

BIOGRAPHICAL SKETCH

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NAME: Lin Li

eRA COMMONS USER NAME (credential, e.g., agency login): LINLI5

POSITION TITLE: Assistant Professor of Physics

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 (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Huazhong University of Science & technology (China)	B.S.	05/2005	Applied Physics
Huazhong University of Science & technology (China)	Ph.D.	03/2011	Biophysics
Clemson University (Clemson, U.S.)	Postdoctoral	07/2013	Molecular Biophysics

A. Personal Statement

I have strong biophysics background as well as solid computer science background, which enable me to develop and improve Biology models from the view of Physics, then implement novel models into computational approaches. During my Ph.D. career, I developed software packages such as ASPDock and SRM (Soft Restrict Method). After I joined in Dr. Alexov's group as a Postdoc Fellow in Clemson, I developed many new algorithms and tools in DelPhi software, such as Gaussian smooth method and MEMPOT (MEMbrane Potential). Working at The University of Texas at El Paso, my research group has developed some novel computational tools, such as structure manipulation package, and web servers to study important biology problems. These new development results in three intellectual properties. I have finished a variety of projects in which I used numerical approaches to study important biological problems. My research interests include virus capsid assembly, protein-protein/DNA/RNA interactions, multiple simulations of molecular motors, etc. Working as computational biophysicist, I have plenty of experience on collaborating with experimental scientists to achieve scientific goals. My expertise and experience show strong evidence of successful achievements for numerical simulations of virus capsid assembly. In the proposed basic research project, my numerical simulations will work with experimental results to reveal the virus capsid assembly mechanisms at the atomic level.

1. **Lin Li**, Li C, Sarkar S, Zhang J, Witham S, Zhang Z, Wang L, Smith N, Petukh M, Alexov E.* ***DelPhi: a comprehensive suite for DelPhi software and associated resources***, *BMC Biophys*, (2012) May14;4(1):9.
2. **Lin Li**, Chuan Li, Zhe Zhang, Emil Alexov, ***On the Dielectric "Constant" of Proteins: Smooth Dielectric Function for Macromolecular Modeling and Its Implementation in DelPhi***, *J Chem Theory Comput*. 2013 Apr 9;9(4):2126-2136.
3. **Lin Li**, Dachuan Guo, Yangyu Huang, Shiyong Liu, Yi Xiao*, ***ASPDock: protein-protein docking algorithm using atomic solvation parameters model***, *BMC Bioinformatics*, 2011, 12(1): 36.

4. **Lin Li**, Zhe Jia, Yunhui Peng, Arghya Chakravorty, Lexuan Sun, and Emil Alexov. **DelPhiForce web server: electrostatic forces and energy calculations and visualization**. *Bioinformatics* (2017).

B. Positions and Honors

Positions and Employment

- 2005 – 2011 Research Associate, Department of Physics and Astronomy, Huazhong University of Science and Technology, China
- 2011 – 2013 Postdoctoral Fellow, Department of Physics and Astronomy, Clemson University
- 2013 – 2017 Research Associate, Department of Physics and Astronomy, Clemson University
- 2017 – Assistant Professor, Department of Physics, University of Texas at El Paso

Honors

- 2002: The First Prize Scholarship in Huazhong University of Science and Technology
- 2002: National Scholarship from Ministry of Education of the P.R. China (top 0.2% in China)
- 2003-2004: Individual Scholarship in Huazhong University of Science and Technology (2 Consecutive years)
- 2005-2009: Excellent Leader of Student Groups in University in Huazhong University of Science and Technology (4 Consecutive years)
- 2011: National Scholarship from Ministry of Education of the P.R. China (top 0.2% in China)
- 2016: FASEB (Federation of American Societies for Experimental Biology) MARC Travel Award

C. Contribution to Science

1. One of my main achievements is the development of new models and algorithms for DelPhi software, which is very widely used software by many biophysics and biochemistry groups around the world to do the energy calculation for biomolecules. I have successfully developed many new algorithms to improve the performance of DelPhi. These developments result in three intellectual properties. One of the new algorithms is called Gaussian smooth algorithm, which models the protein as inhomogeneous material thus more accurate than the previous algorithms. These novel algorithms improve the accuracy of energy calculations for biomolecules, which is important for protein-protein interactions, protein folding, drug design and many other fields.

- a) **Lin Li**, Li C, Sarkar S, Zhang J, Witham S, Zhang Z, Wang L, Smith N, Petukh M, Alexov E.* **DelPhi: a comprehensive suite for DelPhi software and associated resources**, BMC Biophys, (2012) May14;4(1):9.
- b) **Lin Li**, Chuan Li, Zhe Zhang, Emil Alexov, **On the Dielectric "Constant" of Proteins: Smooth Dielectric Function for Macromolecular Modeling and Its Implementation in DelPhi**, J Chem Theory Comput. 2013 Apr 9;9(4):2126-2136.
- c) **Lin Li**, Chuan Li, Emil Alexov, **On the Modeling of Polar Component of Solvation Energy Using Smooth Gaussian-Based Dielectric Function**, Journal of Theoretical and Computational Chemistry, 2014.
- d) (book chapter) Brandon Campbell, **Lin Li**, Emil Alexov, & Ohshima, H. (2016). **Dielectric Properties of Biological Macromolecules and Biomolecule–Water Interfaces**. Encyclopedia of Biocolloid and Biointerface Science 2V Set, 380-390.

2. Another important work of mine is the parallelization of DelPhi. I worked on parallelizing DelPhi to be able to perform the energy calculations on large and complex systems, such as adeno-associated virus, which contains more than a million atoms. Using parallelized DelPhi and hundreds of CPUs, I obtained the periodical and symmetric distribution of electrostatic potential around the entire adeno-associated virus. Such symmetric electrostatic potential distribution indicates that the electrostatic forces play an important role in virus capsid assembly. Those electrostatic features around the whole capsid of a virus are important to reveal the

mechanisms of virus capsid assembly and essential for anti-virus drug design. The parallelized DelPhi is also used on membranes, which reveals the electrostatic features of large pieces of membranes.

- a) Chuan Li, Lin Li, Jie Zhang, Alexov E. *, **Highly efficient and exact method for parallelization of grid-based algorithms and its implementation in DelPhi**, J Comput Chem. (2012)
- b) Lin Li, Lin Wang, Emil Alexov, **On the energy components governing molecular recognition in the framework of continuum approaches**, Frontiers in Molecular Biosciences 2 (2015): 5.
- c) Roberta Dias[§], Lin Li[§], Thereza A. Soares and Emil Alexov, **Modeling the Electrostatic Potential of Asymmetric Lipopolysaccharide Membranes: The MEMPOT Algorithm Implemented in DelPhi**, Journal of computational chemistry (2014). ([§] contributed equally)
- d) Chuan Li, Lin Li, Marharyta Petukh, Emil Alexov, **Progress in developing Poisson-Boltzmann equation solvers**, Molecular Based Mathematical Biology. Volume 1, Pages 42-62

3. I have also developed a docking algorithm (ASPDock) to calculate binding free energy of protein-protein and protein-DNA complexes, which improves the accuracy of the complex structure predictions. ASPDock gives very good success rate in a large set of benchmarks. Besides ASPDock, I developed a Softly Restricting Method which uses biological information to enhance the success rate of protein-protein interaction predictions. Using ASPDock and Softly Restricting Method, I and my team have participated in two rounds of Critical Assessment of PRediction of Interactions (CAPRI). We got high-quality hits for T40 and T41 and the best LRMSD were 2.35 Å and 1.41 Å, respectively. (ranking 6th in 40+ teams).

- a) Lin Li, Dachuan Guo, Yangyu Huang, Shiyong Liu, Yi Xiao*, **ASPDock: protein-protein docking algorithm using atomic solvation parameters model**, BMC Bioinformatics, 2011, 12(1): 36.
- b) Lin Li, Yanzhao Huang, and Yi Xiao, **How to Use Not-Always-Reliable Binding Site Information in Protein-Protein Docking Prediction**, PloS one 8.10 (2013)
- c) Huang, Yangyu, Shiyong Liu, Dachuan Guo, Lin Li, and Yi Xiao. **A novel protocol for three-dimensional structure prediction of RNA-protein complexes**, Scientific reports 3 (2013).

4. Another research direction of mine is the study of important biological systems, such as molecular motors. Molecular motors are extremely important proteins, which are involved in various of functions, such as organelle transport, cytoskeleton dynamics, cell movements and signal transduction. Dysfunctions of molecular motors lead to many human diseases. I have revealed important fundamental mechanisms of molecular motors. For example, one of my recent studies is about dynein, which is a microtubule associate molecular motor. I found that the electrostatic force plays significant roles for dynein's binding to microtubule. The structures of dynein and microtubule result to elegant electrostatic interactions which make the dynein binding to microtubule in an accurate and robust way. With experimental evidences, I have also proved that the electrostatic binding energy is strongly related to the dynein's run length and velocity on microtubule. These findings are novel and exciting. These mechanisms of molecular motors are valuable for human health and fundamental research. The computational approaches I used in molecular motors are also capable of handling virus capsid assembly problems.

- a) Lin Li, Joshua Alper, and Emil Alexov, **Cytoplasmic dynein binding, run length, and velocity are guided by long-range electrostatic interactions**, Scientific Reports 6 (2016).
- b) Lin Li, Joshua Alper, and Emil Alexov. **Multiscale method for modeling binding phenomena involving large objects: application to kinesin motor domains motion along microtubules**, Scientific Reports, 6 (2016): 23249.
- c) Lin Li, Arghya Chakravorty, Emil Alexov. **DelPhiForce, a tool for electrostatic force calculations: Applications to macromolecular binding**, Journal of Computational Chemistry 38.9 (2017): 584-593.

- d) **Lin Li**, Zhe Jia, Yunhui Peng, Subash Godar, Ivan Getov, Shaolei Teng, Joshua Alper, and Emil Alexov. **Forces and Disease: Electrostatic force differences caused by mutations in kinesin motor domains can distinguish between disease-causing and non-disease-causing mutations.** *Scientific Reports* 7 (2017).

Complete List of Published Work in MyBibliography:

<https://www.ncbi.nlm.nih.gov/sites/myncbi/1NMpzOw8vZ9QM/bibliography/47532210/public/?sort=date&direction=ascending>

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

N/A