

Stacia Kathleen Wyman

Home Address

35 Latham Street
Williamstown, MA 01267
(413) 358-3218
stacia@cs.williams.edu

University Address

Department of Computer Science
Williams College
Williamstown, MA 01267
(413) 597-4711

Education

- 2004 Ph.D., Computer Sciences, University of Texas at Austin
(Interdisciplinary Ph.D. in Bioinformatics)
- 1992 M.S., Computer Science, University of Wisconsin, Madison
- 1990 B.A. *cum laude* with honors in Computer Science, Smith College

Honors and Awards

- International Society for Computational Biology Travel Fellowship, 2003
- NSF Integrative Graduate Education and Research Training Fellowship, 2001-2003
- University Co-op Society Fellowship for Excellence in Graduate Research, 2001
- David Bruton Graduate Fellowship, 2000
- First-year Graduate Student Summer Research Fellowship, 1991
- General Electric Graduate Fellowship, 1990-1991
- Best Paper Award, Hawaii Int'l Conference for the System Sciences, 1992
- Elected to Phi Beta Kappa, Sigma Xi, 1990
- First Group Scholar, Smith College, 1987-1990

Academic Experience

- Visiting Assistant Professor, Williams College Department of Computer Science 8/2004-present
- Guest Researcher, Lawrence Berkeley Lab & DOE Joint Genome Institute 6/2004-present
- Research Assistant, Center for Comp. Biology and Bioinformatics, UT Austin 9/2003-8/2004
- Visiting Researcher, Lawrence Berkeley Lab & DOE Joint Genome Institute 6/2002-9/2002
- Research and Teaching Assistant, Dept. of Computer Sciences, UT Austin 9/1999-9/2001
- Research and Teaching Assistant, Dept. of Computer Science, UW Madison 6/1991-1/1992

Professional Experience

- Web Developer and System Administrator, eMerging Media, San Francisco, CA 7/1996-1/1999
- Sequence Analysis Software Developer, Genentech, South San Francisco, CA 7/1994-2/1996
- Network Administrator, Net Daemons Associates, Waltham, MA 1/1993-9/1993

Software

- DOGMA: Dual Organellar Genome Annotator
- Tool for Comparative Repeat Analysis of Small Genomes

Publications

- Wyman, S.K. and St. John, K., "Algorithms for Analyzing and Clustering Repeats in Whole Genomes," in preparation.
- Wyman, S.K. and Holschulte, N., "Comparative Repeat Analysis of Whole Genomes," in preparation.
- Jansen R.K., Raubeson L.A., Boore J.L., dePamphilis C.W., Chumley T.W., Haberle R.C., Wyman S.K., Alverson A.J., Peery R., Herman S.J., Fourcade H.M., Kuehl J.V., McNeal J.R., Leebens-Mack J., Cui L. (book chapter) "Methods for obtaining and analyzing whole chloroplast genome sequences." *Methods Enzymol.* 2005; (**395**):348-84.
- Wyman, S.K., Jansen, R.K., and Boore, J.L., "Automatic annotation of organellar genomes with DOGMA," *Bioinformatics.* 2004;20(**17**):3252-5.
- Wyman, S.K., and Boore, J.L., "Annotating animal mitochondrial tRNAs: an experimental evaluation of four methods," *Proc. of European Conference in Computational Biology (ECCB 2003)*, Paris, France, 2003:44-46.
- Moret, B.M.E., Wyman, S.K., Bader, D.A., Warnow, T., and Yan, M., "A detailed study of breakpoint analysis," *Proc. 6th Pacific Symp. Biocomputing (PSB 2001)*, Hawaii, World Scientific Pub., 2001:583-594.
- Moret, B.M.E., Wang, L.-S., Warnow, T., and Wyman, S.K., "New approaches for reconstructing phylogenies based on gene order," *9th Int'l Conf. on Intelligent Systems for Molecular Biology (ISMB 2001)*, Copenhagen, in *Bioinformatics* **17** 2001: 165S-173S; chosen as one of the 5 best papers at the conference.
- Cosner, M.E., Jansen, R.K., Moret, B.M.E., Raubeson, L.A., Wang, L.S., Warnow, T., and Wyman, S.K. (corresponding author), "An empirical comparison of phylogenetic methods on chloroplast gene order data in Campanulaceae," in *Comparative Genomics: Empirical and Analytical Approaches to Gene Order Dynamics, Map Alignment, and the Evolution of Gene Families*, D. Sankoff and J. Nadeau, eds., Kluwer Academic, Dordrecht 2000:99-121.
- Cosner, M.E., Jansen, R.K., Moret, B.M.E., Raubeson, L.A., Wang, L.S., Warnow, T., and Wyman, S.K. (corresponding author), "A new fast heuristic for computing the breakpoint phylogeny and a phylogenetic analysis of a group of highly rearranged chloroplast genomes," *Proc. 8th Int'l Conf. on Intelligent Systems for Molecular Biology (ISMB 2000)*, San Diego, CA 2000:104-115.
- Istvanick, W., Kryder, A., Lewandowski, G., Meidanis, J., Rang, A., and Wyman, S.K., "Dynamic Methods for Fragment Assembly in Large-scale Genome Sequencing Projects," *Proc. Hawaii International Conference for the System Sciences*, 1992.

Presentations

- “Comparative Chloroplast Genomics of Seed Plants: Annotation and Analysis of Genomic Sequences,” Wyman, S.K., Haberle, R., Chumley, T., Boore, J.L., Jansen, R.K., IMA RECOMB Satellite Workshop on Comparative Genomics, University of Minneapolis, Minneapolis, MN, 2003 (poster).
- “An experimental evaluation of four methods for identifying animal mitochondrial tRNAs,” Wyman, S.K., Boore, J.L., Evolution meeting, Chico State University, Chico, CA 2003.
- “Comparative chloroplast genomics: integrating computational methods, phylogeny, and molecular evolution,” Jansen, R.K., Raubeson, L.A., Haberle, R.C., Wyman, S.K., Chumley, T., Moret, B.M.E., Boore, J.L., Fourcade, M., Wang, L.S., Warnow, T., Plant and Animal Genomics Conference, San Diego, CA, 2003.
- “Inferring phylogenetic relationships using gene order data: a case study of photosynthetic organelles and chloroplast genomes,” Raubeson, L.A., Moret, B.M.E., Tang, J., Warnow, T., Wyman, S.K., Evolution, Chico State University, Chico, CA, 2003.
- “Structure and evolution of two highly rearranged chloroplast genomes in the Campanulaceae”, Haberle, R., Boore, J.L., Fourcade, M.H., Jansen, R.K., Wyman, S.K., Evolution, Chico State University, Chico, CA, 2003.
- “AMICA: A new annotation program for animal mitochondrial and chloroplast genomes,” Wyman, S.K., Haberle, R.C., Raubeson, L.A., Fourcade, M., Boore, J.L., Jansen, R.K., Keck/GCC Bioinformatics Consortium 2002 Bioinformatics Symposium, Rice University, Houston, TX, 2002 (poster).
- “Evolutionary implications of the complete sequence of the *Trachelium caeruleum* (Campanulaceae) chloroplast genome,” Haberle, R.C., Wyman, S.K., Eddie, W.M., Boore, J.L., Jansen, R.K., Botany 2002, Botanical Society of America meeting, Madison, WI, 2002.
- “High-performance algorithm engineering for gene-order phylogenies,” Bader, D.A., Moret, B.M.E., Warnow, T., Wyman, S.K., and Yan, M., DIMACS Workshop on Whole Genome Comparison, Rutgers U., 2001.
- “New approaches for using gene order data in phylogeny reconstruction,” Jansen, R.K., Bader, D.A., Moret, B.M.E., Raubeson, L.A., Wang, L., Warnow, T., and Wyman, S.K., Botanical Society of America meetings Albuquerque, NM, 2001.

References

Jeffrey L. Boore, Ph.D.
Evolutionary Genomics Department Head
and Associate Adjunct Professor, University of California, Berkeley
DOE Joint Genome Institute
2800 Mitchell Drive
Walnut Creek, CA 94598
Email: jlboore@lbl.gov
Phone: 925-296-5691

Robert K. Jansen, Professor and Chair
Section of Integrative Biology
The University of Texas at Austin
Austin, Texas 78712-0253
Email: jansen@mail.utexas.edu
Phone: 512-232-5661/471-8827

David Sankoff, Professor
Department of Mathematics and Statistics
University of Ottawa
585 King Edward Avenue
Ottawa, Ontario, Canada. K1N 6N5
Email: sankoff@uottawa.ca
Phone: 613-562-5800 ext. 3525