UNC CHARLOTTE

Office of the Chancellor

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June 1, 2010

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

Dear Dr. Mabe:

Enclosed is UNC Charlotte's request for authorization to establish a Ph.D. program in Bioinformatics and Computational Biology.

The proposed Bioinformatics and Computational Biology program will play a vital role in supporting the state's biotechnology industry. The program will benefit from the recently completed, state-funded Bioinformatics Building and from collaborations with the North Carolina Research Campus in Kannapolis.

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/ch

Enclosure (5 copies of the proposal)

cc: Provost Joan F. Lorden
Dean Yi Deng

Request for Authorization to Establish

Doctor of Philosophy
Bioinformatics and Computational Biology

May 2010

College of Computing and Informatics

APPENDIX C

THE UNIVERSITY OF NORTH CAROLINA
REQUEST FOR AUTHORIZATION TO ESTABLISH A NEW DEGREE PROGRAM

INSTRUCTIONS: Please submit five copies of the proposal to the Senior Vice President for Academic Affairs, UNC Office of the President. Each proposal should include a 2-3 page executive summary. The signature of the Chancellor is required.

Date: May 27, 2010

Constituent Institution: University of North Carolina at Charlotte

CIP Discipline Specialty Title: Bioinformatics

CIP Discipline Specialty Number: 26.1103 Level: B_____ M_____ 1st Prof _____ D X

Exact Title of the Proposed Degree: Bioinformatics and Computational Biology

Exact Degree Abbreviation (e.g. B.S., B.A., M.A., M.S., Ed.D., Ph.D.): Ph.D.

Does the proposed program constitute a substantive change as defined by SACS? Yes__ No X

a) Is it at a more advanced level than those previously authorized? Yes__ No X

b) Is the proposed program in a new discipline division? Yes____ No X

Proposed date to establish degree program (allow at least 3-6 months for proposal review):
month January *year* 2011

Do you plan to offer the proposed program away from campus *during the first year of operation*?
Yes ____ No X

If so, complete the form to be used to request establishment of a distance education program and submit it along with this request.

Proposed date of initiation of proposed degree program: January 2011

This proposal to establish a new degree program has been reviewed and approved by the appropriate campus committees and authorities.

Chancellor: Phil. J. Dubois 6/1/10

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EXECUTIVE SUMMARY

The Department of Bioinformatics and Genomics at the University of North Carolina at Charlotte requests authorization to establish a Ph.D. Program in Bioinformatics and Computational Biology. This Program is based upon the highly successful Bioinformatics track within the existing Information Technology Ph.D. of the College of Computing and Informatics. The current Bioinformatics track, which has been operating for four years, has 20 Ph.D. students currently enrolled and offers a full curriculum taught by the faculty of the Department. The transformation of this track into an independent Ph.D. program will greatly increase its attractiveness to students interested in Bioinformatics and Computational Biology and will increase participation by faculty in other departments on campus.

Bioinformatics and Computational Biology are at the forefront of 21st century biological sciences, spanning plant genomics to ecology to medicine. This field will be one of the major drivers of the emerging biomedical and biotechnology revolution and will be a critical element in the economic development of the region and State.

UNC Charlotte has a unique role to play in this area. The proposed Program, housed within the College of Computing and Informatics, is focused on applying new computational techniques and hardware on important but very difficult problems in biology and biomedicine. It has a critical role in the development of a robust biotechnology industry in the Charlotte region, and it has a special relationship to the North Carolina Research Campus at Kannapolis.

This request for authorization to establish a Ph.D. program describes the essential elements of the program that have been developed over the past four years. These include recruitment and admission of students, the curriculum, degree requirements, program administration, faculty research and funding. Justification of student demand and need for the program are also provided. The appendix contains biographical sketches of the Core faculty.

I. DESCRIPTION OF THE PROGRAM

The University of North Carolina at Charlotte requests authorization to establish a Ph.D. program in *Bioinformatics and Computational Biology (BCB)*. The program will be administered by the Department of Bioinformatics and Genomics within the College of Computing and Informatics and will involve participating faculty from several other departments as well.

The life sciences have changed dramatically in the last two decades. Initially, the widespread use of high-throughput technologies to generate massive databases has caused biology to become, to a great extent, an information-driven science. Now, more generally, computation is at the heart of many areas of 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[2] (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.*

It is important to note that both Bioinformatics and Computational Biology are grounded in the life sciences, as well as the physical, computational and information sciences. Bioinformatics is directed toward the development and use of computational strategies to extract meaning from data, especially large, complex data sets. Current examples include the assembly and annotation of novel genomes, and the analysis and interpretation of gene expression microarray data. Computational biology focuses more on modeling and simulation. Common examples include structural and physical modeling of proteins to elucidate functional and regulatory mechanisms. There is often considerable synergy between bioinformatics and computational biology, since it is common for modeling and simulation studies to depend on analysis of massive data sets, and for data analysis algorithms to rely on complex theoretical models.

The initial call for bioinformatics training programs came about with the widespread use of high-throughput sequencing associated with the Human Genome Project. Since that time, the size and complexity of the data analysis problems have grown enormously, especially with the widespread use of Next-Gen sequencing systems and the expansion of microarray platforms. Increasingly, the data sets are becoming far too large and complex to be analyzed with ordinary desktop computers, a situation made worse by the current 3 GHz speed limit reached by most processors. Moreover, modeling and simulation studies have come to rely heavily on high performance computing systems. Many organizations, including our Department, now use large high performance computing clusters, multi-core large memory machines, graphic processing units, and hybrid (field programmable gate array) computers to keep up with the demands of growing data sets. Programming and using these computational platforms requires highly specialized training. Moreover, the introduction of single molecule sequencing systems in the next year or so will trigger another data explosion. It is likely that the data production will vastly exceed current analysis capability.

From the National Academy's Bio2010 report, the NIH Roadmaps and the recent report from the National Academy ("A New Biology for the 21st Century: Ensuring the United States Leads the Coming Biology Revolution"), the critical need to integrate biology with computation is widely recognized. However, the problem has been that, from undergraduate through graduate to post-graduate education, biologists and computer scientists have constituted two largely non-overlapping populations. This begins at the undergraduate level, where there is little encouragement for biology students to take computer courses and biology departments rarely allow computer courses to count toward the major. This is equally true for computer science. Moreover, by the time students are in graduate school, the prerequisites are so extensive it is essentially impossible for a biology graduate student to take a graduate computer course, or for a computer science student to take a graduate biology course.

The proposed program provides a mechanism to break this pattern. Because the UNC Charlotte program is centered in a Bioinformatics and Genomics Department, we can design and deliver accelerated courses which allow a student with an undergraduate biology degree to quickly get up to speed in modern computational procedures, while providing other courses that provide the computer science, physics, or mathematics student with the background in molecular biology, genetics, and biochemistry needed to take our core courses. We have refined this approach over the last three years with both our Professional Science Master's courses in Bioinformatics as well as in the Bioinformatics track of the Information Technology Ph.D. program. The result is that students with a variety of different undergraduate backgrounds have been able to successfully complete our core courses as well as the advanced and elective courses in these programs. Far from being a detriment, the interaction of students with different undergraduate majors has clearly enhanced the educational experience.

While the Bioinformatics track in the Information Technology Ph.D. program has been successful, it is difficult to attract applicants who are specifically interested in bioinformatics and computational biology, since they are more likely to go to universities that offer a degree in this field. More specifically, the "Information Technology" designation clearly discourages students with biology backgrounds from applying. Furthermore, because the Bioinformatics track is tied to the admissions, curriculum and graduation criteria for the Computer Science track, both are limited in their ability to tailor their programs to the needs of the students. While our program-wide track approach has been very valuable in the development and refinement of new courses, the organization of admissions and evaluation criteria, and the development of a rigorous research culture for our students, further advancement depends on the establishment of an independent BCB Ph.D. Program.

Educational Objectives

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 much of a contribution. The proposed Ph.D. Program in Bioinformatics and Computational Biology seeks 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 at a high level.

This program has special appeal to students with undergraduate training in computing, life science, 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 science as needed. This is accomplished through the Gateway Courses. The degree program includes additional training beyond an 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.

Relationship to Existing UNC Charlotte Programs

Currently, the Bioinformatics track of the IT Ph.D. program has a close working relationship with the Departments of Biology, Chemistry, Physics and Optical Science, Computer Science, and Mathematics and Statistics. Students in most of these graduate programs may take courses offered by our Bioinformatics faculty, and we expect that Bioinformatics and Computational Ph.D. students will take advanced courses offered by these departments. Faculty in each of the abovementioned departments may serve as mentors, committee members, or provide laboratory rotations for our current students as Participating Faculty. 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. Currently, a Physics faculty member has a wet lab and office in our Bioinformatics Building, and faculty in many departments utilize the two large computer clusters operated by the Department of Bioinformatics and Genomics. We expect these relationships to grow and for new relationships with faculty in other departments to develop as the program expands.

II. JUSTIFICATION FOR THE PROGRAM

Relationship to Institutional Mission

The proposed Ph.D. in Bioinformatics and Computational Biology (BCB) 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) help the University reach "Doctoral/Research University – Extensive" status, 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 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. Currently, the North Carolina Biotechnology Center lists more than 50 biotech companies in the area and nearly 150 biotech-related companies. 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.

Student Demand and Job Prospects

The strongest indication of future student demand has been our success in attracting outstanding students to the existing Bioinformatics Track. We currently have 20 Ph.D. students and will admit 4 more in the fall of 2010. One student graduated in December 2009, and two more will graduate in May 2010. Our experience suggests that student demand is quite substantial. This is despite the fact that our Ph.D. is in Information Technology. We expect even greater demand for a dedicated Ph.D. in Bioinformatics and Computational Biology.

It is noteworthy that we have been able to attract highly qualified North Carolina residents to our program. Nearly half (9 of 20) of our current students are U.S. citizens, and all of these are North Carolina residents. One-third of our students are female and one (5 percent) is an underrepresented minority. Active recruiting measures (see below) will substantially increase the numbers of women and minorities, and especially of North Carolina students. Local students are often recruited through personal interaction with the faculty, including research internships in faculty laboratories. For example, about one-third of the undergraduate 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 very substantial number of inquiries from potential students and arrange interviews. In addition, Ms. Marshall travels to many colleges and universities in our region to recruit outstanding students. Indeed, on a recent visit to North Carolina A & T University, she signed up 12 biology/math/computer science students to visit our graduate open-house event. The strong student demand is mirrored in the other institutions in our State. This year, NCSU's program received around 150 applications for only 6-8 positions, and Duke reported receiving more than 150 applications for only 8 positions. The Bioinformatics and Computational Biology program at Chapel Hill admits students through the unified Biological and Biomedical Sciences Program (BBSP). Of the roughly 1000 applicants to BBSP, it is estimated that more than 100 are competing for only 6-8 slots in the Bioinformatics and Computational Biology Ph.D. program. 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 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 rapidly 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. We believe that many of these jobs will require significant computational skill sets. Our own experience suggests that individuals with this training are in short supply. In the past three years, we have held faculty searches in bioinformatics and computational biology for 12 faculty positions, and received over 400 applications. Despite our explicit requests for individuals trained in bioinformatics and computational biology, *we rarely see an applicant with a degree in this field.*

Impact on Existing Programs at UNC Charlotte

The new Ph.D. program in Bioinformatics and Computational Biology will have a positive effect on other academic programs at UNC Charlotte. First, separating this track from the Computer Science track of the IT Ph.D. program will allow that track to be more readily optimized for their students. Futhermore, a BCB Ph.D. will be a more attractive mechanism for faculty in other departments to train students. The Bioinformatics track currently has two graduate students whose mentors are members of the Physics and Optical Science Department. Since many new faculty hires in Physics have been in the area of molecular biophysics, we expect an increasing number of these faculty to train their students in this program. Similarly, we expect that some faculty in Biology and Chemistry will be more likely to train their students in a "Bioinformatics and Computational Biology" Ph.D. than an "Information Technology" Ph.D. program.

It is important to note that no Ph.D. programs at UNC Charlotte fail to meet the Board of Governor's productivity criteria. Given the substantial number of Ph.D. students in the Bioinformatics track, we see no evidence that the proposed Ph.D. program will fail to meet productivity requirements.

Other Institutions in North Carolina Offering Similar Programs

There are currently three other doctoral programs within North Carolina in Bioinformatics and Computational Biology. North Carolina State University (NCSU), located 170 miles from UNC Charlotte, established the first such program in 1999. This program, directed by Dr. Zhao-Bang Zeng, 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. This program typically graduates 6-7 Ph.D. students each year.

Duke University, located 145 miles from UNC Charlotte, established a Ph.D. in Computational Biology and Bioinformatics in 2003. The Duke program, directed by Dr. John Harer, offers over 15

courses, but only three are required (Genomic Tools and Technologies, Algorithms, and Statistical Methods) 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. While the program covers all major areas, they have particular strength in systems biology. Their goal is to graduate about 8 students per year.

The Ph.D. in Bioinformatics and Computational Biology at Chapel Hill (also 145 miles from UNC Charlotte) was approved in 2008, and is directed by its founder, Dr. Tim Elston. The Chapel Hill program requires two foundation courses, laboratory rotations, a colloquium, and seven 1 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, they list 29 Core faculty in 15 departments, along with 12 additional Resource faculty. These faculty represent a broad range of subject areas. This program plans to produce 6-8 graduates per year.

UNC Charlotte is Unique and Appropriate

While the UNC Charlotte program covers the same core areas of Bioinformatics and Computational Biology as the NCSU, UNC Chapel Hill, and Duke programs, it is unique in several ways. First, it is departmentally based. The Department of Bioinformatics and Genomics has complete freedom in the design of the curriculum, scheduling classes, and in hiring faculty and assigning teaching responsibilities. This structure contrasts with that of NCSU, Duke, and UNC Chapel Hill, which use faculty from various departments to teach courses and mentor and support students. Except for a few core courses, their didactic courses are primarily designed for, and taught by, other graduate programs. 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 these courses as part of their primary teaching responsibilities, and that rigorous control over both student performance and course content 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. This is especially important for attracting both computer science and life science undergraduate applicants and providing them with the means to bridge the disciplinary gap.

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 center 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 be able to place an emphasis on cutting-edge 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, thus seamlessly integrating biological and computational aspects. Our statistics course uses examples drawn from common problems in bioinformatics and incorporates assignments in the R language. We can also place a special emphasis on parallel programming (multi-thread, multi-processor) using high performance computing platforms in our course offerings. Students have ready access to three high performance computer clusters for bioinformatics as well as special purpose FPGA computers, massive GPU clusters, and multi-core large memory computers for bioinformatics applications. The incorporation of high performance computing technologies will be critical as next-gen sequencing throughput approaches the terabyte range, and third-gen sequencing eclipses that. Our program also offers significant training in physics/chemistry-based modeling that is largely absent from the other three programs.

Finally, UNC Charlotte is a major partner providing faculty and service staff in bioinformatics to the North Carolina Research Campus (NCRC) at Kannapolis. This association will provide an opportunity to collaborate with NCRC scientists on a wide range of important problems and allows access to the latest technology. We have already developed relationships with the UNC-CH Nutrition Research Institute (Dr. Zeisel), the NCSU Plants and Human Health Institute (Dr. Lila), and the David H. Murdock Research Institute (Dr. Luther). 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 end 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 BCB Ph.D. Program will play a critical part in that role.

It is important to note that no other North Carolina university offers distance education courses at this level. Indeed, distance education is not appropriate for doctoral level education in this field due to the close mentor-student relationship that is required and the need to access laboratory facilities.

Enrollment at other UNC institutions

As previously noted, UNC Chapel Hill and NCSU offer similar programs. Their five-year history of enrollments and degrees is shown below. The directors of both the NCSU and UNC programs were consulted in the preparation of this request, as was the director of the Duke program. All three institutions reported around 100 to 150 applicants each year for approximately 8 positions in each program, indicating strong student demand. The relatively limited number of faculty directly involved in training will likely restrict each program to around 6 to 8 graduates per year. The directors of both the NCSU and Duke programs report that demand for their graduates is very strong, with roughly half going into academia (usually via a post-doctoral position) and half directly to industry. Dr. Tim Elston, the director of the UNC Chapel Hill program, is optimistic about demand for graduates given the experience UNC Chapel Hill has had with their Graduate Certificate program in Bioinformatics and Computational Biology. All three directors have indicated that both the student demand and demand for graduates is strong enough to support another program graduating 4 or 5 students a year.

Institution: North Carolina State University
Program Title: Bioinformatics (261103)

	2004-05	2005-06	2006-07	2007-08	2008-09
Enrollment	41	40	36	35	31
Degrees-awarded	4	6	7	9	6

Institution: University of North Carolina at Chapel Hill
Program Title: Bioinformatics (261103)

	2004-05	2005-06	2006-07	2007-08	2008-09
Enrollment	na	na	na	na	1*
Degrees-awarded	0	0	0	0	0

*Although this is the reported number, the actual number of enrolled students is 10, since students entering through the BBSP are not reported until their 2nd year.

Projected Enrollment and Credit-Hour Production

Use the format in the chart below to project your enrollment in the proposed program for four years and explain the basis for the projections:

	Year 1 (2010 - 2011)	Year 2 (2011 - 2012)	Year 3 (2012 - 2013)	Year 4 (2013 - 2014)
Full-time	22	24	26	28
Part-time	0	0	0	0
TOTALS	22	24	26	28

Please indicate the anticipated steady-state headcount enrollment after four years:
Full-time 28 Part-time 0 Total 28

All of the current students in the Bioinformatics track of the IT Ph.D. program will transfer into the Ph.D. program in Bioinformatics and Computational Biology. There are currently 20 full-time Bioinformatics track students enrolled, and historically, the headcount for this program has grown by about 2 students per year. By year 4 we expect to graduate 5 students per year.

SCH production (upper division program majors, juniors and seniors only, for baccalaureate programs).
Use the format in the chart below to project the SCH production for four years. Explain how SCH projections were derived from enrollment projections (see UNC website for a list of the disciplines comprising each of the four categories).

The Biological Sciences CIP (26) is in category III of the funding model. The projections are based on each student taking 9 credit hours per semester (the minimum required by our program).

Year 1	**Student Credit Hours**		
Program Category	**UG**	**Masters**	**Doctoral**
Category I			
Category II			
Category III			396
Category IV			

Year 2	**Student Credit Hours**		
Program Category	**UG**	**Masters**	**Doctoral**
Category I			
Category II			
Category III			432
Category IV			

Year 3	**Student Credit Hours**		
Program Category	**UG**	**Masters**	**Doctoral**
Category I			
Category II			
Category III			468
Category IV			

Year 4	Student Credit Hours		
Program Category	**UG**	**Masters**	**Doctoral**
Category I			
Category II			
Category III			504
Category IV			

III. PROGRAM REQUIREMENTS AND CURRICULUM

Program Planning

The Plan described in this Request for Authorization to Establish is based primarily on our experience over the past four years with the Bioinformatics track of the existing IT Ph.D. program. During this period, we have increased our enrollment and course offerings, six of our students have passed their qualifying examinations, and one has graduated. The basic mechanism has remained the same, although a number of adjustments have been made. All of the components of the program are in place and have been tested. These include recruitment and admissions, financial support, academic requirements, timelines, courses, and administrative structure.

Many major universities now offer Ph.D. degrees in Bioinformatics and Computational Biology in one form or another. Many of these programs are based in medical schools and resemble the Duke and UNC Chapel Hill programs in structure. The programs with curricula comparable to that proposed here include:

Boston University – Bioinformatics
University of Michigan – Bioinformatics
Georgia Tech – Computational Biology and Bioinformatics
University of Southern California – Computational Biology and Bioinformatics

On-site consultations with the directors of NCSU's Program in Bioinformatics (Dr. Zhao-Bang Zeng) and UNC Chapel Hill's Bioinformatics and Computational Biology (Dr. Tim Elston) were very helpful in developing UNC Charlotte's plan and understanding the differences in emphasis between these programs. In addition, consultation with Dr. John Harer, director of Duke's Computational Biology and Bioinformatics program, was also useful. All three directors indicated that student demand for these programs and employer demand for graduates exceed their training capacity. It is also clear that while all three of these programs provide excellent training, they each have their own strengths and are likely to produce students with quite different skills and interests. UNC Charlotte's program will make a further contribution to the programmatic diversity of bioinformatics training in the state.

Recruitment

The BCB Ph.D. recruitment plan is directed primarily at recruiting US students, especially North Carolina residents and underrepresented minorities. Currently, there is no shortage of international applicants to our program. Two recruitment strategies for local students have proven successful. One is through the use of the undergraduate bioinformatics courses and research opportunities. The Department offers several undergraduate courses aimed at computer science and life science majors, and will soon offer a concentration in bioinformatics for undergraduates. These efforts are producing much interest among undergraduate students on campus. Many of the students enrolled in these undergraduate bioinformatics courses are also participating in research under supervision from Bioinformatics faculty.

As a result of these efforts, several junior level undergraduate students have expressed an interest in applying to the Ph.D. program.

The other recruiting method involves faculty or advanced graduate students travelling to local colleges and universities with the Program Coordinator to give research talks. Thus far, we have presented talks at Davidson College, Elon College, UNC Asheville, North Carolina A&T University, Guilford University, Queens University, Winthrop University, Johnson C. Smith University, Appalachian State University, Fayetteville State University, and Barton College. Many other schools are being scheduled, including those in Georgia, Virginia, South Carolina, and Tennessee. While the website (bioinformatics.uncc.edu) is an excellent resource, establishing relationships with faculty and counselors in the life sciences and computer science departments is crucial for effective recruiting of local students.

Admission

It is expected that students entering the program will have completed an undergraduate major in either a life science or a quantitative discipline from an accredited institution. The most important qualifications include: excellent GRE scores, satisfactory past academic performance as usually reflected by a grade point average of (or equivalent to) at least 3.0 (on a 4.0 scale), and research experience. Applicants whose native language is not English must score at least 220 computer-based, 557 paper-based, or 83 internet-based in the Test of English as a Foreign Language (TOEFL). Letters of recommendation and statements of purpose are very important in determining the top applicants. Further documentation that will support the application may include: evidence of scholarly and creative activity, including publication list; awards; results in national or international contests related to information technology, etc. The admissions committee consists of at least five tenured or tenure-track Bioinformatics and Genomics faculty members. The admissions committee selects the applicants for an interview. Selected US applicants are invited for an on-campus interview, meetings with the current Bioinformatics students, and will visit with interested bioinformatics faculty labs to learn more about research opportunities and UNC Charlotte. International students are interviewed via phone or web video (e.g. Skype). Applicants will be notified by the end of February with acceptance or rejection letters. Those offered admission will have until April 15 to accept or decline.

Degree Requirements

To earn a Ph.D. degree, students must complete at least 72 post-baccalaureate credit hours. This includes at least 18 hours of dissertation research and at least 9 hours of course work completed at UNC Charlotte. A limited amount of transfer credit is allowed, as specified by the Graduate School. Students are expected to acquire a sufficiently broad body of technical knowledge in the discipline as well as a deep understanding of a specialized area. This is accomplished with a combination of required courses and appropriate electives approved by the student's advisor(s) and dissertation committee.

i. Didactic Coursework

The required coursework is organized in three tiers of formal training: Gateway courses (Table 1), Core courses (Table 2), and Electives (Table 3). The Gateway courses will differ according to the student's background. A student with a strong computer science background would likely take BINF 8100 and BINF 8101, but not BINF 8111 and BINF 8112. A student with a strong background in the life sciences would take BINF 8111 and BINF 8112, but not BINF 8100 and BINF 8101. This determination is made by the Program Director when the student enters the Program. All students, regardless of their background, must take the Core courses, BINF 8200, BINF 8201, and BINF 8202 and nine credit hours of Electives. Students may register for Elective courses listed in Table 3 or for courses outside of the Bioinformatics and Genomics Department

with the permission of the Program Director. The courses offered for the Program will be available to graduate students only.

All of the proposed courses are offered at the 8000 level with second digits following the guidelines for course numbers described in the UNC Charlotte Graduate Catalog. In addition, the Gateway courses have a second digit of "1", Core bioinformatics courses have a second digit of "2" and most Electives have a second digit of "3" or higher. All listed courses have been approved and are currently being offered.

Table 1. Gateway Courses

Course Number (credits)	Title and Description
BINF 8100 (3)	Biological Basis of Bioinformatics. This course provides a foundation in molecular genetics and cell biology focusing on foundation topics for graduate training in bioinformatics and genomics.
BINF 8101 (3)	Energy and Interaction in Biological Modeling. This course covers: (i.) the major organic and inorganic chemical features of biological macromolecules; (ii.) the physical forces that shape biological molecules, assemblies and cells; (iii.) the chemical driving forces that govern living systems; (iv.) the molecular roles of biological macromolecules and common metabolites; (v.) and the pathways of energy generation and storage. Each section of the course builds upon the relevant principles in biology and chemistry to explain the most common mathematical and physical abstractions used in modeling in the relevant context.
BINF 8111 (3)	Bioinformatics Programming I. This course introduces fundamentals of programming for bioinformatics using a high-level object-oriented language such as python. The first weeks cover core data types, syntax, and functional programming, focusing on construction of programs from small, testable parts. Students will learn productive use of the Unix environment, focusing on Unix utilities that are particularly useful in bioinformatics. The course will cover object-oriented programming, introduce analysis of algorithms and sequence alignment methods, and introduce computational environments that are particularly useful in bioinformatics analyses such as R, BioPython, and Web services in bioinformatics. By the end of the class, students will have gained the ability to analyze data within the python interpreter (for example) and write well-documented, well-organized programs.
BINF 8112 (3)	Bioinformatics Programming II. This course is the second semester of Introduction to Bioinformatics Programming I. In this semester, students will practice and refine skills learned in the first semester. New topics introduced will include: programming as part of a team, using sequence analysis algorithms in realistic settings; writing maintainable and re-usable code; Web programming; and graphical user interface development. At the end of the semester, students will be able to evaluate and deploy computer languages, tools, and software engineering techniques in bioinformatics research.

Table 2. Core Courses

Course Number (credits)	Name
BINF 8200 (3)	Statistics for Bioinformatics. This course aims to introduce statistical methods commonly used in bioinformatics. Basic concepts from probability, stochastic processes, information theory, and other statistical methods will be introduced and illustrated by examples from molecular biology, genomics and population genetics with an outline of algorithms and software. R is introduced as the programming language for homework.
BINF 8201 (3)	Molecular Sequence Analysis. Introduction to bioinformatics methods that apply to molecular sequence. Intro to biological databases online. Sequence databases, molecular sequence data formats, sequence data preparation and database submission. Local and global sequence alignment, multiple alignment, alignment scoring and alignment algorithms for protein and nucleic acids, genefinding and feature finding in sequence, models of molecular evolution, phylogenetic analysis, comparative modeling.
BINF 8202 (3)	Computational Structural Biology. This course covers: **(a)** the fundamental concepts of structural biology (chemical building blocks, structure, superstructure, folding, etc.); **(b)** structural databases and software for structure visualization; **(c)** structure determination and quality assessment; **(d)** protein structure comparison and the hierarchical nature of biomacromolecular structure classification; **(e)** protein structure prediction and assessment; and **(f)** sequence- and structure-based functional site prediction.

Table 3. Elective Courses

Course Number (credits)	Name
BINF 8203 (3)	Genomics
BINF 8204 (3)	Mathematical Systems Biology
BINF 8205 (3)	Computational Molecular Evolution
BINF 8210 (3)	Numerical Methods and Machine Learning in Bioinformatics
BINF 8211 (3)	Design and Implementation of Bioinformatics Databases
BINF 8311 (3)	Biophysical Modeling
BINF 8312 (3)	Computational Comparative Genomics
BINF 8313 (3)	Structure, Function, and Modeling of Nucleic Acids
BINF 8601 (1)	Journal Club
BINF 8151 (1)	Professional Communications
BINF 8171 (3)	Business of Biotechnology
BINF 8310 (3)	Advanced Statistics
BINF 8350 (3)	Biotechnology and Genomics Laboratory
BINF 8380 (3)	Bioinformatics Programming III

ii. Research Rotations

Each Ph.D. student must complete two research rotations, BINF 8911, and 8912, in their first year. These rotations provide two semesters of faculty supervised research experience to supplement regular course offerings. The purpose of these courses is to broaden students'

exposure to state-of-the-art technologies currently being utilized within the field of bioinformatics, to guide them towards recognizing important, outstanding questions in specific scientific domains, and to give them hands-on training within those domains. Students select their rotation projects in consultation with the Program Director and selected faculty members. At the end of each rotation, students must prepare a formal presentation on their findings for the faculty and their peers.

iii. Seminar

BINF 8600 (Graduate Research Seminar) is taken every semester until advancing to Ph.D. candidacy. The Bioinformatics Seminar has been required of the current IT Bioinformatics track Ph.D. students and Bioinformatics Professional Science Master's students and will continue to be a part of the BCB Ph.D. program. During the fall and spring semesters, the seminar hosts guest speakers to present talks that focus on bioinformatics, genomics, and computational biology related research. There are also designated seminar slots for the Ph.D. students to present their research rotation work.

iv. Qualifying Exam

Students are required to take a qualifying exam to demonstrate proficiency in the fundamentals of bioinformatics and computational biology, as well as competence in statistics, molecular biology, biochemistry, and genetics. The qualifying exam must be passed prior to the 5th semester of residence. The qualifying exam for the Bioinformatics and Computational Biology Ph.D. is composed of both a written and oral examination. The qualifying exam committee will have the same members in any given semester. The written component will have three sections that emphasize (a.) molecular sequence analysis, (b.) computational structural bioinformatics, and (c.) statistics and research methods. The qualifying exam is based largely on material covered in the Core courses listed above. The written sections are graded numerically, and the examinations and grades are kept by the Program to assess student outcomes. Each student must pass all sections in order to advance; failure to pass requires that the student attempt the failed sections the following semester. Passed sections carry forward from one exam to the next. Two attempts are permitted. After passing the three written sections, students must pass an oral exam over the same and related topics, for which two attempts are also permitted. Students who do not pass both sections of the qualifying exam will be dismissed from the program.

v. Research

Students become engaged in research immediately upon entering the Program through two mandatory research rotations in the first year. A student is expected to identify a research mentor by the beginning of the second year, and take pre-dissertation research credits. Once the qualifying examination is passed (i.e., by the 5^{th} semester), the student should have formed a Dissertation Committee in consultation with the mentor and the Program Director. UNC Charlotte Graduate School rules specify that the committee consist of at least five members, four of whom must be BCB faculty members (Core or Participating, see below) and one appointed by the Graduate School. The committee chair must be a BCB faculty member. Dissertation Committee meetings are held once a semester starting in the fall semester of the third year to ensure sufficient progress is being made to complete the dissertation within five years. Students are required to present an oral progress report at each meeting, followed by a discussion of goals for the following semester.

Each student must present and defend a Ph.D. dissertation proposal no more than three semesters after passing the qualifying exam. The proposal defense will be conducted by the student's Dissertation Committee and will be open to faculty and students. At the discretion of the Dissertation Committee, the defense may include questions that cover the student's program of study and background knowledge in the area of the proposal. A student can retake the proposal defense if he/she does not pass it the first time. The second failed defense of a dissertation proposal will result in the termination of the student's enrollment in the Ph.D. program. A doctoral student advances to Ph.D. candidacy after the dissertation proposal has been successfully defended.

vi. Teaching and Professional Development

Students are required to serve as teaching assistants for at least one Bioinformatics and Computational Biology course after they have passed their qualifying exam. Faculty members supervising teaching assistants will specify their duties, which may include: attending classes, assisting with grading, tutoring, preparing and delivering lectures, and/or proctoring exams.

The Professional Communications course is highly recommended but not required. This course will be useful for Ph.D. students with oral presentations, poster presentations, scientific writing, use of references and avoiding plagiarism. Students will also learn how to properly organize and a run a meeting. Lastly, students will prepare a CV, job application letter with supporting documents, and job talk.

vii. Dissertation proposal, Oral Defense, and Publication(s)

Each student must complete a research proposal approved by the student's Dissertation Advisor(s) that yields a high quality, original and substantial piece of research. The Ph.D. dissertation describes this research and its results. The dissertation defense is a public presentation. A written copy of the dissertation must be made available to each member of the student Ph.D. Dissertation Committee, to the Program Director, and to the UNC Charlotte Library at least three weeks before the public defense. The date of the defense must be publicly announced at least three weeks prior to the defense. The student must present the dissertation and defend it in a manner accepted by the Dissertation Committee. The dissertation will be graded as pass/fail by the Dissertation Committee and must be approved by the Dean of the Graduate School. A student who fails the defense of a dissertation twice will be terminated from the Ph.D. program.

Table 4. Typical Timeline for Student Progression

Admission
• Completed an undergraduate major in either a life science or a quantitative discipline
Year 1
• 2 Gateway courses (3 credits each)
• 2 Core courses (3 credits each)
• Bioinformatics Seminar (BINF 8600) (1 credit/semester)
• 2 research rotations (BINF 8911 and 8912) (2 credits each)
Year 2
• 1 Core course (3 credits)
• Bioinformatics Seminar (BINF 8600) (1 credit/semester)

• Electives (3-9 credits)
• Pre-Dissertation Research (BINF 8911) (6-10 credits)
• Qualifying exam (written and oral)
Years 3-5
• Electives (as needed)
• Bioinformatics Seminar (BINF 8600) (1 credit/semester)
• Dissertation Research (BINF 8911) (9-10 credits/semester)
• Proposal Defense, dissertation, publications(s), and oral defense

Students are expected to excel in all course work. Graduation requirements mandate that students must achieve a minimum grade point average of 3.0 to graduate. Receiving more than two *C* grades or a grade of *U* in any course will result in a suspension from the program.

In accordance with rules of the UNC Charlotte Graduate School, students are allowed to transfer up to 30 semester hours of graduate credit earned at UNC Charlotte or other recognized graduate programs. In cases of applicants with records of exceptionally high quality, the Program Direct may request that the Graduate School approve transfer credit beyond the limit set by the Graduate School. To receive transfer credit, students must file a written request and submit all necessary documents to the Program Director.

All requirements for the degree must be completed within eight years after first registration as a doctoral student. The student must achieve admission to candidacy within six years after admission to the program and complete all requirements within six years after admission to candidacy for the Ph.D. degree. These time limits are maximums; students will typically be expected to complete the degree requirements within five years. To ensure progress, each student will undergo a comprehensive program review by the Program Director each year.

IV. FACULTY

A. List the names of persons now on the faculty who will be directly involved in the proposed program.

Table 5. Core Faculty (primary appointment: Bioinformatics and Genomics)

Name	Rank	Research Interest
Xiuxia Du, Ph.D.	Asst. Professor	Computational proteomics & metabolomics and integration of –omics data for systems biology research.
Anthony Fodor, Ph.D.	Asst. Professor	Metagenomics, microbial ecology and diversity, human associated microbiota.
Cynthia Gibas, Ph.D.	Assoc. Professor	Genomic data analysis and visualization
Jun-tao Guo, Ph.D.	Asst. Professor	Protein structure prediction and protein-DNA interactions.
Dennis Livesay, Ph.D.	Assoc. Professor	Protein sequence/structure/function relationships
Ann Loraine, Ph.D.	Assoc. Professor	Plant genomics, genomic visualization, alternative splicing, mining expression microarray data.
Lawrence Mays, Ph.D.	Professor, Chair	Bioinformatics education.
Jessica Schlueter, Ph.D.	Asst. Professor	Evolution, plant genomics. Genome structure. Polyploidy. Gene expression regulation. Epigenetics.

Shannon Schlueter, Ph.D.	Asst. Professor	Bioinformatic algorithm development for computational recognition and prediction of genomic features.
Susan Sell, Ph.D.	Professor	Genomics of disease susceptibility; expression array-based biomarker development
Zhengchang Su, Ph.D.	Asst. Professor	Computational prediction of transcription factor binding sites & reconstruction of gene regulatory networks.
Jennifer Weller, Ph.D.	Assoc. Professor	Quantifying hybridization assays. Storage/retrieval of massive datasets. Progression of complex disease.

B. Faculty required.

No new faculty will be needed. All required and elective courses are now being taught by current faculty either as part of the existing Professional Science Master's Program in Bioinformatics or as part of the Bioinformatics track of the current IT Ph.D. program. All courses except for BINF 8151 and BINF 8205 have been taught as ITSC 8010 Special Topics courses before. BINF 8991 is currently being taught as ITSC 8991.

C. If the employment of new faculty requires additional funds, please explain the source of funding.

No new faculty required.

D. Explain how the program will affect faculty activity, including course load, public service activity, and scholarly research.

The program will not increase course load significantly, or public service activity, since nearly all courses are now being taught as cross listed courses for the Professional Science Master's program. The program will likely improve the faculties' scholarly research productivity, since it will attract ever more qualified Ph.D. students.

V. LIBRARY

A. Provide a statement as to the adequacy of present library holdings for the proposed program.

A library consultation was requested and received for each of the courses from the University Librarian. The library holdings were classified as "adequate" for all courses.

B. State how the library will be improved to meet new program requirements for the next five years. The explanation should discuss the need for books, periodicals, reference material, primary source material, etc. What additional library support must be added to areas supporting the proposed program?

No additional improvements are required to meet program requirements.

C. Discuss the use of other institutional libraries.

No other institutional libraries will be required for this program.

VI. FACILITIES AND EQUIPMENT

A. Describe facilities available for the proposed program.

The BCB Program is housed within the Bioinformatics Building on the UNC Charlotte Campus. This is a 94,000 GSF building completed in August 2009. Approximately 25 percent of the useable space is devoted to BSL-2 class wet labs, with associated freezer rooms, dishwashers, autoclaves, etc. It also has a 900 square feet BSL-3 suite. The labs have a wide variety of equipment including freezers, centrifuges, PCR machines, DNA sequencer, etc. The building has approximately 50 faculty and staff offices and office space for up to 70 graduate students and post-docs. The building also has several classrooms, a server room, a fully equipped 36-seat computer classroom and 6 conference rooms. The Department of Bioinformatics and Genomics is the only academic department occupying this building.

Computer facilities in the building include more than 50 workstations, a 440-core computer cluster, a four processor TimeLogic FPGA system, several large memory (128GB) computers, and a graphics processor (GPU) platform. An additional 500-core cluster will be operational in the building by June 2010. Students also have access to a 524-core computer cluster maintained by the Department at our Kannapolis (NCRC) site. Computer facilities are supported by the 3-person High-Performance Computing (HPC) technical staff located in the Bioinformatics Building and another 3-person technical support group provided by the College of Computing and Informatics.

B. Describe the effect of this new program on existing facilities and indicate whether they will be adequate, both at the commencement of the program and during the next decade.

The new physical facilities are more than adequate for the program for the present and for the next decade. The computer equipment will be refreshed on a 3 to 4 year cycle, funded by the College and the HPC unit of the University's Information Technology Service group.

C. Discuss any information technology services needed and/or available.

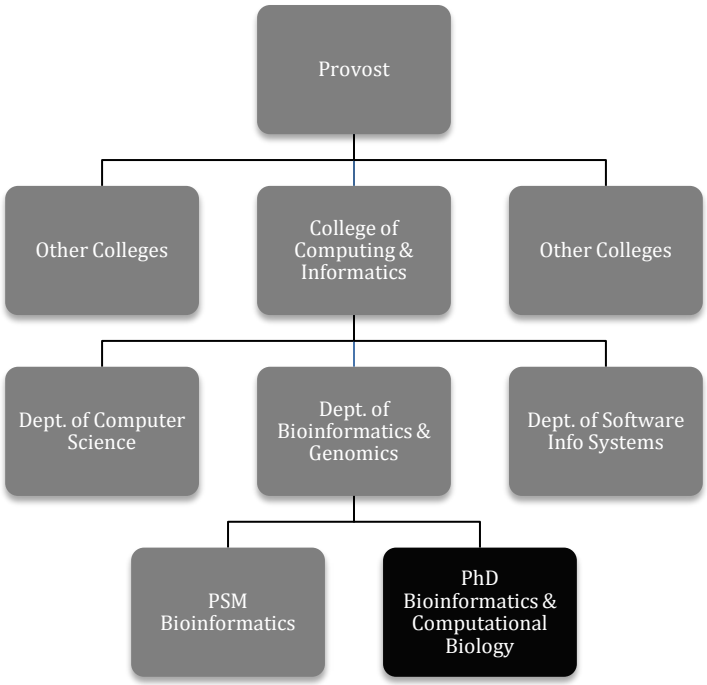
See Section VI. A. above.

D. Discuss sources of financial support for any new facilities and equipment.

See Section VI. A. above.

VII. ADMINISTRATION

The Bioinformatics and Computational Biology Ph.D. program is housed administratively within the Department of Bioinformatics and Genomics in the College of Computing and Informatics. The Professional Science Master's (PSM) in Bioinformatics is the other graduate program within this Department. The administrative structure of the Program and its relationship to other units of the University is shown below:



The Core Faculty of the BCB Ph.D. program are the full-time graduate faculty in the Department of Bioinformatics and Genomics. They are responsible for teaching all required courses and the majority of elective courses. The Department Chair makes these teaching assignments in consultation with the Program Director and Curriculum Committee. Graduate faculty from other departments such as Physics and Optical Science, Chemistry, Mathematics and Statistics, and Biology may be granted Participating Faculty status by recommendation of the Program Director and approval by a majority of the Core Faculty. Participating Faculty may mentor BCB students, serve on dissertation committees or teach courses in the BCB Ph.D. program. The BCB Ph.D. Program Director (currently Dr. Livesay) is nominated by the Department Chair for a three-year term and approved by the Core Faculty. The Program Director may be re-appointed for multiple terms. The Program Coordinator (currently Ms. Marshall) assists the Program Director and the standing committees. The standing committees of the BCB Ph.D. program are the Admissions, Curriculum, and Qualifying Exam committees. Standing committee members are nominated by the Program Director and approved by the Core Faculty. Membership in the standing committees is restricted to members of the Core Faculty. The membership of each standing committee elects its chair. The responsibilities and roles of the key personnel and standing committees are described below:

<u>Program Director:</u>

- Overall responsibility for the success of the Program
- Reports to Graduate School on behalf of the Program

- Approves dissertation committees
- Final signatory authority for Ph.D. processes
- Meets regularly with Program Coordinator, Dept. Chair and standing committee chairs
- Manages financial support for students (with assistance of Program Coordinator)
- Assigns initial advisor to incoming students
- Nominates candidates for Participating Faculty and standing committees

Program Coordinator:

- Responsible for website content and public relations
- Monitors students progress and maintains records
- Coordinates student recruitment activities
- Assists Program Director and Chairs of standing committees
- *Ex-officio* member of standing committees

Admissions Committee:

- Selects applicants for interviews and offers
- Directs recruitment efforts

Curriculum Committee:

- Responsible for creating coursework and other degree requirements
- Coordinates scheduling of course offerings

Qualifying Examination Committee:

- Writes, administers, and grades qualifying exam twice a year

VIII. ACCREDITATION

The BCB Ph.D. Program has no plans for requesting professional accreditation, as there are no specific accreditation agencies relevant to bioinformatics and computational biology.

IX. SUPPORTING FIELDS

There are no specific subject matter fields at UNC Charlotte whose development, expansion or improvement is necessary for the success of the proposed BCB Ph.D. Program.

X. ADDITIONAL INFORMATION

None.

XI. BUDGET

No additional State-appropriated funds are needed to implement this Program. The courses in the Program are taught by existing Bioinformatics and Genomics Department faculty. The Program is administered by these faculty with assistance of support staff provided by the College of Computing and Informatics. Graduate assistantships are provided by the College, the Graduate School, by funding associated with the Department's research efforts at the NCRC in Kannapolis, and by the Department's participation in the GAANN fellowship program. These are adequate for the number of students that are expected to enroll. In addition, a majority of faculty have substantial research grants which are used to

support students in later years of study. Given that our faculty is relatively young, we expect that the size and number of these research grants will grow.

XII. EVALUATION PLANS

A. Criteria to be used to evaluate the proposed program:

The criteria used to evaluate the program will include:

1. Number of applicants
2. Percentage of applicants offered admission who matriculate
3. Percentage of US and NC residents, women, underrepresented minorities
4. Length of time to graduation
5. Graduate assistantship support
6. Percentage of students who graduate
7. Publications by students
8. Job placement

B. Measures to be used to evaluate the program:

Using the criteria enumerated above, within 5 years we would expect:

1. 100 applicants per year
2. 60% of applicants offered admission will matriculate
3. 35% NC residents, 55% US, 50% women, 10% minorities
4. Between 5 and 6 years to graduation
5. 100% assistantship support to all students requesting support
6. 70% graduation in 5 years, 85% within 6 years
7. Three publications per student by the time of graduation
8. Approximately 60% of students go on to postdocs, 40% to industry

C. Projected productivity levels (number of graduates):

The totals below are estimates of the number of students graduating from the current Bioinformatics tract.

Level	Year 1	Year 2	Year 3	Year 4	TOTALS
B					
M					
I/P					
D	3	3	4	5	15

(Key: B-Bachelor's, M-Master's, I/P-Intermediate or Professional, D-Doctoral)

D. Recommended consultant/reviewers: Names, titles, addresses, e-mail addresses, and telephone numbers. May not be employees of the University of North Carolina.

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E. Plan for evaluation prior to fifth operational year.

During the fourth year of operation, the Program will undergo a formal external review by a panel of leading scientists in the field, such as those listed above. The panel will travel to UNC Charlotte, interview faculty and students, and review the records of the Program. The panel will then prepare a written evaluation report and plan for improvements that will be given to the Program Director, the Dean of the College of Computing and Informatics and the Provost.

XIII. REPORTING REQUIREMENTS

Institutions will be expected to report on program productivity after one year and three years of operation. This information will be solicited as a part of the biennial long-range planning revision.

Appendix A

Atkins Library Consultation Report

UNC CHARLOTTE

J. Murrey Atkins Library

Consultation on Library Holdings

To: Larry Mays
College of Computing and Informatics
Department of Bioinformatics and Genomics

From: Reese Manceaux

Date: March 17, 2010

Subject: Proposed Doctoral Degree Program in Bioinformatics

Summary of Librarian's Evaluation of Holdings:

Evaluator: Reese A. Manceaux **Date:** 3/17/10
Check One:

1. Holdings are superior
2. ☑**Holdings are adequate (Please see comments)**
3. Holdings are adequate only if Dept. purchases additional items.
4. Holdings are inadequate

Comments:

Atkins Library has adequate resources to support the courses proposed for the revised undergraduate curriculum for the Department of Bioinformatics and Genomics. The library has an vast set of databases in the proposed areas of study. Journal articles and books that are not held by the Library can be obtained through Interlibrary Loan.

Once budget concerns are addressed, monograph purchases should increase in the area of computational biology as well as other areas related to courses in this program.

A small sampling of subject searching in the Atkins Library online catalog reveals the following holdings in support of these courses. (See the table that follows). A search of a few related subjects retrieved over 1,805 pertinent items. The monograph holdings are adequate. The book collection can be updated, as needed, through acquisitions by the appropriate departments.

In addition, the library purchases subscriptions to many electronic databases that provide major up-to-date research support such as Science Direct, CSA Biological Sciences/Biotechnology and Bioengineering Abstracts, Compendex, IngentaConnect, PubMed, SpringerLink, Web of Science, and Wiley Interscience - many with links to full text articles. The library also has electronic access to periodicals and other electronic resources (e-books, Skillport) that support these courses. All these resources support the overall Bioinformatics and Genomics programs.

Please refer to the table at the end of the document for the top journals in the subject area arranged by JCR Impact Factor.

Atkins Library Sample Holdings in Areas Related to Course
3/17/2010

Subject	Books/EBooks	After Year 2000	Journals
Bioinformatics	114	73	21
Biotechnology	588	172	17
Genomics	76	67	6
Data Mining	159	102	6
Computational Biology	29	23	8
DNA	312	117	9
Genetics	527	107	18
Totals	**1805**	**661**	**85**

Reese A. Manceaux
Evaluator's Signature

March 17, 2010

A current search of the 2008 Journal Citation Reports shows the Bioinformatics journals ranked by impact factor.

Of the top 20, Atkins Library holds ALL 20 electronically (some concurrently in paper).

- **Plos Computational Biology**
- **Bioinformatics**
- **BMC Bioinformatics**
- **BMC Systems Biology**
- **Biostatistics**
- **Journal Of Computational Neuroscience**
- **Journal Of Theoretical Biology**
- **Journal Of Molecular Graphics And Modelling**
- **SAR And QSAR In Environmental Research**
- **Statistical Methods In Medical Research.**
- **IET Systems Biology**
- **Statistics In Medicine**
- **Algorithms For Molecular Biology**
- **IEE Proceedings-Systems Biology**
- **Biometrics**
- **IEEE Transactions On Information Technology In Biomedicine**
- **Bulletin Of Mathematical Biology**
- **Journal Of Mathematical Biology**
- **Journal of Computational Biology**
- **Biometrika**

JCR-Web 4.5 Journal Summary List

Journal Summary List

Journals from: subject categories MATHEMATICAL & COMPUTATIONAL BIOLOGY VIEW CATEGORY SUMMARY LIST

Sorted by: Impact Factor SORT AGAIN

Journals 1 - 20 (of 29) [1 | 2]

MARK ALL UPDATE MARKED LIST

Ranking is based on your journal and sort selections.

Mark	Rank	Abbreviated Journal Title (linked to journal information)	ISSN	JCR Data					
				Total Cites	Impact Factor	5-Year Impact Factor	Immediacy Index	Articles	Cited Half-life
☐	1	PLOS COMPUT BIOL	1553-734X	2730	5.895	6.144	0.826	253	2.1
☐	2	BIOINFORMATICS	1367-4803	30344	4.328	6.481	0.566	643	4.8
☐	3	BMC BIOINFORMATICS	1471-2105	8141	3.781	4.246	0.664	607	2.8
☐	4	BMC SYST BIOL	1752-0509	234	3.706	3.706	0.459	98	1.4
☐	5	BIOSTATISTICS	1465-4644	1625	3.394	5.253	0.643	56	5.1
☐	6	J COMPUT NEUROSCI	0929-5313	1087	2.750	2.286	0.483	58	6.9
☐	7	J THEOR BIOL	0022-5193	12876	2.454	2.490	0.351	402	>10.0
☐	8	J MOL GRAPH MODEL	1093-3263	3798	2.347	2.684	0.352	122	>10.0
☐	9	SAR QSAR ENVIRON RES	1062-936X	718	2.238	2.212	0.222	45	4.9
☐	10	STAT METHODS MED RES	0962-2802	1517	2.177	2.600	0.421	38	9.1
☐	11	IET SYST BIOL	1751-8849	92	2.143	2.314	0.263	38	
☐	12	STAT MED	0277-6715	11113	2.111	2.315	0.438	388	8.8
☐	13	ALGORITHM MOL BIOL	1748-7188	81	2.081		0.231	13	
☐	14	IEE P SYST BIOL	1741-2471	167	2.054			0	2.7
☐	15	BIOMETRICS	0006-341X	12772	1.970	2.352	0.324	136	>10.0
☐	16	IEEE T INF TECHNOL B	1089-7771	1341	1.939	2.825	0.476	84	4.4
☐	17	B MATH BIOL	0092-8240	2279	1.735	2.051	0.471	104	8.8
☐	18	J MATH BIOL	0303-6812	2641	1.577	1.971	0.639	72	>10.0
☐	19	J COMPUT BIOL	1066-5277	2129	1.563	2.272	0.118	85	6.5
☐	20	BIOMETRIKA	0006-3444	11218	1.405	1.887	0.307	75	>10.0

MARK ALL UPDATE MARKED LIST

Done

Appendix B

Budget Projections for the First Four Years of Program Operation

Projected Funding for New Degree Program
Ph.D. in Bioinformatics and Computational Biology
Regular Term 2010-11
(Based on 2009-2010 Change in Student Credit Hours)

Program Category	Change in Student Credit Hours			Instructional - Position Funding Factors			Instructional Positions Required		
	Undergrad	Masters	Doctoral	Undergrad	Masters	Doctoral	Undergrad	Masters	Doctoral
Category I				708.64	169.52	115.56	0.000	0.000	0.000
Category II				535.74	303.93	110.16	0.000	0.000	0.000
Category III				406.24	186.23	109.86	0.000	0.000	0.000
Category IV				232.25	90.17	80.91	0.000	0.000	0.000

** Students transferring from IT PhD to Bioinformatics and Computational Biology*

		Total Positions Required		**0.000**
		Instructional - Position Salary Rate		$80,189
	101-1310	Instructional Salary Amount		$0
		Other Academic Costs	44.89300%	0
	Purpose 101	Total Academic Requirements		$0
Fringe rates for staff				
FICA @ 7.65%				
Retirement @ 8.75%	*Purpose 151*	Library	11.48462%	0
Medical @ $4,527				
	Purposes 152,	General Instit Support	54.04980%	0
	160, 170 180	Neg Adj Factor	50.00000%	n/a
Fringes for faculty salaries				
FICA @ 7.65% *$0*		In-state SCHs	0	
Retirement @ 11.86% *$0*		Financial Aid (in-state)	67.99800%	0
Medical @ $4,527 *$0*				
		Total Requirements		**$0**
$0				

SUMMARY OF ESTIMATED ADDITIONAL COSTS FOR PROPOSED PROGRAM/TRACK

Institution **UNC Charlotte** *Date* **November 19, 2009**

Program (API#, Name, Level) **26.1103 Bioinformatics**

Degree(s) to be Granted **Ph.D.** *Program Year* **2011-12**

	ADDITIONAL FUNDING REQUIRED - BY SOURCE				
	Reallocation of Present Institutional Resources	Enrollment Increase Funds	Federal/State or Other Non-state Funds (Identify)	New Allocations	Total
101 Regular Term Instruction					
1210 SPA Regular Salaries	$0				$0
1110 EPA Non-teaching Salaries					0
1310 EPA Academic Salaries	10,000	0	0		10,000
Coordinator Stipend	10,000				
Graduate Teaching Assistants					
1810 Social Security	765		0		765
1820 State Retirement	0		0		0
1830 Medical Insurance (3432*X)	0				0
2000 Supplies and Materials	0				0
2300 Educational Supplies					0
2600 Office Supplies					0
3000 Current Services	2,000				2,000
3100 Travel	500				
3200 Communications	500				
3400 Printing & Binding	500				
3700 Advertising	500				
5000 Capital Outlay (Equipment)	0				0
5100 Office Equipment					
5200 EDP Equipment					
TOTAL Regular Term Instruction	**$12,765**	**$0**	**$0**	**$0**	**$12,765**
151 Libraries					
5000 Capital Outlay (Equipment)	0	0			0
5600 Library Book/Journal					
TOTAL Libraries	**$0**	**$0**	**$0**	**$0**	**$0**
189 General Institutional Support					
2000 Supplies and Materials					0
2600 Office Supplies					
3000 Current Services					0
3200 Communications					
3400 Printing & Binding					
5000 Capital Outlay (Equipment)					0
5100 Office Equipment					
5200 EDP Equipment					
TOTAL General Inst. Support	**$0**	**$0**	**$0**	**$0**	**$0**
TOTAL ADDITIONAL COSTS	**$12,765**	**$0**	**$0**	**$0**	**$12,765**

NOTE: Accounts may be added or deleted as required.

Projected Funding for New Degree Program
Ph.D. in Bioinformatics and Computational Biology
Regular Term 2011-12
(Based on 2010-2011 Change in Student Credit Hours)

Program Category	Change in Student Credit Hours			Instructional - Position Funding Factors			Instructional Positions Required		
	Undergrad	Masters	Doctoral	Undergrad	Masters	Doctoral	Undergrad	Masters	Doctoral
Category I				708.64	169.52	115.56	0.000	0.000	0.000
Category II				535.74	303.93	110.16	0.000	0.000	0.000
Category III			36	406.24	186.23	109.86	0.000	0.000	0.328
Category IV				232.25	90.17	80.91	0.000	0.000	0.000

** Does not include 20 students (360 credit hours) transferring from IT PhD to Bioinformatics and Computational Biology*

Fringe rates for staff
FICA @ 7.65%
Retirement @ 8.75%
Medical @ $4,527

Fringes for faculty salaries

FICA @ 7.65%	*$2,010*
Retirement @ 11.86%	*$3,116*
Medical @ $4,527	*$1,483*
	$6,610

	Total Positions Required		**0.328**
	Instructional - Position Salary Rate		$80,189
101-1310	Instructional Salary Amount		$26,277
	Other Academic Costs	44.89300%	11,797
Purpose 101	Total Academic Requirements		$38,074
Purpose 151	Library	11.48462%	4,373
Purposes 152, 160, 170 180	General Instit Support	54.04980%	20,579
	Neg Adj Factor	50.00000%	n/a
	In-state SCHs	0	
	Financial Aid (in-state)	67.99800%	0
	Total Requirements		**$63,026**

SUMMARY OF ESTIMATED ADDITIONAL COSTS FOR PROPOSED PROGRAM/TRACK

Institution **UNC Charlotte** *Date* **November 19, 2009**

Program (API#, Name, Level) **26.1103 Bioinformatics**

Degree(s) to be Granted **Ph.D.** *Program Year* **2012-13**

	ADDITIONAL FUNDING REQUIRED - BY SOURCE				
	Reallocation of Present Institutional Resources	Enrollment Increase Funds	Federal/State or Other Non-state Funds (Identify)	New Allocations	Total
101 Regular Term Instruction					
1210 SPA Regular Salaries					$0
1110 EPA Non-teaching Salaries					0
1310 EPA Academic Salaries	0	26,277	0		26,277
1810 Social Security	0	2,010	0		2,010
1820 State Retirement	0	4,888	0		4,888
1830 Medical Insurance					0
2000 Supplies and Materials		1,132			1,132
2300 Educational Supplies		1,032			
2600 Office Supplies		100			
3000 Current Services		1,150			1,150
3100 Travel		750			
3200 Communications		200			
3400 Printing & Binding		100			
3700 Advertising		100			
5000 Capital Outlay (Equipment)		2,617			2,617
5100 Office Equipment		0			
5200 EDP Equipment		2,617			
TOTAL Regular Term Instruction	**$0**	**$38,074**	**$0**	**$0**	**$38,074**
151 Libraries					
5000 Capital Outlay (Equipment)		4,373			4,373
5600 Library Book/Journal		4,373			
TOTAL Libraries	**$0**	**$4,373**	**$0**	**$0**	**$4,373**
189 General Institutional Support					
2000 Supplies and Materials		6,900			6,900
2600 Office Supplies		6,900			
3000 Current Services		6,900			6,900
3200 Communications		3,450			
3400 Printing & Binding		3,450			
5000 Capital Outlay (Equipment)		6,779			6,779
5100 Office Equipment		3,400			
5200 EDP Equipment		3,379			
TOTAL General Inst. Support	**$0**	**$20,579**	**$0**	**$0**	**$20,579**
TOTAL ADDITIONAL COSTS	**$0**	**$63,026**	**$0**	**$0**	**$63,026**

NOTE: Accounts may be added or deleted as required.

Projected Funding for New Degree Program
Ph.D. in Bioinformatics and Computational Biology
Regular Term 2012-2013
(Based on 2011-2012 Change in Student Credit Hours)

Program Category	Change in Student Credit Hours			Instructional - Position Funding Factors			Instructional Positions Required		
	Undergrad	Masters	Doctoral	Undergrad	Masters	Doctoral	Undergrad	Masters	Doctoral
Category I				708.64	169.52	115.56	0.000	0.000	0.000
Category II				535.74	303.93	110.16	0.000	0.000	0.000
Category III			36	406.24	186.23	109.86	0.000	0.000	0.328
Category IV				232.25	90.17	80.91	0.000	0.000	0.000

Fringe rates for staff
FICA @ 7.65%
Retirement @ 8.75%
Medical @ $4,527

Fringes for faculty salaries

FICA @ 7.65%	*$2,010*
Retirement @ 11.86%	*$3,116*
Medical @ $4,527	*$1,483*
	$6,610

	Total Positions Required		**0.328**
	Instructional - Position Salary Rate		$80,189
101-1310	Instructional Salary Amount		$26,277
	Other Academic Costs	44.89300%	11,797
Purpose 101	Total Academic Requirements		$38,074
Purpose 151	Library	11.48462%	4,373
Purposes 152, 160, 170 180	General Instit Support	54.04980%	20,579
	Neg Adj Factor	50.00000%	n/a
	In-state SCHs	0	
	Financial Aid (in-state)	67.99800%	0
	Total Requirements		**$63,026**

SUMMARY OF ESTIMATED ADDITIONAL COSTS FOR PROPOSED PROGRAM/TRACK

Institution **UNC Charlotte** *Date* **November 19, 2009**

Program (API#, Name, Level) **26.1103 Bioinformatics**

Degree(s) to be Granted **Ph.D.** *Program Year* **2013-14**

	ADDITIONAL FUNDING REQUIRED - BY SOURCE				
	Reallocation of Present Institutional Resources	Enrollment Increase Funds	Federal/State or Other Non-state Funds (Identify)	New Allocations	Total
101 Regular Term Instruction					
1210 SPA Regular Salaries					$0
1110 EPA Non-teaching Salaries					0
1310 EPA Academic Salaries	0	26,277	0		26,277
1810 Social Security	0	2,010	0		2,010
1820 State Retirement	0	3,116	0		3,116
1830 Medical Insurance					0
2000 Supplies and Materials		2,166			2,166
2300 Educational Supplies		2,066			
2600 Office Supplies		100			
3000 Current Services		1,950			1,950
3100 Travel		1,200			
3200 Communications		500			
3400 Printing & Binding		100			
3700 Advertising		150			
5000 Capital Outlay (Equipment)		2,500			2,500
5100 Office Equipment		0			
5200 EDP Equipment		2,500			
TOTAL Regular Term Instruction	**$0**	**$38,020**	**$0**	**$0**	**$38,020**
151 Libraries					
5000 Capital Outlay (Equipment)		4,373			4,373
5600 Library Book/Journal		4,373			
TOTAL Libraries	**$0**	**$4,373**	**$0**	**$0**	**$4,373**
189 General Institutional Support					
2000 Supplies and Materials		6,900			6,900
2600 Office Supplies		6,900			
3000 Current Services		6,900			6,900
3200 Communications		3,450			
3400 Printing & Binding		3,450			
5000 Capital Outlay (Equipment)		6,779			6,779
5100 Office Equipment		3,400			
5200 EDP Equipment		3,379			
TOTAL General Inst. Support	**$0**	**$20,579**	**$0**	**$0**	**$20,579**
TOTAL ADDITIONAL COSTS	**$0**	**$62,972**	**$0**	**$0**	**$62,972**

NOTE: Accounts may be added or deleted as required.

Projected Funding for New Degree Program
Ph.D. in Bioinformatics and Computational Biology
Regular Term 2013-2014
(Based on 2012-2013 Change in Student Credit Hours)

Program Category	Change in Student Credit Hours			Instructional - Position Funding Factors			Instructional Positions Required		
	Undergrad	Masters	Doctoral	Undergrad	Masters	Doctoral	Undergrad	Masters	Doctoral
Category I				708.64	169.52	115.56	0.000	0.000	0.000
Category II				535.74	303.93	110.16	0.000	0.000	0.000
Category III			36	406.24	186.23	109.86	0.000	0.000	0.328
Category IV				232.25	90.17	80.91	0.000	0.000	0.000

	Total Positions Required		**0.328**
	Instructional - Position Salary Rate		$80,189
101-1310	Instructional Salary Amount		$26,277
	Other Academic Costs	44.89300%	11,797
Purpose 101	Total Academic Requirements		$38,074
Purpose 151	Library	11.48462%	4,373
Purposes 152, 160, 170 180	General Instit Support	54.04980%	20,579
	Neg Adj Factor	50.00000%	n/a
	In-state SCHs	0	
	Financial Aid (in-state)	67.99800%	0
	Total Requirements		**$63,026**

Fringe rates for staff
FICA @ 7.65%
Retirement @ 8.75%
Medical @ $4,527

Fringes for faculty salaries

FICA @ 7.65%	*$2,010*
Retirement @ 11.86%	*$3,116*
Medical @ $4,527	*$1,483*
	$6,610

SUMMARY OF ESTIMATED ADDITIONAL COSTS FOR PROPOSED PROGRAM/TRACK

Institution **UNC Charlotte** *Date* **November 19, 2009**

Program (API#, Name, Level) **26.1103 Bioinformatics**

Degree(s) to be Granted **Ph.D.** *Program Year* **2013-14**

	ADDITIONAL FUNDING REQUIRED - BY SOURCE				
	Reallocation of Present Institutional Resources	Enrollment Increase Funds	Federal/State or Other Non-state Funds (Identify)	New Allocations	Total
101 Regular Term Instruction					
1210 SPA Regular Salaries					$0
1110 EPA Non-teaching Salaries					0
1310 EPA Academic Salaries	0	26,277	0		26,277
1810 Social Security	0	2,010	0		2,010
1820 State Retirement	0	3,116	0		3,116
1830 Medical Insurance					0
2000 Supplies and Materials		2,166			2,166
2300 Educational Supplies		2,066			
2600 Office Supplies		100			
3000 Current Services		1,950			1,950
3100 Travel		1,200			
3200 Communications		500			
3400 Printing & Binding		100			
3700 Advertising		150			
5000 Capital Outlay (Equipment)		2,500			2,500
5100 Office Equipment		0			
5200 EDP Equipment		2,500			
TOTAL Regular Term Instruction	**$0**	**$38,020**	**$0**	**$0**	**$38,020**
151 Libraries					
5000 Capital Outlay (Equipment)		4,373			4,373
5600 Library Book/Journal		4,373			
TOTAL Libraries	**$0**	**$4,373**	**$0**	**$0**	**$4,373**
189 General Institutional Support					
2000 Supplies and Materials		6,900			6,900
2600 Office Supplies		6,900			
3000 Current Services		6,900			6,900
3200 Communications		3,450			
3400 Printing & Binding		3,450			
5000 Capital Outlay (Equipment)		6,779			6,779
5100 Office Equipment		3,400			
5200 EDP Equipment		3,379			
TOTAL General Inst. Support	**$0**	**$20,579**	**$0**	**$0**	**$20,579**
TOTAL ADDITIONAL COSTS	**$0**	**$62,972**	**$0**	**$0**	**$62,972**

NOTE: Accounts may be added or deleted as required.

Appendix C

Biosketches of Core Faculty

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Du, Xiuxia	Assistant Professor

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	YEAR(s)	FIELD OF STUDY
Hefei University of Technology, China	B.S.	1991	Electrical Engineering
Washington University in St. Louis, Missouri	M.S.	2004	Electrical Engineering
Washington University in St. Louis, Missouri	D. Sc.	2005	Systems Science and Math
Pacific Northwest National Laboratory	Postdoc	2008	Computational Mass Spec

Research and Professional Experience

1994 - 1999 Researcher, Institute of Electrical Engineering, Chinese Academy of Sciences, Beijing, China
2008 - present Assistant Professor, Department of Bioinformatics & Genomics
University of North Carolina at Charlotte

Selected peer-reviewed publications

- Chowdhury, S.; **Du, X.**; Tolic, N.; Wu, S.; Moore, R.; Mayer, M.; Smith, R.; Adkins, J. (2009) Identification of Cross-Linked Peptides after CLICK-Based Enrichment Using Sequential Collision-Induced Dissociation and Electron Transfer Dissociation Tandem Mass Spectrometry, *Anal. Chem.*, DOI**:** 10.1021/ac900853k.
- Ding, S.; Wang, Y.; Jacobs, J. M.; Qian, W.; Yang, F.; Tolmachev, A. V.; **Du, X.**; Wang, W.; Moore, R. J.; Monrow, M. E.; Purvine, S. O.; Waters, K.; Heibeck, T. H.; Adkins, J. N.; Camp, D. G., II; Klemke, R. L.; Smith, R. D. (2008) Quantitative Phosphoproteome Analysis of Lysophosphatidic Acid Induced Chemotaxis Applying Dual-Step ^{18}O Labeling Coupled with Immobilized Metal-Ion Affinity Chromatography, *J. of Proteome Res.*, 7(10); 4215-4224.
- **Du, X.**; Callister, S. J.; Manes, N. P.; Adkins, J. N.; Alexandridis, R. A.; Zeng, X.; Roh, J. H.; Smith, W. E.; Donohue, T. J.; Kaplan, S.; Smith, R. D.; Lipton, M. S. (2008) A Computational Strategy to Analyze Label-Free Temporal Bottom-up Proteomics Data, *J. of Proteome Res.*, 7(7), 2595-2604.
- **Du, X.**; Yang, F.; Manes, N. P.; Stenoien, D. L.; Monroe, M. E.; Adkins, J. N.; States, D. J.; Purvine, S. O.; Camp, D. G., II; Smith, R. D. (2008) Linear Discriminant Analysis-Based Estimation of False Discovery Rate for Phosphopeptide Identifications, *J of Proteome Res.* 7(6), 2195-2203.
- Manes, N. P.; Estep, R. D.; Mottaz, H. M.; Moore, R. J.; Clauss, T. R. W.; Monroe, M. E.; **Du, X.**; Adkins, J. N.; Wong, S. W.; Smith, R. D. (2008) Comparative Proteomics of Human Monkeypox and Vaccinia Intracellular Mature and Extracellular Enveloped Virions, *J. of Proteome Res.,* 7(3), 960-968.
- Yang, F.; Jaitly, N.; Jayachandran, H.; Luo, Q.; Monroe, M. E.; **Du, X.**; Gritsenko, M. A.; Zhang, R.; Anderson, D. J.; Purvine, S. O.; Adkins, J. N.; Moore, R. J.; Mottaz, H. M.; Ding, S.-J.; Lipton, M. S.; Camp, D. G., II; Udseth, H. R.; Smith, R. D.; Rossie, S. (2007) Applying a Targeted Label-free Approach using LC-MS AMT tags to Evaluate Changes in Protein Phosphorylation Following Phosphatase Inhibition, *J. of Proteome Res.,* 6(11), 4489-4497.
- **Du, X.**; Ghosh, B.K.; Ulinski, P. (2006) Encoding of Motion Targets by Waves in Turtle Visual Cortex, *IEEE Transactions on Biomedical Engineering*, vol. 53, No. 8, pp.1688-1695.
- **Du, X.**; Ghosh, B.K.; Ulinski, P. (2005) Encoding and Decoding Target Locations with Waves in the Turtle Visual Cortex, *IEEE Transactions on Biomedical Engineering*, vol. 52, No. 4, pp. 566-577.
- **Du, X.**; Ghosh, B.K. (2003) Information-Theoretic Analysis of Turtle Cortical Waves, Proceedings of the *42nd IEEE Conference on Decision and Control,* pp. 6423--6428.

Synergistic Activities

American Society for Mass Spectrometry Member

Collaborations and Co-Editors

Name	**Current Affiliation**	**Relationship**
Adkins, Joshua N.	PNNL	Collaborator/Co-Author
Alexandridis, Roxana A.	University of Wisconsin-Madison	Co-Author

Anderson, Gordon A.	PNNL	Collaborator/Co-Author
Callister, Stephen J.	PNNL	Collaborator/Co-Author
Camp, David G.	PNNL	Co-Author
Chowdhury, Saiful M.	PNNL	Co-Author
Donohue, Timothy, J.	University of Wisconsin-Madiaon	Co-Author
Fredrickson, Jim K.	PNNL	Co-Author
Jia, Wei	University of North Carolina at Greensboro	Collaborator
Kaplan, Samuel	University of Texas-Houston	Co-Author
Lipton, Mary S.	PNNL	Collaborator/Co-Author
Manes, Nathan P.	George Mason University	Co-Author
Monroe, Matthew E.	PNNL	Collaborator/Co-Author
Purvine, Samuel O.	PNNL	Co-Author
Roh, Jung H.	University of Texas-Houston	Co-Author
Sang, Shengmin	North Carolina Central University	Collaborator
Smith, Richard D.	PNNL	Collaborator/Co-Author
Smith, William E.	University of Texas-Houston	Co-Author
States, David J.	University of Michigan	Co-Author
Stenoien, David L.	PNNL	Co-Author
Wu, Si	Battelle Toxicology	Co-Author
Yang, Feng	PNNL	Co-Author
Zeng, Xiaohua	University of Texas-Houston	Co-Author

Graduate and Postdoctoral Advisors and Advisees

Name	**Degree**	**Affiliation**
Ghosh, Bijoy K.	Ph.D.	Texas Tech University
Jiang, Wenxin	Ph.D.	University of North Carolina at Charlotte (UNCC)
Liang, Guizhao	Ph.D.	UNCC
Ni, Yan	M.S.	UNCC
Smith, Richard D.	Ph.D.	PNNL
Suttlemyre, Kyle	M.S.	UNCC

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors in the order listed on Form Page 2.

Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME Anthony Fodor	POSITION TITLE Assistant Professor Bioinformatics and Genomics University of North Carolina, Charlotte
eRA COMMONS USER NAME AFODOR	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
Vassar College	B.A.	1984-1988	Cognitive Science
Arizona State University	M.S.	1991-1994	Zoology
University of Washington	Ph.D.	1994-1997	Physiology and Biophysics
University of Washington	Postdoctoral	1998	Physiology and Biophysics

Please refer to the application instructions in order to complete sections A, B, and C of the Biographical Sketch.

A. Positions and Honors

Positions and Employment

1998-1999. Software Developer. Xypoint Corporation. Seattle, WA.
1999-2000. Software Developer. Punch Networks. Seattle, WA
2000-2002. Bioinformatics Programmer. Immunex Corporation. Seattle, WA
2001. Java instructor (part-time). Java 2 Enterprise Programming Certificate. University of Washington Extension. Seattle, WA
2002-2005. Research Specialist. Howard Hughes Medical Institute. Stanford University.
2005-present. Assistant Professor. Bioinformatics and Genomics. University of North Carolina, Charlotte.

Honors

1988. Phi-beta kappa prize for the most outstanding academic record in graduating class. Vassar College.

B. Publications (in chronological order)

A.A. Fodor, K.D. Black, and W.N. Zagotta. Tetracaine Reports a Conformational Change in the Pore of Cyclic Nucleotide-gated Channels, Journal of General Physiology, 110(5), 591-600. 1997.

A.A. Fodor, S.E. Gordon, and W.N. Zagotta. Mechanism of Tetracaine Block of Cyclic Nucleotide-gated Channels, Journal of General Physiology, 109(1), 3-14. 1997.

A.A. Fodor and R.W. Aldrich. Influence of Conservation on Calculations of Amino Acid Covariance in Multiple Sequence Alignments. Proteins 56(2): 211-221, 2004.

J.P. Dekker, **A.A. Fodor**, R.W. Aldrich and G. Yellen. A perturbation-based method for calculating explicit likelihood of evolutionary co-variance in multiple sequence alignments. Bioinformatics 20:1565-1572, 2004.

A.A. Fodor and R.W. Aldrich. On Evolutionary Conservation of Thermodynamic Coupling in Proteins. J. Biol. Chem. 279(18):19046-19050, 2004.

A.A. Fodor and R.W. Aldrich. Statistical Limits to the Identification of Ion Channel Domains by Sequence Similarity. Journal of General Physiology, 127(6), 755-766, 2006.

A.L. Meredith, S.W. Wiler, B.H. Miller, J.S. Takahashi, **A.A. Fodor**, N.F. Ruby and R.W. Aldrich. BK calcium-activated potassium channels regulate circadian behavioral rhythms and pacemaker output, Nature Neuroscience, 9, 1041-1049, 2006.

S.J. Pyott, A.L. Meredith, **A.A. Fodor**, AE. Va´zquez, E.N. Yamoah and R.W. Aldrich. Cochlear function in mice lacking the bk channel alpha, beta-1, OR beta-4 Subunits, J. Biol. Chem., Vol. 282, Issue 5, 3312-3324, February 2, 2007.

R.Z. Gharaibeh, **A.A. Fodor** and C.J. Gibas. Using Probe Secondary Structure Information to Enhance Affymetrix GeneChip Background Estimates. Computational Biology and Chemistry. Apr;31(2):92-8. 2007.

A.A. Fodor, T.L. Tickle and C. Richardson, Towards the Uniform Distribution of Null p-values on Affymetrix Microarrays, Genome Biology. May 1;8(5):R69. 2007.

R.Z. Gharaibeh, **A.A. Fodor** and C. J. Gibas. Background correction using dinucleotide affinities improves the performance of GCRMA. BMC Bioinformatics 9:452. 2008.

R.W. Reid and **A.A. Fodor.** Determining gene expression on a single pair of microarrays. BMC Bioinformatics. BMC Bioinformatics 9:489. 2008.

N. Sanapereddy, T. Hamp, L. Gonzalez and H. Hilger, **A.A. Fodor** and S.M. Clinton. Molecular Diversity of a North Carolina Wastewater Treatment Plant As Revealed by Pyrosequencing. Applied and Environmental Microbiology. 75(6):1688-96. 2009.

A.A. Fodor and R.W. Aldrich. Convergent Evolution of Alternative Splices at Domain Boundaries of the BK Channel. Annual Review of Physiology, Vol. 71: 19-36 March, 2009.

T.J. Hamp, W.J. Jones, **A.A. Fodor**. The effects of experimental choices and analysis noise on surveys of the rare biosphere. Applied and Environmental Microbiology. 75(10):3263-70. 2009.

M.M. Tunney, E R. Klem, **A.A. Fodor**, D.F. Gilpin, T.F. Moriarty, S.J. McGrath, M.S. Muhlebach, R.C. Boucher, C. Cardwell, G. Doering, J. S Elborn, M C Wolfgang. Use of culture and molecular analysis to determine the effect of antibiotic treatment on microbial community diversity and abundance during exacerbation in cystic fibrosis patients. Submitted, Thorax.

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Cynthia J. Gibas	Associate Professor
eRA COMMONS USER NAME cgibas	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
Lawrence University	B.A.	1990	Chemistry
University of Illinois at Urbana-Champaign	Ph.D.	1996	Biophysics and Computational Biology
University of Illinois at Urbana-Champaign	Postdoctoral	1998	Molecular and Integrative Physiology

Please refer to the application instructions in order to complete sections A, B, and C of the Biographical Sketch.

A. Positions and Honors

Positions and Employment

1998-1999 Research Programmer, National Center for Supercomputing Applications
1999-2000 Research Assistant Professor, Fralin Biotechnology Center, Virginia Tech
2000-2005 Assistant Professor, Biology, Virginia Tech
2005- Associate Professor, Bioinformatics and Genomics, UNC Charlotte

Honors

1990 NIH NRSA in Cell and Molecular Biology
1994 DOE GAANN Fellowship in Computational Biology

B. Publications

1. Zahn, LM, Ma, X, Altman, NS, Zhang, Q, Wall, PK, Tian, D, Gibas, CJ, Gharaibeh, R, Leebens-Mack, JH, dePamphilis, CW Ma, H. Comparative transcriptomics among floral organs of the basal eudicot Eschscholzia californica: a reference for comparison with core eudicots and basal angiosperms. 2010. Genome Biology. In review.
2. Gharaibeh, RZ*, Fodor, A, Gibas CJ. Accurate estimates of microarray target concentration from a simple sequence-independent Langmuir model. 2010. Algorithms for Molecular Biology. In review.
3. Cain, AA*, Kosara, R, Gibas CJ. GenoSets: Set-Based Visualization of Genomic Data. 2010. Under revision for BMC Bioinformatics.
4. Gharaibeh, RZ*, Newton, JS, Weller, JW, **Gibas CJ**. Application of equilibrium models of solution hybridization to microarray design and analysis. 2010, accepted with revision (PLoS One).
5. Gharaibeh, RZ*, Fodor, A, **Gibas CJ**. Background correction using dinucleotide affinities improves the performance of GCRMA. BMC Bioinformatics, 2008 Oct 23;9:452.
6. Gharaibeh, RZ*, Fodor, A, **Gibas CJ**. Software note: using probe secondary structure information to enhance Affymetrix GeneChip background estimates. Comput Biol Chem. 2007 Apr;31(2):92-8.

7. Karanam, RK, Ravindran, A, Mukherjee, A, **Gibas, CJ**, Wilkinson, AB. Using FPGA-Based Hybrid Computers for Bioinformatics Applications. XCell Journal 58:80-83, 2006.
8. Ratushna V*, Sturgill D*, Ramamoorthy S, Reichow S, He Y, Lathigra R, Sriranganathan N, Halling S, Boyle S, **Gibas CJ**. Molecular targets for rapid identification of Brucella spp. BMC Microbiology 6, 13, Feb 2006.
9. Ratushna, V*, Weller, J, **Gibas C**. Secondary structure in the target as a confounding factor in synthetic oligomer microarray design. BMC Genomics, 6(1), 31, Mar 2005.
10. Kaluszka, A*, **Gibas C**. Genome Organization Analysis Tool. Bioinformatics 20(18): 3662-3664, Dec 2004.
11. Halling S, **Gibas C**, Boyle S. Comparative genomics of Brucella melitensis, B. suis, and B. abortus. In: Frontier in the Molecular and Cellular Biology of Brucella. Ignacio Lopez-Goni et al., eds. Horizon Scientific Press, 2004.
12. **Gibas C**, Sturgill D, Weller J. GenoMosaic: On-Demand Multiple Genome Comparison and Comparative Annotation. In: Proceedings of the IEEE Symposium on Bioinformatics and Bioengineering, 2003.
13. **Gibas CJ**, Jambeck P, Subramaniam S. Continuum electrostatic methods applied to pH-dependent properties of antibody-antigen association. *Methods*. 20(3): 292-309, Mar 2000
14. Herrgard S, **Gibas CJ**, Subramaniam S. Role of an electrostatic network of residues in the enzymatic action of the Rhizomucor miehei lipase family. Biochemistry. 39(11): 2921-30, Mar 2000.
15. **Gibas CJ**, Subramaniam S, McCammon JA, Braden BC, Poljak RJ. PH dependence of antibody/lysozyme complexation. Biochemistry. 36(50): 15599-614, Dec 1997.
16. **Gibas C**, Subramaniam S. Knowledge-based design of a soluble bacteriorhodopsin. Protein Engineering. 10(10): 1175-90, Oct 1997
17. **Gibas CJ**, Subramaniam S. Explicit solvent models in protein pKa calculations. Biophysical Journal. 71(1): 138-47, Jul 1996
18. Blackwell, M, **Gibas, C**, Gygax, S, Roman, D, Wagner, B. The plastoquinone diffusion coefficient in chloroplasts and its mechanistic implications. Biochimica et Biophysica Acta-Bioenergetics. 1183: 533-543, 1994
19. Nedbal, L, **Gibas, C**, Whitmarsh, J. Light saturation curves show competence of the water splitting complex in inactive photosystem-II reaction centers. Photosynthesis Research. 30: 85-94, 1991

C. Research Support

Ongoing Research

NIH 5R01GM072619-02
Biophysical Optimization of Oligonucleotide Microarrays
08/01/05 – 07/31/10
Role: Principal Investigator

The goal of this project is to assess candidate criteria for oligonucleotide microarray design by controlled experimentation, examining properties of the probe, target, and oligonucleotide duplex and comparing observed intensities to predictions based on solution modeling of hybridization. The simulation approach described in the current application was not part of the original aims of this project, but evolved out of our early observations, where we are consistently seeing better predictive results from equilibrium binding simulations than from ad hoc rules based on computed properties.

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors in the order listed on Form Page 2.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Guo, Jun-tao	Assistant Professor
eRA COMMONS USER NAME (credential, e.g., agency login) jguo33	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
Nankai University, Tianjin, P.R. China	B.S.	1990	Biochemistry
Nankai University, Tianjin, P.R. China	M.S.	1993	Biochemistry
University of Kentucky	M.S.	2002	Computer Science
University of Kentucky	Ph.D.	2001	Biochemistry
Oak Ridge National Laboratory/Univ. Georgia	Postdoc.	2001-2004	Bioinformatics

A. Positions and Honors.

Positions and Employment

1993-1995 Lecturer, Department of Biochemistry and Molecular Biology, Nankai University, China
2001-2003 Research Associate, Life Sciences Division, Oak Ridge National Laboratory, Oakridge, TN
2003-2004 Research Associate, Department of Biochemistry and Molecular Biology, University of Georgia, Athens, GA
2004-2007 Assistant Research Scientist, Department of Biochemistry & Molecular Biology, Institute of Bioinformatics, University of Georgia, Athens, GA
2007- Assistant Professor, Department of Bioinformatics and Genomics, Bioinformatics Research Center, University of North Carolina at Charlotte, Charlotte, NC

Honors

1991-1993 Guanghua Graduate Fellowship, Nankai University, Tianjin, P. R. China
1997-1998 Graduate School Academic Year Fellowship, University of Kentucky
2009-2014 NSF CAREER award

B. Selected peer-reviewed publications (in chronological order).

1. Kindy, M.S. Yu, J. Guo, J-T. Zhu, H. "Apolipoprotein Serum Amyloid A in Alzheimer's Disease" *J. Alzheimer's Disease* 1999, 1:155-167
2. Yu, J. Guo, J-T. Zhu, H. Kindy, M.S. "Amyloid Formation in the Rat: Adenoviral Expression of Mouse Serum Amyloid A Proteins" *Amyloid* 2000 Mar. 7(1):32-40
3. De villiers, W.J.S. Varilek, G.W. de Beer, M.C. Guo, J-T. Kindy, M.S. "Increased Serum Amyloid A Levels Reflect Colitis severity and Precede Amyloid Formation in IL-2 Deficient Mice" *Cytokine* 2000 Sept. 12(9):1337-1347
4. Yu, J. Zhu, H. Guo, J-T. de Beer, F.C. Kindy, M.S. “Expression of Mouse Apolipoprotein SAA1.1 in CE/J Mice: Isoform-specific Effects on Amyloidogenesis” *Laboratory Investigation* 2000 Dec. 80(12), 1797-1806
5. Xie, C. Lovell, M. Xiong, S. Kindy, M. Guo, J-T. Xie, J. Amaranth, V. Montine, T.J. Marksbery, W. “Expression of Glutathione-S-Transferase isozyme in the SY5Y neuroblastoma Cell Line Increases Resistance to Oxidative Stress” *Free Radical Biology and Medicine* 2001, Jul. 31(1):73-81.
6. Guo, J-T. Yu, J. Grass, D. de Beer, F.C. Kindy, M.S. " Inflammation Dependent Cerebral Deposition of Serum Amyloid A Protein in a Mouse Model of Amyloidosis" *J. Neurosci.* 2002, July 15, 22(14), 5900-5909
7. Guo, J-T. Xu, D. Kim, D. Xu, Y. "Improving the Performance of DomainParser for Structural Domain Partition Using Neural Networks". *Nucleic Acids Research.* 2003, 31(3), 944-952, 2003

8. Kim, D. Xu, D. Guo, J-T. Ellrott, K. Xu, Y. “PROSPECT II: Protein Structure Prediction Program for the Genome-scale Application”. *Protein Eng*. 16(9), 641-650, 2003
9. Williams, A. Portelius, E. Kheterpal, Guo, J-T. Xu, Y. Cook, K. Wetzel, R. “Mapping Abeta Amyloid Fibril Secondary Structure Using Scanning Proline Mutagenesis”*. J. Mol. Biol.* 335:833-842, 2004
10. Qu, Y. Guo, J-T. Olman, V. and Xu, Y. “Fast protein fold recognition using dipolar couplings”, *Nucleic Acids Research,* 32(2):551-561, 2004
11. Gupta, V. Peterson, C.B. Dice, L. Uchiki, T. Guo, J-T. Xu, Y. Hettich, R. Dealwis, C. "Sml1p Protein is a Dimer in Solution: Characterization of Denaturation and Renaturation of Recombinant Sml1p". *Biochemistry* 2004, 43(26): 8568-8578
12. Guo, J-T. Ellrott, K. Chung, WJ. Xu, D. Passovets, S. Xu, Y. "PROSPECT-PSPP: An Automatic Computational Pipeline for Protein Structure Prediction", *Nucleic Acids Res.*, 2004; 32:W522-5
13. Guo, J-T. Wetzel, R. Xu, Y. "Molecular Modeling of the Core of Abeta Amyloid Fibrils", *Proteins: Structure, Function, and Bioinformatics,* 57(2):357-364, 2004
14. Liu, Z. Mao, F. Guo, J-T. Yan, B. Wang, P. Qu, Y. Xu, Y. "Quantitative Validation of Protein-DNA Interaction using an Optimized Knowlege-based Potential", *Nucleic Acids Research*, 2005, 33(2):546-558
15. Sharp, JS. Guo, J-T. Uchiki, T. Xu, Y. Dealwis, C. Hettich, R. "Application of Photochemical Surface Mapping of C14S Sml1p to Constrained Computational Modeling", Analytical Biochemistry, 340(2):201-212, 2005
16. Wang, P. Yan, B. Guo, J-T. Hicks, C. Xu, Y. "Structural genomics analysis of alternative splicing and its application in modeling structures of alternatively spliced variants", *Proc Natl Acad Sci USA*, 102(52):18920-18925, 2005
17. Guo, J-T. and Xu Y. "Computational approaches to amyloid beta fibril core structures", *Methods in Enzymology*, 412:300-314, 2006
18. Guo,J-T. C. Hall, Ying Xu and R. Wetzel, "Modeling Protein Aggregate Assembly and Structure", *Computational Methods for Protein Structure Prediction and Modeling*, 279-317, 2006
19. Ellrott, K. Guo, J-T. Olman, V. and Xu, Y. "A Generalized Threading Model using Integer Programming with Secondary Structure Element Deletion", *Genome Informatics*, 17(2):248-258, 2006
20. Guo, J-T. JW Jaromczyk, Xu, Y. "Analysis of Chameleon Sequences and Their Implications in Biological Processes", *Proteins: Structure, Function, and Bioinformatics*, 67(3):548-558, 2007
21. Guo, J-T. Ellrott, K. Xu, Y. "A historical perspective of template-based protein structure prediction", *Methods Mol Biol*., 413:3-42, 2008
22. Ellrott, K. Guo, J-T. Olman, V. Xu, Y. "Improving the performance of protein threading using Insertion/Deletion Frequency Arrays", *Journal of Bioinformatics and Computational Biology*, 6(3):585-602, 2008
23. Liu, Z.* Guo, J-T.* Li, T. Xu, Y. "Structure-based recognition of binding sites of transcription factors using an efficient protein-DNA docking approach", *Proteins: Structure, Function, and Bioinformatics*, 72(4), 1114-1124, 2008. *equal contribution
24. Guo, J-T*. Xu, Y. "Toward Modeling of Amyloid Fibril Structures". *Frontiers in Bioscience*, 13:4039-4050, 2008. *corresponding author.
25. Kim, R. and Guo, J-T., “PDA: an automatic and comprehensive analysis program for protein-DNA complex structures”, *BMC Genomics,* 10(Supple 1):S13, 2009

C. Research Support

Ongoing Research Support

DBI-0844749 Guo (PI) 07/15/2009-06/30/2014
NSF CAREER
A Structure-Based Approach to Transcription Factor-Binding Site Prediction via Protein-DNA Docking
Role: PI

This study proposes to develop computational methods and the data and infrastructure resources required for genomic scale prediction of transcription factor binding sites.

Completed Research Support

R01 AG018927-03 Wetzel (PI) 9/01/2001-8/31/2006
NIH/NIA
Hydrogen exchange studies on A-beta amyloid fibrils
Role: key personnel

My role on this grant was to model the amyloid fibril structures by combining experimental data and computational techniques.

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Dennis R. Livesay	Associate Professor
eRA COMMONS USER NAME drlivesay	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
Ball State University	B.S.	1996	Chemistry
University of Illinois at Urbana-Champaign	Ph.D.	2000	Physical Chemistry

A. ACADEMIC POSTIONS and HONORS

Positions

2006-present Associate Professor, Department of Bioinformatics and Genomics; University of North Carolina at Charlotte

2005-2006 Associate Professor, Department of Chemistry; California State Polytechnic University, Pomona

2000-2005 Assistant Professor, Department of Chemistry; California State Polytechnic University, Pomona

Professional and synergistic activities

2007-present Coordinator, Bioinformatics-track of the IT Ph.D. program; UNC Charlotte

2007-present Chair and member, IT Ph.D. Program Steering Committee; UNC Charlotte

2006-present *Chemistry Central Journal:* Editor: Biomacromolecules and Biochemistry sections

2006-present Developed Ph.D. level courses in: *Computational Structural Biology*; *Biophysical Modeling*; and *Energy and Interaction in Biological Modeling*

2005-2006 Graduate advisor; Department of Chemistry, Cal Poly Pomona

2005 Developed and delivered *Introduction to Bioinformatic Methods* short-course at Technology Park Malaysia (Kuala Lumpur, Malaysia)

2004-present Recurring referee for: *Astrobiology*; *BBA-Proteins and Proteomics*; *Bioinformatics*; *Biophysical* Journal; *BMC Bioinformatics*; *BMC Structural* Biology; *Chemical Reviews*; *Chemistry Central Journal*; *FEBS Letters*; *Genome Biology*; *Journal of Computational Chemistry*; *Journal of Molecular Biology; Journal of Molecular Recognition*; *Journal of Structural Biology*; *Nucleic Acids Research*; *PROTEINS: Structure, Function & Bioinformatics*

2003-2006 Member of the Faculty Consensus Group, California State University Program for Education and Research in Biotechnology (CSUPERB)

2002-2004 Co-organizer of Cal Poly Pomona's *Molecular Modeling & Simulation* baccalaureate degree, and two courses (*Bioinformatics* and *Macromolecular Modeling*) in support thereof.

Honors

2009 Nominated and runner-up for Outstanding Faculty Research Award, College of Computing and Informatics, UNC Charlotte

1998 NATO Advanced Study Institute on Hydration Processes in Biology; Les Houches, France

1997 Department of Chemistry Graduate Fellowship; University of Illinois

1996 Undergraduate Award for All-Around Achievement in Chemistry; Ball State University

1996 1st Place; Midwest Regional Undergraduate Research Poster Competition; University of KY

1996 Graduated Cum Laude; Ball State University

1995 Undergraduate Research Fellow; Ball State University

B. PUBLICATIONS (‡ indicates that I am either corresponding or co-corresponding author)

Research Papers

(*1.*) Livesay DR, Linthicum SD, Subramaniam S (1999). *pH dependence of antibody-hapten association.* **Molecular Immunology**, 36:397-410.

(*2.*) Rojnuckarin A, Livesay DR, Subramaniam S (2000). *Reaction rate prediction with weighted ensemble Brownian dynamics and the University of Houston Brownian Dynamics program.* **Biophysical Journal**, 79:686-693. PMCID: PMC1300969.

(*3.*) Livesay DR, Jambeck P, Rojnuckarin A, Subramaniam S (2003). *Conservation of electrostatic properties within enzyme families and superfamilies.* **Biochemistry**, 42:3464-3473.

(*4.*) La D, Silver MA, Edgar RC, Livesay DR‡ (2003). *Using motif-based methods in multiple genome analyses: A case study comparing orthologous mesophilic and thermophilic proteins.* **Biochemistry**, 42:8988-8998.

(*5.*) Torrez M, Schultehenrich M, Livesay DR‡ (2003). *Conferring thermostability to mesophilic proteins through optimized electrostatic surfaces.* **Biophysical Journal**, 85:2845-2853. PMCID: PMC1303565.

(*6.*) Alsop E, Silver MA, Livesay DR‡ (2003). *Optimized electrostatic surfaces parallel increased thermostability: A structural bioinformatic analysis.* **Protein Engineering**, 16:871-874.

(*7.*) Livesay DR, Subramaniam S (2004). *Conserved sequence and structure association motifs in antibody-protein and antibody-hapten complexes.* **Protein Engineering, Design, & Selection**, 17:463-472.

(*8.*) Livesay DR, Dallakayan S, Woods GG, Jacobs DJ (2004). *A flexible approach for understanding protein thermodynamics.* **FEBS Letters**, 576:468-476.

(*9.*) La D, Sutch B, Livesay DR‡ (2005). *Predicting protein functional sites with phylogenetic motifs.* **PROTEINS: Structure, Function, & Bioinformatics**, 58:309-320.

(*10.*) Livesay DR‡, La D (2005). *Probing the evolutionary origins and catalytic importance of conserved electrostatic networks in TIM-barrel proteins.* **Protein Science**, 14:1158-1170. PMCID: PMC2253277.

(*11.*) La D, Livesay DR‡ (2005). *Predicting functional sites with an automated algorithm suitable for heterogeneous datasets.* **BMC Bioinformatics**, 6:116. PMCID: PMC1142304.

(*12.*) La D, Livesay DR‡ (2005). *MINER: Software for phylogenetic motif identification.* **Nucleic Acids Research**, 33:W267-W270. PMCID: PMC1160226.

(*13.*) Livesay DR, Jacobs DJ (2006). *Conserved quantitative stability/flexibility relationships (QSFR) in an orthologous RNase H pair.* **PROTEINS: Structure, Function, & Bioinformatics**, 62:130-143.

(*14.*) Jacobs DJ, Livesay DR, Hules J, Tasayco ML (2006). *Elucidating quantitative stability/flexibility relationships within thioredoxin and its fragments using a Distance Constraint Model*. **Journal of Molecular Biology**, 358:882-904.

(*15.*) Livesay DR‡, Jacobs DJ, Kanjanapangka J, Chea E, Cortez H, Garcia J, Kidd P, Marquez MP, Pande S, Yang D (2006). *Probing the conformational dependence of calculated pKa values.* **Journal of Chemical Theory and Computation**, 2:927-938.

(*16.*) Roshan U, Livesay DR (2006). *Probalign: multiple sequence alignment using partition function posterior probabilities*. **Bioinformatics**, 22:2715-2721.

(*17.*) Chikkagoudar S, Roshan U, Livesay DR (2007). *eProbalign: generation and manipulation of multiple sequence alignments using partition function posterior probabilities.* **Nucleic Acids Research**, 35:W675-W677. PMCID: PMC1933135.

(*18.*) Chea E, Livesay DR‡ (2007). *How accurate and statistically robust are catalytic site predictions based on closeness centrality?* **BMC Bioinformatics**, 8:153. PMCID: PMC1876251.

(*19.*) Livesay DR‡, Kidd PD, Eskandari S, Roshan U (2007). *Assessing the ability of sequence-based methods to provide functional insight within membrane integral proteins: a case study analyzing the neurotransmitter/Na+ symporter family.* **BMC Bioinformatics**, 8:397. PMCID: PMC2194793.

(*20.*) Istomin AY, Jacobs DJ, Livesay DR (2007). *On the role of structural class of a protein with two-state folding kinetics in determining correlations between its size, topology, and folding rate*. **Protein Science**, 16:2564-2569. PMCID: PMC2211710.

(*21.*) Istomin AY, Gromiha MM, Vorov OK, Jacobs DJ, Livesay DR‡ (2008). *New insight into long-range nonadditivity within protein double-mutant cycles*. **PROTEINS: Structure, Function, & Bioinformatics**, 70:915-924.

(*22.*) Roshan U, Chikkagoudar S, Livesay DR (2008). *Searching for evolutionary distant RNA homologs within genomic sequences using partition function posterior probabilities.* **BMC Bioinformatics**, 9:61. PMCID: PMC2248559.

(*23.*) Livesay DR‡, Huynh D, Dallakyan S, Jacobs DJ (2008). *Hydrogen-bond networks determine emergent mechanical and thermodynamic properties across a protein family*. **Chemistry Central Journal**, 2:17. PMCID: PMC2533333.

(*24.*) Vorov OK, Livesay DR, Jacobs DJ (2008). *Conformational entropy of an ideal cross-linking polymer chain*. **Entropy**, 10:285-308. PMCID: PMC2748956.

(*25.*) KC DB, Livesay DR‡ (2008). *Improving position specific predictions of protein functional sites using phylogenetic motifs.* **Bioinformatics**, 24:2308-2316.

(*26.*) Mottonen JM, Xu M, Jacobs DJ, Livesay DR‡ (2009). *Unifying mechanical and thermodynamic descriptions across the thioredoxin protein family*. **PROTEINS: Structure, Function, & Bioinformatics**, 75:610-627. PMCID: In process.

(*27.*) Jasuja R, Ulloor J, Yengo CM, Choong K, Istomin AY, Livesay DR, Jacobs DJ, Swerdloff RS, Mikšovská J, Larsen RW, Bhasin S (2009). *Kinetic and thermodynamic characterization of dihydrotestosterone-induced conformational perturbations in androgen receptor ligand binding domain*. **Molecular Endocrinology**, 23:1231-1241. PMCID: In process.

(28.) Vorov OK, Livesay DR‡, Jacobs DJ (2009). *Helix/coil nucleation: A local response to global demands*. **Biophysical Journal**, 97:3000-3009. PMCID: In process.

(29.) KC DB, Livesay DR. *Topology improves phylogenetic motif functional site predictions.* **IEEE/ACM Transactions on Computational Biology and Bioinformatics**, In press.

Peer-Reviewed Conference Proceedings

(*30.*) Roshan U, Livesay DR‡, La D (2005). *Improved Phylogenetic Motif Detection Using Parsimony*. **Fifth IEEE Symposium on Bioinformatics and Bioengineering**, BIBE05:19-26.

(*31.*) Roshan U, Livesay DR, Chikkagoudar S (2006). *Improving progressive alignment for phylogeny reconstruction using parsimonious guide-trees.* **Sixth IEEE Symposium on Bioinformatics and Bioengineering**, BIBE06:159-164.

(*32.*) Pande S, Raheja A, Livesay DR‡ (2007). *Prediction of Enzyme Catalytic Sites from Sequence Using Neural Networks.* **IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology**, CIBCB07:247-253.

Commentaries, Etc

(*33.*) Livesay DR‡ (2007). *At the crossroads of biomacromolecular research: highlighting the interdisciplinary nature of the field.* **Chemistry Central Journal**, 1:4. PMCID: PMC1975824.

Book Chapters

(*34.*) KC DB, Livesay DR‡ (2009). *A spectrum of phylogenetic-based approaches for predicting protein functional sites*. In **Bioinformatics for Systems Biology**, Krawetz S (Ed.), Humana Press. ISBN: 978-934115-02-2.

(*35.*) Jacobs DJ, Mottonen JM, Vorov OK, Istomin AY, Livesay DR (2010). *Protein thermodynamics modeled using network rigidity*. To appear in **Theoretical Studies Laboratory Expository Lecture Series V**, Zainuddin H (Ed.).

(*36.*) Livesay DR‡, KC DB, La D (2010). *Predicting protein functional sites with phylogenetic motifs: Past, present and beyond*. To appear in **Omics approaches for protein function prediction**, Kihara D (Ed.), Springer.

Patents, Scientific Software, and Databases

(*5.*) Jacobs DJ, Livesay DR. *Computer Implemented System for Protein and Drug Target Design utilizing Quantitative Stability/Flexibility Relationships*. Application number: 61016848, Patent pending

(*4.*) Jacobs DJ, Livesay DR. ***FAST*** (*Flexibility And Stability Test*): this software is currently being developed through NIH-R01 GM 073082. *FAST* will be free to academics for high throughput applications in computational biology, i.e., comparative analysis of proteins, detection of allosteric communication, and rational protein design.

(*3.*) Livesay DR. **MINER**: this web-server is an implementation of our phylogenetic motif-based functional site prediction algorithm. A stand-alone version of MINER is also available.

(*2.*) Livesay DR. **miniMINER**: a streamlined and self-contained Java-based (jar) implementation of the above MINER algorithm without the data analysis tools designed for high-throughput applications.

(*1.*) Roshan U, Livesay DR. **Probalign** and **eProbalign**: stand-alone and web-based, respectively, software that implements our maximal expected accuracy multiple sequence alignment algorithm.

C. RESEARCH SUPPORT

Ongoing Research Support

(*8.*) *Predicting protein stability and flexibility*
Jacobs, D.J. (PI) 2006-2009
NIH R01 GM073082-01A1 Role: Co-investigator

Completed Research Support

(*7.*) *Phylogenetic similarity maximization: A new algorithm for phylogenetic motif detection*
Livesay, D.R. (PI) 2005-2006
CSUPERB-Joint Venture Matching Grant Role: Principle investigator

(*6.*) *The Center for Macromolecular Modeling and Materials Design (CM^3D)*
PI: Ortiz, J.M. (Cal Poly Pomona President) 2006-2007
W.M. Keck Foundation Role: Investigator

(*5.*) *Acquisition of a workstation network for research in parallel and distributed computing*
0321333; Kuang, H. (PI) 2003-2005
NSF-MRI Role: Co-investigator

(*4.*) *Dihedral-angle characterization of conformational flexibility in protein structure*
S06 GM48680-0952; Jacobs, D.J. (PI) 2002-2005
NIH-SCORE Role: Paid consultant

(*3.*) *Investigation of superoxide dismutase surface electrostatics*
S06 GM53933-07; Livesay, D.R. (PI) 2002-2004
NIH-SCORE Role: Principle investigator

(*2.*) *Bioinformatic study correlating protein flexibility with function*
Jacobs, D.J. (PI) 2003
CSUPERB-Joint Venture Matching Grant Role: Co-investigator

(*1.*) *Conferring thermostability to mesophilic protein structures through systematic mutation of surface residues*
36848-GB4; Livesay, D.R. (PI) 2001-2003
ACS-Petroleum Research Fund Role: Principle investigator

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Loraine, Ann Elizabeth	Associate Professor, University of North Carolina, Charlotte
eRA COMMONS USER NAME aloraine	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
University of Texas, Austin, TX	B.A.	1989	Plan II (Liberal Arts)
University of Texas, Austin, TX	B.S.	1989	Zoology
University of California, Berkeley, CA	Ph.D.	1996	Molecular & Cell Biology
University of California, Berkeley, CA	Post-doc	1997	Bioinformatics

A. Positions and Honors.

Positions and Employment

1997-1998 Post-doc, Berkeley Drosophila Genome Project, UC Berkeley
1998-1999 Programmer/Analyst, Berkeley Drosophila Genome Project, UC Berkeley
1999-2000 Bioinformatics Software Engineer, Neomorphic, Inc., Berkeley, CA
2000-2003 Bioinformatics Scientist, Affymetrix, Inc., Emeryville, CA
Spring, 2004 Instructor for Introduction to Statistics for Bioinformatics, Cal State Hayward
Summer, 2004 Consultant, Affymetrix, Inc., Emeryville, CA
2004-2008 Assistant Professor of Genetics, University of Alabama at Birmingham
2004-2008 Assistant Professor of Biostatistics, Section on Statistical Genetics, UAB
2004-2008 Associate Scientist, UAB Comprehensive Cancer Center
2007-present Assistant Adjunct Professor, Computer and Information Sciences, UAB
2008-present Associate Professor, Dept.Bioinformatics and Genomics, UNC Charlotte

Other Experience

2003-present Program Committee Member, Life Sciences Society (formerly IEEE) Computational Systems and Bioinformatics Conference
2005-present Co-founder, Genoviz open source bioinformatics data visualization project
2007-present Publications Chair, LSS Computational Systems Bioinformatics Conference
2009-present Scientific Advisory Board, “FishManOmics” Salmon Fisheries Genomics Project, Genome British Columbia

Honors

1984-1988 University of Texas Dedman Merit Scholar
1987 University-wide Endowed Presidential Scholarship, University of Texas at Austin
1988 Endowed Presidential Scholarship in Plan II, University of Texas at Austin
1989 Phi Beta Kappa Honor Society
1990-1991 NIH pre-doctoral training grant, University of California, Berkeley, CA
1995-1996 NIH pre-doctoral training grant, University of California, Berkeley, CA
2004 IEEE Computer Society Certificate of Appreciation “For successfully obtaining MEDLINE indexing for the IEEE CS Computational Systems Bioinformatics Conference Proceedings”

B. Publications

Mutwil M, Usadel B, Schütte M, **Loraine A**, Ebenhöh O, Persson S. Assembly of an interactive correlation network for the *Arabidopsis* genome using a novel heuristic clustering algorithm. Plant Physiol. 2010 Jan;152(1):29-43.

Loraine A. Co-expression Analysis of Metabolic Pathways in Plants. Methods Mol Biol. 2009;553:247-64.

Helt GA, Nicol JW, Erwin E, Blossom E, Blanchard SG Jr, Chervitz SA, Harmon C, **Loraine AE**. Genoviz Software Development Kit: Java toolkit for building genomics visualization applications. BMC Bioinformatics. 2009 Aug 25;10:266.

Nicol JW, Helt GA, Blanchard SG Jr, Raja A, **Loraine AE**. The Integrated Genome Browser: free software for distribution and exploration of genome-scale datasets. Bioinformatics. 2009 Oct 15;25(20):2730-1.

Cui, X, **Loraine, AE**. Consistency analysis of redundant probe sets on Affymetrix 3-prime expression arrays and applications to differential mRNA processing. PLoS One. 2009. Jan 23.

Dybvig K, Zuhua C, Lao P, Jordan DS, French CT, Tu AH**, Loraine AE**. Genome of Mycoplasma arthritidis. Infect Immun. 2008 Sep;76(9):4000-8.

Srinivasasainagendra V, Page G, Mehta T, Coulibaly I, **Loraine AE**. CressExpress: A tool for large-scale mining of expression data from *Arabidopsis thaliana*. Plant Physiol. 2008 May 8.

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Cui X, **Loraine AE**. Global correlation analysis between redundant probe sets using a large collection of Arabidopsis ATH1 expression profiling data. Proc LSS Comp Sys Bioinform Conf. 2006;223-227.

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Liu G, **Loraine AE**, Shigeta R, Cline M, Cheng J, Valmeekam V, Sun S, Kulp D, Sani-Rose MA. NetAffx: Affymetrix probesets and annotations. Nucleic Acids Res. 2003 Jan 1;31(1):82-6.

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Helt GA, Lewis S, **Loraine AE**, Rubin GM. BioViews: Java-based tools for genomic data visualization. Genome

Res. 1998 Mar;8(3):291-305.
Yalovsky S, **Loraine AE**, Gruissem W. Specific Prenylation of Tomato Rab Proteins by Geranylgeranyl Type-II Transferase Requires a Conserved Cysteine-Cysteine Motif. Plant Physiol. 1996 Apr;110(4):1349-1359.
Loraine AE, Yalovsky S, Fabry S, Gruissem W. Tomato Rab1A homologs as molecular tools for studying Rab geranylgeranyl transferase in plant cells. Plant Physiol. 1996 Apr;110(4):1337-47.

Long abstracts:

Loraine A, Salmi ML, Stout SC, Roux SJ. Gene Ontology-based analysis of gene expression changes in early development in *Ceratopteris*. IEEE Computational Systems Bioinformatics Conference, Stanford, CA, August, 2005.
Budagyan B, **Loraine AE**. Gene length and alternative transcription in the fruit fly. IEEE Computational Systems Bioinformatics, Stanford, August, 2004.

Other:

Kim K, Zakharkin SO, **Loraine AE**, Allison DB. Picking the most likely candidates for further development: Novel intersection-union tests for addressing multi-component hypotheses in comparative genomics. Proc American Statistical Association Joint Statistical Meeting, ENAR Section [CD-ROM], Toronto, Ontario, Canada, Aug 8 - 12, 2004

C. Research Support Current and Past

Current:

UNCC PI: Ann Loraine (Lead PI Alice Cheung, U Mass Amherst)
Title: Collaborative Proposal: Research Coordination Network on Integrative Pollen Biology
Funded by: National Science Foundation MCB
Award amount: $46,907.00
Award Dates: May 1, 2010 – April 30, 2015 (award is pending)
Goal: Develop and promote pollen as a model system in plant biology and develop community cohesion and expertise in integrative research techniques, especially genomics and bioinformatics.

PI: Ann Loraine **Title**: “Visualization software and data server for *Arabidopsis*”
Funded by: National Science Foundation (projected start date March 1, 2008)
Award amount: $600,000
Award Dates: July 1, 2008 – June 30, 2011
Goal: Develop visualization software and data integration techniques for *Arabidopsis* genome data and functional genomics data sets.

PI: Ann Loraine **Title**: “Development of novel and directed tools and processes for bioinformatics-intensive probe of the blueberry genome.”
Funded by: University of North Carolina General Administration
Award amount: $310,888
Award dates: January 1, 2009 – June 30, 2011
Goal: Perform transcriptome sequencing of blueberry and correlate expressed genes with levels of anthocyanin and other bioactive compounds in berry fruit. This is a collaborative project with co-PIs Mary Ann Lila (Faculty Director, Plants for Human Health Institute) and Allan Brown, both from NC State University.

Past:

PI: Ann Loraine **Title:** "Effects of Genistein on alternative splicing in breast cancer"
Funded by: Center for Nutrient-Gene Interaction (UAB) pilot grant

Goal: Investigate how genistein, a soy isoflavone with cancer-preventive properties, affects alternative splicing in cancerous versus non-cancerous breast cell lines.

BIOGRAPHICAL SKETCH			
NAME Lawrence E Mays	POSITION TITLE Professor and Chair		
EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as*			
INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
University of Virginia	B.A.	1967	Psychology
Pennsylvania State University	M.S.	1969	Psychology
University of Virginia	Ph.D.	1973	Psychology
Temple University	M.A.	1976	Computer Science

A. ACADEMIC POSITIONS and HONORS

Positions

1972-1973 Research Associate, Department of Psychology, Temple University
1973-1977 Research Associate, Department of Pharmacology, Temple University
1975-1977 NIH Postdoctoral Research Fellowship, Pharmacology, Temple University
1977-1979 Research Associate, Neurosciences Program University of Alabama at Birmingham
1979-1983 Research Assistant Professor, Department of Physiological Optics, University of Alabama at Birmingham
1983-1985 Research Associate Professor, Department of Physiological Optics, University of Alabama at Birmingham
1985-1991 Associate Professor, Department of Physiological Optics, University of Alabama at Birmingham
1991-1995 Director, Vision Science Research Center, University of Alabama at Birmingham
1991-2004 Professor, Department of Physiological Optics, University of Alabama at Birmingham
1995-2004 Chairman, Department of Physiological Optics, University of Alabama at Birmingham
2002-2004 Director, Center for the Development of Functional Imaging, University of Alabama at Birmingham
2004-2008 Professor of Computer Science, University of North Carolina at Charlotte
2005-Present Director, Bioinformatics Research Center, UNC Charlotte
2006-Present Director, NCRC Bioinformatics Service Center
2008-Present Professor and Chair, Department of Bioinformatics and Genomics, University of North Carolina at Charlotte

Other Experience and Professional Memberships

Society for Neuroscience
AAAS
American Physiological Society
Associate for Research in Vision and Ophthalmology
2001-2004 Member CVP NIH Study Section
Chair, NCRC IACUC
Honors
McKnight Scholar

B. PUBLICATIONS (selected)

Best, P. J., C. E. Olmstead, and L. E. Mays. Activity of midbrain reticular formation units during conditioned emotional response. In: Brain Unit Activity During Behavior, M. I. Phillips (Ed.). Charles Thomas, Springfield, 1973, pp. 155-164.

Olmstead, C. E., P. J. Best, and L. E. Mays. Neural activity in the dorsal hippocampus during paradoxical sleep, slow wave sleep and waking. Brain Res. 60: 381-391, 1973.

Mays, L. E., and P. J. Best. Hippocampal unit activity to tonal stimuli during arousal from sleep and in awake rats. Exp. Neurol. 47: 268-279, 1975.

Mays, L. E., and J. G. McElligott. Neuro-11; A computer system for relating neural spike trains to physiological and behavioral data. Behav. Res. Meth. Instrum. 8: 325-329, 1976.

Sparks, D. L., L. Mays, and J. G. Pollack. Saccade-related unit activity in the monkey superior colliculus. In: Control of Gaze by Brain Stem Neurons, Baker and Berthoz (Eds.). Elsevier, Amsterdam, 1977, pp. 437-444.

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McElligott, J. G., L. E. Mays, and P. M. Gochin. An analysis and display computer system for multichannel neurophysiological data. Brain Theory Newsletter 3: 159-161, 1978.

McElligott, J. G., M. H. Loughnane, and L. E. Mays. The use of synchronous demodulation for the measurement of eye movements by means of an ocular magnetic search coil. IEEE Trans. Biomed. Eng. BME 26: 370-374, 1979.

Mays, L. E., and D. L. Sparks. Dissociation of visual and saccade-related responses in superior colliculus neurons. J. Neurophysiol. 43: 207-232, 1980.

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Mays, L. E. Neurophysiological correlates of vergence eye movements. In: Basic and Clinical Aspects of Binocular Vergence Eye Movements, K. Cuiffreda and C. Schor (Eds.). Butterworths, Boston, 1983, pp. 649-670.

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Sparks, D. L., and L. E. Mays. The spatial localization of saccade targets. I. Compensation for stimulation-induced perturbations in eye position. J. Neurophysiol. 49: 45-63, 1983.

Mays, L. E., and J. D. Porter. Neural control of vergence eye movements: Activity of abducens and oculomotor neurons. J. Neurophysiol. 52: 743-761, 1984.

Mays, L. E. Neural control of vergence eye movements: Convergence and divergence neurons in midbrain. J. Neurophysiol. 51: 1091-1108, 1984.

Mays, L. E., and C. A. Tello. Neurophysiological correlates of convergence and its tonic adjustment. In: Adaptive Processes in Visual and Oculomotor Systems in Advances in the Biosciences, Vol. 57, E. L. Keller and D. S. Zee (Eds.). Pergamon Press, New York, 1986, pp. 143-149.

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Mays, L. E., J. D. Porter, P. D. R. Gamlin, and C. A. Tello. Neural control of vergence eye movements: Neurons encoding vergence velocity. J. Neurophysiol. 56: 1007-1021, 1986.

Sparks, D. L., L. E. Mays, M. R. Gurski, and T. L. Hickey. Long-term and short-term monocular deprivation in the rhesus monkey: Effects on visual fields and optokinetic nystagmus. J. Neurosci. 6: 1771-1780, 1986.

Sparks, D. L., L. E. Mays, and J. D. Porter. Eye movements induced by pontine stimulation: Interaction with visually-triggered saccades. J. Neurophysiol. 58: 300-318, 1987.

Lorden, J. F., G. A. Oltmans, S. Stratton, and L. E. Mays. Neuropharmacological correlates of the motor syndrome of the genetically dystonic (dt) rat. In: Dystonia 2: Advances in Neurology, Vol. 50, S. Fahn, C. D. Marsden, and D. Calne (Eds.). Raven Press, New York, 1988, pp. 277-295.

Stratton, S. E., J. F. Lorden, L. E. Mays, and G. A. Oltmans. Spontaneous and harmaline-stimulated Purkinje cell activity in rats with a genetic movement disorder. J. Neurosci. 8: 3327-3336, 1988.

Lorden, J. F., S. E. Stratton, L. E. Mays, and B. A. Oltmans. Purkinje cell activity in rats following chronic treatment with harmaline. Neuroscience 27: 465-472, 1988.

Gamlin, P. D. R., J. W. Gnadt, and L. E. Mays. Abducens internuclear neurons carry an inappropriate signal for ocular convergence. J. Neurophysiol. 62: 70-81, 1989.

Gamlin, P. D. R., J. W. Gnadt, and L. E. Mays. Lidocaine-induced unilateral internuclear ophthalmoplegia: Effects on convergence and conjugate eye movements. J. Neurophysiol. 62: 82-95, 1989.

Sparks, D. L., and L. E. Mays. Signal transformations required for the generation of saccadic eye movements. Ann. Rev. Neurosci. 13: 309-336, 1990.

Zhang, Y., P. D. R. Gamlin, and L. E. Mays. Antidromic identification of midbrain near response cells projecting to the oculomotor nucleus. Exp. Brain Res. 84: 525-528, 1991.

Mays, L. E., Y. Zhang, M. Thorstad, and P. D. R. Gamlin. Trochlear unit activity during ocular convergence. J. Neurophysiol. 65: 1484-1491, 1991.

Gamlin, P. D. R., and L. E. Mays. Dynamic properties of medial rectus motoneurons during vergence eye movements. J. Neurophysiol. 67: 64-74, 1992.

Zhang, Y., L. E. Mays, and P. D. R. Gamlin. Characteristics of near response cells projecting to the oculomotor nucleus. J. Neurophysiol. 67: 944-960, 1992.

Clendaniel, R. A., and L. E. Mays. Characteristics of antidromically identified oculomotor internuclear neurons during vergence and versional eye movements. J. Neurophysiol. 71(3): 1111-1127, 1994.

Gamlin, P. D. R., R. A. Clendaniel, Y. Zhang, and L. E. Mays. Behavior of Edinger-Westphal neurons during ocular accommodation. J. Neurophysiol. 72(5): 2368-2382, 1994.

Gnadt, J. W., and L. E. Mays. Neurons in monkey parietal area LIP are tuned for eye movement parameters in three-dimensional space. J. Neurophysiol. 73(1): 280-297, 1995.

Mays, L. E. and D. W. Morrisse. Electrical stimulation of the pontine omnipause area inhibits eye blink. J. Am. Optom. Assoc. 66(7): 419-422, 1995.

Benjamin, W. J. and Mays, L. E. Research: Where we go from here. J. Am. Optom. Assoc., 66(7): 394-395, 1995.

Mays, L. E. and P. D. R. Gamlin. A neural mechanism subserving saccade-vergence interactions. In: Eye Movement Research: Mechanisms, Processes and Applications. Findlay, Walker, Kentridge (eds.) Elsevier, 1995, pp. 215-223.

Mays, L. E. and P. D. R. Gamlin. Neuronal circuitry controlling the near response. Cur. Opinion in Neurobiol. 5(6): 763-768, 1995.

Mays, L. E. Has Hering been hooked? Nature Med. 4(8): 889-890, 1998.

Ledoux, M. S., J. F. Lorden, J. M. Smith, and L. E. Mays. Serotonergic modulation of eye blinks in cat and monkey. Neurosci. Letters 253(1):61-64, 1998.

Mays, L.E. and P. D. R. Gamlin. Neuronal circuits for accommodation and vergence in the primate. In: Accommodation and Vergence Mechanisms in the Visual System. Franzén, O; Richter, H; and Stark L (eds.) Birkhauser Verlag, Stockholm, 2000, pp. 1-9.

Walton, M.G. and L. E. Mays. Discharge of saccade-related superior colliculus neurons during saccades accompanied by vergence. J. Neurophysiol 90:1124-1139, 2003.

Mays, L.E. Neural control of vergence eye movements. In: The Visual Neurosciences, L. M. Chalupa and J. S. Werner (eds.) MIT Press, Cambridge, pp. 1415-1427, 2003.

Busettini, C. and L. E. Mays. Pontine omnipause activity during conjugate and disconjugate eye movements in macaques J. Neurophysiol. 90: 3838-3853, 2003.

Busettini, C. and L.E. Mays. Saccade-vergence interactions in macaques. I. Test of the omnipause multiply model. J. Neurophysiol. 94: 2295-2311, 2005.

Busettini, C. and L.E. Mays. Saccade-vergence interactions in macaques. II. Vergence enhancement as the product of a local feedback vergence motor error and a weighted saccadic burst. J. Neurophysiol. 94: 2312-2330, 2005.

Mays, L.E. Accommodation-Vergence Interactions. In: Encyclopedia of Neuroscience. Vol. 1. M.D. Binder, N. Hirokawa and U. Windhorst (eds). Springer-Verlag GmbH, Berlin Heidelberg, 2009, pp. 10-12.

Mays, L.E. Near Response Neurons. In: Encyclopedia of Neuroscience. Vol. 4. M.D. Binder, N. Hirokawa and U. Windhorst (eds). Springer-Verlag GmbH, Berlin Heidelberg, 2009, pp. 2535-2538.

Mays, L.E. Saccade-Vergence Interactions. In: Encyclopedia of Neuroscience. Vol. 5. M.D. Binder, N. Hirokawa and U. Windhorst (eds). Springer-Verlag GmbH, Berlin Heidelberg, 2009, pp. 3562-3564.

C. RESEARCH SUPPORT

Ongoing Research Support

N/A

Completed Research Support

Principal Investigator:	NEI Research Grant R01 EY03463
Title:	"Neural Mechanisms of Vergence Eye Movements"
Period of Support:	09/01/80 - 1/1/2004
Principal Investigator:	Wm. F. Keck Foundation Grant
Title:	Functional MRI Facility
Amount	$1,500,000
Period of Support	07/1/00 – 06/30/04
Principal Investigator:	EyeSight Foundation of Alabama
Title:	Center for Functional Neuroimaging
Amount:	$300,000
Period of Support:	07/01/01 – 06/30/04
Co-Principal Investigator:	NSF Award #DBI-0116467 (Gamlin, PI)
Title:	Acquisition of a High-field Magnetic Resonance Imaging (MRI) System for Neuroscience Research
Amount:	$451,000
Period of Support:	09/01/01 – 08/31/04
Principal Investigator:	Sloan Foundation subgrant (UNC-GA)
Title:	PSM Planning Grant - Bioinformatics
Amount	$3,500
Period of Support	11/18/05 – 5/31/06
Principal Investigator:	NC Biotechnology Center
Title:	Faculty Recruitment Grant
Amount	$150,000
Period of Support	06/1/07 – 05/31/09
Principal Investigator:	Sloan Foundation subgrant (UNC-GA)
Title:	PSM Implementation Grant - Bioinformatics
Amount	$25,000
Period of Support	8/31/07 – 5/31/08
Principal Investigator:	Sloan Foundation subgrant (UNC-GA)
Title:	PSM Planning Grant – Health Info Tech
Amount	$13,000
Period of Support	2/25/09 – 6/15/09

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors in the order listed on Form Page 2.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Schlueter, Jessica A	Assistant Professor
eRA COMMONS USER NAME (credential, e.g., agency login)	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Texas A&M University; College Station, TX	B.S.	05/00	Genetics
Iowa State University; Ames, IA	Ph.D.	05/06	Genetics
USDA-ARS-CICGR; Ames, IA	Postdoctoral	11/06	Soybean genomics
Purdue University; West Lafayette, IN	Postdoctoral	08/09	Agronomy & Bioinformatics

A. Positions and Honors

Positions and Employment

2009-present Assistant Professor; Department of Bioinformatics and Genomics; University of North Carolina at Charlotte, Charlotte, North Carolina
2006-2009 Postdoctoral Research Associate; Department of Agronomy; Purdue University, West Lafayette, Indiana
2006-2006 Postdoctoral Research Geneticist; USDA-ARS-CICGR; Ames, IA

Other Experience

2009-present Planning committee for the Soy 2010 Biennial Molecular and Cellular Biology of the Soybean Conference, Raleigh, NC
2007-present Participant and organizer of the Soybean Genetics and Genomics Strategic Planning Committee
2005-present Recurring journal referee for: *BMC Genomics, Plant Physiology, BMC Plant Biology, BMC Bioinformatics, Crop Science, The Plant Genome, Genome and Genetics.*

Academic & Research Awards

Iowa State University, Research Assistantship, 2001-2006
Iowa State University, Miller Fellowship 2000-2004
Texas A&M University, Biochemistry Research Scholar's Program, 1999-2000.
Texas A&M University, Edmonds Educational Fund Scholarship, 1999-2000
Texas A&M University, University Honor's Program, 1999-2000
Texas A&M University, Academic Incentive Award, 1998-1999

B. SELECTED PEER-REVIEWED PUBLICATIONS

Journal Publications

1. Cordoba, J.M., Chavarro, C.M., Schlueter, J.A., Jackson, S.A. and Blair, M.W. 2010. Integration of physical and genetic maps of common bean through BAC-derived microsatellite markers. *BMC Genomics*, in review.

2. Schmutz, J., Cannon, S.B., Schlueter, J.A., Ma, J., Hyten, D., Song, Q., Mitros, T., Nelson, W., May, G.D., Gill, N., Peto, M., Goodstein, D., Thelen, J.J., Cheng, J., Bhattacharya, M., Sandhu, D., Grant, D.,

Joshi, T., Libault, M., Zhang, X-C., Xu, D., Futrell-Griggs, M., Abernathy, B., Grimwood, J., Wing, R.A., Cregan, P., Stacey, G., Specht, J., Rokhsar, D., Shoemaker, R.C., and Jackson, S.A. 2010. Genome sequence of the paleopolyploid soybean (*Glycine max* (L.) Merr.). *Nature*, 463: 178-183.

3. Joseph, B., Schlueter, J.A., Du, J., Graham, M.A., Ma, J. and Shoemaker, R.C. 2009. Retrotransposonas in the intergenic regions of syntenic regions in soybean and *Medicago truncatula* and their contribution to local genome evolution. *Genome*, in press.

4. Ramasamy, P., Menz, M.A., Metha, P.J., Katile, S., Gutierrez, R.L., Klein, R.R., Klein, P.E., Prom, L.K., Schlueter, J.A., Rooney, W.L., and Magill, C.W. 2009. Moelcular mapping of *cgi*, a gene for resistance to anthracnose (Collectotrichum sublineolum) in sorghum. *Eyphytica*, 165: 597-606.

5. Zhang, C., Mallery, E.L., Huang, S., Fan, Y., Schlueter, J.A., Staiger, C.J, and Szymanski, D.B. 2008. The Arabidopsis SCAR gene family: unequal redundancy and ARP2/3-activation thresholds control shoot morphogenesis. *Plant Cell*, 10.1105/TPC.107.055350.

6. Schlueter, J.A., Scheffler, B.E., Jackson, S.A. and R.C. Shoemaker. 2008 Fractionation of a genomic region containing tandemly duplicated genes across *Glycine max, Medicago truncatula* and *Arabidopsis thaliana*. *J. of Heredity*, doi:10.1093/jhered/esn010.

7. Schlueter, J.A., Goicoechea, J.L, Collura, K., Gill, N., Lin, J-Y., Yu, Yeisoo, Kudrna, D., Zuccolo, A., Vallejos, C.E., Munoz-Torres, M, Blair, M.W., Tohme, J., Tomkins, J., McClean, P., Wing, R.A., and Jackson, S.A. 2008 A BAC-based physical map of *Phaseolus vulgaris, Tropical Plant Biology,* 10.1007/s12042-007-9003-9.

8. Schlueter, J.A., Lin, J.-Y., Schlueter, S.D., Vasylenko-Sanders, I.F., Deshpande, S., Yi, J., Siegfried, M., Roe, B.A., R.T., Scheffler, B.E., Jackson, S.A. and R.C. Shoemaker. 2007 Genome duplication in soybean and the implications for whole genome sequence assemblies. *BMC Genomics*, 8:330.

9. Schlueter, J.A., Scheffler, B.E., Roe, B., Schlueter, S.D. and Shoemaker, R.C., 2007 The FAD2 family of soybean: insights into the structural and functional divergence of a paleopolyploid genome. *The Plant Genome, a Suppl. To Crop Sci.* 47: 14-26.

10. Schlueter, J.A., Scheffler, B.E., Schlueter, S.D. and Shoemaker, R.C., 2006 Sequence conservation of homeologous BACs and expression of homeologous genes in soybean (Glycine max L Merr) *Genetics*, 174(2): 1017-1028.

11. Shoemaker, R.C., Schlueter J.A., and Doyle, J.J., 2006 Paleopolyploidy and gene duplication in soybean and other legumes. *Current Opinions in Plant Biology*, 9: 104-109.

12. Pfeil, B.E., Schlueter, J.A., Shoemaker, R.C., and Doyle, J.J., 2005 Placing paleopolyploidy in relation to taxon divergence: a phylogenetic analysis in legumes using 39 gene families. *Systematic Biology* 54: 441-454.

13. Schlueter, J.A., Dixon, P., Granger, C., Grant, D., Clark, L., Doyle, J.J., and Shoemaker R.C., 2004 Mining EST databases to resolve evolutionary events in major crop species. *Genome*, 47: 868-876.

14. Vaghchhipawala, Z.E., Schlueter, J.A., Shoemaker, R.C., and Mackenzie, S.A., 2004 Soybean FGAM synthase promoters direct ectopic nematode feeding site activity. *Genome*, 47: 404-413.

15. Shoemaker, R.C., Schlueter, J.A., Cregan, P., and Vodkin L., 2003 The status of soybean genomics and its role in the development of soybean biotechnologies. *AgBioForum*, 6: 4-7.

16. Klein, R.R., Rodriguez-Herrera, R., Schlueter, J.A., Klein, P.E., Yu, Z.H., and Rooney, W.L., 2001 Identification of genomic regions that affect grain-mould incidence and other traits of agronomic importance in sorghum, *Theor. Appl. Genet*, 102: 307-319.

C. RESEARCH SUPPORT

Project/Proposal Title: **SoyMapII: Leveraging untapped genetic diversity in soybean**
PI: Scott Jackson CoPI: Randy Shoemaker, Perry Cregan, Jeff Doyle, Jeremy Schmutz
Senior Personnel: Jane Grimwood, Jianxin Ma, Jessica Schlueter
Source of Support: NSF PGRP
Total Award Amount: $5,258,288
Total Award Period: 3/15/2009 – 2/28/2013
Location of Project: Purdue University
Person-Months per Year Committed to the Project: 2 months

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors in the order listed on Form Page 2.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Schlueter, Shannon D	Assistant Professor
eRA COMMONS USER NAME (credential, e.g., agency login)	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Texas A&M University; College Station, TX	B.S.	05/00	Genetics
Iowa State University; Ames, IA	Ph.D.	08/06	Bioinformatics & Computational Biology
Purdue University; West Lafayette, IN	Postdoctoral	08/07	Agronomy & Bioinformatics

A. Positions and Honors

Positions and Employment

2009-present Assistant Professor; Department of Bioinformatics and Genomics; University of North Carolina at Charlotte, Charlotte, North Carolina
2007-2009 Assistant Professor; Department of Computer and Information Technology; Purdue University, West Lafayette, Indiana
2006-2007 Postdoctoral Research Associate; Department of Agronomy; Purdue University, West Lafayette, Indiana

Other Experience

2008-present NSF grant reviews: Graduate Research Fellows Program (NSF crosscutting), Advances in Biological Informatics (NSF BIO/DBI)
2007-present Developed and delivered *Applied Data Mining for Bioinformatics* at Purdue University and UNC-Charlotte
2006-present Recurring journal referee for: *Bioinformatics; BMC Bioinformatics; BMC Genomics; Genome Biology, Nucleic Acids Research;* and *Plant Physiology*

Professional Memberships

Perl Mongers (College Station, Ames, Lafayette, Charlotte) *since 1998*
International Society for Computational Biology *since 2001*
Association for Computing Machinery; SIG: Algorithms and Computational Theory *since 2003*
The Open Bioinformatics Foundation *since 2006*

Academic & Research Awards

2003 Plant Sciences Institute Research Fellow; Iowa State University
2001 NSF-IGERT Graduate Research Fellow; Iowa State University
2000 Graduated Magna Cum Laude with Foundation and University Honors; Texas A&M University
1999 Undergraduate Research Fellow; Texas A&M University
1996 McFadden Honors Scholar; Texas A&M University
1996 Fina All-State Scholar Athlete; Texas A&M University

B. SELECTED PEER-REVIEWED PUBLICATIONS

Journal Publications

1. Kane MD, Sringer JA, Iannotti NV, Gough E, Johns SM, Schlueter SD, Sepúlveda MS. Identification of development and tissue-specific gene expression in the fathead minnow Pimephales promelas, Rafinesque using computational and DNA microarray methods. Journal of Fish Biology. 2008 ;72(9):2341-2353.

2. Schlueter JA, Lin J, Schlueter SD, Vasylenko-Sanders IF, Deshpande S, Yi J, O'Bleness M, Roe BA, Nelson RT, Scheffler BE, Jackson SA, Shoemaker RC. Gene duplication and paleopolyploidy in soybean and the implications for whole genome sequencing. BMC genomics. 2007 ;8330.

3. Schlueter JA, Vaslenko-Sanders IF, Deshpande S, Yi J, Siegfried M, Roe BA, Schlueter SD, Scheffler BE, Shoemaker RC. The FAD2 gene family of soybean: Insights into the structural and functional divergence of a paleoplyploid genome CROP SCIENCE. 2007 ;47(1):S14-S26.

4. Schlueter JA, Scheffler BE, Schlueter SD, Shoemaker RC. Sequence conservation of homeologous bacterial artificial chromosomes and transcription of homeologous genes in soybean (Glycine max L. Merr.). Genetics. 2006 ;174(2):1017-28.

5. Schlueter SD, Wilkerson MD, Dong Q, Brendel V. xGDB: open-source computational infrastructure for the integrated evaluation and analysis of genome features. Genome biology. 2006 ;7(11):R111.

6. Wilkerson MD, Schlueter SD, Brendel V. yrGATE: a web-based gene-structure annotation tool for the identification and dissemination of eukaryotic genes. Genome biology. 2006 ;7(7):R58.

7. Dong Q, Lawrence CJ, Schlueter SD, Wilkerson MD, Kurtz S, Lushbough C, Brendel V. Comparative plant genomics resources at PlantGDB. Plant physiology. 2005 ;139(2):610-8.

8. Schlueter SD, Wilkerson MD, Huala E, Rhee SY, Brendel V. Community-based gene structure annotation. Trends in plant science. 2005 ;10(1):9-14.

9. Dong Q, Schlueter SD, Brendel V. PlantGDB, plant genome database and analysis tools. Nucleic acids research. 2004 ;32(Database issue):D354-9.

10. Schlueter SD, Dong Q, Brendel V. GeneSeqer@PlantGDB: Gene structure prediction in plant genomes. Nucleic acids research. 2003 ;31(13):3597-600.

11. Zhu W, Schlueter SD, Brendel V. Refined annotation of the Arabidopsis genome by complete expressed sequence tag mapping. Plant physiology. 2003 ;132(2):469-84.

12. Klein PE, Klein RR, Cartinhour SW, Ulanch PE, Dong J, Obert JA, Morishige DT, Schlueter SD, Childs KL, Ale M, Mullet JE. A high-throughput AFLP-based method for constructing integrated genetic and physical maps: progress toward a sorghum genome map. Genome research. 2000 ;10(6):789-807.

C. RESEARCH SUPPORT

No ongoing or previous federal or foundation research support as either PI or Co-PI.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Susan M. Sell	Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
University of California , Berkeley	A.B.	1978	Genetics
Pasteur Institute, Paris, France	N/A	1978-1980	Developmental Biology
University of California – Berkeley	Non-Degree	1980-1981	Biochemistry
University of Utah Medical Center, Salt Lake City	PhD	1987	Cellular, Viral and Molecular Biology
Stanford University Medical Center, Palo Alto	Post-Doc	1987-1991	Molecular Immunogenetics
NIH/NIDDK, Phoenix Indian Medical Center	Post-Doc	1991-1995	Molecular Genetics/Genomics

A. ACADEMIC POSITIONS and HONORS

Positions

2009-present Professor, Department of Bioinformatics and Genomics; University of North Carolina at Charlotte (UNC Charlotte)
2006-present Associate Dean of the Graduate School; UNC Charlotte
2006-2009 Associate Professor, Department of Biology; UNC Charlotte
2003-2006 Associate Dean of the Graduate School; University of Alabama, Birmingham (UAB)
1995-2006 Assistant Professor, Department of Nutrition Sciences; Graduate Faculty, Department of Genetics; Adjunct Professor, Department of Computer & Information Sciences; UAB

Professional and synergistic activities

2010 Reviewer, DAAD German Academic Exchange Service Fellowship Program in the Natural Sciences
2009 Moderator, Prader-Willi Syndrome Research Strategy Workshop, Washington, DC [NIH R13 DK085332]
2009 Chair, Plenary Session on *Integrative Training: Crossing Traditional Disciplinary Boundaries and Creating New Frameworks*, Council of Southern Graduate Schools 38th Annual Meeting
2008-present Member, Executive Committee, Council of Southern Graduate Schools
2007-present Graduate Faculty Representative: Bioinformatics and Genomics track; Educational Leadership; Health Services Research; Information Technology; Optical Science & Engineering; Special Education; UNC Charlotte
2006-present Board member, NSF ADVANCE Program; UNC Charlotte
2006-2008 Reviewer, NSF Advance Competitive Awards Program; UNC Charlotte
2005-2006 Board member, Science and Technology Honors Program; UAB
2005-2006 Reviewer, NCI Comprehensive Cancer Center Junior Faculty Development Grants Program; UAB
2003-present Board Member/Reviewer, Foundation for Prader-Willi Research/Competitive Research Awards Program
2003-2006 Director, McNair Scholars [DoEd] and Bridges to the Baccalaureate [NIH R25 GM060187] Training Grants; UAB
2003-2006 Board member, Alabama Space Grant Consortium, a National Space Grant College Fellowship Program
2001-present Editorial Board Member, *Cancer Genetics and Cytogenetics*
2000 Member, NIH Study Section, Special Emphasis Panel, NIH NCRR Specialized Centers
2000 Reviewer, Louisiana Board of Regents Health Excellence Fund Competitive Grant Program
1999 Reviewer, UAB Health Services Foundation Center Grants
1998-2001 UAB Project Director, USDA Biotechnology Experiential Learning Program for Rural Alabama [USDA 97-05546]
1998 Reviewer, Faculty Development Grants; UAB
1997-2000 Advisory Board Member, NIH Specialized Center of Research (SCOR) in SLE; UAB [NIH P50 AR045231]
1997 Reviewer, University of Michigan NIH NIDDK Diabetes Research Center Pilot Feasibility Grants
1996-2006 Preceptor, Cancer Research Experiences for Students (CAReS); UAB [NIH R25 CA076023]
1996 Developed and delivered *Molecular Basis of Disease*, special topics course for UAB Honors Program
1992 Reviewer, NSF Program Evaluation in Biochemical Genetics

Honors

2007-2008 National Postdoctoral Association Leadership Award
1987-1990 Dean's Post-Doctoral Fellowship, Stanford University Medical Center
1984-1987 NIH Pre-Doctoral Training Program in Genetics, University of Utah [NIH T32 GM007464]
1983-1984 University of Utah Graduate Research Fellowship
1979 NATO Advanced Study Institute on Molecular Biology

B. PUBLICATIONS (selected)

Research Papers (* indicates corresponding or co-corresponding author)

(1.) Whalen, RG, Schwartz, K, Bouveret, P, Sell, SM, and Gros, F (1979). *Contractile Protein Isozymes in Muscle Development: Identification of an Embryonic Form of Myosin Heavy Chain.* Proceedings of the National Academy of Sciences, 76:5197-5201.

(2.) Whalen, RG and Sell, SM (1980). *Myosin from Fetal Hearts Contains the Skeletal Muscle Embryonic Light Chain*. Nature, 286:731-733.

(3.) Whalen, RG, Sell, SM, Butler-Browne, GS, Schwartz, K, Bouveret, P, and Pinset-Harstrom, I (1981). *Three Myosin Heavy-Chain Isozymes Appear Sequentially in Rat Muscle Development.* Nature, 292:805-809.

(4.) Whalen, RG, Sell, SM, Eriksson, A and Thornell, LE (1982). *Myosin Subunit Types in Skeletal and Cardiac Tissues and Their Developmental Distribution*. Developmental Biology, 91:478-84.

(5.) Bugaisky, LB, Butler-Browne, GS, Sell, SM, and Whalen, RG (1984). *Structural Differences in the Subfragment1 and Rod Portions of Myosin Isozymes from Adult and Developing Rat Skeletal Muscles*. Journal of Biological Chemistry, 259:7212-18.

(6.) Brough, DE, Rice, SA, Sell, S, and Klessig, DF (1985). *Restricted Changes in the Adenovirus DNA Binding Protein that Lead to Extended Host Range for Temperature-Sensitive Phenotypes*. Journal of Virology, 55:206-212.

(7.) Zylicz, M, Yamamoto, T, McKittrick, N, Sell, S, and Georgopoulos, C (1985). *Purification and Properties of the dnaJ Replication Protein of Escherichia coli*. Journal of Biological Chemistry, 260:7591-7598.

(8.) Yamamoto, T, McIntyre, J, Sell, S, Georgopoulos, C, Skowyra, D, and Zylicz, M (1987). *Enzymology of the Pre-priming Steps in Lambda dv DNA Replication in vitro.* Journal of Biological Chemistry, 262:7996-7999.

(9.) Sell, SM*, Eisen, C, Ang, D, Zylicz, M, and Georgopoulos, CP (1990). *Isolation and Characterization of dnaJ Null Mutants of Escherichia coli.* Journal of Bacteriology, 172:4827-4835.

(10.) Sell, SM* (1992). *V(D)J Recombinase Precursors and Coding Structure of Signal Sequence Directed Rearrangement*. Computers and Chemistry, 16:125-133.

(11.) Sell, SM*, Reese, DE, and Ossowski, V (1994). *Insulin-Inducible Changes in the Insulin Receptor mRNA Splice Variants.* Journal of Biological Chemistry, 269:30769-72.

(12.) Reese, D, LeDuc, R, Sell, SM* (1996). *Evidence for Hormone-Induced Differential Splicing of PTP1B in vivo.* Experimental and Clinical Endocrinology & Diabetes, 104:124-125.

(13.) Sell, SM*, Ren,K (1997). *Automated Capillary Electrophoresis in the Genotyping of Apolipoprotein E.* Genomics, 46: 163-164.

(14.) Sell, SM*, Altungoz, O, Prowse, A, Surti, U, Meloni, A, and Sandberg, AA (1998). *Molecular Analysis of Chromosome 7q21.3 in Uterine Leiomyoma: Analysis using Markers with Linkage to Insulin Resistance*. Cancer Genetics and Cytogenetics, 100:165-168.

(15.) Sell, SM* and Reese, D (1999). *Insulin-inducible Changes in the Relative Ratio of PTP1B Splice Variants*. Molecular Genetics and Metabolism, 66:189-192.

(16.) Sell, SM* and Lugemwa, PR (1999). *Development of a Highly Accurate, Rapid PCR-RFLP Genotyping Assay for the Methylenetetrahydrofolate Reductase Gene*. Genetic Testing [invited], 3:287-289.

(17.) Pratley, RE, Ren, K, Milner, MR, Sell, SM* (2000). *Insulin Increases Leptin mRNA Expression in Abdominal Subcutaneous Adipose Tissue in Humans.* Molecular Genetics and Metabolism, 70:19-26.

(18.) Sell, SM*, Booyse, FM, Blasi, F(2000).*PCR-RFLP Genotyping of the Urokinase Gene*. Genetic Testing, 4:305-307.

(19.) Sell, SM*, Song, C, and Booyse, FM (2001). *PCR-RFLP Genotyping Assay for the Bcl I Polymorphism of the B-Fibrinogen Gene*. Genetic Testing, 5:45-46.

(20.) Yoder, B and Sell, SM*(2001). *Jets: a Modification to Speed Flexible Oligonucleotide Array Construction*. The Pharmacogenomics Journal, 1:163-165.

(21.) Sell, SM*, Patel, S, Stracner, D, Meloni, A (2001). *Allelic Loss Analysis by Capillary Electrophoresis: an Accurate, Automated Method for Detection of Deletions in Solid Tumors*. Genetic Testing, 5:267-268.

(22.) Sell, SM*, White, T, Johnson, P, Johnson, J, Palmer, E, Tullis, C and Lugemwa, PR (2002). *An Improved Assay for Genotyping the Common Alu Insertion in the Tissue-Type Plasminogen Activation Gene, TPA.* Genetic Testing, 6:67-68.

(23.) DelParigi, A, Tschop, M, Heiman, M, Salbe, AD, Vozarova, B, Sell, SM, Bunt, JC and Tataranni, PA (2002). *High Circulating Ghrelin: a Potential Cause for Hyperphagia and Obesity in Prader-Willi Syndorme*. Journal of Clinical Endocrinology and Metabolism, 87:5461-4.

(24.) Sell, SM*, Tullis, C, Stracner, D, Song, C-Y, Gewin, J (2005) *Minimal Deletion Interval Defined on Chromosome 7q in Uterine Leiomyoma*. Cancer Genetics and Cytogenetics, 157:76-69.

(25.) Ptacek, T and Sell, SM* (2005) *A Tiered Approach to Comparative Genomics*. Briefings in Functional Genomics & Proteomics, 4:178-185.

(26.) Chen, D, Song, S, Orthner, HF, and Sell, SM (2005). *Personalized Online Information Search and Visualization.* BMC: Medical Informatics and Decision Making, 5:6-15.

(27.) Ptacek, T, Song, C-Y, Walker, CL, Sell, SM* (2007). *Physical Mapping of Distinct 7q22 Deletions in Uterine Leiomyoma, and Analysis of a Recently Annotated 7q22 Candidate Gene*. Cancer Genetics and Cytogenetics, 174:116-20.

(28.) Bittel, DC, Kibiryeva, N, Sell, SM, Strong, TV, Butler, MG (2007). *Whole Genome Microarray Analysis of Gene Expression in Prader-Willi Syndrome*, American Journal of Medical Genetics, [Epub ahead of print].

(29.) Nishimura, W, Rowan, S, Salameh, T, Maas, R, Bonner-Weir, S, Sell, SM, Sharma, A (2008). *Preferential reduction of beta cells derived from Pax6-MafB-pathway in MafB deficient mice.* Developmental Biology, 314:443-456.

Peer-Reviewed Conference Proceedings

(30). Sell, SM* (1993). *Hepatic Expression of an SH2-Domain PTPase and the Distribution of Insulin Receptor Isotype are Regulated by Insulin*. Experimental and Clinical Endocrinology, 101 Supplement 2:132-133.

Published Commentary

(31.) Weinsier, RL, Hunter, GR, Heini, AF, Goran, MI, Sell, SM (1998).*The Etiology of Obesity: Relative Contribution of Metabolic Factors,* Diet, and Physical Activity. American Journal of Medicine, 105:145-150.

Book Chapter

(32.) Whalen, RG, Bugaisky, LB, Butler-Browne, GS, Sell, SM, Schwartz, K, and Pinset-Harstrom, I (1982). *Characterization of Myosin Isozymes Appearing During Rat Muscle Development.* In Muscle Development: Molecular and Cellular Control (Pearson, M.L. and Epstein, H.F., eds.) pp25-33. CSHL, CSH, NY.

U.S. Patent

(1.) Sell, SM (Issued 2004). *Isolated Polynucleotide Associated with Type II Diabetes Mellitus and Methods of Use Thereof*. U.S. Patent Application Serial No. 10/012,282.

C. RESEARCH SUPPORT

Ongoing Research Support

N/A

Completed Research Support

(24.) *A High Resolution Comparative Analysis of Early Onset Breast Cancer by Race*
Tyesha Farmer, Pre-doctoral Mentee — 2007-2009
NIH F31 CA126473-01A1 — Role: Co-Mentor

(23.) *Proteasome Regulation by O-glycosylation*
Sell, SM (PI)/Kudlow, J (PI) — 2006-2008
NIH R01 CA095021 supplement — Role: Re-entry Mentee

(22.) *Identification of Genetic Factors for Breast Cancer among Young African-American and Caucasian Women*
Fouad, M (PI) — 2004-2005
NIH P50 CA089019 SPORE in Breast Cancer, Developmental Research Program — Role: Co-investigator

(21.) *Markers and Mechanisms of Vascular Disease in Diabetes*
Lopes-Virella MF (PI) 2003-2006
NIH P01 HL055782 Role: Investigator

(20.) *Breast Cancer Gene in Alabama African-Americans*
Strong, T (PI) 2003-2004
AVON Foundation Role: Co-investigator

(19.) *Defective Fas Apoptosis During Aging*
Mountz, JD (PI) 2001-2004
NIH R01 AG116533-06 Role: Investigator

(18.) *Development of UAB Marker Assisted Genetics Facility* 2001-2003
Weaver, C (PI) Role: Director, Speedcongenics
UAB Health Services Foundation Genotyping

(17.) *Polyphenols & Nutrients: Genes, Proteins and Cancer Risk*
Barnes, S (PI) 2001-2002
NIH P20 CA093753 Role: Investigator

(16.) *Screening for Pediatric Type 2 Diabetes Genes*
Sell, SM (PI) 2000-2004
NIH R21 HD40788 Role: Principle Investigator

(15.) *Development of Microarray Technology*
Sell, SM (PI) 2000-2003
Bristol-Myers PINS Award Role: Principle Investigator

(14.) *Genetic Expression of the Diabetes Drug Target: PTP-1B*
Sell,SM (PI) 2000-2002
NIH MO1 RR000032 General Clinical Research Center, Protocol #863 Role: Principle Investigator

(13.) *Prader-Willi Syndrome-Associated Diabetes*
Sell, SM (PI) 2000
Civitan International Research Foundation Role: Principle Investigator

(12.) *NIH/NIDDK Clinical Nutrition Research Unit* 1999-2006
Weinsier, R (PI)/Allison, D (PI) Roles: Co-investigator and
NIH P30 DK056336 Genetics Core Co-Director

(11.) *Genetic Expression of the Diabetes Drug Target: PTP-1B*
Sell, SM (PI) 1999-2002
Diabetes Trust Fund Role: Principle Investigator

(10.) *Neuroanatomical Correlates of Hunger and Satiation in Subjects with PWS using Positron Emission Tomography*
Sell, SM (PI) 1999-2002
Prader-Willi Syndrome Association Role: Principle Investigator

(9.) *Type 2 Diabetes in a Bahamian Island Population*
Sell, SM (PI) 1998-1999
Office of the Provost UAB Faculty Development Program Role: Principle Investigator

(8.) *Allelic Imbalance and FISH Studies of Chromosome 7 in Wilms Tumor*
Meloni, A (PI) 1998-1999
University of Utah Primary Children's Medical Center Foundation Role: Co-investigator

(7.) *Relationship between Obesity and Risk for Diabetes in Subjects with Prader-Willi Syndrome*
Sell, SM (PI) 1998-1999
Prader-Willi Syndrome Association Role: Principle Investigator

(6.) *Age, Race, Sex and Aortic Stiffness: Genetic Markers*
Booyse, F (PI) 1997-2003
NIH R01 AG1426-01A1 Role: Co-investigator

(5.) *Molecular Genetics of Uterine Leiomyoma*
Sell, SM (PI) 1997-1999
NIH P30 CA013148 Comprehensive Cancer Center Junior Faculty Development Role: Principle Investigator

(4.) *Mapping Genes for Fat Distribution in a Founder Population*
Sell, SM (PI) 1997
UAB Faculty Development Grant Role: Principle Investigator

(3.) *Biomarker Development for Hyperinsulinemia*
Sell, SM (PI) 1995-1996
UAB Faculty Development Grant Role: Principle Investigator

(2.) *Insulin Signaling in Skeletal Muscle from Pre-diabetic Subjects*
Sell, SM (PI) 1992-1995
PHS Indian Health Service ISRSA0005 Role: Principle Investigator

(1.) *V(D)J Recombination*
Weisman, I (PI) 1990-1991
NSF Small Grant for Exploratory Research Role: Co-investigator

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Su, Zhengchang	Assistant Professor of Bioinformatics
eRA COMMONS USER NAME zhengchang	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
Yunnan Agricultural University	B.S.	1984	Animal Science
Jilin University	M.S.	1990	Physiology
University of Alabama at Birmingham	Ph.D.	2000	Physiology/Biophysics
University of Alabama at Birmingham	M.S.	2001	Computer Science
University of Alabama at Birmingham	Postdoct	2000-2002	Computational Biology
Oak Ridge National Laboratory	Postdoct	2002-2004	Computational Biology

A. Positions and Honors.

Positions and Employment

1990-1994 Instructor, Animal Physiology, Yunnan Agricultural University, Kunming, China
2004-2006 Assistant research professor, Institute of Bioinformatics, University of Georgia, Athens, GA
2006- Assistant professor of Bioinformatics, the University of North Carolina at Charlotte, Charlotte, NC

Other Experience and Professional Memberships

1994-2004 Member, America Physiological Society
1996-2004 Member, AAAS
2005- Current member: the International Society for Computational Biology

Honors

1994 CC Wu Foundation award, Hong Kong
2004 Best paper award, 14th international workshop of genome informatics, Japan

B. Selected peer-reviewed publications (in chronological order).

(Publications selected from 29 peer-reviewed publications (1-26))

1. Csutora, P., Su, Z., Kim, H.Y., Bugrim, A., Cunningham, K.W., Nuccitelli, R., Keizer, J.E., Hanley, M.R., Blalock, J.E. and Marchase, R.B. (1999) Calcium influx factor is synthesized by yeast and mammalian cells depleted of organellar calcium stores. *Proc Natl Acad Sci U S A*, **96**, 121-126, PMID: 9874782.
2. Manion, M.K., Su, Z., Villain, M. and Blalock, J.E. (2000) A new type of Ca^{2+} channel blocker that targets Ca^{2+} sensors and prevents Ca^{2+}-mediated apoptosis. *Faseb J*, **14**, 1297-1306, PMID: 10877822.
3. Villain, M., Jackson, P.L., Manion, M.K., Dong, W.J., Su, Z., Fassina, G., Johnson, T.M., Sakai, T.T., Krishna, N.R. and Blalock, J.E. (2000) De novo design of peptides targeted to the EF hands of calmodulin. *J Biol Chem*, **275**, 2676-2685, PMID: 10644729.
4. Su, Z., Csutora, P., Hunton, D., Shoemaker, R.L., Marchase, R.B. and Blalock, J.E. (2001) A store-operated nonselective cation channel in lymphocytes is activated directly by Ca^{2+} influx factor and diacylglycerol. *Am J Physiol Cell Physiol*, **280**, C1284-1292, PMID: 11287342.
5. Su, Z., Barker, D.S., Csutora, P., Chang, T., Shoemaker, R.L., Marchase, R.B. and Blalock, J.E. (2003) Regulation of Ca^{2+} release-activated Ca^{2+} channels by INAD and Ca^{2+} influx factor. *Am J Physiol Cell Physiol*, **284**, C497-505, PMID: 12388110.

6. Su, Z., Dam, P., Chen, X., Olman, V., Jiang, T., Palenik, B. and Xu, Y. (2003) Computational inference of regulatory pathways in microbes: an application to phosphorus assimilation pathways in *Synechococcus sp.* WH8102. *Genome Inform* **14**, 3-13, PMID: 15706515.
7. Chen, X., Su, Z., Dam, P., Palenik, B., Xu, Y. and Jiang, T. (2004) Operon prediction by comparative genomics: an application to the *Synechococcus sp.* WH8102 genome. *Nucleic Acids Res*, **32**, 2147-2157, PMID: 15096577
8. Chen, X., Su, Z., Xu, Y. and Jiang, T. (2004) Computational Prediction of Operons in *Synechococcus sp.* WH8102. *Genome Inform*, **15**, 211-222, PMID: 15706507.
9. Dam, P., Su, Z., Olman, V. and Xu, Y. (2004) In silico reconstruction of the carbon fixation pathway in *Synechococcus sp.* WH8102. *J Biol Sys*, **12**, 97-125, PMID.
10. Su, Z., Shoemaker, R.L., Marchase, R.B. and Blalock, J.E. (2004) Ca^{2+} modulation of Ca^{2+} release-activated Ca^{2+} channels is responsible for the inactivation of its monovalent cation current. *Biophys J*, **86**, 805-814, PMID: 14747316.
11. Olman, V., Peng, H.-C., Su, Z. and Xu, Y. (2004), *Proceedings 2004 IEEE Computational Systems Bioinformatics Conference*. IEEE Computer Society Press, Stanford, CA, pp. 363-370.
12. Su, Z., Guo, X., Barker, D.S., Shoemaker, R.L., Marchase, R.B. and Blalock, J.E. (2005) A store-operated nonselective cation channel in human lymphocytes. *Cell Mol Neurobiol*, **25**, 625-647, PMID: 16075382.
13. Wu, H., Mao, F., Su, Z., Olman, V. and Xu, Y. (2005) Prediction of functional modules based on gene distributions in microbial genomes. *Genome Inform*, **16**, 247-259, PMID: 16901107.
14. Wu, H., Su, Z., Olman, V. and Ying Xu. (2005) Prediction of functional modules based on comparative genome analysis and gene ontology. *Nucleic Acids Res*, **33**, 2822-2837, PMID: 15901854.
15. Huang, J., Su, Z. and Xu, Y. (2005) The Evolution of the Phosphonate Degradation Pathways. *J Mol Evol*, **61**, 682-690, PMID: 16245012.
16. Mao, F., Su, Z., Olman, V., Dam, P., Liu, Z. and Xu, Y. (2006) Mapping of Orthologous Genes in the Context of Biological Pathways: an Application of Integer Programming. *Proc. Natl. Acad. Sci. U.S.A*, **103**, 129-134, PMID: 16373500.
17. Su, Z., Olman, V., Mao, F. and Xu, Y. (2006) Comparative genomics analysis of NtcA regulons in cyanobacteria: regulation of nitrogen assimilation and its coupling to photosynthesis. *Nucleic Acid Res*, **33**, 5156-5171, PMID: 16157864.
18. Su, Z., Dam, P., Mao, F., Chen, X., Olman, V., Jiang, T., Palenik, B. and Xu, Y. (2006) Computational inference and experimental validation of nitrogen assimilation regulatory networks in cyanobacterium *Synechococcus sp.* WH8102. *Nucleic Acids Res.*, **34**, 1050-1065, PMID: 16473855
19. Catte, A., Patterson, J.C., Jones, M.K., Jerome, W.G., Bashtovyy, D., Su, Z., Gu, F., Chen, J., Aliste, M.P., Harvey, S.C., Li, L., Weinstein, G. and Segrest, J.P. (2006) Novel changes in discoidal high density lipoprotein morphology: a molecular dynamics study. *Biophys J*, **90**, 4345-4360, PMID: 16581834.
20. Dam, P., Olman, V., Harris, K., Su, Z. and Xu, Y. (2007) Operon prediction using both genome-specific and general genomic information. *Nucleic Acids Res*, **35**, 288-298, PMID: 17170009.
21. Tran, T.T., Dam, P., Su, Z., Poole, F.L., 2nd, Adams, M.W., Zhou, G.T. and Xu, Y. (2007) Operon prediction in Pyrococcus furiosus. *Nucleic Acids Res*, **35**, 11-20, PMID: 17148478.
22. Su, Z., Olman, V. and Xu, Y. (2007) Computational prediction of Pho regulons in cyanobacteria. *BMC Genomics*, **8**, 156 PMID: 17559671.
23. Su, Z., Li, G. and Xu, Y. (2008) Prediction of Regulons through Comparative Genome Analyses. In Xu, Y. and Gogarten, J. (eds.), *Computational Methods for Understanding Bacterial and Archaeal Genomes*, pp. 259-279.
24. Xu, M. and Su, Z. (2009) Computational prediction of cAMP receptor protein (CRP) binding sites in cyanobacterial genomes. *BMC Genomics*, **10**, PMID: 19146659.
25. Zhang, S., Xu, M., Li, S. and Su, Z. (2009) Genome-wide de novo prediction of cis-regulatory binding sites in prokaryotes. *Nucleic Acids Res*, **37**, e72, PMID: 19383880.
26. Xu, M. and Su, Z. (2010) A novel alignment-free method for comparing transcription factor binding site motifs. *PLoS One*, **5**, e8797, PMID: 20098703.

C. Research Support

Ongoing Research Support

1. Zhengchang Su, Brian Cooper 9/1/2009-8/31/2013
   Annotating the *cis*-regulatory binding sites in sequenced prokaryotic genomes

Role: PI

Funding agency: NSF

This project is to develop a fast algorithm for genome-wide prediction of *cis*-regulatory binding sites in all sequenced prokaryotic genomes through parallel computing, and a database system to store these predicted *cis*-regulatory binding sites for the research community to use.

D. Collaborators & Other Affiliations

1. Collaborators and Co-Editors.

Dr. Brian Palenik, Scripps Institute of Oceanography.
Dr. Ian Paulsen, the Institute of Genome Research.
Dr. Bhaya Devaki, Carnegie Institution for Science.
Dr. Brian Cooper, the University of North Carolina at Charlotte
Dr. Sunil Hwang, Carolinas Medical Center

2. Graduate and Postdoctoral Advisors.

Ph.D. thesis advisor:
Dr. J. Edwin Blalock, Department of Biophysics and Physiology, University of Alabama at Birmingham

Postdoctoral advisers:
Dr. Stephen Harvey, School of Biology, Georgia Institute of Technology
Dr. Ying Xu, Department of Biochemistry and Molecular Biology, University of Georgia in Athens

3. Thesis Advisor and Postgraduate-Scholar Sponsor

Shan Li, Ph.D. student, Department of Computer Science, the University of North Carolina at Charlotte
Minli Xu, Ph.D. student, Department of Computer Science, the University of North Carolina at Charlotte
Dr. Di Huang, postdoctoral fellow, Department of Computer Science, the University of North Carolina at Charlotte
Dr. Shaoqiang Zhang, postdoctoral fellow, Department of Computer Science, the University of North Carolina at Charlotte

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel in the order listed for Form Page 2.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Jennifer Walsh Weller, PhD	Associate Professor, Computer Science/Bioinformatics, UNC-Charlotte, Charlotte NC 28223

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
University of Montana	B.Sc.	1979	Chemistry
Oregon State University	M.S.	1986	Biochemistry and Molecular Genetics
University of Montana	Ph.D.	1990	Biochemistry
Michigan State University	Post-doctoral	1990-1992	Molecular Genetics
The Carnegie Institute for Plant Biology at Stanford	Post-doctoral	1992-1994	Molecular Genetics

A. Positions and Honors. List in chronological order previous positions, concluding with your present position. List any honors. Include present membership on any Federal Government public advisory committee.

Associate Professor, Bioinformatics and Genomics Department, UNC-Charlotte, Charlotte, NC 28223 (6/2007-present)
Associate Professor, School of Computational Sciences, George Mason University, Manassas VA, 20110. (6/2002-5/2007)
Director of Bioinformatics for the Epidemic Outbreak Surveillance project, USAF/SGX, Falls Church VA, 22041(6/2002-6/2003, IPA assignment 80% until July 1st, 2003)
Research Assistant Professor, Virginia Bioinformatics Institute, Virginia Tech, Blacksburg VA, 24061. (2000-present).
Adjunct Research Assistant Professor, Biology Dept. Virginia Tech, Blacksburg VA, 24061. (April 2001- present)
Adjunct Professor of Biology, University of New Mexico (2000).
Science Program Leader for Structural Genomics and for Gene Expression, NCGR, Santa Fe, NM 87505 (1999-2000).
Scientist and Senior Scientist at the PE Biosystems Corp. (other company unit names include PE AgGen, PE GenScope and Celera Applied Genomics), Foster City CA 87606 (1994-1999).
Honors, Awards

UM Regents Scholarship (1976-1977)
UM Honors Scholarship (1977-1978)
Hetler Memorial Award (1978)
Watkins-Morton Scholar (1978-1979)
Awardee on MBL Physiology Course Training Grant (1979)
ASM Presidents Fellowship (1981)- attended the Cold Spring Harbor Yeast Genetics Course, summer 1980
Bertha Morton Scholar (1987-1988)
Bertha Morton Scholar (1988-1989)
Fuson Award (1988)
ACS Divisional Award for outstanding student presentation at a meeting (1988).
Touchstone Award for the Northern California Technical Communication Competition (1997)
PE SPOT Award (1998) for technical contributions
NCGR Sustained Achievement Award (Mar. 2000)

B. Selected peer-reviewed publications (in chronological order).

1. DeCenzo,R., Engel, S.R., Gomez, G., Jackson, E., Munkvold, G., Weller, J., and Irelan, N. "Analysis of genetic diversity in Eutypa lata from California grape production regions using fluorescent AFLP and rDNA ITS sequence data. Phytopath. 89(10),884-893 (1999).
2. Iyoda S, Wada A, Weller J, Flood SJ, Schreiber E, Tucker B, Watanabe H. " Evaluation of AFLP, a high-resolution DNA fingerprinting method, as a tool for molecular subtyping of enterohemorrhagic Escherichia coli O157:H7 isolates". Microbiol Immunol. 1999; 43(8):803-6.
3. Zhao S, Mitchell SE, Meng J, Kresovich S, Doyle MP, Dean RE, Casa AM, Weller JW. "Genomic typing of Escherichia coli O157:H7 by semi-automated fluorescent AFLP analysis". Microbes Infect. 2000 Feb; 2(2): 107-13.
4. Waugh,M., Hraber, P., Weller, J., Inman, J., Farmer, A., and Sobral, B. (2000). The *Phytophthora* genome initiative. *Nucleic Acids Research* 28, 87-90.
5. Harger, C., Chen, G., Farmer, A., Huang, W., Inman, J., Kiphart, D., Schilkey, F., Skupski, M.P., Weller, J. (2000). The genome sequence database. *Nucleic Acids Research* 28, 31-32.
6. Mangalam, H., Stewart, J., Zhou, J., Waugh, M., Schlauch, K., Chen, G., Farmer, A., Collelo, G., and Weller, J. (2001), GeneX: an open source gene expression database and integrated tool set. *IBM Systems Journal*, 40 (2) 552-569.
7. Inman, J.T., Flores, H.R., May, G.D., Weller, J.W., and Bell, C.J. (2001) "A High-Throughput Distributed DNA Sequence Analysis and Database System" *IBM Systems Journal*, 40(2) 464-486.
8. Bell, C.J., Dixon, R.A., Farmer, A.D., Flores, R., Inman, J., Gonzales, R.A., Harrison, M.J., Paiva, N.L., Scott, A.D., Weller, J.W. and May, G.D. (2001). The *Medicago* genome initiative: a model legume database. *Nucleic Acids Research*, 29(1): 114-117.
9. Hraber, P.T. and Weller, J.W. "On the species of origin: diagnosing the source of symbiotic transcripts" Genome Biology 2001: 2(9) 37.1-37.13.
10. Mao, C., Cushman, J.C., May, G.D., Weller, J.W. "ESTAP – an automated system for the analysis of EST data" Bioinformatics (2003) 19: 1720-1722.
11. Gibas C.J., Sturgill D.M., Weller, J.W. GenoMosaic: On-Demand Multiple Genome Comparison and Comparative Annotation. 2003. In Proceedings of the Third IEEE Symposium on BioInformatics and BioEngineering, IEEE Press: 158-167.
12. Lee, J.K., Laudeman, T., Kanter, J., James, T., Siadaty, M.S., Knaus, W.A., Prorok, A., Bao, Y., Freeman, B., Puiu, D., Wen, L., Buck, G.A., Schlauch, K., Weller, J., Mangalam, H.J., Fox, J.W. "GeneX Va: VBC Open Source Microarray Database and Analysis Software for Multiple Users in Biomedical Research" Benchmarks, *Biotechniques*. 2004 Apr;36(4):634-8, 640, 642..
13. Ratushna, V., Weller, J., Gibas, C.(2005) "Secondary structure as a confounding factor in synthetic oligomer microarray design" BMC Genomics 6:31.
14. Higgs, B., J. Weller, et al. (2005). "On Spectral Embedding for Extraction of Structure in Biological Data". *Joint Statistical Meeting 2005 - Using Our Discipline to Enhance Human Welfare*, Minneapolis, Minnesota, ASA.
15. Higgs, B., J. Weller, et al. (2005). "Deriving Meaningful Structure from Spectral Embeddings and Clustering." Interface 2005: *Classification and Clustering 37th Symposium on the Interface*, St. Louis, Mo., Interface Foundation of North America.
16. Higgs BW., Solka JL., Weller J. (2005) Deriving Meaningful Biological Structure from Spectral Embedding and Clustering. *Computing Science and Statistics*. 37.
17. Higgs, B.W., Weller, J.W. and Solka, J.L.(2006) "Spectral Embedding Finds Meaningful (Relevant) Structure in Image and Microarray Data" *BMC Bioinformatics* **7**:74.
18. Overall, CC, Solka, JL, Priebe, CE, Weller, JW, Using Scan Statistics for Anomaly Detection in Genetic Regulatory Networks. Quantitative Methods in Defense and National Security (QMDNS). Fairfax, VA, February 7-8, 2007.
19. Overall, CC, Solka, JL, Weller, JW, Priebe, CE "Anomaly Detection in Genetic Networks." *Joint Statistical Meeting* (JSM). Seattle, WA, August 6-10, 2006.
20. Overall, CC, Solka, JL, Weller, JW, Priebe, CE. "Using Scan Statistics for Anomaly Detection in Genetic Networks." *Classification Society of North America* (CSNA). Rutgers, NJ, May 10-13, 2006.
21. Kumari, S., Verma, L., and Weller, J. (2007) "AffyMAPSDetector: A Tool To Detect SNPs In Affymetrix GeneChip™ Expression Arrays" *BMC Bioinformatics* 8:276.

22. Taylor, R.C., Singhal, M., Weller, J., Khoshnevis, S., Shi, L., McDermott, J. (2009) A Network Inference Workflow Reveals Functional Groups, Metabolic Pathways, and Regulons in *Salmonella typhimurium*. *Annals of the NY Academy of Science, Proceedings of the DREAM 2 conference*.1158:143-58.
23. Thompson, K.T., Deshmukh, H., Solka, J.L., Weller, J.W. (2009) "A Whitebox Approach to Microarray Probe response Characterization: the BaFL Pipeline" BMC Bioinformatics 10:449.
24. Carr, D.A. and Weller, J.W. (2009) "DataFATE: an ontologically based model for a scientific information management system" (IEEE Transactions on Computational Biology and Bioinformatics, accepted for publication).

C. Research Support.

COMPLETED

(None)- Weller (PI) 11/30/00 – 11/29/02 20%
VT/SR Noble Foundation/UN-Reno EPSCoR $579,453
Collaborative development of an EST database and analysis pipeline: ESTAP

The major goal of this project was to develop a relational database for EST data, a set of automated validation, cleansing and analysis procedures with selectable parameters and a Web interface allowing the data to be uploaded and subsequently viewed remotely. The principal investigator was responsible for defining the functionality of the pipeline and the database, for providing user interface design, use documentation and test criteria; for quality control and programmer supervision, for bringing in the criticisms of collaborators and ensuring that project resources and timelines were fulfilled. The source code is available from the Virginia Tech licensing office.

COMPLETED

NSF-BDI Weller (PI) 05/01/02 – 04/30/07 1 month summer
NSF/DBI (#BDI-0244167) $750, 691
Open GeneX: An Open Source Toolkit for Gene Expression Analysis
The major goals of this project were to provide a relational database that is consistent with the MAGE-OM on which the MIAME standards for gene expression databases were developed (www.mged.org). In addition I/O interfaces were developed for data and meta-data upload, and an analysis platform was created and tested that allows data to be treated consistently so that methods, experiments and organisms can be compared in a scientifically sound manner. The project was Open Source under the modified BSD license and the codebase is available at a UNCC project site. Four graduate students were funded and four manuscripts have been submitted describing both the code base and computational experiments performed using it.

ONGOING

NIGMS Gibas(PI) Weller (Co-PI) 08/01/06-07/31/10 1 month summer
NIH/NIGMS (R01-GM072619-01 subaward UNCC) $698,672
Biophysical Optimization of Oligonucleotide Arrays: This project aims to use predict and test the effect on the accuracy and robustness with which microarrays predict transcript concentrations when biophysical parameters are included at both the design stage and as part of preprocessing the raw data prior to meta-analysis. Arrays will be designed for which we have predicted outcomes based on probe and target structures and experiments will be performed in which concentrations and specific activities are carefully controlled in order to reduce technical variability as we assess the importance of various factors. The system models the infection of mouse cells by Brucella and a final outcome will be a diagnostic array with more well-characterized sensitivity and specificity than any currently available.

COMPLETED

NC Biotechnology Center Clemons(PI) Dreau (Co-PI) Weller (Co-PI) 05/01/09 $157,245 NA (IDG)
"A laser capture microscope platform for the interdisciplinary biotechnology programs in Charlotte"
An Institutional Development Grant for a shared laser capture microscope (Arcturus) with laser capture, laser cutting and fluorescence imaging capabilities along with strong image tracking and image analysis software capabilities. My interest was to make sure that a state of the art platform existed for the projects of several of my students who have an interest in wet-lab as well as computational experiments. It is increasingly clear that individual cell types have distinct signatures of each molecule class, and that the averaging that occurs in heterogeneous samples obscures essential information. Thus we wish to run our high-throughput platforms on properly purified samples before expending large amounts of effort on the analyses, and this platform makes that possible.

PENDING

NIH/NIAID Woody (PI) 01/01/10 – 12/31/10
R43EB011801-01 $30,000 (subaward amount)
"Elastic Wave Detectors Enabling Rapid Nucleic Acid Hybridization: Pathway to Low Cost Infectious Disease Diagnostics". This project aims to test whether EwD technology will enhance the rate of nucleic acid hybridization without requiring heat, which diminishes duplex stability, or inducing shearing, which diminishes specificity by degrading the template.

Research Interests: The research in my group for the past eight years has focused on developing computational tools for managing and integrating high-throughput genomics data sets, and testing hypotheses about microarray hybridization behavior in the wet lab. The data sets use in developing the tools have all been taken from large adenocarcinoma studies, allowing genotype, expression and alternative splice form data to be modeled. We have been working on biotechnology devices that enhance lab activities for various aspects of high-throughput microarray assays, with students in the Engineering departments at UNCC and with Dr. Woody at InSituTec, a local company. We also are working with partners at the Carolina Medical Research Center who are interested in ovarian cancer (Dr. David Tait) and in ALS (Dr. Jean-Luc Mougeot) to produce integrated genotype, CNV, and exon expression data, in order to add copy number variation and transcriptional regulation data to their data sets. Preliminary data bases have been instantiated for project involving these data types generated for a small number of abdominal cancer samples, ovarian cancer samples and ALS samples.