

John Eargle

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Objective

Research and development position utilizing my expertise in computational biology and bioinformatics.

Education

Ph.D. Biophysics and Computational Biology, University of Illinois at Urbana-Champaign, 2010
B.A. Computer Science / Plan II, University of Texas at Austin, 2001

Skills

Programming languages: C/C++, Java, Ruby, Perl, Python, Tcl, JavaScript, MySQL
Biomolecular modeling and simulation software: VMD, NAMD, Modeller, PropKa, APBS, X3DNA
Bioinformatics software: ClustalW, MAFFT, BLAST, USCS Genome Browser, PAUP*, STAMP, XRNA
Scientific and engineering software: Matlab, BLAS, LAPACK

Professional Experience

Postdoctoral Research Associate, Zaida Luthey-Schulten laboratory, 2010–present

Implemented NetworkView, a 3D network visualization plugin to VMD
Implemented contact-based potentials into NAMD
Mentored two graduate students resulting in two publications
Collaborated with experimentalists resulting in one publication

Graduate Research Assistant, Zaida Luthey-Schulten laboratory, 2004–2010

Implemented MultiSeq, a sequence/structure evolutionary analysis environment for VMD; >5000 users
Implemented sequence/structure bioinformatics library
Implemented VMD plugin to transform QM Hessian between internal and cartesian coordinates
Provided scientific and technical support to MultiSeq users

Volunteer Scientific Programmer, Robin Gutell laboratory, 2001–2003

Developed RNA secondary structure viewer
Compared automated vs. manual rRNA sequence alignments

Teaching Experience

TA, NIH Computational Biophysics Workshops, 2007–2011
TA, NSF Center for the Physics of Living Cells Summer School, UIUC, July 2010
TA, CHEM 470 Computational Chemical Biology, UIUC, Spring 2008
TA, NSF GK-12 Miniworkshop, UIUC, Mar. 2007

Selected Publications

Journal Articles (5 of 9)

Chen K., **Eargle J.**, Sarkar K., Gruebele M., and Luthey-Schulten Z., "The functional role of ribosomal signatures," *Biophysical Journal*, **99**, 3930–3940, 2010
Sethi A.*, **Eargle J.***, Black A., and Luthey-Schulten Z., "Dynamical networks in tRNA:protein complexes," *Proceedings of the National Academy of Sciences*, **106**, 6620–6625, 2009

Eargle J., Black A., Sethi A., Trabuco L., and Luthey-Schulten Z., "Dynamics of recognition between tRNA and elongation factor Tu," *Journal of Molecular Biology*, **377**, 1382–1405, 2008

Roberts E., **Eargle J.**, Wright D., and Luthey-Schulten Z., "MultiSeq: unifying sequence and structure data for evolutionary analysis," *BMC Bioinformatics*, **7**, 382, 2006

Eargle J., Wright D., and Luthey-Schulten Z., "Multiple Alignment of protein structures and sequences for VMD," *Bioinformatics*, **22**, 504–506, 2006

* equal contribution

Web Publications

Eargle J. and Luthey-Schulten Z., "NetworkView," UIUC, 2010,
<http://www.scs.illinois.edu/schulten/tutorials/network>

Magis A., Chen K., **Eargle J.**, Roberts E., and Luthey-Schulten Z., "Evolution of Translation: EF-Tu:tRNA," UIUC, 2009, <http://www.scs.illinois.edu/schulten/tutorials/ef-tu>

Magis A., Chen K., Mathew D., **Eargle J.**, and Luthey-Schulten Z., "Evolution of Translation: The Ribosome," UIUC, 2009, <http://www.scs.illinois.edu/schulten/tutorials/ribosome>

Roberts E., **Eargle J.**, Wright D., Dhaliwal B., Sethi A., O'Donoghue P., and Luthey-Schulten Z., "Evolution of Biomolecular Structure," UIUC, 2006,
http://www.scs.illinois.edu/schulten/tutorials/evolution_classII

Presentations

"Dynamic Interaction Networks in aaRS:tRNA," 2011 International Symposium on Aminoacyl-tRNA Synthetases, Salt Lake City, UT, Sep. 2011

"Simulation and Visualization of Dynamics in RNA:Protein Complexes in Translation," Santa Fe Institute Origins of Life Workshop, Fairfax, VA, June 2011

"Dynamic Signaling Networks of tRNA:Protein Complexes in Translation," Illinois Biophysical Society Symposium, Champaign, IL, May 2009

"Role of Signatures in Ribosomal Assembly," Center for the Physics of Living Cells Symposium, Urbana, IL, Feb. 2009

"Dynamics of Recognition between tRNA and Elongation Factor Tu," 22nd tRNA Workshop, Uppsala, Sweden, Nov. 2007

Press Coverage

"Researchers study signaling networks that set up genetic code," PhysOrg (Apr 2009),
<http://www.physorg.com/news158936293.html>

"Signaling networks that set up genetic code," ScienceDaily (Apr 2009),
<http://www.sciencedaily.com/releases/2009/04/090414141251.htm>

James E. Kloeppel, "Evolutionary software to be released free of charge," UIUC News Bureau (Sep 2006), <http://news.illinois.edu/news/06/0918software.html>

Honors and Awards

NSF Postdoctoral Fellowship, Center for the Physics of Living Cells, 2010–present

NIH Molecular Biophysics Training Grant, 2003–2007

Ullyott Fellowship, 2003

National Merit Scholarship, 1996–2000