

A. PERSONAL INFORMATION

Name: Dennis R. Livesay, PhD

Address: Department of Bioinformatics and Genomics
University of North Carolina at Charlotte
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Charlotte, NC 28223

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Personal: Citizenship: U.S.A.
Marital status: Married with 1 child
Birthdate: 07/04/1974

B. POSTIONS & EDUCATION

Professional Positions: Associate Professor (2008-present)
Department of Bioinformatics and Genomics
University of North Carolina at Charlotte

Other affiliations at UNC Charlotte:
Bioinformatics and Computational Biology PhD Program
Computing and Information Systems PhD Program
Bioinformatics Research Center
Center for Biomedical Engineering Systems

Associate Professor (2006-2008)
Department of Computer Science
University of North Carolina at Charlotte

Associate Professor (2005-2006)
Department of Chemistry
California State Polytechnic University at Pomona

Assistant Professor (2000-2005)
Department of Chemistry
California State Polytechnic University at Pomona

Education: PhD in Physical Chemistry (1997-2000)
University of Illinois at Urbana-Champaign
Dissertation: *Conservation of electrostatically mediated function across protein families and superfamilies*
Advisor: Shankar Subramaniam (now at UCSD)

B.Sc. in Chemistry (1994-1996)
Ball State University

Studied Chemistry (1992-1994)
Indiana University/Purdue University at Indianapolis

C. PROFESSIONAL ACTIVITIES

- Editorial Activity (Books):** Methods in Molecular Biology: Protein Dynamics, Editor (in progress)
- Editorial Activity (Journals):** J Proteome Science and Computational Biology, Editorial Board (2012-present)
 PLoS Computational Biology, Associate Editor (2011-present)
 BMC Bioinformatics, Associate Editor (2010-present)
 Current Protein and Peptide Science, Editorial Board (2010-present)
 Protein and Peptide Letters, Editorial Board (2010-present)
 Advances in Bioinformatics, Editorial Board (2010-present)
 Current Opinion in Pharmacology, Editor of special issue on “*The importance of protein dynamics*” (2010)
 Chemistry Central Journal, Editorial Board (2010-present)
 Chemistry Central Journal, Section Editor: *Biomacromolecules* (2006-2010)
- Tenure Reviews:** I have served as an outside reviewer for 6 different tenure applications.
- Journal Reviews:** Advances in Bioinformatics
 Astrobiology
 BBA – Proteins and Proteomics
 Bioinformatics
 Biophysical Journal
 BMC Bioinformatics
 BMC Structural Biology
 Chemical Reviews
 Chemistry Central Journal
 Communications in Computational Physics
 Current Bioinformatics
 Current Opinion in Pharmacology
 FEBS Letters
 Genome Biology
 Journal of Biophysics and Structural Biology
 Journal of Computational Chemistry
 Journal of Molecular Biology
 Journal of Molecular Recognition
 Journal of Structural Biology
 Nature Communications
 Nature Protocols
 Nucleic Acids Research
 PLoS Computational Biology
 PLoS ONE
 PROTEINS: Structure, Function & Bioinformatics
- Grant Reviews:** Research Corporation – Cottrell College Science Award (2011 and 2012)
 W.M. Keck Foundation (2010)
 NIH-ZRG1 BST-F – S10 proposals (2009)
 NIH-Special Emphasis study section – R15 and R21 proposals (2005)

NIH-MBRS ad hoc study section – SCORE (S01) proposals (2002)
 National Science Foundation (2006)
 CSUPERB Seed Grant Program (2004 & 2005)
 CPP Research Council internal grants (2004)

Synergistic Activities:

(Founding) Director of the Bioinformatics and Computational Biology PhD program; UNC Charlotte (2011-present)
 Bioinformatics representative, IT PhD Program Steering Committee; UNC Charlotte (2007-present)
 Chair, IT PhD Program Steering Committee; UNC Charlotte (2007-2010)
 Coordinator of the Bioinformatics-track of the IT PhD program; UNC Charlotte (2007-2010)
 Developed PhD level courses in: *Computational Structural Biology*; *Biophysical Modeling*; and *Energy and Interaction in Biological Modeling* (2006-2008)
 Graduate advisor, Department of Chemistry; Cal Poly Pomona (2005-2006)
 Developed and delivered *Introduction to Bioinformatic Methods* short-course at Technology Park Malaysia, in Kuala Lumpur, Malaysia (2005)
 One of three co-organizers of Cal Poly Pomona's *Center of Macromolecular Modeling & Material Design* (CM³D), which represents a tight collaboration between six departments and two colleges. The goal of the CM³D is to co-locate research equipment, reduce redundancy and foster interdisciplinary efforts (2003).
 Co-organizer of Cal Poly Pomona's *Molecular Modeling & Simulation* baccalaureate degree (2002)
 While at Cal Poly Pomona, supervised 7 M.Sc. students and 15 B.Sc. students, 8 of which matriculated to PhD programs (2000-2006)

Honors:

UNC Charlotte Leadership, which is a by invitation university-wide workshop to develop the campus' next wave of leaders (2010-2011)
 Outstanding Faculty Research Award, College of Computing and Informatics, UNC Charlotte (2010)
 NATO Advanced Study Institute on Hydration Processes in Biology; Les Houches, France (1998)
 Department of Chemistry Graduate Fellowship; University of Illinois (1997)
 Undergraduate Award for All-Around Achievement in Chemistry; Ball State University (1996)
 1st Place; Midwest Regional Undergraduate Research Poster Competition; University of Kentucky (1996)
 Graduated Cum Laude; Ball State University (1996)
 Undergraduate Research Fellow; Ball State University (1995)

Student Research Awards:

Cal Poly Pomona International Center Merit Scholarship (Swati Pande, 2006)
 Sigma Xi Graduate Research Poster Competition (David La, 2006)
 Howard Hughes Undergraduate Research Fellowship (Eric Chea, 2005)

Don Eden Graduate Student Research Award, which is a CSU-wide competition
(David La, 2004)

Annual Meeting of the Protein Society Research Poster Award (David La and
Melanie Silver, 2002)

D. RESEARCH SUPPORT

Ongoing Support: *Quantitative stability/flexibility relationships in the GABA transport protein*
Livesay DR (PI) 2012
UNC Charlotte (Faculty Research Grant) Role: PI
Amount: \$12,000 (joint proposal with Don Jacobs)

Antibody fragment stability: A focus on domain-domain interactions
Livesay DR (PI) 2011-2012
MedImmune, LLC Role: PI
Amount: \$99,495

Predicting protein stability and flexibility
PI: Jacobs DJ 2006-2011
NIH R01 GM073082 Role: Investigator
Amount: \$1,459,968

NOTE: multiple PI's were not an option at NIH when the above R01 grant was submitted, but I am a *de facto* PI. In fact, the official PI and I make joint decisions regarding all major expenditures and most research issues.

Completed Support: ARRA administrative supplement to: *Predicting protein stability and flexibility*
PI: Jacobs DJ 2010-2011
NIH R01 GM073082-04S2 Role: Investigator
Amount: \$102,125

High performance computing in computational biology
PI: Livesay DR 2010-2011
NIH S10 SRR026514 Role: PI
Amount: \$474,288

Center for macromolecular modeling and material design
PI: Ortiz JM (CPP President) 2006-2007
W.M. Keck Foundation Role: Investigator
Amount: \$500,000

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

Investigation of superoxide dismutase surface electrostatics
PI: Livesay DR 2002-2004
NIH S06 GM53933-07 Role: PI
Amount: \$178,00

Acquisition of a workstation network for research in parallel and distributed computing

PI: Kuang H 2003-2005
 NSF MRI 032-1333 Role: Co-PI
 Amount: \$159,658

Conferring thermostability to mesophilic proteins through systematic mutation of surface residues

PI: Livesay DR 2001-2003
 ACS Petroleum Research Fund 36848-GB4 Role: PI
 Amount: \$25,000

Bioinformatic study correlating protein flexibility with function

PI: Jacobs DJ 2003
 CSUPERB-Joint Venture Matching Grant Role: Co-PI
 Amount: \$25,000 + \$75,000 (in-kind from Cengent Therapeutic)

Dihedral-angle characterization of conformational flexibility in protein structure

PI: Jacobs DJ 2002-2005
 NIH S06 GM48680-0952 Role: Paid consultant
 Amount: \$370,328

+2 allocations of supercomputer time from the National Center for Supercomputing Applications, +3 intramural "mini-grants" and +4 travel awards.

E. PUBLICATIONS ([‡] indicates that I am either corresponding or co-corresponding author)**Summary:**

Journal publications = 37 (corresponding author = 23)
 Peer-reviewed conference papers = 5 (corresponding author = 3)
 Invited book chapters = 4 (corresponding author = 4)
 H-Index = 16^a
 Total citations = 647
 Average # of citations per paper = 15.8^b

^a H = 10-12 is expected for Associate Professors, and H ~ 18 is expected for full professorship.

^b Based only on papers with ≤ 1 citation, meaning newly published papers are not considered.

Research Articles:

(46.) Verma D, Jacobs DJ, Livesay DR[‡] (2012). *Changes in lysozyme flexibility upon mutation are frequent, large and long-ranged*. **PLoS Computational Biology**, 8:e1002409.

(45.) González LC, Wang H, Livesay DR[‡], Jacobs DJ (2012). *Calculating ensemble averaged descriptions of protein rigidity without sampling*. **PLoS ONE**, 7:e29176.

(44.) Vorov OK, Livesay DR[‡], Jacobs DJ (2011). *Nonadditivity in conformational entropy upon molecular rigidification reveals a universal mechanism affecting folding cooperativity*. **Biophysical Journal**, 100:1129-1138.

(43.) KC DB, Livesay DR[‡] (2011). *Topology improves phylogenetic motif functional site predictions*. **IEEE/ACM Transactions on Computational Biology and Bioinformatics**, 8:226-233.

- (42.) Livesay DR[‡] (2010). *Protein dynamics: Dancing on an ever-changing free energy stage*. **Current Opinion in Pharmacology**, 10:706-708 (ALSO EDITOR OF SPECIAL SECTION ON PROTEIN DYNAMICS).
- (41.) Verma D, Jacobs DJ, Livesay DR[‡] (2010). *Predicting the melting point of human c-type lysozyme mutants*. **Current Protein and Peptide Science**, 11:562-572.
- (40.) Mottonen JM, Jacobs DJ, Livesay DR[‡] (2010). *Allosteric response is both conserved and variable across three CheY orthologs*. **Biophysical Journal**, 99:2245-2254.
- (39.) Chikkagoudar S, Livesay DR, Roshan U (2010). *PLAST-ncRNA: Partition function local alignment search tool for non-coding RNA sequences*. **Nucleic Acids Research**, 38:W59-W63.
- (38.) Vorov OK, Livesay DR[‡], Jacobs DJ (2009). *Helix/coil nucleation: A local response to global demands*. **Biophysical Journal**, 97:3000-3009.
- (37.) R. Jasuja, Ulloor J, Yengo CM, Choong K, Istomin AY, Livesay DR, Jacobs DJ, Swerdloff RS, Miksovska J, Larsen RW, Bhasin S (2009). *Kinetic and thermodynamic characterization of dihydrotestosterone-induced conformational perturbations in androgen receptor ligand binding domain*. **Molecular Endocrinology**, 23:1231-1241.
- (36.) Mottonen JM, Xu M, Jacobs DJ, Livesay DR[‡] (2009). *Unifying mechanical and thermodynamic descriptions across the thioredoxin protein family*. **PROTEINS: Structure, Function, & Bioinformatics**, 75:610-627.
- (35.) KC DB, Livesay DR[‡] (2008). *Improving position specific predictions of protein functional sites using phylogenetic motifs*. **Bioinformatics**, 24:2308-2316.
- (34.) Vorov OK, Livesay DR, Jacobs DJ (2008). *Conformational entropy of an ideal cross-linking polymer chain*. **Entropy**, 10:285-308.
- (33.) Livesay DR[‡], Huynh DH, Dallakyan S, Jacobs DJ (2008). *Hydrogen bond networks determine emergent mechanical and thermodynamic properties across a protein family*. **Chemistry Central Journal**, 2:17 (HIGHLY ACCESSED).
- (32.) Roshan U, Chikkagoudar S, Livesay DR (2008). *Searching for evolutionary distant RNA homologs within genomic sequences using partition function posterior probabilities*. **BMC Bioinformatics**, 9:61.
- (31.) Istomin AY, Gromiha MM, Vorov OK, Jacobs DJ, Livesay DR[‡] (2008). *New insight into long-range nonadditivity within protein double-mutant cycles*. **PROTEINS: Structure, Function, & Bioinformatics**, 70:915-924.
- (30.) Istomin AY, Jacobs DJ, Livesay DR (2007). *On the role of structural class of a protein with two-state folding kinetics in determining correlations between its size, topology, and folding rate*. **Protein Science**, 16:2564-2569.
- (29.) Livesay DR[‡], Kidd PD, Eskandari S, Roshan U (2007). *Assessing the ability of sequence-based methods to provide functional insight within membrane*

integral proteins: a case study analyzing the neurotransmitter/Na⁺ symporter family. **BMC Bioinformatics**, 8:397.

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

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

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

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

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

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

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

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

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

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

(18.) La D, Sutch B, Livesay DR[‡] (2005). *Predicting protein functional sites with phylogenetic motifs.* **PROTEINS: Structure, Function, & Bioinformatics**, 58:309-320 (FEATURED ON THE COVER).

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

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

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

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

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

(12.) Livesay DR, Jambeck P, Rojnuckarin A, Subramaniam S (2003). *Conservation of electrostatic properties within enzyme families and superfamilies*. **Biochemistry**, 42:3464-3473 (FACULTY OF 1000 "MUST READ").

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

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

Peer-Reviewed Proceedings:

(9.) González LC, Livesay DR[‡], Jacobs DJ (2011). *Improving protein flexibility predictions by combining statistical sampling with a mean-field virtual pebble game*. **Second ACM Conference on Bioinformatics, Computational Biology and Biomedicine**, 294-298.

(8.) Barlow S, Liu Y, Yang J, Livesay DR, Jacobs DJ, Mottonen J, Verma D (2011). *WaveMap: Interactively discovering features from protein flexibility matrices using wavelet-based visual analytics*. **Computer Graphics Forum**, 30:1001-1010.

(7.) Pande S, Raheja A, Livesay DR[‡] (2007). *Prediction of enzyme catalytic sites from sequence using neural networks*. **IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology**, 247-253.

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

(5.) Roshan U, Livesay DR[‡], La D (2005). *Improved phylogenetic motif detection using parsimony*. **Fifth IEEE Symposium on Bioinformatics and Bioengineering**, 19-26 (<20% ACCEPTANCE RATE).

Book Chapters:

(4.) Jacobs DJ, Livesay DR[‡], Mottonen JM, Vorov OK, Istomin AY, Verma D (2012). *Ensemble properties of network rigidity reveal allosteric mechanisms*. In **Allostery: Methods and Protocols**, A. Fenton (Ed.), Springer, ISBN: 978-1-61779-333-2.

(3.) Livesay DR[‡], Kreth KE, Fodor AA (2012). *A critical evaluation of correlated mutation algorithms and coevolution within allosteric mechanisms*. In **Allostery: Methods and Protocols**, A. Fenton (Ed.), Springer, ISBN: 978-1-61779-333-2.

(2.) Livesay DR[†], KC DB, La D. *Predicting protein functional sites with phylogenetic motifs: Past, present and beyond* (2011). In **Protein Function Prediction for the Omics Era**, D. Kihara (Ed.), Springer, ISBN: 978-94-007-0880-8.

(1.) KC DB, Livesay DR[†]. *A spectrum of phylogenetic-based approaches for predicting protein functional sites* (2010). In **Bioinformatics for Systems Biology**, S. Krawetz (Ed.), Humana Press, ISBN: 978-1-934115-02-2.

F. PATENTS, SCIENTIFIC SOFTWARE, AND DATABASES

Patents: (5.) Jacobs DJ, Livesay DR. *Computer implemented system for protein and drug target design utilizing quantitative stability/flexibility relationships*. Application number: 61016848, Patent pending.

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

(3.) Livesay DR. **webMINER**. This web-server is an implementation of our phylogenetic motif-based functional site prediction algorithm.

(2.) Livesay DR. **miniMINER**. A streamlined Java-based (jar) implementation of the above MINER algorithm without the data analysis tools.

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

G. COMPLETED STUDENT THESES

PhD Theses: (9.) Gonzalez LC (2011). *A virtual pebble game to ensemble average graph rigidity*. Information Technology PhD Program, UNC Charlotte.

Master's Theses: (8.) Pande S (2007). *Predicting enzyme catalytic sites with neural networks*. Department of Biological Sciences, Cal Poly Pomona.

(7.) Kanjanapangka J (2006). *Investigating protein stability and per residue pKa values using Poisson-Boltzmann continuum electrostatic theory*. Department of Biological Sciences, Cal Poly Pomona.

(6.) La D (2005). *Robust large-scale protein functional site prediction using phylogenetic motifs*. Department of Biological Sciences, Cal Poly Pomona.

(5.) Torrez M (2004). *Conferring thermostability to mesophilic proteins through optimized electrostatic surfaces*. Department of Chemistry, Cal Poly Pomona.

(4.) Lin B (2004). *Understanding polymer based sensing films*. Department of Chemistry, Cal Poly Pomona.

Senior Project: (3.) Fregoso S (2005). *Computational redesign of RNase Sa2 surface electrostatics*. Department of Chemistry, Cal Poly Pomona.

(2.) Alsop E (2003). *Optimized electrostatic surfaces parallel increased thermostability: A structural bioinformatics analysis*. Department of Chemistry, Cal Poly Pomona.

(1.) Lam H (2002). *Identification of factors leading to increased thermostability in iron-manganese superoxide dismutase*. Department of Chemistry, Cal Poly Pomona.

H. CURRENT & FORMER LAB MEMBERS (when known, current location is provided in parentheses)

- Post-Docs Advised:** Dr. Dukka Bahadur K.C. (SRA International/NIH)
 Dr. Chuanbin Du, jointly w/ Don Jacobs (Post-Doc, UNC Charlotte)
 Dr. Andrei Istomin, jointly w/ Don Jacobs
 Dr. Jim Mottonen, jointly w/ Don Jacobs (Gastonia Community College)
 Dr. Li Tong, jointly w/ Don Jacobs (Post-Doc, UNC Charlotte)
 Dr. Oleg Vorov, jointly w/ Don Jacobs (R.I.P.)
 Dr. Hui Wang, jointly with Don Jacobs (Goldman Sachs)
- Programmers Advised:** Dr. Jaydutt D. Bhalshankar (Bioinformatics PhD student, India)
- PhD Students:** Dr. Luis Carlos Gonzalez (Faculty, Autonomous Univ of Chihuahua)
 Deeptak Verma (PhD student, UNC Charlotte)
- PhD Rotation Students:** Kyle Kreth (PhD student, UNC Charlotte)
 Cristina Baciú (PhD student, UNC Charlotte)
 Ivetth Corona de la Fuente (PhD student, UNC Charlotte)
 Minli Xu (PhD student, Carnegie Mellon University)
- M.S. Students:** Julie Kanjanapangka (PhD student, City of Hope)
 Dr. David La (Post-Doc in David Baker's lab, University of Washington)
 Brian Lin (PhD student, University of California-Santa Barbara)
 Swati Pande (Statistician, University of California-Berkeley)
 Michael Schultehenrich
 Michael Torrez (Lecturer, Norco Community College)
- Undergraduate Students:** Eric Alsop (PhD student, Arizona State University)
 Kim Archer
 Dr. Eric Chea (FDA)
 Alfonso Faris
 Steve Fregoso
 Julie Kanjanapangka (PhD student, City of Hope)
 Dr. David La (Post-Doc in David Baker's lab, University of Washington)
 Hank Lam
 Eric Kish-Trier (PhD student, University of California-Riverside)
 Paul Ruegger (PhD student, University of California-Riverside)
 Melanie Silver
 Dr. Brian Sutch (Computational Pharmaceuticals Consultant)
 Bhavik Upadhyay (Physical Therapist)
 Leo Xu

I. TEACHING EXPERIENCE († indicates courses that I personally developed)

- Energy & Interaction in Biological Modeling:*** (BINF 8101[†]) Survey of methods in chemistry and biophysics. Topics covered include: (a) the major organic and inorganic chemical features of biological macromolecules; (b) the physical forces that shape biological molecules, assemblies and cells; (c) the chemical driving forces that govern living systems; (d) the molecular roles of biological macromolecules and common metabolites; (e) and the pathways of energy generation and storage. Each section of the course builds upon the relevant biology and chemistry to explain the most common mathematical and physical abstractions used in modeling in the relevant context.
- Biophysical Modeling:*** (BINF 8311[†]) Survey of methods in computational biophysics. Topics covered include: overview of statistical mechanics; molecular mechanical force fields; energy minimization and grid search techniques; (d) dynamics simulations (molecular and coarse-grained); Monte-Carlo methods; classical representations of electrostatics (Poisson-Boltzmann, generalized Born, and Coulombic); Brownian dynamics simulation methods; and the distance constraint model.
- Structural Bioinformatics:*** (BINF 8202[†]) Survey of structural bioinformatics. Topics covered include: the fundamental concepts of structural biology; software for visualization, visualization styles, publication quality images; the hierarchical nature of biomacromolecular structure classification; computational methods to evaluate and compare biomacromolecular structure; inferring structure/function relationships from structure; and computational prediction of protein and nucleic acid structure from sequence.
- Introduction to Proteomics:*** (CHM 561[†]) Overview of modern “omic” methods, with special emphasis on the proteome. Introduction to relevant primary literature. Topics covered include: protein mass spectrometry, 2D-gel electrophoresis, co-affinity assays, yeast-2-hybrid, gene/protein microchips, etc.
- Computational Biochemistry:*** (CHM 417[†]) Survey of bioinformatics, covering theoretical and technical issues germane to common sequence and structure analysis methods. Topics covered include: scoring matrices, dynamic programming, BLAST, multiple sequence alignment, phylogeny reconstruction, hidden Markov models, motif detection, functional site prediction, & structural alignment.
- Macromolecular Modeling:*** (CHM 416[†]) Survey of computational biophysics, covering theoretical foundation and algorithmic implementation of standard biophysical methods. Topics covered include: Poisson-Boltzmann continuum electrostatics, force field development, molecular dynamics, Brownian dynamics, Monte Carlo simulation, protein structure prediction, etc.
- Bioinformatics:*** (BIOL 499) One-quarter introduction to bioinformatics. Team-taught with four other faculty members (three from Biology, one from Computer Science, and myself from Chemistry).
- Biochemistry:*** Year-long biochemistry series. Topics covered include: (CHM 327) Protein structure and function, carbohydrates, lipids, and enzyme kinetics; (CHM 328) Overview of anaerobic and aerobic metabolism – pathways, regulation, and enzyme mechanisms; & (CHM 329) Nucleic acid structure, replication,

transcription, and translation. I have also taught the equivalent first semester biochemistry course at UNC Charlotte.

Blood & Lymphatic Systems: Guest lecturer at Western University of Health Sciences School of Osteopathic Medicine. Six hours of lecture focusing on the proteins and biochemistry of the blood and lymphatic systems.

Other Courses Taught: (CHM 121) General Chemistry; (CHM 321) Elements of Biochemistry; and a variety of biochemistry laboratory courses.

J. FACULTY/SERVICE ACTIVITIES

Service at UNC Charlotte: *(Founding) Director* – Bioinformatics and Computational Biology PhD program (2011-present). Oversee the application and admission process, advise students vis-à-vis courses and selecting an advisor, establish and enforce policy, manage assistantship budget, liaison with the graduate school, and ensure that students complete the program in a timely manner. Much of my effort has been on creation of the program and all of the accompanying processes and regulations. (2011-present).

Member of the College of Computing and Informatics Promotion and Tenure Committee – College-level P&T review (2011-present).

Ad hoc review committee – Graduate School Dean's Outstanding Dissertation Award (2011).

President-elect – College of Computing and Informatics faculty (2011-present).

Member of the Belk Distinguished Professorship search committee – Search committee for an endowed professor in bioinformatics (2010-present). I have also been a member of many other search committees, including for some outside my college.

Chair of the BCB PhD Advising Committee – We have per-semester advising for all Bioinformatics and Computational Biology PhD students (2011-present).

Chair of the BCB PhD Admissions Committee – (2011-present).

Member of the Departmental Promotion and Tenure Committee – Department-level P&T review (2009-2011).

Member of Faculty Council – Campus-wide faculty governance committee (2008-present).

Member of Faculty Competitive Grants Committee – This is a standing campus-wide grants review committee for instances when internal competitions are necessary (2008-present).

Chair, IT PhD Steering Committee – This committee is responsible for developing policy and processing applications of new members to the IT PhD program (2007-2010).

IT PhD Program (Bioinformatics Track) Graduate Coordinator – Oversee the application and admission process, advise students vis-à-vis courses and

selecting an advisor, establish and enforce policy, and ensure that students complete the program in a timely manner (2007-2010).

Department of Computer Science Awards Committee – The committee is responsible for nominating and preparing application packets of CS faculty to college, university, and outside awards (2007-2009).

Ad hoc Committee on Diversity within the Graduate School – This committee (Chaired by Susan Sell, Associate Dean of the Graduate School) is responsible for investigating the state of diversity within the graduate school, what proactive steps are being taken to improve diversity, and what should be done. Specifically, I was part of a sub-group that critically examined recruitment of students from underrepresented minority groups (2006-2007).

CPP Departmental Service:

Department of Chemistry Graduate Coordinator – Oversee the application and admission process, advise students vis-à-vis courses and selecting an advisor, establish and enforce policy, and ensure that students complete the program in a timely manner (2005-2006).

Joint Chemistry-Physics Committee for Interdisciplinary Development – This committee is responsible for planning future CM³D efforts, which (despite the committee name) now includes 11 faculty members from six departments and two colleges (2003-2006).

Senior Thesis Committee (Co-chair) – Advised students on technical aspects of performing research and writing of a Senior Thesis (2002-2006).

5 Yr Chemistry Program Evaluation - Program Quality Subcommittee (2003-2005).

Graduate Program / Research Committee – Develop policy vis-à-vis scholarly research and the graduate program (2003-2006).

Curriculum Development committee – Development and long-term planning of our *Molecular Modeling and Simulation* degree. See also *Teaching Experience* above (2001-2003).

Undergraduate Advising Committee – Advised chemistry majors (every quarter) on future course selections as necessary for successful completion of their degree (2000-2005).

CPP College of Science:

High Performance Computing & Networking Committee – The College of Science has targeted computer-based research as a key area for development. This College-level committee was set up to develop technology policy and plan for future infrastructure procurement (2004-2006)

CPP & the CSU System:

University Research Council – College of Science representative. The Council analyzes policy issues, reviews RSCA proposals, evaluates Student Travel Fund applications, judges the student poster presentation, and advises the Office of Research and Sponsored Programs on a host of other issues (2003-2004).

Cal Poly Pomona Representative to CSUPERB Faculty Consensus Group – The California State University Program in Education and Research in Biotechnology (CSUPERB) is a multi-campus initiative created in 1987 designed to leverage

system-wide resources and catalyze interdisciplinary, inter-campus, biotechnology endeavors (2003-2006).

Community Service:

Instructor – Boy Scouts of America Chemistry Merit Badge – As part of Cal Poly Pomona's annual Boy Scout Merit Badge Day, I taught two half-day courses annually that allowed the students to earn their Chemistry merit badge. The course introduced all sub-disciplines of chemistry and included hands-on demonstrations like making slime, quantifying vitamin C concentrations from various commercial juices, determining pH of various solutions using an indicator extracted from red cabbage, etc (2000-2005).

K. NON-SCIENTIFIC REPORTS COMMENTING ON OUR RESEARCH

The Poly Post:
(Pomona, CA)

Livesay Leaves Cal Poly for North Carolina. The Poly Post is the independent student newspaper at Cal Poly Pomona. The article described our recent accomplishments and the fact that I was leaving Cal Poly Pomona for a new position at UNC Charlotte (April 11, 2006).

The Republic:
(Columbus, IN)

East Grad's Chemistry Skills Focused on Battling Diseases. The Republic is the only daily newspaper in Columbus, IN. The article described my current work, our successes and the influences of my high school and community college teachers on my career development (April 6, 2006).

PolyTrends:
(Pomona, CA)

More Than Innovative, Research Center is Surprisingly Interdisciplinary. PolyTrends is a bi-annual publication of Cal Poly Pomona Development Office designed to highlight "excellence on campus." The article described the Center for Macromolecular Modeling & Materials Design and our recent W.M. Keck Foundation grant (January, 2006).

The New Straight Times:
(Kuala Lumpur)

Expert to Discuss Bioinformatics in KL. The New Straight Times is the leading English-language paper in Malaysia. The article briefly described my Bioinformatics Short Course at Technology Park Malaysia (May 5, 2005).

Panorama:
(Pomona, CA)

Taking a Byte out of Complex Research. Panorama is a quarterly community newsletter published by the Cal Poly Pomona Development Office. This article described our funded NSF-MRI grant, which allowed us to create a new state-of-the-art computer lab and a 64-CPU research cluster (Winter, 2004)