BIOGRAPHICAL SKETCH

NAME:	**Thomas E. Cheatham, III**
eRA COMMONS USER NAME:	**cheatham**
POSITION TITLE:	**Professor & Director of Research Computing and CHPC, UIT**

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

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
Middlebury College, Middlebury, VT.	B.A.	03/1989	Chemistry (honors)
Middlebury College, Middlebury, VT.	B.A.	03/1989	Math & Comp. Sci.
University of California, San Francisco, CA.	Ph.D.	05/1997	Pharmaceutical Chem.
NHLBI, National Institutes of Health	[postdoc]	12/1999	Comp. Biophysics

A. Personal Statement

Our lab is deeply interested and driven to understand biomolecular structure, flexibility and dynamics, and their relation to function, design and drug-ability. Our main approach is the application and development of biomolecular simulation methods, including molecular dynamics (MD), estimation of free energies, enhanced sampling, and detailed analysis of results. We aim to accurately model biomolecular structure and dynamics, to validate and assess the results, and to improve the molecular mechanical force fields. Exploration is enabled through large-scale simulation—using local, national and special purpose hardware (including extensive allocations of computer time on the Frontera system at TACC and various NSF XSEDE resources). Training is a critical component of our research efforts since few students have sufficient background in structural biology, high performance scientific computing and code development, and chemistry required to perform our research. Our lab has mentored high school students from Judge Memorial and also the Juan Diego Summer program, a number of undergraduate volunteers, graduate students and postdocs throughout the years at Utah.

Working together, we have exposed serious problems with the force fields for nucleic acids and overcome a number of these. We have also demonstrated the ability to reproducibly—from independent initial conditions—fully converge the conformational and dynamic distribution of tetranucleotides, RNA tetraloops, and the internal portions of DNA helices. The methods also prove, when coupled with NMR derived restraints (distance, torsion, residual dipolar coupling), extremely capable of finding structures that well satisfy the experimental data and overcome force field limitations. As one can model anything, a critical aspect is assessment and validation of the results and we do this with a number of experimental groups. Also, as a principal AMBER developer and the main lab developing the analysis codes “ptraj” and “cpptraj”, we access the latest methods.

B. Positions and Honors

Positions and Employment

1988—1990 Programmer/Analyst, Division of Applied Sciences, Harvard University, Cambridge, MA.
1997—2000 National Research Council Research Associate, NHLBI, NIH, Advisor: Bernard Brooks, PhD
1/00—7/02 Research Assistant Professor, Department of Medicinal Chemistry, University of Utah
7/00—6/19 Adjunct Assistant Professor, Department of Bioengineering, University of Utah
7/02—6/09 Assistant Professor, Department of Medicinal Chemistry, University of Utah (60%)
7/02—6/09 Assistant Professor, Dept. of Pharmaceutics and Pharmaceutical Chem., U of Utah (40%)
7/19— Adjunct Professor, Department of Bioengineering, University of Utah
7/09— Associate Professor, Department of Medicinal Chemistry, University of Utah (60%)
7/09—7/11 Associate Professor, Dept. of Pharmaceutics and Pharmaceutical Chem., U of Utah (40%)
7/11—6/14 Associate Professor and Director of Graduate Studies, Department of Medicinal Chemistry
7/14— Professor and Director of Graduate Studies (-2017), Department of Medicinal Chemistry and Director, Research Computing & Center for High Performance Computing, U of Utah IT

Other Experience and Professional Memberships

5/00—2/06	Associate/Assistant Editor, Molecular Modeling and Computational Chemistry Results
7/2001—	Member, Board of Editors, Journal of Biomolecular Structure and Dynamics
3/02—6/08	TeraGrid Resource Allocation Committee NSF Review Panels, Chair (2007, 2008)
11/2002	Site review team, DOE evaluation of EMSL at PNNL
3/2003	NIH Ad hoc reviewer on BBCA study section
2/2004	NIH Ad hoc reviewer on ZAI1 AR-M (M1) NIAID study section
10/05, 3/06	NIH Ad hoc reviewer on ZRG1 BCMB-Q Computational Biophysics study section
3/2006	NIH Ad hoc reviewer on ZRG1 F04B-A (20) Biophysics Fellowships study section
6/2006—	NSF Cyberinfrastructure User Advisory Committee / Teragrid Science Advisory Board
7/2008	NIH Ad hoc reviewer on ZRG1 BCMB-B (90) Special topics in biological sciences
2/09, 10/07	NIH Ad hoc reviewer on ZRG1 MSFD Computational Biophysics
6/2009	NIH Ad hoc reviewer on ZRG1 MSFD Computational Biophysics
6/2009	NIH Ad hoc reviewer on ZRG1 BCMB-P(58) RRFA-09-003 Challenge Grants, mail
10/2009—	Member, Board of Editors, *Journal of Molecular Modeling and Graphics*
6/2010	NIH Ad hoc reviewer on ZRG1 MSFD Computational Biophysics
6/2010—	President (2012-2014), Vice-president (2010-2012) Intl. Soc. of Quantum Bio. and Pharmacol.
7/2010—	National Institute of Computational Sciences User Advisory Committee, U Tennessee
9/10-7/11	Chair, Teragrid Science Advisory Board
3/2011	NIH NCI Intramural lab site review team
4/2011	External thesis examiner, University of Bergen, Norway
7/11-6/15	NIH Charter Member ZRG1 MSFD study section
3/2012	NIH Ad hoc reviewer ZHJ1 F04 Fellowship panel: Chem, Biochem, Biophys, Bioeng F30-33
3/2012	NSF OCI Review Panel
1/12—	NSF XSEDE User Advisory Committee, Chair (2012-2015)
6/12—	NSF XSEDE Science Advisory Board
6/12—5/15	NSF XSEDE Senior Management Team
2012	Supercomputing12 Program Committee
2012—	International HPC Summer School, Organizing Committee and Mentor
10/12,5/13	NSF CHE/OCI Review Panel
9/12-8/14	University of Utah Academic Senate
2012—	University of Utah Cyberinfrastructure and Research Computing Governance, Chair
2013—	XSEDE ’14 Technical Program Committee, Science Track Chair
2013-2016	Scientific Advisory Committee of the Swedish National Infrastructure for Computing
10/2013	NIH ZRG1 MID-B NIAID Study Section
1/14,12/14	Great Lakes Consortium for Petascale Computation Blue Waters Allocations Review Panel
3/2014	NSF Review Panel, CHE
2014—	U. Illinois Blue Waters Petascale Resource Science and Engineering Team Advisory Committee
2014—	Supercomputing 14/15/16 Education Program Executive Committee
2014—	Blue Waters Science and Engineering Team Advisory Committee (SETAC)
2015-2021	Utah Education Network Advisory Council
2017	Advanced Research Computing on Campuses (ARCC) @ PEARC17, Chair
2017-2018	Rocky Mountain Advanced Computing Consortium (RMACC), Vice Chair, Board Member 2018-
2016—	Campus Research Computing Consortium (CaRCC), Interim Chair (2016-2017), Council Chair
2018—	Center for Computational Engineering and Sciences, UNICAMP, Brazil, Intl Advisory Board
2018—	Internet2 E-CAS “Exploring Cloud for Acceleration of Science” Advisory Board
10/19	NIH ZRG1 MSFD study section

Honors

1994-1995	UCSF Department of Pharmaceutical Chemistry Award for Outstanding Service
1995-1996	UCSF Pharmacy School, Frank Goyan Award for Excellence in Achievement in Phys. Chem.
1995-1996	UCSF Chancellor's Graduate Research Fellow
1998	Finalist, Computerworld-Smithsonian Awards in the category of science
2005-2010	Nominated for College of Pharmacy Teaching Award, University of Utah
2007	Hewlett-Packard Outstanding Junior Faculty Award, ACS COMP division
2012-2013	University of Utah College of Pharmacy P2 Teacher of the Year

C. Contribution to Science

Full biography: http://scholar.google.com/citations?user=fCEXKK4AAAAJ

(1) **Reproducibility and convergence in simulations of biomolecules**: Thanks to considerable access to large-scale parallel, GPU, and special-purpose computational resources, optimization of the codes, and application of enhanced sampling and ensemble methods, the Cheatham lab has shown the ability to nearly "converge" the conformational distributions of a number of biomolecular systems, including RNA tetranucleotides, the internal helices of DNA duplexes, and RNA tetraloop structures, in addition to modeling the influence of ions on the conformational distributions. Although it is nearly impossible to *prove* convergence, the results are compelling and demonstrate that independent simulations with different codes or vastly different initial conditions give reproducible results, equivalent distributions of conformations sampled, and nearly equivalent principal modes of motion.

- R Galindo-Murillo, DR Roe, and TE Cheatham, III. "Convergence and reproducibility in molecular dynamics simulations of the DNA duplex d(GCACGAACGAACGAACGC)." *Biochimica Biophys. Acta* 1850, 1041-1058 (2015).
- R Galindo-Murillo, DR Roe, and TE Cheatham, III. "On the absence of intrahelical DNA dynamics on the μs to ms timescale." *Nature Commun.* 5:5152 (2014).
- C Bergonzo, N Henriksen, DR Roe, J Swails, AE Roitberg, and TE Cheatham, III. "Multi-dimensional replica exchange molecular dynamics yields a converged ensemble of an RNA tetranucleotide." *J. Chem. Theory Comp.* 10, 492-499 (2014).
- C Bergonzo, KB Hall, and TE Cheatham, III. "Stem-loop V of Varkud satellite RNA exhibits characteristics of the Mg^{2+} bound structure in the presence of monovalent ions." *J. Phys. Chem. B* 119, 12355-12364 (2015).

(2) **AMBER code and workflow development**: AMBER is a suite of programs for biomolecular simulation. With over 1000 site-licensed versions of the code per release, a large community of researchers uses AMBER. At present, an extremely useful feature is the extreme and optimized performance on GPU resources. AMBER implements a variety of enhanced sampling and free energy estimation methods and makes excellent use of ensembles of independent simulations, for example with replica-exchange MD.

- AMBER 18 (released April, 2018) and AmberTools 17 (April, 2017) available at http://ambermd.org.
- TE Cheatham, III and DR Roe. "The impact of heterogeneous computing on workflows for biomolecular simulation and analysis." *Computing in Science and Engineering* 17:2, 30-39 (2015).
- DA Case, TE Cheatham, III, TA Darden, H Gohlke, R Luo, KM Merz, Jr., A Onufriev, C Simmerling, B Wang, and R Woods. "The AMBER biomolecular simulation programs" *J. Comp. Chem.* 26, 1668-1688 (2005).
- DR Roe and TE Cheatham, III "Parallelization of CPPTRAJ enables large scale analysis of molecular dynamics trajectory data." *J. Comp. Chem.* 39, 2110-2117 (2018) doi:10.1002/jcc.25382.

(3) **Force fields for biomolecular simulation**: Since the early 90's, Cheatham has been involved in the development, assessment and validation of force fields for biomolecular simulation, most notably the nucleic acid and ion force fields in AMBER (http://www.ambermd.org). A large community uses AMBER to better understand biomolecular structure, dynamics, interactions, folding, and energetics, including widespread use in computer-aided drug-design and also structure refinement. The Cheatham group is known for pushing the methods to their limits and exposing and overcoming limitations in the force fields.

- C Bergonzo and TE Cheatham, III. "Improved force field parameters lead to a better description of RNA structure" J. Chem. Theory Comp. 11, 3969-3972 (2015).
- M Zgarbova, F Javier Luque, J Sponer, TE Cheatham, III, M Otyepka, and P Jurecka, "Toward improved description of DNA backbone: Revisiting epsilon and zeta torsion force field parameters." *J. Chem. Theory Comp.* 9, 2339-2354 (2013).
- In Suk Joung, and TE Cheatham, III. "Determination of alkali and halide monovalent ion parameters for use in explicitly solvated biomolecular simulations" *J. Phys. Chem. B* 112, 9020-9041 (2008).
- TE Cheatham, III, P Cieplak & PA Kollman. "A modified version of the Cornell *et al.* force field with improved sugar pucker phases and helical repeat." *J. Biomol. Struct. Dyn.* 16, 845-862 (1999).

(4) **Molecular dynamics trajectory analysis and dissemination methods**: Since the early 90's, Cheatham has been involved in the development of the MD trajectory analysis methods in AMBER. The current codes developed by our group are open-source, freely available, and applicable to MD trajectories from most of the common MD simulation codes. A wide variety of analysis methods are enabled and applicable to both internal and external data-sets in the programs "ptraj" and CPPTRAJ. These codes used by a large community of users to better interpret their simulation results. In addition, the Cheatham lab has developed methods to automatically annotate the simulation results, and to search and disseminate the results.

- JC Thibault, DR Roe, JC Facelli, and TE Cheatham, III. "Data model, dictionaries, and desiderata for biomolecular simulation data indexing and sharing." *J. Cheminformatics* 6 (2014).
- R Galindo-Murillo, C Bergonzo, and TE Cheatham, III. "Molecular modeling of nucleic acid structure: Setup and analysis." *Current Protocols Nucleic Acid Chemistry* 56: 7.10.1-7.10.21 (2014).
- DR Roe and TE Cheatham, III. "PTRAJ and CPPTRAJ: Software for processing and analysis of molecular dynamics trajectory data." *J. Chem. Theory Comp.* 9, 3084-3095 (2013).
- JC Thibault, JC Facelli, and TE Cheatham, III. "iBIOMES: Managing and sharing biomolecular simulation data in a distributed environment." *J. Chem. Inf. Model.* 53, 725-736 (2013).

(5) **Nucleic acid and protein simulation**: Cheatham has considerable experience in the application of biomolecular simulation methods to nucleic acids and focuses on means to fully validate, assess, and improve the simulation results. He also provides training and learning materials, tutorials, and guides on how to perform reliable simulations of nucleic acids.

- JC Robertson and TE Cheatham, III. "DNA backbone BI/BII distribution and dynamics in E2 protein-bound environment determined by molecular dynamics simulation." *J. Phys. Chem. B* 119, 14111-14119 (2015).
- R Galindo-Murillo, C Bergonzo, and TE Cheatham, III. "Molecular modeling of nucleic acid structure." *Current Protocols Nucleic Acid Chemistry* 54: 7.5.1-7.5.13 (2013). See also three additional education units in this series.
- TE Cheatham, III and DA Case. "Twenty-five years of nucleic acid simulations." Biopolymers 99, 969-977 (2013).
- TE Cheatham, III & PA Kollman. "Molecular dynamics simulations of nucleic acids". Ann. Rev. Phys. Chem. 51, 435-471 (2000).

D. Additional Information: Research Support and/or Scholastic Performance

ACTIVE

University of Texas at Austin (10/01/19-9/34/24) ***"Portable applications driven approach to scalability on Frontera and future exascale systems"***
PI: Berzins, sub-contract to NSF OAC-1818253, PI: Stanzione.

This is a subcontract for Frontera support.

NIH R01 GM-081411 (9/23/19-8/30/23) ***"Biomolecular simulation for the end-stage refinement of nucleic acid structure"***
PI: Cheatham.

Core NIH grant for assessment, validation and improvement of force fields for nucleic acids and experimental and computational ensembles of model RNA systems.

NSF OAC-1659425 (4/01/17-3/31/20) ***"CC* Cyber Team: Creating a Community of Regional Data and Workflow Cyberinfrastructure Facilitators"***
PI: Hauser, Co-PIs: Burns, Williams, Siegel, and Cheatham.

This is a collaborative grant for data facilitation in the region with Colorado State U and U Colorado Boulder as partners.

NSF OAC-19196675 (10/01/19-9/30/22) ***"MRI: Development of ACCORD, a Community Cyberinstrument for Broadening Access to Research on Sensitive Data"***
PI: Hutchins (UVa), Co-PIs: Sosonkina, Crawford, Midkiff, and Cheatham.

This $2.5M equipment grant is for a compute infrastructure for U of Virginia and partners for research on protected or sensitive data and Cheatham serves as a consultant.

COMPLETED WITHIN PAST THREE YEARS:

NSF ACI-1443054 (10/01/15 to 9/30/19) ***"CIF21 DIBBS: Middleware and high performance analytics libraries for scalable data science."***
PI: Cheatham; sub-contract from U Indiana (G. Fox, PI).

Development of software tools to support data analytics.

NSF- OCI-1036208 (2/01/11-7/31/19) ***"PRAC- Hierarchical molecular dynamics sampling for assessing pathways and free energies of RNA catalysis, ligand binding, and conformational change."***
PI: Cheatham, Co-PIs: Simmerling (Stony Brook U), Case (Rutgers), Roitberg (U Fl), York (Rutgers)

This is a travel grant for collaboration to enable use of the Blue Waters computational platform at U Illinois. We received a 12 million node hour allocation per year on this resource. In NCE without allocation since 7/31/18.

NIH S10OD021644 (4/01/17 to 3/31/18) ***"From genomics to natural language processing: A protected environment for research computing in the health sciences"***
PI: Cheatham

A large compute environment for protected or restricted data with HPC, storage, VM, analytics and strong security.

NSF ACI-1341935 (3/01/14-8/31/18) ***"Advanced Cyberinfrastructure – Research and Educational Facilitation: Campus-based computational research support"*** PI: Bottum (Clemson U), Utah PI: Cheatham.

This is funding for the ACI-REF (research and education facilitators) program at ~six universities.

NSF XSEDE MCA01S027 (10/01/16-9/30/17, renewed annually) ***"Insight into biomolecular structure, dynamics, interactions, and energetics from simulation"***, PI: Cheatham

This is a large XRAC computer allocation that provides computational support (~12,000,000 core hours for 2015 for the research in the Cheatham lab. Renewed annually. Overlap: Provides computational hours.

NSF ACI-1521728 (4/01/15-3/30/17) ***"RAPID: Optimizing experimental approaches to Ebola membrane fusion inhibitor peptide design through high-throughput biomolecular simulation workflows on Blue Waters."*** PI: Cheatham.

A RAPID award for computationally modeling and design novel peptidic viral membrane fusion inhibitors.

NSF ACI-1338155 (9/01/13 to 8/31/17) ***"MRI: Development of Apt, a testbed instrument with adaptable profiles for network and computational science."*** PI: Ricci (Utah), Co-PI: Cheatham

Major goals: This is for a computational cluster / test bed at the University of Utah. Co-PIs: van der Merwe, Corbato, Eide, and Facelli. Cheatham is Co-PI.