

Curriculum Vitae

Peter Hraber

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Education

- Postdoctoral Fellow Theoretical Biology & Biophysics, LANL 2006-8
- Postdoctoral Fellow Santa Fe Institute 2001-2
- PhD University of New Mexico 2001
- MS University of New Mexico 1997
- MA St. John's College 1991
- BFA *cum laude* Rochester Institute of Technology 1989

Employment Experience

Postdoctoral Fellow, T-10, Los Alamos National Laboratory (2006-present)

- Investigated techniques to analyze viral genomes and host-pathogen interactions.
- Developed network-accessible resources for pathogen signature discovery.
- Deployed methods for inferential testing of phylogenetic tree and network topologies.
- Documented and communicated findings, and prepared grant proposals.

Research Scientist, Exagen Diagnostics, Inc. (2004-2006)

- Used machine-learning methods to develop markers for clinical disease prognosis.
- Implemented information-system disaster recovery and HIPAA compliance policies.
- Managed desktop systems and built high-performance cluster.
- Collaborated to acquire, analyze, and archive clinical data.

Postdoctoral Fellow, Santa Fe Institute (2001-2002)

- Collaborated to develop computational solutions for challenges in systems biology.
- Developed methods for statistical genetics with information based selection criteria.
- Communicated results at meetings and in publications.

Computational Biologist, National Center for Genome Resources (1999-2000)

- Developed information systems for gene sequencing and functional genomics.
- Designed and built databases of biomolecular structure and gene expression.
- Communicated research findings at conferences and in print.
- Developed proposals and projects.

Software Developer, National Center for Genome Resources (1997-1999)

- Implemented genome sequence analysis algorithms and database applications.
- Provided bioinformatics services via the internet with object-oriented development.
- Presented analysis applications to students and scientists.
- Coordinated team development activities.

Publications

1. E Schultes, P Hraber, T LaBean. No molecule is an island: Molecular evolution and the study of sequence space. In J Kok, ed. *Algorithmic Bioprocesses*, in press.
2. P Hraber, C Kuiken, M Waugh, S Geer, W Bruno, T Leitner. Automatic classification of HCV and HIV-1 sequences with the branching index. *Journal of General Virology*, in press.
3. C Kuiken, P Hraber, J Thurmond, K Yusim. The hepatitis C sequence database in Los Alamos. *Nucleic Acids Research* 36:D512-D516, 2008.
4. P Hraber, C Kuiken, K Yusim. Evidence for human leukocyte antigen heterozygote advantage against hepatitis C virus infection. *Hepatology* 46(6):1713-1721, 2007.
5. P Hraber, R Leach, L Reilly, J Thurmond, K Yusim, C Kuiken. Los Alamos hepatitis C virus sequence and human immunology databases: an expanding resource for antiviral research. *Antiviral Chemistry and Chemotherapy* 18(3):113-124, 2007.
6. N Frahm, K Yusim, T Suscovich, S Adams, J Sidney, P Hraber, H Hewitt, C Linde, D Kavanagh, T Woodberry, L Henry, K Faircloth, J Listgarten, C Kadie, N Jojic, K Sango, N Brown, E Pae, M Zaman, F Bihl, A Khatri, M John, S Mallal, F Marincola, B Walker, A Sette, D Heckerman, B Korber, C Brander. Extensive HLA class I allele promiscuity among viral CTL epitopes. *European Journal of Immunology* 37(9):2419-2433, 2007.
7. L Davis, C Harris, L Tang, P Doherty, P Hraber, Y Sakai, T Bocklage, K Doeden, B Hall, I Rabinowitz, T Williams, J Hozier. Amplification patterns of three genomic regions predict distant recurrence in breast carcinoma. *Journal of Molecular Diagnostics*, 9(3):327-336, 2007.
8. P Hraber, B Korber, S Wolinsky, H Erlich, E Trachtenberg, TB Kepler. HLA and HIV infection progression: application of the minimum description length principle to statistical genetics. *Lecture Notes in Bioinformatics* 4345:1-12, 2006.
9. P Hraber, W Fischer, W Bruno, T Leitner, C Kuiken. Comparative analysis of hepatitis C virus phylogenies from coding and non-coding regions: the 5' untranslated region (UTR) fails to classify subtypes. *Virology Journal* 3(1):103, 2006.
10. P Hraber. Editorial (Introduction to "Collectives Formation and Specialization in Biosystems"). *Advances in Complex Systems* 9(4):295-298, 2006.
11. E Trachtenberg, B Korber, C Sollars, TB Kepler, P Hraber, E Hayes, R Funkhouser, M Fugate, J Theiler, Y Hsu, K Kunstman, S Wu, J Phair, H Erlich, S Wolinsky. Advantage of rare HLA supertype in HIV disease progression. *Nature Medicine* 9:928-935, 2003.
12. P Hraber, J Weller. On the species of origin: diagnosing the source of symbiotic transcripts. *Genome Biology* 2(9):e37.1-14, 2001.

13. D Qutob, P Hraber, B Sobral, M Gijzen. Comparative analysis of expressed sequences in *Phytophthora sojae*. *Plant Physiology* 123:243-254, 2000.
14. M Waugh, P Hraber, J Weller, Y Wu, G Chen, J Inman, D Kiphart, B Sobral. The *Phytophthora* Genome Initiative Database: informatics and analysis for distributed pathogenomic research. *Nucleic Acids Research* 28(1):87-90, 2000.
15. S Kamoun, P Hraber, B Sobral, D Nuss, 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.
16. E Schultes, P Hraber, T LaBean. Estimating the contributions of selection and self-organization in RNA secondary structure. *Journal of Molecular Evolution* 49(1):76-83, 1999.
17. E Schultes, P Hraber, T LaBean. A parameterization of RNA sequence space. *Complexity* 4:61-71, 1999.
18. 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, JJ Zhuang, P Schad. The Genome Sequence DataBase (GSDB): improving data quality and access. *Nucleic Acids Research* 26:21-26, 1998.
19. E Schultes, P Hraber, T LaBean. Global similarities in nucleotide base composition among disparate functional classes of single-stranded RNA imply adaptive evolutionary convergence. *RNA* 3:808-822, 1997.
20. P Hraber, T Jones, S Forrest. The ecology of Echo. *Artificial Life* 3(3):165-190, 1997.
21. P. Hraber, B Milne. Community assembly in a model ecosystem. *Ecological Modelling* 103:267-285, 1997.
22. B Milne, A Johnson, T Keitt, C Hatfield, J David, P Hraber. Detection of critical densities associated with Pinyon-Juniper woodland ecotones. *Ecology* 77(3):805-821, 1996.
23. M Mitchell, J Crutchfield, P Hraber. Evolving cellular automata to perform computations: mechanisms and impediments. *Physica D* 75:361-391, 1994.
24. M Mitchell, J Crutchfield, P Hraber. Dynamics, computation, and the "Edge of chaos": a re-examination. In G Cowan, D Pines, D Meltzer, eds. *Complexity: Metaphors, Models, and Reality*. Addison-Wesley (Reading, MA) 1994.
25. M Mitchell, P Hraber, J Crutchfield. Revisiting the edge of chaos: evolving cellular automata to perform computations. *Complex Systems* 7:89-130, 1993.

Talks and Invited Presentations

- HLA and HIV infection progression: application of the minimum description length principle to statistical genetics. 7th International Symposium on Biomedical Data Analysis (Thessaloniki, Greece) 2006.
- Dissecting genetics of host-pathogen interactions. Rocky06–4th Annual Rocky Mountain Bioinformatics Conference (Aspen/Snowmass, CO) 2006.
- Challenges in computational biomarker discovery. Rocky05–3rd Annual Rocky Mountain Bioinformatics Conference (Aspen/Snowmass, CO) 2005.
- Information-based models of complex biological processes. Invited keynote at the 3rd Meeting of the International Society for Ecological Informatics (Rome, Italy) 2002.
- Symbiosis and macroevolution. International Workshop on Evolutionary Innovation (Prague, Czech Republic) 2002.
- The *Phytophthora* Genome Initiative: a database and analysis system for collaborative pathogenomic research. Society for Industrial Microbiology, 50th Anniversary Annual Meeting (Arlington, VA) 1999.
- Community assembly in a model ecosystem. University of Michigan (Ann Arbor, MI) 1997.

Teaching and Mentoring

- Mentored student working groups in Immunology (2002) and Genomics (2001) at the Santa Fe Complex Systems Summer School.
- Guest-lectured and coordinated computational laboratory exercises for Biology 544, *Genomes and Genome Analysis*, University of New Mexico, 2001.
- Mentored and collaborated with Allison Styer, undergraduate student of biology and computer science at Carnegie-Mellon University, during a summer internship at NCGR, on “Screening ESTs for secreted peptides with PexFinder,” 2000.
- Teaching assistant, Department of Biology, University of New Mexico, 1995-6.

Funding Awards

- Granted ESF travel award to participate in “From Genome to Life: International Summer School in Functional Genomics” (Corsica, France) 2002.
- Granted NSF travel award to attend “Artificial Intelligence and Heuristic Methods for Bioinformatics” NATO Advanced Study Institute (San Miniato, Italy) 2001.
- Research grant from Santa Fe Institute for “Validation of the Echo model” 1996.

Editorial Service

- Reviewer for *Artificial Life*, *Complex Systems*, *Complexity*, *Ecological Modelling*, *Evolutionary Computation*, *Human Immunology*, *JTB*, and *Virology*.
- Guest Editor, *Advances in Complex Systems*.
- Associate Editor, *Ecological Informatics*.