LONG SIGNATURE SHEET

UNC CHARLOTTE

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Grad School
4-7-10 ap

Proposal Number: BINF 3/10/2010

Proposal Title Request for Authorization to Establish BCB Ph.D.

Originating Department Department of Bioinformatics and Genomics

TYPE OF PROPOSAL: UNDERGRADUATE______ GRADUATE ✓ UNDERGRADUATE & GRADUATE___

DATE RECEIVED	DATE CONSIDERED	DATE FORWARDED	ACTION	SIGNATURES
2/23/10	3/2/10	3/2/10	approved	DEPARTMENT CHAIR
3/2/10	3/8/10	3/9/10	approved	COLLEGE CURRICULUM COMMITTEE CHAIR
~~3/9/10~~	~~3/16~~/10			TEACHER EDUCATION COMMITTEE CHAIR (Teacher Education Program proposals only)
3/9/10	3/16/10	3/16/10	approved	COLLEGE FACULTY CHAIR
3/16/10	3/16/10	3/16/10	approved	COLLEGE DEAN
				UNDERGRADUATE COURSE & CURRICULUM COMMITTEE CHAIR (for undergraduate courses)
3-17-10	4/6/2010	4-7-10	approved	GRADUATE COUNCIL CHAIR (for graduate courses) Rob Roy McGregor
				FACULTY GOVERNANCE SECRETARY (noting Faculty Council approval on Consent Calendar)
				FACULTY EXECUTIVE COMMITTEE (if decision is appealed)

Revised 4/08/03
OAA/jdp

APPENDIX C

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

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

Date: January 16, 2010

Constituent Institution: University of North Carolina at Charlotte

CIP Discipline Specialty Title: Bioinformatics

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

Exact Title of the Proposed Degree: Bioinformatics and Computational Biology

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

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

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

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

Proposed date to establish degree program (allow at least 3-6 months for proposal review):
month August *year* 2010

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

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

Proposed date of initiation of proposed degree program: August 2010

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

Chancellor: ______________________________

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EXECUTIVE SUMMARY

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

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

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

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

I. DESCRIPTION OF THE PROGRAM

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

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

In 2000, the National Institutes of Health formed a committee to develop working definitions of these terms[2] (http://www.bisti.nih.gov/CompuBioDef.pdf). The Committee offered the following definitions, recognizing that no definition could completely eliminate overlap with other activities:

> ***Bioinformatics:*** *Research, development, or application of computational tools and approaches for expanding the use of biological, medical, behavioral or health data, including those to acquire, store, organize, archive, analyze, or visualize such data.*
>
> ***Computational Biology:*** *The development and application of data-analytical and theoretical methods, mathematical modeling and computational simulation techniques to the study of biological, behavioral, and social systems.*

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

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

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

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

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

Educational Objectives

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

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

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

Relationship to Existing UNC Charlotte Programs

Currently, the Bioinformatics track of the IT Ph.D. program has a close working relationship with the Departments of Biology, Chemistry, Physics and Optical Science, Computer Science, and Mathematics and Statistics. Students in most of these graduate programs may take courses offered by our Bioinformatics faculty, and we expect that Bioinformatics and Computational Ph.D. students will take advanced courses offered by these departments. Faculty in each of the abovementioned departments may serve as mentors, committee members, or provide laboratory rotations for our current students as Participating Faculty. For example, we note that two of our students have dissertation advisors in the Physics and Optical Science Department working on computational biology problems. Other students work closely with Biology faculty on issues related to biomarkers for cancer. Still other students are, or will be working with Chemistry faculty on analysis of mass spectrometry data. Currently, a Physics faculty member has a wet lab and office in our Bioinformatics Building, and faculty in many departments utilize the two large computer clusters operated by the Department of Bioinformatics and Genomics. We expect these relationships to grow and for new relationships with faculty in other departments to develop as the program expands.

II. JUSTIFICATION FOR THE PROGRAM

Relationship to Institutional Mission

The proposed Ph.D. in Bioinformatics and Computational Biology (BCB) is connected to a number of University goals, including those which a) increase the number of Ph.D. programs in high demand fields, b) extend the campus infrastructure supportive of research, c) help the University reach "Doctoral/Research University – Extensive" status, d) and increase both faculty and student research that will address regional problems. The proposed Ph.D. is also closely aligned with the recommendations of the UNC Tomorrow Commission. It is in an inherently interdisciplinary field that will help foster collaborative research and educational efforts within a number of existing programs, and will help attract outstanding students and extramural funding.

The development of a Ph.D. in Bioinformatics and Computational Biology is well aligned with the commitment to develop applied sciences and technologies in the Charlotte area. The region is well on its way to becoming a major biotechnology center in the State with the development of the North Carolina Research Campus (NCRC) at Kannapolis. Currently, the North Carolina Biotechnology Center lists over 50 biotech companies in the area and nearly 150 biotech-related companies. The expertise provided by this program is critical in a wide range of biotechnology research problems and applications, from genomics to health care and beyond.

Student Demand and Job Prospects

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

It is noteworthy that we have been able to attract highly qualified North Carolina residents to our program. Nearly half (9 of 20) of our current students are U.S. citizens, and all of these are North Carolina residents. One-third of our students are female and one (5%) is an underrepresented minority. We think that active recruiting measures (see below) will substantially increase the numbers of women and minorities, and especially of North Carolina students. Informally, we find that local students are often recruited through personal interaction with the faculty, including research internships in faculty laboratories. For example, about one-third of the undergraduate interns that have participated in research activities in the Microarray Core Facility since 2006 (supervised by Dr. Cynthia Gibas) have so far applied or are in the process of applying to the Ph.D. program. We have more demand for such internships than we can currently meet, another indication of strong student interest in Bioinformatics and Computational Biology.

We employ a full-time Graduate Coordinator (Ms. Elise Marshall) to answer the very substantial number of inquiries from potential students and arrange interviews. In addition, Ms. Marshall travels to many colleges and universities in our region to recruit outstanding students. Indeed, on a recent visit to North Carolina A & T University, she signed up 12 biology/math/computer science students to visit our graduate open-house event. The strong student demand that we observed is mirrored in the other institutions in our State. This year, NCSU's program received around 150 applications for only 6-8 positions, and Duke reported receiving over 150 applications for only 8 positions. The Bioinformatics and Computational Biology program at Chapel Hill admits students through the unified Biological and Biomedical Sciences Program. Of the roughly 1000 applicants to BBSP, it is estimated that more than 100 are competing for only 6-8 slots in Bioinformatics and Computational Biology Ph.D. program. Clearly, there is a strong student demand that is not being met by the current programs in our State. Nationwide, Black and Stephan ("Bioinformatics: Recent Trends in Programs, Placement and Job

Opportunities", Report to the Alfred P. Sloan Foundation, June, 2004) report that although the number of training programs is rising rapidly, it still falls short of student demand.

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

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

In many respects, the growth of biotechnology mirrors that of the electronics industry in the mid- 20th Century. The Milken Institute (www.milkeninstitute.org/pdf/biopharma_report.pdf) projects that over 7,000 new biopharma jobs will be created in North Carolina by 2014. We believe that many of these jobs will require significant computational skill sets. Our own experience suggests that individuals with this training are in short supply. In the past three years, we have held faculty searches in bioinformatics and computational biology for 12 faculty positions, and received over 400 applications. Despite our explicit requests for individuals trained in bioinformatics and computational biology, *we rarely see an applicant with a degree in this field.*

Impact on Existing Programs at UNC Charlotte

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

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

Other Institutions in North Carolina Offering Similar Programs

There are currently three other doctoral programs within North Carolina in Bioinformatics and Computational Biology. North Carolina State University (NCSU), located 170 miles from UNC Charlotte, established the first such program in 1999. This program, directed by Dr. Zhao-Bang Zeng, was developed from their strength in the area of statistical genetics, and many of their faculty have appointments in either the Department of Statistics or Genetics. The NCSU program consists of courses in bioinformatics, molecular genetics, functional genomics, statistics, computational methods, a journal club, electives and dissertation research. Although there are a number of options within this curriculum, there is a strong emphasis on statistics and statistical/quantitative genetics. This program typically graduates 6-7 Ph.D. students each year.

Duke University, located 145 miles from UNC Charlotte, established a Ph.D. in Computational Biology and Bioinformatics in 2003. The Duke program, directed by Dr. John Harer, offers over 15 courses, but only three are required (Genomic Tools and Technologies, Algorithms, and Statistical

Methods) in addition to a seminar. A Student Advisory Committee advises first and second year students with respect to courses, rotations, and advisor selection. The Duke program lists 40 faculty with appointments in several different departments. While the program covers all major areas, they have particular strength in systems biology. Their goal is to graduate about 8 students per year.

The Ph.D. in Bioinformatics and Computational Biology at Chapel Hill (also 145 miles from UNC Charlotte) was approved in 2008, and is directed by its founder, Dr. Tim Elston. The Chapel Hill program requires two foundation courses, laboratory rotations, a colloquium, and seven 1 credit "core modules" that cover most topics in bioinformatics and computational biology. A substantial number of electives are offered. Except for the short "core modules", existing departments, such as Chemistry, Computer Science, Cell Biology, etc., currently offer all of the courses. Currently, they list 29 Core faculty in 15 departments, along with 12 additional Resource faculty. These faculty represent a broad range of subject areas. This program plans to produce 6-8 graduates per year.

UNC Charlotte is Unique and Appropriate

While the UNC Charlotte program covers the same core areas of Bioinformatics and Computational Biology as the NCSU, UNC, and Duke programs, it is unique in several ways. First, it is departmentally based. The Department of Bioinformatics and Genomics has complete freedom in the design of the curriculum, scheduling classes, and in hiring faculty and assigning teaching responsibilities. This structure contrasts with that of NCSU, Duke, and UNC which use faculty from various departments to teach courses and mentor and support students. Except for a few core courses, their didactic courses are primarily designed for, and taught by other graduate programs. The departmentally based structure at UNC Charlotte insures that the proper mix of faculty for the program can be hired, that the department can assign faculty to teach these courses as part of their primary teaching responsibilities, and that rigorous control over both student performance and course content will be maintained. This later point is especially important for a Bioinformatics and Computational Biology curriculum, which involves a complex mix of topics from a variety of disciplines. By exercising precise control over our curriculum, we can insure that our students will have the proper prerequisites, minimize gaps and overlap between courses, and schedule the courses appropriately. This is especially important for attracting both computer science and life science undergraduate applicants and providing them with the means to bridge the disciplinary gap.

UNC Charlotte is different from other North Carolina universities offering similar programs in that our program is *based in the College of Computing and Informatics*, as opposed to a Statistics or Genomics center or department. While these other programs are certainly comprehensive, and all programs, including UNC Charlotte's, will cover most of the same topics, UNC Charlotte will be able to place an emphasis on cutting-edge computational approaches. For example, our courses emphasize structured, object-oriented programming applications in bioinformatics. Students write data parsers, visualization tools, genome browsers, and alignment code, thus seamlessly integrating biological and computational aspects. Our statistics course uses examples drawn from common problems in bioinformatics and incorporates assignments in the R language. We can also place a special emphasis on parallel programming (multi-thread, multi-processor) using high performance computing platforms in our course offerings. Students have ready access to three high performance computer clusters for bioinformatics as well as special purpose FPGA computers, massive GPU clusters, and multi-core large memory computers for bioinformatics applications. The incorporation of high performance computing technologies will be critical as next-gen sequencing throughput approaches the terabyte range, and third-gen sequencing throughput eclipses that. Our program also offers significant training in physics/chemistry-based modeling that is largely absent from the other three programs.

Finally, UNC Charlotte is major partner providing faculty and service staff in bioinformatics to the North Carolina Research Campus (NCRC) at Kannapolis. This association will provide an opportunity to collaborate with NCRC scientists on a wide range of important problems and allows us access to the latest technology. We have already developed relationships with the UNC-CH Nutrition Research Institute (Dr. Zeisel), the NCSU Plants and Human Health Institute (Dr. Lila) and the David H. Murdock Research Institute (Dr. Luther). When fully developed, the NCRC is expected to house over one hundred biotechnology companies and laboratories working in a variety of fields, including nutrigenomics, metabolomics, plant genomics and translational medicine. We expect that in 10 years, the Charlotte area will be the southwestern end of a biotechnology corridor reaching to the Triangle. UNC Charlotte has an important role to play in the extension of biotechnology across the State, and the BCB Ph.D. Program will play a critical part in that role.

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

Enrollment at other UNC institutions

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

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

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

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

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

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

Projected Enrollment and Credit-Hour Production

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

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

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

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

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

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

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

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

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

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

III. PROGRAM REQUIREMENTS AND CURRICULUM

Program Planning

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

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

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

University of Southern California – Computational Biology and Bioinformatics

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

Recruitment

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

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

Admission

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

Applicants will be notified by the end of February with acceptance or rejection letters. Those offered admission will have until April 15 to accept or decline.

Degree Requirements

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

i. Didactic Coursework

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

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

Table 1. Gateway Courses

Course Number (credits)	Title and Description
BINF 8100 (3)	Biological Basis of Bioinformatics. This course provides a foundation in molecular genetics and cell biology focusing on foundation topics for graduate training in bioinformatics and genomics.
BINF 8101 (3)	Energy and Interaction in Biological Modeling. This course covers: (i.) the major organic and inorganic chemical features of biological macromolecules; (ii.) the physical forces that shape biological molecules, assemblies and cells; (iii.) the chemical driving forces that govern living systems; (iv.) the molecular roles of biological macromolecules and common metabolites; (v.) and the pathways of energy generation and storage. Each section of the course builds upon the relevant principles in biology and chemistry to explain the most common mathematical and physical abstractions used in modeling in the relevant context.
BINF 8111 (3)	Bioinformatics Programming I. This course introduces fundamentals of programming for bioinformatics using a high-level object-oriented language such as python. The first weeks cover core data types, syntax, and functional

	programming, focusing on construction of programs from small, testable parts. Students will learn productive use of the Unix environment, focusing on Unix utilities that are particularly useful in bioinformatics. The course will cover object-oriented programming, introduce analysis of algorithms and sequence alignment methods, and introduce computational environments that are particularly useful in bioinformatics analyses such as R, BioPython, and Web services in bioinformatics. By the end of the class, students will have gained the ability to analyze data within the python interpreter (for example) and write well-documented, well-organized programs.
BINF 8112 (3)	Bioinformatics Programming II. This course is the second semester of Introduction to Bioinformatics Programming I. In this semester, students will practice and refine skills learned in the first semester. New topics introduced will include: programming as part of a team, using sequence analysis algorithms in realistic settings; writing maintainable and re-usable code; Web programming; and graphical user interface development. At the end of the semester, students will be able to evaluate and deploy computer languages, tools, and software engineering techniques in bioinformatics research.

Table 2. Core Courses

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

Table 3. Elective Courses

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

ii. Research Rotations

Each Ph.D. student must complete two research rotations, BINF 8911, and 8912, in their first year. These rotations provide two semesters of faculty supervised research experience to supplement regular course offerings. The purpose of these courses is to broaden students' exposure to state-of-the-art technologies currently being utilized within the field of bioinformatics, to guide them towards recognizing important, outstanding questions in specific scientific domains, and to give them hands-on training within those domains. Students select their rotation projects in consultation with the Program Director and selected faculty members. At the end of each rotation, students must prepare a formal presentation on their findings for the faculty and their peers.

iii. Seminar

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

iv. Qualifying Exam

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

v. Research

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

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

vi. Teaching and Professional Development

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

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

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

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

Table 4. Typical Timeline for Student Progression

Admission
• Completed an undergraduate major in either a life science or a quantitative discipline
Year 1
• 2 Gateway courses (3 credits each)
• 2 Core courses (3 credits each)
• Bioinformatics Seminar (BINF 8600) (1 credit/semester)
• 2 research rotations (BINF 8911 and 8912) (3 credits each)
Year 2
• 1 Core course (3 credits)
• Bioinformatics Seminar (BINF 8600) (1 credit/semester)
• Electives (3-6 credits)
• Pre-Dissertation Research (BINF 8911) (6-10 credits)
• Qualifying exam (written and oral)
Years 3-5
• Electives (as needed)
• Bioinformatics Seminar (BINF 8600) (1 credit/semester)
• Dissertation Research (BINF 8911) (9-10 credits/semester)
• Proposal Defense, dissertation, publications(s), and oral defense

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

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

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

IV. FACULTY

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

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

Name	Rank	Research Interest
Xiuxia Du, Ph.D.	Asst. Professor	Computational proteomics & metabolomics and integration of –omics data for systems biology research.
Anthony Fodor, Ph.D.	Asst. Professor	Metagenomics, microbial ecology and diversity, human associated microbiota.
Cynthia Gibas, Ph.D.	Assoc. Professor	Genomic data analysis and visualization
Jun-tao Guo, Ph.D.	Asst. Professor	Protein structure prediction and protein-DNA interactions.
Dennis Livesay, Ph.D.	Assoc. Professor	Protein sequence/structure/function relationships
Ann Loraine, Ph.D.	Assoc. Professor	Plant genomics, genomic visualization, alternative splicing, mining expression microarray data.
Lawrence Mays, Ph.D.	Professor, Chair	Bioinformatics education.
Jessica Schlueter, Ph.D.	Asst. Professor	Evolution, plant genomics. Genome structure. Polyploidy. Gene expression regulation. Epigenetics.
Shannon Schlueter, Ph.D.	Asst. Professor	Bioinformatic algorithm development for computational recognition and prediction of genomic features.
Susan Sell, Ph.D.	Professor	Genomics of disease susceptibility; expression array-based biomarker development
Zhengchang Su, Ph.D.	Asst. Professor	Computational prediction of transcription factor binding sites & reconstruction of gene regulatory networks.
Jennifer Weller, Ph.D.	Assoc. Professor	Quantifying hybridization assays. Storage/retrieval of massive datasets. Progression of complex disease.

B. Faculty required.

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

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

No new faculty required.

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

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

V. LIBRARY

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

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

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

No additional improvements are required to meet program requirements.

C. Discuss the use of other institutional libraries.

No other institutional libraries will be required for this program.

VI. FACILITIES AND EQUIPMENT

A. Describe facilities available for the proposed program.

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

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

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

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

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

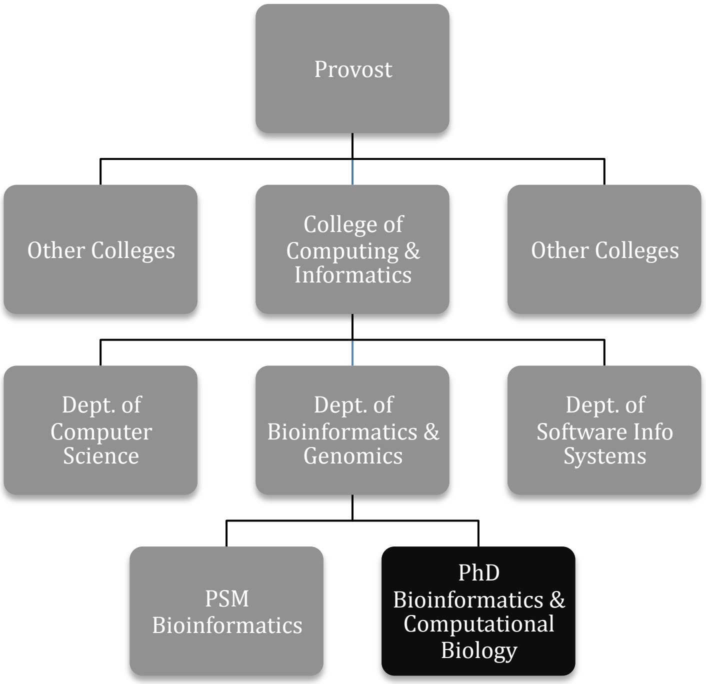
See Section VI. A. above.

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

See Section VI. A. above.

VII. ADMINISTRATION

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



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

Program Director:
- Overall responsibility for the success of the Program
- Reports to Graduate School on behalf of the Program
- Approves dissertation committees
- Final signatory authority for Ph.D. processes
- Meets regularly with Program Coordinator, Dept. Chair and standing committee chairs
- Manages financial support for students (with assistance of Program Coordinator)
- Assigns initial advisor to incoming students
- Nominates candidates for Participating Faculty and standing committees

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

Admissions Committee:
- Selects applicants for interviews and offers
- Directs recruitment efforts

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

Qualifying Examination Committee:
- Writes, administers, and grades qualifying exam twice a year

VIII. ACCREDITATION

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

IX. SUPPORTING FIELDS

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

X. ADDITIONAL INFORMATION

None.

XI. BUDGET

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

XII. EVALUATION PLANS

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

The criteria used to evaluate the program will include:

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

B. Measures to be used to evaluate the program:

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

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

C. Projected productivity levels (number of graduates):

No applicant to the new BCB PhD program can graduate within 4 years. The totals below are estimates of the number of students graduating from the current Bioinformatics tract.

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

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

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

Bruce Weir, Ph.D.
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Distinguished Professor of Biomolecular Engineering
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Elliot Lefkowitz, Ph.D.
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University of Alabama at Birmingham
1530 3rd Avenue South
Birmingham, AL 35294
(2050 934-1946
ElliotL@uab.edu

E. Plan for evaluation prior to fifth operational year.

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

XIII. REPORTING REQUIREMENTS

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

Department of Bioinformatics & Genomics

Ph.D. in Bioinformatics and Computational Biology

Department of Bioinformatics and Genomics

365 Bioinformatics Building
704-687-8541
bioinformatics.uncc.edu

Chair

Dr. Lawrence Mays

Graduate Faculty

Xiuxia Du, Assistant Professor
Anthony Fodor, Assistant Professor
Cynthia Gibas, Associate Professor
Jun-tao Guo, Assistant Professor
Dennis Livesay, Associate Professor
Ann Loraine, Associate Professor
Jessica Schlueter, Assistant Professor
Shannon Schlueter, Assistant Professor
Susan Sell, Professor
Zhengchang Su, Assistant Professor
Jennifer Weller, Associate Professor

PH.D. IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

The Department of Bioinformatics and Genomics admits students seeking the Ph.D. degree in Bioinformatics and Computational Biology.

Ph.D. in Bioinformatics and Computational Biology Requirements

Students will be required to demonstrate competence in the areas of biochemistry, cellular and molecular biology, genetics, statistics, and computer science related to core concepts in bioinformatics. The student's advisor and at least one other dissertation committee member must be faculty in the Bioinformatics track. Students must complete at least 72 post-baccalaureate credit hours. This includes at least 18 hours of dissertation research and at least 9 hours of course work completed at UNC Charlotte. Students are expected to acquire a sufficiently broad body of technical knowledge in the discipline as well as a deep understanding of a specialized area. This is accomplished with a combination of required courses and appropriate electives approved by the student's advisor(s) and dissertation committee.

Course Requirements

Plans of Study for Bioinformatics Ph.D. students are developed on an individual basis, by the student and his or her advisory committee. The required coursework is organized in three tiers of formal training: Gateway courses, Core courses, and Electives. The Gateway courses will differ according to the student's background. A student with a strong computer science background would likely take BINF 8100 and BINF 8101, but not BINF 8111 and BINF 8112. A student with a strong background in the life sciences would take BINF 8111 and BINF 8112, but not BINF 8100 and BINF 8101. This determination is made by Program Director when the student enters the Program. All students, regardless of their background, must take the Core courses, BINF 8200, BINF 8201, and BINF 8202 and nine credit hours of Electives. Students may register for Elective courses, or for courses outside of the Bioinformatics and Genomics Department with the permission of the Program Director.

Gateway Courses:

- BINF 8100 Biological Basis of Bioinformatics
- BINF 8101 Energy and Interaction in Biological Modeling
- BINF 8111 Bioinformatics Programming I
- BINF 8112 Bioinformatics Programming II

Core Courses:

- BINF 8200 Statistics for Bioinformatics
- BINF 8201 Molecular Sequence Analysis
- BINF 8202 Computational Structural Biology

Elective Courses:

- BINF 8203 Genomics
- BINF 8204 Mathematical Systems Biology
- BINF 8205 Computational Molecular Evolution
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- BINF 8911 Research Rotation I
- BINF 8912 Research Rotation II

Seminar

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

- BINF 8600 Graduate Research Seminar

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Dissertation Proposal, Oral Defense, and Publication(s)

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

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

COURSES IN BIOINFORMATICS

BINF 8100. Biological Basis of Bioinformatics. (3)
Prerequisites: Admission to graduate standing in Bioinformatics and undergraduate training in Computer Science or other non-biological discipline. This course provides a foundation in molecular genetics and cell biology focusing on foundation topics for graduate training in bioinformatics and genomics. (Fall)

BINF 8101. Energy and Interaction in Biological Modeling. (3)
Prerequisites: Admission to graduate standing in Bioinformatics. This course covers: (i.) the major organic and inorganic chemical features of biological macromolecules; (ii.) the physical forces that shape biological molecules, assemblies and cells; (iii.) the chemical driving forces that govern living systems; (iv.) the molecular roles of biological macromolecules and common metabolites; (v.) and the pathways of energy generation and storage. Each section of the course builds upon the relevant principles in biology and chemistry to explain the most common mathematical and physical abstractions used in modeling in the relevant context. (Spring)

BINF 8111. Bioinformatics Programming I. (3)
Prerequisite: Admission to graduate standing in Bioinformatics. This course introduces fundamentals of programming for bioinformatics
using a high-level object-oriented language such as python. The first weeks cover core data types, syntax, and functional programming, focusing on construction of programs from small, testable parts. Students will learn productive use of the Unix environment, focusing on Unix utilities that are particularly useful in bioinformatics. The course will cover object-oriented programming, introduce analysis of algorithms and sequence alignment methods, and introduce computational environments that are particularly useful in bioinformatics analyses such as R, BioPython, and Web services in bioinformatics. By the end of the class, students will have gained the ability to analyze data within the python interpreter (for example) and write well-documented, well-organized programs. (Fall)

BINF 8112. Bioinformatics Programming II. (3)
Prerequisite: BINF 8111*/ITSC 8111. This is a continuation of Bioinformatics Programming I (BINF 8111). This course is the second semester of Introduction to Bioinformatics Programming I. In this semester, students will practice and refine skills learned in the first semester. New topics introduced will include: programming as part of a team, using sequence analysis algorithms in realistic settings; writing maintainable and re-usable code; Web programming; and graphical user interface development. At the end of the semester, students will be able to evaluate and deploy computer languages, tools, and software engineering techniques in bioinformatics research. (Spring)

BINF 8151/GRAD 8151. Professional Communications. (1) This course covers: Principles and useful techniques for effective oral presentations, poster presentations, scientific writing, use of references and avoiding plagiarism. Students in the class will critique and help revise each other's presentations and learn how to avoid common pitfalls. In addition, students will learn how to properly organize and run a meeting. Students will prepare a CV, job application letter and job talk. (Fall).

BINF 8171. **Business of Biotechnology. (3)** This course introduces students to the field of biotechnology and how biotech businesses are created and managed. The students should be able to define biotechnology and understand the difference between a biotech company and a pharmaceutical company. Additional concepts covered will include platform technology, biotechnology's history, biotechnology products and development processes, current technologies used by biotech companies today, biotechnology business fundamentals, research and development within biotech companies, exit strategies, and careers in the biotech field. (Summer)

BINF 8200. Statistics for Bioinformatics. (3)
This course aims to introduce statistical methods commonly used in bioinformatics. Basic concepts from probability, stochastic processes, information theory, and other statistical methods will be introduced and illustrated by examples from molecular biology, genomics and population genetics with an outline of algorithms and software. R is introduced as the programming language for homework. (Fall)

BINF 8201. Molecular Sequence Analysis. (3)
Prerequisite: BINF 8100*/ITSC 8100 or equivalent. BINF 8100 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, genefinding and feature finding in sequence, models of molecular evolution, phylogenetic analysis, comparative modeling. (Fall)

BINF 8202. Computational Structural Biology. (3)
Prerequisite: BINF 8101*, 8201*/ITSC 8101, 8201 or equivalents. This course covers: **(a)** the fundamental concepts of structural biology (chemical building blocks, structure, superstructure, folding, etc.); **(b)** structural databases and software for structure visualization; **(c)** structure determination and quality assessment; **(d)** protein structure comparison and the hierarchical nature of biomacromolecular structure classification; **(e)** protein structure prediction and assessment; and **(f)** sequence- and structure-based functional site prediction. *(Fall)*

BINF 8203. Genomics. (3)
Prerequisite: BINF 8100*/ITSC 8100 or equivalent. This course surveys the application of high-throughput molecular biology and analytical biochemistry methods and data interpretation for those kinds of high volume biological data most commonly encountered by bioinformaticians. The relationship between significant biological questions, modern genomics technology methods, and the bioinformatics solutions that enable interpretation of complex data is emphasized. Topics include: Genome sequencing and assembly, annotation, and comparison. Genome evolution and individual variation. Function prediction. Gene ontologies. Transcription assay design, data acquisition, and data analysis. Proteomics methods. Methods for identification of molecular interactions. Metabolic databases, pathways and models. (Spring)

BINF 8204. Mathematical Systems Biology. (3)
Prerequisites: BINF 8200* and 8210*/ITSC 8200 AND 8210 or equivalents. This course introduces basic concepts, principles and common methods used in systems biology. The class emphasizes on molecular networks, models and applications, and covers the following topics: the structure of molecular networks; network motifs, their system properties and the roles they play in biological processes; complexity and robustness of molecular networks; hierarchy and modularity of molecular interaction networks; kinetic proofreading; optimal gene circuit design; the rules for gene regulation. (Spring)

BINF 8205. Computational Molecular Evolution. (3)
Pre-requisites: BINF 8201*/ITSC 8201 (Molecular Sequence Analysis) and BINF 8200*/ITSC 8200 Statistics for Bioinformatics (or permission of the instructor). This course will cover major aspects of molecular evolution and phylogenetics with an emphasis on the modeling and computational aspects of the fields. Topics will include: models of nucleotide substitution, models of amino acid and codon substitution, phylogenetic reconstruction, maximum likelihood methods, Bayesian methods, comparison of phylogenetic methods and tests on trees, neutral and adaptive evolution and simulating molecular evolution. Students will obtain an in-depth knowledge of the various models of evolutionary processes, a conceptual understanding of the methods associated with phylogenetic reconstruction and testing of those methods and develop an ability to take a data-set and address fundamental questions with respect to genome evolution. (On demand)

BINF 8210. Numerical Methods and Machine Learning in Bioinformatics. (3)
Prerequisites: Ability to program in a high-level language (Perl, Java, C#, Python, Ruby, C/C++), Calculus. This course focuses on commonly used numerical methods and machine learning techniques. Topics will include: solutions to linear systems, curve fitting, numerical differentiation and integration, PCA, SVD, ICA, SVM, PLS. Time permitting, hidden markov chains and Monte Carlo simulations will be covered as well. Students will learn both the underlying theory and how to apply the theory to solve problems. *(Fall)*

BINF 8211. Design and Implementation of Bioinformatics Databases. (3)
In this course students will acquire skills needed to access and utilize public biomedical data repositories, and will be expected to design, instantiate, populate, query and maintain a personal database to support research in an assigned domain of bioinformatics. The course content includes common data models and representation styles, use of open-source relational DBMS, and basic and advanced SQL. The course focuses on how data integration is achieved, including the use of standardized schemas, exchange formats and ontologies. We will examine large

public biomedical data repositories such as GenBank and PDB, learn how to locate and assess the quality of data in Web-accessible databases, and look at representation, standards and access methods for such databases. *(Spring)*

BINF 8310. Advanced Statistics for Genomics. (3)
Prerequisite: BINF 8200*/ITSC 8200 or equivalent. The first half of this course emphasizes canonical linear statistics (t-test, ANOVA, PCA) and their non-parametric equivalents. The second half of the course emphasized Bayesian statistics and the application of Hidden Markov Models to problems in bioinformatics. 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. *(Spring)*

BINF 8311. Biophysical Modeling. (3)
This course covers: **(a)** an 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 Coulombic); **(g)** free energy decomposition schemes; and **(h)** hybrid quantum/classical (QM/MM) methods. *(On demand)*

BINF 8312. Computational Comparative Genomics. (3)
Prerequisite: BINF 8201*/ITSC 8201 or equivalent. This course introduces computational methods for comparative genomics analyses. 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)*

BINF 8313. Structure, Function, and Modeling of Nucleic Acids. (3)
Prerequisite: BINF 8100-8101 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)*

BINF 8350. Biotechnology and Genomics Laboratory. (3) Prerequisite: none. This course teaches basic wet-lab techniques commonly used in biotechnology to generate genomics data. Lectures will cover methods for sample isolation, cell disruption, nucleic acid and protein purification, nucleic acid amplification, protein isolation and characterization, molecular labeling methods and commonly used platforms for characterizing genome-wide molecular profiles. In particular we will discuss and learn to perform: tissue culture and LCM isolation of cells, DNA sequencing methods, DNA fingerprinting methods, RT-qPCR and microarrays of cDNA, 1D and 2D gels for protein separation, protein activity assays, and proteomics platforms. Lectures will describe emerging methodologies and platforms, and will discuss the ways in which the wet-lab techniques inform the design and use of bioinformatics tools, and how the tools carry out the processing and filtering that leads to reliable data. The course will also discuss the commercial products beginning to emerge from genomics platforms. (Spring)

BINF 8380. Programming III. (3)
Prerequisite: BINF 8112 or equivalent. This course emphasizes implementation of bioinformatics algorithms in the context of parallel processing. Topics covered depend on instructor expertise and student interest but may include development of multi-threaded applications, developing for multi-core processors and utilization of large clusters and “cloud” supercomputers. Students will be expected to complete a significant independent project (Fall).

BINF 8600. Seminar. (1)
Prerequisites: Admission to graduate standing in Bioinformatics. Departmental seminar. Weekly seminars will be given by bioinformatics researchers from within the university and across the world. *(Fall, Spring)*

BINF 8601. 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)*

BINF 8911 Research Rotation I (2), BINF 8912 Research Rotation II (2).
Faculty supervised research experience in bioinformatics to supplement regular course offerings.

UNC CHARLOTTE

J. Murrey Atkins Library

Consultation on Library Holdings

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

From: Reese Manceaux

Date: March 17, 2010

Subject: Proposed Doctoral Degree Program in Bioinformatics

Summary of Librarian's Evaluation of Holdings:

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

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

Comments:

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

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

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

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

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

Atkins Library Sample Holdings in Areas Related to Course

3/17/2010

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

Totals	**1805**	**661**	**85**

Reese A. Manceaux

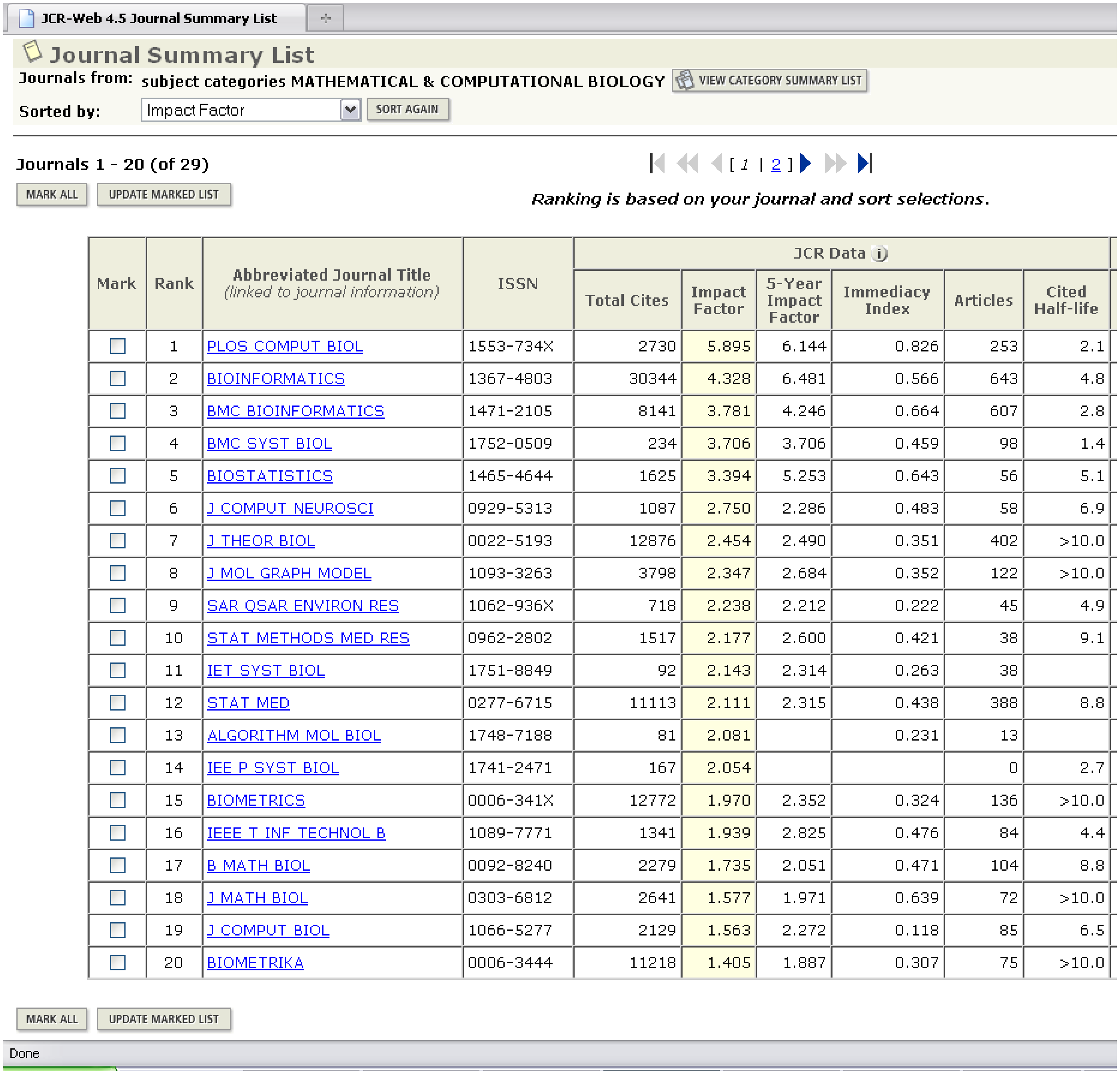
Evaluator's Signature

March 17, 2010

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

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

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



Journal Summary List

Journals from: subject categories MATHEMATICAL & COMPUTATIONAL BIOLOGY

Sorted by: Impact Factor

Journals 1 - 20 (of 29)

Ranking is based on your journal and sort selections.

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

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

March 12, 2010

Professor Larry Mays
Chair and Director
Department of Bioinformatics
and Genomics

Dear Larry

I am writing to express my support for the request to establish a free-standing doctoral degree in Bioinformatics and Computational Biology at UNC Charlotte. It is a very strong proposal that will provide the highest caliber training for North Carolina students in a fast emerging area of intellectual pursuit that is clearly one of high priority for North Carolina. You have identified several unique strengths of the UNC Charlotte situation as it pertains to this program and these combine to make the program, the locale, and the university environment a great home for the future recruits. Among these strengths is the opportunity to leverage faculty strengths and interests from supporting departments such as Mathematics and Statistics and I am excited at the prospect of the highly multi-disciplinary activity between the life/physical sciences and the computational/mathematical sciences that will be appropriately brought together and enhanced through the mentoring of doctoral students in this new program.

Alan Dow, Chair
Mathematics and Statistics