UNC CHARLOTTE
The University of North Carolina at Charlotte
9201 University City Boulevard
Charlotte, NC 28223-0001

March 16, 2007

Office of the Chancellor
Telephone: 704/687-2201
Facsimile: 704/687-3219

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

Dear Dr. Martin:

Enclosed is UNC Charlotte's request for authorization to establish a Professional Science Master's in Bioinformatics program.

The proposed Bioinformatics program is an interdisciplinary program at the intersection of the disciplines of biology, chemistry, mathematics and statistics, computing and informatics, physics, and engineering. Two major initiatives support the establishment of the proposed new program. The first is the 2005 initiative by the North Carolina State Legislature to fund construction of a $35 million bioinformatics facility on the Charlotte Research Institute campus. The second is our commitment to the North Carolina Research Campus in Kannapolis, 18 miles from UNC Charlotte.

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,

Phil

Philip L. Dubois
Chancellor

PLD/cfh

Enclosure (5 copies of the proposal)

cc: Provost Joan F. Lorden
Dean Mirsad Hadzikadic

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: March 16, 2007

Constituent Institution: The University of North Carolina at Charlotte

CIP Discipline Specialty Title: Bioinformatics

CIP Discipline Specialty Number: 26.1103 Level: B ☐ M ☒ 1st Prof ☐ D ☐

Exact Title of Proposed Program: Professional Science Master's (PSM) in Bioinformatics

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

Does the proposed program constitute a substantive change as defined by SACS? Yes ☒ No ☐

a) Is it at a more advanced level than those previously authorized? Yes ☐ No ☒

b) Is the proposed program in a new discipline division? Yes ☒ No ☐

Proposed date to establish degree program (allow at least 3-6 months for proposal review):

July 31, 2007

Do you plan to offer the proposed program away from campus *during the first year of operation*?

Yes ☐ No ☒

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

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Executive Summary

Overview
The program in Bioinformatics leading to the Professional Science Master's degree (PSM) is an interdisciplinary program at the intersection of the disciplines of Biology, Chemistry, Mathematics and Statistics, Computing and Informatics, Physics, and Engineering. It is expected that students entering the program will have completed an undergraduate major in either a life science or a quantitative discipline, with substantial coursework or a minor in a complementary discipline. The degree includes additional training and demonstrated competence in both life sciences and scientific programming. The program is structured to provide students with the skills and knowledge to develop, evaluate, and deploy bioinformatics and computational biology applications. The program is designed to prepare students for employment in the biotechnology sector, where the need for knowledgeable life scientists with quantitative and computational skills has exploded in the past decade. It will serve as an important qualification for individuals who will seek employment in North Carolina's biotechnology industry and research incubators, significant engines of economic growth in the state. The program will also provide an excellent foundation for advanced graduate study in the life sciences, biotechnology, and medicine.

Bioinformatics has wide applicability to medicine, pharmaceuticals, and agriculture. UNC Charlotte is uniquely positioned to contribute to all these areas. Located near several major medical centers including the Carolinas Medical Center, the Presbyterian Hospital, and the Salisbury VA Hospital, the University has collaborative programs underway with all three, providing access to patient populations. In addition, UNC Charlotte will provide the bioinformatics expertise for the North Carolina Research Campus (NCRC) at Kannapolis, located only eighteen miles from campus. When fully developed, the NCRC is expected to house over one hundred biotechnology companies and laboratories working in a variety of fields, including metabolomics, plant genomics, and translational medicine. These facilities will provide outstanding opportunities for internships, master's level projects, and ultimately employment for students in the proposed program.

Notification of Intent to Plan the proposed program was posted September 12, 2006. The proposed date for implementation is August, 2007. North Carolina has one other program leading to a Master of Bioinformatics that is specifically designed to prepare students for professional employment requiring master's-level credentials (NC State).

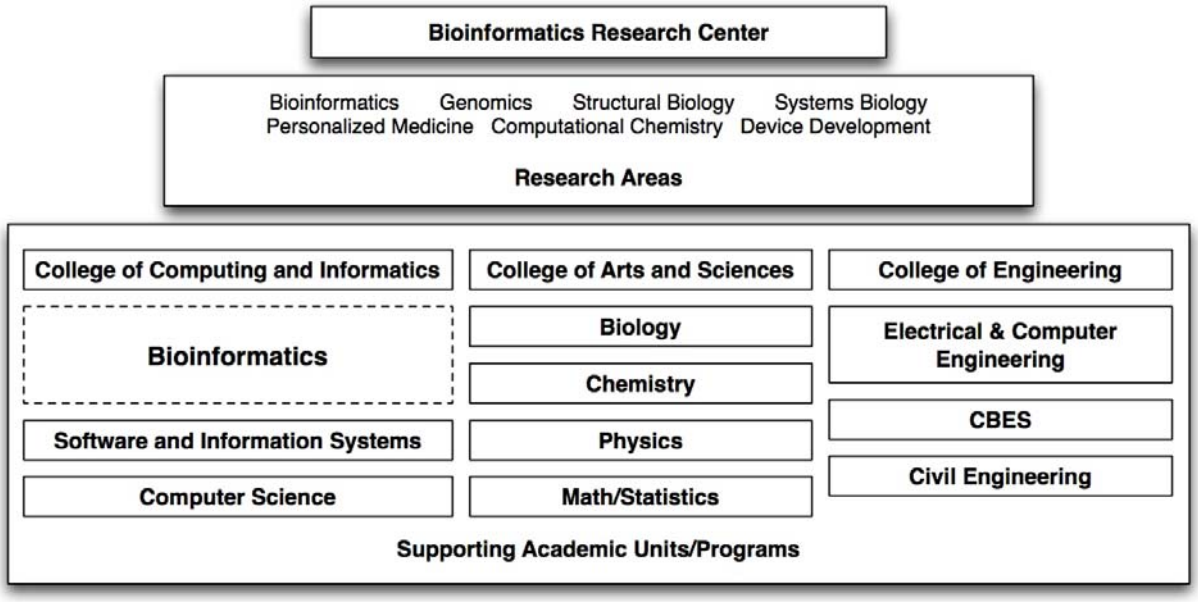
Program Objectives
The proposed PSM in Bioinformatics program has the following educational objectives:

- To provide students with a rigorous foundation in scientific computation;
- To provide an understanding of the biological context for development and application of bioinformatics methods;
- To train students in the structure and application of current state-of-the-art bioinformatics algorithms;
- To instill research, writing and critical thinking skills by teaching rigorous scholarly inquiry and research methods at a level appropriate for graduate education;

- To support and increase the base of technology in the rapidly growing biotechnology industry in the Charlotte area, in North Carolina, and across the nation; and
- To support activities of the UNC Charlotte Bioinformatics Research Center.

Relationship of Proposed New Program to Existing Programs

Bioinformatics is an interdisciplinary field of study that, when most successful, integrates relevant basic science, information technology, and engineering disciplines as depicted by the following diagram.



The proposed new degree program at UNC Charlotte clearly establishes this unique collaborative environment, and is designed to accommodate students and faculty from a variety of disciplines. Graduates of the program will be clearly identifiable as bioinformaticians. Student demand for the proposed program has been steadily building at UNC Charlotte. Currently, master's-level students with an interest in Bioinformatics enroll in the Department of Computer Science M.S. program. However, Computer Science does not provide a formal training option for these students, and an appropriate Bioinformatics training program will need to draw broadly on expertise outside of the College of Computing and Informatics as well as within it. Over 20 faculty members in several academic departments work in areas of Bioinformatics or closely allied disciplines. Their graduate students are enrolled in Biology, Chemistry, and Physics as well as Computer Science. Implementation of the proposed program will allow students seeking training in Bioinformatics a degree option that has an appropriate label and appropriate interdisciplinary content. We are already receiving inquiries from prospective students and there is no question as to future student demand for the proposed program.

Special Conditions in Support of the Proposed Program

Two major initiatives at UNC Charlotte and in the Charlotte region support establishment of the proposed new program at this time. The first of these was a 2005 initiative by the North Carolina State Legislature to fund construction of a $35 million Bioinformatics facility on the UNC Charlotte research and technology campus. UNC Charlotte has formed a Bioinformatics Research Center and made a commitment to acquire substantial Bioinformatics expertise by

hiring five faculty in 2005 and 2006, with further commitments to hire several additional Bioinformatics Faculty in preparation for the opening of the Bioinformatics building in August, 2009. The second initiative is the development of the North Carolina Research Campus (NCRC) in Kannapolis, eighteen miles from UNC Charlotte. Research activities in experimental genomics, proteomics, and systems biology at the NCRC will generate vast volumes of data. In 2006, UNC Charlotte proposed a significant role for its Bioinformatics Research Center in support of the NCRC. The Bioinformatics Research Center will develop a satellite facility on the NCR Campus and hire research faculty specifically to collaborate with scientists at the NCRC. One element of the proposal for UNC Charlotte Bioinformatics Research Center involvement in NCRC is that Professional Science Master's students in Bioinformatics will have the opportunity to intern with NCRC researchers and companies in the course of their degree, and a permanent staff member will be hired to coordinate PSM training activities between UNC Charlotte and NCRC. Permanent state funds to support these efforts have been awarded and are projected to increase to approximately $4.7M annually over the next four years. Implementation of the proposed new degree program is critical to the success of these initiatives.

Concluding Remarks

Establishment of the proposed new program will result in a substantial increase in the number of graduate students working in the critical area of Bioinformatics and in allied fields as part of the Bioinformatics Research Center initiative. These uniquely skilled people are urgently needed today and into the foreseeable future, as massively parallel experimental platforms that are now widely used in the life sciences generate terabytes of biological and clinical data annually. A source of skilled graduates in Bioinformatics will attract biotechnology and health-related businesses to the Charlotte area and to the newly formed North Carolina Research Campus. The establishment of the proposed program will result in an increase in the number and quality of our research laboratories. This will in turn attract faculty and students from the United States and abroad to create a major intellectual resource for the greater Charlotte region.

I. DESCRIPTION OF THE PROGRAM

The proposed program in Bioinformatics leading to the Professional Science Master's degree (PSM) is an interdisciplinary program at the intersection of the disciplines of Biology, Chemistry, Computer Science, Software and Information Systems, Physics, Mathematics and Statistics.

Bioinformatics has wide applicability to medicine, pharmaceuticals, and agriculture. UNC Charlotte is uniquely positioned to contribute to all these areas. Located near several major medical centers including the Carolinas Medical Center, the Presbyterian Hospital, and the Salisbury VA Hospital, the University has collaborative programs underway with all three, providing access to patient populations. In addition, UNC Charlotte will provide the bioinformatics expertise for the North Carolina Research Campus (NCRC) at Kannapolis, located only eighteen miles from campus. When fully developed, the NCRC is expected to house over one hundred biotechnology companies and laboratories working in a variety of fields, including metabolomics and plant genomics. These facilities will provide outstanding opportunities for internships, master's-level projects, and ultimately employment for students in the proposed program.

Notification of intent to plan the proposed program was posted September 12, 2006. The proposed date for implementation is August, 2007.

A. Description of the Program

Bioinformatics is by nature an interdisciplinary degree. As such, it may appeal to students with undergraduate training in computing, life science, or physical science disciplines. It is expected that students entering the program will have completed an undergraduate major in either a life science or a quantitative discipline, with substantial coursework or a minor in a complementary discipline. 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 proposed Professional Science Master's in Bioinformatics program has been designed to accommodate students entering with different backgrounds and to provide an accelerated introduction to either computing or life science as needed.

The proposed degree program includes additional training beyond introduction to the complementary discipline, and graduation from the program requires demonstrated competence in both life science concepts and scientific programming. The program is structured to provide students with the skills and knowledge to develop, evaluate, and deploy bioinformatics and computational biology applications. The first generation of bioinformatics 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 both strong programming, numerical and statistical analysis skills, and a substantive understanding of cellular and molecular biology, genomics, evolution and individual variation.

The program is designed to prepare students for employment in the biotechnology sector, where the need for knowledgeable life scientists with quantitative and computational skills has exploded in the past decade. Because the program is structured as a Professional Science Master's, some additional requirements are called for. Students must choose an elective that will develop their ability to work effectively in an industry setting, and must also seek an internship in an industry setting during one of the summer sessions between academic years in the program. If the student is returning for retraining while employed, bioinformatics work for the employer during enrollment in the program may satisfy the internship requirement. The proposed program will serve as an important qualification for individuals who will seek employment in North Carolina's biotechnology industry and research incubators, significant engines of economic growth in the state. The program will also provide an excellent foundation for advanced graduate study in the life sciences, biotechnology, and medicine.

B. Educational Objectives of the Proposed Program

The proposed Professional Science Master's program in Bioinformatics has the following educational objectives:

- To provide students with a rigorous foundation in scientific computation;
- To provide an understanding of the biological context for development and application of bioinformatics methods;
- To train students in the structure and application of current state-of-the-art bioinformatics algorithms;
- To instill research, writing and critical thinking skills by teaching rigorous scholarly inquiry and research methods at a level appropriate for graduate education;
- To support and increase the base of technology in the rapidly growing biotechnology industry in the Charlotte area, in North Carolina, and across the nation;
- To prepare students for work in an industry setting by providing training and experience relevant to that goal; and
- To support activities of the UNC Charlotte Bioinformatics Research Center.

C. Relationship of the Proposed New Program to Existing Programs

The new program will complement programs in information technology, biology, statistics, chemistry, and mathematics. Bioinformatics is an interdisciplinary field which, when most successful, integrates computer science and information technology methods with a significant base of biological knowledge. As such, although Bioinformatics at UNC Charlotte is housed in the College of Computing and Informatics, interaction with scientific disciplines in the College of Arts and Sciences is required to build a successful program. This will be achieved by participation of faculty from the Bioinformatics Program (which will pursue status as an independent department in 2007-8) and other fields in the Bioinformatics Research Center. An interdisciplinary faculty will provide a unique opportunity for students to build on undergraduate degrees in a variety of areas to prepare for employment in North Carolina's growing biotechnology industry. Graduates of the program will be clearly identifiable as bioinformaticians, and will be well prepared to understand both the biological basis, and the quantitative and computational aspects, of the problems they will encounter in the workplace.

II. JUSTIFICATION FOR THE PROGRAM

A. Describe the proposed program as it relates to:

1. <u>The institutional mission and strategic plan</u>

The following is the Mission Statement for the University of North Carolina at Charlotte:

> *UNC Charlotte is the only Doctoral/Research University – Intensive in the Charlotte region, fully engaged in the discovery, dissemination, synthesis, and application of knowledge. It provides for the educational, economic, social, and cultural advancement of the people of North Carolina through on- and off-campus programs, continuing personal and professional education opportunities, research, and collaborative relationships with private, public, and nonprofit institutions. UNC Charlotte has a special responsibility to build the intellectual capital of this area. As such it serves the research and doctoral education needs of the greater Charlotte metropolitan region.*
>
> *The primary commitment of UNC Charlotte is to extend educational opportunities and to ensure success for qualified students of diverse backgrounds through informed and effective teaching in the liberal arts and sciences and in selected professional programs offered through Colleges of Architecture, Arts and Sciences, Business Administration, Education, Engineering, Information Technology, and Health and Human Services, and through programs and services designed to support students' intellectual and personal development. The University offers an extensive array of baccalaureate and master's programs and a number of doctoral programs.*
>
> *With a broad institutional commitment to liberal education as the foundation for constructive citizenship, professional practice, and lifelong learning, UNC Charlotte is prepared to focus interdisciplinary resources to address seven broad areas of concern to the Charlotte region: 1) Liberal Education; 2) Business and Finance; 3) Urban and Regional Development; 4) Children, Families, and Schools; 5) Health Care and Health Policy; 6) International Understanding and Involvement; and 7) Applied Sciences and Technologies.*

The proposed Professional Science Master's (PSM) Degree in Bioinformatics is consistent with UNC Charlotte's Mission Statement. It represents a carefully targeted expansion of the programs at the master's level. Moreover, Bioinformatics is 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 PSM Degree in Bioinformatics is well aligned with the institutional 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. Bioinformatics expertise is critical in a wide range of biotechnology research problems and applications, from genomics to health care and beyond. In recognition of our initiative in Bioinformatics and its importance to the success of the North

Carolina Research Campus (NCRC), UNC Charlotte has been designated as the lead institution in the area of Bioinformatics for Kannapolis. A major goal of the PSM Degree in Bioinformatics is to provide well-trained people for six to ten educational institutions and the hundreds of companies that will come to the NCRC and greater Charlotte area.

2. Student demand

Even without advertising, student demand for a Bioinformatics master's degree is high. Approximately half of the inquiries come from students who have majored in biology or chemistry and are interested in developing quantitative, statistical, and computational skills. Most of the other inquiries come from computer science majors who are looking for a meaningful application area for their skills. These students are well aware of the strong demand for well-trained bioinformatics specialists and realize that they need a different skill set than is provided by traditional computer science or biology master's programs. It is very rare for a computer science major to have completed the biology prerequisites needed for entry into a biology master's program, or for the biology major to have the prerequisites for computer science. Even if they did, current biology and computer science graduate programs do not provide the specialized training needed for a career in bioinformatics. Most prospective students understand that a master's in computer science or biology will not allow them to accomplish their career goals. As we note below, there is only one other formal Bioinformatics master's program in North Carolina (NC State), although there are several other programs in related fields that have a bioinformatics component. It is clear that the UNC Charlotte program, originating in the College of Computing and Informatics, will place a heavier emphasis on the development and use of computational tools than programs that have grown from statistics or biological science departments. This appears to be the emphasis desired by most of our prospective students.

Survey: UNC Charlotte student interest in Bioinformatics graduate training

A voluntary interest survey of current UNC Charlotte undergraduates who are currently enrolled in majors likely to prepare them for Bioinformatics was conducted from November 30 to December 12, 2006. The survey was distributed to students via e-mail from their department chairs, and yielded 44 responses. Forty-two of the respondents indicated some level of interest in Bioinformatics as a career path. A majority of the students interested in the field (69 percent) were current Biology majors. Of those interested in Bioinformatics, 41 would consider enrolling in a Bioinformatics master's program at UNC Charlotte (27 percent Yes; 67 percent Maybe). Seventy-three percent of respondents indicated a preference for an industry internship experience in the course of their master's degree training, while 27 percent preferred a standard scientific research experience. The majority of the respondents were interested in employment in the academic (26 percent), medical (28 percent) or biotechnology industry (21 percent) sectors, given a range of choices that also included business management, engineering, law, and "other, please specify."

3. Societal need

The latest comprehensive analysis of manpower needs comes from "Bioinformatics: Recent Trends in Programs, Placements and Job Opportunities" (Black, G.C. & Stephan, P.E., Report to the Alfred P. Sloan Foundation, June 2004). This report roughly covers the period from 2000 to 2003 and is a follow up of their 1999 report on the same topic. In their earlier report, Black and Stephan reported a huge gap between the supply of individuals trained in bioinformatics and

demand, especially demand by industry. Unfortunately, the earlier report captured the "dot.com" exuberance of the late 1990's, while the latest report was a snapshot of the "dot.bomb" recession in technology, and especially in the collapse of many ill-conceived free-standing bioinformatics companies of that era. The last three or four years have seen considerable recovery in demand in bioinformatics jobs. In fact, currently (Nov. 2006) BioPlanet.com, a popular comprehensive bioinformatics/computational biology forum that allows free posting of Bioinformatics jobs, lists over 1000 jobs in their "Bioinformatics Forum." This represents more than a five-fold increase in BioPlanet job ads over the 2002-2003 period sampled by Black and Stephan.

The best indication of bioinformatics manpower needs in North Carolina comes from the continuing success of the biotechnology enterprise in this state. Currently, North Carolina is ranked third in the US in terms of biotechnology activity with approximately 800 biotechnology companies. North Carolina has a large investment is expanding biotechnology throughout the State. Indeed, the North Carolina Biotechnology Center just opened its fifth branch office on the Charlotte Research Institute campus at UNC Charlotte. This is in recognition of the growth in biotechnology in the Charlotte region as well as future plans for expansion. The rise of the NCRC at Kannapolis is the most dramatic example of the rise of biotechnology in the Charlotte area. The NCRC represents a $1B investment in biotechnology that will bring together bioscientists from Duke University, UNC Chapel Hill, UNC Charlotte, NC State, NC Central, NC A&T, and UNC Greensboro. The laboratories at NCRC will be equipped with over $50M in state-of-the-art research facilities including at least four NMRs (two 850MHz), five mass specs, four microarray labs, high-throughput sequencing facilities, X-ray crystallography, MRIs, and other high throughput analysis equipment. In addition to university scientists, the NCRC will house the Dole Food Laboratories and perhaps 200 other commercial biotechnology companies. The capacity for data production will be phenomenal and the data analysis and interpretation needs will be astounding. The UNC Charlotte Bioinformatics Research Center will be on-site providing bioinformatics services from the opening day of the NCRC and will work closely with the other universities and commercial partners to train bioinformatics specialists to supply these personnel needs. A coordinator for the PSM program will be recruited in 2007, and that staff member will be on-site part time at the NCRC building with the task of developing relationships with industry partners for internship training and placement of graduates.

Survey: current job opportunities for Master's-level Bioinformaticians

We analyzed the jobs posted on the BioPlanet website's Bioinformatics jobs forum (http://www.bioplanet.com). When the analysis was conducted (December 3, 2006), there were 1067 bioinformatics jobs posted on BioPlanet. About 644 (60.4 percent) of the posted jobs required a master's degree, and the rest (39.0 percent) required a doctoral degree. Of the 644 master's-level jobs, 443 jobs were in industry (biotechnology and pharmaceutical companies, and hospitals), and 201 jobs in academia. Thus, it appears that master's level bioinformatics professionals are in high demand both in industry and in academia. Obviously, the jobs posted on this website represent only a portion of the current job market; there are many other internet job listing services relevant to the life science. The real size of the market is likely to be larger.

4. Impact on existing undergraduate and/or graduate academic programs

The proposed program will significantly enhance instructional and research programs at UNC Charlotte at both the undergraduate and graduate levels. The program will be interdisciplinary with active participation initially by six academic departments (Biology, Computer Science, Physics and Optical Science, Chemistry, Mathematics and Statistics, and Software and

Information Systems). The program will expand to include other units with interests and applications in bioinformatics. Increased visibility provided by this program will better allow UNC Charlotte to attract and retain highly qualified students and faculty in this and related areas. The increased levels of external support will allow the University to provide more and better opportunities and programs for students choosing bioinformatics, biology, chemistry, or computer science as a field of study.

B. Discuss potential program duplication and program competitiveness

1. Identify similar programs offered elsewhere in North Carolina. Indicate the location and distance from the proposing institution. Include a) public and b) private institutions of higher education.

a) public institutions

North Carolina State University offers both master's and doctoral degrees in Bioinformatics through their Statistical Genetics and Bioinformatics Program. Their master's degree is listed as a PSM by the Sloan Foundation. This is the only program that is comparable to the proposed UNC Charlotte degree (by description and CIP number).

UNC Chapel Hill offers a certificate-granting program which works with various degree-granting UNC Chapel Hill departments to offer a specialization in Bioinformatics and Computational Biology. The degrees (master's or Ph.D.) are granted through the various home departments.

b) private institutions

Duke University offers a Ph.D. in Computational Biology and Bioinformatics. They do not offer a master's degree in this field as such.

2. Differences and duplication with other programs

The proposed program is similar to the master's degree in Bioinformatics offered by NC State. The UNC Charlotte degree program is needed because 1) NC State is 150 miles from Charlotte; 2) the Charlotte program will operate in partnership with the North Carolina Research Campus in nearby Kannapolis; 3) the Charlotte program, stemming from the College of Computing and Informatics, has a much stronger emphasis on promoting computational expertise than the NC State program, which developed from a program in statistical genetics; and 4) none of the NC State bioinformatics courses are offered on-line or through any other distance education format, and it would be impractical to ask Charlotte area students to study in Raleigh for two years before assuming internships in Kannapolis.

C. Enrollment

Headcount enrollment

As mentioned above, the only program in North Carolina similar to the proposed PSM in Bioinformatics is a program currently offered at NC State. The NC State program grew out of a program in statistical genetics, and has remained relatively

small, with enrollments fluctuating between seven and sixteen students per year. Since there is little other data to help assess the demand for Bioinformatics programs in North Carolina, we turned to master's programs at other universities in the region and nationwide to help assess likely student demand for a Computing and Informatics-based Bioinformatics degree. For example, George Mason University (Falls Church, VA) reports annual enrollments in its Bioinformatics master's program at 40-45, nearly triple the number enrolled at NC State. Therefore it is likely that the relatively low enrollments in the Bioinformatics master's program at NC State are an anomaly.

Program Title: Master in Bioinformatics

University	**Data**	**Year**				
		2000-01	**2001-02**	**2002-03**	**2003-04**	**2004-05**
NCSU	Fall Enrollment	7	16	11	14	8
	Degrees awarded	1	5	11	4	4

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 (2007-08)	Year 2 (2008-09)	Year 3 (2009-10)	Year 4 (2010-11)
Full-time	8	17	27	38
Part-time	2	5	8	12
TOTALS	**10**	**22**	**35**	**50**

Please indicate the anticipated steady-state headcount enrollment after four years:

Full-time 38 Part-time 12 Total 50

SCH production

Year 1: 2002-03	**Student Credit Hours (SCH)**		
Program Category	**UG**	**Master's**	**Doctoral**
Category I			
Category II			
Category III		168	
Category IV			

Year 2	**Student Credit Hours (SCH)**		
Program Category	**UG**	**Master's**	**Doctoral**
Category I			
Category II			
Category III		366	
Category IV			

Year 3	**Student Credit Hours (SCH)**		
Program Category	**UG**	**Master's**	**Doctoral**
Category I			
Category II			
Category III		564	
Category IV			

Year 4	**Student Credit Hours (SCH)**		
Program Category	**UG**	**Master's**	**Doctoral**
Category I			
Category II			
Category III		828	
Category IV			

III. Program Requirements and Curriculum

A. Program Planning

In planning the proposed Professional Science Master's in Bioinformatics programs, we examined the offerings of several universities with PSM in Bioinformatics programs, as well as a selection of strong Master of Science programs from institutions not having a formal PSM program. We chose a variety of programs, some housed in departments of computer science or mathematics, others in life sciences departments. We examined the course listings of each department chosen, as well as course descriptions and syllabi where available. Among the programs chosen, we identified a core of common required courses, as well as institution-specific electives that were unique and of high interest, which we may be able to replicate at UNC Charlotte. A full comparison of offerings and course content in the various programs is shown in Appendix I.

1. Institutions with Similar Offerings.

The institutions considered to have model programs in Bioinformatics were:

PSM Programs

- Arizona State, Computational Biosciences and Bioinformatics (interdisciplinary center)
- Boston University, Bioinformatics (interdisciplinary center)
- Georgia Tech, Bioinformatics (Biology)
- University of Michigan, Bioinformatics (Medical School)
- University of California at Santa Cruz, Bioinformatics (Engineering)

Master's Programs

- George Mason University, Bioinformatics (School of Computational Science)
- Indiana University, Bioinformatics (School of Informatics)
- Johns Hopkins University (School of Arts and Sciences)
- N.C. State University, Bioinformatics (Department of Statistics)

2. Institutions Visited or Consulted.

Faculty members in the UNC Charlotte Program in Bioinformatics are familiar with many of the programs listed above and have colleagues at several of these institutions. Especially helpful in developing this proposal was Dr. Jennifer Weller, of the Bioinformatics Department at George Mason University (GMU). The GMU program is one of the most mature and successful bioinformatics programs in the country. Bioinformatics at GMU maintains a constant enrollment of approximately 90 students, a mixture of returning professionals and Ph.D. and M.S. students, and places graduates successfully in the DC/Northern Virginia area and nationwide. We have also visited and consulted Dr. Zhao-Bang Zhang, director of the NC State Bioinformatics Research Center. We discussed his center and the emphasis of and demand for the NC State Master of Bioinformatics.

As recommended by the Sloan Foundation, we have formed an external advisory committee for the Professional Science Master's in Bioinformatics program. We will continue pursuing additional advisors for the program, emphasizing participation from companies in the Charlotte region and elsewhere in North Carolina. Current committee members, Dr. Jennifer Weller (GMU), Dr. James Bradburne (Clearpath BioMedical, VA) and Dr. Satyendra Kumar (Merck Research Labs), met with the Bioinformatics Faculty on Nov. 27, 2006, to recommend changes in this proposal before it was submitted for approval at the college level. Their vitae are included in Appendix A. A written statement of their recommendations at the time of the initial review is included in Appendix B.

Subsequent to review by the external advisory committee, we modified the Justification section of this proposal, and assessed UNC Charlotte student demand for the program by conducting a voluntary survey of undergraduates in relevant disciplines. We designed syllabi to avoid perceived overlaps, and added a visualization component to the statistics syllabus. We appreciate the need for a "branding" of expertise in the Bioinformatics program; however, our focus for the current hiring cycle has been to continue to broaden the expertise of our faculty rather than to begin deepening it in particular areas. This focus will shift in coming years, as the external advisory committee recommended. To address concerns that the internship focus is too strongly on Kannapolis, we have obtained funding to support a program coordinator for the PSM program; one of the coordinator's responsibilities will be to identify appropriate internships both locally (in UNC Charlotte and Carolinas Medical Center core labs and at local companies outside the Kannapolis umbrella) and in the broader mid-Atlantic and southeast region, including DC/Northern VA, Atlanta, and the Research Triangle. To alleviate the concern that PSM student advising will consume excessive faculty time, the PSM program coordinator will be hired in late Spring 2007 and will be in place and prepared to advise the first class of students.

B. Admission. List the following:

1. Admissions requirements.

The minimum admission requirements for the program are:

a. A baccalaureate degree in Biology, Biochemistry, Chemistry, Physics, Mathematics, Statistics, Computer Science, Engineering, or another related field which provides a sound background in life sciences, computing, or both.
b. A minimum undergraduate GPA of 3.0 (4.0 scale) and 3.0 in the major.
c. A minimum combined score of 1000 on the verbal and quantitative portions of the GRE, and acceptable scores on the analytical section of the GRE.
d. A combined TOEFL score of 220 (computer-based) or 557 (paper-based) is required if the previous degree was from a country where English is not the common language.
e. Positive letters of recommendation.

2. Documents to be submitted for admission (listing or sample).

a. Official transcripts from all colleges and universities attended.
b. Official GRE scores.
c. Official TOEFL scores.
d. The UNC Charlotte application for graduate admission form.
e. Three letters of recommendation.
f. An essay detailing the applicant's motivation and career goals, along with any specific research and training interests.

C. Degree requirements. List the following:

1. Total hours required

The minimum requirement for the PSM in Bioinformatics degree is 37 credit hours beyond the baccalaureate degree, and a minimum of 33 hours of formal course work. This includes a minimum of:

- 15 credit hours of **Core Bioinformatics** courses, one of which must be BINF 6200, *Statistics for Bioinformatics.*
- 6 credit hours of **Fundamental Biosciences** or **Fundamental Computing** courses.
- 1 credit hour of Seminar.
- 3 credit hours of an approved elective in information management, project management, IT ethics, or research ethics.
- 3 credit hours of BINF 6400 (Internship Project) or, recognizing that some students will inevitably develop an interest in research and may want to prepare for further graduate study by writing a Master's Thesis, 6 credit hours of BINF 6900 (Master's Thesis).

The remaining nine hours of required coursework may be selected from the Bioinformatics Core, Bioinformatics Advanced Electives, or the listing of approved electives in other departments offered by the Bioinformatics Program and other departments.

2. **Proportion of courses open only to graduate students to be required**
   At UNC Charlotte, courses having 5000 numbers are open to graduate students and advanced undergraduate students. Courses with 6000, 7000, and 8000 numbers are open to graduate students only. A minimum of 24 credit hours presented towards a PSM in Bioinformatics degree must be numbered 6000 or higher.

3. **Grades required**
   A student in the PSM in Bioinformatics Program must maintain a minimum GPA of 3.0 for continued enrollment in the program. Accumulation of three C grades will result in the suspension of the student's enrollment in the program. Accumulation of one U grade will result in the suspension of the student's enrollment in the program.

4. **Amount of transfer credit accepted**
   Up to six hours of approved coursework may be transferred from appropriately accredited master's and doctoral programs. Only courses in which the student earned a grade of B or better may be transferred.

5. **Seminar requirement.**
   Each student must enroll in the Bioinformatics Program seminar for a minimum of one semester. Each student must give a Bioinformatics seminar describing results of the internship or research project in the second year of their degree program.

6. **Language requirements.**
   The program has no language requirement.

7. **Time limits for completion of degree**
   Students are expected to take no more than six years to complete the program as per Graduate School rules.

D. List existing courses by title and number and indicate (*) those that are required. Include an explanation of numbering system. List (under a heading marked "new") and describe new courses proposed.

The PSM in Bioinformatics requires the addition of several new graduate courses and the formalization of existing courses that have been taught as ITCS special topics courses.

[N]Indicates course will be a new addition to the Catalog as part of the proposed Bioinformatics curriculum.
[O]Indicates course has been offered as an ITCS special topics course in 2005-6, 2006-7 or 2007-8 academic year.

New course development is focused in three areas:

1. Fundamental Biosciences and Fundamental Computing Courses

These courses are designed to provide an accelerated introduction to prerequisite knowledge in a field complementary to the student's undergraduate training. They are demanding courses designed for a graduate audience to acquire a broad range of knowledge of a field outside their original training, in a highly focused format. These courses are intended to preclude the need for students entering the PSM in Bioinformatics program to take an extensive series of

undergraduate courses (essentially amounting to a second degree) as prerequisite. The Fundamentals courses are distinguished from standard Biology and Computer Science graduate level offerings in that they have no prerequisite other than admission to the Bioinformatics graduate program. They are designed to emphasize those areas of biology and computing most relevant to the bioinformatician. At least two of the four courses are required for each student, depending on their prior training.

[N]**BINF 6100. Biological Basis of Bioinformatics. (3)**
Prerequisites: Admission to graduate standing in Bioinformatics and undergraduate training in Computer Science or other non-biological discipline. Provides a foundation in molecular genetics and cell biology focusing on foundation topics for graduate training in bioinformatics and genomics. (Fall)

[N]**BINF 6101. Energy and Information in Biological Modeling. (3)**
Prerequisites: Admission to graduate standing in Bioinformatics. This course covers: the major organic and inorganic chemical features of biological macromolecules, the physical forces that shape biological molecules, assemblies and cells, the chemical driving forces that govern living systems, the molecular roles of biological macromolecules and common metabolites, and the pathways of energy generation and storage. Each section of the course builds upon the relevant biology and chemistry to explain the most common mathematical and physical abstractions used in modeling in the relevant context. (Spring)

[N,O]**BINF 6111. Bioinformatics Programming I. (3)**
Prerequisites: Admission to graduate standing in Bioinformatics. Students in this course will learn how to use object-oriented programming to solve common problems in bioinformatics. Topics covered will include creation and manipulation of relational databases and interfacing with standard bioinformatics programs such as CLUSTAL, BLAST and HMMer. Emphasis will be placed on the creation of memory and time efficient algorithms to handle the large data sets of post-genomic biology. (Fall)

[N]**BINF 6112. Bioinformatics Programming II. (3)**
Prerequisite: BINF 6111. This is a continuation of Bioinformatics Programming I (BINF 6111). While the previous course emphasized fundamentals of Bioinformatics programming, this course emphasizes efficiency in speed, data structures and file size. Students will learn how to optimize code and databases so that the demanding analyses of modern biology can be performed in acceptable amounts of time while minimizing hardware requirements. Topics covered will include algorithm optimization, optimization of database queries and parallel processing to allow bioinformatics calculations to be performed on clusters. (Spring)

2. Core Bioinformatics Courses

These courses provide coverage of core methods and concepts in Bioinformatics, as identified through a survey of multiple Bioinformatics graduate programs. Twelve credit hours of coursework from this category are required towards the degree; one of those must be Statistics for Bioinformatics. Seminar does not count towards the Core Bioinformatics course requirement.

[N]**BINF 6200. Statistics for Bioinformatics. (3)**
Prerequisite: BINF 6100 and 6111 or equivalents. The aim of this 3-credit course is to introduce students to statistical methods used in further, more technical courses. Basic relevant concepts from probability, stochastic processes, information theory, statistics and experimental design 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. (Fall)

[N,O]**BINF 6201. Molecular Sequence Analysis. (3)**
Prerequisite: BINF 6100 or equivalent. 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, gene finding and feature finding in sequence, models of molecular evolution, phylogenetic analysis, comparative modeling. (Fall)

[N,O]**BINF 6202. Computational Structural Biology. (3)**
Prerequisite: BINF 6101, 6201 or equivalents. This course will cover: **(a)** the fundamental concepts of structural biology (chemical building blocks, structure, superstructure, folding, etc.); **(b)** software for visualization, visualization styles, publication quality images; **(c)** the hierarchical nature of biomacromolecular structure classification; **(d)** computational methods to evaluate and compare biomacromolecular structure; **(e)** inferring structure/function relationships from structure; and **(f)** computational prediction of protein and nucleic acid structure from sequence. *(Fall)*

[N,O]**BINF 6203. Genomics, Transcriptomics & Proteomics. (3)**
Prerequisite: BINF 6100 or equivalent, and BINF 6201.This course surveys the application and interpretation of high-throughput molecular biology and analytical biochemistry methods used to produce the kinds of high-volume biological data most commonly encountered by bioinformaticians. The relationship between significant biological questions, modern biotechnology methods, and the bioinformatics solutions that enable interpretation of complex data is emphasized. Topics include: Genome sequencing and assembly, genome annotation, genome comparison. Genome evolution. Function prediction and gene ontologies. Microarray assay design, data acquisition, data analysis. Proteomics and methods and data analysis. Methods for identification of molecular interactions. Metabolic databases, pathways and models. (Spring)

[N]**BINF 6204. Mathematical Systems Biology. (3)**
Prerequisites: BINF 6200 and 6210 or equivalents. Introduction to concepts and common methods in systems biology. The class emphasizes molecular networks, models and applications, and covers the following topics: complexity and robustness of cellular systems; hierarchy and modularity of molecular interaction networks; biologically data acquisition for system level modeling; introduction to systems biology markup language (SBML); Bayesian inference of biological systems; stoichiometric and constraint-based modeling; modeling molecular interaction networks with nonlinear ordinary differential equations; quantitative approaches to the analysis of genetic regulatory networks; stochastic modeling of intracellular kinetics; multilevel modeling. (Spring)

[N]**BINF 6210. Numerical Methods in Bioinformatics. (3)**
Prerequisites: Ability to program in a high-level language (Perl, Java, C#, Python, Ruby, C/C++). Calculus. This course will focus on mathematically complex problems and show students how to implement efficient numerical methods to solve those problems. The focus on the class will depend on instructor expertise but may include: applying linear models and principal component analysis to analysis of microarrays, application of ordinary and partial differential equations to modeling cellular pathways, applying Markov Chains to gene finding and gene predictions algorithms and application of stochastic models and Monte Carlo simulations to molecular dynamics and protein folding. *(Fall)*

[N]**BINF 6211. Design and Implementation of Bioinformatics Databases. (3)**
Prerequisite: BINF 6111 and 6112 or equivalent. Students will acquire skills needed to exploit public biological databases and establish and maintain personal databases that support their own research; such skills include learning underlying data models and the basics of DBMS, and SQL. Particular topics will include formats and schemas in important bioinformatics databases (Genbank, EMBL, PDB), XML schema and XML exchange methods, using CGI for the query interface, using generic database tools to browse and manage databases (Tomcat and Pgadmin), relevant database applications of SOAP and CORBA, the types of models used in designing databases, and how ontologies (such as GO) affect database design and queries. *(Spring)*

3. Advanced Bioinformatics Electives

These courses provide detailed coverage of specific topics in Bioinformatics. The following courses, already offered by the Bioinformatics Faculty, are representative of the types of electives that may be offered but do not cover the entire range of possible electives.

[N,O]**BINF 6310. Analysis of Microarray Data. (3)**
This course focuses on recent literature concerning algorithms for analysis of microarray data. The course will start with a review of normal statistics (t-test, ANOVA, etc.) and their non-parametric, robust equivalents. It then turns to primary literature for a survey of the techniques of analyzing microarray data: background subtraction, normalization across samples, assignment of p-values, evaluation of algorithms on control data sets, clustering algorithms, self organizing maps, bootstrap estimations of significance and over-representation of gene ontology terms. Special attention will be given to the problem of appropriate correction of significance for multiple measurements. Students should have fluency in a high-level programming language (PERL, Java, C# or equivalent) and will be expected in assignments to manipulate and analyze large public data sets. The course will utilize the R statistical package with the bioconductor extension. *(On demand)*

[N]**BINF 6311. Biophysical Modeling. (3)**
This course will cover: **(a)** overview of mechanical force fields; **(b)** energy minimization; **(c)** dynamics simulations (molecular and coarse-grained); **(d)** Monte-Carlo methods; **(e)** systematic conformational analysis (grid searches); **(f)** classical representations of electrostatics (Poisson-Boltzmann, Generalized Born and Colombic); **(g)** free energy decomposition schemes; and **(h)** hybrid quantum/classical (QM/MM) methods. *(On demand)*

[N,O]**BINF 6312. Computational Comparative Genomics. (3)**
Prerequisite: BINF 6210 or equivalent. Computational methods for comparative genomics analysis. The course covers the following topics: the architecture of prokaryotic and eukaryotic genomes; the evolutionary concept in genomics. databases and resources for comparative genomics; principles and methods for sequence analysis; evolution of genomes; comparative gene function annotation; evolution of the central metabolic pathways and regulatory networks; genomes and the protein universe; cis-regulatory binding site prediction; operon and regulon predictions in prokaryotes; regulatory network mapping and prediction. *(On demand)*

[N]**BINF 6313. Structure, Function, and Modeling of Nucleic Acids. (3)**
Prerequisite: BINF 6100-6101 or equivalent. The course covers the following topics: atomic structure, macromolecular structure-forming tendencies and dynamics of nucleic acids; identification of genes which code for functional nucleic acid molecules, cellular roles and metabolism of nucleic acids; 2D and 3D abstractions of nucleic acid macromolecules and methods for structural modeling and prediction; modeling of hybridization kinetics and equilibria; hybridization-based molecular biology protocols, detection methods and molecular genetic methods, and the role of modeling in designing these experiments and predicting their outcome. *(On demand)*

4. Internship, Seminar and Thesis courses

These courses are required as components of the PSM training.

[N]**BINF 6400. Internship Project. (1-3)**
Prerequisites: Admission to graduate standing in Bioinformatics. Project chosen and completed under the guidance of an industry partner, which results in an acceptable technical report. *(Fall, Spring)*

[N]**BINF 6600. Seminar. (1)**
Prerequisites: Admission to graduate standing in Bioinformatics. Bioinformatics Program seminar. Weekly seminars will be given by bioinformatics researchers from within UNC Charlotte and across the world. *(Fall, Spring)*

[N]**BINF 6601. Journal Club. (1)**
Prerequisites: Admission to graduate standing in Bioinformatics. Each week, a student in the class is assigned to choose and present a paper from the primary bioinformatics literature. *(Fall, Spring)*

[N]**BINF 6900. Master's Thesis. (1-3)**
Prerequisites: Twelve graduate credits and permission of instructor. Project chosen and completed under the guidance of a graduate faculty member, which results in an acceptable master's thesis and oral defense. *(On demand)*

Complete draft Catalog copy for the program is included in the curriculum proposal that accompanies this Request to Establish.

IV. FACULTY

A. Faculty Directly Involved in Proposed Program

Direct supervision of the Professional Science Master's in Bioinformatics Program will be the responsibility of the Bioinformatics Faculty, with involvement of faculty having primary appointments in other departments as their interest so dictates, via membership in the Bioinformatics Research Center. Members will be added to the Bioinformatics Faculty via new hires and to the Bioinformatics Research Center Faculty from current UNC Charlotte faculty as they meet criteria for membership and agree to actively participate. The Bioinformatics Faculty listed below includes only existing members of the Bioinformatics Program. A full listing of all faculty members participating in the Bioinformatics Research Center is included in IX, Supporting Fields, below, and full vitae for members of the Bioinformatics Program and all Bioinformatics Research Center Faculty are included in Appendix J.

Licensure Track: All tracks, educational research component

Faculty Name	Highest Degree and Institution	Other degrees and Institutions
Dr. Anthony Fodor	Ph.D. 1997, Physiology and Biophysics, University of Washington	M.S. 1994, Arizona State
Dr. Cynthia Gibas	Ph.D., 1996, Biophysics and Computational Biology, University of Illinois	B.A., Chemistry, Lawrence University.
Dr. Dennis Livesay	Ph.D. Physical Chemistry, University of Illinois	B.S, Chemistry, Ball State University
Dr. Lawrence Mays	Ph.D., 1973, Psychology, University of Virginia	M.A., 1976, Computer Science, Temple University
Dr. Zhengchang Su	Ph.D. 2000, Physiology & Biophysics, University of Alabama at Birmingham	M.S. 2001, Computer Science, University of Alabama at Birmingham

B. Estimate the need for new faculty for the proposed program for the first four years. If the teaching responsibilities for the proposed program will be absorbed in part or in whole by the present faculty, explain how this will be done without weakening existing programs.

Since the inception of the UNC Charlotte Bioinformatics initiative in 2005, five faculty members have been hired into the Bioinformatics Program, including the Director and four faculty members at Associate or Assistant rank. At the time the new Bioinformatics facility was planned, a program of accelerated hiring into the Bioinformatics Program was initiated, with plans to hire approximately 15 faculty members over five years. Subsequent to that, the program will grow at a normal rate, as demand and University allocations dictate. While current faculty and faculty who will be hired in Spring 2007 will be able to provide core courses to the initial classes of PSM in Bioinformatics students, it will be necessary to follow through on the plan of

hiring multiple faculty into the Bioinformatics Program over the next three years in order to provide diversity in expertise and offer desirable electives that will strengthen the appeal of the program. The Bioinformatics Program is currently recruiting three new tenure-track faculty, which will bring the number of primary Bioinformatics Faculty able to teach in the PSM to eight by Fall 2007. Planned hiring in Biology, Physics, Chemistry, and other departments is expected to create synergy with Bioinformatics hires and increase Bioinformatics Research Center participation.

C. If acquisition of new faculty requires additional funds, please explain where and how these funds will be obtained.

New faculty positions to support growth of the proposed program will occur through normal University allocations, on the accelerated schedule described above, which is designed to allow the Bioinformatics Program to grow rapidly in preparation for the opening of the new Bioinformatics Research Center facility in 2009.

Additional funding for tenure-track and research faculty positions stipulated as spending the majority of their time at the NCRC satellite facility will be provided by a special appropriation by the state legislature. The amount of this appropriation is to increase annually for five years, topping out at 4.7 million dollars in continuing state funds. While the purpose of this funding is specifically to support research at the NCRC, in practical terms these additional positions will enhance the expertise of the Bioinformatics Faculty on the UNC Charlotte campus. The NCRC funding will provide full salaries and start-up funds for ten additional new faculty members in bioinformatics (three new positions in 2007-08, two new positions in 2008-9, two new positions in 2009-10 and three new positions in 2010-11). This support, combined with the assistance of the PSM coordinator, will constitute adequate staffing for the master's program. The two facilities are only eighteen miles apart and NCRC faculty will maintain offices in the Bioinformatics Research Center and participate in the UNC Charlotte community in order to have access to students and local expertise.

D. Impact of proposed new program on faculty activity.

Implementation of the new program will have no negative impact on faculty activity. All members of the Bioinformatics Program and of the Bioinformatics Research Center Faculty are currently engaged in the activities required to support the Professional Science Master's in Bioinformatics Program. Many of the core courses described in the previous section have already been offered at least once as special topics courses, and all Bioinformatics Faculty are already research active. One way in which teaching/advising workload will increase is by the requirement to advise students as they enter the PSM program and prepare to graduate. Given the planned size of the Bioinformatics Faculty, however, and the participation of collaborating faculty in the Bioinformatics Research Center, the expected advising load per faculty member is expected to be fewer than five PSM students annually. There may be some requirement for faculty to generate research projects for PSM students when sufficient internship opportunities cannot be found, however, this is likely to result in a net increase in scholarly research activity.

V. LIBRARY

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

Consultation with the library staff was initiated on November 20, 2006. The evaluation by Joanne S. Klein was completed on November 29, 2006. Her assessment is attached as Appendix E. Her conclusion is that the holdings are adequate.

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

There are no plans to increase library holdings specifically for Bioinformatics at this time. Expansion of relevant holdings will be sought as funds become available.

C. Discuss the use of other institutional libraries

Holdings of other major libraries in the North Carolina system and beyond are accessible to faculty and students through interlibrary loan.

VI. FACILITIES AND EQUIPMENT

A. Description of Facilities Available for the Proposed New Program

Current facilities are adequate to support the proposed program during its first three years. During the past five years, the University has developed a significant infrastructure to support collaborative research between faculty in the College of Computing and Informatics and those in the Department of Biology. In 2005, the College of Computing and Informatics, the Department of Biology, and many Engineering faculty members relocated into the newly constructed Woodward Hall. Current activity in Bioinformatics is concentrated in Woodward Hall and Cameron Hall. Space in Woodward Hall is occupied by the offices and laboratories of Bioinformatics faculty members Dr. Cynthia Gibas and Dr. Anthony Fodor (220 sq. ft. office space, 450 sq. ft. wet lab space, and 500 sq. ft. dry lab space). A large section of Cameron Hall is currently undergoing renovation to prepare for the majority of Bioinformatics activity, including housing faculty now housed in Woodward and new faculty hired in 2007 and 2008. The Cameron Hall space available for Bioinformatics includes 2000 sq. ft office space for faculty and students, 3000 sq. ft. of wet lab space, and 5000 sq. ft of general purpose lab space. This space is currently occupied by the Bioinformatics Program office, by the offices and laboratories of Dr. Dennis Livesay and Dr. Zhengchang Su, and by the UNC Charlotte Functional Genomics Core Facility (PI: Dr. Cynthia Gibas), a recently-funded full-service glass-slide microarray facility which is staffed by a full-time technician. An inventory of major laboratory and computing equipment is presented in Appendix F.

B. Facilities to become available by 2009.

While present space is sufficient for existing personnel and bioinformatics graduate students, the planned Bioinformatics program will soon grow beyond the ability of these facilities to

accommodate it. Two major initiatives at UNC Charlotte and in the Charlotte region will provide facilities for the expansion of the UNC Charlotte Bioinformatics programs. The first of these was a 2005 initiative by the North Carolina State Legislature to fund construction of a $35 million Bioinformatics facility on the Charlotte Research Institute (CRI) campus at UNC Charlotte. Construction will begin in Spring 2007 on a 75,000 sq. ft. building to house the planned Department of Bioinformatics and the Bioinformatics Research Center. Additional space available upon completion of this building will include (1) research laboratories and office space to accommodate as many as 40 faculty, 60 postdocs and 100 graduate students, (2) core laboratory space and equipment for experimental genomics, proteomics, structural and systems biology, including an animal facility, microarray facility, a mass-spec facility, small labs adapted for patch-clamp experiments, spectroscopy, and microscopy, an X-ray crystallography facility, and a BSL-3 suite, (3) high-performance computing facilities and a server room with enhanced cooling capability to accommodate high-density architectures, and (4) state-of-the-art auditorium, conference room, and computer laboratory facilities. This building is scheduled for completion in August, 2009.

The second initiative is the development of the North Carolina Research Campus (NCRC) in Kannapolis, eighteen miles from UNC Charlotte. Research activities in experimental genomics, proteomics, and systems biology at the NCRC will generate vast volumes of data. In 2006, UNC Charlotte proposed a significant role for its Bioinformatics Research Center in support of the NCRC. The Bioinformatics Research Center will staff a 3000 S.F. satellite facility in the NCRC Core Laboratory facility and hire research faculty and staff specifically to collaborate with scientists at the NCRC beginning in Fall 2007. One element of the proposal for UNC Charlotte Bioinformatics Research Center involvement in NCRC is that Professional Science Master's students in Bioinformatics will have the opportunity to intern with NCRC researchers and companies in the course of their degree, and a permanent staff member will be hired to coordinate PSM training activities between UNC Charlotte and NCRC. Permanent state funds to support these efforts have been awarded and are projected to increase to approximately $4.7M annually over the next four years. Availability of the new building on campus and the satellite office at NCRC should provide adequate physical facilities for the planned Department of Bioinformatics and the PSM in Bioinformatics Program until at least 2020.

C. Information Technology Services Needed for Proposed New Program.

Information technology services currently provided by the University and the computing support group within the College of Computing and Informatics have so far been adequate to support the new program. Funding has also been provided by the State Legislature for a $500,000 bioinformatics research computer to complement the $3.7M computational facility at NCRC. However, as the program develops, the Bioinformatics Research Center will require its own dedicated computing support staff. The Bioinformatics Research Center maintains a 75-node OS X-based computing cluster plus servers and workstations for four research groups. This will only increase as the size of the faculty and the number of students increases.

D. Sources of Financial Support.

In recognition of the critical role played by the NCRC at Kannapolis in the development of Charlotte's PSM in Bioinformatics, the projected state budget allocation to UNC Charlotte includes significant funding on a permanent basis. For 2007-2008, the projected budget provides approximately $40,000 to help support PSM students in internships, and this amount rises to

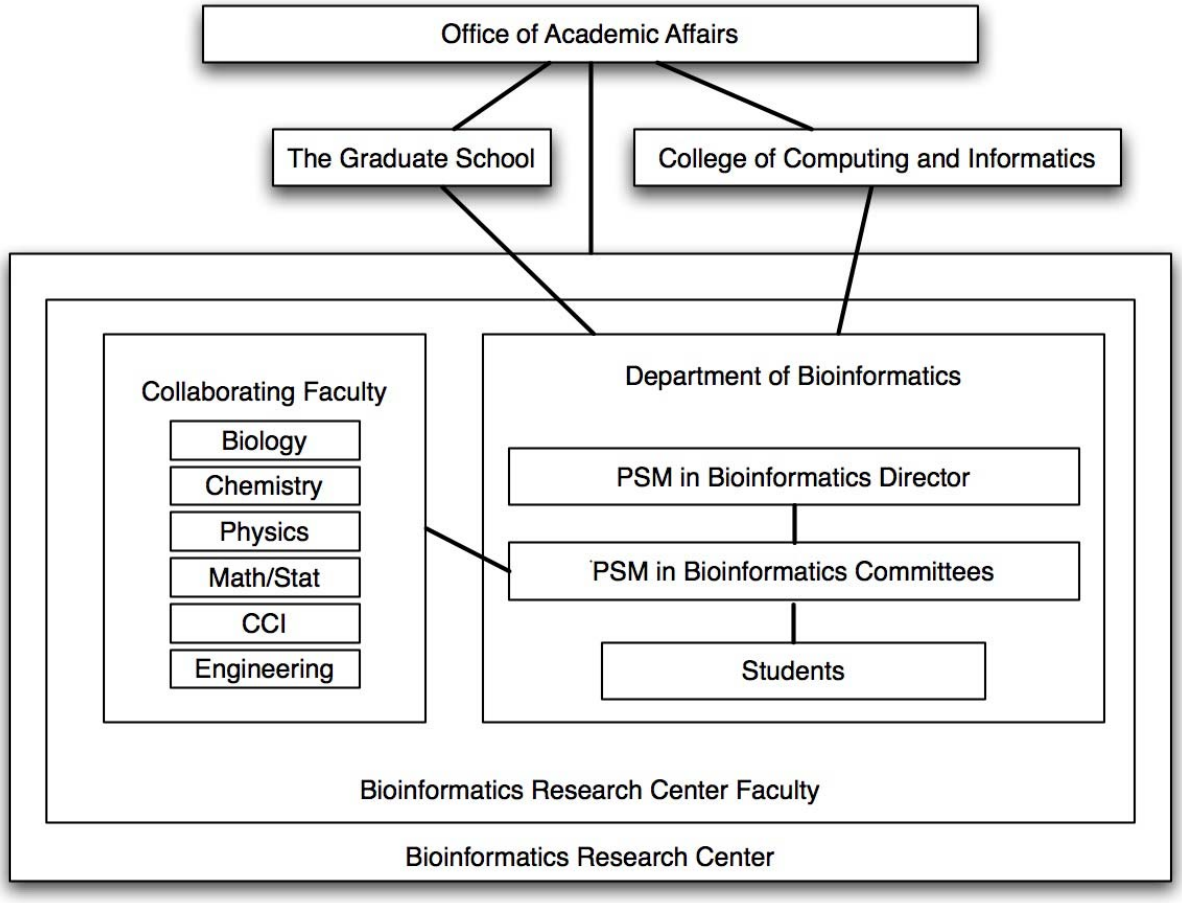
$200,000 for 2010 and beyond. In addition, the budget provides $63,000 (salary and fringe) for a PSM coordinator. This State appropriation provides funding for one new Bioinformatics (tenure-track) faculty member and one Bioinformatics support specialist (Ph.D. level, non-tenure) in 2006-2007. By 2010-2011, this recurring funding will support ten new tenure-track faculty in Bioinformatics and six Bioinformatics support specialists. These personnel will contribute to the training of PSM students in Bioinformatics.

VII. ADMINISTRATION

The interdisciplinary Professional Science Master's Program in Bioinformatics will be administered by the current Bioinformatics Program of the Department of Computer Science, and subsequently through the planned Department of Bioinformatics. Formation of a Department of Bioinformatics is in progress. The Director of the Bioinformatics Program will have administrative responsibility for all programs administered through that department and will also serve as the Director of the Bioinformatics Research Center. Membership on the Bioinformatics Faculty is restricted to those having a primary appointment in the Bioinformatics Program and significant published scholarship in the field. Membership on the Bioinformatics Research Center Faculty is more broadly defined, and may include those having primary appointments in other academic units and a willingness to teach in the Bioinformatics Professional Science Master's Program, collaborate in research which involves a substantive bioinformatics component, and serve on dissertation and advisory committees.

A. Organizational chart

The organizational chart for the administration of the Professional Science Master's Program in Bioinformatics is shown below. On the recommendation of the Bioinformatics Faculty, the Director of the Bioinformatics Program will recommend a Professional Science Master's in Bioinformatics Program Director to the Dean of the College of Computing and Informatics. The Professional Science Master's in Bioinformatics Program Director will appoint a Professional Science Master's in Bioinformatics committee from among the Bioinformatics Faculty and collaborating faculty in the Bioinformatics Research Center.



B. The Bioinformatics Research Center Faculty

In accordance with the criteria developed for each graduate program or unit and approved by the Graduate Council, and upon recommendation of the appropriate department chair, the Dean of the Graduate School appoints graduate faculty members for renewable five-year terms. Members of the graduate faculty offer courses and seminars and supervise research and dissertation at an advanced level of scholarship.

Faculty having primary appointments in Bioinformatics will automatically be members of the Bioinformatics Research Center Faculty. Any member of the graduate faculty with an interest in Bioinformatics and a willingness to teach and/or serve on committees in the Bioinformatics Research Center may apply to the Director of the Bioinformatics Program for membership in the Bioinformatics Research Center Faculty. Appointments will be for five-year terms with reappointments made according to guidelines established by the Director of the Bioinformatics Program with advice from the faculty, and administered by the Dean of the Graduate School. The Bioinformatics Research Center Faculty will serve as the constituency of the program for matters appropriate for faculty governance, and will meet as appropriate to vote on such issues.

C. The Professional Science Master's in Bioinformatics Program Committee

The Professional Science Master's in Bioinformatics Program Committee will have at least one representative from each of the departments having more than one faculty representative on the

Bioinformatics Research Center Faculty. The Director of the Bioinformatics Program will have ex-officio membership on the committee. At least three members of the committee will have their primary appointment in Bioinformatics. Membership on the committee will be for a two-year period.

The Committee works with the Director of the Bioinformatics Program to set policy and:

- Recommends to the Graduate School applicants for admission to the program
- Approves the student's advisory committee and internship or project plan
- Assures that the qualifying and comprehensive exams are administered appropriately
- Recommends to the Graduate School qualified candidates for the degree
- Assures that all requirements are fulfilled by each candidate
- Recommends course additions and alterations as appropriate
- Approves participation of faculty in the program
- Plans and evaluates the program

D. Professional Science Master's in Bioinformatics Program Director

The Director of the Bioinformatics Program will have final administrative responsibility for all programs administered through that department, under the direction of the Dean of the College of Computing and Informatics. The Professional Science Master's in Bioinformatics Program Director will have direct administrative responsibility for the PSM in Bioinformatics Program, in consultation with the Director of the Bioinformatics Program, the PSM in Bioinformatics Program Committee, and the Bioinformatics Faculty. The duties of the Director include:

- Curriculum and conduct of the program
- Chairing meetings of the PSM in Bioinformatics Program Committee
- Communicating assessment of the program and personnel to the Bioinformatics Research Center Director and to chairs of participating programs
- Overseeing recruitment efforts for the program
- Recommending operating budgets to the Director of the Bioinformatics Program and supervising expenditures
- Coordinating scheduling of courses among the participating units
- Assuring proper maintenance of graduate student records
- Representing the program to external constituencies

A Professional Science Master's program coordinator will be hired to assist the Director in management of the program and to lead efforts in tracking student outcomes, identifying appropriate internship partnerships, and supporting placement of graduates.

E. The College of Computing and Informatics

The Program in Bioinformatics is a subset of the Department of Computer Science in the College of Computing and Informatics. The Dean of the College has administrative responsibility for supervision of all departments and programs housed within the College.

F. The Graduate School

At the University of North Carolina at Charlotte, the Dean of the Graduate School is the administrative officer with primary responsibility for the supervision of graduate programs. The Dean is responsible for the executive and administrative affairs of the Graduate School in accordance with policies determined by the UNC Charlotte Graduate Council, the Graduate faculty, and the Faculty Council. The Graduate School is responsible for monitoring the quality of graduate programs, the final admission of graduate students, appointments to the Graduate faculty, and the enhancement of research activities essential to the conduct of graduate programs.

The Graduate Dean's main duties include the following:

- Admission of students
- Appointment of dissertation and thesis committees
- Approval of programs of study
- Admission of students to candidacy
- Final approval of dissertations

G. Student's Advisory Committee

Upon admission to the Professional Science Master's in Bioinformatics Program, the student is assigned an appropriate Faculty Advisor from among the Bioinformatics Faculty, based on the student's prior training and stated interests. The Faculty Advisor will recommend a Plan of Study for the student's first year of enrollment in the Program, and assist the student in identification of an appropriate internship or research project. Before the beginning of the third semester following admission to the program, the student must form a three-member Advisory Committee with members chosen from among the Bioinformatics Research Center Faculty. The assigned Faculty Advisor may chair this committee or the student may select a new Faculty Advisor from among the Bioinformatics Research Center Faculty at the time the committee is formed. The PSM in Bioinformatics Program Director must approve the composition of the committee.

Subject to the approval of the Dean of the Graduate School, the functions of the committee are to:

- Approve the student's plan of study
- Evaluate the student's academic progress each semester
- Evaluate the internship project or research project plan
- Certify the candidate's qualifications for the degree subject to the approval of the Dean of the Graduate School

VIII. ACCREDITATION

There is no agency that accredits graduate programs in Bioinformatics at this time. As Bioinformatics accreditation mechanisms become available, either through the International Society of Computational Biology or otherwise, appropriate accreditation will be sought.

Professional Science Master's programs are so designated by the Sloan Foundation and can be designated as affiliates of the Sloan PSM Initiative if they meet the majority of the PSM guidelines (http://www.scienceMaster's.com/affiliation.asp). We have closely followed the Sloan Foundation's startup checklist (http://www.scienceMaster's.com/startup_checklist.asp) in designing this program and the artifacts of that process are included in the appendix material to this document. By designing this program specifically to follow the PSM model we are laying the groundwork to seek official designation as a PSM program and financial support for future phases of program development.

IX. SUPPORTING FIELDS

The proposed program is interdisciplinary and, as such, involves curriculum and research activity in six academic departments housed in two colleges and in the Bioinformatics Research Center. Supporting academic departments include:

1. The Bioinformatics Program in the College of Computing and Informatics. Independent department status will be pursued for Bioinformatics in 2007-2008. When approved this will be the home department of the PSM program.
2. The Departments of Computer Science and Software and Information Systems in the College of Computing and Informatics.
3. The Departments of Biology, Chemistry, Physics and Optical Science, and Mathematics and Statistics in the College of Arts and Sciences.

Faculty strength in these areas is adequate to implement the program, especially considering the initiative to build and staff the Bioinformatics facility and the Kannapolis satellite office within the next three years. Table 2 lists the current members of the Bioinformatics Research Center Faculty by home department and research specialization. The interdisciplinary nature of the proposed program is evident from the mix of disciplines represented by members of the Bioinformatics Research Center Faculty. Each has a Ph.D. in a relevant discipline.

Faculty Name	**Academic Rank**	**Home Department**
Lawrence Mays	Professor	C.S./Bioinformatics Program
Cynthia Gibas	Associate Professor	
Dennis Livesay		
Anthony Fodor	Assistant Professor	
Zhengchang Su		
Mark Clemens	Professor	Biology
Ian Marriott	Associate Professor	
Iain McKillop		
Susan Sell		
Didier Dreau	Assistant Professor	
Julie Goodliffe		
Christine Richardson		
Chris Yengo		
Nury Steuerwald	Research Associate Professor	

Brian Cooper	Associate Professor	Chemistry
Joanna Krueger		
Taghi Mostafavi	Associate Professor	Computer Science
Kayvan Najarian	Assistant Professor	
Xintao Wu		
Alex Gordon	Assistant Professor	Mathematics and Statistics
Andriy Baumketner	Assistant Professor	Physics and Optical Science
Don Jacobs	Assistant Professor	Physics and Optical Science

Support from the academic units listed above is essential to the success of the proposed program since subject matter taught within these academic units is needed to support the proposed degree program. Bioinformatics, an emerging discipline, spans traditional departmental boundaries. Some universities have created separate Bioinformatics departments to house their programs. These departments have variously been created within Colleges or Schools of Science, Life Sciences, Computational Science, and Engineering, depending on institutional history and structure. Other universities have housed Bioinformatics within departments of Biology, Biochemistry, or Computer Science, or have created interdisciplinary centers without substantial additional hiring to add expertise specifically in Bioinformatics. UNC Charlotte has opted to develop a new Department of Bioinformatics, recruiting faculty whose main research focus is on development of Bioinformatics methods, while also taking advantage of existing expertise in allied departments to create a broader interdisciplinary unit called the Bioinformatics Research Center.

While the Bioinformatics Program is a program of the College of Computing and Informatics, close ties with researchers in other disciplines will broaden the training experience for students in the proposed program and model the type of interdisciplinary interactions that are necessary for a successful career in Bioinformatics. Collaborations with Biology faculty using high-throughput molecular biology platforms in their research will provide unique data streams and analysis challenges for Bioinformatics Faculty and students. Collaborations within the College of Computing and Informatics will strengthen the computational science, visualization, IT and data management skills of students in the program. And collaborations with Physics and Optical Science, Chemistry, and Mathematics and Statistics will provide a quantitative foundation for modeling molecular and cellular systems.

The exploitation of all of these relationships is necessary for Bioinformatics research and training programs at UNC Charlotte. While existing resources are adequate to initiate the program, realization of its full potential awaits resources already committed to strengthening the Bioinformatics Faculty and facilities, as well as the growth of allied departments and focus areas.

X. ADDITIONAL INFORMATION

There is no additional information pertinent to the review of the proposed program.

XI. BUDGET

A projected budget spreadsheet for Years 1-3 of the program is included as Appendix H.

XII. EVALUATION PLANS

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

- Number of graduates from the program
- Successful placement of students in the program into internships with local biotechnology companies
- Successful placement of the majority of graduates in positions in government/university/nonprofit research labs and in industry
- Successful placement of graduates not immediately seeking employment in advanced degree programs consistent with their bioinformatics training.

B. Measures to be used to evaluate the program:

Measures to be used to evaluate the quality and effectiveness of the proposed program include:

- We expect to reach a steady-state enrollment of approximately 50 students in the program within seven-ten years, with up to one third of those students being part-time. Expected time to degree is 2-2 1/2 years beyond the baccalaureate degree for a full- time student. We expect to graduate approximately 20 students/year from the program once steady state is reached.
- One component of the Professional Science Master's training experience is an industry internship. While availability of industry internships will fluctuate, we can evaluate success based on whether we are taking full advantage of potential opportunities that do exist in the region. The program will be considered successful if designated staff in the Bioinformatics Research Center satellite office are actively in contact with, and securing internship opportunities for students in, companies and core divisions at the North Carolina Research Campus and at companies in the broader region. When sufficient internships are not available for all students, the ability of the Bioinformatics Research Center Faculty to provide appropriate master's-level research projects will be assessed, based on reports and publications generated through such research.
- The program will be deemed successful if graduates pursue successful careers in government laboratories and industry.
- We recognize that some students entering a Professional Science Master's program may later develop an interest in academic research and doctoral training. The program will be deemed successful if those students not immediately seeking employment in their field after graduation are recruited into research laboratories at UNC Charlotte for training in the College of Computing and Informatics Bioinformatics track, or placed successfully in graduate programs at other institutions to continue their training.

C. Projected productivity levels (numbers of graduates):

	Year 1 (2007-2008)	Year 2 (2008-2009)	Year 3 (2009-2010)	Year 4 (2010-2011)	TOTALS
B					
M	0	7	13	17	37
I/P					
D					

D. Recommended consultants/reviewers:

In addition to our current group of external reviewers, Dr. Jennifer Weller of George Mason University, Dr. Satyendra Kumar of Merck Research, and Dr. James Bradburne of Clearpath Biomedical, whose CVs are included in this document as Appendix A, and whose initial evaluation of the program is included as Appendix B, we suggest the following as potential external reviewers of the proposed program:

Mark Borodovsky
Georgia Institute of Technology
Phone: (404) 894-8432
Fax: (404) 894-0519
mark.borodovsky@biology.gatech.edu

Gregory A. Buck, Ph.D., Director of Bioinformatics
Director, Center for the Study of Biological Complexity
Professor, Microbiology and Immunology
Virginia Commonwealth University
Ph: (804) 827-0026 (Main Number)
Ph: (804) 828-2318 (Office)
Fax: (804) 828-1961 (Main Office)
Fax: (804) 828-1937 (Office)
Email: buck@hsc.vcu.edu

Additional reviewers can be suggested upon the request of the consulting units.

E. Plan for evaluation prior to sixth operational year.

Maturation of the proposed program is expected to take about ten years. Only a few similar programs have been in place for longer than five years. Of these, some have reached steady state with a relatively large number of students seeking terminal master's degrees each year (for example, the Bioinformatics program at George Mason University which serves the Biotech-heavy DC/Northern Virginia area) while others have not yet grown to their full potential. The measures for evaluating program success, as described above, are not likely to be fully realized in four years. Evaluation of the program must therefore assess progress toward the steady-state goals.

From the inception of the program, we will maintain a database of enrollment and student outcome data for every student entering the Professional Science Master's program. Application, admission, graduation, and post-graduate placement data will be collected. Bioinformatics Research Center staff will track the progress of alumni and their satisfaction with their employment outcomes for up to five years after graduation, when possible, by using mailed or e-mailed surveys. Staff will encourage self-reporting for alumni over longer periods by creating a self-service alumni website that encourages graduates to submit their contact information and current employment information, network via online discussion, and contact other alumni.

Based on employment data supplied by graduates, Bioinformatics Research Center staff will make contact with frequent employers of our graduates and initiate formal or informal surveys of employer satisfaction with the goal of establishing reliable placement networks in the long term.

Fourth year milestones are listed below.

1. During the fourth year of the proposed program, enrollment will be assessed to determine whether it is meeting projections. Full-time enrollment in the program should approach 35 by the fourth year.
2. During the fourth year of the program, internship outcomes for students will be assessed. If contact is consistently being made with NCRC tenants and other biotechnology employers in the area regarding internships, and if productive relationships yielding internships for the majority of Bioinformatics students are in place, the program will be deemed successful. The expected volume of internships available will be assessed relative to the growth and success of biotechnology in the region, i.e. if there has for some reason been very little growth in biotechnology business despite the NCRC project, then fewer internship opportunities will be expected.
3. The program should have produced 30-35 graduates by the fourth year of operation. Placement outcomes for those students should be satisfactory for 85 percent of graduates.
4. A panel composed of a subgroup of the suggested program reviewers will visit the UNC Charlotte campus to assess the overall success of the program. These visits will be scheduled during the second year and the fourth year of program operation. The evaluation reports prepared by this panel will be reviewed by the Bioinformatics Research Center director, by the Deans of the College of Computing and Informatics and the College of Arts and Sciences, and by the Provost.
5. Necessary changes in the program will be implemented after each review to ensure that program goals are achieved.

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.

Proposed date of initiation of proposed degree program: 07/31/2007

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

Chancellor Philip Dubois **Date** 3/19/07

APPENDIX A
EXTERNAL ADVISORY COMMITTEE

BIOSKETCHES

JAMES A. BRADBURNE, PH.D.
801 Spring Mountain Way, Fort Valley VA 22652
(540) 933-6828

CURRICULUM VITAE

PROFESSIONAL EXPERIENCE

ClearPath Biomedical, Fort Valley, VA **July 2005 – Present**
Principle

ClearPath Biomedical provides business solutions in the medical research and pharmaceutical industry. ClearPath helps clients define and navigate best path scenarios.

Dec. 2005 – Present (Fort Valley, VA)

- Provide consulting services on intellectual property, licensing, funding and partnering for drug product design, research and clinical development, with a focus on early to mid-stage programs. Specialize in peptide and protein therapeutics. Current projects include freedom to operate and minefield analyses for a next generation drug product of a public pharmaceutical company.

July 2005 – Nov. 2005 (Redwood City, CA)

- Teamed with CEO and Board of Gryphon Therapeutics to sell the company. Efforts included the negotiation and sale of all intellectual property and product programs, as well as managing the due diligence process and transfer of know how and technology.

Gryphon Therapeutics, South San Francisco, CA **July 1999 – June 2005**
Executive Vice President

July 2000 – June 2005

- Part of core executive team that raised ~$27M in private equity and closed a product deal with Hoffman La Roche – the largest preclinical product deal at that point in the industry – with an overall value of up to ~$155M, plus certain future royalty, milestones and co-development rights.
- Negotiated and closed a critical collaboration agreement with Avecia (a global contract manufacturing organization) for the manufacture of Gryphon's protein therapeutics.
- Teamed with the CEO to negotiate and close a collaboration agreement with GeneProt (a leading proteomics company), with upfront cash to Gryphon >$5M, plus royalty, milestones and future product rights.
- Primary day-to-day responsibilities included the development and implementation of the company's intellectual property and legal strategies. Devised, wrote, prosecuted and managed patents and trademarks (over 200 active cases). Conducted freedom to operate and minefield analyses for all research and products. Responsible for writing, negotiating and closing general licensing, CRO and CMO business agreements.
- Managed strategic aspects of design and development efforts for all products. Named as an inventor on multiple patents related to peptide synthesis and ligation, water-soluble polymers, and synthetic proteins.

July 1999 – July 2000

- Part of strategic team that restructured Gryphon to execute on a new business model.
- Drove operational consolidation and financial recapitalization, including procurement of critical bridging revenue (~$1.5M) and investors to seed the new business (~$5M).
- Conceived the company's primary approach for making its therapeutics, and wrote the business plan.
- Managed the design, synthesis and testing of the initial lead product for critical proof of concept data.

PROFESSIONAL EXPERIENCE CONTINUED

Cooley Godward, LLP, Palo Alto, CA **June 1997 – June 1999**
Patent Agent and Technology Advisor, Intellectual Property Group

- Managed biotechnology, bioinformatic and medical device intellectual property portfolios in connection with patent procurement, product and client counseling, due diligence, patentability, validity and infringement analysis, and minefield studies. Clients included Gryphon Sciences, NaviCyte, The Regents of the University of California, Mayer Laboratories, Lynx Therapeutics, and Roche-Boehringer Mannheim.

- Patent litigation advisor with responsibilities that included client counseling, argument development and theory, discovery, witness preparation and depositions, interrogatory and brief writing, and preparation and presentation of technology tutorials for trial counsel and the court. One of four core team members that successfully represented Genencor International against Novo-Nordisk on protein chemistry and industrial enzyme technology patents, with a pivotal settlement in favor of our client worth over $5 billon.

Rae-Venter Law Group, P.C., Palo Alto, CA **Sept. 1995 – May 1997**
Patent Agent and Technology Advisor

- One of the three founding professionals of this start-up patent firm, with a focus on molecular biology and biochemistry. Responsibilities included patent prosecution, intellectual property due diligence, patent infringement and validity analysis, client counseling and management. Internal responsibilities included management and auditing the firm's patent docket.

Weil, Gotshal & Manges, Washington, D.C. **April 1992 – Aug. 1995**
Patent Agent and Technology Advisor, Biotechnology Group

- Prepared and prosecuted domestic and foreign patent applications in molecular biology and biochemistry. Served as patent litigation support and technology advisor in cases involving Genentech, Eli Lilly, and The Regents of the University of California on multiple pioneering patents covering recombinant somatostatin, insulin, and growth hormone.

Georgia Institute of Technology, Atlanta, GA **1987 – 1992**
Teaching Assistant

- Teaching Assistant for graduate and undergraduate courses including Biochemistry, Recombinant DNA Technology, Microbial Physiology, Plant Physiology, Microbiology, Cell Biology, Biology for Engineers, and General Biology.

Georgia Tech Research Institute, Atlanta, GA **1987 – 1989**
Research Technician

- Researched genetic markers linked to environmental stress in the nematode *Caenorhabditis elegans*.

Virginia Polytechnic Institute and State University, Blacksburg, VA **1986 – 1987**
Research Technician

- Researched genes associated with water stress and phosphorous tolerance in the cyanobacterium *Nostoc commune*.

BAR MEMBERSHIP

United States Patent and Trademark Office, Registration No. 38,389 **1994**

EDUCATION

Georgia Institute of Technology, Atlanta, GA, Ph.D., Molecular Biology & Biochemistry **1992**
Thesis title: "Signal transduction and regulation of *nif* gene expression in *Bradyrhizobium japonicum*"
Honors: Sigma Xi - The Scientific Research Society

Georgia Institute of Technology, Atlanta, GA, M.S., Applied Biology **1989**
Thesis title: "Gibberillic acid and reflected light effects on light-harvesting chlorophyll protein"
Honors: Graduate Student Senator representing Schools of Biology, Chemistry, Physics and Mathematics

Virginia Polytechnic Institute and State University, Blacksburg, VA, B.S., Biochemistry **1986**
Honors: Gamma Beta Phi Honor Society

SELECTED PUBLICATIONS

Publication: *International Patent Application* (2005) Publication No. WO 097168
Title: "Synthetic chemokines, methods of manufacture, and uses"
Inventors: Bradburne JA, Paliard X, and Miranda LP

Publication: *Chem. Biol.* (2005) *12(3)*:371-383
Title: "Synthetic erythropoietic proteins: tuning biological performance by site-specific polymer attachment"
Authors: Chen SY, Cressman S, Mao F, Shao H, Low DW, Beilan HS, Cagle EN, Carnevali M, Gueriguian V, Keogh PJ, Porter H, Stratton SM, Wiedeke MC, Savatski L, Adamson JW, Bozzini CE, Kung A, Kent SB, Bradburne JA, and Kochendoerfer GG

Publication: *J. Am. Chem. Soc.* (2005) *127(5)*:1350-1351
Title: "Site-specific polymer attachment to a CCL-5 (RANTES) analogue by oxime exchange"
Authors: Shao H, Crnogorac MM, Kong T, Chen SY, Williams JM, Tack JM, Gueriguian V, Cagle EN, Carnevali M, Tumelty D, Paliard X, Miranda LP, Bradburne JA, Kochendoerfer GG

Publication: *International Patent Application* (2004) Publication No. WO 060307
Title: "Synthetic neutropoiesis stimulating protein"
Inventors: Chen SY, Kochendoerfer GG, Bradburne JA, and Miranda LP

Publication: *Science* (2003) *299(5608)*:884-887
Title: "Design and chemical synthesis of a homogeneous polymer-modified erythropoiesis protein"
Authors: Kochendoerfer GG, Chen SY, Mao F, Cressman S, Traviglia S, Shao H, Hunter CL, Low DW, Cagle EN, Carnevali M, Gueriguian V, Keogh PJ, Porter H, Stratton SM, Wiedeke MC, Wilken J, Tang J, Levy JJ, Miranda LP, Crnogorac MM, Kalbag S, Botti P, Schindler-Horvat J, Savatski L, Adamson JW, Kung A, Kent SB, Bradburne JA

SELECTED PUBLICATIONS CONTINUED

Publication: *International Patent Application* (2003) Publication No. WO 018417
Title: "Nucleophile-stable thioester generating compounds, methods of production and use"
Inventors: Botti P, Bradburne JA, Kent SBH
(E.g., Issued Dec. 2005 in the United States as US 6,977,292 B2)

Publication: *International Patent Application* (2002) Publication No. WO 004015
Title: "Polymer-modified bioactive synthetic chemokines, and methods for their manufacture and use"
Inventors: Bradburne JA, Kochendoerfer GG, Wilken, JG

Publication: *International Patent Application* (2002) Publication No. WO 019963
Title: "Synthetic erythropoiesis stimulating protein"
Inventors: Kochendoerfer GG, Botti P, Bradburne JA, Chen SY, Cressman, S, Hunter CL, Kent SBH, Low DW

Publication: *International Patent Application* (2002) Publication No. WO 020034
Title: "Pseudo-native chemical ligation"
Inventors: Hunter CL, Botti P, Bradburne JA, Chen SY, Cressman S, Kent SBH, Kochendoerfer GG, Low DW
(E.g., Issued April 2006 in the United States as US 7,030,218 B2)

Publication: *International Patent Application* (2002) Publication No. WO 020557
Title: "Extended native chemical ligation"
Inventors: Botti P, Bradburne JA, Kent SBH, Low DW

Publication: *International Patent Application* (2002) Publication No. WO 020033
Title: "Polymer-modified synthetic proteins"
Inventors: Kochendoerfer GG, Botti P, Bradburne JA, Chen SY, Cressman S, Hunter CL, Kent SBH, Low DW, Wilken J
(E.g., Issued Oct. 2006 in the United States as US 7,118,737 B2)

Publication: *FEMS Microbiol. Lett.* (1994) *123(1-2):*91-98
Title: "*nif* gene expression in a Nif+, Fix- *Bradyrhizobium japonicum* variant"
Authors: Bradburne JA, Mathis JN, Israel DW

Publication: *Appl. Environ. Microbiol.* (1993) *59(3)*:663-668
Title: "*In vivo* labeling of *E. coli* cell envelope proteins with N-hydroxysuccinimide esters of biotin."
Authors: Bradburne JA, Godfrey P, Choi JH, Mathis JN

Publication: *Plant Physiol.* (1989) *91(3):*800-803
Title: "Reflected far-red light effects on chlorophyll and light-harvesting chlorophyll protein (LHC-II) Contents under Field Conditions"
Authors: Bradburne JA, Kasperbauer MJ, Mathis JN

Publication: *Plant Physiol.* (1989) *91(1):*19-22
Title: "Gibberellic acid effects on greening in pea seedlings"
Authors: Mathis JN, Bradburne JA, Dupree MA

SATYENDRA KUMAR, PhD
5042 Finsbury Road
Baltimore, MD - 21237
email: chrom23@gmail.com
Phone: 703-599-1458 (M)

SUMMARY

Experienced and resourceful technology professional with broad experience in Information Technology, M/C Learning/AI, Bioinformatics/Biotechnology, Image Processing and Technical Management.

Over 13 years of experience in providing Information Technology solutions with primary focus on Application Architecture, Software/Framework Development, Team Leadership and Project Management. Strong interpersonal and leadership skills with experience in managing technical professionals working in a cross-functional environment including science, software and business development.

CAREER PROFILE

- Professional background founded on expertise in information technology and experience in biotechnology and pharmaceutical industries. Strong background in computer science, bioinformatics, algorithms, system and molecular biology, and biomedical engineering.
- Management experience in matrixed organizations, including leading groups of software and science professionals working on multiple projects requiring software, algorithms and bioinformatics skills. Responsibilities included resource allocation, professional development, skill-assessment of the direct reports and budget for the line organization.
- Designed, developed and architected applications spanning several industries including Bioinformatics, Drug Discovery and Development, Medicine, Multimedia, Insurance, e-Commerce, Defense, Education and Government.
- Mentored and provided leadership in successful development, integration and deployment of applications using iterative, use-case drive process, OO methodology, and J2SE/J2EE/RDBMS/XML technologies.

COMPUTER SKILLS

- **J2EE:** EJB, Servlets/JSP, Java Server Faces, JDBC, JNDI, JMS, JTS, JAI, Java Mail
- **Application Servers:** WebSphere 6.0, Tomcat 5.5, JBoss 4, SJSAS 8.1, Web Logic 8
- **Languages:** Java, AspectJ, C++, C, PL/SQL, Perl, SML
- **IDEs:** RAD/WSAD, Eclipse, JBuilder, JDeveloper, PL/SQL Developer, Dreamweaver
- **Frameworks/Tools:** Struts, Tiles, Hibernate, JProbe, Log4J
- **XML Technologies:** XML, DTD, Schema, DOM, SAX, XSLT
- **Web Services:** Axis, JWSDP 1.5, SOAP, WSDL, UDDI, JAXP, JAX-RPC, JAXM, JAXR
- **OO Methodologies:** RUP, UML, ER Modeling, CRC, Design/Meta Patterns
- **Case Tools:** Rational Rose, Together J, Magic Draw, Visio, Oracle Designer
- **GUI/Rich Client:** Swing, SWT/JFace, Eclipse Plug-in, Eclipse RCP
- **Graphics Packages:** OpenGL, Java2D, Java3D, SRGP
- **Databases:** Oracle 9.0, MySQL, Microsoft Access
- **Systems:** Windows XP, Windows 2000, Linux, Sun Solaris

MACHINE LEARNING / SEMANTIC WEB / BIOINFORMATICS TOOLS & DB

- **MATLAB:** Signal/Image Processing, Wavelets, Optimization, Neural Net, Statistics, Bioinformatics
- **Statistics:** Parametric and Non-Parametric Statistics - Probability Distributions, ANOVA, Hypothesis Testing, Correlation/Regression, Multivariate Statistics
- **Semantic Web:** RDF, RDFS, OWL-DL, Jena2 RDQL/OWL/Reasoner, Protégé, BioPAX
- **M/C Learning/AI:** Graphical Models (Bayesian/HMM), Decision Tree, Nearest Neighbor, Reinforcement Learning, Clustering, Logic/Inference, Planning
- **Algorithms:** Sequence Alignment, Structure Prediction, Phylogenetic Analysis, Gene Expression Analysis & Classification, Dynamic Programming, Hidden Markov Models

- **System Biology:** Boolean, Probabilistic Boolean and Bayesian Networks, Gene Regulatory and Signal Transduction Networks, Data Integration - SRS, TAMBIS
- **NCBI:** Entrez Databases & Pipelines, RefSeq, dbSNP, Gene, UniGene, OMIM, OMIA
- **Protein/Other DBs:** SWISS-PROT, PIR, PDB, Bind/KEGG, GeneCards, PROSITE, PFAM, BLOCKS, CATH, SCOP
- **Analysis Tools:** BLAST/FASTA, PSI BLAST, CLUSTALW, T-COFFEE, JalView, PHYLIP, PAUP, MEGA, DAMBE, mVISTA, GRAIL, GeneID, GENSCAN, FGENES, JPred, TMHMM, 3DPSSM, Swiss-Model, SWISS-PDB Viewer, RASMOL, MFold, HaploView

EXPERIENCE

2006 - Present

Senior Research Scientist, Applied Computer Science and Mathematics, Merck Research Labs

Lead Research Engineer/Consultant, NLP and Speech Recognition, Streamsage Inc.

- **ChoiceStream Personalization System [Struts, XML-RPC, Oracle, Tomcat]**
  Developed a Struts based web-application to integrate the ChoiceStream personalization system with the Comcast's TV Planner Portal. The user-profile information was persisted using Oracle database and a highly modular, middle tier object model was developed to access ChoiceStream system using XML/RPC. The integration enabled TV Planner to make appropriate show recommendations, suggest shows similar to those the user may be interested in, and manage profile related information.

2001 - 2006 Staff Software Engineer/Line Manager, Informatics Department, Celera Genomics

- **Content Management System [LiveLink, Struts, Oracle, Tomcat]**
  Developed LiveLink API for integrating enterprise applications with the LiveLink Document Management System. Led development of a Struts based, content management web-application using LiveLink API. The application was used to browse and search documents stored in the Oracle database using LiveLink based processes and workflows for the DMPK and Toxicology departments.
- **Inventory Management System [Struts, Tiles, RAD 6.0, Tomcat]**
  Worked with a team of developers to implement an Inventory Management System for tracking the compounds being used for clinical trials. The web application provided functionality for searching, reporting and editing entries in the Inventory Management System.
- **Portfolio/Alliance Management System [JSF, RAD 6.0, Oracle, WebSphere App Server]**
  Developed an Alliance Management System for managing various projects associated with the Celera Therapeutics Portfolio. The system allowed business development group to request, access and distribute business development and finance related information from/to the management teams of the different therapeutics programs.
- **HTAMPS Application [Struts, Portal, WSAD 5.0, WebSphere Portal Server]**
  As a lead developer, implemented a web-based application for automating HTAMPS assay processing workflow. The application supported compound submission for new assay requests, analyzing and publishing assay results, tracking submissions through assay life-cycle, email-notification for select life-cycle events and access-control to the workflow processes based on the role of the requestor.
- **Study Management System [Struts, Portal, WSAD 5.0, WebSphere Portal Server]**
  Developed a Study Management System to support creation and management of studies conducted by the DMPK, Toxicology, Pharmacology and Pharmaceutical Sciences departments. The application was used to create, edit, list and search scientific studies and associated meta-data. The application allowed users to associate study specific results by uploading relevant files for the study.
- **Biomarker Profiler System [Swing, Visualization, Oracle, JBuilder]**
  Worked with a team of scientists and developers to implement a thick client application that supported management, quality control, and analysis of real-time PCR expression data generated by Celera Diagnostics. Specifically responsible for implementing functionality related to data normalization, fold-difference analysis, growth curve and melt profile visualization, and exporting data for analysis by 3rd party tools. The application was deployed in three phases to manage its complex functionality.

- **Proteins to Targets Application - P2T [XML, SAX/DOM, JSP, Oracle]**
  Led a team of software engineers to develop a web-based application to support Celera's Proteomics Pipeline. Primary goal of this application was to load LCMS and MSMS maps into a relational database, map the features in LCMS maps to proteins/peptides and make this information available to the scientists for identification and curation of protein targets.
- **Integrated Pathway Data Model and Database [Data Model, ER, Oracle Designer]**
  Designed and developed a generic pathway data-model for storage of protein-protein interactions, arbitrary set of atomic, composite and multi-valued properties, protein complexes, pathway interactions and hierarchy of pathways. The data-model was developed using ER modeling technique (Oracle Designer) and was used to populate an example database using actual data from a curated pathway. The database schema supported storage of complementary data (including gene/protein synonyms and signal transduction ontology).

1999 - 2001 Enterprise Architect, Professional Services - Sun Java Center, Sun Microsystems

- **Enterprise Application Architecture [J2EE, XML, RUP, MVC]**
  Led the enterprise application architecture development effort for a major insurance company. Mentored the architecture team in J2EE and XML technologies and established a RUP based application development process. Worked with the architecture team to develop architecture definition and design. The multi-tier architecture was based on the layers and MVC architecture pattern. The base-architecture supported a diverse set of clients including web, voice and wireless and helped achieve seamless integration with the legacy applications.
- **Federated Image Exploitation System [J2SE, JAI, XML, DAG]**
  Worked for the Defense Science and Technology Organization of the Department of Defense of a NATO member country. Led a team of architects and computer scientists to develop the architecture for a distributed, scalable and fault-tolerant Image Exploitation System. The architecture was based on Java Advance Imaging framework and supported non-functional requirements including distribution of DAG, load balancing, caching, security, failover and distributed exception/event handling.
- **e-Fulfillment Application Architecture [J2EE, RUP, UML, EJB, Servlets]**
  Led the architecture and design of an e-Commerce application software for a large fulfillment and logistic provider. Responsible for mentoring the team in the use of UML, RUP, Servlets and EJB component model. Designed the common business objects for reuse across multiple application components and use-cases. The application was implemented using J2EE framework and RUP methodology was used during the development cycles.
- **Web Application Framework**
  Worked for the finance department of a major insurance company as a lead member of the architecture team. The framework architecture was based on J2EE and consisted of a number of sub-frameworks including persistent, security, logging, bean-XML mapping and dynamic content generation. The framework was used to provide common business functionality and system services across multiple lines of businesses. Also responsible for mentoring the development team on UML, meta-patterns, framework development methodology and appropriate use of J2EE design patterns/best practices.
- **Swing & Performance Tuning**
  Worked for the claims department of a major insurance company to identify potential areas of performance bottleneck and memory leakage of a 3-tier Swing based application. Using reverse engineering and refactoring techniques, the application response time was reduced by more than 80%. Mentored the development team in a number of areas including OO design methodology, coding styles for Java and Swing, application refactoring and design patterns.

1994 - 1999 Teaching/Research Assistant, Image Processing Lab, BME - The University of Akron

- **Image Processing Framework [Morphology, OOSE, C++]**
  Project lead responsible for domain analysis, design and implementation stages of development cycle. The **multidimensional image processing framework** was used to implement binary/gray scale morphology toolbox that supported operations such as dilation, erosion, opening, closing, deblurring, and edge detection.

- **Registration/Fusion Algorithms [C++, Wavelets, Multi-resolution Decomposition]**
  Developed and implemented novel algorithms for registration of brain images. Algorithms were based on morphological image analysis and wavelet based **multi-resolution decomposition**.

  Developed and implemented wavelet based fusion algorithms to integrate **multimodality brain images**. **Orthogonal** and **biorthogonal wavelet filters** were evaluated for their effectiveness in the fusion.
- **Illumination and Shading [Graphics, OpenGL]**
  Rendered a 3D **interactive**, **animated scene** in C and OpenGL. The actors in the scene were rendered using diffusive, ambient, specular and emissive lighting, Goraud and Phong shading, and texture mapping.
- **Library Maintenance System [OOP, C++, STL, UML]**
  Led a team of three members to design and implement a library maintenance system. The system supported standard operations including check-in, check-out, performing search and placing holds. **UML** was used to capture **design artifacts** and **STL** was used during the implementation stage.
- **Multithreaded ATM [C++, POSIX Threads, Synchronized Queues]**
  Played lead role in the design and development of a multithreaded ATM server using **POSIX threads**. Work distribution was modeled after the **Master-Slave** paradigm. A **thread pool** was used to schedule transactions. The server utilized a **Producer Consumer Queue** to process priority based transactions.
- **Human Resource Management Database [ER Modeling, Oracle, Java, JDBC]**
  Designed and developed a company personnel database using Oracle. **Entity Relation Modeling** was used during the design phase. **Semantic** and **referential integrity** constraints were used to meet business requirements. Front end was implemented in Java with **JDBC** to connect to the database.
- **Distributed Fault Tolerance [IPC, Sockets]**
  Implemented a **two-phase commit** protocol for achieving atomic-commit during distributed transaction management. **BSD Sockets** were used to exchange messages between the coordinator and the work processes.
- **Multitasking Operating System [Process Control, IPC, Synchronization, Interrupt Handling]**
  Designed and implemented various features of an operating system on an IBM-370 architecture. The features included **Memory Management**, **Multi Programming Process Control**, **Inter Process Communication** and **Synchronization**. The operating system had the capability of process creation and destruction, **scheduling** and **interrupt handling**.

1992 - 1994 Research Assistant, Vascular Dynamics Lab, BME - The University of Akron

- **Vascular Hemodynamics [C, MATLAB]**
  Developed software modules to analyze turbulent, shear and normal forces downstream of an in-vitro model of a stenosed coronary artery.
- **Physiological System Modeling [MATLAB, VIS-SIM]**
  Developed a **contractility-impedance model** of the cardiovascular system to evaluate parameters required to **diagnose cardiac dysfunction**.

  Developed a model to study **ventricular-vascular coupling** (VVC). The model was used to determine **afterload** characteristics that will maintain optimal VVC during cardiac dysfunction.

  Developed and validated a model of **esophagus** peristalsis to help diagnose **swallowing and respiratory disorders**.

1991 - 1992 Software Engineer, DOE Project - Govt. of India, SBME – IIT Bombay

- **Object Detection Software [C, MATLAB]**
  Designed and implemented an object detection software toolbox to perform object detection and matching. Used to apply multi-level thresholds, segmentation, correlation and **Fourier Mellin Invariant Descriptor** (FMID with log-polar sampling) on 2D images.

WHITE PAPERS

- **Knowledge Representation** in Bioinformatics - Ontology Modeling and Inferencing with RDF, RDFS and OWL
- **Gene Regulatory Networks** and Network Biology
- **Jena 2 Framework** for Creating, Storing, Querying and Reasoning with Ontology Languages
- Using **Protégé** to Model and Instantiate **BioPAX Ontology**
- Network Analysis of the **Integrated Signaling Pathways in Cancer**

PRESENTATIONS

- **Gene Expression Analysis** and Classification using Oligonucleotide Microarray Data
- Molecular and Neurochemical Basis of the **Alzheimer's Disease**
- **DNA Repair** Mechanism of DNA **Polymerase Y** Family
- **Phylogenetic Analysis** of Human **GPCR Family**
- **CYP-450 Enzymes** - Drug Metabolism, Polymorphism and Targeted Medicine
- **Regulation of VEGF Transcription** - Role in Angiogenesis and Cancer Therapeutics
- **Java Server Faces** (JSF) - An MVC/Bean Component based Framework for Building Dynamic and Modular Web Applications

EDUCATION

PhD, Biomedical Engineering (Specialization: Image Processing), 1999. GPA: 4.0/4.0
The University of Akron, Akron, Ohio.
Dissertation: Retrospective Registration of Multimodality Brain Images using Multiresolution Decomposition.

Advanced Post Masters Certificate, Computer Science, 2006. GPA: 4.0/4.0
Johns Hopkins University, Baltimore, Maryland.
Specialization: M/C Learning, Bioinformatics

MS, Computer Science (Specialization: Software Engineering), 1999. GPA: 4.0/4.0
The University of Akron, Akron, Ohio.
Project: Idioms, Patterns and Frameworks in the Development of Reusable Object Oriented Software Components.

MS, Biomedical Engineering (Specialization: Vascular Dynamics), 1994. GPA: 4.0/4.0
The University of Akron, Akron, Ohio.
Thesis: Turbulent Hemodynamic Forces Downstream of the Stenosed Coronary Arteries: An *in-vitro* Study Using 3D-LDA.

B Tech, Mechanical Engineering, 1991
Indian Institute of Technology, Bombay, Mumbai, India.
Project: Role of Micro-circulation in Physiological Thermal Regulation: An *in-vivo* Study using LDA.

PROFESSIONAL TRAINING

- **Enterprise Application Development using Struts and J2EE**, Trivera Technologies
- **Portal Based Application Development Using RAD**, IBM Educational Services
- **Oracle 9i: Programming Using PL/SQL**, Oracle University
- **Architecting and Designing J2EE Applications**, Sun Educational Services
- **Object Oriented Analysis & Design Using the UML** - Rational University
- **Rational Unified Process** - Rational University
- **GUI Construction with Java Foundation Classes** - Sun Educational Services
- **Implementing Java Security** - Sun Educational Services
- **Entrez System and Powerscripting**, National Center for Biotechnology Information

CONFERENCES

- Attended **Java One Conference, '99, '00**, San Francisco, California
- Attended **SIGS Conference for Java Development '98**, **'99,** San Jose, California.

- Attended **SIGS Conference - XML One '99,** Santa Clara, California.
- Presented a research paper entitled - Registration of Brain Images using Phase Only Feature Correlation, during the **BMES ’98 Conference**, Cleveland, Ohio.
- Attended **ACM Object Oriented Programming, Systems, Language and Applications (OOPSLA’ 97) Conference**, Atlanta, Georgia.

CURRICULUM VITAE
Sept 2006

Dr. Jennifer Walsh Weller

Current Position/Address:
Associate Professor
Dept. of Bioinformatics and Computational Biology
George Mason University
10900 University Blvd MS 5B3
School of Computational Sciences, PWI rm 328E
Manassas, VA 20110
TEL: 703-993-8329
email: jweller@gmu.edu

Professional research experience:

Current

June 2002 – present. Associate Professor in the School of Computational Science at George Mason University at the Prince William campus in Manassas VA. My research and teaching interests are focused on the design, generation and analysis of gene expression data from high-throughput platforms, understanding and controlling sources of variation in the data, and the storage, organization integration of this data with other data types (genetic, phenotypic, environmental, clinical etc). I am PI on one active grant from the NSF (OpenGeneX) and co-PI on an active grant from NIGMS (with PI Gibas).

Government

May 2002-June 2003. Scientific Advisor and Director of Bioinformatics for the Epidemic Outbreak Surveillance project funded by the USAF/SGX. The project is described briefly below.

Academic

June 2002-July 2003. On institutional leave from GMU in order to serve as Scientific Advisor for the EOS project. The project designed and did prototype testing of a microarray to monitor the outbreak of several respiratory infections, including adenovirus and influenza virus causative agents, among basic military trainees. The study used standard clinical assessment, antibody, PCR and custom Affymetrix GeneChip^{TM} platforms to establish the cause of illness.

September 2000- May 2002. Research Assistant Professor at the Virginia Bioinformatics Institute at Virginia Tech University. At the time I joined it, this institute was 'virtual'. My primary roles were to oversee the design of the experimental laboratories with the architects, design core capabilities and hire personnel for the Core Genomics Laboratory (of which I was interim Director), recruit faculty and support personnel for the institute, and work with other new faculty to initiate programs and obtain funding. Six grants in which I played a major creative and writing role were funded in the first 18 months. I also had a position as adjunct assistant professor in the Biology Department (desirable in order to meet collaborators and students). I was primary author and PI of an NSF grant for the 'OpenGeneX' project, awarded by the NSF in May 2002, which transferred to GMU with me and which is ongoing at this time (terminates May 2006).

NFP

June 1999-August 2000. Senior Research Scientist in the molecular genetics group at NCGR, the National Center for Genome Resources, in Santa Fe, NM, promoted in August, 1999 to Program Leader for Structural Genomics, acting as interim program leader for Gene Expression and then promoted to group leader of the Gene Expression group in February 2000. The projects I managed included a large EST pipeline and analysis project for the SR Noble Foundation ('MGI' and 'XGI'), and the internally-funded project for a gene expression information system ('GeneX'). I was primary author and PI on an NSF grant for the Gene Expression development, which was awarded in October of 2000 (transferred to NCGR at their request). I oversaw one PhD student from the University of New Mexico, Peter Hraber, who successfully defended his thesis in May 2001.

Industrial

1997-1999 Senior Research Scientist at PE GenScope, a Center of Excellence of PE Biosystems; the group provided transcript imaging data to the pharmaceutical industry. Scientific duties included establishment of PCR protocols to meet standards of reproducibility for the cDNA-AFLP technology; protocol development for production of the samples for bulk cloning in a sequencing project that provided baseline sequence data and SNP information for rat, mouse and human tissues. A major accomplishment was the production of 30,000 gene tags for the rat genome in six months, giving GenScope the largest such data-base in the world at that time. Laboratory management duties included training of technical associates, maintaining day-to-day operations of the molecular biology laboratory, and maintenance of database entry, editing and updating for the sequencing project. Production team duties included improving the sequencing project technology sufficiently to save half of the budgeted cost in two months; cutting the time to project completion by one-third, establishing ISO9000 accountability and GLP and GMP standards within our operating unit; writing SOPs, and working with software engineers to describe and implement sample handling, data flow and data processing and report production requirements into the LIMS and proprietary data analysis programs PE GenScope produced.

In January 1999 PE GenScope became part of Celera Applied Genomics, headed by Dr. Craig Venter.

1994-1997 Research Scientist at Perkin-Elmer/Applied Biosystems Division- Agricultural Applications Group in Foster City CA. My primary research and development duties were to convert the PCR-based molecular genetic markers called AFLPs from a manual, radioactive detection mode to a fluorescence-based automated system. I provided support for data analysis in the technical manual in the form of tutorials. Several extensive collaborations were undertaken, and data exchange managed, to demonstrate the utility of the technology. One such joint project was the generation of an *Arabidopsis thaliana* map having 1000 markers, of which I provided half. A strong customer education component was a responsibility of the job, including providing research communications, giving scientific seminars, giving presentations at meetings, designing the training course for the Applications Specialists and the training of telephone support personnel to give knowledgeable and accurate help to customers. I was the sole R & D scientist involved in this effort.

Graduate Courses Taught at GMU

BINF 633	Molecular Biotechnology and Bioinformatics Tools*
BINF 636	Microarray Design Analysis
BINF 637	DNA Forensics*
BINF 702	Research Methods (Biostatistics)
BINF 704	Graduate Research Colloquium
BINF 705	Research Ethics
BINF 733	Microarray Data Analysis
BINF 739	Databases for Bioinformatics (will become BINF650)

* Graduate courses also taught as Visiting Scientist at Korea University, Seoul, Korea Summer 2006.

Academic Research Experience

1990-1994 Postdoctoral Research Associate, MSU-DOE Plant Research Labs, Michigan State University and The Carnegie Institute for Plant Biology at Stanford University with Dr. Shauna Somerville. Two projects were initiated. The first was to generate subtractive cDNA and genomic libraries from near- isogenic barley lines that are resistant/susceptible to the powdery mildew disease, *Erysiphe graminis* f. sp. *hordei*, as a strategy for isolating the gene for resistance at the Ml-a locus, using the RDA technology. The second project was the genetic and physical mapping of the Ml-a locus using DNA fragment polymorphisms generated using random 10-mers as primers in the PCR reaction (RAPD or DAF markers).

1987-1988 Instructor of Biochemistry, University of Montana. Courses taught:

Biochemistry 382
Biochemistry Lab 485,486,490
Biochemistry 483

Evaluations may be obtained from:

Dept. of Chemistry
University of Montana
Missoula, MT 59812
USA

1986-1989. Graduate student in the laboratory of Dr. Walter E. Hill at the University of Montana. Research involved probing the detailed structure of specific regions of 16S rRNA *in situ* in the 30S ribosomal subunit of *E.coli*, using cDNA oligomers. Regions of interest were then tested for various functional activities in the presence and absence of the cDNA oligomers.

1979-1982. Graduate student in the laboratory of Dr. Kensal van Holde at Oregon State University. Structural changes occurring in chromatin during gene expression were investigated. Metabolically manipulable genes in *Saccharomyces cerevisiae* allowed specific induction and repression of targeted genes.

August 1979- September 1979. Graduate student with Dr. Barbara Hamkalo during the Woods Hole MBL Physiology post-course. Oocytes of the surf clam, *Spissula solidissima* were spread on em grids; areas active in transcription during early development were studied.

1976-1979 Undergraduate research assistant in the laboratory of Dr. Walter E. Hill at the University of Montana. Research involved physical studies of the 30S subunit of the *E. coli* ribosome, with and without the protein S1.

Educational Training:

B.Sc. Chemistry, 1979 - University of Montana

Marine Biological Laboratories Physiology Course, Woods Hole, MA. 1979

Cold Spring Harbor Laboratory Yeast Genetics Course, Cold Spring Harbor, New York. 1980

M.Sc. Biochemistry and Molecular Genetics - Oregon State University (1979-1982, degree awarded 1986)

Ph.D. Biochemistry - University of Montana, April, 1990

Postdoctoral experience- with Dr. Shauna Somerville at two institutions:

DOE-Plant Research Laboratories
Plant Biology Building
Michigan State University
East Lansing, MI 48824 USA
Telephone: (517)-353-9182

The Carnegie Institute for Plant Biology
290 Panama St.
Stanford University
Stanford CA 94305 USA
Telephone: 415-325-1521

Honors and Awards:

UM Regents Scholarship (1976-1977)
UM Honors Scholarship (1977-1978)
Hetler Memorial Award (1978)
Watkins-Morton Scholar (1978-1979)
Awardee on MBL Physiology Training Grant (1979)
ASM Presidents Fellowship (1981)
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)

Adjunct Professor of Biology at the University of New Mexico (Feb. 2000)
Adjunct Professor of Biology at Virginia Tech (March 2001)

Membership in Professional Societies:

The American Association for the Advancement of Science
The American Society for Microbiology
The International Society of Computational Biologists (ISCB/ISMB)

General Research Interests:

The biophysics, molecular biology and biology of gene expression and regulation, at the transcriptional and translational level; signal transduction in the host/pathogen response; the application of molecular genetic markers in large or previously unmapped genomes and the use of molecular markers to assess the composition and diversity of populations. The development of computational tools that allow the tracking, merging and multi-component analysis of biological and genetic information.

Publications

Articles in reviewed journals or proceedings:

1. Davie, J.R.,Saunders, C.A., Walsh, J.M., and Weber, S., "Histone acetylation in the yeast, S. cerevisiae", Nucleic Acids Research, 9, 3205-3215 (1981).
2. Weller, R., Weller, J.W., and Ward, D.M. "16S rRNA Sequences Retrieved As Randomly Primed cDNA from a Hot Spring Cyanobacterial Mat Community", Applied and Environmental Microbiology, 57, 1146-1151 (1991).
3. Weller, J. and Hill, W.E "Probing the initiation complex formation on *E. coli* ribosomes using short complementary DNA oligomers". Biochimie.73(7-8):971-81 (1991).
4. Weller, J.W. and Hill, W.E. "Using Complementary Oligodeoxyribonucleotides to 16S rRNA as Probes of Dynamic Changes in rRNA Conformation in the 30S Subunit of the E. coli Ribosome". Biochemistry, 31, 2748-2757 (1992).
5. Weller, J.W. and Hill, W.E.,"The Structure of the Decoding Region of 16S rRNA in situ as Determined With Hexameric cDNAs". Journal of Biological Chemistry, 269 (30), 19369-19374 (1994).
6. 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).
7. 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.
8. 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.
9. Waugh, M., Hraber, P., Weller, J.W., Inman, J., Farmer, A. Sobrall, B.W. "The Phytophthora Genome Initiative" NAR Database Issue, 2000.

10. 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.
11. 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.
12. 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.
13. Mangalam, H., Stewart, J., Zhou, J., Schlauch, K., Waugh, M., Chen, G., Farmer, A., Colello, G., Weller, J. "GeneX: An Open Source gene expression database and integrated tool set" IBM Systems Journal, 40(2) 552-569.
14. 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.
15. 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.
16. 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..
17. 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.
18. Ratushna, V., Weller, J., Gibas, C. "Secondary structure as a confounding factor in synthetic oligomer microarray design" *BMC Genomics*(2005) 6:31.
19. 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.
20. 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 Amercia.
21. Higgs BW., Solka JL., Weller J. (2005) Deriving Meaningful Biological Structure from Spectral Embedding and Clustering. *Computing Science and Statistics*. 37.
22. 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.
23. Kumari, S., Verma, L., and Weller, J, "AffyMAPSDetector: A Tool To Detect SNPs In Affymetrix GeneChip^{TM} Expression Arrays" submitted to *BMC Bioinformatics*.
24. Deshmukh, H. and Weller, J. "Probe based data cleansing for Affymetrix arrays based on biophysical characteristics" submitted to *Bioinformatics*.

Book Chapters

Hill, W.E., Weller, J.W., Gluick, T., Merryman, C., Marconi, R.T., Tassanakajohn, A.,Tapprich, W.E., "Probing Ribosome Structure and Function by Using Short Complementary DNA Oligomers" in The Ribosome. Structure, Function and Evolution.(Eds. Hill, W.E.,

Dahlberg, A., Garrett, R., Moore, P.B., Sclessinger, D., and Warner, J.R.) pp 253-261. 1990 ASM Publications, Washington, D.C.

Bates, S.R.E., Knorr, D.A., Weller, J.W. and Ziegle, J.S. "Instrumentation for Automated Molecular Marker Acquisition and Data Analysis." in The Impact of Plant Molecular Genetics (Ed. Sobral, B.) 1996 Birkhauser, Boston

Weller, J.W. and Reddy, A.S., "Fluorescent Detection and Analysis of RAPD Amplicons Using the ABI Prism™ DNA Sequencers" in Fingerprinting Methods Based on Arbitararily Primed PCR in the Springer Lab Manual series (Eds. Bova, R. and M.R. Micheli) pp 81-92. 1997 Springer-Verlag, Berlin Heidelberg New York.

Weller, J.W. and Robertson, J.R. , "An Introduction to PCR Primer Design and Optimization of Amplification Reactions" in Forensic DNA Profiling Protocols from the Methods in Molecular Biology series (Ed. Lincoln, P.J. and J.Thomson) pp121-154 . 1998 The Humana Press, Totowa, New Jersey.

Giese, H., Hippe-Sanwald,S., Somerville,S. and Weller,J. "*Eriysiphe graminis*" in The Mycota series (Eds. Carroll,G.C. and Tudzynski,P.) Chapt 4 Part B, 1997 Springer-Verlag, Berlin Heidelberg.

Selected Abstracts and Presentations

Chen, S. Yee, A., Weller, J., MacFadden, S., Read, S., Johnson, R., Gyles, C., De Grandis, S. (1996) "Molecular Typing of Verotoxigenic Eschericia coli Using Amplified Fragment Length Polymorphism (AFLP) Analysis". American Society of Microbiology. Miami, Florida, 1996.

Flood, S.J.A., Weller, J., Sharaf, M., Green, R., Wada, A., Izumiya, H., Watanabe, H., Paszko-Kolva, C. (1996) "Investigation of E. coli O157:H7 Epidemic Samples from Japan using Genomic Fingerprinting Techniques and Genetic Based Typing Methods" . American Society of Microbiology. Miami, Florida, 1996.

Casa,A.M., Mitchell,S.E., Dean,R., Kresovich,S.K. Jester,C., Weller,J.W. and Ferreira, ME.(1997) "Fluorescence-Based AFLP Genotyping of Cultivated Rice and Its Wild Relatives" Plant Genome V, Abstract #74. San Diego CA, Jan 11-16, 1997.

Walsh-Weller, J., Johnston,E., and Millam,J. (1997) "AFLP Fluorescent Markers for Mapping a Family of Yellow-Naped Amazons: a Comparison of the Marker Density and Inheritance Patterns of Fluorescent AFLP Markers and VNTR-RFLP Markers" Plant Genome V, Abstract #83. San Diego CA, Jan 11-16, 1997.

Walsh-Weller,J., Sharaf,M., Inagaki, Y., Izumiya,H., and Watanabe,H. (1997) "Application of Fluorescent AFLP Analysis to the Classification and Identification of *E coli* O157:H7 Strains from the Recent Outbreak in Japan" Plant Genome V, Abstract #84. San Diego CA, Jan 11-16, 1997.

Bodeau, J., Baumhueter, S., Spier,E., Weller,J., Hwang,S., Gilbert,D. (1998) "PE GenScope: Transcript Imaging", Functional Genomics meeting, Seattle, Washington Sept 10-11, 1998.

Sturgill, D., Weller, J.W., and Gibas, C. (2002) " Systematic Genomic Comparison of Three Brucella Spp. and a Data Model for Feature-Based Multiple Genome Analysis." ISMB Aug 2002, Edmonton Canada (Weller name inadvertently left off of printed abstract for poster 192A).

Deshmukh, H., Mangalam, H., Weller, J. (2004) "PyROOo: an interface to GeneX for S preadsheet Functions" MGED 7, Toronto, Canada, Sept 8-11, 2004.

Carr, D.A., Deshmukh, H., Weller, J. (2005). ISMB 2005, Detroit MI. June 24-28, 2005

Deshmukh, H., Carr, D.A., Weller, J. (2005). ISMB 2005, Detroit MI. June 24-28, 2005
Kumari, S., Verma, L., ., Weller, J. (2005). ISMB 2005, Detroit MI. June 24-28, 2005

Weller, Jennifer. "AffyMAPSDetector: Finding and Applying SNP information for probes in Affymetrix GeneChips" Seminar at NCI Nov. 3rd, 2005.

Grant Funding History (* currently active, **)

Joint development project (VBI/U Nevada at Reno/SR Noble Foundation), PI J Weller "Collaborative development of an EST database and analysis pipeline: ESTAP", 2000-2002, $399,354.

NSF CISE, PI Ramakrishnan, "Expresso, a microarray experiment management system", co-PI for 5% effort (salary recovery) 2001-2005.(not currently actively engaged)

NSF PGRP, PI Mendes, " An Integrated Approach to Functional Genomics and Bioinformatics in a Model Legume", senior personnel for 10% effort (salary recovery while at VBI, did not migrate to GMU), 2001-2005.

GenXpediter: An upload tool for gene expression data to the GeneX database Virginia Tech $17,100 VT and $5700 matching VBI 12/31/01-12/30/02. Current ASPIRES program and Virginia Tech

* NSF-BDI "Open GeneX: Expanding the Toolkit of an Open Source Gene Expression Informatics System."George Mason University $751,260 05/01/02 – 04/30/04. Weller commitment: 2.4 months per year

** NIH ZRG1 BST-D "Biophysical Optimization of Oligonucleotide Microarrays" R01 GM072619-01. co-PI (with Dr. Cynthia Gibas of VPISU, Blacksburg, VA). Scores are as follows, the budget is currently under administrative review: *SRG Action:* Priority Score: 153 Percentile: 9.7 # (funding level cutoff is 16% for this section).

Research Advisor
PhD and MS students

Peter Hraber (primary advisor; PhD awarded June 2001, University of New Mexico).
Brandon Higgs (PhD awarded Dec 2005, GMU)
Thomas Heiman (PhD awarded Dec 2005, GMU)
Hrishikesh Desmukh (PhD awarded May 2006, GMU)

Yuying Tian (MS awarded May 2002 VPISU)
Sunita Kumari (MSc awarded May 2004, GMU)
Sarah Bittenbender (MSc awarded Aug 2005, GMU)
Karen Schwartz (MSc awarded May 2005 GMU)
Vasuki Palanigobu (MSc awarded Aug 2005 GMU)
Farhana Alam (MSc awarded Dec 2005)
Rachel Brower (MSc May 2006)
Shaun Rabah (MSc, May 2006)

Postdoctoral Fellows

Dr. Karen Schlauch (Nov 2000-July 2002, now a professor at Boston College School of Medicine)

Detailed Research Interests

Wet-lab: My primary research focus in the first five years of my professional life was method development for genome-wide assessment of transcript prevalence. While chips and arrays are convenient and readily available ways to assess the levels of all known transcripts, albeit at a price, there are methods such as SAGE, MPSS and cDNA-AFLP that allow one to assess not only previously characterized transcripts but to obtain data about unknown transcripts as well. I was also been involved in a project with the optical sciences and engineering research group at VPISU (Virginia Tech) to work on micro-bead based arrays using Q-dot identifiers. These methods share the characteristic that they generate very large amounts of data that require a significant amount of pre-processing before they can be assessed for biological meaning.

Informatics: As various projects began to produce large amounts of gene expression data several years ago, it became clear that the available informatics tools to handle such data and to manipulate it and obtain informative results were extremely limited. I accepted a position at NCGR to begin developing such resources. This was the genesis of the GeneX project, which is still an ongoing and funded project in my group. Because in non-model systems ESTs are usually the basis of microarray construction, and since the existing EST analysis pipelines incorporated an inadequate level of sequence quality control, I was also the PI for an EST analysis pipeline that incorporates such controls, called ESTAP. My primary professional contributions to these projects include data modeling, use-case and requirements gathering, schema design and instantiation and analysis tool integration. In addition there are the inevitable project management and coordination activities required by a PI. As we have expanded efforts to design and interpret data from microarrays my collaborator and I, Dr. Cynthia Gibas, have been returning to our early biophysical training and are incorporating biophysical constraints into oligomer design and data analysis methods, the subject of a recent joint proposal to the NSF.

Statement of Teaching Interests (short version)
Teaching is an activity that I find enjoyable as well as challenging and it is a necessary activity in order to refine my own communication and thinking skills. Thus I have always sought opportunities to design and present workshops, seminars, and short courses at my places of employment and local community. In the past four years I have developed two and participated in teaching another three semester-length graduate-level courses for the bioinformatics program at GMU, including a research methods that includes biostatistics, BINF 703 for microarray design, BINF 636 that uses bioinformatics tools as a way to discuss modern biotechnology, BINF 637 which is a DNA Forensics course, BINF 733 on microarray analysis methods, and a course in the design and implementation of biological databases, BINF 739. Our department is currently organizing a semester course on the biophysics of proteins and nucleic acids. I have not taught University undergraduates since I was an instructor at the University of Montana. Teaching evaluations are available upon request.

Service Contributions

Meetings Organized

Oct 17, 2002 Organizer of the Virginia Bioinformatics Consortium Genex-dev meeting at George Mason University. Developers from Virginia, Cal Tech, and New Mexico met for a day to discuss progress and needs for continued progress in a gene expression database and information system.

Interface 2004, May 29-30, Baltimore MD (organized keynote and workshop speakers)

Curriculum Development

New courses developed

Microarray Methods, BINF 636 – a course aimed at teaching students the wet lab, instrumentation and manufacture, bioinformatics and experimental design methods required to construct a microarray that can answer fundamental scientific questions.

Data modeling for Bioinformatics, BINF 739 (with Dr. Curt Jamison) – a course emphasizing data models that meet basic design requirements of the scientific methods and implementation using the ER model and relational DBMS, as well as an introduction to the structure of the most widely used biological databases.

Academic programs developed or substantially modified

Molecular Biotechnology, BINF 633 – This course was previously taught as primarily a DNA molecular biology methods class, I added strong components of biochemistry and instrumentation with data readout and quality control as part of the analysts /bioinformaticians challenge.

Journal editing: ad hoc reviewer for a number of journals including Bioinformatics, Genome Research, Genome Biology, BMC Genetics, Functional Genomics.

Grant Review panelist

NIH; SSS-H ZRG1 (2004),BMDA ZRG1 (2004), BDMA (2006)
NSF: PGRP (2004, 2005), INFORM (2003-2005), BDI (2006)

SCS committees/ responsibilities

BINF Faculty hiring committee 2003-2004
BINF Graduate student admissions committee 2003- present)
BINF and SCS Weekly and BI-Semester Faculty meetings
BINF Laboratory Safety and Organization committee (2004- present)
BINF Curriculum Committee (2005- present, now chair)

Service to other universities (program review, etc.)

Nov 5, 2002 Invited panelist/advisor for the Louisiana CERT-CIBI group, an NSF-EPSCoR funded consortium in the planning grant stage of developing a medical bioinformatics program in their state.

NSF-EPSCoR program review as member of the scientific advisory board for UN-Reno. May 20, 2004 (I was a member of this Board in 2002 and 2003 as well).
NSF Maize Chromatin Scientific Advisory Board member (Mar 2005- present)
NSF workshop for Arabidopsis Data Integration (invited participant), meeting in April 2005 at TIGR, organized by Chris Town.
Office of Naval Research, NSWCDD B-10; external reviewer of in-house laboratory research (IHLR) projects, Oct 2004.

Entrepreneurial Activities

I have met with representatives from Celera Pharmacogenomics, MITRE Corp., GeneLogic Corp., IDD (a cancer diagnostics lab in San Antonio TX) and BoozAllenHamilton in order to discuss activities of mutual interest that might lead to funding of graduate students, transfer of research ideas to the industrial setting and to find out what computational tools scientists in industry most feel they need. This has not resulted in any contracts as of yet, but has given rise to several jointly submitted grant proposals (SBIRs).

Synergistic Activities:

1. Project Leader for the gene expression analysis system GeneX (http://www.ncgr.org/research/genex) currently funded by NSF-BDI. GeneX is an open source database and query/analysis interface developed at NCGR.
2. Project leader of an EST analysis system development team for collaborative EST sequencing projects at NCGR (http://www.ncgr.org/research/mgi and http://www.ncgr.org/research/pgi) and at the Virginia Bioinformatics Institute at the Virginia Polytechnic Institute and State University (http://www.vbi.vt.edu/estap).
3. Development of a high-density *Arabidopsis thaliana* genetic map using the Landsberg er. x Columbia gl. RI lines using AFLP markers (~1000 markers) has been made available to the community through the TAIR Web site (http://www.arabidopsis.org).
4. Lectured in "Dreamcatchers", a three-evening mini-course in science (molecular genetics of corn, with hands-on sample prep and PCR) in June 2000, for Native American middle-

school age children, an enrichment program sponsored by the AISES and Sandia National Labs.

5. Instructor in the "Database Design and Development for Genomics Research" course sponsored by the BioPharmaceutical Center Institute in Madison WI, June 29-July1, 2000. A beginners course for biologists interested in bioinformatics and for computer scientists interested in bioinformatics.
6. Organizing committee for an O'Reilly conference on Bioinformatics schedules for January 2002 (http://conferences.oreilly.com/biocon/cfp.html).
7. Workshop organizer and one of two instructors for a course titled "The analysis and informatics of gene expression data" funded by the NSF and the SR Noble Foundation, Aug 19-21, 2002 in Ardmore OK.
8. Scientific advisor on bioinformatics to the USAF Surgeon General's office for the Epidemic Outbreak Surveillance project May 15, 2002 – June 30, 2003, Falls Church VA.
9. Conference organizer for Interface 2004, Baltimore, MD, May 26-29, 2004

APPENDIX B
EXTERNAL ADVISORY COMMITTEE

LETTER OF EVALUATION OF PROPOSED PROGRAM

Nov 28th, 2006

To: Dr. Larry Mays and Dr. Cynthia Gibas, organizers of the PSM-Bioinformatics proposal for UNC-Charlotte.

Subject: Action Recommendation by the External Advisory Board concerning the proposed Professional Science Masters program in Bioinformatics at UNCC.

External Advisory Board members: Dr. James Bradburne, Dr. Satyendra Kumar, Dr. Jennifer Weller

The EAB complements the department members involved in preparing the proposal for producing a well-written, lucid and convincing justification of the proposed program and having a strong educational plan for implementing it. The board members believe that the program should have little difficulty in attracting students and providing them with the training necessary to make them competitive in a biotechnology environment that is increasingly relying on computational skills in order to diminish the number of false leads and time to market of products. The criticisms in the remaining part of this document are offered in the interest of improving the program and making it more competitive, not as a way to question the viability of the program.

With respect to justification of the program, the board members offer the following suggestions: the argument for the demand from students and employers should be elaborated by pursuing data through questionnaires for both of undergraduate students and companies throughout the region. The student questionnaires should target not only the participating departments and disciplines, but those spanning both the life science and non-life science areas, particularly engineering. The corporate questionnaires should be afforded the same targeting flexibility. For example, in addition to biotechnology, companies with any significant medical, environmental or health and safety components should be part of the sampling. To ensure fast turn-around on responses it was suggested that the questionnaires be posted on the department Web page and some coaxing of responses might be achieved by telephoning hiring managers at a number of companies to request their attention.

The educational program itself has an excellent foundation: the core courses provide a solid and flexible basis for many types of specialization. Some of the questions concerning content were related to the rather general course descriptions (we realize that Syllabi are not yet worked out). For example, there seems to be a lot of overlap between the Cell and Molecular Biology course and the Biochemistry and Biophysics course, and the descriptions mentioned nucleic acids and proteins rather more explicitly than the other macromolecules, and signaling seemed to get the lion's share of the small molecule attention. Similarly the descriptions for OO Programming/Algorithms and Database courses need to be revised for course contents. Two areas that we strongly urge the curriculum committee to incorporate are network analysis, perhaps as part of systems biology, and data summarization and visualization, perhaps as part of statistics.

Although there are not a large number of such programs nationwide the trend for creating such degree programs is on the upswing. We urge the department to consider 'branding' its program by focusing on certain areas of excellence in the upper-level electives, perhaps by attempting to hire new faculty in these areas. There was considerable discussion as to what such a focus area would be, since in the absence of details on the demand from students and companies for bioinformatics expertise, as well as specific information about the companies that may come to Kannapolis it is not possible to tune the program very precisely, and there is the example of the rather narrowly-focused statistical genetics-based bioinformatics MSc at NC State, which may serve a narrow niche very well but has limited interest beyond that need. Areas discussed as likely to be needed across a wide range of research facilities and biotechnology companies included domains related to nutrition, metabolism and drug development such as toxicology, immunology, and clinical studies. More focused areas might include computational chemistry, cancer biology, molecular targets in cancer and host-pathogen interactions, in addition perhaps to device development. All of these areas appear to have broad applicability and will require complex systems or organism level understanding. Higher-level electives will provide the theoretical bases for these areas and internships will help in attaining the practical experience in working with the underlying technology/techniques.

The board members expressed concern that the internship program was unnecessarily focused on the development and success of the yet to be tenanted Kannapolis center. For a number of reasons, both the start-up and the training ability of these companies may be significantly delayed compared to the timeline of the suggested program. For example, the hiring and relocation of scientists may be more of a barrier than is realized, and most start-ups are small with the scientists rarely having time to train individuals with little to offer towards a looming delivery deadline. Internships should be investigated further afield than in the neighborhood of Charlotte, including other areas in North Carolina and in the region (such as Atlanta and DC/VA/MD). For example, internships at NCBI will allow interns to return to local companies with valuable skills.

The board members discussed how the risk of providing for internship sites might be diminished. For example, Dr. Gibas has lab expertise in designing microarrays, and Dr. Fodor in the analysis of such data. For most companies these are intermittent activities, in which they could save the hiring of dedicated personnel for short-term needs if well-trained interns or teams could help solve a problem or crunch through a dataset. A feed-forward part of the process might be to require such interns to not only perform the task but, on the business development side, identify either other potential customers (including a reasonable cost of the service and restrictions on data security) or a way to improve the process. In this way it might be possible for the department/university to become a useful service via the intern program, and things that faculty currently do as favors (free service) to their peers could be considered as intern projects done for or through companies.

The board members all concur that in the first few years of the PSM Program a majority of the students most likely will do faculty-guided projects and this use of faculty time

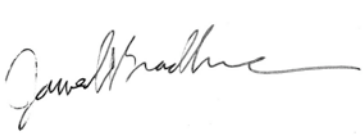
will be substantial. Because of this and the considerable administrative overhead to setting up the program, screening students and maintaining records as well as developing relationships with entities willing to train interns, we suggest that the PSM Program Coordinator be hired as quickly as possible. It is important that this individual manage the growth of the program in parallel with availability of faculty, their skills and time. This individual will need to design a strategy for development of the program as Kannapolis comes on-line, including activities such as meet and greet when companies arrive, and presentation of successful outcomes of internships along with the more basic 'what bioinformatics could do for you' overview. The faculty who are responsible for content cannot at the same time manage this part of the process. If the money for the Coordinator position is not available immediately the group should consider hiring a part-time consultant who will shoulder the screening/administrator burden.

The board had only minor revisions to suggest to the proposed degree requirements, and these have been conveyed to Dr. Gibas through an edited copy of the proposal, so the details have not been presented here (see the four pages of notes on the wiki site for details). The wiki site also has a proposed list of elective courses that can be developed to support the various specialization tracks outlined in the proposal.

The EAB congratulates the UNCC Bioinformatics faculty and staff for an excellent presentation and well-run discussions, and wishes them all success in this endeavor.

Jennifer W. Weller, Ph.D.
Bioinformatics and Computational Biology
George Mason University
Manassas VA 20110

Satyendra Kumar, Ph.D.
Senior Research Scientist
Applied Computer Science & Mathematics
Merck & Co.
West Point, PA 19486



James Bradburne, PhD
Clear Path Biomedical
801 Spring Mountain Way
Fort Valley, VA 22652

APPENDIX C
LETTERS OF SUPPORT

CHARLOTTE RESEARCH INSTITUTE
UNC CHARLOTTE

9201 University City Boulevard
Charlotte, NC 28223-0001
704.687.8284 (phone)
704.687.8285 (fax)
www.charlotteresearchinstitute.org

January 8, 2007

Larry Mays, Ph.D.
Director of Bioinformatics Research Center
204 Cameron Hall
UNC Charlotte
9201 University City Blvd.
Charlotte, NC 28223

Dear Dr. Mays,

The Charlotte Research Institute strongly supports your efforts to create a Professional Science Master's Degree Program in Bioinformatics. This degree program will fill a significant need for the biotechnology cluster that is developing in the Charlotte Region.

My organization works daily with regional, national, and international companies to create new research ventures, university partnerships with regional and national enterprises, and spin-off companies. We find that some of the best partnerships come when well-prepared graduates take research results directly to implementation at partner companies. The graduates of this new degree program will have deep knowledge in both cutting edge science and the workings and opportunities of the marketplace. They will have a significant impact on the growth of bioinformatics business in the Charlotte Region.

The proposal comes at a very opportune time. With the North Carolina Research Campus now under construction only 18 miles north of UNC Charlotte, this degree program will begin just as the first of an expected 100-200 biotechnology companies arrive in the Charlotte Region. This will be both an attraction for companies moving to the region and a resource as these businesses grow.

Again, I strongly support this proposed degree program and look forward to working with you to make it a strong resource for North Carolina and the Charlotte Region.

Sincerely,

Robert G. Wilhelm, Ph.D.
Executive Director
Charlotte Research Institute

UNCCHARLOTTE
The University of North Carolina at Charlotte
9201 University City Boulevard
Charlotte, NC 28223-0001

Department of Biology
704/687-8686

January 10, 2007

Lawrence Mays, Ph.D.
Professor of Computer Science
College of Computing and Informatics
The University of North Carolina at Charlotte

Dear Larry:

The Department of Biology is most pleased to support the proposed Professional Science Master's Degree in Bioinformatics. There is a critical need for such a program in our region, and this would train students to be successful at the interface between biology and computer science. I actually suspect that most of the students entering your new program will be our own successful biology majors, as well as biology majors from other institutions. We need more interdisciplinary programs of this kind developed at UNC Charlotte to best serve the students. Again, we are most excited about this proposal.

Sincerely,

Michael C. Hudson, Ph.D.
Professor and Chair of Biology
The University of North Carolina at Charlotte
9201 University City Blvd.
Charlotte, NC 28223
704-687-8694
704-687-3128 (fax)
mail to: mchudson@email.uncc.edu
http://www.bioweb.uncc.edu/Faculty/Hudson/

UNC CHARLOTTE
The University of North Carolina at Charlotte
9201 University City Boulevard
Charlotte, NC 28223-0001

Fax: 704/687-6416
E-Mail: adow@email.uncc.edu

Chairman
Mathematics & Statistics
704/687-4556

January 3, 2007

TO: Professor Larry Mays
Bioinformatics Research Center
UNC - Charlotte
Cameron Applied Research Center
9201 University City Blvd
Charlotte, NC 28223

Dear Larry:

I am writing in support of the proposed Professional Science Master's Degree in Bioinformatics. It is a very well designed proposal that should be excellent preparation for students in an exciting interdisciplinary field with tremendous opportunities for growth and employment. This kind of degree will be very attractive to math undergraduates who are looking for a quick entry into a great career as a professional scientist.

I am naturally interested in the selection of mathematical and statistics orientated courses in the curriculum since I think a solid foundation in these is an important component of such a degree. The courses look appealing to me and although I know you have your own highly qualified faculty to handle these courses, I can see that they would make for enjoyable and fruitful opportunities for program collaboration.

Many of our current doctoral students choose to complete the interdisciplinary Masters of Mathematical Finance program while completing their doctoral degree. The proposed Professional Science Master's Degree in Bioinformatics would also be a wonderful choice for doctoral students looking into a more interdisciplinary research focus.

I strongly support the implementation of this degree and look forward to increasing cross-fertilization for our students and programs.

Sincerely,

Alan Dow

Alan Dow

From: "Chu, Bill" <billchu@uncc.edu>
Date: Sun, 14 Jan 2007 15:39:36 -0500
To: "Mays, Lawrence" <lemays@uncc.edu>
Conversation: SIS department support of the professional master's program in Bioinformatics
Subject: SIS department support of the professional master's program in Bioinformatics

Dear Dr. Mays,

The Sofware and Information Systems Departments supports the proposed Master's program in Bioinformatics. We believe it is an excellent program with great promise of success.

Sinerely,

Bill Chu
Professor and Chair
Department of Software and Information Systems
UNC Charlotte

UNC CHARLOTTE
The University of North Carolina at Charlotte
Computer Science

To: Lawrence Mays, Ph.D.
Director, Bioinformatics Research Center
College of Computing and Informatics
University of North Carolina at Charlotte

From: Larry F. Hodges, Ph.D.
Professor and Chair
Department of Computer Science
College of Computing and Informatics
University of North Carolina at Charlotte

Date: January 11, 2007

RE: Professional Science Masters Degree Proposal

I fully support the proposed new Profession Science Masters (PSM) Degree in Bioinformatics. The fusion of courses in computing and the biological sciences will provide a number of exciting educational opportunities for our students in both computer science and the biological sciences at UNC Charlotte. This program will also strengthen our relationship with the North Carolina Research Campus being developed in Kannapolis as we prepare well-trained graduates for the jobs created by the over 100 biotechnology companies and labs that are expected to locate there.

APPENDIX D
BIOINFORMATICS IN THE NEWS

CHARLOTTE AREA
2004-2007

UNC CHARLOTTE IN THE NEWS

07/01/2006

Charlotte Research Institute opens Kannapolis satellite office near North Carolina Research Campus

LINCOLN TRIBUNE - Jason Saine

UNC Charlotte business portal to support bioinformatics development

CHARLOTTE - The Charlotte Research Institute (CRI) today celebrated "Charlotte Research Institute Day in the City of Kannapolis" with the opening of its satellite office at 201 Oak Ave., near the North Carolina Research Campus (NCRC) site.

Lynne Scott Safrit of Castle and Cooke North Carolina and CRI Executive Director Bob Wilhelm hosted a luncheon nearby the CRI office that featured a presentation on UNC Charlotte's role in the campus and its commitment to the support and redevelopment of Kannapolis in bioinformatics.

The opening of the office signifies increased efforts to leverage the resources of the NCRC and UNC Charlotte with partners in research and business development.

"Opening this office is a milestone in UNC Charlotte's involvement in an enormous endeavor that will transform Kannapolis and bring much greater attention and business to North Carolina's biotechnology industry," Wilhelm said.

To recognize the CRI's commitment in accelerating UNC Charlotte's development as a top-tier research university, Kannapolis Mayor Robert S. Misenheimer proclaimed June 29, 2006 "Charlotte Research Institute Day in the City of Kannapolis." Misenheimer also cited the CRI for its collaboration with industry, academia and government in the areas of bioinformatics, precision metrology, e-business technology, optoelectronics and optical communications.

"UNC Charlotte and the Charlotte Research Institute are charting new territory in research and development that will affect the way we live for generations to come," said UNC Charlotte Chancellor Philip Dubois, who delivered opening remarks. "But more importantly, the economic impact associated with the discovery of these technological advances will enhance the quality of life in Kannapolis and the Charlotte region right now. We're pleased to partner with the City of Kannapolis and play a part in the development of the North Carolina Research Campus."

Other speakers included Safrit; Lawrence Mays, director of UNC Charlotte's Center for Bioinformatics Research; and W. Steven Burke of the North Carolina Biotechnology Center.

UNC Charlotte's new Bioinformatics Center will provide computational research and educational programs to support the biotechnology efforts of the North Carolina Research Center in plant genomics, health and translational research, specifically with gene-related research in the areas of functional genomics, statistical genetics and proteomics. The university currently offers a bioinformatics track in its Information Technology doctoral program and plans to establish a master's program in bioinformatics to train highly qualified professionals to work in the biotechnology field.

The university provides additional resources for the NCRC through several organizations including:

- College of Information Technology
- College of Arts & Sciences
- College of Health and Human Services
- William States Lee College of Engineering
- Information and Technology Services - High Performance Computing and Network Communication
- Office of Technology Transfer – intellectual property, licensing, business startup.

For more information about the Charlotte Research Institute at UNC Charlotte, visit: http://www.charlotteresearchinstitute.com.

About the Charlotte Research Institute

NEWS RELEASES

UNC CHARLOTTE IN THE NEWS

NEWS BRIEFS

NEWS RELEASE

September 12, 2005

UNC Charlotte announces support of Kannapolis "Biopolis"
Plans announced at site of future North Carolina Research Campus

CHARLOTTE – The University of North Carolina at Charlotte today announced its commitment to support the redevelopment of Kannapolis in three main areas – bioinformatics, research in nutrition and health behavior, and education – as part of the newly-announced North Carolina Research Campus that will transform Kannapolis into a hotbed of high-tech jobs on the former Pillowtex corporate headquarters site.

The announcement was made at a 10 a.m. news conference attended by Philip L. Dubois, Chancellor of UNC Charlotte; Molly Corbett Broad, President of the University of North Carolina; David H. Murdock, Chairman and CEO of Dole Food Company and architect of the Kannapolis redevelopment plan, and other dignitaries.

According to Dubois, UNC Charlotte's new Bioinformatics Center is well positioned to provide computational research and educational programs to support the biotechnology efforts of the North Carolina Research Center in plant genomics, health, and translational research, specifically with gene-related research in the areas of functional genomics, statistical genetics, and proteomics. The university currently offers a bioinformatics track in its Information Technology doctoral program and plans to establish a master's program in bioinformatics to provide highly trained professionals to work in the biotechnology field.

UNC Charlotte's College of Health and Human Services also will provide support in the areas of nutrition and health behavior to bolster research programs spearheaded by sister institutions UNC Chapel Hill and NC State. UNC Charlotte currently offers a Ph.D. program in health services research – the only one in the state – to produce future experts who will focus on the heath of populations (people or communities) and how health technologies, organizational structures and processes, personal behaviors, and various social factors impact heath and well-being.

In addition, UNC Charlotte's College of Education will support the formation of a residential science and mathematics high school for high-achieving young women by providing a curriculum development team, graduate assistants in classrooms to strengthen and enhance instruction, and research to help determine effective science education programs and techniques for talented high school women.

"As this region's only research university, we are honored to play a leading role in shaping the success of the North Carolina Research Campus to enhance the intellectual capital – and economic development – of our region," Dubois said. "Under the leadership of Bioinformatics Center Director Larry Mays, College of Health and Human Services Dean Karen Schmaling, and College of Education Dean Mary Lynne Calhoun, our faculty across the board will provide invaluable expertise to our university partners and others involved in this effort," he added.

Chancellor Dubois noted that according to a memo from UNC President Broad, the North Carolina Research Campus is a key element in reshaping the Kannapolis region's economy. The centerpiece of the plan is a "biopolis" that will be a collaboration of the University's leading research campuses including UNC Charlotte, NC State and UNC-Chapel Hill.

The North Carolina Research Campus will include:

The Institute for Advanced Fruit and Vegetable Science – led by N.C. State and created in conjunction with Dole Food Company – to develop enabling technologies for research and education to help bolster the economic and horticultural potential for fruit and vegetable production in the southeastern United States;

A Nutrition Institute led by UNC Chapel Hill to focus on examining the relationship between nutrition and the brain, obesity, and cancer; and

A residential science and mathematics high school to attract and prepare young women for careers in science-related professions.

###

Media contact: Tony Hoppa, (704) 687-2143

APPENDIX E
LIBRARY CONSULTATION REPORT

UNC CHARLOTTE
J. Murrey Atkins Library

Consultation on Library Holdings

To: Dr. Anthony Fodor
College of Computing and Informatics

From: Joanne S. Klein
Reference Librarian, Engineering and Information Technology

Date: November 29, 2006

Subject: New Master's in Bioinformatics

Summary of Librarian's Evaluation of Holdings:

Evaluator: Joanne S. Klein **Date:** 11/29/06

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

Comments:

A search of the Atkins Library online catalog reveals the following holdings in support of this program. See the tables that follow. A search in the areas of Bioinformatics and related subjects retrieved 6139 pertinent items. Of this total, 1795 have been acquired since 2000, so this is a current and relevant collection. Because there is some overlap of subject headings, the actual total number of titles will be less than this, but the collection, especially if bolstered by ongoing purchases, is quite adequate to support this program. The Library owns or has electronic access to 388 journals and 1086 other electronic resources that support this program. See the second table which lists some of the most relevant journals in the collection. In addition, the library has approximately 20 electronic databases, many with links to full text articles, supporting the overall Computing and Informatics programs.

Joanne S. Klein
Evaluator's Signature

November 29, 2006
Date

Revised 12/19/2006
OAA jdp

Atkins Library Holdings in Areas Related to Bioinformatics
11/29/06

Subject Heading	All Books	Post 2000	Journals	Electronic Resources
Bioinformatics	56	40	4	23
Biomolecule*	67	15	3	14
Biophysical model*	11	7	0	0
Biotechnology	791	191	33	184
Cellular biology	192	50	19	40
Computational biology	75	48	5	25
Cytogenetic*	86	7	4	13
Genetics	1804	414	91	225
Genom*	386	208	27	77
Medical informatics	152	71	9	42
Microarray data	10	10	1	2
Molecular biology	878	181	67	216
Molecular sequenc*	87	40	1	10
Molecular structur*	371	126	29	61
Nucleic acid*	123	32	9	16
Nucleotide sequenc*	40	15	0	7
Oncogene*	33	6	5	7
Protein*	770	241	63	88
Proteom*	45	42	9	19
RNA	112	46	5	9
Ultrastructur* biology	50	5	4	8
Totals	**6139**	**1795**	**388**	**1086**

Revised 12/19/2006
OAA jdp

J. Murrey Atkins Library
Journal Holdings Specific to Bioinformatics
(* Journals Requested by Faculty)
November 29, 2006

Title	Format	Call#	Holdings
Algorithms for Molecular Biology	Electronic	n/a	v. 1 (2006) - present
Anatomical Record	HardCopy Electronic	QL801.A45 n/a	v.160 (1968) – v. 275 (2004) v. 247 (1997) – v. 281 (2004)
Annals of the New York Academy of Sciences	HardCopy Electronic	Q11.N5 n/a	v. 4 (1887) – present Some missing issues v. 300(1998) - present
*Annals of Statistics	HardCopy Electronic	HA1.A83 n/a	v. 1 (1973) – present v. 1 (1973) – present
*Annual Review of Biochemistry	HardCopy Electronic	QP501.A7 n/a	v.1(1932) – v. 73 (2004) Some missing issues v. 65(1996) - present
*Annual Review of Biophysics & Biomolecular Structure	Electronic	n/a	v. 25 (1996) – present
*Annual Review of Genetics	HardCopy Electronic	QH426.A54 n/a	v. 1(1967) – v. 37 (2003) v. 30(1996) - present
Annual Review of Genomes and Human Genetics	Electronic	n/a	v.2 (2001) - present
*Applied and Environmental Microbiology	HardCopy Electronic	QR1.A6 n/a	v. 31 (1976) – present v. 31 (1976) - present
*BMC Biochemistry	Electronic	n/a	v. 1 (2000) – present
*BMC Bioinformatics	Electronic	n/a	v. 1 (2000) – present
*BMC Evolutionary Biology	Electronic	n/a	v. 1 (2001) – present
*BMC Genomics	Electronic	n/a	v. 1 (2000) - present
BMC Medical Informatics and Decision Making	Electronic	n/a	v. 1 (2001) - present
*BMC Microbiology	Electronic	n/a	v. 1 (2001) - present
*BMC Molecular Biology	Electronic	n/a	v. 1 (2000) - present
*BMC Structural Biology	Electronic	n/a	v. 1 (2001) - present
*Biochemical Journal	HardCopy Micro Electronic	QP501.B47 QP501.B47 n/a	v.217 (1984) – present Some missing issues v.321 (1997) – v. 336 (1998) v. 1 (1906) - present
*Biochemistry	HardCopy Electronic	QP501.B5x n/a	v. 1 (1962) – present v. 1 (1962) - present
Biochimica et Biophysica Acta	Electronic	n/a	v. 1598 (2002) -

Revised 12/19/2006
OAA jdp

			present
*BioEssays	Electronic	n/a	v. 18 (1996) – present
*Bioinformatics	Electronic	n/a	v. 12 (1996) - present
*Biophysical Chemistry	Electronic	n/a	v. 60 (1995) - present
*Biophysical Journal	Electronic	n/a	v. 1 (1960) – 1 year ago
*Biopolymers	Electronic	n/a	v. 39 (1996) - present
*Biostatistics	Electronic	n/a	v. 1 (2000) - present
Bio/technology	HardCopy Micro	TP248.3.B557 TP248.3.B557	v. 7 (1989) – v.14 (1996) v. 1 (1983) - v. 6 (1988)
Biotechnology and Bioengineering	HardCopy Micro Electronic	QH324.B5 QH324.B5 n/a	v. 62 (1999) – v. 89 (2005) v. 45 (1995) – v. 56 (1997) v. 49 (1996) - present
*Briefings in Bioinformatics	Electronic	n/a	v. 1 (2001) - present
Bulletin of Mathematical Biology	Electronic	n/a	v. 57 (1995) - present
*Cancer Cell	Electronic	n/a	v. 1 (2001) - present
Cancer Genetics and Cytogenetics	Electronic	n/a	v. 81 (1995) - present
*Cell	HardCopy	QH573.C38	v. 32 (1983) - present
Cell Growth and Differentiation: The Molecular Biology Journal of the American Association for Cancer Research	HardCopy Electronic	RC261.A1C43 n/a	v. 12 (2001) – v.13 (2002) v. 10 (1999) - present
Cell Preservation Technology	HardCopy Electronic	TP248.27.A53C465 n/a	v. 3 (2005) – present v. 1 (2002) - present
Cells, Tissues, Organs	Electronic	n/a	v. 164 (1999) – 1 year ago
*Chembiochem	Electronic	n/a	v. 1 (2000) - present
*Chemistry: a European Journal	HardCopy Electronic	QD1.A6725 n/a	v. 1 (1995) – v. 11(2004-5) v. 4 (1998) - present
*Clinical Chemistry	HardCopy Electronic	RB37.A1C55 n/a	v. 1 (1955) – v. 35 (1989) v. 32 (1986) – 1 year ago
Clinical Data Management	Electronic	n/a	v. 6 (1999) – v. 7 (2000)
*Comparative and Functional Genomics	Electronic	n/a	v. 2 (2001) – v. 6 (2005)
*Computational Biology and Chemistry	HardCopy Electronic	QD39.3.C6C6 n/a	v. 27 (2003) – present v. 27 (2003) – present
Computers and Biomedical Research	HardCopy	R855.A1.C647	v. 31 (1998) – v.33

	Electronic	n/a	(2000) v. 29 (1995) – v. 33 (2000)
Computers, Informatics Nursing	HardCopy	RT50.5.C645	v. 20 (2002) - present
Computing and Visualization in Science	Electronic	n/a	v. 1 (1997) - present
Critical Reviews in Biotechnology	HardCopy Electronic	TP248.13.C74 n/a	v. 9 (1989) – present V. 22 (2002) - present
*Current Biology	Electronic	n/a	v. 15 (1995) – present
Current Genomics	Electronic	n/a	v. 1 (2000) – 1 year ago
*Current Opinion in Structural Biology	Electronic	n/a	v.5 (1995) – present
Current Proteomics	Electronics	n/a	v. 1 (2004) – 1 year ago
Cytogenetic and Genome Research	HardCopy Electronic	QH426.C95 n/a	v. 96 (2002) - (2003) v. 96 (2002) – 1 year ago
Cytogenetics and Cell Genetics	HardCopy Electronic	QH426.C95 n/a	v. 12 (1973) – v. 95 (2001) v. 83 (1998) – v. 95 (2001)
Cytotechnology	Electronic	n/a	v. 1 (1997) - present
DNA Research: An International Journal for Rapid Publication of Reports on Genes and Genomes	Electronic	n/a	v. 1 (1994) - present
DNA Sequence: The Journal of DNA Sequencing and Mapping	Electronic	n/a	v. 13 (2002) – 1 year ago
E Health International	Electronic	n/a	v. 1 (2002) only
*EMBO Journal	HardCopy Micro Electronic	QH506.E46 QH506.E46 n/a	v. 15 (1996) – v. 24 (2004) v. 9 (1990) – v. 14 (1995) v. 17 (1997) – present
*Ecology	HardCopy Micro Electronic	QH540.E3 QH540.E3 n/a	v. 46 (1965) – present v. 1 (1920) – v. 45 (1964) v. 1 (1920) – present
*European Journal of Biochemistry	Micro Electronic	QP501.E89 n/a	v. 1 (1967) – v. 71 (1976) v. 1 (1967) – v. 271(2004)
*FASEB Journal	HardCopy Electronic	QH301.F33 n/a	v. 1 (1987) – v. 4(1991) v. 1 (1987) – 1 year ago
*FEBS Journal	Electronic	n/a	v. 272 (2005) – 1 year ago
*FEBS Letters	Electronic	n/a	v. 1 (1968) – present

Functional and Integrative Genomes	Electronic	n/a	v. 1 (2000) - present
*Gene	Electronic	n/a	v. 152 (1995) – present
Genes and Development	Electronic	n/a	v. 11 (1997) - present
Genes to cells	Electronic	n/a	v. 1 (1996) – 6 months ago
Genescreen: An International Journal of Medical Genomics	Electronic	n/a	v. 1 (2000) – (2001)
Genome	HardCopy Electronic	QH431.A1C25 n/a	v. 29 (1987) – v. 38 (1995) v. 44 (2001) – 6 months ago
*Genome Biology	Electronic	n/a	v. 1 (2000) – present
*Genome Research	Electronic	n/a	v. 7 (1997) – present
Genomics and Genetics Weekly	Electronics	n/a	v. 1 (1998) - present
Genomics and Proteomics	Electronic	n/a	v. 2 (2002) - present
Health Management Technology	Electronic	n/a	v. 19 (1998) - present
Healthcare Informatics	Electronic	n/a	v. 19 (2002) - present
Human Molecular Genetics	Electronic	n/a	v. 5 (1996) - present
IEE Proceedings Nanobiotechnology	Electronic	n/a	v. 150 (2003) - present
IEEE/ACM Transactions on Computational Biology and Bioinformatics	Electronic	n/a	v. 1 (2004) - present
IEEE Transactions on Nanobioscience	HardCopy Electronic	QH506.I34 n/a	v. 1 (2002) – v. 2 (2003) v. 1 (2002) - present
Immunome Research	Electronic	n/a	v. 1 (2005) - present
In Silico Biology	Electronic	n/a	v. 1 (1998) – 6 months ago
International Journal of Medical Informatics	Electronic	n/a	v. 44 (1997) - present
Internet Journal of Genomics and Proteomics	Electronic	n/a	v. 1 (2002) - present
Internet Journal of Molecular Design	Electronic	n/a	v. 1 (2002) - present
Journal of Agricultural Genomics	Electronic	n/a	v. 1 (1995) – (2000)
Journal of Biomedical Informatics	HardCopy Electronic	R858.A1C647 n/a	v. 34 (2001) – present v. 34 (2001) - present
*Journal of the American Chemical Society	HardCopy Micro Electronic	QD1.A5 QD1.A5 n/a	v. 38 (1916) – present v. 1 (1879) – v. 37 (1915) v. 1 (1879) – present
Journal of the American Medical Informatics Association	Electronic	n/a	v. 1 (1994) - present
*Journal of Bacteriology	HardCopy Micro Electronic	QR1.J6 QR1.J6 n/a	v. 59 (1950) – present v. 4 (1932) – v. 60 (1950) v. 177 (1995) – 6

			months ago
Journal of Biochemical and Molecular Toxicology	Electronic	n/a	v. 12 (1998) - present
*Journal of Bioinformatics and Computational Biology	Electronic	n/a	v. 1 (2003) - present
* Journal of Biological Chemistry	HardCopy Micro Electronic	QP501.J7 QP501.J7 n/a	v. 235 (1960) – present Some missing issues v. 68 (1926) – v. 234 (1959) v. 1 (1905) – present
Journal of Cellular Physiology	HardCopy Micro Electronic	QP1.W533 QP1.W533 n/a	v. 60 (1962) – v. 166 (1996) v. 1 (1932) – v. 59 (1962) v. 170 (1997) - present
Journal of the Chemical Society, Faraday Transactions II: Molecular and Chemical Physics	HardCopy	QD1.C616	v. 82 (1986) – v. 85 (1988)
Journal of Chemical Technology and Biotechnology	Electronic	n/a	v. 64 (1995) - present
*Journal of Chemical Theory and Computation	Electronic	n/a	v. 1 (2005) – present
*Journal of Computational Biology	Electronic	n/a	v. 6 (1999) – present
*Journal of Computational Chemistry	Electronic	n/a	v. 17 (1996) – present
Journal of Experimental Zoology Part B: Molecular and Developmental Evolution	Electronic	n/a	v. 295 B (2003) - present
*Journal of General Physiology	HardCopy Micro Electronic	QP1.J73 QP1.P73 n/a	v. 47 (1963/4) – present v. 1 (1919) – v. 46 (1963) v. 109 (1997) – present
*Journal of Molecular Biology	HardCopy Electronic	QH301.J73 n/a	v. 1 (1959) – present v. 245 (1995) – present
*Journal of Molecular Evolution	Electronic	n/a	v. 45 (1997) – present
*Journal of Molecular Recognition	Electronic	n/a	v. 10 (1997) – present
*Journal of Physiology	HardCopy Micro Electronic	QP1. J75 QP1. J75 n/a	v. 184 (1966) – present v. 1 (1878) – v. 183 (1966) v. 1 (1878) – present
*Journal of Proteomic Research	Electronic	n/a	v. 1 (2002) – present
Journal of Structural Biology	HardCopy Electronic	QH573.J6 n/a	v. 103 (1990) – present

			v. 114 (1995) - present
Journal of Structural and Functional Genomics	Electronic	n/a	v. 1 (2000) – present
Journal of Ultrastructure and Molecular Structure Research	HardCopy	QH573.J6	v. 94 (1986) – v. 102 (1988)
Mammalian Genome: Official Journal of the International Mammalian Genome Society	Electronic	n/a	v. 7 (1997) - present
Medical Informatics and the Internet in Medicine	Electronic	n/a	v. 24 (1999) - present
Microbiology and Molecular Biology Reviews	HardCopy Electronic	QR1.B25 n/a	v. 61 (1997) – present v. 59 (1995) – 1 year ago
Molecular and Cellular Biology	HardCopy Micro	QH506.M64 QH506.M64	v. 19 (1999) – present v. 15 (1995) – v. 18 (1998)
*Molecular Biology and Evolution	HardCopy Electronic	QH506.M652 n/a	v. 1 (1983-4) v. 1 (1983) – present
Molecular bioSystems	Electronic	n/a	v. 1 (2005) - present
Molecular Cancer Therapeutics	HardCopy Electronic	RC270.8.M65 n/a	v. 1 (2001) –present v. 1 (2001) –present
*Molecular Cell	Electronic	n/a	v. 1 (1997) – present
Molecular Cell Biology Research Communications	HardCopy	QH573.M67	v. 1 (1999) – v. 4 (2000)
Molecular Engineering	Electronic	n/a	v. 7 (1997) – v. 8 (1999)
Molecular Genetics and Genomes	HardCopy Electronic	QH431.M552 n/a	v. 265 (2001) – (2005) v. 250 (1996) – (2005)
*Molecular Microbiology	HardCopy Micro Electronic	QR74.M65 QR74.M65 n/a	v. 27 (1998) – present v. 1 (1987) – v. 22 (1996) v. 17 (1995) – present
*Molecular Systems Biology	Electronic	n/a	v. 1 (2002) – 1 year ago
Mutation Research	Electronic	n/a	v. 382 (1997) – (2001)
Natural Computing	Electronic	n/a	v. 1 (2002) - present
*Nature	HardCopy Micro Electronic	Q1.N2 Q1.N2 n/a	v. 161 (1948) – present Some missing issues v. 165 (1950) – v. 204 (1964) v. 385 (1997) – present

*Nature Reviews: Genetics	Electronic	n/a	v. 1 (2000) – 1 year ago
*Nature: Biotechnology	HardCopy Electronic	TP248.3.B557 n/a	v. 14 (1996) – present v. 16 (1998) - present
*Nature: Cell Biology	HardCopy Electronic	QH573.N38 n/a	v. 6 (2004) – present v. 1 (1999) – present
*Nature: Genetics	Electronic	n/a	v. 1 (1998) – present
*Nature: Medicine	HardCopy Electronic	RB113.N37 n/a	v. 5 (1999) – present Some missing issues v. 4 (1998) – present
*Nature: Neuroscience	Electronic	n/a	v. 1 (1998) – 1 year ago
*Nature Reviews: Cancer	Electronic	n/a	v. 1 (2001) – 1 year ago
*Nature: Structural and Molecular Biology	HardCopy Electronic	QH506.N4 n/a	v. 11 (2004) – present v. 5 (1998) – present
*Nucleic Acids Research	Electronic	n/a	v. 1 (1974) – present
*OMICS	Electronic	n/a	v. 5 (2000) – present
*Oncogene	Electronic	n/a	v. 14 (1997) – 1 year ago
Physiological Genomics	Electronic	n/a	v. 1 (1999) – 1 year ago
Plant Journal for Cell and Molecular Biology	HardCopy Micro Electronic	QK728.P53 QK728.P53 n/a	v. 9 (1996) present v. 1 (1991) – v. 8 (1995) v. (1991) - present
Plant Molecular Biology	HardCopy Electronic	QK728.P54 n/a	v. 30 (1996) – v. 53 (2003) v. 33 (1997) - present
*PLOS: Biology	Electronic	n/a	v. 1 (2003) – present
*PLOS: Computational Biology	Electronic	n/a	v. 1 (2005) – present
*PLOS: Genetics	Electronic	n/a	v. 1 (2005) – present
*Proceedings of the National Academy of Sciences	HardCopy Micro Electronic	Q11.N26 Q11.N26 n/a	v. 38 (1952) – present Some missing issues v.1 (1915) – v. 52 (1964) v. 1 (1915) – present
Progress in Biophysics and Molecular Biology	Electronic	n/a	v.63 (1995) - present
Protein Engineering	Electronic	n/a	v. 9 (1996) – v. 16 (2003)
*Protein Engineering Design and Selection	Electronic	n/a	v. 17 (2004) – present
*Protein Science	HardCopy Electronic	QP551.P69761 n/a	v. 8 (1999) – present v. 1 (1992) – present
*Protein: Structure, Function and Bioinformatics	Electronic	n/a	v. 24 (1996) – present
Proteome Science	Electronics	n/a	v. 1 (2003) - present
Proteomics	Electronic	n/a	v. 1 (2001) - present

*RNA	Electronic	n/a	v. 1 (1995) – present
*Science	HardCopy Electronic	Q1.S35 n/a	v. 58 (1923) – present Some missing issues v. 275 (1997) – present
SIGBIO Newsletter	HardCopy Electronic	R853.D37 S55 n/a	v. 6 (1982) –v. 21 (2001) Some missing issues v. 1 (1976) – v. 21 (2001)
Somatic Cell and Molecular Genetics	Electronic	n/a	v. 24 (1998) – v. 27 (2002)
Spectrochimia Acta, Part A: Molecular and Biomolecular Spectroscopy	HardCopy Electronic	QD95.S633 n/a	v. 51 (1995) – present v. 51 (1995) - present
Statistical Applications in Genetics and Molecular Biology	Electronic	n/a	v. 1 (2002) - present
*Structure	Electronic	n/a	v. 3 (1995) – present
Theochem	Electronic	n/a	v. 321 (1995) - present
*Trends in Biotechnology	HardCopy Electronic	TP248.13.T74 n/a	v. 16 (1998) – present v. 13 (1995) - present
*Trends in Genetics	HardCopy Electronic	QH426.T74 n/a	v. 15 (1999) – present v. 11 (1995) – present
*Trends in Microbiology	HardCopy Electronic	QR1.T74 n/a	v. 6 (1998) – present v. 3 (1995) – present
Ultramicroscopy	HardCopy Electronic	QH212.E4U57 n/a	v. 52 (1993) – present v. 61 (1995) – present
Ultrastructural pathology	Electronic	n/a	v. 23 (1999) – 1 year ago

APPENDIX F
LISTING OF MAJOR EQUIPMENT AVAILABLE TO SUPPORT PROGRAM

I. Existing infrastructure facilities for Bioinformatics

A. Building space.

The Bioinformatics Program is currently housed in approximately 6800 sq. ft. in Cameron Hall. Laboratories and offices within this space will be renovated to accommodate new faculty hires until the Bioinformatics building opens in August 2009.

B. Core laboratory facilities.

B.1 The UNCC Functional Genomics Core Facility is a joint project by UNCC and Carolinas Medical Center researchers and primarily funded by NC Biotech. The facility grant was awarded in August of 2006. The facility is supervised by Dr. Cynthia Gibas and staffed by a full-time technician and will be accessible to all UNCC researchers on a cost-recovery basis beginning in December 2006. Major equipment includes: (1) a Matrix PlateMate 2x2 robotic system for automated microvolume pipetting, including plate replication and reformatting, reagent addition, serial dilution, and reaction setup; (2) a BioRad BioOdyssey Calligrapher benchtop microarray fabrication system for printing of small- to medium- batches of microarrays on standard slides, on membranes or in microplates; (3) a Tecan HS-4800 automated hybridization and wash station for processing of multiple microarrays under controlled conditions and (4) a Tecan LS-Reloaded microarray scanner with capabilities for multi-slide and microplate scanning and up to three dye chemistries simultaneously in red, green and blue wavelength ranges. Major equipment already in the core facility includes a Bio-Rad iQ5 Real Time PCR system with 5-color detection capabilities, an Agilent eBioanalyzer for QC of nucleic acid and protein samples, a NanoDrop UV-Vis spectrophotometer for quantitation of nucleic acids in extremely small sample volumes, and ThermoElectron and Agilent hybridization ovens, carousels, and chambers for manual hybridization of oligonucleotide microarrays. Additional common equipment including centrifuges, refrigeration, water purification, autoclaves and ventilated hoods are located in shared space connected to faculty laboratories.

B.2 The Mass Spectrometer Facility is a joint project by UNC Charlotte and Carolinas Medical Center researchers and primarily funded by NC Biotech. The facility was awarded in May 2006. The facility is located at Molecular core laboratory in Cannon Research Center at CMC, supervised by Dr. M. Taghi Mostafavi and managed by the core facility manager and a full-time mass spectrometer specialist (starting in Spring 2007). In addition a part time IT staff and a molecular biology technician will support researchers from both institutes for use of this facility. Major equipment includes: (1) LTQXL Linear Quadruple Ion Trap Mass Spectrometer bundle that include high performance 2-D Linear Ion Trap Mass Spectrometer with Xcalibur and Bioworks 3.3 Software; (2) NLC-2D-20-1 Nano LC 2-dimensional binary gradient pump system with external 10-port column switching valve, configured for 20 ul/min max flow in first dimension and 1 uL/ min max; (3) NLC-AS1 AS-1 temperature controlled autosampler with 96 well capacity that includes six port injection valve flow in second dimension; (4) New Objective NanoSpray Probe with PicoView 550 for LTQXL Ion Trap Mass spectrometer; Data are

accessible by all researchers at UNC Charlotte and CMC through network connected to a computational server with Bioworks software.

B.3 Microarray Facility: also a joint project by UNC Charlotte and Carolina Medical Center researchers located in Molecular Biology Core Facilities in Cannon Research Center, CMC. This facility is manage by Dr. Nury Steuerwald at UNC-Charlotte and the manager of core facility, Z. Bahrani-Mostafavi, at CMC. Major equipment includes: (1) Genechip Fluidics Station 400; (2) Genechip Hybridization Oven 640; (3) Affymetrix Genechip Scanner 3000. The facility includes the latest software by affymetrix for data analysis and genomics study. The core facility laboratory house technicians to prepare samples and provide data from the microarray system to researcher of both institutions.

C. Core computing Facilities.

The Bioinformatics Research Center provides faculty with access to high performance cluster computing on a 73-node Apple XServe cluster and a 4-node prototyping cluster. The cluster is equipped with a 3 TB RAID storage array. The cluster is loaded with common bioinformatics software accessible either through the BioTeam Inquiry web interface or via UNIX command line. Researchers also have access to a 50-node Linux cluster through Information Technology Services.

APPENDIX G
NEW INFRASTRUCTURE FACILITIES PLANNED FOR BIOINFORMATICS

I. Planned infrastructure facilities for Bioinformatics

A. Bioinformatics Research Center building (completion August 19, 2009).

The Bioinformatics Research Center will be located in a $35M, 75,000 g.s.f. building under construction on the Charlotte Research Institute Campus of UNC Charlotte. The building offers space for both wet and dry laboratories.

B. Core laboratory facilities.

The planned Bioinformatics Research Center Facility includes core facilities for gene expression, proteomics, microscopy, crystallography, and computing.

C. Instructional facilities.

The planned Bioinformatics Research Center Facility includes auditoriums, conference rooms, and a computer classroom suitable for offering Bioinformatics graduate courses.

D. North Carolina Research Center satellite office (move-in Jan.-May 2007).

The BRC has also taken a leadership role in developing Bioinformatics programs in collaboration with the developers of the North Carolina Research Campus, a billion-dollar, 350-acre research park that will be home to the research programs of a large number of private biotechnology companies as well as university and medical research programs. The BRC will develop a Center of Excellence in Bioinformatics at the North Carolina Research Campus at Kannapolis, eventually hiring several faculty with research interests at both locations. This will be a research, educational and service Center with a focus on the development of novel analytical methods for knowledge discovery in large biological datasets. Research at the Center will enable basic and applied researchers to ask and answer complex questions in molecular and population biology, to manage

and navigate the vast data sets that are generated by modern molecular biology methods, and to translate the results into practical benefits through understanding of the interacting effects of health, nutrition, development, and behavior.

APPENDIX H
BUDGET SCHEDULE FOR PROPOSED PROGRAM

SUMMARY OF ESTIMATED ADDITIONAL COSTS FOR PROPOSED PROGRAM/TRACK

Institution **UNC Charlotte** *Date* **January 15, 2007**

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

Degree(s) to be Granted **Master of Science** *Program Year* **2007-08**

	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	$55,000				$55,000
Bioinformatics Coordinator	55,000				
1110 EPA Non-teaching Salaries					0
1310 EPA Academic Salaries	131,000	0	170,000		301,000
Assistant Professors (2)			170,000		
Associate Professor	95,000				
Graduate Assistants (2 @ 18k)	36,000				
1810 Social Security	14,229		13,005		27,234
1820 State Retirement	14,529		18,972		33,501
1830 Medical Insurance (3432*X)	7,708		7,708		15,416
2000 Supplies and Materials	1,200				1,200
2300 Educational Supplies	200				200
2600 Office Supplies	1,000				1,000
3000 Current Services	3,500				3,500
3100 Travel	2,000				
3200 Communications	500				
3400 Printing & Binding	1,000				
5000 Capital Outlay (Equipment)	24,000				24,000
5100 Office Equipment	0				
5200 EDP Equipment	24,000				
TOTAL Regular Term Instruction	**$251,166**	**$0**	**$209,685**	**$0**	**$460,851**
151 Libraries					
5000 Capital Outlay (Equipment)		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**
999 Multiactivity					
0123 Non-Resident Graduate Assistant Tuition Waivers (2)	**$21,206**	**$0**	**$0**	**$0**	**21,206**
TOTAL ADDITIONAL COSTS	**$272,372**	**$0**	**$209,685**	**$0**	**$482,057**

NOTE: Accounts may be added or deleted as required.

SUMMARY OF ESTIMATED ADDITIONAL COSTS FOR PROPOSED PROGRAM/TRACK

Institution **UNC Charlotte** *Date* **January 15, 2007**

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

Degree(s) to be Granted **Master of Science** *Program Year* **2008-09**

	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	65,659	65,341	170,000		301,000
Assistant Professors (2)			170,000		
Associate Professor	29,659	65,341			
Graduate Assistants (2 @ 18k)	36,000				
1810 Social Security	5,023	4,999	13,005		23,027
1820 State Retirement	3,310	7,292	18,972		29,574
1830 Medical Insurance	377	3,477	7,708		11,562
2000 Supplies and Materials		1,000			1,000
2300 Educational Supplies		500			
2600 Office Supplies		500			
3000 Current Services		3,750			3,750
3100 Travel		2,500			
3200 Communications		500			
3400 Printing & Binding		750			
5000 Capital Outlay (Equipment)		8,815			8,815
5100 Office Equipment		750			
5200 EDP Equipment		8,065			
TOTAL Regular Term Instruction	**$74,369**	**$94,674**	**$209,685**	**$0**	**$378,728**
151 Libraries					
5000 Capital Outlay (Equipment)		10,873			10,873
5600 Library Book/Journal		10,873			
TOTAL Libraries	**$0**	**$10,873**	**$0**	**$0**	**$10,873**
189 General Institutional Support					
2000 Supplies and Materials		17,100			17,100
2600 Office Supplies		17,100			
3000 Current Services		17,100			17,100
3200 Communications		8,550			
3400 Printing & Binding		8,550			
5000 Capital Outlay (Equipment)		16,971			16,971
5100 Office Equipment		8,500			
5200 EDP Equipment		8,471			
TOTAL General Inst. Support	**$0**	**$51,171**	**$0**	**$0**	**$51,171**
999 Multiactivity					
0123 Non-Resident Graduate Assistant Tuition Waivers	**$21,206**	**$0**	**$0**	**$0**	**$21,206**
TOTAL ADDITIONAL COSTS	**$95,575**	**$156,718**	**$209,685**	**$0**	**$461,978**

NOTE: Accounts may be added or deleted as required.

SUMMARY OF ESTIMATED ADDITIONAL COSTS FOR PROPOSED PROGRAM/TRACK

Institution **UNC Charlotte** *Date* **January 15, 2007**

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

Degree(s) to be Granted **Master of Science** *Program Year* **2009-2010**

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	53,991	77,009	170,000		301,000
Assistant Professors (2)			170,000		
Associate Professor	17,991	77,009			
Graduate Assistants (2 @ 18k)	36,000				
1810 Social Security	4,130	5,891	13,005		23,026
1820 State Retirement	2,008	8,594	18,972		29,574
1830 Medical Insurance		4,098	7,708		11,806
2000 Supplies and Materials		1,500			1,500
2300 Educational Supplies		750			
2600 Office Supplies		750			
3000 Current Services		4,500			4,500
3100 Travel		3,000			
3200 Communications		500			
3400 Printing & Binding		1,000			
5000 Capital Outlay (Equipment)		9,989			9,989
5100 Office Equipment		750			
5200 EDP Equipment		9,239			
TOTAL Regular Term Instruction	**$60,129**	**$111,581**	**$209,685**	**$0**	**$381,395**
151 Libraries					
5000 Capital Outlay (Equipment)		12,815			12,815
5600 Library Book/Journal		12,815			
TOTAL Libraries	**$0**	**$12,815**	**$0**	**$0**	**$12,815**
189 General Institutional Support					
2000 Supplies and Materials		20,100			20,100
2600 Office Supplies		20,100			
3000 Current Services		20,100			20,100
3200 Communications		10,050			
3400 Printing & Binding		10,050			
5000 Capital Outlay (Equipment)		20,109			20,109
5100 Office Equipment		10,100			
5200 EDP Equipment		10,009			
TOTAL General Inst. Support	**$0**	**$60,309**	**$0**	**$0**	**$60,309**
999 Multiactivity					
0123 Non-Resident Graduate Assistant Tuition Waivers	**$21,206**	**$0**	**$0**	**$0**	**$21,206**
TOTAL ADDITIONAL COSTS	**$81,335**	**$184,705**	**$209,685**	**$0**	**$475,725**

NOTE: Accounts may be added or deleted as required.

APPENDIX I
TABLE COMPARING PSM AND MASTER'S COURSE OFFERINGS IN ESTABLISHED BIOINFORMATICS PROGRAMS

	Proposed UNCC	Georgia Tech	UCSC	Boston University	University of Michigan	Arizona State	NC State	Indiana University	Johns Hopkins
HOURS	36 credit hours; 30 coursework	37 semester hours	Quarter system…	32 credits	2yrs	42 hours (6= internship)	33-36 hours	36 cr	
PREREQS		Intro biology Intro programming Organic Chemistry Calculus Physics	"Please learn to program before entering the graduate program"		BS in bio, CS, math or eng	Genetics, cell, organic, biochem, differential equations, statistics, and OO design	Genetics, Intro programming, calculus, linear algebra, stats for bio	6 ug hrs bio 6 ug hrs computing	Organic, Biochem, Programming, Data Structures, calculus, prob & stats
INTERN?	Yes			Yes	Yes	Yes			
Course that introduces cell/molecular biology at grad level	Intro to Cellular and Molecular Biology for Bioinformatics	Prokaryotic Molecular Genetics	Advanced Molecular Genetics		1 Mol Bio elective		Molecular Genetics (can be subbed with Macromolecular Synthesis and Regulation)		Molecular Biology AND Gene Organization and Expression
		Eukaryotic Molecular Genetics							
Course that introduces biochem or protein structure at grad level	Introduction to Biophysical Systems for Bioinformatics	Biochemistry I	Chemistry 200B (protein structure + function)			Intro to Structural and Mol Bio	Macromolecular Structure (can be subbed with Population Genetics)		
		Biochemistry II							
Systems biology/mathematical modeling course	Mathematical Systems Biology	Modeling and Dynamics (Math)			1 Systemic Modeling	Modeling and Comp. Bio			
Course that introduces statistics used in bio research at the grad	Statistics for Bioinformatics	Probability and Statistics	Statistics		1 Probability and Stat	Multivariate Stats	Experimental Stats for Bio		

level									
								Intro Informatics	
“Capstone type course/project course”	Internship Project			Computational Genomics II (project course?)		Apps and Complex Problem Solving in Comp Bio		Bioinformatics, Theory & App.; Bioinformatics in Mol Bio & Genetics	
Course that introduces computing/ programming in a bioinformatics context. Some as described seem very nonrigorous	Bioinformatics Programming – OO Design	Intro Computing Concepts in Bioinformatics		Applications in Bioinformatics	Fundamentals of Bioinformatics		Bioinformatics I		Foundations of Algorithms OR Computer Concepts for Bioinformatics
		Applications of AI							
Course that introduces sequence analysis, phylogenetic analysis, comparative modeling, etc.	Molecular Sequence Analysis	Bioinformatics	Intro to Bioinformatics +Lab	Sequence Analysis			Bioinformatics II AND Comp Methods for Mol. Bio	Intro Bioinformatics	
Course that applies physical chemistry (esp. stat mech, stat therm) in a biological context	Introduction to Biophysical Systems for Bioinformatics & Numerical Methods in Bioinformatics	Biophysics			1 Biophysics & Struc Bio				
Database course (some are designed specifically for bioinformatics, some not)	Bioinformatics Programming – Data Structures and Visualization & Design and	Intro Database Systems OR Visualization		Biological Database Systems	1 Databases & Computing			Information Management	Principles of Database Systems OR Biological Databases AND

	Implementation of Bioinformatics Databases								Database Tools
"Bioinformatics" or computational biology with a molecular modeling focus. Some include MD/QSAR/etc.	Computational Structural Biology	Macromolecular Structure OR Drug Design	Protein Bioinformatics						
Hands-on mol bio lab experience	Recombinant DNA Techniques								
Course that introduces high-throughput laboratory methods and supporting informatics approaches	Genomics & Proteomics		Computational Genomics	Computational Genomics I			Intro to Genomic Science		
						Experimental Design			
Everyone's got a different approach to ethics	Research Ethics		Ethics	Biotech Law and Ethics		Business Issues and Ethics			
	Seminar		Seminar	Seminar	Journal Club		Journal Club		
			MS Thesis					MS Thesis	
			2 electives					18 electives from several major areas	4 concentration classes from one of several major areas; 1 CS elective, 1 Biotech elective

APPENDIX J
CURRICULUM VITAE FOR BIOINFORMATICS RESEARCH CENTER FACULTY

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
Baumketner, Andriy	Assistant Professor
eRA COMMONS USER NAME	

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
Institute for Condensed Matter Physics, National Academy of Sciences of Ukraine	Ph.D.	2000	Theoretical Physics
Lviv State University	M.Sc.	1995	Physics

A. Positions and Honors

Employment and Affiliations

Assistant Professor — University of North Carolina Charlotte, August 2006-present.
Postdoctoral researcher — University of California Santa Barbara, August 2002-August 2006
Adviser – J.-E. Shea
Postdoctoral researcher — Kanazawa University, Kanazawa, Japan, January 2000-March 2002.
Adviser – Y. Hiwatari
Junior researcher — Institute for Condensed Matter Physics, NAS of Ukraine, December 1999-present

Other Experience

Awards — "Diploma cum Laude" from Lviv State University, Ukraine, 1995
G. Soros Graduate Student, Ukraine, 1997
Fellowships — University of Jyvaskyla, Finland, 1999
International Center for Theoretical Physics (ICTP), Trieste, Italy, 2000
Research Grants — NSF- High Performance Computing and TeraGrid allocation.
PI – J.-E. Shea, grants # MCB040044(2004), #MCA05S027P(2005)

Professional Service

Referee — Physical Review Letters; Physical Reviews E

B. SELECTED PEER-REVIEWED PUBLICATIONS

Journal Publications

8.) J.-E. Shea, M. Friedel, A. Baumketner (2006). Simulations of protein folding. Rev. Comp. Chem. 22:169.

7.) D.B. Teplow, N.D. Lazo, G. Bitan, S. Bernstein, T. Wyttenbach, M. T. Bowers, A. Baumketner, J.-E. Shea, B. Urbanc, L. Cruz, J. Borreguero, H.E. Stanley (2006). Elucidating amyloid beta-protein folding and assembly: A multidisciplinary approach. Acc. Chem. Res., 39:635.

6.) A. Baumketner, J.-E. Shea (2006). Folding landscapes of the Alzheimer amyloid-beta(12-28) peptide. J. Mol. Biol., 362:567.

5.) M. Friedel, A. Baumketner, J.-E. Shea (2006). Effects of surface tethering on protein folding mechanisms. PNAS, 103:839.

4.) A. Baumketner, S.L. Bernstein, T. Wyttenbach, N.D. Lazo, D.B. Teplow, M.T. Bowers, J.-E. Shea (2006). Structure of the 21-30 fragment of amyloid Beta protein. Protein Science, 15:1239.

3.) P. Soto, A. Baumketner, J.-E. Shea (2006). Aggregation of polyalanine in a hydrophobic environment. J. Chem. Phys., 124:134904.

2.) A. Baumketner, S.L. Bernstein, T. Wyttenbach, G. Bitan, D.B. Teplow, M.T. Bowers, J.-E. Shea (2006). The structure of the wild type Amyloid-Beta monomer: a computational and experimental study. Protein Science, 15:420.

1.) A. Baumketner, J.-E. Shea (2006). The thermodynamics of folding of a beta hairpin peptide probed through replica exchange molecular dynamics simulations. Theor. Chem. Acc. 116:262.

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
Clemens, Mark G.	Professor and Vice Chair for Research
eRA COMMONS USER NAME Mark_clemens	

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
St. Louis University, St. Louis, MO	BS	1975	Phyical Therapy
St. Louis University, St. Louis MO	PhD	1979	Physiology
Yale University, New Haven CT	Postdoc	1980-81	Shock, Metabolism

PAST EXPERIENCE

Associate Research Scientist (Surgery) Yale University School of Medicine 1981-1984
Research Scientist (Surgery) Yale University School of Medicine 1984-1986
Assistant Professor (Surgery and Physiology) Johns Hopkins School of Med. 1986-91
Associate Professor (Surgery and Physiology) Johns Hopkins School of Med. 1991-1996
Professor and Chairman (Biology) University of North Carolina at Charlotte 1996-2005
Professor and Vice Chair for Research (Biology) University of North Carolina at Charlotte 2005- present

HONORS

National Merit Scholar, St. Louis University 1968-72; Charles Ohse Award, Yale University 1983; Robert Garrett Scholar, Johns Hopkins University 1986-96; Associate Editor, SHOCK 1993-present; Basic Science Councilor, The Shock Society 1992-95; Publications Committee Chairman, The Shock Society 1993-94, Scientific Program Committee, The Shock Society 1995-1999 (Chair 1998), First Citizens Bank Scholar Award 2005.

Federal Government Public Advisory Committee Service

NIH (NHLBI) Special Emphasis Review Panel: "Hemoglobin-Based Oxygen Carriers: Mechanisms of Toxicity" (1993); NIH (Surgery Anesthesiology and Trauma study section), ad hoc member, 1998, 99, 00-05; Regular member SAT study section Oct 2005-. Veteran's Administration grant reviewer, 1993-1999. Special Emphasis Panels (NIHLB May 2000; April 2001; NIGMS August 2000, December 2000); SEP, NIGMS P01/ P50 reviews, 2000-2005 (Chair, 2004, 2005), Regular member SAT study section 2005-2009

Publications (partial listing)

Selected publications (from a total of 145)

1. Bauer I, Bauer M, Pannen BHJ, Leinwand MJ, Zhang JX and Clemens MG. Chronic ethanol consumption exacerbates liver injury following hemorrhagic shock: Role of sinusoidal perfusion failure. Shock 4:324-331, 1995
2. Bauer M, Paquette NC, Zhang JX, Bauer I, Pannen BHJ, Kleeburger SR and Clemens MG. Chronic ethanol consumption increases hepatic sinusoidal contractile response to endothelin-1. Hepatology 22: 1565-1576, 1995.
3. Pannen BHJ, Bauer M, Zhang JX, Robotham JL, Clemens MG. Endotoxin pretreatment enhances the portal venous contractile response to endothelin-1. Am. J. Physiol.270:H7-H15, 1996.
4. Gingalewski C, Wang K, Clemens MG, and DeMaio A. Posttranscriptional regulation of the connexin 32 gene in liver during acute inflammation. J. Cell Pysiol.166:461-467, 1996.
5. Jaeschke H, Smith CW, Clemens MG, Ganey PE and Roth RA. Mechanisms of inflammatory liver injury:

Adhesion molecules and cytotoxicity of neutrophils Toxicol Appl Pharmacol 139(2):213-26, 1996

6. Miller LS, Morita Y, Rangan U, Kondo S, Clemens MG and Bulkley GB. Suppression of cytokine-induced neutrophil accumulation in rat mesenteric venules *in vivo* by general anesthesia. International Journal of Microcirculation: Clinical and Experimental 16(3):147-54, 1996
7. Pannen BHJ, Bauer M, Zhang JX, Robotham J and Clemens MG. A time-dependent balance between endothelin and nitric oxide regulates portal vascular resistance following endotoxin pretreatment. Am. J. Physiol. 271: H1953-H1961, 1996
8. Bauer M, BHJ Pannen, I Bauer, C Herzog, GA Wanner, R Hanselmann, JX Zhang, MG Clemens and R Larsen. *In vivo* evidence for a functional link between stress response and vascular control in hepatic portal circulation. Am. J. Physiol. 271:G929-G935, 1996.
9. Pannen BHJ, Bauer M, Zhang JX, Robotham J and Clemens MG. A time-dependent balance between endothelin and nitric oxide regulates portal vascular resistance following endotoxin. Am. J. Physiol. 271: H1953-H1961, 1996.
10. Rai R, JX Zhang, MG Clemens and AM Diehl. Gadolinium chloride alters acinar distribution of phagocytosis and balance between pro- and anti-inflammatory cytokines. Shock 6(4):243-7, 1996
11. Pannen PHJ, M Bauer, E N ldge-Schomburg, JX Zhang, JL Robotham, MG Clemens, and KK Geiger. Regulation of hepatic blood flow during resuscitation from hemorrhagic shock: Role of nitric oxide and endothelins. Am J Physiol Jun;272(6 Pt 2):H2736-45, 1997.
12. Yang SQ; Lin HZ; Lane MD; Clemens M; Diehl AM. Obesity increases sensitivity to endotoxin liver injury: implications for the pathogenesis of steatohepatitis. Proc Natl Acad Sci U S A 1997 Mar 18;94(6):2557-62
13. Bauer I; Bauer M; Clemens MG; Pannen BH; Wolf B, Miescher EA; Alte C; Rensing H; Wanner GA. Expression pattern of heme oxygenase isoenzymes 1 and 2 in normal and stress-exposed rat liver. Hepatology 27(3):829-38, 1998.
14. Clemens MG; Zhang JX; Bauer I; Pannen BH; Bauer M Remodeling of hepatic microvascular responsiveness after ischemia/reperfusion. Shock 8(2):80-5, 1997.
15. Pannen BH; Geiger KK; Clemens MG; Bauer M, Al-Adili F. Role of endothelins and nitric oxide in hepatic reperfusion injury in the rat. Hepatology 27(3):755-64, 1998
16. Clemens, MG. Does altered regulation of ecNOS in sinusoidal endothelial cells determine increased intrahepatic resistance leading to portal hypertension? Hepatology 1998 Jun; 27(6): 1745-1747.
17. Benedikt H. J. Pannen, Nicola K hler, Burkhard Hole, Michael Bauer, Mark G. Clemens, Klaus K. Geiger. Protective Role of Endogenous Carbon Monoxide in Hepatic Microcirculatory Dysfunction after Hemorrhagic Shock in Rats. Journal of Clinical Investigation 1998 Sep 15; 102(6): 1220-1228.
18. Garcia-Pagan J-C, Zhang JX, Sonin N, Nakanishi K, Clemens Mark G. Ischemia / reperfusion induces an increase in the hepatic portal vasoconstrictive response to endothelin-1. Shock 11: 325-329, 1999
19. Sonin NV, Garcia-Pagan JC, Nakanishi K, Zhang JX, Clemens MG. Patterns of vasoregulatory gene expression in the liver response to ischemia / reperfusion and endotoxemia. Shock 11: 175-179, 1999
20. Susumu Kobayashi, Elizabeth Miescher, and Mark G. Clemens A synergistic effect of extracellular hypocalcemia for hyperoxic reoxygenation injury in rat hepatocytes. Transplantation 67:451-457, 1999.
21. Clemens, MG Nitric Oxide in liver injury. Hepatology 30: 1-5, 1999
22. Clemens, MG and JX Zhang. Regulation of sinusoidal perfusion: *in vivo* methodology and control by endothelins. Seminars in Liver Disease 1999;19(4):383-96
23. Lee S-M, M-J Park, T-S Cho and MG Clemens. Hepatic injury and lipid peroxidation during ischemia and reperfusion. Shock 2000;13(4):279-84
24. Clemens MG. Liver circulation in portal hypertension. Hepato-Gastroenterology 46 (Supplement II): 1429-1433, 1999.

25. Bauer M, Bauer I, Sonin N, Kresge N, Baveja R, Harding D, Yokoyama Y, Zhang JX, Clemens MG. Functional significance of endothelin-B receptor expression in endotoxemia. Hepatology 2000 Apr;31(4):937-47
26. Yokoyama Y, Baveja R, Sonin N, Nakanishi, Zhang JX, and Clemens MG. The role of endothelin receptor remodeling in microvascular response after ischemia / reperfusion. Shock 13(1):72-8, 2000.
27. DeMaio A, Gingalewski C, Theodorakis N, Clemens MG. Interruption of hepatic gap junctional communication in the rat during inflammation induced by bacterial lipopolysaccharide. Shock Jul;14(1):53-9, 2000
28. Baveja R, Zhang JX, and Clemens MG. Endothelin-1 induces microheterogeneity of hepatic tissue PO_2 *in vivo* Shock (in press)
29. Yokoyama Y, Baveja R, Sonin N, Clemens MG, Zhang JX Hepatic neovascularization after partial portal vein ligation: novel mechanism of chronic regulation of blood flow. Am J Physiol Gastrointest Liver Physiol. 280(1): G21-G31, 2001
30. Clemens, M.G. Nitric Oxide in the Liver. *In* The Liver: Biology and Pathobiology; I. Arias, Ed. (in Press)
31. Lee C, Zhang JX, deSilva H, Coger R and Clemens MG. Heterogeneous flow patterns during hypothermic machine perfusion preservation of livers. Transplantation 70: 1797-1811, 2000.
32. McConnell NA, Yunus RS, Gross SA, Bost KL, Clemens MG, Hughes FM Jr. Water permeability of an ovarian antral follicle is predominantly transcellular and mediated by aquaporins. Endocrinology 2002 Aug;143(8):2905-12
33. Baveja R, Yokoyama Y, Korneszczuk K, Zhang JX, Clemens MG. Endothelin 1 impairs oxygen delivery in livers from LPS-primed animals. Shock 2002 May;17(5):383-8
34. Yokoyama Y, Alterman DM, Sarmadi AH, Baveja R, Zhang JX, Huynh T, Clemens MG. Hepatic vascular response to elevated intraperitoneal pressure in the rat. J Surg Res 2002 Jun 15;105(2):86-94
35. Baveja R, Keller S, Yokoyama Y, Sonin N, Clemens MG, Zhang JX. LPS-induced imbalanced expression of hepatic vascular stress genes in cirrhosis: possible mechanism of increased susceptibility to endotoxemia. Shock 2002 Apr;17(4):316-21
36. Yokoyama Y, Baveja R, Kresge N, Sonin N, Nakanishi K, Zhang JX, Gitzelmann CA, Clemens MG Endothelin receptor remodeling induces the portal venous hyper-response to endothelin-1 following endotoxin pretreatment.. Shock 2002 Jan;17(1):36-40
37. Yokoyama Y, Wawrzyniak A, Baveja R, Sonin N, Clemens MG, Zhang JX. Altered endothelin receptor expression in prehepatic portal hypertension predisposes the liver to microcirculatory dysfunction in rats. J Hepatol 2001 Jul;35(1):29-36
38. Baveja R, Zhang JX, Clemens MG. In vivo assessment of endothelin-induced heterogeneity of hepatic tissue perfusion. Shock 2001 Mar;15(3):186-92
39. Lee CY, Zhang JX, Jones JW Jr, Southard JH, Clemens MG. Functional recovery of preserved livers following warm ischemia: improvement by machine perfusion preservation. Transplantation 2002 Oct 15; 74(7):944-51
40. Paxian M, Keller SA, Cross B, Huynh TT, Clemens MG. High resolution visualization of oxygen distribution in the liver in vivo. Am J Physiol Gastrointest Liver Physiol. 2004 Jan;286(1):G37-44.
41. Rensing H, Bauer I, Zhang JX, Paxian M, Pannen BH, Yokoyama Y, Clemens MG, Bauer M. Endothelin-1 and heme oxygenase-1 as modulators of sinusoidal tone in the stress-exposed rat liver. Hepatology. 2002 Dec;36(6):1453-65.
42. Yokoyama Y, Xu H, Kresge N, Keller S, Sarmadi AH, Baveja R, Clemens MG, Zhang JX. Role of thromboxane A2 in early BDL-induced portal hypertension. Am J Physiol Gastrointest Liver Physiol 2003 Mar;284(3):G453-60
43. Paxian M, Keller S, Huynh T, and Mark G. Clemens Perflubron emulsion improves hepatic microvascular integrity and mitochondrial redox state following hemorrhagic shock. Shock. Nov; 20(5): 449-57, 2003 .
35. Paxian M, Keller S, Baveja R, Korneszczuk K, Huynh T, and Mark G. Clemens. Functional link between ET_B receptors and eNOS maintain tissue oxygenation in the normal liver. Microcirculation 11(5):435-49, 2004
36. Ashburn J H,. Rajiv Baveja, Nicole Kresge, Katarzyna Korneszczuk, Steve Keller, Amel Karaa, Yukihiro Yokoyama, Jian X. Zhang, Toan Huynh, and Mark G. Clemens. Remote trauma sensitizes hepatic microcirculation to endothelin via caveolin inhibition of eNOS activity. Shock 22(2):120-30, 2004

37. Lee SM, Clemens MG. Glucagon increases gap junctional intercellular communication via cAMP in the isolated perfused rat liver. Shock. 22(1):82-7, 2004.
38. Lee CY, Jain S, Duncan HM, Zhang JX, Jones JW Jr, Southard JH, Clemens MG. Survival transplantation of preserved non-heart-beating donor rat livers: preservation by hypothermic machine perfusion. Transplantation. 2003 Nov 27; 76(10): 1432-6.
39. Xu H, Lee CY, Clemens MG, Zhang JX. Prolonged Hypothermic Machine Perfusion Preserves Hepatocellular Function but Potentiates Endothelial Cell Dysfunction in Rat Livers. Transplantation 15;77(11):1676-82, 2004.
40. Jain S, Purohit S, Zhang J, Clemens MG, and Lee CY. Visualization of endothelial cell structure during machine perfusion preservation of livers. Proceedings of IMECE 2002, 1-6, 2002.
41. Jain S, Xu H, Duncan H, Jones JW Jr, Zhang JX, Clemens MG, Lee CY. Ex-vivo study of flow dynamics and endothelial cell structure during extended hypothermic machine perfusion preservation of livers. Cryobiology. 2004 Jun;48(3):322-32
42. Keller SA, Paxian M, Ashburn JH , Clemens MG, and Toan Huynh. Kupffer Cell Ablation Improves Hepatic Microcirculation after Trauma and Sepsis. J. Trauma Apr;58(4):740-9, 2005.
43. Keller SA, Paxian M, Lee SM,Clemens MG, and Toan Huynh. Kupffer Cell Ablation Attenuates Cyclooxygenase-2 Expression after Trauma and Sepsis. J Surg ResMar;124(1):126-33, 2005.
44. Kamoun WS, Shin MC, Karaa A, Clemens MG. Quantification of hepatic microcirculation heterogeneity of perfusion: Effects of endothelin-1. Microvasc Res. 2005 May;69(3):180-6.
45. Jain S, Lee CY, Baicu S, Duncan H, Xu H, Jones JW Jr, Clemens MG, Brassil J, Taylor MJ, Brockbank KG. Hepatic function in hypothermically stored porcine livers: comparison of hypothermic machine perfusion vs cold storage. Transplant Proc. 2005 Jan-Feb;37(1):340-1.
46. Xu H, Korneszczuk K, Karaa A, Lin T, Clemens MG, Zhang JX. Thromboxane A2 from Kupffer cells contributes to the hyperresponsiveness of hepatic portal circulation to endothelin-1 in endotoxemic rats. Am J Physiol Gastrointest Liver Physiol. 2005 Feb;288(2):G277-83.
47. Merkel SM, Kamoun W, Karaa A, Korneszczuk K, . Schrum LW and Mark G. Clemens. LPS Inhibits Endothelin-1-Mediated eNOS Translocation to the Cell Membrane in Sinusoidal Endothelial Cells. Microcirculation 12: 433-442, 2005.
48. Karaa A, Kamoun W and Clemens MG. Oxidative stress disrupts nitric oxide synthase activation in liver endothelial cells. Free Radical Biology and Medicine Nov 15;39(10):1320-31, 2005
49. Kamoun WS, Shin MC., Keller S, Karaa A, Huynh T, Clemens MG. Induction of Biphasic Changes in Perfusion Heterogeneity of Rat Liver Following Sequential Stress in Vivo. Shock . Oct;24(4):324-31, 2005.
50. Zinchenko YS., Schrum LW., Clemens M, and Coger RN. Hepatocyte and Kupffer Cells Co-cultured on Micropatterned Surfaces to Optimize Hepatocyte Function. Tissue Engineering (In Press)
51. Karaa A, Kamoun WS, Clemens MG. Chronic Ethanol Sensitizes the Liver to Endotoxin via Effects on Endothelial Nitric Oxide Synthase Regulation. Shock Nov;24(5):447-54, 2005.
52. Kamoun WS, Karaa A, Kresge N, M. Merkel S, Korneszczuk K, Clemens MG. LPS Inhibits Endothelin-1 Induced Endothelial Nitric Oxide Synthase Activation through a Negative Feedback Involving Caveolin-1. Hepatology Jan;43(1):182-90, 2006

Ongoing research support

R01 (DK38201, Years 18-22).
NIH / NIDDK Dec 1, 20055 – Nov 30, 2010.
"Hepatic sinusoidal perfusion in shock"
This study addresses the hypothesis that inflammatory or oxidative stress cause induction of stress-related genes that modulate vascular reactivity. Specifically, the goals were to characterize the expression of endothelin, nitric oxide synthase and heme oxygenase-1 in the liver following endotoxemia or ischemia and to determine the functional implications for the control of blood flow and oxygen delivery in the liver.
Role: Principal investigator:

R01 DK58503 Sept 30, 2001- July 31, 2006

NIH / NIDDK
Engineering Aspects of Liver Support Systems.
This project is an engineering partnership that focuses on the development of improved bioartificial liver support as well as machine perfusion preservation of donor livers.
Role: Principal Investigator

2RO1 DK 060606 0/ 1/ 03 - 5 /31/ 06
NIH / NIDDK
Proastanoids and liver microcirculation in stresses
This project investigates the role of arachadonic acid metabolites, especially thromboxanes in producing microvascular dysfunction following stresses such as cirrhosis and endotoxemia.
Role: Co-Investigator

1R41DK074194-01 May 2006 – Dec 2006
NIH / NIDDK
Recovery and preservation of donation by cardiac death livers
This project tests the efficacy of hypothermic machine preservation in restoring hepatic function following a period of warm ischemia in a swine model. The ultimate goal is to develop a method for recovering donor liver function following cardiac death of the donor.
Role: PI, 10% effort

Completed research support

The Whitaker Foundation Biomedical Engineering Research Grant: 5/01 -5/04.
Machine Perfusion Preservation of Livers for Transplantation.
Goals: The goals of this proposal are to understand the flow dynamics during hypothermic machine perfusion preservation of livers and determine if the effect of shear stress contributes to tissue damage during prolonged preservation.
Role: Collaborator

1R03 AA13282-01 Aug 1, 2001- July 31, 2003
NIH/ NIAAA
Alcohol as a modulator of prefibrotic liver disease
This study investigates the interaction between chronic combined hyperlipidemia and alcohol consumption in the development of hepatic microvascular dysfunction and fibrotic liver disease in the mouse. Dates:
Role: Principal Investigator

BES 9984648: 4/00 - 3/03
National Science Foundation
CAREER: Understanding the Role of Matrix in the Cryopreservation of Liver Systems
The major goal of this proposal is to investigate the effects of cell-ECM interactions on the viability of hepatocytes after storage at low temperature. There is no overlap between this project and the application being considered.
Role: Collaborator

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel on page 1 of the Detailed Cost Estimate form for the initial budget period.

NAME	POSITION TITLE
Brian T. Cooper	Associate Professor, Bioanalytical Chemistry

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
Purdue University; West Lafayette, IN	B.S.	1989	Chemistry
University of Arizona; Tucson, AZ	Ph.D.	1994	Analytical Chemistry
Iowa State University; Ames, IA	Postdoc	1994–1997	Bioanalytical Chemistry

RESEARCH AND PROFESSIONAL EXPERIENCE: Concluding with present position, list, in chronological order, previous employment, experience, and honors. Include present membership on any Federal Government public advisory committee. List, in chronological order, the titles, all authors, and complete references to all publications during the past 3 years and representative earlier publications pertinent to this application. PAGE LIMITATIONS APPLY. DO NOT EXCEED THREE PAGES FOR THE ENTIRE BIOGRAPHICAL SKETCH PER INVESTIGATOR.

Professional Experience

1989	Purdue University. Undergraduate research assistant
1989–1993	University of Arizona. Graduate teaching/research associate
1993	Naval Research Laboratory, Washington, DC. Graduate research assistant
1994–1997	Iowa State University. Postdoctoral research associate
1997–2003	UNC Charlotte. Assistant Professor, Analytical Chemistry
1998–	UNC Charlotte Regional Analytical Chemistry Laboratory. Director of Mass Spectrometry
2003–	UNC Charlotte. Associate Professor, Analytical Chemistry
2004–	UNC Charlotte. Chemistry Graduate Coordinator

Honors

1990	Honorable Mention, NSF Graduate Fellowship competition, University of Arizona
1994–1996	National Institutes of Health (NIH) Postdoctoral Fellowship, Iowa State University
1999	Oak Ridge Associated Universities Junior Faculty Enhancement Award, UNC Charlotte
2000–2004	NSF Faculty Early Career Development (CAREER) Award

Representative Publications/Presentations

1. Cooper, B. T.; Buckner, S. W. "Relaxation of Vibrationally Excited Gas-Phase $Cr(CO)_5^-$," *J. Am. Soc. Mass Spectrom.* **1999**, *10*, 950–957.
2. Cooper, B. T. *J. Am. Chem. Soc.* **2000**, *122*, 3981. Book review of *Microcharacterization of Proteins*, 2nd Ed., Kellner, R.; Lottspeich, F.; Meyer, H. E., Eds., Wiley-VCH: Weinheim, 1999.
3. Gunawardena, H. P.; Childs, A. J.; Ross, C. L.; Cooper, B. T. "Protein MEKC: Surfactant Binding and Monoclonal Antibody Analysis," invited talk, Eastern Analytical Symposium, Atlantic City, NJ, October 2001.
4. Cooper, B. T. *J. Am. Chem. Soc.* **2002**, *124*, 13638–13639. Book review of *Applied Electrospray Mass Spectrometry*, Pramanik, B. N.; Ganguly, A. K.; Gross, M. L., Eds., Marcel Dekker: New York, 2002.
5. Cooper, B. T.; McKinnon, T. A.; Sanzgiri, R.; Hamper, A. M. "Probing Antibody Conformational Microheterogeneity by Surfactant Affinity Capillary Electrophoresis (SurfACE)," poster, HPCE Meeting, San Diego, CA, January 2003.

6. Emory, J. M.; Carlin, C. M.; Cooper, B. T. “Single-Molecule Electrophoresis in Microfabricated Glass Channels,” poster, National ACS Meeting, New Orleans, LA; March 2003.
7. Dixon, K. A.; Cooper, B. T. “Nanoflow Electrospray of Tryptic Digests from Gels Containing Ammonium versus Sodium Dodecyl Sulfate,” poster, ASMS Meeting, Montréal, QC, June 2003.
8. Sullivan, H. M.; Cooper, B. T. “Liquid-liquid Partition Chromatography (LLPC) in an Open-Tubular Format,” poster, National ACS Meeting, San Diego, CA; March 2005.
9. Bullock, K. A.; Xu, Y.; Cooper, B. T. “Affinity Capillary Electrophoresis of Long-Chain Fatty Acid Binding to Serum Albumin,” poster, National ACS Meeting, San Diego, CA; March 2005.
10. Bailey, S. E.; Sanzgiri, R. D.; Cooper, B. T. “Surfactant Affinity Capillary Electrophoresis of Monoclonal Antibodies: Parallel Versus Sequential Binding Mechanisms,” poster, National ACS Meeting, San Diego, CA; March 2005.
11. Sanzgiri, R. D.; McKinnon, T. A.; Cooper, B. T. Intrinsic Charge Ladders of a Monoclonal Antibody in Hydroxypropylcellulose-coated Capillaries,” *Analyst*, **2006**, *131*, 1034–1043.
12. Shelton, S. W.; Cooper, B. T. “Measuring Protein Charge and Size under Simulated Intracellular Conditions,” poster, MSB Meeting, Vancouver, BC, January 2007.

Funding History

1. NIH National Research Service Award (Postdoctoral Fellowship): “Conformational Change Upon Channel Protein Gating,” $45,300, February 1994–February 1996 (Iowa State University).
2. NSF (Major Research Instrumentation, Co-PI): “Acquisition of Liquid Chromatography-Mass Spectrometry instrumentation for the Regional Analytical Chemistry Laboratory,” $139,340 + UNC Charlotte ($147,935) and industrial (Clariant: $10,000; Goulston: $15,000) matches; September 1998–August 2001.
3. ORAU Ralph E. Powe Junior Faculty Award: “Protein Charge States in Aqueous Solution,” $5,000 + $5000 UNC Charlotte match; July 1999–June 2000.
4. NSF: “CAREER: Rapid Ultrasensitive Protein Mapping and Bioanalytical Extension Activities,” $278,800 + $24,000 UNC Charlotte match; February 2000–February 2004 (plus one-year no-cost extension).
5. Research Corporation: “Capillary Electrophoretic Investigations of Conformational Isomerism in Monoclonal Antibodies,” $36,912 + $7,000 UNC Charlotte match; May 2001–May 2003 (plus no-cost extension).

Current and Pending Grants

1. NCBC Institutional Development Grant: “Acquisition of an Automated Tandem Mass Spectrometer: Enabling Proteomics Research in the Charlotte Region,” $248,175 + UNC Charlotte (COIT) and CMC ($150,484 total) matches + UNC Charlotte (COAS, $20,000) post-award supplemental funding, June 2006–June 2007.

Research Students

Career totals:

2 PhD students (Bioinformatics PhD program, interdisciplinary Biology PhD program)
18 MS students (9 completed MS theses; 3 pending; includes 1 co-advisee)
30 BS/BA students (includes 5+ biology and 2 engineering students and 2 co-advisees)
3 high school students

Current group: 1 PhD (rotation) student, 3 Master’s students, 3 undergraduate students.

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
DRÉAU, Didier	Assistant Professor
eRA COMMONS USER NAME	

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 Rennes I, Rennes, France	B.S.	1988	Physiology & Cell Biology
University Blaise Pascal, Clermont-Fd, France	M.S.	1990	Molecular & Cell Biology
College of Agriculture of Rennes, Rennes, France	Ph.D.	1994	Molecular & Cell Biology (Immunology)

A. Positions and Honors.

Positions and Employment

1989-1991 Undergraduate student in Molecular Biology (Mechanism of gene regulation) National Institute for Health and Medical Research (INSERM, Unit 384) Clermont-Ferrand, France
1991-1994 Ph.D. student in Immunology (Allergy mechanisms), Young Ruminant Laboratory, National Institute for Agriculture Research (INRA), Rennes, France and Laboratory of Infectious Pathology and Immunology National Institute for Agriculture Research (INRA), Tours, France
1994-1997 Post-doctoral Fellow with Dr. G. Sonnenfeld (mentor) -"Immunology and stress" and with Dr. W. D. Holder, (mentor)-"Immune responses in melanoma patients treated with Immunotherapy", Dept. General Surgery Research, Carolinas Medical Center, Charlotte NC
1998-2000 Research scientist, Dept General Surgery, Carolinas Medical Center, Charlotte NC
2000-2002 Research Scientist, Faculty, Dept General Surgery, Carolinas Medical Center, Charlotte NC
2003-2004 Research Scientist, Department of Biology, University of North Carolina at Charlotte, Charlotte, NC
2004-Present Assistant Professor, Department of Biology, University of North Carolina at Charlotte, Charlotte, NC

Other Experience and Professional Memberships

1994-1997 Research Fellowship in Infection and Immunology, Carolinas Medical Center, Charlotte NC
1997-1999 Research Fellowship in Cancer Immunology, Carolinas Medical Center, Charlotte NC
1994-2004 Adjunct Assistant Professor, Biology, University of North Carolina at Charlotte, NC
1995-Present Ad hoc reviewer for *Am. J. Dermopathol, Human & Exp. Toxicol*., *Gastroenterology* and *J. Interferon & Cytok Res*
1998-Present Member of the *American Association for Cancer research*
2000-Present Member of the Graduate Faculty, University of North Carolina at Charlotte, NC
2001-Present Member (Founding) and user of the Charlotte Genomics Consortium, a micro-array facility
2005-Present Member of the Bioinformatics Research Center at UNC Charlotte

B. Selected publications.

Peer-reviewed publications

1- Tourmente S., Chapel S., Dréau D., Drake M.E. , Bruhat A., Couderc J.L., Dastugue B., 1993. Enhancer and silencer elements within the first intron mediate the transcriptional regulation of the ß3 tubulin gene by 20-hydroxyecdysone in Drosophila Kc cells. Insect. Biochem. Mol. Biol. 23: 137-143.

2- Bruhat A., Dréau D., Drake M.E., Tourmente S., Chapel S., Couderc J.L., Dastugue B., 1993. Intronic and 5' flanking sequences of the drosophila ß3 tubulin gene are essential to confer ecdysone responsiveness. Mol. Cell. Endocr. 94:61-71.

3- Dréau D., Larré C., Lallès J.P., 1994. Semi quantitative purification and assessment of purity of three soybean proteins, glycinin, ß-conglycinin and a-conglycinin, by SDS-PAGE electrophoresis, densitometry and immunoblotting. J. Food Sci. Technol., 31: 489-493.

4- Dréau D., Lallès J.P., Philouze-Romé V., Toullec R., Salmon H., 1994. Local and systemic immune responses to soybean protein ingestion in early weaned pigs. J. Anim. Sci., 72: 2090-2098.

5- Dréau D., Lallès J.P., Salmon H., Toullec R., 1995. IgM, IgA, IgG1 and IgG2 specific levels in blood and gut secretion of calves fed soyabean products. Vet. Immunol. Immunopathol., 47: 57-68.

6- Dréau D., Lallès J.P., Toullec R., Salmon H., 1995. B and T lymphocyte densities are enhanced in the gut of piglets fed heat-treated soyabean proteins. Vet. Immunol. Immunopathol., 47: 69-79.

7- Lallès J.P., Dréau D., Huet A., Toullec R., 1995. Systemic and local gut-specific antibody responses in preruminant calves sensitive to soya. Res. Vet. Sci., 59: 56-60.

8- Dréau D., Lallès J.P., Lejan C., Toullec R., Salmon H., 1995. Hypersensitivity to soybean proteins in early weaned piglets: humoral and cellular components. Adv. Exp. Med. Biol. 371B: 865-871.

9- Lallès J.P., Dréau D., Salmon H., Toullec R., 1996. Identification of soyabean allergens and immune mechanisms of dietary sensitivities in preruminant calves. Res. Vet. Sci., 60: 111-116.

10- Lallès J.P., Dréau D., Féménia F., Parodi A.L., Toullec R., 1996. Feeding heated soyabean flour increases the density of B and T lymphocytes in the small intestine of preruminant calves. Vet. Immunol. Immunopathol., 52: 105-115.

11- Dréau D., Morton D., Foster M., Swiggett J.P., Sonnenfeld G., 1997. Immune alterations in male and female mice after 2-deoxy-D-glucose administration. Physiol Behav, 62 (6): 1325-1331.

12- Dréau D., Morton D., Fowler N., Foster M., Sonnenfeld G., 1998. Effects of 2-deoxy-D-glucose administration on immune parameters in mice. Immunopharmacology, 39 (3): 201-213.

13- - Dréau D., Bosserhoff A.-K., White R.L., Holder W.D, 1999. Melanoma-inhibitory activity protein concentrations in the blood of melanoma patients treated with immunotherapy. Oncology Research, 11: 55-61.

14- Dréau D., Lallès J.P., 1999. Contribution to the study of gut hypersensitivity reactions to soyabean proteins in preruminant calves and early-weaned piglets. Livest. Prod. Sci., 60: 209-218.

15- Dréau D., Sonnenfeld G., Morton D.S., Fowler N., Lyte M., 1999. Effects of social conflict on immune responses and *Escherichia coli* growth within peritoneal implant chambers in mice. Physiol Behav, 67: 133-140.

16- Dréau D., Morton D.S., Foster M., Fowler N., Sonnenfeld G., 2000. Effects of 2-deoxy-D-glucose administration on cytokine production in BDF_1 mice. J. Interf. Cytok. Res., 20: 247-255.

17- Dréau D., Culberson C., Wyatt S., Holder W.D, 2000. Human Papilloma virus in melanoma biopsy specimens and its relation to melanoma progression. Ann. Surg., 231: 664-671.

18- Dréau D., Foster M., Morton D.S., Fowler N., Kinney K., Sonnenfeld G, 2000. Immune alterations in three mouse strains following 2-deoxy-D-glucose administration. Physiol Behav, 70:1-8.

19- Bosserhoff A.K., Dréau D., Hein R., Landthaler M., Holder W.D., Buettner R., 2001. Melanoma inhibitory activity (MIA), a serological marker of malignant melanoma. Recent Results in Cancer Res., 158:158-168.

20- Dréau D., Foster M., Hogg M., Swiggett J., Holder W.D., White R.L, 2001. Angiogenic and immune parameters during Interferona2b adjuvant treatment in melanoma patients. Oncol. Res, 12:241-251.

21- Brar, S.S., Grigg, C., Wilson, K.S., Holder, W.D.,Jr., Dréau, D., Austin, C., Foster, M., Ghio, A.J., Whorton, A.R., Stowell, G.W., Whittall, L.B. Whittle, R.R., White, D.P., Kennedy, T.P., 2004. Disulfiram inhibits activating transcription factor/cyclic AMP-responsive element binding protein and human melanoma growth in a metal-dependent manner in vitro, in mice and in a patient with metastatic disease. Mol Cancer Ther, 3:1049-1060.

22- Carbonell A.M., Matthews B.D., Dréau D., Foster M., Austin C.E., Kercher K.W., Sing R.F., Heniford B.T., 2005. The susceptibility of prosthetic biomaterials to infection. Surg Endosc. 19:430-435.

23- Dréau D., Karaa A., Culberson C., Wyan H., McKillop I.H., Clemens M.G., 2006. Bosentan® inhibits tumor vascularization and bone metastasis in an immune competent skin-fold chamber model of breast carcinoma cell metastasis. Clin Exp Metastasis, 23:41-53.

Invited Presentations:

1- Dréau D., Lallès J.P., Lejan C., Toullec R., Salmon H., 1993. Influence de la portée sur l'hypersensibilité du porcelet aux protéines de soja lors du sevrage. (French) “Journées de Rech Porcine en France” vol. 25, p 209-214.

2- Dréau D., Lallès J.P., Chevaleyre C., Toullec R., Salmon H., 1993. Effects of antigenic soyabean on gut tissues in early weaned piglets. In “Rec. Adv. ANF in legume seeds”, EAAP Publication, Pudoc Scientific Publisher, Wageningen, Pays-Bas. vol. 70, p 271-274.

3- Dréau D., Lallès J.P., Philouze-Romé V., Toullec R., Salmon H., 1994. Effect of maternal transfer on specific IgG1 levels in early-weaned piglets fed soyabean. In “Proceeding of the 6th International Symposium on Digestive Physiology in Pigs”, vol. 2, p. 308-311.

4- Dréau D., Lyte M., Fowler N., Morton D., Sonnenfeld G., 1997. Social conflict stress, immune responses and resistance to infection. In E. Faist Ed. "The Immune Consequences of Trauma Shock and Sepsis". Monduzzi Editore, Editore, Bologna, Italy. p. 119-122.

5- Dréau D., Wyan H., Culberson C., Clemens M.G., 2006. Endothelin-1 and the development of breast cancer bone metastases. 2006 Komen Mission Conference, June 11-13, 2006, Washington, DC.

Manuscripts Under Review / In Preparation:

1- Dréau D., Foster M., Hogg M., Nunes P., Wuthier R.E. Inhibitory effects of Fusarochromanone on melanoma growth. In preparation.

Recent Presentations and Meetings:

1- Bosserhoff A.K., Hein R., Dréau D., Stoltz W, Landthaler M, Buettner R., 1999. MIA, a serological marker of malignant melanoma. J. Invest. Dermatol., 113:515.

2- Dréau D., Foster M, Hogg, M., Swiggett J., Culberson, C., Holder, W.D., 2000. Production of vascular endothelial growth factor and interleukin-8 by high and low MIA-producing melanoma cells in vitro, Proc. Am. Assoc. Cancer Res., 41, 209.

3- Evans L., Austin, C., Dréau D., Morton D., Coleman S., Swiggett J., Loebsack A., Holder, W.D., Klitzman B., Halberstadt C., 2000. Characteristics of green fluorescent protein-labeled human pre-adipocytes, NC Biothechnology Annual Meeting (Durham, NC).

4- Mostafa G., Matthews B., Dréau D., Austin C., Foster M., Culberson C., Henniford T., 2002. Ischemia/reperfusion with CO_2 pneumoperitoneum in a porcine model. Annual meeting of the society of american gastrointestinal endoscopic surgeons (SAGES), New York, March 13-15 [Research Award 2002].

5- Dréau D., Karaa A., Culberson C. Clemens M.G., 2005. Vascularization changes during the development and progression of bone metastases in a new immunocompetent model of mouse mammary carcinoma. FASEB meeting, April 2005, San Diego, CA.

6- Dréau D., Wyan H., Karaa A., Culberson C., McKillop I.H., Clemens M.G., 2006. Endothelin and breast cancer metastases to bone in vivo. 97th AACR Annual Meeting, April 1-5, 2006, Washington, DC.

C. Research Support.

Completed Research Support

1- Research grant 03/01/1999-06/30/2003
Charlotte-Mecklenburg Health Services Foundation, Inc.
Conversion, maturation and sensitization of human dendritic cells to cancer antigens
The major goal of this project was to optimize the conditions for use of dendritic cells to initiate a specific immune response in cancer patients.
Role: Co-Principal Investigator (R.L. White, Co-PI)

2- Research grant 09/01/2000-06/30/2003
Charlotte-Mecklenburg Health Services Foundation, Inc.
Genetic mutations in tumor suppressor genes and oncogenes in melanoma
The major goal of this project was to determine the frequency of Ras mutations and genetic alterations at the locus 9p21 are present in melanoma biopsy and derived cell lines.
Role: Principal Investigator

3- Research grant 06/01/2002-06/30/2003
Charlotte-Mecklenburg Health Services Foundation, Inc.
Differences in the expression of genes involved in metastases following transplantation of melanoma tumor cells in SCID mice
The major goal of this project is to determine whether the variations in gene expression between melanoma cell lines with different potential for metastatic growth in vivo using microarray technology.
Role: Principal Investigator

4- Research grant 07/01/2002-03/30/2003
Charlotte-Mecklenburg Health Services Foundation, Inc.
Anti-tumorigenic effects of fusarochromanone on the growth of solid tumors in vivo
The major goal of this project is to determine whether in vivo effects of fusarochromanone are associated with both anti-angiogenic and anti-tumoral effects on human melanoma growth in a SCID mouse model.
Role: Principal Investigator

5- Research grant 07/01/2002-02/28/2003
AAI/Research (Wilmington, NC)
Effects of gold dithiocarbamate (GTC) on the growth of human melanoma tumor cells in a SCID mouse model
The major goal of this project is to determine whether in vivo effects of gold dithiocarbamate are associated with significant anti-tumoral effects on human melanoma growth in a SCID mouse model.
Role: Principal Investigator

6- Research equipment grant 07/01/2001-N/A
North Carolina Biotechnology Center, Research Triangle Park, NC
The Charlotte Genomics Consortium: development of a Microarray facility
This consortium equipped the Charlotte research community with a facility for microarray analyses
Role: Co-Investigator (M.G. Clemens, PI)

Ongoing Research Support

1- Research grant 01/10/2005-06/15/2006
University of North Carolina at Charlotte
Skin-fold chamber model of breast cancer bone metastases
The major goal of this project is to refine an immunocompetent murine model of early events associated with breast cancer metastases to bone.
Role: Principal Investigator

2- Research grant 03/15/2005-02/14/2010
Department of Defense – Era of Hope Scholars Program
3D test systems: new tools for unlocking the mysteries of breast cancer
The major goal of this project is to develop an in vitro 3D system to study breast cancer. Our aspect of the proposed research focuses on the analyses of cell-cell interactions associated with the development of breast cancer using in vitro systems.
Role: Co-Investigator (K.J.L. Burg PI)

3- Research grant 05/01/2005-04/30/2007
The Susan B. Komen Breast Cancer Foundation
Endothelin-1 Effects on the Development of Breast Cancer Bone Metastases
The major goal of this project is to determine the role of the endothelin axis in the development of bone metastases in an immunocompetent model of breast cancer metastases to bone.
Role: Principal Investigator

4- Research grant 06/01/06-05/31/08
The brain Tumor Fund
Alterations of gene expression and the development of brain metastases

The major goal of this project is to determine the genetic differences in primary tumor between patients developing or not brain cancer metastases.
Role: Principal Investigator

There is no overlap between this project and the application being considered

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
Fodor Anthony A.	Assistant Professor
eRA COMMONS USER NAME AFODOR	

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
Vassor College, Poughkeepsie, NY	B.A.	1988	Cognitive Science
University of Washington, Seattle, WA	Ph.D.	1997	Physiology & Biophysics
Stanford University, Palo Alto, CA	Post-Doc	2002-2005	Computational Biology

A. Positions and Honors.

Positions and Employment

1999-2000 Lead Developer, Punch Networks, Seattle, WA
2000-2001 Java Instructor, Java 2 Enterprise Programming Certificate, University of Washington, Seattle, WA, (Part-time)
2000-2002 Software Developer, Department of Bioinformatics, Immunex Corporation (Now Amgen), Seattle, WA
2002-2005 Research Specialist, Howard Hughes Medical Institute, Department of Molecular and Cellular Physiology, Stanford University, Palo Alto, CA
2005-present Assistant Professor, Bioinformatics Research Center, Department of Computer Science, University of North Carolina-Charlotte, Charlotte, NC

Other Experience and Professional Memberships

Honors

1988 Phi Beta Kappa prize for most outstanding academic record in graduating class
National Institutes of Health T32 Training Grant

B. Selected peer-reviewed publications.

Journal Publications

1. **Fodor A.A.**, Gordon S.E., Zagotta, W.N. *Mechanism of tetracaine block of cyclic nucleotide-gated channels. Journal of General Physiology.* 1997 Jan;109(1):3-14.
2. **Fodor A.A.**, Black K.D., Zagotta, W.N. *Tetracaine reports a conformational change in the pore of CNG Channels. Journal of General Physiology.* 1997 Nov;110(5):591-600.
3. **Fodor A.A.**, Aldrich, R.W. *On evolutionary conservation of thermodynamic coupling in proteins.* Journal of of Biological Chemistry. 2004 Apr 30;279(18):19046-50.
4. Dekker J.P., **Fodor A.A.**, Aldrich R.W., Yellen G. *A perturbation-based method for calculating explicit likelihood of evolutionary co-variance in multiple sequence alignments.* Bioinformatics. 2004 Jul 10;20(10):1565-72.
5. **Fodor A.A.**, Aldrich R.W. *Influence of conservation on calculations of amino acid covariance in multiple Sequence alignments. Proteins: Structure, Function and Bioinformatics.* 2004 Aug 1;56(2):211-21.
6. **Fodor A.A.**, Aldrich R.W. *Statistical Limits to the Identification of Ion Channel Domains by Sequence Similarity.* JGP 127(6), 755-766, 2006.

7. Meredith A.L., Wiler S.W., Miller B.H., Takahashi, J.S., **Fodor A.A.**, Ruby, N.F., Aldrich, R.W. BK *Calcium-activated potassium channels regulate circadian behavioral rhythms and pacemaker output.* Nature Neuroscience, 9, 1041-1049, 2006.
8. Pyott S.J., Meredith A.L., **Fodor A.A.**, Va'zquez A.E., Yamoah E.N., Aldrich, R.W. *Cochlear function in mice lacking the bk channel alpha, beta-1, OR beta-4 Subunits.* In revision. JBC.

C. Research Support

Ongoing Research Support

North Carolina Biotechnology Center — Role: Participant
UNCC Functional Genomics Core Facility

Completed Research Support

None.

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
Gibas, Cynthia J.	Associate Professor
eRA COMMONS USER NAME	

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, Appleton, WI	B.A.	1990	Chemistry
University of Illinois at Urbana-Champaign, Urbana, IL	Ph.D.	1996	Biophysics and Computational Biology
University of Illinois at Urbana-Champaign Urbana, IL	Post-Doc	1996-1998	Molecular and Integrative Physiology

A. Positions and Honors.

Positions and Employment

1996-1998 Postdoctoral Research Associate in Molecular and Integrative Physiology, University of Illinois at Urbana-Champaign, Urbana, IL
1998-1999 Research Programmer, National Center for Supercomputing Applications
1999-2000 Research Assistant Professor, Fralin Biotechnology Center, Virginia Tech, Blacksburg, VA
2000-2005 Assistant Professor, Virginia Tech, Blacksburg, VA
2005-present Associate Professor, Computer Science/ Bioinformatics Research Center, University of North Carolina-Charlotte, Charlotte, NC

Honors

1990 National Institutes of Health NRSA in Cell and Molecular Biology
1994 Department of Education GAANN Fellowship in Computational Biology

B. Selected peer-reviewed publications.

1. **Gibas C.J.**, Subramaniam S. (1996). *Explicit solvent models in protein pKa calculations.* Biophysical Journal, 71(1):138-47.
2. **Gibas C.J.**, Subramaniam S. (1997). *Knowledge-based design of a soluble bacteriorhodopsin.* Protein Engineering, 10(10):1175-90.
3. **Gibas C.J.**, Subramaniam S., McCammon J.A., Braden B.C., Poljak R.J. (1997). *PH dependence of antibody/lysozyme complexation.* Biochemistry, 36(50):15599-614.
4. Herrgard S., **Gibas C.J.**, Subramaniam S. (2000). *Role of an electrostatic network of residues in the enzymatic action of the Rhizomucor miehei lipase family.* Biochemistry, 39(11):2921-30.
5. **Gibas C.J.**, Jambeck P., Subramaniam S. (2000). *Continuum electrostatic methods applied to pH-dependent properties of antibody-antigen association.* Methods, 20(3):292-309.
6. **Gibas C.**, Sturgill D., Weller J. (2003). *GenoMosaic: On-demand multiple genome comparison and comparative annotation.* In: Proceedings of the IEEE Symposium on Bioinformatics and Bioengineering.
7. Halling S., **Gibas C.**, Boyle S. (2004). *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.
8. Kaluszka A.*, **Gibas C.** (2004). *Genome organization analysis tool.* Bioinformatics, 20(18):3662-3664.
9. Ratushna V.*, Weller J., **Gibas C.** (2005). *Secondary structure in the target as a confounding factor in synthetic oligomer microarray design.* BMC Genomics, 6(1), 31.

10. Ratushna V.*, Sturgill D.*, Ramamoorthy S., Reichow S., He Y., Lathigra R., Sriranganathan N., Halling S., Boyle S. **Gibas C.J.** (2006). *Molecular targets for rapid identification of Brucella spp.* BMC Microbiology 6, 13.
11. Karanam R.K., Ravindran A., Mukherjee A., **Gibas C.J.**, Wilkinson A.B. (2006). *Using FPGA-based hybrid computers for bioinformatics applications.* XCell Journal, 58:80-83.

C. Research Support.

Ongoing Research Support

Biophysical Optimization of Oligonucleotide Microarrays
5R01GM072619-02
PI: Gibas C.J. — August 2005 – July 2010
National Institutes of Health — Role: PI

UNCC Functional Genomics Core Laboratory
PI: Gibas, C.J. — August 2006 – August 2007
North Carolina Biotechnology Center — Role: PI

Completed Research Support

Isolation of Genes for Transgenic Production of a Diabetes Treatment
PI: Gillaspy — July 2001 – December 2002
Commonwealth Health Research Board — Role: Co-PI

BIOGRAPHICAL SKETCH

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

NAME	POSITION TITLE
Alexander Y. Gordon	Assistant 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
Moscow State University (Moscow, Russia)	M.S.	1970	Mathematics
Moscow Institute of Electronic Engineering _(Moscow, Russia)	Ph.D.	1988	Mathematics

A. Positions and Honors

Positions and Employment

1971-1989 Software Engineer, Senior Software Engineer, Project Leader, Automated Control Systems Department, Moscow Transport Administration (Moscow, Russia)
1990-1993 Senior Research Fellow, Moscow Research and Design Institute of Urban Transportation (Moscow, Russia)
1993-1994 Senior Research Fellow, International Institute of Earthquake Prediction Theory and Mathematical Geophysics of Russian Academy of Sciences (Moscow, Russia)
1994-1994 Visiting Research Fellow, Observatory of Nice (Nice, France)
1995-1998 Visiting Assistant Professor, Lecturer, Visiting Research Assistant Professor, Department of Mathematics, University of North Carolina at Charlotte (Charlotte, NC)
1999-2002 Senior Software Engineer/Research Mathematician, ``PDH International'' (Hallandale, FL)
2002-2004 Analyst/Programmer Lead, University of Rochester, Department of Biostatistics and Computational Biology, University of Rochester (Rochester, NY)
2004-2006 Assistant Professor, Department of Biostatistics and Computational Biology, University of Rochester (Rochester, NY)
2006 - Assistant Professor, Department of Mathematics and Statistics, University of North Carolina at Charlotte (Charlotte, NC)

Member of the Moscow Mathematical Society (1988);
Member of the International Association of Mathematical Physics (1994).

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

Selected Papers (out of 35 peer reviewed papers):

1. Gordon, A. Y. On the point spectrum of one-dimensional Schroedinger operator, *Russian Mathematical Surveys*, 1976, 31: 257--258 (in Russian).

2. Gordon, A.Y. An algorithm for the solution of the minimax scheduling problem. In ``*Studies in Discrete Optimization*'', Moscow, ``Nauka'', 1976: 327--333 (in Russian).

3. Gordon, A.Y. Continuous spectrum of a one-dimensional Schroedinger operator, *Functional Analysis and its Applications*, 1979, **13**, 218—219.

4. Gordon, A.Y. An example of an analytic flow on a torus with a mixed spectrum, In *Theory of Functions, Functional Analysis and their Applications*, 1980, No. 33, Kharkov University Press, Kharkov, 40—45. English translation: *Selecta Mathematica Sovetica*, 1989, **8**, 292--298, Birkhaeuser Verlag, Basel.

5. Gordon, A.Y. A sufficient condition for the continuity of the spectrum of a discrete Schroedinger operator. *Functional Analysis and its Applications* **20**, 1986, 313--315.

6. Gordon, A.Y. A deterministic potential with pure point spectrum. *Mathematical Notes*, 1990, **48**, 1197--1203.

7. Gordon, A.Y. On the inverse problem of the best approximation by the entire functions of exponential type. In: ``*Studies in the theory of functions of several real variables*". -- Yaroslavl University Press, Yaroslavl, 1990 (in Russian). -- English version in: *Lecture Notes in Mathematics* **1043** (Linear and Complex Analysis Problem Book), Springer--Verlag, 1984, 592--594.

8. Gordon, A.Y., Molchanov, S. A., and Tzagani, B. Spectral theory of one-dimensional Schroedinger operators with strongly fluctuating potentials. *Functional Analysis and its Applications*, 1991, **25,** 236--238.

9. Gordon, A.Y. On exceptional values of boundary phase for Schroedinger equation on the half-axis. *Russian Mathematical Surveys*, 1992, **47**, 260—261

10. Gordon, A.Y., Maslov, V.P., and Molchanov, S.A. Behavior of generalized eigenfunctions at infinity and the Schroedinger conjecture. *Russian Journal of Mathematical Physics*, 1993, **1**, 71--104.

11. Gordon, A.Y., Jaksic, V., Molchanov, S.A., and Simon, B. Spectral properties of random Schrodinger operators with unbounded potentials. *Communications in Mathematical Physics*, 1993, **157,** 23--50.

12. Gordon, A.Y. Pure point spectrum under one-parameter perturbations and instability of Anderson localization. *Communications in Mathematical Physics*, 1994, **164**, 489--505.

13. Gordon, A.Y. Strong unboundedness of unbounded analytic functions. *Proceedings of the American Mathematical Society*, 1994, **122**, 525--529.

14. Gordon, A.Y. A fast algorithm for the solution of the inviscid Burgers equation. In: "*Computational Seismology*" **29**, Moscow, 1997, 179--189 (in Russian).

15. Gordon, A.Y. Instability of dense point spectrum under finite rank perturbations. *Communications in Mathematical Physics*, 1997, **187**, 583--595.

16. Gordon, A.Y., Jitomirskaya, S., Last, Y., and Simon, B. Duality and singular continuous spectrum in the almost Mathieu equation. *Acta Mathematica*, 1997, **178**, 169--183.

17. Gordon, A.Y. Purely continuous spectrum for generic almost-periodic potential. -- In*: Contemporary Mathematics*, 1998, **217**, 183--189.

18. Figotin, A., Gordon, A.Y., Molchanov, S.A., Quinn, J.E., and Stavrakas, N. Occupancy numbers in testing random number generators. -- *SIAM Journal of Applied Mathematics*, 2002, **62**, 1980--2011.

19. Derfel, G., Gordon, A.Y., and Molchanov, S.A. Random matrices over Z/pZ and testing random number generators. -- *Random Operators and Stochastic Equations*, 2004, **12**, 1-10.

20. Xiao, Y., Frisina, R., Gordon, A.Y., Klebanov, L., and Yakovlev, A Multivariate search for differentially expressed gene combinations. - *BMC Bioinformatics*, 2004, 5:134.

21. Dow, A., Ganguli, S., Gordon, A.Y., and Molchanov, S. A problem by E. Landis and generic behavior of non-generic sets. *Applicable Analysis* 84 (2005), pp. 927-952.

22. Glazko, G., Gordon, A., and Mushegian, A. The choice of optimal distance measure in genome-wide data sets. - *Bioinformatics* 2005 21: iii3-iii11.

23. Qiu, X., Xiao, Y., Gordon, A., and Yakovlev, A. Assessing stability of gene selection in microarray data analysis. - *BMC Bioinformatics* 2006 7:50

24. Klebanov, L., Gordon, A., Xiao, Y., Land. H., and Yakovlev, A. A permutation test motivated by microarray data analysis. *Computational Statistics and Data Analysis* 50 (2006), pp. 3619-3628.

25. Xiao, Y., Gordon, A. and Yakovlev, A. The L1-version of the Cramer-von Mises test for two-sample comparisons in microarray data analysis - *EURASIP Journal on Bioinformatics and Systems Biology* Volume 2006, Article ID 85769, pp. 1-9. doi:10.1155/BSB/2006/85769

26. Xiao, Y., Gordon, A. and Yakovlev, A. C++ package for the Cramer-von Mises two-sample test. - Accepted for publication in *Journal of Statistical Software*.

27. Gordon, A.Y. Explicit formulas for generalized family-wise error rates and unimprovable step-down multiple testing procedures. - Accepted for publication in *Journal of Statistical Planning and Inference*.

28. Gordon, A.Y. Unimprovability of the Bonferroni procedure in the class of general step-up multiple testing procedures. - *Statistics and Probability Letters* 77 (2007), pp. 117-122. doi:10.1016/j.spl.2006.07.001 (available online at www.sciencedirect.com)

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
Donald J. Jacobs	Assistant Professor
eRA COMMONS USER NAME DJACOBS1	

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
Fulton-Montgomery Comm. College, Johnstown, NY	A.S.	1983	Engineering Science
Union College, Schenectady, NY	B.S.	1985	Physics
Purdue University, West Lafayette, IN	Ph.D.	1992	Physics
Inst. of Theor. Physics, Univ. of Utrecht, Netherlands	Post-Doc	1992-1994	Physics
Michigan State University, Lansing, MI	Res-Assoc	1994-1997	Physics

A. PROFFESIONAL EXPERIENCE

Positions

2005-present Assistant Professor of Physics, University of North Carolina at Charlotte (UNCC)
2005 (Fall) Unpaid leave, Associate Professor of Physics; California State University, Northridge (CSUN)
1999-2005 Assistant Professor of Physics; CSUN
1999-2001 Acting president to MolFlex LLC
1998-1999 President and Director of Research, MolFlex LLC
1998-1999 Assistant Research Professor of Physics, Michigan State University
1994-1996 Part-time Instructor (50% time), Michigan State University

Honors

2005 Sabbatical leave granted for fall 2005 based on Outstanding Scholarly Merit (CSUN) **(unused)**
1992 Edward F. Akeley Memorial Award for outstanding theoretical Physics Thesis
1985 Graduated *Magna Cum Laude,* Union College, Schenectady, New York
1983 Who's Who Among Students in American Junior Colleges

Professional activities

2006-current Currently supervising two post doctorial researchers, and one Senior Research Associate, one MS student and 3 Undergraduate Students.
2005-current Focus leader within the Center for Biomedical Engineering Systems on Biomedical Modeling, Imaging & Processing, UNC-Charlotte.
2005-current Member of Bioinformatics and Interdisciplinary Biology Ph.D. Programs at UNC-Charlotte.
2005-current Leading the development of a new Ph.D. program in Applied Physics, emphasizing Biophysics
2001-2005 Program developer and coordinator for Undergraduate Biomedical Physics Program at CSUN
2001-2005 Member of the Center for Supramolecular Studies and Interdisciplinary Mathematical Research and Education Center, CSUN
2001-2005 Society of Physics Students Advisor, CSUN
2001 Steering committee for the California Science Project Site at CSUN
1999-current Reviewed over 28 manuscripts, half of which for Physical Review Letters. Reviewed 3 NSF proposals: ITR-ASE (2004) and 2 DMR (2005). Reviewed 3 Physics textbooks: Two calculus-based introductory books and an upper level biophysics by Phil Nelson.

1999-2005 Thesis Advisor for 5 completed MS thesis.

2003-2005 Supervised 2 Post-doctoral Researchers: Dr. G. Wood (Now Assistant Prof. of Physics at CSU Channel Island) & Dr. S. Dallakayan (Now Level III Scientific Programmer at Scripps Institute)

B. PUBLICATIONS (#,$ indicates Jacobs lab graduate student and research associates respectively)

1. Wei Cai, Shaozhong Deng and D.J. Jacobs, *Extending the Fast Multipole Method to Charges Inside or Outside a Dielectric Sphere*, Journal of Computational Physics, (preprint 06_06) **in press**.
2. D.J. Jacobs, *Predicting Protein Flexibility and Stability using Network Rigidity: A new Modeling Paradigm*. **Invited Review:** Recent Research Developments in Biophysics, **5**, 71-131 ISBN 81-7895-215-7 Publisher: Transworld Research Network, Trivandrum, India, (2006)
3. D.R. Livesay, D.J. Jacobs, J. Kanjanapangka, H. Cortez, J. Garcia, P. Kidd, M.P. Marquez, S. Pande, D. Yang, and E. Chea, *Elucidating the conformational dependence of calculated pKa values.* Journal of Chemical Theory and Computation, **2**(4), 927-938 (2006)
4. D.J. Jacobs, D.R. Livesay, J. Hules# and M.L. Tasayco, *Elucidating quantitative stability/flexibility relationships within thioredoxin and its fragments using a distance constraint model.* Journal of Molecular Biology. Journal of Molecular Biology. **358**, 882-904 (2006)
5. D.R. Livesay and D.J. Jacobs *Conserved quantitative stability/flexibility relationships (QSFR) in an orthologous RNase H pair*. Proteins: Structure, Function, and Bioinformatics. **62**, 130-43 (2006)
6. D. J. Jacobs and S. Dallakayan$, *Elucidating Protein Thermodynamics from the Three Dimensional Structure of the Native State Using Network Rigidity*. Biophysical Journal, **88**, 903-915 (2005)
7. D.R. Livesay, S. Dallakyan$, G.G. Wood$ and D.J. Jacobs, *A flexible approach for understanding protein stability*. FEBS Letters, **576**, 468-476 (2004)
8. M.S. Lee#, G.G. Wood$ and D.J. Jacobs, *Investigations on the alpha-helix to coil transition in HP-heterogeneous polypeptides using network rigidity*. J. Phys. Cond. Mat. **16**, S5035-S5046 (2004)
9. B.M. Hespenheide, D.J. Jacobs and M.F. Thorpe, *Structural rigidity in the capsid assembly of cowpea chlorotic mottle virus*. J. Phys. Cond. Mat. **16**, S5055-S5064 (2004)
10. D.J. Jacobs and G.G. Wood$, *Understanding the α-Helix to Coil Transition in Polypeptides Using Network Rigidity: Predicting Heat and Cold Denaturation in Mixed Solvent Conditions*. Biopolymers, **75** 1-31 (2004).
11. D.J. Jacobs, S. Dallakayan$, G.G. Wood$ and A. Heckathorne#, *Network rigidity at finite temperature: Relationships between thermodynamic stability, the nonadditivity of entropy, and cooperativity in molecular systems*. Phys Rev E **68**, 061109 (2003).
12. D.J. Jacobs, A. Rader, L.A. Kuhn and M.F. Thorpe, *Graph Theory Predictions of Protein Flexibility*. Proteins: Structure, Function, and Genetics **44**: no. 2, 150-155 (2001). **(Featured on cover page)**
13. M.F. Thorpe, A. Rader, M. Lei, D.J. Jacobs, L.A. Kuhn, *Predicting Flexibility in Proteins using Constraint Theory*. Journal of Molecular Graphics and Modeling **19**, 60-69, (2001).
14. M.F. Thorpe, D.J. Jacobs, M.V. Chubynsky and J.C. Phillips, *Self organization in network glasses*. J. Non-Crystalline Solids Volumes **266-269**, pages 859-866 (2000).
15. P.M. Duxbury, D.J. Jacobs, M.F. Thorpe and C. Moukarzel, *Floppy Modes and the Free Energy: Rigidity and Connectivity percolation on Bethe Lattices*. Phys. Rev. E **59**, 2084-2092 (1999).
16. D.J. Jacobs, *Generic Rigidity in Three-dimensional Bond-bending Networks*. J. Phys. A Math. Gen. **31**, 6653-6668 (1998).
17. D.J. Jacobs and M.F. Thorpe, *Comment on "Infinite-Cluster Geometry in Central-Force Networks"*, Phys. Rev. Lett. **80**: no. 24, 5452 (1998).
18. D.J. Jacobs and B. Hendrickson, *An Algorithm for Two Dimensional Rigidity Percolation: The Pebble Game*. J. Comput. Phys. **137**, 346-365 (1997).
19. D.J. Jacobs and M.F. Thorpe, *Generic Rigidity Percolation: The Pebble Game*. Phys. Rev. E **53**, 3682-3693 (1996).
20. D.J. Jacobs & M.F. Thorpe, *Generic Rigidity: The Pebble Game*. Phys. Rev. Lett. **75**, 4051-4054 (1995).

21. J.R. Dorfman, M.H. Ernst, R. Nix and D.J. Jacobs, *Mean Field Theory for Lyapunov Exponents and Kolmogorov-Sinai Entropy in Lorentz Lattice Gases*, Phys. Rev. Lett. **74**, 4417-4410 (1995).
22. J.R. Dorfman, M.H. Ernst and D.J. Jacobs, *Dynamical Chaos in the Lorentz Lattice Gas*. J. Stat. Phys. **81**, 497-513 (1995).
23. S. Mukherjee, D.J. Jacobs and H. Nakanishi, *Diffusion on Loopless Critical Percolation Cluster*. J. Phys. A **28**, 291-296 (1995).
24. D.J. Jacobs, S. Mukherjee and H. Nakanishi, Diffusion on DLA cluster in Two and Three Dimensions, J. Phys. A **27**, 4341-4348 (1994).
25. D.J. Jacobs, and A. Masters, *Domain Growth in a One-dimensional Diffusive Lattice Gas with Short Range Attraction*. Phys. Rev. E **49**, 2700-2710 (1994).
26. D.J. Jacobs and H. Nakanishi, *A Persistent Random Walk Model for the Frequency-Dependent Electrical Conductivity*. Physica A **197**, 204-222 (1993).
27. S. Muralidhar, D.J. Jacobs, D. Ramkrishna and H. Nakanishi, *Diffusion on Percolation Clusters: Influence of Cluster Anisotropy*, Phys. Rev. A **43**, 6503-6517 (1991).
28. S. Muralidhar, D. Ramkrishna, H. Nakanishi and D.J. Jacobs, *Anomalous Diffusion: A Dynamic Perspective*. Physica A **167**, 539-553 (1990).
29. D.J. Jacobs and H. Nakanishi, Autocorrelation Functions for Discrete Random Walks on Disordered Lattice, Phys. Rev. A **41**, 706-719 (1990).

+ 11 more publications in conference proceedings

Patents, Scientific Software and Databases

1. **D.J. Jacobs** and M.F. Thorpe, *Computer Implemented System for Identifying Rigid and Flexible Regions in Macromolecules*, US patent # 6014449, Active in year 2000 (filed in 1997).
2. **D.J. Jacobs**, L.A. Kuhn and M.F. Thorpe, **Software: *FIRST*** (*Floppy Inclusion and Rigid Substructure Topography*). Original release of FIRST resulted from work done at MolFlex (NIH-SBIR with D.J. Jacobs PI). Recent versions are distributed by L.A. Kuhn at MSU under ***ProFlex,*** and by M.F. Thorpe at Arizona State University. FIRST is freeware to academics and licensed to commercial users for profit.
3. **D.J. Jacobs**, *Computer Implemented System for Quantifying Stability and Flexibility Relationships in Macromolecules,* patent discloser filed at patent office (April, 2006)
4. **D.J. Jacobs** and D.R. Livesay, *Computer Implemented System for Protein and Drug Target Design utilizing Quantitative Stability/Flexibility Relationships to control function*, patent discloser submitted to UNC Charlotte Intellectual Property office.
5. **D.J. Jacobs** and D.R. Livesay, **Software: *FAST*** (*Flexibility And Stability Test*). This software is currently being developed through NIH-R01 GM 073082-0181 (D.J. Jacobs PI). FAST will be made freely available to academics and licensed to commercial users and/or used for a spin off company.
6. **D.J. Jacobs** and D.R. Livesay, **Database: *QSFRdb*** (*Quantitative Stability and Flexibility Relationship database*). This publicly available database is being developed through NIH-R01 GM 073082-0181 (D.J. Jacobs PI), which will be used for data mining of thermodynamic/mechanical properties across large numbers of proteins.

C. RESEARCH SUPPORT

In preparation

NIH-R01 *Synergistic Application of Bioinformatics and Biophysical Techniques*

Livesay, D.R. (PI) Dept. of Computer Science and Bioinformatics Research Center, UNC-Charlotte
Role: Co-investigator

NIH-R01 *Fusion of Biochemical Analysis and Advanced Signal Processing for Functional Classification of Proteins*

Najarian, Kayvan (PI) Dept. of Computer Science, UNC-Charlotte
Role: Co-investigator

NSF(DMR)/NIH(NIGMS) Mathematical Biology Initiative: *Numerical Methods for Fast and Accurate Calculation of Electrostatic Interactions in Biomolecular Simulations*
Cai, Wei (PI) Department of Mathematics and Statistics, UNC Charlotte
Role: Co-PI (with Co-PIs Dr. Shaozhong Deng and Andrij Baumketner at UNC Charlotte)

Current

UNC GA Undergrad Research Opportunity Expansion: *Investigations of conformational changes in myosin*
Jacobs, D.J. (PI) Dept. of Physics and Optical Science
Role: Principle investigator $3,500 summer 2006 student stipend for Miss Whitney Hubbard.
In close collaboration with Dr. Chris Yengo (Biology Dept.) who uses Florescence spectroscopy.

Internal SEED grant: *Using Information Visualization to Identify Sequence Pattern Signatures for Alpha Helix Stability within Model HP-Polypeptides*
Yang, Jing. (PI) Computer Science Department, UNC Charlotte
Role: Co-investigator $12,000 from July 1, 2006 to Dec 31, 2007

NIH-R01 GM 073082-01A1: *Predicting protein stability and flexibility*
Jacobs, D.J. (PI) Dept. of Physics and Optical Science
Role: Principle investigator $1,284,144 over 4 yrs from March 1, 2006 to February 28, 2010

NIH-R01 GM073082-01A1S1: *Supplement to: Predicting protein stability and flexibility*
Subproject thesis: *Investigations of Underlying Mechanisms of Allostery in Proteins*
Role: Principle investigator $282,943 over 2 ½ years from Sept. 1, 2006 to February 28, 2009

Recently Completed:

NIH-SCORE *Dihedral-angle characterization of conformational flexibility in protein structure*
S06 GM48680-0952; Zavala, M.E. (Adm. Director)
Role: Principle Investigator $370,328 October 2002 to June 2005

D. RECENT PRESENTATIONS AT SCIENTIFIC MEETINGS

Invited talks

1. Three invited lectures: *Modeling Protein Conformational Flexibility Using Network Rigidity, Modeling Thermodynamic Stability in Polypeptides and Proteins with Non-additive Free Energy Decomposition,* and *Predicting Protein Stability, Flexibility and Molecular Cooperativity***,** TSL Lecture Series 5, Computational Physical Sciences 2006, Universiti Putra Malaysia (Dec 12-15, 2006)
2. *The Role of Mechanics in Understanding Protein Stability, Flexibility and function*. 7th World Congress on Computational Mechanics, Molecular & Cell Biology Symposium, Los Angeles, CA (July 16-22, 2006)
3. *FIRST: A look under the hood*, Workshop on Rigidity, Flexibility and Motion in Biomolecules, Tempe, AZ (May 15-18, 2006)
4. *Predicting Protein Stability Using Network Rigidity at Finite Temperatures.* Second International Conference on Multiscale Materials Modeling (MMM-II), in focus session "Multiscale Modeling of Biomaterials" at UCLA, Los Angeles, CA (October 11-15, 2004)
5. *Protein Stability and Flexibility: Application to Network Rigidity.* Modeling Protein Flexibility and Motions Workshop at Banff International Research Station for Mathematical Innovation and Discovery (BIRS), Banff Canada (July 17-22, 2004)
6. *Network Rigidity at Finite Temperatures and Free Energy Landscapes.* American Mathematical Society, in focus session: Geometry of Protein Modeling, Lawrenceville, NJ (April 17-18, 2004)
7. *Predicting Protein Stability from a Free Energy Decomposition*. Mathematics and Computer Science Workshop: The Geometry of Modeling Proteins, Bellairs Research Institute of McGill University, Holetown, Barbados, West Indies (January 16-23, 2004)

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
Krueger, Joanna K.	Associate Professor
eRA COMMONS USER NAME JKKRUEGE	

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
Kalamazoo College, Kalamazoo, MI.	B.A.	1985	Chemistry
Princeton University	M.A.	1988	Chemistry
Princeton University	Ph.D.	1991	Chemistry
University of TX Southwestern Medical School	Post-Doc	1992-1995	
Los Alamos National Laboratory	Post-Doc	1995-1999	

A. Positions and Honors

Positions and Employments

1983-1985 Research Assistant at KALSEC (Kalamazoo Spice Extraction Company)
1985 Senior Research Student at Texas A & M University
1991-1992 Research Assistant at U.T. Southwestern Medical Center, Dallas, TX.
1992-1995 Post-Doctoral Associate (NIH Fellow, 1993-1995). University of Texas Southwestern Medical Center, Dallas, TX.
1995-1999 Post-Doctoral Associate (NIH Fellow, 1995-1996). Los Alamos National Laboratory
1999-2005 Assistant Professor, Department of Chemistry, University of North Carolina-Charlotte, Charlotte, NC
2005-present Associate Professor, Department of Chemistry, University of North Carolina-Charlotte, Charlotte, NC

Honors

1982-1985 F.W. and Elsie L. Heyl Scholarship – Full tuition paid undergraduate scholarship
1993-1994 Cardiology Training Fellowship – National Institutes of Health
1994-1996 National Institutes of Health NRSA – A two-year post-doctoral fellowship awarded by the National Heart, Lung and Blood Institute
2001-2002 Oak Ridge Associated Universities Ralph E. Powe Junior Faculty Enhancement Award
2003-2008 National Science Foundation CAREER Award

B. Selected peer-reviewed publications

1. Bassel-Duby R., Hernandez M. L., Gonzalez M. A., **Krueger J. K.**, and Williams R. S. (1993). *A 40-Kilodalton Protein Binds Specifically to an Upstream Sequence Element Essential for Muscle-Specific Transcription of the Human Myoglobin Promoter.* Mol. Cell. Biol. 12 (11): 5024-5032.
2. Stull J. T., **Krueger J. K.**, Zhi G. and Gao Z. -H. (1995). *Molecular Properties of Myosin Light Chain Kinases.* In: International Symposium on Regulation of the Contractile Cycle in Smooth Muscle*.* April 26, 1995, MIE, Japan.
3. **Krueger J. K.**, Padre R. C., and Stull J. T. (1995). *Intrasteric Autoinhibition of Myosin Light Chain Kinase* J. Biol. Chem*.* 270(28): 16848-853.
4. Stull J. T., **Krueger J. K.**, Kamm K. E., Gao Z.-H., Zhi G. and Padre R. C. (1996). *Myosin Light Chain Kinase". In: Biochemistry of Smooth Muscle Contraction.* (Barany, M., Ed.) pp. 119-128, Academic Press, Inc., San Diego.

5. Stull J. T., Kamm K. E., **Krueger J. K.**, Lin P.-J., Luby-Phelps K., and Zhi G. (1997). *Ca^{2+}/Calmodulin-dependent Myosin Light Chain Kinase*. Chapter for *Advances* in Second Messengers and Phosphoproteins (J. Corbin and S. Francis, Eds.) Vol. 31, pp. 141-149, *Raven* Press, New York.
6. **Krueger J.K.**, Olah G. A., Rokop S., Zhi G., Stull J. T. and Trewhella J. (1997). *Structures of Calmodulin and a Functional Myosin Light Chain Kinase in the Activated Complex: A Neutron Scattering Study.* Biochemistry 36: 6017-23.
7. **Krueger J. K.**, Bishop N. A., Blumenthal D. K., Zhi G., Beckingham K., Stull J. and Trewhella J. (1998). *Calmodulin Binding to Myosin Light Chain Kinase Begins at Substoichiometric Ca^{2+} Concentrations: A Small-Angle Scattering Study of Binding and Conformational Transitions.* Biochemistry 37(51): 17810-17.
8. Stull J. T., Lin P. J., **Krueger J. K.**, Trewhella J., and Zhi G. (1998). *Myosin Light Chain Kinase: Functional Domains and Structural Motifs.* Acta Physiol. Scand. 164: 471-482.
9. Improta S., **Krueger J. K.**, Gautel M., Atkinson R., Lefevre J.-F., Moulton S., Trewhella J. and Pastore A. (1998). *The Assembly of Immunoglobulin-like Modules in Titin: Implications For Muscle Elasticity.* J. Mol. Biol. 284(3): 761-777.
10. **Krueger J. K.**, Zhi G., Stull J.T., and Trewhella J. (1998). *Neutron Scattering Studies Reveal Further Details of the Ca^{2+}/Calmodulin-Dependent Activation Mechanism of Myosin Light Chain Kinase.* Biochemistry 37(40): 13997-14004.
11. Trewhella J., Gallagher S. C., **Krueger J. K.**, and Zhao J. (1998). *Neutron and X-ray Solution Scattering Provide Insights into Biomolecular Structure and Function.* Science Progress 81(2): 101-122.
12. **Krueger J.K.**, McCrary B., Wang A. H.-J., Shriver J. W., Trewhella J., and Edmondson S. P. (1999). *Solution Structure of Sac7d/DNA Complex Studied by Small-Angle X-ray Scattering.* Biochemistry 38(32): 10247-10255.
13. **Krueger J. K.**, Gallagher S. C., Wang A., and Trewhella J. (2000). *Calmodulin Remains Extended upon Binding to Smooth Muscle Caldesmon: A Combined Small-Angle Scattering and Fourier Transform Infrared Spectroscopy Study.* Biochemistry, 39(14): 3979-3987.
14. **Krueger J. K.**, Gallagher S. C., Zhi G., Geguchadze R., Persechini A., Stull J. and Trewhella J. (2001). accelerated publication) *Activation of Myosin Light Chain Kinase Requires Translocation of Bound Calmodulin.* J. Biol. Chem. 276(7): 4535-4538.
15. Trewhella J., and **Krueger J.K.** (2001). *Small-angle Solution Scattering Reveals Information on Conformational Dynamics in Calcium Binding Proteins and in Their Interactions with Regulatory Targets*. In Methods of Molecular Biology. (H.J. Vogel, Ed.) Vol 173, pp. 137 – 160. *Humana Press*.
16. Heller W. T., **Krueger J. K.**, and Trewhella J. (2003*). Further Insights into Calmodulin-Myosin Light Chain Kinase Interaction from Solution Scattering and Shape Restoration.* Biochemistry 42(36): 10579-588.
17. **Krueger J. K.** and Wignall G. D. (2004*). Small Angle Neutron Scattering from Biological Molecules*. In Neutrons in Biology - Techniques and Applications (J. Fitter, T. Gutberlet, J. Katsaras, Eds.) Springer Publications Biophysical Studies Series
18. Ashish Garg, R.; Anguita J.; **Krueger J.K.** (2006). *Binding of Full-length HIV-1 gp120 to CD4 Induces Structural Reorientation Around the gp120 Core.* Biophys. J. 91(*6*):L69-71.
19. Gautam J.K., Ashish, Comeau L.D., **Krueger J.K.**, and Smith M.F. Jr. (2006). *Structural and Functional Evidence for the role of the TLR2 DD loop in TLR1/TLR2 Heterodimerization and Signaling.* J. Biol. Chem. 281(40):30132-42.

C. Research Support

Ongoing Research Support

CAREER: Integrated Structural Biology Approach to Building Atomic Models of Actin Complexes
0237676
PI: Krueger, J.K. April 2003 – March 2008
National Science Foundation Role: PI

The major goal of this project is to build an atomic-resolution model of actin:gelsolin complexes using interatomic distance constraints provided by small-angle x-ray and neutron scattering data.

Completed Research Support

Distance Constraints for Building an Atomic Model of Gelsolin:2Actin Complexes Determined by Chemical Cross-linking and Peptide Mapping
PI: Krueger, J.K. March 2003 – April 2005
Cottrell College Science Award Research Corporation Role: PI

The major goal of this project is to provide lysine-lysine distance constraints within actin:gelsolin complexes using major chemical cross-linking and a peptide technique, which involves protein digestion, μLC separation and MS detection.

Principal Investigator/Program Director (Last, First, Middle):	Lightfoot, J. Timothy

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
Lightfoot, J. Timothy	Professor
eRA COMMONS USER NAME jtlightf	

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
Northeast Louisiana University, Monroe, LA	BS	1981	Physical Education/Math
Northeast Louisiana University, Monroe, LA	MEd	1982	Exercise Physiology
University of Tennessee, Knoxville, TN	PhD	1986	Exercise Physiology
Johns Hopkins University, Baltimore, MD	Post-doc	1989	Physiology

PROFESSIONAL EXPERIENCE:

1983-86 Department of Physical Education, University of Tennessee, Knoxville, Tennessee; **Graduate Teaching Assistant**

1985 The Bionetics Corporation, National Aeronautics and Space Administration, Kennedy Space Center; **Research Consultant**

1986-1989 Division of Physiology, The Johns Hopkins University, Baltimore, Maryland; **Post-doctoral Research Fellow**

1989-1993 Department of Exercise Science, Florida Atlantic University, Boca Raton, FL; **Assistant Professor** and Member of Graduate Faculty

1994-1996 Department of Exercise Science, Florida Atlantic University, Boca Raton, FL; **Associate Professor**, Department Chair, and Member of Graduate Faculty

1996-2005 Department of Kinesiology, University of North Carolina-Charlotte, Charlotte, NC; **Professor** and Department Chair

2005-current Department of Kinesiology, University of North Carolina-Charlotte, Charlotte, NC; **Professor**

ACADEMIC HONORS/PROFESSIONAL ACTIVITIES:

American Physiological Society, Research Career Enhancement Award, 2001; Graduate Teacher of the Year, College of Nursing and Health Professions, UNC Charlotte, 2000-2001; Registered Clinical Exercise Physiologist - October, 1999; Florida Atlantic University College of Education "Teacher of the Year" 1994-1995; Florida Atlantic University College of Education, Researcher of the Year, 1994; Fellow of the American College of Sports Medicine, 1992; American College of Sports Medicine - Preventive and Rehabilitative Exercise Specialist - July, 1988; NIH Institutional Grant, Post-Doctoral Research Fellowship, HL 07534-03, 1986; Pre-Doctoral Fellowship 1984, Awarded through the Bionetics, Corporation, NASA, Kennedy Space Center, Florida.

SELECTED PUBLICATIONS (from approximately 40)

Lightfoot, JT. Experimentally evolving exercise endurance: One step at a time. Journal of Applied Physiology (Invited editorial; June 29 – Epub), 2006.

Jung, AP, TS Curtis, MJ Turner, **JT Lightfoot.** Influence of age of exposure to a running wheel on activity in inbred mice. Medicine and Science in Sports and Exercise. 38(1): 51-56, 2006.

Turner, MJ, SR Kleeberger, **JT Lightfoot.** Influence of genetic background on daily running-wheel activity differs with aging. Physiologic Genomics. 22: 76-85, 2005.

JT Lightfoot, MJ Turner, M Daves, A Vordermark, SR Kleeberger. Genetic influence on daily wheel running activity level. Physiologic Genomics. 19: 270-276, 2004.

Howden, R, **JT Lightfoot**, SJ Brown, IL Swaine. A wide range of baroreflex stimulation does not alter forearm blood flow. European J. Appl Physiology. 93:124-129, 2004.

Howden, R, **JT Lightfoot**, SJ Brown, IL Swaine. The effects of breathing 5% CO2 on human cardiovascular responses and tolerance to orthostatic stress. Experimental Physiology. 89(4): 465-471, 2004.

Howden, R, **JT Lightfoot**, SJ Brown, IL Swaine. The effects of isometric exercise training on resting blood pressure and orthostatic tolerance in humans. Experimental Physiology. 87(4): 507-515, 2002.

JT Lightfoot, MJ Turner, KA DeBate, SR Kleeberger. Interstrain variation in murine aerobic capacity. Med. Sci. Sports Exerc. 33(12): 2053-2057, 2001.

Howden, R., PA Tranfield, **JT Lightfoot**, SJ Brown, and IL Swaine. The reproducibility of maximum tolerance to lower body negative pressure and its quantification. Eur. JAP 84:462-468, 2001.

JT Lightfoot, L Katz, K DeBate. Naloxone decreases tolerance to a hypotensive, hypovolemic stress in healthy humans. Critical Care Medicine 28(3): 684-691, 2000.

Marks, B L, D Torok, **JT Lightfoot**. A Comparison of Body Fat Estimates Obtained at Health Fitness Screenings. Worksite Health. Fall, 27-32, 1999.

Marks, B L, **JT Lightfoot**. Reproducibility of resting heart rate variability with short sampling periods. Canadian Journal of Applied Physiology 24(4): 337-348, 1999.

Lightfoot, JT, D Char, J McDermott, C Goya. Immediate post-exercise massage does not attenuate delayed onset muscle soreness. J Strength and Conditioning Research. 11: 119-124, 1997.

Lightfoot, JT, B Tuller, DF Williams. Ambient noise interferes with auscultatory blood pressure measurement during exercise. Medicine and Science in Sports and Exercise 28 (4): 502-508, 1996

Lightfoot, JT and KM Tsintgaras. Quantification of tolerance to lower body negative pressure in a healthy population. Medicine and Science in Sports and Exercise 27(5): 697-706, 1995.

Lightfoot, JT, RP, Claytor, T Journell, D Torok, and M Turner. Resistance training increases lower body negative pressure tolerance. Medicine and Science in Sports and Exercise 26(8): 1003-1011, 1994.

Lightfoot, JT, SA Rowe, SM Fortney. Occurrence of presyncope in subjects without ventricular innervation. Clinical Science 85(12): 1993.

Fortney, SM, C Tankersley, **JT Lightfoot**, J Fleg, D Drinkwater, J Clulow, G Gerstenblith, F O'Conner, E Lakatta, L Becker. Cardiovascular responses to lower body negative pressure in trained and untrained older men. Journal of Applied Physiology 73: 2693-2700, 1992.

Lightfoot, JT, N Thakor, S Biswijit, DF Hanley. Presyncope caused by central hypovolemia is not preceded by evoked potential alterations. Clinical Physiology 12: 267-275, 1992.

Lightfoot, JT. Can blood pressure be measured during exercise?: A review. Sports Medicine 12: 290-301, 1991

Other Support

Active

NIH RO1AR050085 (Lightfoot, JT, PI) 7/01/05 – 6/30/10 Amt. Of 12-month effort = 25%
NIAMSD $197,000. Annual Direct Costs
"Genetic Factors Responsible for Exercise Endurance"
The overall objective of this proposal is to determine the specific genes involved in the control of inherent exercise endurance.

NIH AR050085-S1 (Lightfoot, JT, PI) 8/15/06 – 7/30/10 Amt. Of 12-month effort = 0%
NIAMSD $52,245. Annual Direct Costs
"Minority Postdoctoral Supplement for - Genetic Factors Responsible for Exercise Endurance"
The overall objective of this proposal is to provide post-doctoral research training for Dr. Trudy Moore.

NIH AG022417 (Turner, MJ, PI) 9/01/03 – 8/30/05
NIA $50,000. Annual Direct Costs
"Aging, Physical Activity, and Cardiac Apoptosis"
Role on Project: Unpaid Co-Investigator
The overall objective of this proposal is to complete genetic segregation and linkage analyses of inbred mouse strains that have shown differential patterns of age-related change in daily physical activity.

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
Livesay, Dennis R.	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. Positions and Honors

Positions and Employment

2006-present Associate Professor; Bioinformatics Research Center and Department of Computer Science; University of North Carolina at Charlotte
2005-2006 Associate Professor; Department of Chemistry and Center for macromolecular Modeling & Materials Design; California Sate Polytechnic University, Pomona
2000-2005 Assistant Professor; Department of Chemistry; California State Polytechnic University, Pomona

Other Experience

2006-present Section Editor (Biomacromolecules): *The Chemistry Central Journal*
2006-present Advisory board member; *Center for Macromolecular Modeling & Material Design*, California State Polytechnic University, Pomona
2005-2006 Graduate Program Director: Department of Chemistry, California State Polytechnic University, Pomona
2005 Developed and delivered *Introduction to Bioinformatic Methods* short-course at Technology Park Malaysia (Kuala Lumpur, Malaysia)
2004-present Recurring journal referee for: *Astrobiology; Bioinformatics; BMC Bioinformatics; Chemical Reviews; FEBS Letters; Genome Biology, Journal of Computational Chemistry; Nucleic Acids Research;* and *Proteins: Structure, Function & Bioinformatics*
2003-2006 Faculty Consensus Group, California State University Program for Education and Research in Biotechnology (CSUPERB)
2003-2004 College of Science representative to California State Polytechnic University Research Council
2003 Co-organizer of California State Polytechnic's *Center of Macromolecular Modeling & Material Design*
2002-present NIH grant reviews: NIH-Special emphasis study section (R15 and R21 proposals), NIH-MBRS ad hoc study section (SCORE S01 proposals)
2002 Co-organizer of California State Polytechnic, Pomona's *Molecular Modeling & Simulation* baccalaureate degree

Professional Memberships

2003-present American Association for the Advancement of Science
2002-present The Protein Society

2001-2006 California State University Program for Education and Research in Biotechnology
2000-present The American Chemical Society
1998-present The Biophysical Society

Academic & Research Awards

1998 Hydration in Biology NATO Advanced Study Institute travel award; Les Houches, France
1997 Department of Chemistry Graduate Fellowship; University of Illinois at Urbana-Champaign
1996 Undergraduate Award for All-Around Achievement in Chemistry; Ball State University
1996 1st Place; Midwest Regional Undergraduate Research Poster Competition; University of Kentucky
1996 Graduated Cum Laude; Ball State University
1995 Undergraduate Research Fellow; Ball State University

B. SELECTED PEER-REVIEWED PUBLICATIONS (¹·² indicates Livesay lab graduate and undergraduate students, respectively)

Journal Publications

1. Livesay DR, Linthicum SD, Subramaniam S (1999). *pH dependence of antibody-hapten association.* Molecular Immunology, 36(6):297-410.
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(2):686-693.
3. Livesay DR, Jambeck P, Rojnuckarin A, Subramaniam S (2003). *Conservation of electrostatic properties within enzyme families and superfamilies.* Biochemistry, 42(12):3464-3473 (*Faculty of 1000 "must read").*
4. La D², Silver MA², Edgar RC, Livesay DR (2003). *Using motif-based methods in multiple genome analyses: A case study comparing orthologous mesophilic and thermophilic proteins.* Biochemistry, 42(30):8988-8998.
5. Torrez M¹, Schultehenrich M¹, Livesay DR, (2003). *Conferring thermostability to mesophilic proteins through optimized electrostatic surfaces.* Biophysical Journal, 85(5):2845-2853, 2003.
6. Alsop E², Silver MA², Livesay DR (2003). *Optimized electrostatic surfaces parallel increased Thermostability: A structural bioinformatic analysis.* Protein Engineering, 16912):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(5):463-472.
8. Livesay DR, Dallakayan S., Woods G.G., Jacobs DJ (2004). *A flexible approach for understanding Protein thermodynamics.* FEBS Letters, 576(3):468-476.
9. La D¹, Sutch B², Livesay DR (2005). *Predicting protein functional sites with phylogenetic motifs.* Proteins: Structure, Function, & Bioinformatics, 58(2):309-320 (*Featured on the cover).*
10. Livesay DR, La D¹ (2005). *Probing the evolutionary origins and catalytic importance of conserved Electrostatic networks in TIM-barrel proteins.* Protein Science, 14(5):1158-1170.
11. La D¹, Livesay DR (2005). *Predicting functional sites with an automated algorithm suitable for heterogeneous datasets.* BMC Bioinformatics, 6(1):116.
12. La D¹, Livesay DR (2005). *MINER: Software for phylogenetic motif identification.* Nucleic Acids Research, 33(web server issue):W267-W279.
13. Livesay DR, Jacobs DJ (2006). *Conserved quantitative stability/flexibility relationships (QSFR) in an orthologous RNase H pair.* Proteins: Structure, Function & Bioinformatics, 62(1):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(3):882-904.
15. Livesay DR, Jacobs DJ, Kanjanapangka J¹, Chea E², Cortez H², Garcia J², Kidd P¹, Marquez MP¹, Pande S¹, Yang D¹ (2006). *Probing the conformational dependence of calculated pKa values.* Journal of Chemical Theory and Computation, 2(4):927-938.

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

Peer-reviewed CS conference proceedings

17. Pande S[1], Raheja A, Livesay DR (2007). *Prediction of Enzyme Catalytic Sites from Sequence Using Neural Networks.* 2007 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, CIBCB07, In press.
18. Roshan U, Livesay DR, Chikkagoudar S. *Improving progressive alignment for phylogeny reconstruction using parsimonious guide-trees.* Sixth IEEE Symposium on Bioinformatics and Bioengineering, BIBE06, In press.
19. Roshan U, Livesay DR, La D[1] (2005). *Improved Phylogenetic Motif Detection Using Parsimony.* Fifth IEEE Symposium on Bioinformatics and Bioengineering, BIBE05:19-26.

C. RESEARCH SUPPORT

Ongoing Support

1. *Predicting protein stability and flexibility*
   NIH R01 GM073082-01A1
   PI: Jacobs, D.J. 2006-2009
   National Institutes of Health Role: Co-PI
   Grant amount: $960,000 (my subcontract amount is ~46%)

   The grant is supporting continued development of the Distance Constraint Model, which is a biophysical model that harmoniously calculates stability and flexibility metrics. In addition, a QSFR (quantitative stability/flexibility relationships) database will be built that provides a user-friendly interface to our results.

Completed Support

2. *Center for macromolecular modeling and material design*
   PI: Ortiz, J.M. (CPP President) 2006-2007
   W.M. Keck Foundation Role: Investigator
   Grant amount: $500,000

   This equipment grant purchased several pieces of state-of-the-art materials science apparatus, including an atomic force microscope. A small amount of money was also used to supplement the center's computational resources.

3. *Phylogenetic similarity maximization: A new algorithm for phylogenetic motif detection*
   PI: Livesay, D.R. 2005-2006
   CSUPERB-Joint Venture Grant Role: PI
   Grant amount: $21,200 + 2 programmers in Bangalore, India (in-kind from Agiline, Inc.)

   Phylogenetic motifs are a bioinformatic method developed in my lab for predicting protein functional sites from sequence. This proposal refined our initial approach with an algorithm that improved the statistical significance of the predicted sites.

4. *Acquisition of a workstation network for research in parallel and distributed computing*
   032-1333
   PI: Kuang, H. 2003-2005
   National Science Foundation-Major Research Instrumentation Role: Co-PI
   Grant amount: $159,658

This equipment grant provided funds to purchase a large computational cluster.

5. *Investigation of superoxide dismutase surface electrostatics*
S06 GM53933-07
PI: Livesay, D.R. 2002-2004

National Institutes of Health Role: PI
Grant amount: $178,000

This grant used computational biology and bioinformatic techniques to investigate superoxide dismutase electrostatics and its role in evolution of the family.

6. *Conferring thermostability to mesophilic proteins through systematic mutation of surface residues*
36848-GB4
PI: Livesay, D.R. 2001-2003
3 ACS-Petroleum Research Fund Role: PI
Grant amount: $25,000

This grant developed our Poisson-Boltzmann continuum electrostatics model for optimizing protein electrostatic surfaces.

7. *Bioinformatic study correlating protein flexibility with function*
PI: Jacobs, D.J. 2003
CSUPERB-Joint Venture Matching Grant Role: Co-PI
Grant amount: $25,000 + $75,000 (in-kind from Cengent Therapeutic)

This grant investigated changes in stability and flexibility on inhibitor binding in HIV protease.

8. *Dihedral-angle characterization of conformational flexibility in protein structure*
S06 GM48680-0952;
PI: Jacobs, D.J. 2002-2005
National Institutes of Health-SCORE Role: Paid consultant
Grant amount: $370,328

My role on Don Jacobs' SCORE grant was to provide advice on modeling schemes vis-à-vis protein structures. This grant funded initial development of the minimal DCM, which is a biophysical modeling scheme that harmoniously calculates stability and flexibility metrics. Don Jacobs and I now share an R01 (see above) to continue development and application of the model.

+ 2 allocations of supercomputer time from the National Center for Supercomputing Applications, + 3 Cal Poly Pomona intramural mini-grants (~$1,000 each) and + 3 travel awards.

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
Marriott, Ian	Associate Professor
eRA COMMONS USER NAME imarriot	

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 Birmingham, United Kingdom	B.Sc. (Hons)	1989	Physiology
Tulane University Medical Center, New Orleans, LA	M.S.	1994	Physiology
Tulane University Medical Center, New Orleans, LA	Ph.D.	1996	Physiology
Tulane University Medical Center, New Orleans, LA	Post-doc	1996-1998	Immunology

A. Positions and Honors.

Positions and Employment

1996-1998 Research Associate, Department of Microbiology and Immunology, Tulane University Medical Center, New Orleans, LA
1998-2000 Research Assistant Professor, Department of Biology, University of North Carolina-Charlotte, Charlotte, NC
2000-2004 Assistant Professor, Department of Biology, University of North Carolina-Charlotte, Charlotte, NC
2004-present Associate Professor, Department of Biology, University of North Carolina-Charlotte, Charlotte, NC

Other Experience and Professional Memberships

1998 American Association of Immunologist's Advanced Immunology Course, Berkeley, CA
1998 Becton Dickinson Immunocytometry Systems Flow Cytometry Training Course, San Jose, CA
2002-present Editorial Board Membership, Journal of Immunology
2003-present Departmental Advisory Committee member
2004-present Editorial Board Membership, Current Immunology Reviews
2004-present Departmental Review, Committee member, Department of Biology, University of North Carolina-Charlotte, NC
2004 NIH Study Section: NCCAM special Emphasis Panel, ZAT1 DB-17, "Botanicals Centers"
2005 NIH Study Section: NIDCR Special Grants Review Committee
2005-2006 NIH Study Sections: NCCAM Special Emphasis Panel, ZAT1 DB-18, DB-19, DB-21 and DB-22 "Basic Science"
2005-present Departmental Advisory Committee member, Department of Kinesiology, University of North Carolina-Charlotte, NC
NIH Study Section: NIAMS Specialized Centers (P50s), ZAR1 MLB-G M1 1 "Centers of Research Translation"
2006-present Coordinator, M.S. Program in Department of Biology, University of North Carolina-Charlotte, NC

Ad Hoc Reviewer

Journal of Immunology, American Journal of Physiology, American Journal of Pathology, Glia, Journal of Neuroimmunology, bone, Journal of Neurochemistry, Biotechnology and Applied Biochemistry, Microbes and Infection, Journal of Cellular Physiology, International Immunopharmacology, BMC Infectious Disease, Dept. of Veterans Affairs Merit Review, USDA extramural grant program, Wellcome Trust, Los Alamos national Laboratory directed research internal funding, Medical Research Council UK

Memberships

American Association of Immunologists; International Society for Neurochemistry

Honors

1990-1993	Science and Engineering Research Council (UK), Overseas Research Scholarship
1993-1995	Tulane University, Chancellors Fellowship
1995-1996	American Heart Association Graduate Student Research Fellowship
1998	Leah Seidman Schaffer Award for Postdoctoral Research in Microbiology and Immunology, Tulane University Medical Center, New Orleans, LA
1998	Chancellor's Award for Excellence in Research and Presentation by a Postdoctoral Fellow, Tulane University Medical Center, New Orleans, LA
2002	American Association of Immunologists Pfizer-Showell Travel Award for Early-Career Scientists
2003	American Association of Immunologists Junior Faculty Travel Award

B. Selected peer-reviewed publications.

(Publications selected from 49 peer-reviewed publications)

1. Rasley A., Bost K.L., Olson J.K., Miller S.D., and **Marriott I.** (2002) *Expression of functional NK-1 receptors in murine microglia.* Glia. 37: 258-267.
2. Gasper N.A., Petty C.C., Schrum L.W., **Marriott I.,** and Bost K.L. (2002). *Bacterium induced CXCL10 secretion by osteoblasts can be mediated in part through Toll-Like Receptor 4.* Infect. Immun. 70: 4075-82.
3. Rasley A., Anguita J., and **Marriott I.** (2002). *Borrelia burgdorferi induces inflammatory mediator production by murine microglia.* J. Neuroimmunol. 130: 22-31.
4. **Marriott I.**, Hughes F.M.Jr., and Bost K.L. (2002). *Bacterial infection of osteoblasts induces IL-1 and IL-18 transcription but not protein synthesis.* J. Interf. Cytok. Res. 22: 1049-1055.
5. Taylor W.R., Rasley A., Bost K.L., and **Marriott I.** (2003). *Murine gammaherpesvirus-68 infects microglia and induces high levels of pro-inflammatory cytokine production. J. Neuroimmunol.* 136: 75-83.
6. Elsawa S.F., Taylor W.R., Petty C.C., **Marriott I.**, Weinstock J.V., and Bost K.L. (2003*). Limited CTL response and increased viral burden in substance P receptor deficient mice infected with murine gammaherpesvirus 68.* J. Immunol. 170: 2605-2612.
7. Shrum L.W., **Marriott I.**, Thomas E.K., Butler B.R., Hudson M.C., and Bost K.L. (2003). *Functional CD40 expression induced following bacterial infection of mouse and human osteoblasts.* Infect. Immun. 71: 1209-1216.
8. Alexander E.H., Rivera F.A., **Marriott I.**, Anguita J., Bost K.L., and Hudson M.C. (2003). *Staphylococcus aureus-induced tumor necrosis factor-related apoptosis-inducing ligand expression mediates apoptosis and caspase-8 activation in infected osteoblasts.* BMC Microbiology. 3: 5.
9. Bowman C.C., Rasley A., Tranguch S.L, and **Marriott I.** (2003). *Cultured astrocytes express Toll-like receptors for bacterial products.* Glia. 43: 281-291.
10. Madrazo D.R., Tranguch S.L., and **Marriott I.** (2003). *Signaling via Toll-like receptor 5 can initiate inflammatory mediator production by murine osteoblasts.* Infect. Immun. 71: 5418-5421.
11. Schrum L.W., Bost K.L., Hudson M.C., and **Marriott I.** (2003). *Bacterial infection induces expression of functional MHC Class II molecules in murine and human osteoblasts.* Bone. 33: 812-821.
12. **Marriott I.**, Gray D.L., Tranguch S.L., Fowler V.G. Jr., Stryjewski M., Levin S., Hudson M.C., and. Bost K.L. (2004). *Osteoblasts express the inflammatory cytokine, interleukin-6, in a murine model of Staphylococcus aureus osteomyelitis and infected human bone tissue.* Am. J. Pathol. 164: 1399-1406.
13. Rasley A., **Marriott I.**, Halberstadt C.R., Bost K.L., and Anguita J. (2004). *Substance P augments B. burgdorferi-induced PGE_2 production by murine microglia.* J. Immunol. 172: 5707-5713.

14. Rasley A., Bost K.L., and **Marriott I.** (2004). *Murine gammaherpesvirus-68 elicits robust IL-12p40 expression, but not IL-12p70 production, by murine microglia and astrocytes.* J. Neurovirol. 10: 171-180.
15. Nelson D.A., **Marriott I.**, and Bost K.L. (2004). *Expression of hemokinin-1 mRNA by murine dendritic cells.* J. Neuroimmunol. 155: 94-102.
16. **Marriott I.** (2004). *The role of tachykinins in central nervous system inflammatory responses.* Front. Biosci. 9: 2153-2165.
17. **Marriott I.** (2004). *Osteoblast responses to bacterial pathogens: a previously unappreciated role for bone-forming cells in host immune responses and disease progression.* Immunol. Res. 30: 291-308.
18. **Marriott I.**, Rati D.M., McCall S.H., and Tranguch S.L. (2005). *Induction of Nod1 and Nod2 intracellular pattern recognition receptors in murine osteoblasts following bacterial challenge.* Infect. Immun. 73: 2967.
19. **Marriott I.**, Gray D.L., Rati D.M., Fowler V.G. Jr., Stryjewski M.E., Levin L.S., Hudson M.C., and Bost K.L. (2005). *Osteoblasts produce monocyte chemoattractant protein-1 in a murine model of Staphylococcus aureus osteomyelitis and infected human bone tissue.* Bone. 37:502-510.
20. Sterka D. Jr., Rati D.M., and **Marriott I.** (2006). *Functional expression of NOD2, a novel pattern recognition receptor for bacterial motifs, in primary murine astrocytes.* Glia. 53:322-330.
21. Rasley A., Tranguch S.L., Rati D.M., and **Marriott I.** (2006). *Murine microglia express the immunosuppressive cytokine, interleukin-10, following exposure to Borrelia burgdorferi or Neisseria meningitidis*. Glia. 53:583-592.
22. **Marriott I.**, Bost K.L., and Huet-Hudson Y.M. (2006). *Sexual dimorphism in expression of receptors for bacterial lipopolysaccharides in murine macrophages: a possible mechanism for gender-based differences in endotoxic shock susceptibility.* J. Reprod. Immunol. 71:12-27.
23. **Marriott I.**, and Huet Hudson Y.M. (2006). *Sexual dimorphism in innate immune responses to infectious organisms*. Immuno Res. 34:177-192.
24. Konat G.W., Kielian T., **Marriott I.**, and Pahan K. (2006). *Toll-like receptors in the nervous system*. J. Neurochem. 99: 1-12.
25. Gasper-Smith N., **Marriott I.**, and Bost K.L. (2006). *Murine gammaherpesvirus 68 limits naturally occurring CD4+CD25+ T regulatory cell activity following infection.* J. Immunol. 177: 4670-4678.
26. Sterka D. Jr. and **Marriott I.** *Characterization of nucleotide-binding oligomerization domain (NOD) protein expression in primary murine microglia.* J. Neuroimmunol. In Press.

C. Research Support

Ongoing Research Support

Substance P exacerbation of CNS inflammation
R01NS050325
PI: Ian Marriott — 2006-2010
National Institutes of Health — Role: PI

Macrophage activation & substance P receptor expression
R01A132976
PI: Kenneth Bost — 2002-2007
National Institutes of Health — Role: Co-PI

Completed Research Support

Osteoblast-derived inflammatory mediators in bone infection
R01AR48842
PI: Ian Marriott — 2002-2006
National Institutes of Health — Role: PI

Bacterial infection induces cytokine production by osteoblasts
R03AR47585
PI: Ian Marriott — 2001-2004
National Institutes of Health — Role: PI

Limited IL-12 eta2 receptor expression during salmonellosis
R01A147181
National Institutes of Health 2001-2004
Role: Co-PI

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
Lawrence E. Mays, Ph.D.	Professor
eRA COMMONS USER NAME	

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 Virginia	B.A.	1967	Psychology
The Pennsylvania State University	M.S.	1969	Psychology
University of Virginia	Ph.D.	1973	Psychology
Temple University	M.A.	1976	Computer Science
Temple University	Post Doc	1676-77	Neuroscience
University of Alabama at Birmingham	Post Doc	1977-79	Neuroscience

A. Positions and Honors

Appointments

2004-Present Professor, Department of Computer Science, University of North Carolina at Charlotte

2002-2004 Director, Center for the Development of Functional Imaging, University of Alabama at Birmingham
1995-2004 Chairman, Department of Physiological Optics, University of Alabama at Birmingham
1991-2004 Professor, Department of Physiological Optics, University of Alabama at Birmingham
1991-1995 Director, Vision Science Research Center, University of Alabama at Birmingham
1985-1991 Associate Professor, Department of Physiological Optics, University of Alabama at Birmingham
1983-1985 Research Associate Professor, Department of Physiological Optics, University of Alabama at Birmingham
1979-1983 Research Assistant Professor, Department of Physiological Optics, University of Alabama at Birmingham

B. SELECTED PEER-REVIEWED PUBLICATIONS

1. Busetini C, Mays LE. Pontine omnipause activity during conjugate and disconjugate eye movements in macaques. *J Neurophysiol* 90:3838-3853, 2003.

2. Mays LE. Neural control of vergence eye movements. In: *The Visual Neurosciences*, Chalupa LM and Werner JS (eds.), MIT Press, Cambridge, pp. 1415-1427, 2003.

3. Walton MG, Mays LE. Discharge of saccade-related superior colliculus neurons during saccades accompanied by vergence. *J Neurophysiol* 90:1124-1139, 2003.

4. Mays LE and Gamlin PDR. Neuronal circuits for accommodation and vergence in the primate. In: *Accomodation and Vergence Mechanisms in the Visual System*, Franzen O, Richter H and Stark L (eds.), Birkhauser Verlag, Stockholm, pp. 1-9, 2000.

5. Ledous MS, Lorden JF, Smith JM, Mays LE. Serontonergic modulation of eye blinks in cat and monkey. *Neurosci Lett* 253(1):61-64, 1998.

6. Mays LE. Has Hering been hooked? *Nature Med* 4(8):889-890, 1998.

C. SYNERGISTIC ACTIVITIES

9/1/1980-12/31/2003	PI – NIH Research Grant R01 EY03463
7/1/2000-6/30/2004	PI – W.F. Keck Foundation Grant ($1,500,000)
7/1/2001-6/30/2004	PI – Eyesight Foundation Grant ($300,000)
9/1/2001-8/31/2004	Co-PI – NSF DB1-0116467 ($451,000)
2001-2005	Member NIH CVP Study Section

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
McKillop, Iain H.	Associate Professor
eRA COMMONS USER NAME imckillop	

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 Sheffield, Sheffield, UK	B.Sc. Dual Hons.	1991	Pharmacology and Physiology
University of Sheffield, Sheffield, UK	Ph.D.	1994	Physiology
Johns Hopkins Medical Institutes, Baltimore, MD	Post-Doc	1994-1995	
Georgetown University, Washington, DC	Post-Doc	1995-1997	

A. Positions and Honors.

Positions and Employment

1991-1994 Post-Graduate Student, Department of Medicine, University of Sheffield, Sheffield, UK
1994-1995 Post-Doctoral Fellow, Department of Surgery, Johns Hopkins Medical Institutes, Baltimore, MD
1995-1997 Post-Doctoral Fellow, Department of Surgery, Georgetown University, Washington, DC
1997-1999 Instructor, Department of Surgery, Georgetown University, Washington, DC
1999-2002 Assistant Professor, Department of Surgery, University of Rochester Medical Center, Rochester, NY
2002-present Associate Professor, Department of Biology, University of North Carolina-Charlotte, Charlotte, NC

Other Experience and Professional Memberships

1992-1995 Member of the British Society of Vascular Biology
1996-present Member of the American Society of Cell Biology
1997-present Member of the American Cancer Society
1999-present member of the American Association for the Study of Liver Disease
1999-present Ad hoc reviewer; *Hepatology*
2000-present Associate member of the European Association for the Study of the Liver
2002-present Ad hoc reviewer; *Journal of the American College of Surgeons*
2002-present Invited reviewer; NIH-NIAAA Special Emphasis Panel (ZAA1-DD)
2002-present Invited reviewer; NIH-NIAAA (AA1)
2003-present Ad hoc reviewer; *Alcohol and Alcoholism*
2003-present Civilian Res. And Development Foundation-Cooperative Grants Program [CRDF-CRG] grant reviewer
2004-present Ad hoc reviewer; *Liver International*
2004-present Ad hoc reviewer; *Molecular Carcinogenesis*
2005-present Ad hoc reviewer; *Life Sciences*
2005-present Ad hoc reviewer; *Journal of Viral Hepatitis*
2005-present Ad hoc reviewer; *Cancer Letters*
2005-present NIH-NIGMS Minority Biomedical Research Support (MBRS) program grant reviewer
2006-present Invited Grant Reviewer; Israel Science Foundation (ISF)
2006-present Invited Grant Reviewer; Italian Association for Cancer Research (AICR)
2006-present NIH DMP (Drug discovery & Molecular Pharmacology) study section

Honors

1991-1994	Baxter Health Care Post-Graduate Research Award
2003	Invited participant NIH-NIAAA Symposium "Role of fatty liver, dietary fatty acid supplements & obesity in the progression of ALD"
2004	Invited speaker/ participant NIH-NIAAA sponsored symposia "Alcohol and Cancer"

B. Selected peer-reviewed publications.

1. Haylor J.L., Oldroyd D.D., **McKillop I.H.**, (1995). *Control of renal vascular tone by endothelin and nitric Oxide.* Neph. Dial Transplant, 20 (3): 1-19.
2. **McKillop I.H.**, Haylor J., El Nahas A.M. (1995). *IGF-I stimulates renal function in the isolated perfused rat kidney: Inhibition by nitroarginine methyl ester and aminoguanidine.* Exp. Nephrology, 3: 49-57.
3. **McKillop I.H.**, Haylor J., El Nahas A.M. (1996). *Mediation of the renal response to IGF-I is by calcium dependent NO in the isolated rat kidney.* Biology of Nitric Oxide: Eds Moncada, Higgs and Ignarro.
4. Schmidt, C.M., **McKillop I.H.**, Cahill P.A., Sitzmann J.V. (1997). *Alterations in guanine nucleotide regulatory protein expression and activity in human HCC.* Heptology, 26: 1189-1194.
5. **McKillop I.N.**, Schmidt C.M., Cahill P.A., Sitzmann J.V. (1997). *Altered expression of mitogen activated protein kinases in experimental hepatocellular carcinoma.* Heptology, 26: 1484-1491.
6. Schmidt C.M., **McKillop I.H.**, Cahill P.A., Sitzmann J.V. (1997). *Increased MAPK expression and activity in primary human hepatocellular carcinoma.* Biochem. Biophys. Res. Comm., 236: 54-58.
7. Hendrickson R.J., Cahill P.A., **McKillop I.H.**, Sitzmann J.V., Redmond E.M. (1198). *Ethanol inhibits smooth muscle cell growth and MAPK activity in vitro.* Eur. J. Pharmacol., 362: 251-259.
8. Schmidt C.M., **McKillop I.H.**, Cahill P.A., Sitzmann J.V. (1998). *The role of adenylyl cyclase linked mitogen activated protein kinase signaling in the regulation of human hepatocellular carcinoma growth.* Surg. Forum, X: 450-452.
9. **McKillop I.H.**, Wu Y., Cahill P.A., Sitzmann J.V. (1998). *Altered expression of inhibitory guanine nucleotide regulatory proteins (Gi-proteins) in experimental HCC.* J. Cell Physiol., 175 (3): 295-304.
10. Schmidt C.M., **McKillop I.H.**, Cahill P.A., Sitzmann J.V. (1999). *The role of cAMP-MAPK signaling in the regulation of human HCC growth in vitro.* Eur. J. Gastro. Hepatol. 11: 1393-1399.
11. **McKillop I.H.**, Schmidt C.M., Cahill P.A., Sitzmann J.V. (1999). *Guanine nucleotide regulatory protein activation of mitogen activated protein kinase in experimental hepatocellular carcinoma.* Eur. J. Gastro Hepatol., 11(7): 761-768.
12. Cappadona C., Redmond E.M., Theodorakis N.G., **McKillop I.H.**, Hendrickson R. J., Chhabra A., Sitzmann J.V., Cahill P.A. (1999). *Phenotype dictates the growth response of vascular smooth muscle cells to pulse pressure in vitro.* Exp. Cell Res., 250(1): 174-186.
13. Sunitha I., Shen R., **McKillop I.H.**, Resau J., Avigan M. (1999). *A src-related kinase in the brush border membranes of gastrointestinal cells is regulated by c-met.* Exp. Cell Res., 250 (1) 86-98 (Cover of Issue).
14. **McKillop I.H.**, Schmidt C.M., Cahill P.A., Sitzmann J.V. (1999). *Enhanced Gi-protein mediated mitogenesis following chronic ethanol exposure in HCC.* Hepatology 29 (2): 412-420.
15. **McKillop I.H.**, Schmidt C.M., Cahill P.A., Sitzmann J.V. (1999). *Altered Gq/G11 Guanine nucleotide regulatory protein expression in HCC: Role in cellular mitogenesis.* Hepatology 29 (2): 371-378.
16. Haylor J., **McKillop I.H.**, Oldroyd S., El Nahas A.M. (2000) *IGF-I inhibitors reduce compensatory hyperfiltration in the isolated rate kidney following uninephrectomy.* Neph. Dial. Transplant, 15:87-92.
17. Kovach S.J., Sitzmann J.V., **McKillop I.H.** (2001). *Inhibition of alcohol dehydrogenase (ADH) blocks enhanced Gi-protein expression following chronic ethanol exposure in experimental hepatocellular carcinoma in vitro.* Eur. J. gastro. Hepatol. 13: 1209-1216.
18. Kovach S.J., Sitzmann J.V., **McKillop I.H.** (2001). *Regulation of cAMP responsive elements (CRE's) in a rat model of HCC.* Surg. Forum, LII: 45-46.
19. Price J.A., Kovach S.J., Johnson T., Koniaris L.J., Cahill P.A., Sitzmann J.V., **McKillop I.H.** (2002). *Insulin-like growth factor-I (IGF-I) is a co-mitogen for hepatocyte growth factor (HGF) in a rat model of hepatocellular carcinoma.* Hepatology, 36: 1089-1097.
20. Zimmers T.A., **McKillop I.H.**, Pierce R., Yoo J.Y., Murtha-Riel P., Koniaris L.G. (2003). *Massive liver growth induced by interlueukin-6 over expression in mice.* Hepatology, 38: 326-334.

21. Zimmers T.A., **McKillop I.H.**, Schwartz S., Koniaris L.G. (2003). *Liver regeneration.* J. Am. Coll. Surg., 197 (4): 634-659.
22. Zimmers T.A., Pierce R., **McKillop I.H.**, Koniaris L.G. (2003). *Resolving the role of IL-6 in liver regeneration.* Hepatology, 38 (6) 1590-159.
23. Moran D.M., Mayes N., Koniaris L.G., Cahill P.A., **McKillop I.H.** (2005). *Interleukin-6 inhibits cell proliferation in a rat model of hepatocellular carcinoma.* Liver Int., 25: 445-457.
24. **McKillop I.H.**, Schrum L.W. (2005). *Alcohol and liver cancer.* Alcohol, 35: 195-203.
25. Kovach S.J., Price J.A., Theodorakis N.G., Sitzmann J.V., **McKillop I.H.** (2006). *Role of cyclic AMP responsive elements (CRE's) in cell proliferation in a rat model of hepatocellular carcinoma (HCC).* J. Cell Physiol., 206 (2): 411-419.
26. **McKillop I.H.**, Schrum L.W. (2006). *Alcohol and hepatocellular carcinoma.* Alcohol, Tobacco, and Cancer, Ed. Cho, CH & Purhohit, V. Basel: Karger. pp95-109.
27. Dréau D., Karaa A., Culberson C., Wyan H. **McKillop I.H.**, Clemens M.G. (2006). *Vascular changes associated with the development of bone metastases in an immunocompetent model of mouse mammary carcinoma.* Clin. Exp. Metast., 23(1): 41-53.
28. **McKillop I.H.**, Moran D.M., Jin X., Koniaris L.G. (2006). *Molecular Pathogenesis of hepatocellular carcinoma.* In press. J. Surg. Res. *(ePub available PMID# 17023002).*
29. Moran D.M., Koniaris L.G., Cahill P.A., Halberstadt C.R., **McKillop I.H.** (2006). *Microencapsulation of engineered cells to deliver sustained high circulating levels of interleukin-6 to study hepatocellular carcinoma progression.* In press. Cell Transplantation, 05-06 (*Ref #CT-1556).*
30. Jablonski E.M., Mattocks A.M., Sokolov E., Koniaris L.G., Hughes F.M., Fausto N. Pierce R.H. **McKillop I.H.** (2006). *Decreased aquaporin expression leads to increased resistance to apoptosis in hepatocellular carcinoma.* In press. Cancer Letters 09-06 *(Ref# CAN_8781).*
31. Moran D., Koniaris L.G., Cahill P.A., **McKillop I.H.** (2006). *Interleukin-6 (Il-6) mediates G0/G1 growth arrest in hepatocellular carcinoma through a STAT3 dependent mechanism.* Manuscript reviewed and re-submitted with minor changes. Liv Int., 10/06 (*Ref #05-00339*).
32. Schmidt C.M., Sokolov E., Shaw C.M., Thodorakis N.G., Cahill P.A., Sitzmann J.V., **McKillop I.H.** (2006). *Inhibitory guanine nucleotide regulatory proteins (Gi-proteins) regulate mitogen activated protein kinase activity and mitogenesis in human hepatocellular carcinoma.* Manuscript reviewed and re-submitted with minor changes. Comparative Hepatology, 10/06 (*Ref #2130724275997148*).
33. Hennig M., Klein P.J., Menze A., Matos J., **McKillop I.H.**, Sitzmann J.V., Schmidt C.M. (2006). *Chronic ethanol exposure MEK-ERK dependent growth in human hepatocellular carcinoma (HCC).* Manuscript under review. Surgery 10/06 (*Ref # 20060028*).
34. Zimmers T.A., Jin X., **McKillop I.H.**, Pierce R.H. Koniaris L.G. (2006). *Effect of in vivo loss of Gdf-15/MIC-1 on hepatocellular carcinogenesis.* Manuscript under review. J.Surgical Res. 08/06 (*Ref #JSR-D-06-00305*).

C. Research Support.

Ongoing Research Support

N/A

Completed Research Support

Regulation of Benign and Malignant Hepatocyte Growth
R01CA90895
PI: McKillop, I.H. September 2002 – August 2006
National Institutes of Health Role: PI

The major goals of this research project are to address the regulation of mitogen activated protein kinases following G-protein and/ or tyrosine kinase linked receptor activation. This study determined the downstream nuclear effects of ERK activation and cellular proliferation in *in vitro* models of HCC.

Role of Ethanol on Hepatocellular Carcinoma Progression
R21AA12765
PI: McKillop, I.H. June 2001 – May 2004
National Institutes of Health Role: PI

The major goal of this project was to identify the direct and indirect effects of alcohol on the rate of progression of HCC growth using *in vitro* cell culture models of HCC. The data generated during this project forms the basis of the current proposal which aims to address *in vivo* mechanisms of the effects of ethanol on HCC progression from transformed cell foci.

Role of G-proteins in Hepatocellular Cancer Growth and Differentiation
NRSA FA32 CA79198-01CA

PI: McKillop, I.H. January 1999 – May 2001
National Institutes of Health Role: Fellow

The major goal of this project was to identify altered expression and activity of Gi-proteins and MAPK cascade components in human and animal models of HCC.

BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
M. Taghi Mostafavi	Associate 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
Oklahoma State University	.B. S. M. S. Ph.D.	1980 1982 1986	Computing. and info. Science Electrical Engineering Elec. & Com. Engr. with minor in Com. & info. Sc.

RESEARCH AND PROFESSIONAL EXPERIENCE:

Professional Experience:

Associate Professor, Dept. of Computer Science, College of Computing and Informatics, UNC-Charlotte, 2000-present
Associate Professor, Dept of Computer Science, College of Engineering, UNC-Charlotte, 1993-2000
Assistant Professor**,** Department of Computer Science, College of Engineering, UNC-Charlotte, 1986-1993
Design Consultant, VLSI Design and Test Group, Microelectronics Center of North Carolina, 1988-1989, Responsible for design and development of a silicon compilation for a high level language, 1988-1989.
Teaching Assistant, Department of Electrical and Computer Engineering, Responsible for design of a Computer Engineering teaching laboratory and design of a new graduate course for testing VLSI circuits, Oklahoma State University, 1984-1986.
System Analyst Programmer, Department of Agricultural Economics, Responsible for Design and development of programs for computer systems and supervising and supporting over 100 faculty members, graduate students, and computer staff for their computer programming and computer usage needs, Oklahoma State University, 1980-1986

Research Interests:

Medical Instrumentation, Bioinformatics/Biomedical Information Systems**,** Computer and parallel Architecture.

Funded Research: (total to date, $3,248,175.00)
Federal (NSF) Funds: (total to date $ 1,771,831.00)

Other Current and active funded projects:

1) "Acquisition of an Automated Tandem Mass Spectrometer: Enabling Proteomics Research in the Charlotte Region," Mostafavi (PI), Brian Cooper (Co-PI), North Carolina Biotechnology Center, $248,175.00, May 1, 2006-April 31, 2008.

2) "Effective Ovarian Cancer Data Analysis: Method and Procedure, " Mostafavi (PI), Hemby Cancer Research Endowment, $25,000, Jan. 2006-May 2008.

3) "Center for Biomedical Information System (Bioinformatics)," Mostafavi et al, was submitted in 1998, 2000, 2001, Approved in principal by COIT in 2002, and 2003, approved and supported with $35 million for new building in Fall 2004, State of North Carolina.

4) "Mass Spectrometry Facility," Charlotte-Mecklenburg Health Services Foundation, $96,300, 2004-2007**.**

Research Laboratories:

- Bioinformatics Laboratory at Carolinas Medical Center
- Biomedical Instrumentation Laboratory, Sponsor American Heart Association, UNC-Charlotte
- Mass Spectrometry Facility supported by North Carolina Biotechnology Center, 2006-2007

Patent awarded:

M. Taghi Mostafavi, "Specialized Image Processing System Architecture and Method for Image Data Arrays," U.S. Patent No. 5,642,444, June 24, 1997.

10 Selected Refereed Publications among over 60:

- K. Ashenayi, T. Heng, M.R. Sayeh and T. Mostafavi, "Single-Layer Perceptron Capable of Classifying 2N+1 Distinct input Patterns," Journal of Modeling and Simulation, Vol. 10, No. 4, pp 124-128, 1990.

- T. Mostafavi, S. Vishin, and W. Dettloff, "A parallel Processor ASIC Design for Real Time Pattern Recognition," IEEE International Conference of EURO ASIC 90, Paris, France, pp 306-309, May 29 1990.

- T. Mostafavi, "Most: A Model and Algorithm for Automatic Test Pattern Generation at the Transistor Level," International Conference Control and Modeling, Tehran, pp 951-955, July 1990.

- T. Mostafavi, "Linear Interconnection Architecture in Parallel Implementation of Neural Network Models," SPIE, Vol. 1396, pp193-201, 1990.

- T. Mostafavi, "Specialized Interconnected Architecture for VLSI Implementation of Neural Network Models," Intelligent Engineering Systems Through Artificial Neural Networks, pp 67-72, Vol. 2, Nov. 1992.

- T. Mostafavi, "A Parallel Model for Fast Computation of Pattern Matching in Integrated Engineering," Proceeding of the International Congress on Computational Methods in Engineering, pp 49-56, May 1993.

- M. Taghi Mostafavi and Satish Pragalsingl, "An Optical Calibrating Technique for Non-Contact Metrology," Proceeding of ASEP, Monterey, California, Nov. 1996, pp 196-201.

- K.R. Subramanian, M.J. Thubrikar, M.T. Mostafavi, and B. Fowler, "Accurate 3D reconstruction of curved coronary vessels from intra-vascular ultrasound images," Journal of Medical Engineering and Technology, Vol. 24, number 4, pp 131-140, July/august 2000.

- Timothy L. Tickle,.. , and M. Taghi Mostafavi, " Pax8, a Human Paired Box Gene, is Over expressed in Ovarian Cancer," American Association for cancer Research, April 2006,Washington DC.

- Tim Tickle and M. Taghi Mostafavi, "Analysis of Ovarian Cancer Microarray Data Using an Application Specific Data Base System, AACR conference, Anaheim CA, April 2005.

Graduate Students Supervised:

- Supervised and served on committee for over 60 graduate students theses and projects
- Currently supervising two Ph.D. students

Professional Societies:

Institute of Electrical and Electronics Engineers; IEEE Computer Society; Association of Computing Machinery; International Neural Network Society;SME; ASPE,; IMBE; ISTD;Eta Kappa Nu.

NAME	POSITION TITLE
Kayvan Najarian	Assistant Professor, Department of Computer Science University of North Carolina at Charlotte, Charlotte, NC

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	YEAR(s)	FIELD OF STUDY
University of British Columbia, Vancouver, Canada	Ph.D.	1996-2000	Electrical & Computer Engineering
Amirkabir University of Technology, Tehran, Iran	M.Sc.	1992-1994	Biomedical Engineering
Sharif University of Technology, Tehran, Iran	B.Sc.	1985-1990	Electrical and Computer Engineering

Appointments

July 2001 - present	Assistant Professor, Computer Science Department, College of Information Technology, University of North Carolina at Charlotte, U.S.A.
July 2000- July 2001	Visiting Assistant Professor, Computer Science Department, College of Information Technology, University of North Carolina at Charlotte, U.S.A.
1998-2000	Data Mining Engineer, Knowledge Junction Systems Inc., Vancouver, Canada. (Designed and developed AI algorithms for data mining, knowledge extraction, pattern recognition, data classification and time-series analysis of engineering and business databases)

Other Experience and Professional Memberships

- Member of Institute of Electrical and Electronics Engineers (IEEE), Communication Society of Institute of Electrical and Electronics Engineers, Signal Processing Society of Institute of Electrical and Electronics Engineers, Computer Society of Institute of Electrical and Electronics Engineers, Association for Computing Machinery (ACM), North Carolina Biotechnology Network, Charlotte DNA Microarray Consortium

- Member of Technical Committee of Conferences on Signal and Image Processing, Biomedical Engineering, and Signal Processing, Pattern Recognition, and Applications, Member of Technical Committee of Systemics, Cybernetics and Informatics (SCI) Conferences, Member of Program Committee of International Workshop on Bioinformatics Research and Applications, Technical Committee of the International Conference on Dynamical Systems and Differential Equations.

- Member of Editorial Board of BMC Medical Imaging, Referee for International Journal of Bioinformatics Research and Applications, Referee for Journal of IEEE Trans. on Neural Networks, IEEE Trans. on System, Man, and Cybernetics, IEEE Trans. on Medical Imaging, IEEE Trans. on Signal Processing, IEEE Sensors Journal, International Journal of System Sciences, Referee for Journal of Adaptive Control and Signal Processing, European Journal of Control, European Journal of Control Sensors and Actuators, Journal of Intelligent Information Systems, Automatica (IFAC Journal on Control), International Conference for Robotics and Automation (ICRA), and Journal of Mechatronics.

- Reviewer and panel member for National Science Foundation (NSF), U.S. Civilian Research and Development Foundation (CRDF), Australian Research Council (ARC), Canadian Foundation for Innovation (CFI), and Natural Sciences and Engineering Research Council of Canada (NSERC).

Honors

- Nominated for “2001 Canadian Association of Graduate Studies UMI Distinguished Dissertation Award”.
- Winner of the best non-medical Ph.D. dissertation award from University of British Columbia at Vancouver, 2000.
  - Selection made out of 300 non-medical Ph.D. dissertations.

Selected peer-reviewed publications (since 2001)

Books:

- K. Najarian and R. Splinter, "Biomedical Signal and Image Processing", The CRC Press, ISBN: 0849320992, 2005.
- K. Najarian, A Computational Approach to Systems Biology and Bioinformatics, The CRC Press, in progress, to appear in 2007.

Book Chapters:

- K. Najarian and A. Darvish, "Neural Networks and Their Applications in Biomedical Engineering", in Wiley Encyclopedia of Biomedical Engineering, Wiley and Sons, 2006.
- K. Najarian and A. Darvish, "Maximum Likelihood Estimation; Applications in Analysis of Biomedical Signals and Images in Wiley Encyclopedia of Biomedical Engineering, Wiley and Sons, 2006.
- K. Najarian and B. Ford, "Protein Structure, Folding, and Conformation", in Wiley Encyclopedia of Biomedical Engineering, Wiley and Sons, 2006.
- K. Najarian and C. Eichelberger, "Software Engineering", in Wiley Encyclopedia of Biomedical Engineering, Wiley and Sons, 2006.
- K. Najarian and C. Eichelberger, "Genetic Algorithms of Processing and Classification", in Wiley Encyclopedia of Biomedical Engineering, Wiley and Sons, 2006.
- K. Najarian and C. Eichelberger, "Back-Propagation Algorithm", in Wiley Encyclopedia of Biomedical Engineering, Wiley and Sons, 2006.

Selected journal papers:

- K. Najarian, K. Gopalakrishnan, and R.H. Zadeh, "Signal Processing for Functional Analysis of Protein Mutants", International Journal of Bioinformatics Research and Applications (IJBRA), vol. 1, no. 1, pp. 102-120, 2005.
- A. Darvish and K. Najarian, "Prediction of Regulatory Pathways Using Metabolic Control and Mason Rule: Application to Identification of Galactose Regulatory Pathway", Biosystems (special issue on Systems Biology), Volume 83, Issues 2-3, pp. 125-135, February-March 2006.
- K. Najarian, “Fixed-Distribution PAC Learning Theory for Neural FIR Models”, Journal of Intelligent Information Systems, vol. 25, no. 3, pp. 1573-7675 , 2005.
- J. Dargahi, S. Najarian, and K. Najarian, "Development and 3-dimensional modeling of a biological tissue grasper tool equipped with a tactile sensor", The IEEE Canadian Journal of Electrical and Computer Engineering, 2005.
- K. Najarian, M. Zaheri, A.A. Rad, S. Najarian, and J. Dargahi, “A Novel Mixture Model Method for Identification of Differentially Expressed Genes from DNA Microarray Data”, BMC Bioinformatics, vol. 5, no. 201, 2004.
- A.A. Tzacheva, K. Najarian, and J.P. Brockway, "Breast Cancer Detection in Gadolinium Enhanced MR Images by Static Region Descriptors and Neural Networks", Journal of Magnetic Resonance Imaging, vol. 17, Issue 3, pp. 337-342, March 2003.
- C.M. Wilson, D. Brown, K. Najarian, E.N. Hanley Jr, and H.E. Gruber, Computer Aided Vertebral Visualization and Analysis: A Pilot Study Using the Sand Rat, a Small Animal Model of Disk Degeneration, accepted for publications in BMC Musculoskeletal Disorders, vol. 4, no. 4, 2003.

- D.S. Warren, and K. Najarian, "Learning Theory Applied to Sigmoid Network Classification of Protein Biological Function Using Primary Structure", Discrete and Continuous Dynamical Systems, Sup. vol., pp. 898-904, 2002.
- K. Najarian, "FIR Volterra Kernel Neural Models and PAC Learning", Complexity, vol. 7, no. 6, pp. 48-55, July/August 2002.
- K. Najarian, "Learning-Based Complexity Evaluation of Radial Basis Function Networks", Neural Processing Letters, vol. 16, no. 2, pp. 137-150, October 2002.

Selected conference papers:

- Z. Li and K. Najarian, "Similarity calculation for anti-HIV drugs based on spanning tree matching algorithm", Proc of the 23rd American Chemical Society (ACS) National Meeting, Atlanta, GA, March 26-30, 2006.
- C. Eichelberger and K. Najarian, “Simulating Protein Computing: Character Recognition”, Proc. of IEEE Conference on Granular Computing, Atlanta, GA, U.S.A., 2006.
- Z. Li and K. Najarian, "Classification of pap smear based on features of nuclear Paper", The SPIE's International Symposium on Medical Imaging, San Diego, California. U.S.A, February 12-17, 2005.
- A. Darvish, K. Najarian, D.H. Jeong and W. Ribarsky, "System Identification and Nonlinear Factor Analysis for Discovery and Visualization of Dynamic Gene Regulatory Pathways", Proceedings of the 2005 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, San Diego, U.S.A., Nov. 2005.
- E. Bak, K. Najarian, and J. Brockway, "Efficient Segmentation Framework of Cell Images in Noise Environment", Proceedings of The 26th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (IEEE/EMBS 2004), San Francisco, CA, U.S.A., Sept 1–5, 2004.
- A. Darvish, E. Bak, and K. Najarian, "A New Hierarchical Method for Identification of Dynamic Regulatory Pathways from Time-Series DNA Microarray Data", Proceedings of The 3rd annual Computational Systems Bioinformatics conference (CSB2004), Stanford, CA, U.S.A., August 16–20, 2004.
- G. Zhang, L. Mays, and K. Najarian, "Comparison of Haploview and Hap Based on Haplotype Analysis Using Genotype Data on Chromosome 19", Proceedings of The International Conference on Molecular Systems Biology, Tahoe City, CA, U.S.A., Aug 21-25, 2004.
- Darvish, R.H. Zadeh, and K. Najarian, "Discovering Dynamic Regulatory Pathway by Applying an Auto Regressive Model to Time Series DNA Microarray Data", Proceedings of The 26th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (IEEE/EMBS 2004), San Francisco, CA, U.S.A., Sept 1–5, 2004.
- A. Lal, Sr. Radhakrishnan, S.S. Srinivas, K. Najarian and L. E. Mays, "Splice Site Detection using Pruned Maximum Likelihood Model", Proceedings of The 26th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (IEEE/EMBS 2004), San Francisco, CA, U.S.A., Sept 1–5, 2004.
- Lal, Sr. Radhakrishnan, S.S. Srinivas, K. Najarian and L.E. Mays, "Splice Site Detection using Pruned Maximum Likelihood Model", Proceedings of The 26th IEEE/EMBS conference, San Francisco, CA, U.S.A., Sept 1–5, 2004.
- K. Gopalakrishnan, and K. Najarian, "Computational Analysis and Classification of p53 Mutants According to Primary Structure", Proceedings of The 3rd annual Computational Systems Bioinformatics Conference (CSB2004), Stanford, CA, U.S.A., August 16–20, 2004.
- A. Darvish, and K. Najarian, "Prediction of Regulatory Pathways Using mRNA Expression and Protein-Protein Interaction Data: Application to Prediction of Galactose Regulatory Pathway", Proceedings of The 5th International Conference on Systems Biology, Heidelberg, Germany, Oct 2004.
- K. Gopalakrishnan, and K. Najarian, “Prediction of Protein Function Using Signal Processing of Biochemical Properties”, Proceedings of The Computational Systems Bioinformatics Conference (CSB2003), Stanford University, Stanford, CA, U.S.A., Aug 11-14, 2003.

- Z. Li, K. Najarian, E-S. Bak, “Cytological Classification Using Intelligent Techniques,” Proceedings of Optics in the Southeast Topical Meeting, Huntsville, Alabama, October 2002.
- D.S. Warren, and K. Najarian, "Neural Networks for Length-Dependent and Length-Independent Functional Classification and Prediction of Small Sequences of Lipase, Protease, and Isomerase”, Proceedings of The Fourth International Conference on Dynamical Systems and Differential Equations, Wilmington, U.S.A., May 2002.
- K. Najarian, E. Bak, Z. Li, J. Fan, J. Brockway, and S. Harris, “Computer-based automated classification of PAP smear tests using neural and fuzzy classifiers,” Proceedings of The 6th World Multi-Conference on Systemics, Cybernetics, and Informatics (SCI’2002), Orlando, FL, U.S.A., July 2002.
- Z. Li and K. Najarian, “Automated Classification of Pap Smear Tests Using Neural Networks”, Proceedings of The International Joint Conference on Neural Networks (IJCNN’2001), Washington DC, July 2001.

C. Research Support

Ongoing Research Support

- Genetic Factors Responsible For Maximal Aerobic Capacity 05-09

$1,468,968
National Institute of Health
PI: Tim Lightfoot (UNC Charlotte), Co-I’s: Kayvan Najarian, L. Leamy, M. Turner, and I. Sokolova
Abstract and Significance: The overall objective of this proposal is to determine the specific genes involved in the control of inherent aerobic capacity. More specifically, this research is to find the genes that are involved in determination of aerobic capacity of the heart measured by factors such as cardiac output.

- An Intelligent Computer Assisted System for Head Injury Trauma 06-08

$42,000
Carolinas Healthcare System
PI: Kayvan Najarian
Abstract and Significance: Advanced computational methods based on nonlinear regression trees will be designed to provide a rule-based system to provide trauma surgeons with predictions on the outcome of different treatments. This research will consider the national and North Carolina trauma databases and apply nonlinear regression trees to identify the success of certain treatments and procedures in terms of the patients’ long-term health and independence.

- Signal Processing and Nonlinear Pattern Recognition for Detection of Abnormal Behavior 06-07

$84,000
Bank of America
PI: Kayvan Najarian, Co-PI: William Ribarsky
Abstract and Significance: Advanced wavelet methods and Support Vector Machines are used to analyze customer transaction records and identify unlicensed businesses involved in suspicious financial transactions.

- Undergraduate Research Opportunities in Cognitive Science 06-09

$305,186
National Science Foundation
PI: Paula Goolkasian, Senior Personnel/Senior Scientists: Kayvan Najarian, P. Foos, L. Hodges, J. Welbourne, A. Blanchard, H. Richter, N. Gordon, J. Gaultney, M. Croy, and M. Faust
Abstract and Significance: This REU project will provide undergraduates with an opportunity to work on a research team during the academic year and to interact with faculty mentors and graduate students while doing research. By involving the students early in their college education we may be able to increase the number of students who consider careers in science.

Pending Research Support

- Computer-Assisted Decision Making System for Traumatic Brain Injury 07-09

$144,000
National Institute of Health
PI: Kayvan Najarian, Co-PI: Toan Huynh (CHS)
Abstract and Significance: Our main hypothesis is that there is diagnostically useful complex knowledge in the data gathered from head injured patients in typical intensive care units (ICU) that can help trauma experts improve their decisions for care. We propose that this knowledge can be extracted using advanced signal processing and pattern recognition methods. In this study, we aim to utilize advanced computational methods to design a rule-based system that creates reliable predictions on the occurrence of short term and long term complications for brain injured patients using all the features extracted from all signals and images at ICU.

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
James D. Oliver, Ph.D.	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 Arizona	B.S.	1968	Microbiology
Georgetown University	Ph.D	1973	Microbiology/Bio-chemistry
University of Ottawa, Canada	(Post-Doc)	1973-74	Biochemistry

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

Positions

1974-present Assistant, Associate, Full Professor, Dept. Biology, University of North Carolina at Charlotte
1994-2004 Director, Interdisciplinary Biotechnology Program, UNC Charlotte
1990 Visiting Professor, University of Göteborg, Sweden
1998 Visiting Professor, Royal Veterinary and Agricultural University, Copenhagen, Denmark
2006 Visiting Professor, National University of Ireland, Galway

Honors & Professional Activities

National

1988- 1993 Member, Editorial Board, Applied and Environmental Microbiology
1995- present Special Advisor to the Chairman, *Vibrio vulnificus* Committee, Interstate Shellfish Sanitation Commission
1999 Burrows Welcome Fund Visiting Professor in the Microbiological Sciences
2000 National Science Foundation Policy Working Group on Microbial Genomics
2000 National Marine Pathogen Plan Workshop
2000- present Standard Methods Committee, American Water Works Association

International

2000- present Working Party on Culture Media, International Committee on Food Microbiology and Hygiene, International Union of Microbiological Sciences
2004 Consultant, Food and Agriculture Organization of the United Nations World Health Organization; Risk Assessment of *Vibrio vulnificus* in Raw Oysters
2005 Member, Editorial Board, FEMS Microbiology Ecology

B. Selected peer-reviewed publications (most recent, selected from a total of 121 papers)

1. Optimization of conditions for the polymerase chain reaction amplification of DNA from culturable and nonculturable cells of *Vibrio vulnificus*. 1996. Coleman, S. and J.D. Oliver. FEMS Microbiol. Ecol. 19:127-132.
2. Phenotypic characterization of *Vibrio vulnificus* biotype 2: A LPS-based homogeneous O-serogroup within *Vibrio vulnificus* species. 1996. Biosca, E., J.D. Oliver, and C. Amaro. Appl. Environ. Microbiol. 62:918-927.
3. The viable but nonculturable state in the human pathogen, *Vibrio vulnificus*. 1995. Oliver, J.D. FEMS Lett. (Mini-review). 133:203-208.
4. Effect of low temperature on starvation-survival of the eel pathogen *Vibrio vulnificus* biotype 2. 1996. Biosca, E.G., C. Amaro, E. Marco-Noales, and J.D. Oliver. Appl. Environ. Microbiol. 62:450-455.

5. Detection of *Vibrio vulnificus* biotypes 1 and 2 in eels and unamended oysters by PCR amplification. 1996. Coleman, S.S., D.M. Melanson, E.G. Biosca, and J.D. Oliver. Appl. Environ. Microbiol. 62:1378-1382.
6. Detection of the viable but nonculturable state in *Escherichia coli* O157:H7. 1997. Rigsbee, W., L.M. Simpson, and J.D. Oliver. J. Food Safety 16:255-262.
7. Resuscitation of *Vibrio vulnificus* from the viable but nonculturable state. 1997. Whiteside, M.D. and J.D. Oliver. Appl. Environ. Microbiol. 63:1002-1005.
8. Comparison of ribotyping and randomly amplified polymorphic DNA polymerase chain reaction (RAPD-PCR) for characterization of *Vibrio vulnificus*. 1997. Høi, L., A. Dalsgaard, J.L. Larsen, J.M. Warner, and J.D. Oliver. Appl. Environ. Microbiol. 63:1674-1678.
9. Randomly amplified polymorphic DNA analysis of starved and viable but nonculturable *Vibrio vulnificus* cells. 1998. Warner, J.M. and J.D. Oliver. Appl. Environ. Microbiol. 64:3025-3028.
10. Randomly amplified polymorphic DNA (RAPD) analysis of clinical and environmental strains of *Vibrio vulnificus* and other *Vibrio* species. 1999. Warner, J.M. and J.D. Oliver. Appl. Environ. Microbiol. 65:1141-1144.
11. Comparative study of biological properties and electrophoretic characteristics of lipopolysaccharide from eel-virulent and eel-avirulent *Vibrio vulnificus* strains. 1999. Biosca, E.G., R.M. Collado, J.D. Oliver, and C. Amaro. Appl. Environ. Microbiol. 65:856-858.
12. Pathogenesis of *Vibrio vulnificus*. Linkous, D. and J.D. Oliver. 1999. FEMS Microbiol. Lett. 174:207-214.
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14. The use of modified GFP as a reporter for metabolic activity in *Pseudomonas putida*. 2001. Lowder, M. and J.D. Oliver. Microb. Ecol. 41:310-313.
15. Essential role for estrogen in protection against *Vibrio vulnificus* induced endotoxic shock. 2001. Merkel, S.M., S. Alexander, J.D. Oliver, and Y.M. Huet-Hudson. Infect. Immun. 69:6119-6122.
16. Effects of refrigeration and alcohol on the load of *Aeromonas hydrophila* in oysters. 2002. Birkenhauer, J.B. and J.D. Oliver. J. Food Protect. 65:560–562.
17. Use of diacetyl to reduce the load of *Vibrio vulnificus* in the Eastern oyster, *Crassostrea virginica*. 2003. Birkenhauer, J.B. and J.D. Oliver. J. Food Protect. 66:38-43.
18. A comparison of thiosulphate-citrate-bile salts-sucrose (TCBS) agar and thiosulphate-chloride-iodide (TCI) agar for the isolation of *Vibrio* species from estuarine environments. 2003. Pfeffer, C. and J.D. Oliver. Lett. Appl. Microbiol. 36:150-151.
19. Analysis of *Vibrio vulnificus* from market oysters and septicemia cases for virulence markers. 2003. DePaola, A., J.L. Nordstrom, A. Dalsgaard, A. Forslund, J. Oliver, T. Bates, K.L. Bordage, and P.A. Gulig. Appl. Environ. Microbiol. 69: 4006-4011.
20. The ecology of *Vibrio vulnificus* in estuarine waters of eastern North Carolina. 2003. Pfeffer, C.S., M.F. Hite and J.D. Oliver. Appl. Environ. Microbiol. 69:3526-3531.
21. RpoS-dependent stress response and exoenzyme production in *Vibrio vulnificus*. Hülsmann, A., T.M. Rosche, I.-S. Kong, H.M. Hassan, D.M Beam, and J.D. Oliver. 2003. Appl. Environ. Microbiol. 69:6114-6120.
22. Survival of *Helicobacter pylori* in a natural freshwater environment. 2003. Adams, B.L., T.C. Bates, and J.D. Oliver. Appl. Environ. Microbiol. 69:7462-7466.
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24. Biochemical and virulence characterization of viable but nonculturable cells of *Vibrio parahaemolyticus*. 2004. Wong, H.-C. and J.D. Oliver. J. Food Prot. 67:2430-2435.
25. The viable but nonculturable state of *Vibrio parahaemolyticus*. 2004. Bates, T.C. and J.D. Oliver. J. Microbiol. 42:74-79.
26. Role of catalase and *oxyR* in the viable but nonculturable state of *Vibrio vulnificus*. 2004. Kong, I.-S., T.C. Bates, A. Hülsmann, H. Hassan, and J.D. Oliver. FEMS Microbiol. Ecol. 50:133-142.

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32. The viable but nonculturable state in bacteria. 2005. Oliver, J.D. J. Microbiol. 43:93-100.
33. Cloning, sequencing and expression of a GroEL-like protein gene of *Vibrio vulnificus*. 2005. Wong, H.-c., K.H. Lu, and J.D. Oliver. Taiw. J. Agric. Chem. Food Sci. 43:1-7.
34. RpoS involvement in osmotically-induced cross protection in *Vibrio vulnificus*. 2005. Rosche, T.M., T.C. Bates, D.J. Smith, E.E. Parker, and J.D. Oliver. FEMS. Microbiol. Ecol. 53:455-462.
35. Intrapopulational variation in *Vibrio vulnificus* levels in *Crassostrea virginica* is associated with the host size but not with disease status or developmental stability. 2005. Sokolova, I.M., L. Leamy, M. Harrison, and J.D. Oliver. J. Shellfish Res. 24:503-508.
36. Engineering behavior of biofilm amended earthen barriers used in waste containment. 2005. Daniels, J.L., R. Cherukuri, H.A. Hilger, J.D. Oliver, and S. Bin. Int. J. Manage. Environ. Qual. 16: 691-704.
37. *In situ* and *in vitro* gene expression by *Vibrio vulnificus* during entry into, persistence within, and resuscitation from the viable but nonculturable state. 2006. Smith, B.E. and J.D. Oliver. Appl. Environ. Microbiol. 72:1445-1451.
38. *In situ* gene expression by *Vibrio vulnificus*. 2006. Smith, B.E. and J.D. Oliver. Appl. Environ. Microbiol. 72:2244-2246.
39. An AFLP approach to identify genetic markers associated with resistance to *Vibrio vulnificus* and *Perkinsus marinus* in eastern oysters. 2006. Sokolova, I.M., J.D. Oliver, and L.J. Leamy. J. Shellfish Res.
40. Evidence for an intermediate colony morphology of *Vibrio vulnificus*. 2006. Rosche, T.M., B. Smith, and J.D. Oliver. Appl. Environ. Microbiol. 72: 4356-4359.
41. Capsular polysaccharide phase variation in *Vibrio vulnificus*. 2006. Hilton, T., T. Rosche, B. Froelich, B. Smith, and J.D. Oliver. Appl. Environ. Microbiol. 72:6986-6993.

Book Chapters:

1. Formation of viable but nonculturable cells. Oliver, J.D. pp. 239-272 In: "Starvation in Bacteria", S. Kjelleberg (ed.). Plenum Press. 1993.
2. *Vibrio* species. Oliver, J.D. and J. Kaper. 1997. pp.228-264 *In*: Food Microbiology: Fundamentals and Frontiers, M.P. Doyle (ed.). Amer. Soc. Microbiol.
3. *Vibrio cholerae*. Oliver, J.D. 1998. pp. 9-102 - 9-104, *In*: Standard Methods for the Examination of Water and Wastewater, 20th Ed. Amer. Public Health Assoc.
4. *Vibrio cholerae, V. vulnificus*, and other human pathogenic *Vibrio* species. Dalsgaard, A. and J.D. Oliver. 1997. *In*: World Health Organization Guidelines for Recreational Water and Bathing Beach Quality.
5. *Vibrio vulnificus*. Dalsgaard, A., L. Høi, D. Linkous, and J.D. Oliver. 2000. pp. 439-470 In: Bacterial Pathogens, vol. 1 of Foodborne Disease Handbook. Marcel Dekker Pub., Inc., NY.
6. The viable but nonculturable state and cellular resuscitation. 2000. Oliver, J.D. In: Microbial Biosystems: New Frontiers. C.R. Bell, M. Brylinsky, and P. Johnson-Green. Atlantic Canada Soc. Microb. Ecol. Pub. pp. 723-730.
7. Problems in detecting dormant (VBNC) cells, and the role of DNA elements in this response. Oliver, J.D. 2000. pp. 1-15 In: Tracking Genetically Engineered Microorganisms. J.K. Jansson, J.D. van Elsas, and M. Bailey, ed.

8. Public health significance of viable but nonculturable bacteria. Oliver, J.D. 2000. In: "Non-Culturable Microorganisms in the Environment", R.R. Colwell and D.J. Grimes (ed.). Amer. Soc. Microbiol. Press, Washington, D.C.
9. *Vibrio vulnificus*. 2000. Dalsgaard, A., L. Høi, D. Linkous, and J.D. Oliver. pp. 439-470 In: Bacterial Pathogens, vol. 1 of Foodborne Disease Handbook. Marcel Dekker Pub., Inc., NY.
10. The viable but nonculturable state and cellular resuscitation. 2000. Oliver, J.D. In: Microbial Biosystems: New Frontiers. C.R. Bell, M. Brylinsky, and P. Johnson-Green. Atlantic Canada Soc. Microb. Ecol. Pub. pp. 723-730.
11. Problems in detecting dormant (VBNC) cells, and the role of DNA elements in this response. 2000. Oliver, J.D. p. 1-15 *In*: Tracking Genetically Engineered Microorganisms. J.K. Jansson, J.D. van Elsas, and M. Bailey, ed. Landes Bioscience, Georgetown, Tx.
12. *Vibrio* species. 2001. Oliver, J.D. and J. Kaper. pp. 263-300 *In*: Food Microbiology: Fundamentals and Frontiers, 2nd ed. M.P. Doyle, L.R. Beuchat, T.J. Montville (ed.). Amer. Soc. Microbiol.
13. Culture media for the isolation and enumeration of pathogenic *Vibrio* species in foods and environmental samples. 2003. Oliver, J.D. pp. 249-269 In: Handbook of Culture media for Food Microbiology, 2nd ed. J.E.L. Corry, G.D.W. Curtis, and R.M. Baird (eds.). Vol. 37 of Progress in Industrial Microbiology. Elsevier. Amsterdam.
14. Viable but nonculturable bacteria in food environments. 2005. Oliver, J.D. In: Food-borne pathogens: Microbiology and Molecular Biology. P.M. Fratamico, A.K. Bhunia, and J.L. Smith (eds.). Caister Academic Press, Norfolk, UK.
15. *Vibrio vulnificus*. 2005. Oliver, J.D. In: Oceans and Health: Pathogens in the Marine Environment. (pp. 253-276). S. Belkin and R.R. Colwell (eds.). Springer Science, New York.
16. *Vibrio vulnificus*. 2006. Oliver, J.D. pp. 349-366 In: Biology of Vibrios. F.L.Thompson, B. Austin, and J. Swing. (eds.). Amer. Soc. Microbiol. Press, Washington, D.C.
17. *Vibrio* species. 2006. Oliver, J.D. and J. Kaper. *In*: Food Microbiology: Fundamentals and Frontiers, 3nd ed. M.P. Doyle, L.R. Beuchat, T.J. Montville (ed.). Amer. Soc. Microbiol. (in press)

C. Research Support. List selected ongoing or completed (during the last three years) research projects (federal and non-federal support). Begin with the projects that are most relevant to the research proposed in this application. Briefly indicate the overall goals of the projects and your role (e.g. PI, Co-Investigator, Consultant) in the research project. Do not list award amounts or percent effort in projects.

Gulf Oyster Industry Program. 2004-2006. “Research to Induce Loss of Virulence in Cells of *Vibrio vulnificus* in Oysters”. PI. Goal was to examine the molecular and physiological aspects of capsule loss.

NOAA (Oceans and Human Health Initiative). 2005-2007. “Ecology and Significance of Two *Vibrio vulnificus* Genotypes”. PI. Goal is to characterize the ecology, physiology, and molecular genetics of the recently realized two genotypes of this human pathogen.

NC Sea Grant. 2006-2008. “Hypoxia Impacts on Sustainable Oyster Populations”. Co-PI with Amy Ringwood and Inna Sokolova, UNC Charlotte, and Patricia McClellan-Green, North Carolina State Univ. Goal is to understand the role of anoxia on oyster physiology and on the presence of *Vibrio vulnificus* in oysters.

Dept. Energy. 2005-2008. “Bio-Tarp: Reducing landfill methane emissions with bioactive alternate daily cover”. Co-PI with Helene Hilger, Dept. Civil Engineering. Goal is to study the use of a methanotroph-embedded tarp for the elimination of methane from landfills.

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
Richardson, Christine	Associate Professor
eRA COMMONS USER NAME	

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
Princeton University, Princeton, N.J.	A.B.	1986-1990	Molecular Biology
Columbia University, New York, N.Y.	Ph.D.	1990-1995	Genetics & Developmt.
Sloan-Kettering Institute, New York, N.Y.	Post-Doc	1995-1999	Cell Biology & Genetics
Sloan-Kettering Institute, New York, N.Y.	Res. Assoc.	1999-2001	Cell Biology & Genetics

A. Positions and Honors.

RESEARCH EXPERIENCE:

1989 Summer Research Intern - Cleveland Clinic, Ft. Lauderdale, FL.
Dr. Fred Lucas, supervisor

1990 - 1995 Graduate Student – Dept of Genetics & Development, Columbia University, NYC, NY
Prof. Arthur Bank, thesis advisor

1995 - 1999 Post-doctoral Fellow – Dept of Cell Biology and Genetics, Sloan-Kettering Institute, NYC, NY
Prof. Maria Jasin, advisor

1999 - 2001 Research Associate – Dept of Cell Biology and Genetics, Sloan-Kettering Institute, NYC, NY
Prof. Maria Jasin, advisor

2001- 2005 Assistant Professor -- Department of Pathology, Institute for Cancer Genetics, Comprehensive Cancer Center, Columbia University, NYC, NY

2006 - Associate Professor – Department of Biology, Bioinformatics Research Center, University of North Carolina, Charlotte, NC

HONORS:

Columbia University -
- Pre-doctoral Fellow of the March of Dimes
- Trainees Travel Research Competition Award, N.Y. Society of Medical Oncologists and Hematologists

Sloan-Kettering Institute -
- Fellow of the Leukemia Society of America
- Special Fellow of the Leukemia and Lymphoma Society
- Short-Term Scientific Exchange Award, Leukemia and Lymphoma Society

Columbia University –
- American Cancer Society Beginning Research Scholar

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

RELEVANT PUBLICATIONS (TOTAL 35)

Richardson, C., and Bank, A. Preselection of transduced murine hematopoietic stem cell populations leads to increased long-term stability and expression of the human multiple drug resistance gene. *Blood* 86(7): 2579-2589, 1995.

Richardson, C., and Bank, A. Developmental stage-specific expression and regulation of an amphotropic retroviral receptor in hematopoietic cells. *Mol. Cell. Biol.* 16(8): 4240-4247, 1996.

Richardson, C., Ward, M., Bank, A. Retrovirus transfer of MDR gene into live mice. In Becker, Y. and Darai, G. (Eds.): Frontiers of Virology: Gene Transfer by Retroviral Vectors for Gene Therapy. Springer-Verlag, 1995.

Jasin, M., Moynahan, M.E., Richardson, C. Targeted transgenesis: A commentary. *Proc. Natl. Acad. Sci.* 93: 8804-8808, 1996.
Richardson, C., Moynahan, M., Jasin, M. Double-strand break repair by interchromosomal recombination: Suppression of chromosomal translocations. *Genes & Development* 12: 3831-3842, 1998.
Elliott, B., Richardson, C., Winderbaum, J., Nickoloff, J., Jasin, M. Gene conversion tracts from double-strand break repair in mammalian cells. *Mol. Cell. Biol.* 18(1): 93-101, 1998.
Richardson, C., Elliott, B., Jasin, M. Chromosomal double strand breaks introduced in mammalian cells by expression of I-*Sce* I endonuclease. In Henderson, D. and Walker, J. (Eds.): Methods in Molecular Biology--DNA Repair Protocols: Eukaryotic Systems. Totowa, N.J.: Humana Press, 453-464, 1999.
Richardson, C., Moynahan, M.E., Jasin, M. Homologous recombination between heterologs during repair of a double-strand break: Suppression of translocations in normal cells. In Anti-Cancer Proteins and Drugs. New York: New York Academy of Sciences, 183-186, 1999.
Richardson, C., and Jasin, M. Frequent chromosomal translocations induced by DNA double-strand breaks. *Nature* 405: 697-700, 2000.
Richardson, C., and Jasin, M. Coupled homologous and nonhomologous repair of a double-strand break preserves genomic integrity in mammalian cells. *Mol. Cell. Biol*. 20(23): 9068-9075, 2000.
Richardson, C. and Jasin, M. Eukaryotic recombination: Initiation by double-strand breaks. In Encyclopedia of Life Sciences. London: Macmillan Reference, 2000.
Richardson, C. and Jasin, M. Recombination between two chromosomes: Implications for genomic integrity in mammalian cells. In Cold Spring Harbor Symposia on Quantitative Biology: Biological Responses to DNA Damage. New York: Cold Spring Harbor Laboratory Press, 553-560, 2000.
Richardson, C. (*corresponding author), Stark, J., Ommundsen, M., and Jasin, M. Rad51 over-expression promotes alternative double-strand break repair pathways and genome instability, *Oncogene* 23 (2): 546-553, 2004.
Richardson, C., Horikoshi, N., and Pandita, T. The DSB response network in meiosis. *DNA Repair*, 3 (8-9): 1149-1164, 2004.
Elliott, B., Richardson, C., Jasin, M. Chromosomal translocation mechanisms at intronic alu elements in mammalian cells. *Mol. Cell*, 17: 885-894, 2005.
Richardson, C. Rad51, genomic stability, and tumorigenesis. *Cancer Letters*, 218: 127-139, 2005.
Libura, J., Slater, D.J., Felix, C.A., Richardson, C. t-AML-like MLL Rearrangements are induced by etoposide in primary human CD34+ cells and remain stable after clonal expansion. *Blood*, 105 (5): 2124-2131, 2005.
Pulte D, Lopez, RJ, Baker ST, Ward MN, Ritchie E, Richardson C, O'Neill D, and Bank, A. Ikaros Increases Normal Apoptosis in Adult Erythroid Cells. *Amer J Hem* 81(1); 12-18, 2006.
Mantha, S., Ward, M., McCafferty, J., Herron, A., Palomero, T., Ferrando, A., Bank, A., Richardson, C. Activating *Notch1* mutations are an early event in T-cell malignancy of *Ikaros* point mutant *Plastic*/+ mice. *Leuk Res*, epub, ahead of print, 2006.
Weinstock, D., Elliott, B., Richardson, C., Jasin, M. Modeling oncogenic translocations: Distinct roles for double-strand break repair pathways in translocation formation in mammalian cells. *DNA Repair*, 5: 1065-1074, 2006.
Sung, P.A., Libura, J., Richardson, C. Etoposide and illegitimate DNA double-strand break repair in the generation of *MLL* chromosomal translocations. *DNA Repair*, 5: 1109-1118, 2006.
Felix, C., Robinson, B., Germano, G., Kolaris, C., Raffini, L., Nigro, L., Roumm,. E., Megonigal, M., Slater, D., Whitmarsh, R., Saginario, C., Lovett, B., Libura, J., Pegram, L., Zheng, N., Pang, S., Zhou, X., Rappaport, E., Richardson, C., Cheung, N., Blair, I., Osheroff, N. Translocation mechanism in secondary leukemias following topoisomerase II poison. In Proceedings of the Third International Symposium on Secondary Leukemias. Rome, Italy: 2006.

C. Research Support.

CURRENT SUPPORT

RSG-02-181-01-MGO Richardson (P.I.) 7/1/2002 - 6/30/2007
American Cancer Society 25% effort
Research Scholar Grant for Beginning Investigators
Influence of Repetitive Elements on Repair of DSBs and Translocations
The aim of this work is to examine the influence of endogenous repetitive elements such as Alu elements in

the generation of translocations and other genome rearrangements during the repair of double-strand breaks.
Role: P.I.

5R01CA100159-02 Richardson (P.I.) 6/1/2003 – 4/30/2008
NIH/NCI 25% effort
Etiology of translocations in hematopoietic cells
The major goals of this project are to use the I-*Sce*I model system developed by the PI to examine products of DSB repair and recombination in hematopoietic early progenitor and myeloid cell lineages and the frequency that this type of damage to promote illegitimate recombination.
Role: P.I.

1 R01 HL70370-01 Bank (P.I.) 12/01/2004 – 11/30/2009
NIH/NHLBI 5% effort
Gene Delivery into Human Hematopoietic Cells
The aims of this project are to develop more efficient vectors to transfer genes to human hematopoietic stem cells and to produce lentiviral packaging systems that are more amenable for human use.
Role: Co-investigator

COMPLETED SUPPORT

Concern Foundation Richardson (P.I.) 7/1/2002 - 6/30/2004
Mouse Model to Examine the Etiology of Genome Rearrangements Induced by DNA Damage
The aim of this project is to develop transgenic mouse lines containing GFP reporter constructs to determine the frequency of double-strand break induced repair and rearrangements in vivo.
Role: P.I.

Stewart Trust Richardson (P.I.) 7/1/2003 – 6/30/2004
Pilot Project for Cancer Research
Control of DNA Repair and Genome Rearrangements in Hematopoietic Progenitor Cells
The goal of this pilot project is to examine aberrant *Rad51* over-expression in human and murine hematopoietic progenitor cells, and determine a role for Rad51 on repair of DNA damage by genotoxic agents and the potential to promote genome rearrangements.

Martin Estrin Pilot Award Richardson (P.I.) 7/1/2003 – 6/30/2004
Control of DNA Repair and Genome Rearrangements using Mouse Model
The goal of this pilot project is to examine aberrant *Rad51* over-expression in transgenic mouse model, and determine a role for Rad51 on repair of DNA damage and the potential to promote genome rearrangements following exposure of mice to genotoxic agents.

*VFFCR CCCU51535401 Richardson (Co-Investigator) 7/1/2003 – 6/30/2004
V-Foundation
The Role of Genome Rearrangements and Instability in the Initiation and Progression of Prostate Cancer
This project examines the frequency of aberrant homologous recombination in epithelial cells, specifically prostate derived cell lines, and the influence of decreased BRCA1 and increased PEG-3 in leading to chromosomal alterations and instability.

LSS#3075-00 7/1/1999-6/30/2002
Special Fellow of the Leukemia and Lymphoma Society
The Effect of Genetic Mutations on Chromosomal Translocations
This project involved double strand break repair in mouse cells and in cells mutant for DNA repair.

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
Sass, Ronald Richard	Associate Professor
eRA COMMONS USER NAME	
Sass	

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
Michigan State University	Ph.D.	1999	Comp. Sci. & Eng.
Michigan State University	M.S.	1992	Computer Science
University of Toledo	B.S.	1989	Comp. Sci. & Eng.

A. Positions and Honors.

Positions and Employment

1996-1997 Visiting Instructor at Michigan State University,
1997-1998 Visiting Assistant Professor and Research Associate at Clemson University
1998-2004 Assistant Professor at Clemson University
2004-2006 Assistant Research Professor at University of Kansas
2006-present Associate Professor at University of North Carolina, Charlotte

Other Experience and Professional Memberships

1988- present Member, ACM (Association for Computing Machinery)
1988- present Member, Tau Beta Pi
1998- present Member, IEEE-CS Institute of Electrical and Electronics Engineers, Computer Society
2000- present Member, IEEE-ComSoc Institute of Electrical and Electronics Engineers, Communication Society
2006- present Chair, IEEE-CS Charlotte Section
2003- present Member, AAAS (American Association for the Advancement of Science)
2004- present Program Committee, International Symposium on Field-Programmable Custom Computing Machines

Honors

1995 DOE/Ford Hybrid Electric Vehicle challenge, 1st Prize Best use of digital electronics
2005 IBM Faculty Award

B. Selected peer-reviewed publications.

(Publications selected from 30 peer-reviewed publications)

[1] Ron Sass. Embedded Systems Design with Platform FPGAs: Principles, Practices, and Economics. Morgan-Kaufmann, an imprint of Elsevier, San Francisco, CA, USA, will appear Fall 2007.

[2] Ron Sass, Parag Beeraka, Jason Agron, Jeff Young, David Andrews, Brian Greskamp, Srinivas Beeravolu, and Christian Trefftz. Run-Time Reconfigurable Java Virtual Machine on a Platform FPGA.

Submitted to FCCM #06: Proceedings of the 13th Annual IEEE Symposium on Field-Programmable Custom Computing Machines (FCCM#06), Washington, DC, USA, 2006. IEEE Computer Society.

[3] Erik Anderson, Jason Agron, Wesley Peck, Jim Stevens, Fabrice Bai-jot, Ed Komp, Ron Sass, and David Andrews. Enabling a Uniform Programming Model Across the Software/Hardware Boundary. Submitted to FCCM #06: Proceedings of the 13th Annual IEEE Symposium on Field-Programmable Custom Computing Machines (FCCM#06), Washington, DC, USA, 2006. IEEE Computer Society.

[4] Nathan DeBardeleben, Ron Sass, Daniel Stanzione, Jr., and Walter Ligon, III. Building Problem Solving Environments with the Arches Framework. Submitted to Journal of Systems and Software, 2006.

[5] Ron R Sass and David Andrews. Essential and Elective Topics: A Proposal for the Content of Reconfigurable Computing Courses. To appear in ISVLSI#06: Proceedings of the IEEE Computer Society Annual Symposium on VLSI: International Workshop on Reconfigurable Computing Education (RC-Education), Washington, DC USA, March 2006. IEEE Computer Society.

[6] Jason Agron, Wesley Peck, Erik Anderson, Ed Komp, Ron Sass, and David Andrews. Run-Time Support for Hybrid CPU/FPGA Systems on Chip. Submitted to ACM Trans. on Embedded Computing Sys., 2006.

[7] Ron Sass, Brian Greskamp, Brian Leonard, Jeff Young, and Srinivas Beeravolu. Online Architectures: A Theoretical Formulation and Experimental Prototype. To appear in Journal of Microprocessors and Microsystems, 2006.

[8] David Andrews, Wesley Peck, Jason Agron, and Ron Sass. hthreads: A Hardware/Software Co-Designed Multithreaded RTOS Kernel. In ETFA2005: 10th IEEE International Conference on Emerging Technologies and Factory Automation, page T3.3, September 2005.

[9] Pradeep Nalabalapu and Ron Sass. Bandwidth Management with a Reconfigurable Data Cache. In IPDPS #05: Proceedings of the 19th IEEE International Parallel and Distributed Processing Symposium (IPDPS#05) - Workshop 3: Reconfigurable Architectures Work-shop (RAW#05), page 159.1, Washington, DC, USA, April 2005. IEEE Computer Society.

[10] Krishna Muriki, Keith D. Underwood, and Ron Sass. RC-BLAST: To-wards a Portable, Cost-Effective Open Source Hardware Implementation. In IPDPS #05: Proceedings of the 19th IEEE International Parallel and Distributed Processing Symposium (IPDPS'5) – Workshop 7 page 196.2, Washington, DC, USA, April 2005. IEEE Computer Society.

[11] Jeff Young and Ron Sass. FERP Interface and Interconnect Cores for Stream Processing Applications. In Lecture Notes in Computer Science: Proceedings of First International Conference on Embed-ded and Ubiquitous Computing, volume 3207, pages 291-00, Aizu-Wakamatsu City, Japan, September 2004.

[12] Keith D. Underwood, Walter B. Ligon, III, and Ron R. Sass. An Analysis of the Cost-Effectiveness of an Adaptable Computing Cluster. Cluster Computing, 7(4):357#371, 2004.

[13] Nathan DeBardeleben, Walter B. Ligon, III, and Ron Sass. Arches: An Infrastructure for PSE Development. In HIPS '4: Proceedings of the Eighth International Workshop on High-Level Parallel Programming Models and Supportive Environments, Santa Fe, New Mexico, USA, April 2004. IEEE Computer Society.

[14] Keith D. Underwood, Walter B. Ligon, III, and Ron R. Sass. Analysis of a Prototype Intelligent Network Interface. Concurrency and Computation: Practice & Experience, 15(7/8):751-77, 2003.

[15] Ranjesh G. Jaganathan, Keith D. Underwood, and Ron Sass. A Configurable Network Protocol for Cluster Based Communications us-ing Modular Hardware Primitives on an Intelligent NIC. In SC #03: Proceedings of the 2003 ACM/IEEE conference on Supercomputing, page 22, Washington, DC, USA, 2003. IEEE Computer Society.

[16] Shyamnath Harinath and Ron Sass. Reconfigurable Mapping Functions for Online Architectures. In IPDPS #03: Proceedings of the 17th International Symposium on Parallel and Distributed Processing, page 173.1, Washington, DC, USA, 2003. IEEE Computer Society.

[17] Keith D. Underwood, Ron R. Sass, and Walter B. Ligon, III. Cost-Effectiveness of an Adaptable Computing Cluster. In Supercomputing '01: Proceedings of the 2001 ACM/IEEE conference on Supercomputing (CDROM), page 54, New York, NY, USA, 2001. ACM Press.

[18] Keith D. Underwood, Ron R. Sass, and Walter B. Ligon, III. A Reconfigurable Extension to the Network Interface of Beowulf Clusters. In CLUSTER #01: Proceedings of the 3rd IEEE International Conference on Cluster Computing, pages 212-221, Newport Beach, CA, October 2001.

[19] Ron R. Sass, Keith D. Underwood, and Walter B. Ligon, III. Design of Adaptable Computing Cluster. In MAPLD '01: Proceedings of the 4th Annual Military and Aerospace Applications of Programmable Devices and Technologies International Conference (CDROM), page D5, 2001.

[20] Keith D. Underwood, Ron R. Sass, and Walter B. Ligon, III. Acceleration of a 2D-FFT on an Adaptable Computing Cluster. In FCCM#01: Proceedings of the 9th Annual IEEE Symposium on Field-Programmable Custom Computing Machines, pages 180-189, Washington, DC, USA, 2001. IEEE Computer Society.

[21] Kim Hazelwood, Walter B. Ligon, III, Gregory Monn, N. Pothen, Ron R. Sass, Daniel Stanzione, Jr., and Keith D. Underwood. Creating applications in RCADE. In Proceedings of the IEEE Aerospace Conference, Video, and Data Communications, pages 337-349, 1999.

[22] Walt B. Ligon III, Brian Boysen, Nathan DeBardeleben, Kim Hazel-wood, Ron Sass, Daniel Stanzione, Jr., and Keith D. Underwood. A Development Environment for Configurable Computing. In Proceedings of the SPIE International Symposium on Voice, Video, and Data Communications, September 1998.

[23] Marwan Krunz, Ron Sass, and Herman D. Hughes. Study of VBR MPEG-coded Video Traffic and Associated Multiplexing Performance. International Journal of Computer Systems Science & Engineering, 11(3):135-143, May 1996.

C. Research Support.

Ongoing Research Support

CNS 04-10790 Sass (PI) 9/01/04-8/31/07
NSF
Dynamic Hardware Reconfiguration to Accelerate Java-Based Embedded Systems
Role: PI

CNS 05-51688 Sass (PI) 3/01/06-2/28/08
NSF
Cluster-on-a-Chip Reconfigurable Computing Cluster
Role: PI

Completed Research Support

GSFC Ligon (PI) 9/01/97-8/30/00
NASA
Reconfigurable Computing Systems for Regional Validation Center Applications
Role: Co-Investigator

GSFC Ligon (PI) 4/01/98-3/31/01
NASA
An Application Development Framework for Reconfigurable Computing Systems

Role: Co-PI

EIA 99-85986 Sass (PI) 9/01/99-8/31/00
NSF
CISE Research Instrumentation: Adaptable Computing Cluster
Role: PI

NAG5-11329 Sass (PI) 9/01/01-8/31/04
NASA
Alternative Computing Roadmap Project
Role: PI

Sass (PI) 8/1/05-7/31/06
IBM
Automatic Synthesis of Hardware Features to Augment the POWER Architecture
Role: PI

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel in the order listed on Form Page 2.
Photocopy this page or follow this format for each person.

NAME	POSITION TITLE
Steuerwald, Nury	Senior Scientist

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
Florida International University, Miami, FL	B.S.	1983	Computer Science
Florida International University, Miami, FL	Ph.D.	1999	Molecular Biology

RESEARCH AND PROFESSIONAL EXPERIENCE:

Employment / Experience

1979-1992	Senior Systems Engineer, Electronic Data Systems, Miami, FL
1992-1993	Research Associate, San Francisco Center for Reproductive Medicine, San Francisco, CA
1993	Research Associate, Pacific Fertility Center San Francisco, CA
1995 - 1998	Research Associate, Embryologist, Institute for Assisted Reproduction, Charlotte, NC
2000 - 2002	Senior Scientist, A.R.T. Institute of Washington
1998 - present	Senior Scientist, A.R.T. Institute of NY/NJ, West Orange, NJ
2000 - present	Adjunct Research Faculty, UNC Charlotte
2002 - present	Senior Scientist, Reprogenetics, West Orange, NJ
2005 – present	Charlotte Genomics Consortium, co-Director, UNC Charlotte and Carolinas Medical Center

Honors: Graduated with Highest Honors 1983, 1999. Awarded mathematical sciences scholarship. Awarded presidential scholarship.

Professional Service:

Referee for scientific journals: Human Reproduction, Molecular Human Reproduction, Reproduction, Biotechniques.

Ad hoc reviewer: NIH - National Institute of Child Health and Human Development 2003, 2004,; The Wellcome Trust 2006

Selected Publications/Presentations

- **Steuerwald N.,** Steuerwald M.D., Mailhes J.B. (2005) Post-ovulatory aging of mouse oocytes leads to decreased MAD2 transcripts and increased frequencies of premature centromere separation and anaphase. Mol Hum Reprod Sep;11(9):623-30. Epub 2005 Oct 5.
- **Steuerwald N.** (2005) Meiotic checkpoints for assessment of aneuploid gametes. Cytogenet Genome Res 111(3-4):256-9.
- **Steuerwald N**, Bermudez MG, Wells D, Munne S, Cohen J Microarray technology to assess gene expression profiles of human oocytes and embryos. 6th International Symposium on Preimplantation Genetics, London, England, May 19-22, 2005.
- Munne A, Velilla E, Colls P, Garcia Bermudez M, **Steuerwald N**, Garrisi J, Cohen J (2005) Self correction of chromosomally abnormal embryos in culture and implications for stem cell production. Fertil Steril. Nov;84(5):1328-34.
- Wells D, Bermudez MG, **Steuerwald N**, Thornhill A., Walker DL, Malter H, Delhanty JDA, Cohen J (2005) Association of abnormal morphology and altered gene expression in human preimplantation embryos. Fertil. Steril. 84(2):343-55.
- Wells D, Bermudez MG, **Steuerwald N**, Thornhill A., Walker DL, Malter H, Delhanty JDA, Cohen J (2005) Expression of genes regulating chromosome segregation, the cell cycle and apoptosis during human preimplantation development. Hum. Reprod. 20(5):1339-48. Epub 2005 Feb 10.

- Bermudez, M.G., Wells, D., Malter, H., Munne, S., Cohen, J., and **Steuerwald, N**. Expression profiles of human oocytes and embryos using microarray technology. Gordon Conference: Mammalian gametogenesis and embryogenesis; 2004 July 6-11; Connecticut College.
- Bermudez, M.G., Wells, D., Malter, H., Munne, S., Cohen, J., and **Steuerwald, N**. (2004) Expression profiles of individual human oocytes using microarray technology. *Reprod. Biomed. Online* **8**(3) March.
- Tranguch, S., **Steuerwald, N.**, Huet-Hudson Y.M. (2003) Nitric Oxide Synthase Production and Nitric Oxide Regulation of Preimplantation Embryo Development. *Biol. Reprod.* **68**, 1538-44. Epub 2002 Nov 27.
- Malter HE, **Steuerwald, N**, Cohen J Interference with Survivin gene function in mouse embryos: towards a molecular model for human embryo fragmentation. 59th annual meeting of the American society of Reproductive Medicine, San Antonia, Tx, Oct 11-15th, 2003 (O-206).
- Barritt, J.A., Kokot, M., Cohen, J., **Steuerwald, N.**, Brenner, C.A. (2002) Quantification of human ooplasmic mitochondria. *Reprod. BioMed. Online* 4(3) 243-247.
- Malter HE, **Steuerwald, N**, Cohen J (2002) Gene silencing in mouse embryos using short interfering oligoribonucleotide-based double-stranded constructs.58th annual meeting of the American society of Reproductive Medicine, Seattle, WA, Oct 12-17th, 2002.
- **Steuerwald, N**, Cohen, J, Herrera, RJ, Sandalinas, M, Brenner, CA (2001) Association between spindle assembly checkpoint expression and maternal age in human oocytes. Molecular Human Reproduction 7(1) 49-55.
- **Steuerwald, N.** Cell cycle checkpoints in meiosis and preimplantation development. Annual review of preimplantation embryology; 2001 January 7-10; Cancun, Mexico.
- **Steuerwald, N.,** Cohen, J. and Brenner, C.A. Association between spindle assembly checkpoint gene expression and maternal age in human oocytes. Gordon Conference: Mammalian gametogenesis and embryogenesis; 2000 July 1-6; Connecticut College.
- **Steuerwald, N.,** Wells, D., Munne, S., Escudero, T., Cohen, J. and Brenner, C.A. Association between spindle assembly checkpoint gene expression and maternal age in human oocytes. 56st. annual meeting of the American Society for Reproductive Medicine; 2000 September; San Diego, CA., Fertil. Steril. 74(3) (Suppl. 1), S51.
- **Steuerwald, N**., Cohen, J., Herrera, R., Brenner, C. (2000) Quantification of mRNA in single oocytes and embryos by real-time rapid cycle fluorescence monitored RT-PCR. *Mol. Hum. Reprod.* **6**,448-453.
- **Steuerwald, N.,** Cohen, J., Herrera, R., Brenner, C. (1999) Quantification of mtDNA in single oocytes, polar bodies and subcellular components by real-time rapid cycle fluorescence monitored PCR. *Zygote*. Aug;8(3):209-15.
- Cohen, J., Brenner, C., Warner, C., **Steuerwald, N**., Sadowy, S., Barritt, J., Sandalinas M. and Munné, M. Genetics of the fertilizing egg. In: Towards reproductive certainty, Fertility & Genetics beyond 1999. The Parthenon Publishing Group, New York, NY. 1999. pp. 231-246.
- **Steuerwald, N.,** Cohen, J., Herrera, R., Brenner, C. (1999) Analysis of gene expression in single oocytes and embryos by real-time rapid cycle fluorescence monitored RT-PCR. *Mol. Hum. Reprod.* **5**,1034-1039.
- Crain, J., Wiemer, K.E., **Steuerwald, N.**, Young, E. (1998) Outcome comparison of IVF treatment using highly purified subcutaneous FSH (Fertinex™) versus intramuscular menotropins. *Am J Obstet Gynecol*. **179**, 299-307.
- Wiemer, K. and **Steuerwald, N.** Embryo microsurgery: assisted hatching, embryo biopsy, removal of blebs and fragments. In: Infertility and reproductive medicine clinics of North America. W.B. Saunders Company, Philadelphia, PA. Volume 9, number 2, April 1998.
- Wiemer, K.E., Garrisi, G.J., **Steuerwald, N.,** Alikani, M., Reing, A.M. , Ferrara, T.A., Noyes, N., and Cohen, J. (1996) Beneficial aspects of co-culture with assisted hatching when applied to multiple failure IVF patients. *Hum. Reprod.* **11,** 249-2433.
- Morgan, K., Wiemer, K., **Steuerwald, N.,** Hoffman, D., Maxson, W., and Godke, R. (1995) Use of videocinematography to assess morphological qualities of conventionally cultured and co-cultured embryos. *Hum. Reprod.* **10,** 2371-2376.
- Wiemer, K.E., Dale, B., Hu, Y., **Steuerwald, N.** Maxson, W. S., and Hoffman, D.I. (1995) Blastocyst development in co-culture: development and morphological aspects. *Hum. Reprod.* **10,** 3226-3232.
- **Steuerwald, N.,** Lambert, H., Steinleitner, A.J., and Herrera, R.J. (1994) Gender determination by multiplex PCR amplification of alphoid repeat sequences from single cells. *Biotechniques* **16,** 82-84.
- Chiang, M.H., **Steuerwald, N.,** Lambert, H., and Main, E.K.; Steinleitner, A. (1994) Detection of human leukocyte antigen class I messenger ribonucleic acid transcripts in human spermatozoa via reverse transcription-polymerase chain reaction. *Fertil. Steril.* **61,** 276-280.

Research Support

- Ongoing, C. Gibas (PI), 8/01/06 - 7/31/07, (20060301)
  - North Carolina Biotechnology Center; $222,000
  - Title: UNCC Functional Genomics Core
  - This grant funded the purchase of a custom microarray facility
  - Role: Co-Investigator
- Ongoing, NM Steuerwald (PI), 06/01/2004 – 05/31/06 (4-R44-HD044292-02)
  - National Institutes of Health, $539,038
  - Title: Comprehensive aneuploidy diagnosis in single cells
  - The objective of the proposed research is to develop clinically applicable DNA microarray methods for detecting chromosome imbalance (e.g. aneuploidy) in isolated cells.
  - Role: PI
- Ongoing, NM Steuerwald (PI), 03/01/2004 – 02/31/07 (1-R03-HD-44618-01A1)
  - National Institutes of Health, $100,000
  - Title: Analysis of cell cycle checkpoints in human oocytes
  - The purpose of this grant is to determine whether cell cycle checkpoints, which are necessary for accurate chromosome segregation, are functional in human oocytes. The expression of a number of critical cell cycle checkpoint genes will be analyzed.
  - Role: PI
- Ongoing, Corporate funding, Tyho-Galileo Research Laboratories
- Completed, YM Huet-Hudson (PI), 04/01/2003-03/31/2005 (1-R03-HD-042094-01A1)
  - National Institutes of Health, $100,000
  - Title: Regulation of early embryo development by nitric oxide.
  - The purpose of the proposed experiments is to elucidate the integrated mechanisms regulated by NO in early embryonic development.
  - Role: Co-PI
- Completed, R.A. Meyer, Jr. and M. Clemens (PI), 7/01/01 - 6/30/02, (2001IDG1015)
  - North Carolina Biotechnology Center; $233,000
  - Title: DNA Microarray Facility –The Charlotte Genomics Consortium
  - This grant funded the purchase of an Affymetrix microarray facility
  - Role: Co-Investigator, executive member of The Charlotte Genomics Consortium

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
Zhengchang Su	Assistant Professor of Computational Biology
eRA COMMONS USER NAME	

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
Jinling 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, Department of Animal Physiology, Yunnan Agricultural University
2004-2006 Assistant research professor**,** Institute of Bioinformatics and Department of Biochemistry and Molecular Biology, University of Georgia in Athens.
2006- Assistant professor, Bioinformatics Program, Department of Computer Sciences, University of North Carolina at Charlotte.

.

Other Experience and Professional Memberships

1999-present member, American Society of Physiology
1999-present member, America Advancement Association of Sciences

Honors

1994 Abroad-studying award, C. C. Wu Culture and Education Foundation, Hong Kong
2004 Best Paper Award of the 15th International Conference on Genomics Informatics, Pacifico Yokohama, Japan

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

(Publications selected from 25 peer-reviewed publications)

1. P. Dam, V Olman, K. Harris, Z. Su, Ying Xu, Operon prediction using both genome-specific and general genome information, Nucleic Acids Research, 2006 (in press).
2. Andrea Catte, James Patterson; Gilbert Weinstein; Zhengchang Su; Ling Li; Jianguo Chen; Martin Jones; Marcela Aliste; Stephen Harvey; Jere Segrest . Novel Minimal Surface Conformations of Nascent High Density Lipoproteins through Molecular Dynamics. Biophysical Journal, 2006, 90(12):4345-60.
3. Zhenchang Su , Fenglou Mao, Phuongan Dam, Hongwei Wu, Victor Olman, Ian Paulsen, Brian Plaenik and Ying Xu. Computational inference and experimental validation of nitrogen assimilation regulatory network in cyanobacterium *Synechococcus sp*. WH8102. Nucleic Acids Research, 2006, 34(3): 1050-1065.
4. Fenglou Mao, Zhengchang Su, Victor Olman, Phuongan Dam, Zhijie Liu, Ying Xu. Mapping of Orthologous Genes in the Context of Biological Pathways: an Application of Integer Programming. Proceedings of National Academy of Sciences U S A, 2006,103 (1): 129-134.

5. Hongwei Wu, Zhengchang Su, Victor Olman and Ying Xu. Prediction of functional gene modules based on comparative genome analysis and gene otology application, Nucleic Acids Research, 2005, 18; 33(9):2822-37.
6. Jinling Huang, Zhengchang Su and Ying Xu, The evolution of Microbial phosphonate Degradation Pathways. 2005, Journal of Molecular Evolution, 2005, 61:682-690.
7. Zhengchang Su, Victor Olman, Fenglou Mao, and Ying Xu. Comparative genomics analysis of NtcA regulons in cyanobacteria: regulation of nitrogen assimilation and its coupling to photosynthesis. Nucleic Acids Research, 2005, 33(16): 5156-5171.
8. Phuongan Dam and Zhengchang Su and Victor Olman Ying Xu. In sillco reconstruction of the carbon fixation pathway in Synechococcus sp. WH8102. Journal of Biological Systems, 2004 12:97-125.
9. X. Chen, Z. Su, P. Dam, B. Palenik, Y. Xu and T. Jiang. Operon prediction by comparative genomics. Nucleic Acid Research, 2004, 32(7):2147-57.
10. Victor Olman, Hanchun Peng, Zhengchang Su, Ying Xu. Mapping of Microbial Pathways through Constrained Mapping of Orthologous Genes. Proceedings of IEEE Computational Systems Biology Conference, 2004, 363-370.
11. Zhengchang Su, Richard L. Shoemaker Richard B. Marchase and J. Edwin Blalock. Ca^{2+} dependent inactivation of monovalent cation current through Ca^{2+} release activated Ca channels. Biophysical Journal, 2004, 86(2):805-14.
12. Zhenchang Su , Phuongan Dam, Xin Chen Vicor Olman, Tao Jiang, Brian Plaenik and Ying Xu. Computational inference of regulatory pathway in microbes. An application to phosphorus assimilation pathway. Genome Informatics, 2003, 14:1-10.
13. Csutora P, Su Z, Kim HY, Bugrim A, Cunningham KW, Nuccitelli R, Keizer JE, Hanley MR, Blalock JE, Marchase RB. Calcium influx factor is synthesized by yeast and mammalian cells depleted of organellar calcium stores. Proceedings of National Academy of Sciences U S A, 1999, 6(1):121-6.

C. Research Support.

Ongoing Research Support

NSF/DBI-0542119, Ying Xu (PI) 7/2006-6/2010
NSF
Computational Prediction of Biological Networks in Microbes and Applications to Cyanobacteria
The study will develop novel tools for inference of biological networks in bacteria.
Role: Co-investigator

Completed Research Support

NNSFC 39160031 Zhengchang Su(PI). 01/1992-12/1994
National Natural Sciences Foundation of China
Mechanisms of the effects of immune response products on the neuroendocrine system
The goal of this project was to understand which neural transmitter systems were involved in the actions of cytokine-induced changes in neuroendocrine functions.
Role: PI

Genome to Life Project, Ying Xu (PI) 7/2003-6/2006
DOE
Carbon Sequestration in *Synechococcus sp.*: From Molecular Machines to Hierarchical Modeling
The goal of this project was to reconstruct the regulatory pathways in Synechococcus sp. WH8102 through mining various forms of high-throughput data.
Role: Co-investigator

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
Wu, Xintao	Assistant Professor
eRA COMMONS USER NAME	

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 Science and Technology of China	B.S.	1994	Information Science
Chinese Academy of Space Technology	M.E.	1997	Computer Engineering
George Mason University, Fairfax, VA	Ph.D.	2001	Information Technology

A. Positions and Honors.

Positions and Employment

1998-2001 Research Assistant, Department of Information and Software Engineering, George Mason University, Fairfax, VA
2001-Present Assistant Professor, Department of Computer Science, University of North Carolina-Charlotte, Charlotte, NC

Other Experience and Memberships

2003 NSF ITR Small Project Panel
2003-2004 PC Member, SDM
2005-2006 PC Member, ISMIS
2005-2006 PC Member, ICDM
2006 NSF IIS Career Panel
2006-2007 PC Member, PAKDD

Honors

2002 Junior Faculty Research Grant Award, University of North Carolina-Charlotte, Charlotte, NC
2004 Junior Faculty Research Grant Award, University of North Carolina-Charlotte, Charlotte, NC
2005 Excellence in Undergraduate Teaching Award, College of Information Technology, University of North Carolina-Charlotte, Charlotte, NC
2006-2010 National Science Foundation Career Award

B. Selected peer-reviewed publications.

1. **Wu X.**, Barbara D., Zhang L., Ye, Y. (2003). *Gene interaction analysis using all k-way interaction loglinear model: a case study on yeast data.* ICML Workshop on Machine Learning in Bioinformatics, Washington, DC pp. 38-45.
2. **Wu X.**, Ye Y., Subramanain K., Zhang L. (2003) *Interactive gene interaction analysis using graphical Gaussian model.* The 3rd ACM SIDKDD Workshop on Data Mining in Bioinformatics (BIOKDD03), Washington, DC, pp. 63-69.
3. **Wu X.**, Barbara D., Ye Y. (2003) *Screening and interpreting multi-item associations using loglinear modeling.* In Proceedings of the 9th ACM SIGKDD International Conference on Knowledge Discovery and

Data Mining, Washington, DC. pp. 276-285.
4. Barbara, D., **Wu X.** (2003) *Approximate median polish algorithm for large multidimensional data sets.* Journal of Knowledge and Information System, 5(4):416-438.
5. **Wu X.**, Ye Y., Zhang L. (2003) *Graphical modeling based gene interaction analysis for microarray data.* SIGKDD Explorations, 5(2):91-100.
6. **Wu X.**, Wu Y., Wang Y., Li Y. (2005) *Privacy aware market basket data set generation: a feasible approach for inverse frequent set mining.* Proceedings of the 5th SIAM International Conference on Data Mining (SDM05), Newport Beach, CA, pp. 103-115.
7. Ye Y., **Wu X.** (2005) *Efficient causal interaction learning with applications in microarray.* Proceedings of the 15th International Symposium on Methodologies for Intelligent Systems (ISMIS05), Saratoga Springs, NY, pp. 382-390.
8. **Wu X.** (2006) *Incorporating large unlabeled data to enhance EM classification.* Journal of Intelligent Information System, 26(3):211-226.
9. Guo S., **Wu X.**, Li Y. (2006) *On the lower bound of reconstruction error for spectral filtering based privacy preserving data mining.* Proceedings of the 10th European Conference on Principles and Practice of Knowledge Discovery in Databases (PKDD06), Berlin, Germany, pp. 520-527.
10. **Wu X.**, Ye, Y. (2006) *Exploring gene causal interactions using an enhanced constraint-based method.* Pattern recognition, 39:2439-2449.

C. Research Support.

Ongoing Research Support

CAREER: Towards Privacy and Confidentiality Preserving Databases
0546027
PI: Wu, X. — January 2006 – December 2010
National Science Foundation — Role: PI

Completed Research Support

Privacy Preserving Database Application Testing
0310974
PI: Wu, X. — September 2003 – August 2006
National Science Foundation — Role: PI

Towards an Efficient and Effective Gene Interaction Analysis System for Microarray Data.
PI: Wu, X. — 2004
Junior Faculty Research Grant, UNC-Charlotte — Role: PI

Advanced data Mining and Knowledge Discovery Curriculum: A Proposal
PI: Wu, X. — 2004
CID Grant, UNC-Charlotte — Role: PI

Using Fractals to Compress Real Data Sets
PI: Wu, X. — 2002

Junior Faculty Research Grant, UNC-Charlotte — Role: PI

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
Yengo, Christopher M.	Assistant Professor
eRA COMMONS USER NAME cmyengo	

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
Indiana University	B.S.	1991	Exercise Science
University of Wyoming	M.S.	1996	Exercise Physiology
University of Vermont	Ph.D.	2000	Mol. Phys. & Biophysics
University of Pennsylvania School of Medicine	Post-Doc	2000-2003	Physiology

A. Positions and Honors.

Positions and Employment

1994-1996 Graduate Teaching Assistant, University of Wyoming, College of Health Sciences, Laramie, WY
1996-2000 Graduate Teaching Fellow, University of Vermont School of Medicine, Department of Molecular Physiology and Biophysics, Burlington, VT
2000-2003 Postdoctoral Fellow, University of Pennsylvania School of Medicine, Department of Physiology Philadelphia, PA
2004-present Assistant Professor, Department of Biology, University of North Carolina-Charlotte, Charlotte, NC

Other Experience and Professional Memberships

2006 Journal Reviewer, *Biochemistry*
2006 American Heart Association Grant Review Panelist

Awards

1996 American College of Sports Medicine, Rocky Mountain Regional Meeting – 2nd Place Prize, Student Poster Presentations
1996 Vaughn Award – Outstanding Graduate Student; Department of Allied Health and Physical Education, University of Wyoming, Laramie, WY
1996 Travel Grant Award – University of Wyoming, Graduate College, Laramie, WY
1999 Travel Grant Award – University of Vermont, Graduate College, Laramie, WY
2001 Travel Award – Alpbach Workshop on Molecular Motors, Alpbach, Austria
2001 NIH National Research Service Award
2004 American Heart Association, Scientist Development Award

B. Selected peer-reviewed publications

1. **Yengo, C.M.**, Fagnant P.M., Chrin L., Rovner A.S., and Berger C.L. (1998). *Smooth muscle myosin mutants containing a single tryptophan reveal molecular interactions at the actin-binding interface*. Proc. Natl. Acad. Sci. U.S.A. 95, 12944-12940.

2. **Yengo C.M.**, Chrin L., Rovner A.S., and Berger C.L. (1999). *Intrinsic tryptophan fluorescence identifies specific conformational changes at the actomyosin interface upon actin-binding and ADP-release.* Biochemistry 38, 14515-14523.
3. **Yengo C.M.**, Chrin L.R., and Berger C.L. (2000). *Interaction of Lys-553 of myosin with the C-terminus and DNAse I binding loop of actin examined by fluorescence resonance energy transfer.* J. Structural Biology 131, 187-196.
4. **Yengo C.M.**, Chrin L., Rovner A.S., and Berger C.L. (2000). *Tryptophan 512 is sensitive to structural changes in the rigid relay loop of smooth muscle myosin during the MgATPase cycle.* J. Biol. Chem. 275, 25481-25487.
5. **Yengo C.M.**, and Berger C.L. (2002). *Fluorescence resonance energy transfer in acto-myosin complexes*. Results and Problems in Cell Differentiation 36, 21-30.
6. **Yengo C.M.**, De La Cruz E.M., Chrin L. and Berger C.L. (2002). Actin-*induced closure of the actin binding cleft of smooth muscle myosin.* J. Biol. Chem*.* 277, 24114-24119.
7. **Yengo C.M.**, De La Cruz E.M., Safer D., Ostap E.M., and Sweeney, H.L. (2002). *Kinetic characterization of the weak binding states of myosin V.* Biochemistry 41, 8508-8517.
8. Coureux P.D., Wells A.L., Ménétrey J., trey J., **Yengo C.M.**, Morris C.A., Sweeney H.L., and Houdusse A. (2003*). A structural state of the myosin V motor without bound nucleotide*. Nature 425, 419-423.
9. Chakrabarty T., **Yengo C.M.**, Sweeney H.L., and Selvin P. (2003). *Does the S2 rod of Myosin II uncoil upon two-headed binding to actin? A leucine-zippered HMM study.* Biochemistry 42, 12886-92.
10. **Yengo C.M.**, and Sweeney H.L. (2004). *Functional role of loop 2 in myosin V*. Biochemistry 43, 2605-2612.
11. Ramamurthy B., **Yengo C.M.**, Straight A.F., Mitchison T.J., and Sweeney H.L. (2004). *Kinetic mechanism of blebbistatin inhibition of nonmuscle myosin IIB.* Biochemistry 43, 14832-14839.
12. Wallace K.N., Dolan A.C., Seiler C., Smith E.M., Yusuff S., Chaille-Arnold L., Judson B., Sierk R., **Yengo C.M.**, Sweeney H.L., Pack M. (2005). *Mutation of smooth muscle myosin causes invasion and cystic expansion of zebrafish intestine.* Dev. Cell 8, 717-726.
13. Ménétrey J., Bahloul A., Wells A.L., **Yengo C.M.**, Morris C.A., Sweeney H.L., Houdusse A. (2005). *The structure of the myosin VI motor reveals the mechanism of directionality reversal.* Nature 435, 779-785.
14. Sun M., Oakes J.L., Ananthanarayanan S.K., Hawley K.H., Tsien R.Y., Adams S.R. and **Yengo C.M.** (2006). *Dynamics of the upper 50 kDa domain of myosin V examined with fluorescence resonance energy transfer*. J. Biol. Chem*.* 281, 5711-5717.
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C. Research Support

Ongoing Research Support

Investigating the molecular basis of human deafness associated with mutations in myosin-1a
PI: Tyska, Matthew J. — Feb. 2006- Jan. 2008
March of Dimes — Role: Collaborator
Basil O'Connor Starter Scholar Research Award

Enzymatic and motor properties of myosin III
R03 EY016419-01
PI: Yengo, C.M. — April 2005 – March 2007
National Institutes of Health — Role: PI

Mechanism of Energy Transduction in Myosin
2975-04-0013
PI: Yengo, C.M. — January 2004 – December 2007
American Heart Association — Role: PI
Scientist Development Award

Completed Research Support

Mechanism of Myosin IX Motility
Sponsor: H. Lee Sweeney
National Institutes of Health
National Research Service Award

February 2001 – December 2003
Role: Post-Doctoral Fellow