrepresented minority) in the Fall of 2008. Current Ph.D. students have an average quantitative GRE of 701, verbal GRE of 502, and the average undergraduate GPA is 3.3. Four of these students have come with newly hired faculty from other institutions, but most have sought us out. Thus far, our only recruiting effort has been the announcement of the Ph.D. program on our website. This suggests that student demand is quite substantial. It is noteworthy that we have not had to rely heavily upon international students for our numbers. Half of our current students are U.S. citizens, and about half of these are from North Carolina. One-third of our students are female. Active recruiting measures (see below) will substantially increase the numbers of women and especially of North Carolina students. Informally, we find that local students are being rapidly recruited through personal interaction with the faculty, including research internships in faculty laboratories. For example, two of six interns who have participated in research activities in the Microarray Core Facility since 2006 (supervised by Dr. Cynthia Gibas) have so far applied or are in the process of applying to the Ph.D. program. We have more demand for such internships than we can currently meet, another indication of strong student interest in Bioinformatics and Computational Biology.

We employ a full-time Graduate Coordinator (Ms. Elise Marshall) to answer the substantial number of inquiries from potential students and to arrange interviews. In addition, Ms. Marshall travels to many colleges and universities in our region to recruit outstanding students. On a recent visit to North Carolina A & T, she signed up 12 biology/math/computer science students to visit our graduate open-house event.

The strong student demand that we observed is mirrored in the other institutions in our state. The Bioinformatics and Computational Biology program at Chapel Hill had 49 applicants for the 2007-08 year, but only seven could be enrolled. Last year, NCSU's program received 210 applications for only 10 positions, and Duke reported receiving 85 applications for only eight positions. There is a strong student demand that is not being met by the current programs in our State. Nationwide, Black and Stephan ("Bioinformatics: Recent Trends in Programs, Placement and Job Opportunities", Report to the Alfred P. Sloan Foundation, June, 2004) report that although the number of training programs is rising rapidly, it still falls short of student demand.

North Carolina is widely regarded as third in the nation (behind CA and NY) in the biotechnology sector. The 2006 Ernst & Young biotechnology report ("Beyond Borders: Global Biotechnology Report 2006") noted that:

The biotechnology industry has not just endured-it has thrived. It now is a global powerhouse with over \$60 billion in revenues and hundreds of marketed products. The industry is rapid maturing and is closer to profitability than at any time in its past. The market valuations of its most successful companies are challenging those of big pharma.

In many respects, the growth of biotechnology mirrors that of the electronics industry in the mid- 20th Century. The Milken Institute (www.milkeninstitute.org/pdf/biopharma_report.pdf) projects that over 7,000 new biopharma jobs will be created in North Carolina by 2014. Many of these jobs will require significant computational skill sets. In a recent meeting with Pfizer at the NCRC, several company leaders cited the need for greater computational expertise and noted their difficulty with appropriate qualifications. Our own experience also suggests that individuals with this training are in short supply. In the past three years, UNC Charlotte's 12 faculty searches in bioinformatics and computational biology have received more than 400 applications. Despite explicit requests for individuals trained in bioinformatics and computational biology, *an applicant with a degree in this field is rarely seen.*

- 5. There are no plans to offer the program away from campus during the first year of operation.**
- 6. Describe the procedures to be used to plan the proposed program. List the names, titles, e-mail addresses and telephone numbers of the person(s) responsible for planning the proposed program.**

Dr. Dennis Livesay (Program Director)
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Dr. Cynthia Gibas
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Dr. Ann Loraine
Associate Professor of Computer Science
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Proposed Curriculum

The proposed curriculum will add two to four additional graduate courses to the existing bioinformatics offerings. The courses currently approved and offered are:

ITSC 8100	Biological Basis of Bioinformatics
ITSC 8111	Bioinformatics Programming I
ITSC 8112	Bioinformatics Programming II
ITSC 8200	Statistics for Bioinformatics
ITSC 8201	Molecular Sequence Analysis
ITSC 8202	Computational Structural Biology
ITSC 8203	Genomics, Transcriptomics & Proteomics
ITSC 8204	Mathematical Systems Biology
ITSC 8210	Numerical Methods for Bioinformatics
ITSC 8211	Design & Implementation of Biological Databases
ITSC 8310	Analysis of Microarray Data
ITSC 8311	Biophysical Modeling
ITSC 8312	Computational Comparative Genomics
ITSC 8313	Structure, Function, & Modeling of Nucleic Acids
ITSC 8600	Seminar
ITSC 8601	Journal Club
ITSC 8880	Research Rotation
ITSC 8990	Pre-dissertation Research
ITSC 8991	Dissertation Research

Currently, the 8100 series courses are required for some students, depending on educational background. The 8200 series courses are Core courses. All students take 8200-8203 and 8600 and are required to take two research rotations (8880). This year, the seminar series brought 32 scientists to campus to speak and meet with students. The 8300 series are advanced courses. In addition, a number of courses in other departments will be permitted as electives. A minimum of 72 semester hours are required for the Ph.D., including 36 hours of coursework and 18 dissertation research hours. Additional electives are offered by other departments, including Biology, Computer Science, and Philosophy (Ethics). Students must pass a qualifying examination by the end of their 5th semester. We anticipate that there will be modest changes to the curriculum.

7. Describe the method of financing the proposed new program (e.g., potential sources of funding) and indicate the extent to which additional state funding may be required.

Day-to-day operation of the program will be overseen by our Graduate Coordinator, Ms. Elise Marshall, who also oversees our recently established Professional Science Master's Degree in Bioinformatics. These tasks involve student recruitment, initial review of applications, maintenance of student records, tracking student progress, and assistance with job placement. No additional staffing will be required for this program.

The University is committed to expand current faculty of 8 to 25 over the next few years. Moreover, we find that faculty from other departments such as Chemistry, Physics, and Biology wish to mentor Ph.D. students in Bioinformatics and Computational Biology. The number of potential faculty mentors for these students will reach 50 by 2013. This will be adequate for the program.

The current Bioinformatics concentration within the IT Ph.D. program currently has funding for full-time stipends for about 14 students. These amounts seem sufficient for the proposed program.

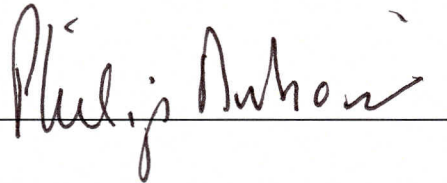
The Bioinformatics Building on the Highway 29 side of the campus is scheduled to open in August 2009. This building will provide ample space for our faculty, staff, post-docs and students.

Our goal is to attain an NIH pre-doctoral training grant (T32) in the next 5-8 years. The critical criteria are 1) an outstanding U.S. applicant pool, 2) training faculty with a strong record of extramural (esp. NIH) funding, and 3) excellent publication and placement record. A number of our faculty now have NIH grants, and we are actively working on increasing this funding stream. Moreover, we are actively recruiting U.S. students with excellent GRE scores and the potential to be productive scientists. The establishment of an independent Ph.D. in Bioinformatics and Computational Biology would greatly strengthen these efforts. Our recruitment efforts have also involved development of connections with several of North Carolina's outstanding HBCUs. Charlotte is a top destination city for African-Americans, and the Bioinformatics Division

has a strong commitment to diversity and to developing a program of professional training that reflects the demographics of the region in its students and, eventually, its faculty. The Division's commitment to diversity also shows at the faculty level; three of the eight faculty recruited since the inception of the program are women. The pursuit of diversity in the program affords us the opportunity to take advantage of fellowship programs for minority recruitment.

This intent to plan a new program has been reviewed and approved by the appropriate campus committees and authorities.

Chancellor

A handwritten signature in cursive script, appearing to read "Philip A. Anderson", written over a horizontal line.

Appendix

Participating Faculty Research Interests

Dr. Andriy Baumketner (Physics and Optical Science) The research interests of my group are in theoretical approaches to problems in biological and chemical physics. Our recent efforts have focused on: a) atomistic simulations of protein folding b) computational studies of protein aggregation c) modeling of confinement effects on folding thermodynamics and kinetics d) interactions of proteins with surfaces f) theoretical models of folding kinetics.

Dr. Wei Cai (Mathematics and Statistics) My group is involved in the development of efficient multiscale numerical methods for molecular dynamics modeling of protein folding, fast algorithms for treating electrostatic interactions and multiphysics models based on classical and quantum mechanics for bio-systems.

Dr. Mark Clemens (Biology) My primary research focus is in vascular control in the liver relevant to liver disease. Areas related to bioinformatics include analysis of perfusion heterogeneity as a function of inflammatory stress or tumor formation and analysis of randomness characteristics of sentry behavior of natural killer T cells as a function of proximity to metastatic tumor target cells.

Dr. Brian Cooper (Chemistry) Our group aspires to meet new challenges in protein analysis and characterization resulting from the ongoing revolution in biotechnology. Much of our research involves developing novel methods or applications for capillary electrophoresis (CE), including characterizing the *microheterogeneity* of monoclonal antibodies (mAbs) and other proteins, using *charge ladders* to measure protein charge and size, and using *affinity capillary electrophoresis* (ACE) to study protein–ligand binding. We also use and develop new methods for electrospray and MALDI mass spectrometry, capillary liquid chromatography, and ultrasensitive fluorescence detection.

Dr. Didier Dréau (Biology) Dr. Dréau's research centers on the mechanisms of cancer metastasis, and the vascular and immune interactions associated with solid tumor growth. The understanding of metastasis processes and the definition of specific signatures encompassing molecular, cellular, tissue and physiological system pathways can uniquely be achieved by developing new and integrated bioinformatics approaches.

Dr. Xiuxia Du (Computer Science/Bioinformatics Research Center) My lab addresses computational and statistical problems for mass spectrometry-based proteomics, metabolomics, lipidomics, and interactomics. These include: (1) the development of algorithms to identify protein-protein interactions using chemical crosslinking; (2) statistical analysis (e.g. estimation of false discovery rate) of peptide and protein identifications; (3) the development of algorithms to analyze time-course data. The long-term goal is to conduct systems level analysis of the dynamics of biological systems using –omics data and facilitate studies of the mechanisms of normal and abnormal biological functions.

Dr. Anthony Fodor (Computer Science/Bioinformatics Research Center) Dr. Fodor's research program focuses on algorithm and method development in bioinformatics. He is particularly interested in the application of new high-throughput sequencing technology to the study of

complex microbial communities. Microbial ecosystems currently under study in his lab include human and mouse gut microbes, bacteria within the activated sludge of a North Carolina wastewater treatment plant and the microbial community within the South Fork of the Eel River in Mendocino County, California

Dr. Cynthia Gibas (Computer Science/Bioinformatics Research Center) Dr. Gibas' research is based in biophysics and focused broadly on the design and optimization of high-throughput experiments. Current active projects include database and visualization infrastructure for genome comparison; DNA array design for comparative functional genomics and host-pathogen interaction experiments; and modeling and optimization of nucleic acid hybridization behavior in high-throughput genomics experiments.

Dr. Julie Goodliffe (Biology) My lab examines the genome-wide control of Myc activity in the *Drosophila* embryo. We have discovered several nuclear, chromatin remodeling proteins that are involved in Myc's ability to both activate and repress its targets (Polycomb, Ash1, Pho). These proteins have well-known roles in cell fate specification, and we are interested in understanding the mechanism by which these proteins, and others, control Myc activity throughout embryogenesis.

Dr. Alexander Gordon (Mathematics and Statistics) The appearance in biology of the new powerful technology of microarrays raised many challenging statistical questions. Most of my research in statistics is in the area of multiple testing procedures and their application to the detection of differentially expressed genes in microarray data analysis. I am also involved in developing fast algorithms for computing exact (rather than asymptotic) theoretical distributions of nonparametric statistics. These studies, too, are motivated by biological applications. Some of my collaborative research focuses on various kinds of distance measures and their application to biological problems.

Dr. Jun-Tao Guo (Computer Science/Bioinformatics Research Center) The Guo group is interested in template-based protein structure prediction, protein-DNA interaction, and their applications in deciphering biological regulatory networks through an integrated methodology of computational prediction and wet-lab experiment. The group is also interested in the evolution of regulatory pathways.

Dr. Donald Jacobs (Physics and Optical Science) My research interests are best described as a mixture of statistical and computational physics supplemented with algorithm development. Thanks to funding from the National Institute of Health (NIH), we have a very active on-going project to develop innovative theory/models to understand protein stability and flexibility. The primary research focus of this project is to implement a novel computational method to facilitate accurate and fast predictions of stability, flexibility and dynamics of proteins, and to quantitatively determine relationships between these distinct physical properties. These computational methods will be useful to facilitate targeted-drug design predictions. My future research plan is to leverage the new methods we are developing today into innovative next-generation state-of-art protein design software.

Dr. Ana Jofre (Physics and Optical Science) My research is in single molecule biophysics. I am using femtoliter volume water droplets, hydrosomes, to encapsulate and isolate single molecules,

which I probe by fluorescence excitation. I am using this technique to probe single protein conformations. The hydrosomes are optically trappable and can be manipulated with optical tweezers. Such manipulation enables the hydrosomes to be used as microreactors, whereby a droplet containing a single molecule can be fused with another droplet containing the corresponding reagent.

Dr. Robert Kosara (Computer Science) My research is in information visualization, specifically in the visualization of large and complex data sets. My work includes the visualization of purely categorical data sets, the interactive visual exploration of such data, and the visualization of sequences of data.

Dr. Joanna Krueger (Chemistry) My lab visualizes biomolecular interactions through molecular modeling of small-angle X-ray and neutron solution scattering data with interpretation supported by an integration of numerous structural biology tools- such as selected-site mutagenesis, chemical cross-linking with peptide mapping, spectroscopy (FTIR, CD, UV-VIS, FRET, MS) and available high resolution crystal and/or NMR structure information.

Dr. Larry Leamy (Biology) My research program has centered on quantitative genetics of skeletal traits in mice and QTL analyses of complex phenotypes, including epistasis and QTL by environmental interactions.

Dr. Timothy Lightfoot (Kinesiology) My research deals with the underlying genetic factors that control and regulate both exercise endurance and daily physical activity levels. This work is conducted using mouse models and a wide-variety of exercise, molecular, cellular, and bio-informatic techniques.

Dr. Dennis Livesay (Computer Science/Bioinformatics Research Center) The Livesay research group is interested in elucidating hidden sequence/structure/function relationships across protein families and superfamilies. Specifically, the group is developing and applying a number of bioinformatic and computational biology techniques to understand how function is conserved despite, at times, appreciable evolutionary drift. Similarly, the group is also attempting to understand and quantify how evolution delicately balances stability and flexibility characteristics within proteins.

Dr. Ann Loraine (Computer Science/Bioinformatics Research Center) My lab develops and applies new methods for mining and visualizing genome-scale data sets. Public databases (e.g., GEO) contain thousands of expression microarray experiments, each one focused on a relatively narrow problem. But when considered together, these data offer the chance to uncover previously unknown aspects of gene regulation and function. We aim to harvest, process, and re-deploy these data for all-new analyses, focusing on secondary metabolic pathways in plants.

Dr. James Oliver (Biology) The major areas of study in my laboratory involve *Vibrio vulnificus* and other pathogenic marine *Vibrio spp.*, *Helicobacter pylori*, the “viable but nonculturable” state, and bacterial stress responses and their relationship to survival and virulence. We are currently studying the various genotypes of *Vibrio vulnificus*, and how we can use bioinformatics to understand differences in their virulence and physiological ecology.

Dr. William Ribarsky (Computer Science) William Ribarsky is the Bank of America Endowed Chair in Information Technology at UNC Charlotte, the founding director of the Charlotte Visualization Center and Principal Investigator for the DHS SouthEast Regional Visualization and Analytics Center. His research interests include visual analytics; 3D multimodal interaction; bioinformatics visualization; virtual environments; visual reasoning; and interactive visualization of large-scale information spaces.

Dr. Christine Richardson (Biology) The long-term goal of my research is to determine the initial events that promote genome instability and hematopoietic malignancies. To complement genetic models in the lab, we have several ongoing microarray projects aimed at (1) determining the transcriptional response of hematopoietic cells to DNA damaging agents and environmental toxins, and (2) identifying new biomarkers and prognostic indicators in specific leukemia and lymphoma patient sub-populations.

Dr. Ronald Sass (Electrical and Computer Engineering) My area of research is in Reconfigurable Computing. This field investigates custom-computing machine architectures to support High-Performance Computing applications. Specifically, we have collaborated with other researchers in the area of bioinformatics to provide solutions to difficult computational problems.

Dr. Susan Sell (Biology) The overall theme of my genomics research program has been the identification of susceptibility genes, regions of genomic instability, SNPs, and biomarkers for common disorders. The unifying strategy has been the utilization of genetically homogeneous populations; this strategy significantly increases the power to uncover new susceptibility genes and biomarkers for common disorders. The projects include: 1) bioinformatics-driven identification of regions of genomic instability associated with type 2 diabetes and cancer; 2) bioinformatics-driven development of a new expression-based diabetes biomarker panel; and 3) a collaborative high-resolution comparative analysis of genomic instability in early-onset breast cancer in Alabama American-American women.

Dr. Min Shin (Computer Science) My research area is in image processing and computer vision. Areas related to bioinformatics include tracking of cells (red blood cells and natural killer T cells) and segmentation of a large network of vessels to analyze the microcirculation as well as the motion behavior of NKT cells with respect to tumor.

Dr. Richard Souvenir (Computer Science) My interests lie in the fields of computer vision and machine learning, specifically modeling and searching high-dimensional data sets. This work has been applied to human motion and biomedical image analysis.

Dr. Zhengchang Su (Computer Science/Bioinformatics Research Center) Dr. Su's research interests are to develop novel algorithms and tools for 1) inference of signaling networks/pathways; 2) characterization of transcriptional regulatory sequences; and 3) classification, molecular modeling and simulation of membrane proteins.

Dr. Jennifer Weller (Computer Science/Bioinformatics Research Center) The Weller group generates and analyzes data from gene expression and genotyping microarray platforms. We have developed a novel relational database model and associated tools for integrating complex

annotations with analysis algorithm output in order to visualize multiple dimensions, mine for novel alleles, and uncover complex factors affecting the molecular phenotypes in these data sets.

Dr. Xintao Wu (Software Information Systems) Xintao Wu's major research interests include data mining, statistical modeling, and their applications in high throughput data-rich areas such as microarray data analysis.

Dr. Jing Yang (Computer Science) My research is on large-scale multi-dimensional data visual exploration that generates public domain multi-dimensional visual exploration software that is free for research and educational purposes. Currently research is focused on high dimensional visualization and its applications on image analysis and simulations.

Dr. Christopher Yengo (Biology) The Yengo group studies the structure and function properties of molecular motor proteins. These proteins are capable of converting chemical energy into mechanical work to drive the processes of muscle contraction, intracellular transport, and cell division. The Yengo group is examining the structural mechanism of energy transduction in myosin motor proteins using spectroscopic and biophysical methods. In addition, studies of uncharacterized non-muscle myosin proteins that function in vision and hearing are in progress to understand their enzymatic, structural and regulatory properties. The regulation of smooth muscle myosin contraction and its role in disease conditions is also under investigation.