

# Hai Minh Nguyen

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BioMaPS Institute, Rutgers University, Piscataway, NJ 08854  
Cell: (631) 512-0455, Email: [hainm.comp@gmail.com](mailto:hainm.comp@gmail.com), Website: <http://hainm.github.io/>

## EDUCATION

<i>Doctor of Philosophy, Chemistry</i> Stony Brook University, 2014 Advisor: <a href="#">Carlos Simmerling</a>	<i>Bachelor of Science, Chemistry</i> Hanoi University of Science, 2006
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## EXPERIENCE

<i>Postdoctoral Associate</i> Rutgers University, PI: <a href="#">David A. Case</a> <ul style="list-style-type: none"><li>• Developing PHENIX/AMBER interface for protein refinement with alternative conformation</li><li>• Applied new Generalized Born solvation models and a Python-based API for recombining Rosetta and Amber force fields for improving structure prediction and design</li><li>• Developing softwares (pytraj, nglview) for molecular dynamics simulation data analysis and visualization</li></ul>	03/2015-present
<i>Postdoctoral Associate</i> Stony Brook University, PI: <a href="#">Carlos Simmerling</a> <ul style="list-style-type: none"><li>• Added code and introduced newly optimized Generalized-Born solvation parameters for nucleic acid simulation to AMBER suite program</li></ul>	11/2014-2/2015
<i>Research Assistant</i> Stony Brook University, PI: <a href="#">Carlos Simmerling</a> <ul style="list-style-type: none"><li>• Developed solvent model for protein and nucleic acid simulations</li><li>• Developed and validated force field</li><li>• Improved salt bridge description for HIV-1 protease simulation</li></ul>	2018-2014

## COMPUTER SKILLS

*Languages:*

- Proficient: Python
- Experience: Javascript, C/C++, FORTRAN

*Others:*

- GIT, software continuous integration, parallel programming (MPI, multiprocessing), AMBER, VMD, PyRosetta, rdkit, docker, Linux, OSX

## RELEASED SOFTWARE

*Lead developer:*

- pytraj: Python API for cpptraj: a data analysis package for biomolecular simulation  
<https://github.com/Amber-MD/pytraj>
- pymdgm: Python API for mdgm simulation package  
<https://github.com/Amber-MD/pymdgm>
- nglview: Jupyter widget to interactively view molecular structures and trajectories,  
<https://github.com/AROSE/nglview>

*Contributing:*

- AMBER program suite: biomolecular simulation program,  
<http://ambermd.org>
- cpptraj: Biomolecular simulation trajectory/data analysis,  
<https://github.com/Amber-MD/cpptraj>
- parmed: Parameter/topology editor and molecular simulator,  
<https://github.com/ParmEd/ParmEd>
- MDAnalysis: an object-oriented python toolkit to analyze molecular dynamics trajectories,  
<http://www.mdanalysis.org/>

## PUBLICATIONS

*Google Scholar statistics (210 citations):* <http://goo.gl/CpC2zg>

*Peer Review*

1. **Nguyen, H.**; Prez, A.; Bermeo, S.; Simmerling, C., (2015) Refinement of Generalized Born Implicit Solvation Parameters for Nucleic Acids and Their Complexes with Proteins. *J Chem Theory Comput.*
2. **Nguyen, H.**; Maier, J.; Huang, H; Perrone, V; Simmerling, C., (2014) Folding simulations for proteins with diverse topologies are accessible in days with a physics-based force field and implicit solvent. *Journal of the American Chemical Society.*
3. **Nguyen, H.**; Roe, D. R.; Simmerling, C., (2013) Improved Generalized Born Solvent Model Parameters for Protein Simulations. *Journal of Chemical Theory and Computation*, 9 (4), 2020-2034.
4. Shang, Y., **Nguyen, H.**, Wickstrom, L., Okur, A., and Simmerling, C. (2011) Improving the description of salt bridge strength and geometry in a Generalized Born model, *Journal of Molecular Graphics and Modeling* 29, 676-684.

*Software*

1. **H. Nguyen**, A. Rose, D. Dotson, M.K. Scherer, ngview v0.5,  
<http://dx.doi.org/10.5281/zenodo.55409>
2. **H. Nguyen**, D.R. Roe, J. Swails, D.A. Case, (2016) PYTRAJ v1.0.0.dev1: Interactive data analysis for molecular dynamics simulations.  
<http://dx.doi.org/10.5281/zenodo.44612>
3. D.A. Case, R.M. Betz, W. Botello-Smith, D.S. Cerutti, T.E. Cheatham, III, T.A. Darden, R.E. Duke, T.J. Giese, H. Gohlke, A.W. Goetz, N. Homeyer, S. Izadi, P. Janowski, J. Kaus, A. Kovalenko, T.S. Lee, S. LeGrand, P. Li, C. Lin, T. Luchko, R. Luo, B. Madej, D. Mermelstein, K.M. Merz, G. Monard, **H. Nguyen**, H.T. Nguyen, I. Omelyan, A. Onufriev, D.R. Roe, A. Roitberg, C. Sagui, C.L. Simmerling, J. Swails, R.C. Walker, J. Wang, R.M. Wolf, X. Wu, L. Xiao, D.M. York and P.A. Kollman (2016), AMBER 2016, University of California, San Francisco.
4. A. Case, J.T. Berryman, R.M. Betz, D.S. Cerutti, T.E. Cheatham, III, T.A. Darden, R.E. Duke, T.J. Giese, H. Gohlke, A.W. Goetz, N. Homeyer, S. Izadi, P. Janowski, J. Kaus, A. Kovalenko, T.S. Lee, S. LeGrand, P. Li, T. Luchko, R. Luo, B. Madej, K.M. Merz, G. Monard, P. Needham, **H. Nguyen**, H.T. Nguyen, I. Omelyan, A. Onufriev, D.R. Roe, A. Roitberg, R. Salomon-Ferrer, C.L. Simmerling, W. Smith, J. Swails, R.C. Walker, J. Wang, R.M. Wolf, X. Wu, D.M. York and P.A. Kollman (2015), AMBER 2015, University of California, San Francisco.

## CONTRIBUTED TALKS

1. Pytraj, ngview: bring AmberTools to Python ecosystem, University of California, San Francisco, 03/2016.
2. Improved generalized Born solvent model parameters for protein and nucleic acid simulations, Icahn School of Medicine at Mount Sinai, 08/2014 (invited speaker)
3. Improved generalized Born solvent model parameters for protein and nucleic acid simulations, Memorial Sloan Kettering, 02/2014 (invited speaker)
4. Implicit solvent developments in AMBER. AMBER developer meeting, Stony Brook University, 01/2014.
5. Improved Generalized Born solvent model parameters for protein and nucleic acid simulations, Hai Nguyen, Carlos Simmerling, 244th ACS conference, Philadelphia, 08/2012.

## SELECTED POSTERS

1. Hai Nguyen, Daniel R. Roe, Jason Swails, David A. Case, "Pytraj: Interactive data analysis for molecular dynamics simulations", Biophysical Society 60th Annual Meeting, February 29, 2016.
2. Hai Nguyen, James Maier, He Huang, Victoria Perrone, Alberto Perez, Carlos Simmerling, Simulating protein and nucleic acid dynamics on the microsecond to millisecond timescale, Biophysical Society 59th Annual Meeting, February 8, 2015.
3. Hai Nguyen, James Maier, He Huang, Victoria Perrone, Alberto Perez, Carlos Simmerling, Simulating protein and nucleic acid dynamics on the microsecond to millisecond timescale, The New York Structural Biology Discussion Group 10th Winter Meeting, January 21, 2015.
4. Hai Nguyen, James Maier, He Huang, Victoria Perrone, Alberto Perez, Carlos Simmerling, Simulating protein and nucleic acid dynamics on the microsecond to millisecond timescale, Stony Brook University Chemistry Research Day, October 31, 2014.
5. Hai Nguyen, James Maier, He Huang, Victoria Perrone, Alberto Perez, Carlos Simmerling, Simulating protein and nucleic acid dynamics on the microsecond to millisecond timescale, Stony Brook University ICBDD 8th Annual Symposium, October 9, 2014.
6. Hai Nguyen, Daniel R. Roe, Lauren Wickstrom, Carlos Simmerling, Improvement of an Implicit Solvent Model, workshop "From Computational Biophysics to Systems Biology (CBSB12)", Knoxville, June 3, 2012
7. Hai Nguyen, Daniel R. Roe, Lauren Wickstrom, Carlos Simmerling, Improvement of an Implicit Solvent Model, ACS conference, Boston, August 24, 2010
8. Hai Nguyen, Daniel R. Roe, Carlos Simmerling, An Improvement of Implicit Solvent Model, Chemistry Research Day, Stony Brook University, November 13, 2009
9. Hai Nguyen, Daniel R. Roe, Carlos Simmerling, An Improvement of Implicit Solvent Model, 3rd Annual ICBDD Symposium, Stony Brook University, October 6, 2009
10. Hai Nguyen, Daniel R. Roe, Carlos Simmerling, An Improvement of Implicit Solvent Model, Inaugural Symposium for the Laufer Center for Computational Biology and Genome Sciences, Stony Brook University, September 25, 2009

**ACADEMIC  
REFERENCES**

**David A. Case**

Professor  
Rutgers University  
Piscataway, NJ  
david.case@rutgers.edu  
<http://casegroup.rutgers.edu>

**Carlos Simmerling**

Professor  
Stony Brook University  
Stony Brook, NY  
carlos.simmerling@gmail.com  
<http://simmerlinglab.org>

**Sagar D. Khare**

Assistant Professor  
Rutgers University  
Piscataway, NJ  
khare@chem.rutgers.edu  
<http://sagardkharelaboratory.org/>