

CURRICULUM VITAE

Zhengchang Su

Associate Professor

Department of Bioinformatics and Genomics
College of Computing and InformaticsThe University of North Carolina at Charlotte, Charlotte, NC 28223
704.687.7996 (office); 980.621.3171 (cell); zcsu@uncc.edu; <https://sulab.uncc.edu/>

1 Education

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

2 Professional Experience

1. June, 2012-present: **Associate Professor**, Department of Bioinformatics and Genomics, the University of North Carolina at Charlotte
2. July, 2006-June 2012: **Assistant Professor**, Department of Bioinformatics and Genomics, the University of North Carolina at Charlotte
3. August, 2004-July, 2006: **Group Leader and Research Assistant Professor**, Oak Ridge National Laboratory, University of Georgia in Athens.
4. August 1990-November 1994: **Instructor**, Department of Animal Physiology, Yunnan Agricultural University.

3 Career Highlights

1. Research:
 - Research achievements and interests
 - 1) Development of new algorithms and tools for *de novo* genome-wide prediction of transcription factor binding sites in genomes
 - 2) Development of new algorithms and tools for the reconstruction of gene regulatory networks in prokaryotes
 - 3) Development of experimental and computational methods for the characterization of transcriptional regulatory networks in single eukaryotic cells
 - Acquired two NSF grants and two institutional grants as the PI in the last four years, total amount of funding: **\$1,666,998**
 - Published **40** peer-reviewed papers, total number of citations: **868**, average citations: **21.7** citations/paper (not time-corrected)

- Received Outstanding Faculty Research Award in 2011, College of Computing and Informatics, UNC Charlotte
 - Research was covered in news presses: NSF news, GenomeWeb and the Computing Community Consortium (CCC)
2. Teaching:
- Developed and taught three graduate courses, received evaluations from students above the college and departmental averages in almost all categories
 - Mentored four Ph. D. students, co-mentored two Master's students
 - Mentored three postdoctoral fellows
 - Mentored three undergraduate students
 - Sponsored one visiting scholar and one visiting student
3. Services:
- Reviewer for NIH grants;
 - Reviewer for numerous journals and conferences
 - Programs committee members on international conferences
 - Members of three College and seven Departmental committees
 - Trained three high school students
 - Siemens Competition Mentor 2010, Siemens Foundation

4 Publications

4.1 Peer Reviewed Journal Publications (Google Scholar citation as of 6/6/2011)

1. Shaoqiang Zhang, Shan Li, Meng Niu, Phuc Pham and **Zhengchang Su**. MotifClick: prediction of cis-regulatory binding sites via merging cliques. **BMC Bioinformatics** 2011; **12**:238. (<http://www.biomedcentral.com/content/pdf/1471-2105-12-238.pdf>)
2. Shan Li, Minli Xu and **Zhengchang Su**. Computational analysis of LexA regulons in Cyanobacteria. **BMC Genomics**. 2010, 11:527. (<http://www.biomedcentral.com/1471-2164/11/527>). Google Scholar citations: **5**, total accesses to this article since publication: **1452**.
3. Xu M, **Su Z**. A novel alignment-free method for comparing transcription factor binding site motifs. **PLoS One**. 2010; 5(1):e8797. (<http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0008797>). Google Scholar citations: **1**.
4. Zhang S, Li S, Pham PT, **Su Z**. Simultaneous prediction of transcription factor binding sites in a group of prokaryotic genomes. **BMC Bioinformatics**. 2010; 11:397. PMID: 2920276. (<http://www.biomedcentral.com/1471-2105/11/397>). Google Scholar citations: **4**, total accesses to this article since publication: **1945**, labeled as **Highly accessed** by the journal.
5. Zhang S, Xu M, Li S, **Su Z**. Genome-wide de novo prediction of cis-regulatory binding sites in prokaryotes. **Nucleic Acids Res**. 2009; 37(10):e72. (<http://nar.oxfordjournals.org/content/37/10/e72.full.pdf+html>). Google Scholar citations: **14**.
6. Xu M, **Su Z**. Computational prediction of cAMP receptor protein (CRP) binding sites in cyanobacterial genomes. **BMC Genomics**. 2009; 10(23). (<http://nar.oxfordjournals.org/content/37/10/e72.full.pdf+html>). Google Scholar citations: **11**.

7. **Su Z**, Olman V, Xu Y. Computational prediction of Pho regulons in cyanobacteria. **BMC Genomics**. 2007 Jun 8;8:156. (<http://www.biomedcentral.com/content/pdf/1471-2164-8-156.pdf>). Google Scholar citations: **32**.
8. Tran TT, Dam P, **Su Z**, Poole FL, 2nd, Adams MW, Zhou GT, et al. Operon prediction in *Pyrococcus furiosus*. **Nucleic Acids Res**. 2007; 35(1):11-20. (<http://nar.oxfordjournals.org/content/35/1/11.full.pdf+html>). Google Scholar citations: **28**.
9. Dam P, Olman V, Harris K, **Su Z**, Xu Y. Operon prediction using both genome-specific and general genomic information. **Nucleic Acids Res**. 2007;35(1):288-98. (<http://nar.oxfordjournals.org/content/35/1/288.full.pdf+html>). Google Scholar citations: **62**.
10. Catte A, Patterson JC, Jones MK, Jerome WG, Bashtovyy D, **Su Z**, et al. Novel changes in discoidal high density lipoprotein morphology: a molecular dynamics study. **Biophys J**. 2006;90(12):4345-60. (<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1471865/pdf/4345.pdf>). Google Scholar citations: **59**.
11. **Zhenchang Su**, Fenglou Mao, Phuongan Dam, Hongwei Wu, Victor Olman, Ian Paulsen, Brian Plaenik and Ying Xu. Computational inference and experimental validation of nitrogen assimilation regulatory network in cyanobacterium *Synechococcus sp.* WH8102. **Nucleic Acids Res.**, 2006, 34(3): 1050-1065. (<http://nar.oxfordjournals.org/cgi/reprint/34/3/1050>). Google Scholar citations: **36**.
12. Fenglou Mao, **Zhengchang Su**, Victor Olman, Phuongan Dam, Zhijie Liu, Ying Xu. Mapping of Orthologous Genes in the Context of Biological Pathways: an Application of Integer Programming. **Proceedings of National Academy of Sciences U S A**, 2006,103 (1): 129-134. (<http://www.pnas.org/cgi/content/full/103/1/129>). Google Scholar citations: **33**.
13. **Zhengchang Su**, Xiaochuan Guo, Richard L. Shoemaker, Richard B. Marchase, and J. Edwin Blalock. A Store-operated Nonselective Cation Channel in Human Lymphocytes. **Cellular and Molecular Neurobiology**, 2005, 25(3-4):625-47. (<http://www.springerlink.com/media/h82ppwqrlgc5ac159dgc/contributions/k/2/7/8/k278221410h4714n.pdf>). Google Scholar citations: **8**.
14. Hongwei Wu, **Zhengchang Su**, Victor Olman and Ying Xu. Prediction of functional modules based on comparative genome analysis and Gene Ontology application. **Nucleic Acids Research**, 2005, 18; 33(9):2822-37. (<http://nar.oxfordjournals.org/cgi/content/full/33/9/2822>). Google Scholar citations: **93**.
15. Jinling Huang, **Zhengchang Su** and Ying Xu, The evolution of Microbial phosphonate Degradation Pathways. 2005, **Journal of Molecular Evolution**, 2005, 61:682-690. (<http://www.springerlink.com/media/hhwxvwmtmm4r53lhktb6/contributions/f/1/8/0/fl80m36015464473.pdf>). Google Scholar citations: **29**.
16. **Zhengchang Su**, Victor Olman, Fenglou Mao, and Ying Xu. Comparative genomics analysis of NtcA regulons in cyanobacteria: regulation of nitrogen assimilation and its coupling to photosynthesis. **Nucleic Acids Research**, 2005, 33(16): 5156-5171. (<http://nar.oxfordjournals.org/cgi/content/full/33/16/5156>). Google Scholar citations: **62**.
17. Phuongan Dam and **Zhengchang Su** and Victor Olman Ying Xu. In silico reconstruction of the carbon fixation pathway in *Synechococcus sp.* WH8102. **Journal of Biological Systems**, 2004 12:97-125. Google Scholar citations: **8**.
18. X. Chen, **Z. Su**, P. Dam, B. Palenik, Y. Xu and T. Jiang. Operon prediction by comparative genomics. **Nucleic Acid Research**, 2004, 32(7):2147-57. (<http://nar.oxfordjournals.org/cgi/content/full/32/7/2147>). Google Scholar citations: **72**.

19. **Zhengchang Su**, Richard L. Shoemaker Richard B. Marchase and J. Edwin Blalock. Ca^{2+} dependent inactivation of monovalent cation current through Ca^{2+} release activated Ca channels. **Biophysical Journal**, 2004, 86(2):805-14. (<http://www.biophysj.org/cgi/content/full/86/2/805>). Google Scholar citations: **14**.
20. **Zhengchang Su**, Douglas S. Barker, Peter Csutora, Theresa Chang, Richard L. Shoemaker, Richard B. Marchase and J. Edwin Blalock. Regulation of Ca^{2+} release activated Ca^{2+} channel by INAD and Calcium influx factors. **American Journal Physiology**, 2003, 4(2):C497-505. (<http://ajpcell.physiology.org/cgi/content/full/284/2/C497>). Google Scholar citations: **13**.
21. **Zhengchang Su**, Peter Csutora, Dacia Hunton, Richard L. Shoemaker, Richard B. Marchase, and J. Edwin Blalock. A Store-operated Non-selective Cation Channel in Lymphocytes is Activated Directly by Ca^{2+} Influx Factor (CIF) and Diacylglycerol. **American Journal of Physiology**, 2001, 280(5):C1284-92. (<http://ajpcell.physiology.org/cgi/content/full/280/5/C1284>). Google Scholar citations: **45**.
22. Villain M, Jackson PL, Manion MK, Dong WJ, **Su Z**, Fassina G, Johnson TM, Sakai TT, Krishna NR, Blalock JE. De novo design of peptides targeted to the EF hands of calmodulin. **Journal of Biological Chemistry**, 2000, 275(4):2676-85. (<http://www.jbc.org/cgi/content/full/275/4/2676>). Google Scholar citations: **41**.
23. Manion MK, **Su Z**, Villain M, Blalock JE. A new type of $\text{Ca}(2+)$ channel blocker that targets $\text{Ca}(2+)$ sensors and prevents $\text{Ca}(2+)$ -mediated apoptosis. **FASEB Journal**, 2000, (10):1297-306. (<http://www.fasebj.org/cgi/content/full/14/10/1297>). Google Scholar citations: **17**.
24. Csutora P, **Su Z**, Kim HY, Bugrim A, Cunningham KW, Nuccitelli R, Keizer JE, Hanley MR, Blalock JE, Marchase RB. Calcium influx factor is synthesized by yeast and mammalian cells depleted of organellar calcium stores. **Proceedings of National Academy of Sciences USA**, 1999, 6(1):121-6. (<http://www.pnas.org/cgi/content/full/96/1/121>). Google Scholar citations: **117**.
25. **Z. C. Su**, D. Y. Zheng and R. Q. Zhang. Effects of the products of immune response on the functions of the nervous and endocrine systems. **Progress in Physiological Sciences**, 1992, 23: 327-331. Google Scholar citations: **5**.
26. **Z. C. Su** and Y. S. Zhang. The role of nucleus ambiguus in modulation of cellular immunity of periaqueductal gray (PAG) in rabbits. **Journal of Immunology**, 1992, 8:18-22. Google Scholar citations: **3**.

4.2 Peer Reviewed Conference Publications

27. Shaoqiang Zhang, Lifen Jiang and Zhengchang Su. A Novel Information Contents Based Similarity Metric for Comparing TFBS Motifs.
28. Shaoqiang Zhang, Huazhi Sun, **Zhengchang Su** and Guojun Li. A simulated annealing heuristic for resource allocation and scheduling with precedence constraints. The 11th International Symposium on Pervasive Systems, Algorithms, and Networks, Dalian, China, 2011. (<http://cnhpc.dlut.edu.cn/ISPAN2011/acceptedpaperlist.html>)
29. H. Wu, F. Mao, **Z. Su**, V Olman, Ying Xu, Prediction of functional modules based on gene distributions in microbial genomes. **Genome Informatics**, 2005, 16:247-259. (<http://www.jsbi.org/pdfs/journal1/GIW05/GIW05F005.pdf>). Google Scholar citations: **10**.
30. Victor Olman, Hanchun Peng, **Zhengchang Su**, Ying Xu. Mapping of Microbial Pathways through Constrained Mapping of Orthologous Genes. **Proceedings of IEEE Computational Systems Biology Conference**, 2004, 363-370.

(http://conferences.computer.org/bioinformatics/csb2004/pdf/036_olman_victor_pmap.pdf).
Google Scholar citations: **5**.

31. Xin Chen, **Zhengchang Su**, Ying Xu, Tao Jiang. Computational prediction of operons in *Synechococcus* sp. WH8102. **Genome Informatics** 2004, 15(2):211-222. (<http://www.jsbi.org/journal/GIW04/GIW04F022.pdf>). **Best Paper Award**, Google Scholar citations: **35**.
32. **Zhengchang Su**, Phuongan Dam, Xin Chen Victor Olman, Tao Jiang, Brian Plaenik and Ying Xu. Computational inference of regulatory pathway in microbes. An application to phosphorus assimilation pathway. **Genome Informatics**, 2003, 14:1-10. (<http://www.jsbi.org/journal/GIW03/GIW03F001.pdf>). Google Scholar citations: **29**.

4.3 Peer Reviewed Extended Abstracts/Short Papers

33. **Zhengchang Su**, Phuongan Dam, Xin Chen, Victor Olman, Tao Jiang, Brian Plaenik and Ying Xu. Computational reconstruction of nitrogen assimilation pathway in *Cyanobacterium Synechococcus* sp. WH8102. Proceeding of 2004 IEEE Computational Systems Bioinformatics Conference, 2004, p640-41, Stanford, CA.
34. Victor Olman, Jizhu Lu, PhuongAn Dam, **Zhengchang Su** and Ying Xu. CUBIC: Search for Binding Sites. Proceedings of the 2004 IEEE Computational Systems Bioinformatics Conference. p666 – 667.
35. Peng Wang, **Zhengchang Su**, Phuongan Dam and Ying Xu. A knowledge base for computational pathway reconstruction. Proceedings of the 2004 IEEE Computational Systems Bioinformatics Conference. p612- 613.
36. Peng Wang, **Zhengchang Su**, Juntao Guo and Ying Xu. Structural Analysis of FGFR1 Kinase Activation through Molecular Dynamics Simulation. Proceedings of the 2004 IEEE Computational Systems Bioinformatics Conference. p700 – 701.
37. Fenglou Mao, , Victor Olman, **Zhengchang Su**, David Chuang and Ying Xu. Pathway mapping with operon information: an integer-programming method. Proceedings of the 2004 IEEE Computational Systems Bioinformatics Conference. p642- 643.
38. Phuongan Dam, **Zhengchang Su**, Victor Olman and Ying Xu. In silico construction of the carbon fixation pathway in *Synechococcus* sp. WH8102. Proceedings of the 2004 IEEE Computational Systems Bioinformatics Conference. p614- 615.
39. **Zhengchang Su**, Phuongan Dam, Xin Chen, Victor Olman, Tao Jiang, Brian Plaenik and Ying Xu. Computational inference of regulatory pathway in microbes. Proceeding of 2003 IEEE Computational Systems Bioinformatics Conference, 2003, p631, Stanford, CA.

4.4 Peer Reviewed Books and Book Chapters

40. Zhengchang Su, Goujun Li, and Ying Xu. Prediction of Regulons through Comparative Genome Analyses. In *Computational Methods for Understanding Bacterial and Archaeal Genomes*. Y. Xu and JP Gogarten, Eds.

4.5 Manuscripts under Review

41. Chen Xu and **Zhengchang Su**. Prediction of the cooperative cis-regulatory elements of broadly expressed neuronal genes in *Caenorhabditis elegans* (**Submitted**)
42. Shan Li and **Zhengchang Su**. Co-evolution of a transcription factor and its *cis*-regulatory binding sites: a lesson learned from the PhoB and its binding sites in bacteria. (**Submitted**)

43. Ridhi Dua, Shaoqiang Zhang, Anthony Wilkinson and **Zhengchang Su**. Prediction of transcription factor binding sites in prokaryotes via load efficient balance using MPI parallel computing (**In preparation**).
44. Xia Dong, Shan Li and **Zhengchang Su**. Transcriptional complexity in E coli K12 revealed by a stand-specific RNA-seq technique (**In preparation**)
45. Shan Li, Xiao Dong and **Zhengchang Su**. Reconstruction of transcription units/operons in prokaryotes using short reads of RNA-seq (**In preparation**)

4.6 Other Publications

45. **Zhengchang Su**, Victor Oman, Fenglou Mao and Ying Xu. Prediction of cis-regulatory binding site with high accuracy. Annual Meeting of International Society of Computational Biology, 2005, Detroit, MI.
46. **Zhengchang Su**, Phuongan Dam, Victor Olman, and Ying Xu. Prediction of protein-protein interactions in *Synechococcus* sp. WH 8102. Fourth International Conference of Bioinformatics, Atlanta, GA, 2003.
47. M. K. Manion, **Z. C. Su**, M. Villian, and J. E. Blalock. A new type of Ca^{2+} channel blocker that prevents apoptosis. *FASEB Journal*, 1999. Abstract 106.9.
48. **Z.C. Su**, R.L Sheomaker R. B. Marchase and J.E. Blalock. Ca^{2+} release activated Ca^{2+} channels are activated by removal of a inhibitory factor(s). *FASEB Journal*, 1999. Abstract 916.8.
49. M. Villian, **Z. C. Su**, M. K. Manion, and J. E. Blalock. Ca regulation by novel EF hand-binding peptide. *FASEB Journal*, 1996. Abstract 2272.
50. M. K. Manion, **Z. C. Su**, M. Villian, and J. E. Blalock. A novel peptide which binds EF hand motif and inhibits A Ca^{2+} Pchannel involved in HIV gp120-mediated apoptosis. *FASEB Journal*, 1996. Abstract 1842.
51. **Z. C. Su**, Y. W. Maio, M. K. Wang, L. X. Zheng X, Y, Qin and D. Y. Zheng. Interleukin-2 acts within the brain to induce fever and stimulate ACTC release by an indirect way in free-moving rats. *FASEB Journal*, 1995.
52. **Z. C. Su**, Y.W. Miao, W. Z. M. K. Wang, L. X. Zheng X, Y, Qin and D. Y. Zheng. Fever and ACTH release induced by central injection of IL-1b are mediated by prostaglandin and M-cholinergic and α -adrenergic receptors but not by opioid and β -adrenergic receptors. Third Congress of Federation of Asian and Oceanian Physiological Societies, S19-7(o), Shanghai, China. 1994.
53. **Z. C. Su**, Y.W. Miao, W. Z. M. K. Wang, L. X. Zheng X, Y, Qin and D. Y. Zheng. Central administration of recombinant rat g-interferon elicits adrenocorticotropin release in free-moving rats: Involvement of opioid and α - adrenergic receptors. *Novel Facts in Neuroendocrinology*, Satellite Symposium of the Third congress of FAOPS: 28-29: Xi'an, China. 1994.

5 Extramural Funding

5.1 Peer Reviewed National and International Grants

1. Title of Grant: CiC (SEA): Large Scale Prediction of Transcription Factor Binding Sites for Gene Regulation using Cloud Computing
 PI: Zhengchang Su
 Co-investigators: Srinivas Akella
 Funding Agency: NSF& Microsoft Research

Program: Computing in Cloud (CiC)
Amount Funded: **\$425,000**
Dates of Funding Period: 04/01/2011-03/31/2013
Category: Research

2. Title of Grant: Annotating the *cis*-Regulatory Binding Sites in Sequenced Prokaryotic Genomes
PI: Zhengchang Su
Co-investigators: Brian Cooper
Funding Agency: NSF/EF0849615
Program: Emerging Frontier (EF) and Advances in Biological Informatics (ABI)
Amount Funded: **\$1,202,998**
Dates of Funding Period: 09/01/2009-08/31/2013
Category: Research

5.2 Peer Reviewed Institutional Grants

1. Title of Grant: Development of a novel method for charactering the molecular determinants of cell fate specification during the embryogenesis in *C. elegans*
PI: Zhengchang Su
Co-investigators: Aidong Lu
Funding Agency: UNC Charlotte
Program: FRG
Amount Funded: **\$12,000**
Dates of Funding Period: 01/01/2011-12/31/2012
2. Title of Grant: Reconstruction of gene regulatory network in *Staphylococcus aureus* USA 300
PI : Zhengchang Su,
Co-investigators: Sunil Hwang
Funding agency: Carolinas Medical Center and UNC-Charlotte
Program: Carolinas Medical Center and UNC-Charlotte Collaborative Fund
Amount funded: **\$43,000.**
Dates of Funding Period: 03/01/2009-02/28/2010.
Category: Research

5.3 Awards and Donations

- 2011: Outstanding Faculty Research Award, College of Computing and Informatics, UNC Charlotte
- 2010: Siemens Competition Mentor, Siemens Foundation
- 2004: Best Paper Award of the 15th International Conference on Genomics Informatics, Pacifico Yokohama, Japan.
- 1994: C. C. Wu Culture and Education Foundation, Hong Kong, China

5.4 Pending Grants

1. Title: Determining the molecular and gene regulatory signatures of each cell in the embryogenesis of *C. elegans*
PI: Zhengchang Su
Funding agency: NIH
Amount: \$1,500,000 (direct cost)
Dates of Funding Period: 9/1/2012-8/31/2017

This project is to determine the expressed signature genes in each single cell generated during the embryogenesis of *C. elegans* and to reconstruct the gene regulatory networks in each cell using innovative experimental and computational methods.

2. Title: Deciphering the complexity of the transcriptomes in *E. coli* K12

PI: Zhengchang Su

Funding agency: NIH

Amount: \$1,495,238

Dates of Funding Period: 9/1/2012-8/31/2016

This project is to characterize the unknown components of the gene regulatory networks in *E. coli* K12, their dynamics and relationships to the transcriptomes, proteomes and metabolome under various stress conditions using a combination of high throughput experimental and computational methods.

6 Student Supervision

6.1 Postdoctoral fellows and Visiting Researchers

Student Name	Role	Period	Project Title	Type of researcher	Current status
Chuanbin Du	Project advisor	Jun.'11 - present	Algorithms for prediction of transcription factor binding sites in eukaryotes	Postdoctoral fellow	Still in the lab
Shaoqiang Zhang	Project advisor	Apr. '07 – Jul.' 10	Algorithms for prediction of transcription factor binding sites in prokaryotes	Postdoctoral fellow	Associate professor, Tianjing Normal University (Tianjing, China)
Di Huang	Project advisor	Apr. '07- Sep. '08	Classification of trans-member proteins	Postdoctoral fellow	Staff scientist, NCBI/NIH (Bethesda, MD)
Xia Dong	Sponsor	Feb.'10- present	Transcriptome analysis in bacteria using directional RNA-seq techniques, single cell transcriptome analysis	Visiting scholar	Professor, Yunnan Agricultural University (Kunming, China)
Yingwu Mei	Project advisor	Aug. '09- Jul.'10	Classification of trans-member proteins	Visiting student	Jilin University (Changchun, China)

6.2 Doctoral Students Supervised

Student Name	Role	Enroll time	Dissertation title	Graduation time	Current status
Shan Li	Dissertation advisor	Spring '07	Evolution and dynamics of transcriptional	Not graduate yet	Passed dissertation

			regulation in prokaryotes		proposal defense
Minli Xu	Dissertation advisor	Fall '07		Dropped in fall 2009	A graduate at CMU
Meng Niu	Dissertation advisor	Fall '08	Prediction of cis-regulatory modules in eukaryotes	Not graduate yet	Passed qualifying exam
Chen Xu	Dissertation advisor	Fall '10	Reconstruction of gene regulatory networks by data integration	Not graduate yet	Just started in the lab
Shatavia Morrison	Rotation adviser	Spring '09	Prediction of transcription factor binding sites in bacteria	Not graduate yet	In Dr. Cynthia Gibas' lab
Matthew Brown	Rotation adviser	Fall '11	Modular structure of transcription factor binding sites in eukaryotes	Not graduate yet	

6.3 Masters Students Supervised

Student Name	Role	Enroll time	Dissertation title	Graduation time	Current status
Colin Simpson	Thesis Co-advisor	Fall '08	Detection of DNA-protein interactions using capillary electro-mobility shift assay	Thesis defense expected in summer 2011	Scientist, CEM (Matthews, NC)
Ridhi Dua	Thesis Co-advisor	Fall'09,	Parallelizing the algorithm eGleClubs (extended ensemble clusters of binding sites)	Spring 2011	Software Engineer, Bank of America (Charlotte, NC)

6.4 Bachelors Students Supervised

Student Name	Role	Time period	Project title	Department	Current status
Cuong Tran	Project advisor	Spring '11 ~ present	Single cell transcriptome analysis using RNA-seq	Biology	Junior

Van Luong	Project co-advisor	Fall'09 ~ spring '11	Detection of protein-DNA interaction using capillary electrophoresis mobility shift assay	Chemistry	Graduated in spring '11
Shaunaq Parikh	Project co-advisor	Summer '10 ~ present	Detection of protein-DNA interaction using capillary electrophoresis mobility shift assay	Chemistry	Senior

7 Teaching

7.1 Major Accomplishments

1. Proposed and developed curriculums of three graduate courses: BINF6312/8312, Computational Comparative Genomics; BINF6200/8200, Statistics for Bioinformatics; and BINF6204/8204, Mathematical Systems Biology. They are all the first of their kinds offered on the UNC Charlotte campus.
2. Taught three graduate courses: BINF6201/8201, Molecular Sequence Analysis; BINF6204/8204, Mathematical Systems Biology; and BINF6312/8312, Computational Comparative Genomics.
3. These courses formed an important part of the foundation for the subsequent establishment of the Professional Science Master's Program in Bioinformatics in 2007 and the Ph.D. Program in Computational Biology and Bioinformatics in 2010.
4. Successful integration of research programs with teaching activities and mentoring different levels of students.

7.2 Courses Taught

7.2.1 Graduate Courses

Course Taught	Semesters	Course No.	Course Level	Average Enrolment	Course Type
Computational Comparative Genomics	Fall '07, fall '08	BINF6312/8312	Graduate	4	New course
Mathematical Systems Biology	Spring '08, spring'10	BINF6204/8204	Graduate	5	New course
Molecular Sequence Analysis	Fall '09, fall'10, fall 11	BINF6201/8291	Graduate	18	Existing course

8 Service and Outreach

8.1 Major Accomplishments

1. Delivered 14 invited talks in conferences and universities
2. Served on two conference program committees
3. Reviewer of proposals for two NIH study sections
4. Reviewer for 15 conferences and journals
5. Served on seven Department committees and three College committees;
6. Supervised three high school students
7. Siemens Competition Mentor 2010, Siemens Foundation

8.2 External Service

8.2.1 Invited Talks

1. June, 2011, Deciphering gene transcription regulatory networks in prokaryotes. State University of New York at Buffalo.
2. June, 2011, Large scale prediction of transcription factor binding sites for gene regulation using cloud computing, Cloud Futures 2011, Redmond, WA.
3. April, 2011, Large scale annotation of *cis*-regulatory sequences in prokaryotic genomes. J. Craig Venter Institute, Rockville, MD.
4. March, 2011, Large scale annotation of *cis*-regulatory sequences in prokaryotic genomes. University of Maryland at Baltimore.
5. June, 2010, Deciphering gene transcription regulatory networks in prokaryotes. Institute of Microbiology and Epidemiology, Beijing China.
6. June, 2011, Large scale annotation of *cis*-regulatory sequences in prokaryotic genomes. Minghai Biotechnology Inc. Beijing, China
7. April, 2010: Large scale annotation of *cis*-regulatory sequences in prokaryotic genomes. West Virginia University
8. February, 2010: Large scale annotation of *cis*-regulatory sequences in prokaryotic genomes. The University of North Carolina at Charlotte.
9. October, 2007: Prediction of *cis*-regulatory elements in prokaryotes. The University of North Carolina at Charlotte.
10. July, 2007: Computational reconstruction of biological pathways. Yunnan Agricultural University.
11. January, 2006: Prediction of signal transduction pathway in cancer stem cells. Department of Biochemistry and Molecular Biology, University of Georgia.
12. November, 2005, Computational prediction of regulatory pathways in prokaryotes. Northwest Pacific National Laboratories.
13. October, 2005: Computational inference of pathways in marine cyanobacteria. Department of Marine Sciences, University of Georgia

14. September, 2005: An efficient algorithm for cis-regulatory elements prediction. Department of Biochemistry of Molecular Biology, University of Georgia.
15. September, 2004. Inference of molecular networks in bacteria: Computational Biology Institute, Oak Ridge National Laboratories.

8.2.2 Journal/Conference Reviewer

1. PLOS ONE
2. Nucleic Acid Research
3. BMC Genomics
4. Mathematical Biosciences
5. Proteins
6. Bioinformatics
7. BMC Bioinformatics
8. Journal of Computational Biology and Bioinformatics
9. The eighth international bioinformatics workshop in Wuhan, China, June 4-6, 2010.
10. IEEE International Conference on Bioinformatics and Biomedicine, Washington DC, 2009.
11. The sixth international bioinformatics workshop in Kunming, China, June 7-9, 2008.
12. 15th International Workshop on Genome informatics, Japan, 2005.
13. 2005 IEEE Computational Systems Bioinformatics Conference, Stanford, CA, 2005.
14. 14th International Workshop on Genome informatics, Japan, 2004.
15. 2003 IEEE Computational Systems Bioinformatics Conference, Stanford, CA, 2003.

8.2.3 Program Committees

1. Program committee, the eighth international bioinformatics workshop in Wuhan, China, June 4-6, 2010. <http://cs.whu.edu.cn/ibw2010/Committee.html>
2. Program committee, the sixth international bioinformatics workshop in Kunming, China, June 7-9, 2008. <http://yunda.org/science/activity/ibw2008/>

8.2.4 Editorial Boards/Panels

1. April 2009, NIH special emphasis Panel/Scientific Review Group ZRG1 GGG-F (58)
2. April 2010, NIH Special Emphasis Panel/Scientific Review Group 2010/08 ZRG1 GGG-F (55)

8.2.5 Professional Affiliations/Memberships

1. American Association for the Advancement of Science
2. The American Physiological Society
3. International Society of Computational Biology