

PETER T. HRABER
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EDUCATION

PhD in Biology, University of New Mexico (Albuquerque, NM) 2001.
Dissertation entitled “Discovering molecular mechanisms of mutualism with computational approaches to endosymbiosis”. Coadvisors: M.A. Nelson, UNM Biology, and J.W. Weller, George Mason University.

Participated in Lipari School for Computer Science Researchers (Italy) 1999.

MS in Biology, University of New Mexico (Albuquerque, NM) 1996.

MA in Liberal Arts, St. John’s College (Santa Fe, NM) 1991.

BFA *cum laude*, Rochester Institute of Technology (Rochester, NY) 1989.

EXPERIENCE

Postdoctoral Fellow, Santa Fe Institute (Spring 2001–Autumn 2002).
Collaborated to develop and validate novel computational solutions to problems in analysis of genome-scale data sets. Developed and applied methods for statistical inference using the minimum description length principle. Mentor: Tom Kepler (Duke University).

Computational Biologist, National Center for Genome Resources (Spring 1999–Autumn 2000).
Developed information and analysis systems to support functional genomics investigations and DNA sequencing in model plants and pathogens. Designed and implemented databases to store and analyze data from gene expression experiments and biomolecular structure. Reported progress of these projects to a variety of audiences. Completed “From the Laboratory to Leadership” training program. Participated in grant writing and project management.

Software Developer, National Center for Genome Resources (Autumn 1997–Spring 1999).
Designed and implemented analysis algorithms and database applications. Provided bioinformatics services via the internet using object-oriented development techniques. Coordinated group activities for several projects, including an analysis system for genome sequencing.

Research Assistant, University of New Mexico (Autumn 1994–Autumn 1997).

Developed and tested simulation algorithms. Presented analysis applications and results at conferences and in publications. Thesis project investigated the influence of ecological and evolutionary dynamics in model ecosystems using agent-based simulation. Other research areas included molecular evolution, RNA structure/function relations, species abundance distributions, spatial data analysis, multivariate analysis, and statistical inference.

Research Assistant, Santa Fe Institute (Autumn 1992–Autumn 1994).

Developed and tested simulation algorithms. Designed and conducted simulation experiments. Analyzed, summarized, and archived experimental data. Project involved implementing a genetic algorithm and other heuristic searches to evolve (or discover) cellular automata rules to perform computational tasks.

PUBLICATIONS

- P.T. Hraber, B.T. Korber, S. Wolinsky, H. Erlich, E. Trachtenberg, and T.B. Kepler. HLA and HIV infection progression: Application of the minimum description length principle to statistical genetics. Santa Fe Institute preprint #03-04-023. Submitted.
- E. Trachtenberg, B.T. Korber, C. Sollars, T.B. Kepler, P.T. Hraber, E. Hayes, R. Funkhouser, M. Fugate, J. Theiler, M. Hsu, K. Kunstman, S. Wu, J. Phair, H. Erlich, and S. Wolinsky. Advantage of rare HLA supertype in HIV disease progression. *Nature Medicine* 9:928-935, 2003.
- P.T. Hraber and J.W. Weller. On the species of origin: Diagnosing the source of symbiotic transcripts. *Genome Biology* 2(9):research37.1-37.14, 2001.
- D. Qutob, P.T. Hraber, B.W.S. Sobral, and M. Gijzen. Comparative analysis of expressed sequences in *Phytophthora sojae*. *Plant Physiology*, 123:243–254, 2000.
- M. Waugh, P.T. Hraber, J.W. Weller, Y. Wu, G. Chen, J. Inman, D. Kiphart, and B.W.S. Sobral. The *Phytophthora* genome initiative database: Informatics and analysis for distributed pathogen research. *Nucleic Acids Research* 28(1):87–90, 2000.
- E. Schultes, P.T. Hraber, and T.H. LaBean. Estimating the contributions of selection and self-organization in RNA secondary structure. *Journal of Molecular Evolution*, 49(1):76–83, 1999.
- E. Schultes, P.T. Hraber, and T.H. LaBean. A parameterization of RNA sequence space. *Complexity* 4:61–71, 1999.

- S. Kamoun, P.T. Hraber, B.W.S. Sobral, D. Nuss, and F. Govers. Initial assessment of gene diversity for the oomycete pathogen *Phytophthora infestans* based on expressed sequences. *Fungal Genetics and Biology*, 28:94–106, 1999.
- C. Harger, M. Skupski, J. Bingham, A. Farmer, S. Hoisie, P. Hraber, D. Kiphart, L. Krakowski, M. MacLeod, J. Schwertfeger, G. Seluja, A. Siepel, G. Singh, D. Stamper, P. Steadman, N. Thayer, R. Thompson, P. Wargo, M. Waugh, J.J. Zhuang, and P.A. Schad. The Genome Sequence DataBase (GSDB): Improving data quality and data access. *Nucleic Acids Research* 26(1):21–26, 1998.
- P.T. Hraber and B.T. Milne. Community assembly in a model ecosystem. *Ecological Modelling* 103:267–285, 1997.
- P.T. Hraber, T. Jones, and S. Forrest. The ecology of Echo. *Artificial Life* 3(3):165–190, 1997.
- E. Schultes, P.T. Hraber, and T.H. LaBean. Global similarities in nucleotide base composition among disparate functional classes of single-stranded RNA imply adaptive evolutionary convergence. *RNA* 3:808–822, 1997.
- B.T. Milne, A.R. Johnson, T.H. Keitt, C.A. Hatfield, J. David, and P.T. Hraber. Detection of critical densities associated with Pinyon–Juniper woodland ecotones. *Ecology* 77(3):805–821, 1996.
- M. Mitchell, J.P. Crutchfield, and P.T. Hraber. Evolving cellular automata to perform computations: Mechanisms and impediments. *Physica D* 75:361–391, 1994.
- M. Mitchell, P.T. Hraber, and J. P. Crutchfield. Revisiting the edge of chaos: Evolving cellular automata to perform computations. *Complex Systems* 7:89–130, 1993.

BOOK CHAPTER

- M. Mitchell, J.P. Crutchfield, and P.T. Hraber. Dynamics, computation, and the “Edge of chaos”: A re-examination. Pages 493–513 in G. Cowan, D. Pines, and D. Meltzer, *editors*. *Complexity: Metaphors, Models, and Reality*. Addison–Wesley, Reading, MA, 1994.

HONORS

- “Information-based models of complex ecological processes,” Invited keynote talk at the third meeting of the International Society for Ecological Informatics (Rome, Italy) 2002.
- Granted ESF travel award to participate in “From Genome to Life” International Summer School in Functional Genomics (Corsica, France) 2002.
- “Symbiosis and macroevolution,” Invited talk at International Workshop on Evolutionary Innovation (Prague, Czech Republic) 2002.
- Granted NSF travel award to attend “Artificial Intelligence and Heuristic Methods for Bioinformatics” Advanced Study Institute (Italy) 2001.
- “Community assembly in a model ecosystem,” Invited talk at University of Michigan (Ann Arbor, MI) 1997.

ACTIVITIES

- Member (2002) of International Societies for Computational Biology, Molecular Plant-Microbe Interactions, and Ecological Informatics, and the Santa Fe Institute Library Committee and Emergency Response Team.
- Mentored student working groups in genomics (2001) and immunology (2002) at the Santa Fe Institute Complex Systems Summer School.
- Guest-lectured and coordinated computational laboratory exercises for Biology 544, Genomes and Genome Analysis, Autumn 2000. Lectures and lab exercises were entitled “The why and how of sequence similarity searching” and “Putting it together with fragment assembly.”
- Mentored and collaborated with Allison Styer, undergraduate student of biology and computer science at Carnegie–Mellon University, during her summer (2000) internship at the National Center for Genome Resources. Her research topic was “Screening ESTs for secreted peptides with PexFinder.”
- Coordinated exercises and lectures for the laboratory component of Biology 322, Principles of Ecology, taught by Professor B.T. Milne, Department of Biology, University of New Mexico. Also guest-lectured in the main course on “Using the World-Wide Web as an ecological resource,” Autumn 1996.
- Reviewer for *Advances in Complex Systems*, *Artificial Life*, *Complex Systems*, *Complexity*, *Ecological Modelling*, *Evolutionary Computation*, and *Journal of Theoretical Biology*.