

Pranjal Vachaspati

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EDUCATION

University of Illinois

PhD in Computer Science

Fall 2014 - Present

Urbana, IL

Computer Science: Algorithms, Parallel Computing, Sparse Numerical Techniques, Phylogenetics, Computational Complexity, Machine Learning, Bioinformatics, Combinatorial Optimization

MIT

B.S. in Physics

Class of 2014; 4.2 GPA

Cambridge, MA

Computer Science: Numerical Simulation, Computer Vision, Machine Learning, Computer Architecture, Complexity Theory

Physics: Solid State Physics, Junior Lab, Quantum Mechanics, Statistical Mechanics & Thermodynamics, Special Relativity, Electricity and Magnetism

Princeton University

High School Program

Jan 2009 - May 2010

Princeton, NJ

Computer Science: Systems Engineering, Algorithms and Data Structures

PUBLICATIONS

12. S. Christensen, E. Molloy, P. Vachaspati, and T. Warnow. “TRACTION: Fast non-parametric improvement of estimated gene trees”. WABI 2019.
11. P. Vachaspati and T. Warnow. “SVDquest: Improving SVDquartets species tree estimation using exact optimization within a constrained search space”. *Molecular Phylogenetics and Evolution*, 2018.
10. P. Vachaspati and T. Warnow (2018). SIESTA: Enhancing searches for optimal supertrees and species trees. *BMC Genomics*, 2018.
9. S. Christensen, E. Molloy, P. Vachaspati, and T. Warnow. “OCTAL: Optimal Completion of Gene Trees in Polynomial Time”. *Algorithms for Molecular Biology*, 2018.
8. P. Vachaspati and T. Warnow. “Enhancing Searches for Optimal Trees Using SIESTA”. *RECOMB International Workshop on Comparative Genomics*, 2017
7. S. Christensen, E. Molloy, P. Vachaspati, and T. Warnow. “Optimal Completion of Incomplete Gene Trees in Polynomial Time”. *17th International Workshop on Algorithms for Bioinformatics (WABI) 2017*.
6. B.M. Boyd, J.M. Allen, N.P. Nguyen, P. Vachaspati, Z.S. Quicksall, T. Warnow, L. Mugisha, K.P. Johnson, and D.L. Reed. “Primates, Lice, and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice”. *Molecular Biology and Evolution*, 2017.

5. J.M. Allen, B. Boyd, N.P. Nguyen, P. Vachaspati, T. Warnow, D.I. Huang, P.G. Grady, K.C. Bell, Q.C. Cronk, L. Mugisha, and B.R. Pittendrigh. “Phylogenomics from Whole Genome Sequences Using aTRAM”. *Systematic biology*, 2017. Vancouver
4. P. Vachaspati and T. Warnow. “FastRFS: Fast and accurate Robinson-Foulds Supertrees using constrained exact optimization”, *RECOMB-Comparative Genomics and Bioinformatics*, 2016.
3. P. Vachaspati and T. Warnow. “ASTRID: Accurate Species TREes from Internode Distances”, *RECOMB-Comparative Genomics and BMC Genomics*, 2015.
2. R. Davidson, P. Vachaspati, S. Mirarab, and T. Warnow. “Phylogenomic species tree estimation in the presence of incomplete lineage sorting and horizontal gene transfer”, *RECOMB-Comparative Genomics, and BMC Genomics*, 2015.
1. P. Vachaspati, W. Detmold (2014). “Fast Evaluation of Multi-Hadron Correlation Functions”. *LATTICE 2014*.
0. S. Li, P. Vachaspati, D. Sheng, N. Dural, M. V. Romalis. “Very large optical rotation generated by Rb vapor in a multi-pass cell”. *Phys. Rev. A* 84, 061403(R) (2011)

PRESENTATIONS

6. “Enhancing Searches for Optimal Trees Using SIESTA”. *RECOMB International Workshop on Comparative Genomics*, 2017, Barcelona, Spain.
5. “FastRFS: Fast and accurate Robinson-Foulds Supertrees using constrained exact optimization”, *RECOMB-Comparative Genomics 2016*, Montreal, Canada.
4. “ASTRID: Accurate Species TREes from Internode Distances”, *Evolution 2016*, Austin, TX.
3. “ASTRID: Accurate Species TREes from Internode Distances”, *RECOMB-Comparative Genomics 2015*, Frankfurt, Germany.
2. “Fast Evaluation of Multi-Hadron Correlation Functions”. *LATTICE 2014*, New York, NY.
1. “Multi-pass cells for quantum non-demolition Faraday rotation measurements in Rb vapor”, *DAMOP 2010*, Houston, TX.

PROFESSIONAL EXPERIENCE

- | | |
|--|-------------------|
| University of Illinois at Urbana-Champaign | Fall 2014-Present |
| <i>Research Assistant for Professor Tandy Warnow</i> | Urbana, IL |
| <ul style="list-style-type: none"> • Designed and evaluated methods for phylogenetic species tree estimation in the presence of various sources of gene tree incongruence | |
| AvaTech | Summer 2014 |
| <i>Data Consultant</i> | Cambridge, MA |
| <ul style="list-style-type: none"> • Developed signal processing techniques to reduce noise in avalanche safety equipment | |
| Milliman, Inc. | Summer 2014 |
| <i>Machine Learning Intern</i> | Cambridge, MA |
| <ul style="list-style-type: none"> • Analyzed machine learning techniques for life insurance pricing and underwriting | |

MIT Center for Theoretical Physics Fall 2012 - Summer 2014
Research Assistant for Professor Will Detmold Cambridge, MA

- Developed lattice quantum chromodynamics simulations on CPUs and GPUs
- Designed efficient evaluation strategies for computing multi-hadronic wavefunctions

Discovery Engine Summer 2011
Software Development Intern San Francisco, CA

- Developed infrastructure for general purpose web search and large-scale data manipulation, network filesystems, and compiler tools.
- Gained expertise in distributed systems, tools for working on large projects, and API design

Princeton University Department of Physics Summer 2008 - Summer 2010
Research Assistant for Professor Michael Romalis Princeton, NJ

- Investigated the use of optical multipass cells to improve the sensitivity of atomic magnetometers

AWARDS AND RECOGNITION

Graduate Research Fellowship 2016-2021
National Science Foundation **Ira and Debra Cohen Fellow** 2015-2016
University of Illinois at Urbana-Champaign College of Engineering Urbana, IL **Saburo Muroga Fellow** 2015-2016
University of Illinois at Urbana-Champaign College of Engineering Urbana, IL **Roy J. Carver Fellow** 2014-2015
University of Illinois at Urbana-Champaign College of Engineering Urbana, IL

SKILLS

Languages: C++, C, Python, Javascript, CSS, HTML, Go, Mathematica, MATLAB, Java, Haskell, Lex, Yacc, L^AT_EX, English, Hindi
Tools: Emacs, Git, Linux/Bash, GCC, GDB, GNU Make, Eclipse

Last Updated August 15, 2019.

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