

School of Computer and Communication Sciences
Ecole Polytechnique Fédérale de Lausanne
CH-1005 Lausanne, Switzerland

email: bernard.moret@epfl.ch
web page: people.epfl.ch/bernard.moret
research lab: lcbb.epfl.ch

+41 21 693 1391 (office) +41 79 832 3808 (cell) +41 21 693 7555 (FAX)

Personal Data:

Born 1953 in Switzerland, U.S. & Swiss citizen.

Languages:

English, French, German, Russian.

Education:

Ph.D. in Electrical Engineering, 1980, The University of Tennessee.
M.S. in Electrical Engineering, 1977, The University of Tennessee.
Diploma of Electrical Engineering, 1975,
EPFL (Swiss Federal Institute of Technology, Lausanne).
Baccalaureates *ès* Latin-Greek and *ès* Latin-Mathematics, 1970,
City Gymnasium, Lausanne.

Professional Experience:

- 2006– *Professor of Bioinformatics*, School of Computer and Communication Sciences, EPFL (Swiss Federal Institute of Technology, Lausanne), Switzerland.
- 2006– *Group Leader*, Swiss Institute of Bioinformatics.
- 2009–2012 *”Chef de Section, Informatique”* (Director, BS & MS programs in CS), EPFL.
- 2003–2006 *Director*, CIPRES (www.phylo.org), a major community project to build a Cyber Infrastructure for Phylogenetic Research to support the reconstruction of the Tree of Life, counting 18 institutions (incl. UC Berkeley, UC San Diego, U. Pennsylvania, UT Austin, and Yale U.) and over 50 researchers, funded by the US National Science Foundation.
- 1993–2006 *Professor of Computer Science and of Electrical and Computer Engineering*, The University of New Mexico. Teaching and research in the design and analysis of data structures and algorithms (particularly for computational biology and computational geometry), experimental algorithmics, and complexity theory.
- 1991–1993 *Chairman*, Department of Computer Science, The University of New Mexico. During this period, the department doubled its production of PhDs, tripled the number of graduate students supported, quadrupled its research funding, received renewed accreditation from CSAB, and initiated major changes in undergraduate education.
- 1985–1993 *Associate Professor of Computer Science*, The University of New Mexico.
- 1980–1984 *Assistant Professor of Computer Science*, The University of New Mexico.
- 1979–1980 *Instructor*, The University of Tennessee. Teaching introductory programming and advanced data structures.
- 1976–1980 *Research Assistant*, The University of Tennessee. Research in pattern recognition, scene analysis, measures of system complexity, and decision trees, under the guidance of Drs. R.C. Gonzalez and M.G. Thomason.
- 1975–1976 *Software Development Engineer*, Omega Electronic, Bienne, Switzerland. Conception and realization of control systems for sports timing and public display applications.

Current Professional Activities:

- Chair *Steering Committee:* Workshop on Algorithms in Bioinformatics (WABI), 2001–present.
- Organizer “*Computational challenges in comparative genomics*”, session and tutorial at the 15th Pacific Symp. on Biocomputing PSB’10 (with W. Miller, P. Pevzner, and D. Sankoff).
- Member *Steering Committee:* ALENEX (Workshop on Algorithm Engineering and Experiments): 2002–present.
Program Committees (so far): 9th Comput. Systems Bioinf. Conf. CSB’10, 6th Int’l Symp. Bioinf. Res. & Appl. ISBRA’10, 14th Conf. Research in Comput. Mol. Bio. RECOMB’10.

Recent Professional Activities:

- Editor-in-Chief ACM Journal of Experimental Algorithmics 1995–2003 (founding editor).
- Chair *NIH Study Section* on Biodata Management and Analysis (BDMA) 2006–2008.
NIH Site Visit Committee for NCCR program (Dec. 2005).
Steering Committee: WAE (Workshop on Alg. Engin. & Experiments) 2000–2002.
Program Committees: 6th Workshop on Algs. in Bioinformatics WABI’06, 1st Workshop on Algs. in Bioinformatics WABI’01, 2nd Workshop on Alg. Engineering & Experiments ALENEX’00.
- Member *NIH Study Section:* BDMA 2004–2008 (charter member).
Editorial Boards: IEEE/ACM Transactions on Computational Biology and Bioinformatics 2003–2008; Journal of Graph Algorithms and Applications 2005–2008.
Steering Committee: ESA (European Symp. on Algs.) 1999–2002.
Program Committees (international confs.):
BIBE (Conf. Bioinformatics & Bioeng.) 2009;
BIBM (IEEE Conf. on Bioinformatics & Biomedicine) 2007–2009;
COCOON (Computing & Combinatorics Conf.) 2003, 2006;
CSB (Comput. Systems Bioinformatics Conf.) 2009;
GIW (Int’l Conf. on Genome Informatics) 2007–2009;
ISBRA (Int’l Symp. on Bioinformatics Res. & Appls.) 2008–2009;
ISMB (Conf. on Intelligent Systems for Mol. Bio.) 2006–2009;
PRIB (IAPR Conf. on Pattern Recognition in Bioinformatics) 2007–2008;
RECOMB-CG (RECOMB Workshop on Comparative Genomics) 2005, 2006, 2008–2009;
SODA (SIAM Symp. on Discrete Algs.) 1999;
WABI (Workshop on Algs. in Bioinformatics) 2001–2009;
WAE (Workshop on Alg. Engin.) 1998, 1999, 2001;
WEA (Workshop on Experimental Algs.) 2005, 2007.
- Organizer “*Computational challenges in comparative genomics*”, session and tutorial at the 14th Pacific Symp. on Biocomputing PSB’09 (with W. Miller, P. Pevzner, and D. Sankoff).
“*Beyond Gap Models: Reconstructing Alignments and Phylogenies Under Genomic-Scale Events*”, session and tutorial at the 13th Pacific Symp. on Biocomputing PSB’08 (with M. Brudno, R. Linder, and T. Warnow).
DIMACS Workshop on Reticulate Evolution, DIMACS, Oct. 2004 (with M. Janowitz and R. Linder).
1st RECOMB Workshop on Comparative Genomics RECOMB-CG’03, Minneapolis, Oct. 2003 (with J. Lagergren and D. Sankoff).
2nd Schloss Dagstuhl Seminar on Experimental Algorithmics (Germany), Sept. 2002 (with J. Bentley, R. Fleischer, and E.M. Schmidt).
1st Schloss Dagstuhl Seminar on Experimental Algorithmics (Germany), Sept. 2000 (with R. Fleischer and E.M. Schmidt).

Sponsored Research Projects (since 1990):

- PI on "Models and algorithms for genome evolution," funded by the Swiss National Science Foundation, 2008–2011, supporting one PhD student (EPFL).
- PI on "Models and algorithms for noncoding genes," an IPhD project sponsored by SystemsX.ch, 2008–2011, supporting one PhD student (EPFL).
- PI and overall project director (until Oct. 2006, thereafter foreign collaborator and executive committee member) on "Building the Tree of Life: A National Resource for Phyloinformatics and Computational Phylogenetics," on National Science Foundation cooperative agreement EF 03-31654 (2003–2008, \$11.6M), leading 15 other institutions (incl. UC Berkeley, UC San Diego, UT Austin, U. Pennsylvania, Yale U., etc.) and over 40 faculty on a community project (CIPRES) to build a Cyber Infrastructure for Phylogenetic Research to support the eventual reconstruction of the Tree of Life.
- PI on "Reconstructing Complex Evolutionary Histories," on National Science Foundation grant EIA 01-23177 (2001–2006, \$793K).
- Local PI on "Comparative Chloroplast Genomics: Integrating Computational Methods, Molecular Evolution, and Phylogeny," on subcontract to U. Texas at Austin (R. Jansen, PI) under National Science Foundation grant DEB 01-20709 (2001–2006, \$195K at UNM).
- Co-PI on "PERCS: Productive, easy-to-use, reliable computing systems," on subcontract from IBM under a DARPA grant (2002–2006, \$700K); D. Bader, PI.
- Co-I on National Science Foundation grant DBI 04-20513 (2004–2006, \$350K), for purchase of a large SMP computer for computational science research at UNM; H. Guo (Chemistry), PI.
- PI on "Computing Optimal Phylogenetic Trees under Genome Rearrangement Metrics," on National Science Foundation grant EIA 01-13095 (2001–2004, \$162K).
- Local PI on "Genome Erosion in Infectious Microorganisms," on subcontract to U. Arizona (H. Ochman, PI), under National Institutes of Health grant 2R01GM056120-05A1 (2004–2005, \$81K at UNM).
- Sponsoring Scientist for Sloan Foundation Postdoctoral Fellowship in Computational Molecular Biology, awarded to Dr. Tiffani Williams to work under my guidance (2002–2004, \$140K).
- PI on "Postdoc: A Hierarchical Methodology for SMP Clusters," on National Science Foundation grant EIA 02-03584 (2002–2004, \$66K plus matching), supporting one postdoc (Dr. Tanya Berger-Wolf).
- PI on "Algorithms for Irregular Discrete Computations on SMPs," on National Science Foundation grant ACI 00-81404 (2000–2003, \$453K).
- PI on "Research in Real-Time Retargeting," on Office of Naval Research grant N00014-97-1-0244 (1997–1999, \$165K).
- PI on "Joint Routing," on Office of Naval Research grant N00014-95-1-1010 (1995–1999, \$127K).
- Co-I on National Science Foundation Research Infrastructure grant EIA 95-03064 (1995–2000, \$1.2M); J. Hollan, PI.
- PI on "Routing Algorithms," on Office of Naval Research contract N00014-92-C-2144 (1992–96, \$480K).

Books:

- Moret, B.M.E. *The Theory of Computation*. Addison-Wesley, Reading, MA, 1998 (473pp.).
- Moret, B.M.E., and H.D. Shapiro. *Algorithms from \mathcal{P} to \mathcal{NP} . Volume I: Design and Efficiency*. Benjamin-Cummings Publishing Co., Menlo Park, CA, 1991 (592pp.).

Edited Volumes:

- (with P. Blicher) *Proc. 6th Workshop on Algorithms in Bioinformatics (WABI'06)*, LNCS **4175**, Springer Verlag, 2006 (410pp.)
- (with R. Fleischer and E.M. Schmidt) *Experimental Algorithmics*, LNCS **2547**, Springer Verlag, 2002 (279pp.)
- (with O. Gascuel) *Proc. 1st Workshop on Algorithms in Bioinformatics (WABI'01)*, LNCS **2149**, Springer Verlag, 2001 (310pp.)
- Special issue for the 10th ACM-SIAM Symp. on Discrete Algorithms SODA'99, *Journal of Algorithms* **38**, 1, 2001 (333pp.)
- (with A. Goldberg) *Proc. 2nd Workshop on Algorithm Engineering & Experiments (ALENEX'00)*, 2000 (300pp.)

Book Chapters:

- Moret, B.M.E., "Large-scale phylogenetic reconstruction," in *Comparative Genomics: Basic and Applied Research*, J.R. Brown, ed., CRC Press/Taylor & Francis (2007), 29–48.
- Williams, T.L., Bader, D.A., Yan, M., and Moret, B.M.E., "High-performance phylogeny reconstruction under maximum parsimony," in *Parallel Computing for Bioinformatics and Computational Biology*, A.Y. Zomaya, ed., John Wiley & Sons (2006), 369–394.
- Moret, B.M.E., and Warnow. T., "Advances in phylogeny reconstruction from gene order and content data," in *Producing the Biochemical Data II*, vol. 395 of *Methods in Enzymology*, E.A. Zimmer and E.H. Roalson, eds., Elsevier (2005), 673–700.
- Moret, B.M.E., Tang, J., and Warnow. T., "Reconstructing phylogenies from gene-content and gene-order data," in *Mathematics of Evolution and Phylogeny*, O. Gascuel, ed., Oxford Univ. Press (2005), 321–352.
- Roshan, U., Moret, B.M.E., Warnow, T., and Williams, T.L., "Performance of supertree methods on various dataset decompositions," *Phylogenetic Supertrees: Combining information to reveal the Tree of Life*, O.R.P. Bininda-Emonds, ed., Kluwer Pub. (2004), 301–328.
- Moret, B.M.E., "Towards a discipline of experimental algorithmics," in *Data Structures, Near Neighbor Searches, and Methodology: 5th and 6th DIMACS Implementation Challenges*, Goldwasser, M.H., Johnson, D.S., and McGeoch, C.C., eds., *DIMACS Monographs* **59**, 197–213, AMS Publishing, 2002.
- Moret, B.M.E., and Warnow, T., "Reconstructing optimal phylogenetic trees: A challenge in experimental algorithmics," *Experimental Algorithmics*, LNCS **2547**, 163–180, Springer Verlag (2002).
- Bader, D.A., Moret, B.M.E., and Sanders, P., "High-performance algorithm engineering for parallel computation," *Experimental Algorithmics*, LNCS **2547**, 1–23, Springer Verlag (2002).
- Cosner, M.E., Jansen, R.K., Moret, B.M.E., Raubeson, L.A., Wang, L.S., Warnow, T., and Wyman, S., "An empirical comparison of phylogenetic methods on chloroplast gene order data in Campanulaceae," in *Comparative Genomics*, D. Sankoff and J. Nadeau, eds., Kluwer Pub., Dordrecht (2000), 99–121.

Refereed Publications (since 1990):

- Rajan, V., Xu, A.W., Lin, Y., Swenson, K.M., and Moret, B.M.E., "Heuristics for the inversion median problem," *Proc. 8th Asia-Pacific Bioinformatics Conf. APBC'10*, accepted, to appear in *BMC Bioinformatics* (2010).
- Lin, Y., Rajan, V., Swenson, K.M., and Moret, B.M.E., "Estimating true evolutionary distances under rearrangements, duplications, and losses," *Proc. 8th Asia-Pacific Bioinformatics Conf. APBC'10*, accepted, to appear in *BMC Bioinformatics* (2010).
- Zhang, X., and Moret, B.M.E., "Refining transcriptional regulatory networks using network evolutionary models and gene histories," *BMC Algorithms in Molecular Biology*, accepted, to appear (2009). (*special issue on best papers from WABI'09*).
- Swenson, K.M., Lin, Y., Rajan, V., and Moret, B.M.E., "Hurdles and sorting by inversions: Combinatorial, statistical, and experimental results," *J. Comput. Biol.* **16**, 20 (2009), 1–13.
- Zhang, X., and Moret, B.M.E., "Improving inference of transcriptional regulatory networks based on network evolutionary models," *Proc. 9th Workshop on Algs. in Bioinformatics WABI'09*, in *LNCS 5724*, 412–425 (2009).
- Pattengale, N.D., Alipour, M., Bininda-Emonds, O.R.P., Moret, B.M.E., and Stamatakis, A., "How many bootstrap replicates are necessary?" *Proc. 13th Int'l Conf. on Research in Comput. Molecular Biol. RECOMB'09*, in *LNCS 5541*, 184–200 (2009).
- Swenson, K.M., Rajan, V., Lin, Y., and Moret, B.M.E., "Sorting signed permutations by inversions in $O(n \log n)$ time," *Proc. 13th Int'l Conf. on Research in Comput. Molecular Biol. RECOMB'09*, in *LNCS 5541*, 386–399 (2009).
- Swenson, K.M., and Moret, B.M.E., "Inversion-based genomics signatures," *Proc. 7th Asia-Pacific Bioinformatics Conf. APBC'09*, in *BMC Bioinformatics* **10** (Suppl. 1):S7 (2009).
- Swenson, K.M., To, Y., Tang, J., and Moret, B.M.E., "Maximum independent sets of commuting and noninterfering inversions," *Proc. 7th Asia-Pacific Bioinformatics Conf. APBC'09*, in *BMC Bioinformatics* **10** (Suppl. 1):S6 (2009).
- Swenson, K.M., Lin, Y., Rajan, V., and Moret, B.M.E., "Hurdles hardly have to be heeded," *Proc. 6th RECOMB Workshop on Comparative Genomics RECOMB-CG'08*, in *LNCS 5267*, 239–249 (2008).
- Zhang, X., and Moret, B.M.E., "Boosting the performance of inference algorithms for transcriptional regulatory networks using a phylogenetic approach," *Proc. 8th Workshop on Algs. in Bioinformatics WABI'08*, in *LNCS 5251*, 245–258 (2008).
- Lin, Y., and Moret, B.M.E., "Estimating true evolutionary distances under the DCJ model," *Proc. 16th Conf. on Intelligent Systems for Comput. Biology ISMB'08*, in *Bioinformatics* **24**, 13 (2008), i114–i122.
- Swenson, K.M., Marron, M., Earnest-DeYoung, J.V., and Moret, B.M.E., "Approximating the true evolutionary distance between two genomes," *ACM J. Experimental Algorithmics* **12**, 3.5 (2008), 17pp. (*special issue on best papers from ALENEX'05*).
- Zhang, X., Zaheri, M., and Moret, B.M.E., "Using phylogenetic relationships to improve the inference of transcriptional regulatory networks," *Proc. 1st Conf. Biomedical Eng. & Informatics BMEI'08*, 186–193, IEEE Comput. Soc. Press (2008).
- Yue, F., Cui, L., dePamphilis, C.W., Moret, B.M.E., and Tang, J., "Inferring ancestral chloroplast genomes with inverted repeat," *BMC Genomics* **9**, Suppl. 1, S25 (2008).
- Swenson, K.M., Arndt, W., Tang, J., and Moret, B.M.E., "Phylogenetic reconstruction from complete gene orders of whole genomes," *Proc. 6th Asia-Pacific Bioinformatics Conf. APBC'08*, in *Advances in Bioinformatics and Computational Biology*, Vol. 6, 241–250, Imperial Press (2008).
- Kothari, M., and Moret, B.M.E., "An experimental evaluation of inversion- and transposition-based genomic distances," *Proc. 3rd IEEE Symp. Comput. Intelligence in Bioinformatics & Comput. Biol. CIBCB'07*, 151–158, IEEE Press (2007).
- Pattengale, N.D., Gottlieb, E.J., and Moret, B.M.E., "Efficiently computing the Robinson-Foulds metric," *J. Comput. Biol.* **14**, 6 (2007), 724–735 (*special issue on best papers from RECOMB'06*).

Refereed Publications (since 1990), cont'd:

- Wang, L.-S., Jansen, R.K., Moret, B.M.E., Raubeson, L., and Warnow, T., "Distance-based genome rearrangement phylogeny," *J. Molecular Evol.* **63**, 4 (2006), 473–483.
- Pattengale, N.D., and Moret, B.M.E., "A sublinear-time randomized approximation scheme for the Robinson-Foulds metric," *Proc. 10th Int'l Conf. on Research in Comput. Molecular Biol. RECOMB'06*, in *LNCS 3909*, 221–230, Springer Verlag (2006).
- Morin, M.M., and Moret, B.M.E., "NETGEN: generating phylogenetic networks with diploid hybrids," *Bioinformatics* **22** (2006), 1921–1923.
- Cui, L., Yue, F., dePamphilis, C.W., Moret, B.M.E., and Tang, J., "Inferring ancestral chloroplast genomes with inverted repeat," *Proc. Int'l Conf. on Bioinformatics & Comput. Biol. BIOCOMP'06*, 75–81, CSREA Press (2006).
- Swenson, K.M., Pattengale, N.D., and Moret, B.M.E., "A framework for orthology assignment from gene rearrangement data," *Proc. 3rd RECOMB Workshop on Comparative Genomics RECOMBCG'05*, in *LNCS 3678*, 153–166, Springer Verlag (2005).
- Liu, T., Tang, J., and Moret, B.M.E., "Quartet methods for phylogeny reconstruction from gene orders," *Proc. 11th Comput. & Combinatorics Conf. COCOON'05*, in *LNCS 3595*, 63–73, Springer Verlag (2005).
- Tang, J., and Moret, B.M.E., "Linear programming for phylogenetic reconstruction based on gene rearrangements," *Proc. 16th Symp. on Combinatorial Pattern Matching CPM'05*, in *LNCS 3537*, 406–416, Springer Verlag (2005).
- Swenson, K.M., Marron, M., Earnest-DeYoung, J.V., and Moret, B.M.E., "Approximating the true evolutionary distance between two genomes," *Proc. 7th Workshop on Algorithm Engineering and Experiments ALENEX'05*, SIAM Press (2005), 121–129.
- Moret, B.M.E., "Computational challenges from the Tree of Life," *Proc. 7th Workshop on Algorithm Engineering and Experiments ALENEX'05*, SIAM Press (2005), 3–16.
- Earnest-DeYoung, J.V., Lerat, E., and Moret, B.M.E., "Reversing gene erosion: Reconstructing ancestral bacterial genomes from gene-content and order data," *Proc. 4th Workshop on Algs. in Bioinformatics WABI'04*, in *LNCS 3240*, 1–13, Springer Verlag (2004).
- Marron, M., Swenson, K.M., and Moret, B.M.E., "Genomic distances under deletions and insertions," *Theor. Comput. Sci.* **325**, 3 (2004), 347–360 (*special issue on best papers from COCOON'03*).
- Moret, B.M.E., Nakhleh, L., Warnow, T., Linder, C.R., Tholse, A., Padolina, A., Sun, J., and Timme, R., "Phylogenetic networks: modeling, reconstructibility, and accuracy," *IEEE/ACM Trans. Comput. Biology & Biocomp.* **1**, 1 (2004), 13–23.
- Roshan, U., Moret, B.M.E., Williams, T.L., and Warnow, T., "Rec-I-DCM3: A fast algorithmic technique for reconstructing large phylogenetic trees," *Proc. 3rd IEEE Computational Systems Bioinformatics Conf. CSB'04*, IEEE Press (2004), 98–109.
- Tang, J., Moret, B.M.E., Cui, L., and dePamphilis, C.W., "Phylogenetic reconstruction from arbitrary gene-order data," *Proc. 4th IEEE Conf. on Bioinformatics & Bioengineering BIBE'04*, IEEE Press (2004), 592–599.
- St. John, K., Warnow, T., Moret, B.M.E., and Vawter, L., "Performance study of phylogenetic methods: (unweighted) quartet methods and neighbor-joining," *J. Algs.* **48**, 1 (2003), 173–193 (*special issue on best papers from SODA'01*).
- Tang, J., and Moret, B.M.E., "Phylogenetic reconstruction from gene rearrangement data with unequal gene contents," *Proc. 8th Workshop on Algs. & Data Structures WADS'03*, in *LNCS 2748*, 37–46, Springer Verlag (2003).
- Marron, M., Swenson, K.M., and Moret, B.M.E., "Genomic distances under deletions and insertions," *Proc. 9th Int'l Combinatorics & Comput. Conf. COCOON'03*, in *LNCS 2697*, 537–547, Springer Verlag (2003).
- Tang, J., and Moret, B.M.E., "Scaling up accurate phylogenetic reconstruction from gene-order data," *Proc. 11th Int'l Conf. on Intelligent Systems for Molecular Biology ISMB'03*, in *Bioinformatics* **19**, i305–i312, 2003.

Refereed Publications (since 1990), cont'd:

- Williams, T., and Moret, B.M.E., "An investigation of phylogenetic likelihood methods," *Proc. 3rd IEEE Symp. Bioinformatics & Bioengineering BIBE'03*, IEEE Press (2003), 79–86.
- Nakhleh, L., Sun, J., Warnow, T., Linder, R., Moret, B.M.E., and Tholse, A., "Towards the development of computational tools for evaluating phylogenetic network reconstruction methods," *Proc. 8th Pacific Symp. Biocomputing PSB'03*, World Scientific Pub. (2003), 315–326.
- Moret, B.M.E., Tang, J., Wang, L.-S., and Warnow, T., "Steps toward accurate reconstructions of phylogenies from gene-order data," *J. Comput. Syst. Sci.* **65**, 3 (2002), 508–525 (*special issue on Comput. Biol.*).
- Moret, B.M.E., Wang, L.-S., and Warnow, T., "Towards new software for computational phylogenetics," *IEEE Computer* **35**, 7 (July 2002), 55–64 (*special issue on bioinformatics*).
- Moret, B.M.E., Bader, D.A., and Warnow, T., "High-performance algorithm engineering in computational phylogeny," *J. Supercomputing* **22** (2002), 99–111 (*special issue on best papers from ICCS'01*).
- Doddi, S., Marathe, M.V., and Moret, B.M.E., "Point set labeling with specified positions," *Int'l J. Comput. Geometry & Applics.* **12**, 1–2 (2002), 29–66 (*special issue on best papers from SoCG'00*).
- Moret, B.M.E., Siepel, A.C., Tang, J., and Liu, T., "Inversion medians outperform breakpoint medians in phylogeny reconstruction from gene-order data," *Proc. 2nd Workshop on Algs. in Bioinformatics WABI'02*, in *LNCS 2452*, 521–536, Springer Verlag (2002).
- Moret, B.M.E., Roshan, U., and Warnow, T., "Sequence-length requirements for phylogenetic methods," *Proc. 2nd Workshop on Algs. in Bioinformatics WABI'02*, in *LNCS 2452*, 343–356, Springer Verlag (2002).
- Nakhleh, L., Moret, B.M.E., Roshan, U., St. John, K., Sun, J., and Warnow, T., "The accuracy of fast phylogenetic methods for large datasets," *Proc. 7th Pacific Symp. Biocomputing PSB'02*, World Scientific Pub. (2002), 211–222.
- Wang, L.S., Jansen, R.K., Moret, B.M.E., Raubeson, L., and Warnow, T., "Fast phylogenetic methods for the analysis of genome rearrangement data: an empirical study," *Proc. 7th Pacific Symp. Biocomputing PSB'02*, World Scientific Pub. (2002), 524–535.
- Bader, D.A., Moret, B.M.E., and Yan, M., "A linear-time algorithm for computing inversion distance between signed permutations with an experimental study," *J. Comput. Biol.* **8**, 5 (2001), 483–491.
- Moret, B.M.E., and Shapiro, H.D., "Algorithms and experiments: the new (and the old) methodology," *J. Univ. Comput. Sci.* **7**, 5 (2001), 434–446.
- Siepel, A., and Moret, B.M.E., "Finding an optimal inversion median: experimental results," *Proc. 1st Workshop on Algs. in Bioinformatics WABI'01*, in *LNCS 2149*, 189–203, Springer Verlag (2001).
- Bader, D.A., Illendula, A.K., Moret, B.M.E., and Weisse-Bernstein, N., "Using PRAM algorithms on a uniform-memory-access shared-memory architecture," *Proc. 5th Workshop on Algorithm Engineering WAE'01*, in *LNCS 2141*, 129–144, Springer Verlag (2001).
- Bader, D.A., Moret, B.M.E., and Yan, M., "A linear-time algorithm for computing inversion distance between signed permutations with an experimental study," *Proc. 7th Workshop on Algs. & Data Structs. WADS'01*, in *LNCS 2125*, 365–376, Springer Verlag (2001).
- Bader, D.A., Moret, B.M.E., and Vawter, L., "Industrial applications of high-performance computing for phylogeny reconstruction from gene-order data," *Proc. SPIE Conf. Commercial Appl. for High-Perf. Comput. ITCOM 2001*, Denver (2001), 159–168.
- Moret, B.M.E., Wang, L., Warnow, T., and Wyman, S.K., "New approaches for reconstructing phylogenies from gene-order data," *Proc. 9th Int'l Conf. on Intelligent Systems for Molecular Biology ISMB'01*, in *Bioinformatics 17* (2001), S165–S173.
- Moret, B.M.E., Bader, D.A., and Warnow, T., "High-performance algorithm engineering in computational phylogeny," *Proc. Int'l Conf. Computational Science ICCS'01*, in *LNCS 2074*, 1012–1021, Springer Verlag, 2001.
- Warnow, T., Moret, B.M.E., and St. John, K., "Absolute phylogeny: true trees from short sequences," *Proc. 12th Ann. Symp. Discrete Algs. SODA'01*, SIAM Press (2001), 186–195.

Refereed Publications (since 1990), cont'd:

- St. John, K., Warnow, T., Moret, B.M.E., and Vawter, L., "Performance study of phylogenetic methods: (unweighted) quartet methods and neighbor-joining," *Proc. 12th Ann. Symp. Discrete Algs. SODA'01*, SIAM Press (2001), 196–205.
- Moret, B.M.E., Wyman, S., Bader, D.A., Warnow, T., and Yan, M., "A detailed study of breakpoint analysis," *Proc. 6th Pacific Symp. Biocomputing PSB'01*, World Scientific Pub. (2001), 583–594.
- Cosner, M.E., Jansen, R.K., Moret, B.M.E., Raubeson, L.A., Wang, L.S., Warnow, T., and Wyman, S., "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'00*, San Diego (2000), 104–115.
- Doddi, S., Marathe, M.V., and Moret, B.M.E., "Point set labeling with specified positions," *Proc. 16th Ann. ACM Symp. on Comp. Geometry SoCG'00*, ACM Press (2000), 182–190.
- Goldberg, A.V., and Moret, B.M.E., "Combinatorial Algorithms Test Sets (CATS): the ACM/EATCS platform for experimental research," *Proc. 10th Ann. ACM/SIAM Symp. on Discrete Algs. SODA'99*, SIAM Press (1999), 913–914.
- Heileman, G.L., Abdallah, C.T., Moret, B.M.E., and Smith, B.J., "Dynamical system representation of open address hash functions," *Proc. 10th Ann. ACM/SIAM Symp. on Discrete Algs. SODA'99*, SIAM Press (1999), 919–920.
- McGeoch, C.C., and Moret, B.M.E., "How to present a paper on experimental work with algorithms," *SIGACT News* **30**, 4 (1999), 85–90.
- Collins, M., and Moret, B.M.E., "Improved lower bounds for the link length of rectilinear spanning paths in grids," *Inf. Proc. Letters* **68**, 6 (1998), 317–319.
- Moret, B.M.E., "ACM's Journal of Experimental Algorithms: Bridging Theory and Practice," *J. Electronic Publishing* **3** (1997), available on-line as www.press.umich.edu/jep/03-01/JEA.html.
- Moret, B.M.E., M. Collins, J. Saia, and L. Yu, "Ice rinks and cruise missiles: sweeping a simple polygon," *Proc. 1st Workshop on Algorithm Engineering WAE'97*, 1997, 104–111.
- Doddi, S., Marathe, M.V., Mirzaian, A., Moret, B.M.E., and Zhou, B., "Map labeling and its generalizations," *Proc. 8th Ann. ACM/SIAM Symp. on Discrete Algs. SODA'97*, SIAM Press (1997), 148–157.
- Boroujerdi, A., and Moret, B.M.E., "Persistent linked structures at constant worst-case cost," *J. Inf. & Comput.* **2**, 1 (1996), 68–78.
- Chen, Z., Holle, A.T., Moret, B.M.E., Saia, J., and Boroujerdi, A., "Network routing models applied to aircraft routing problems," *Proc. Winter Simulation Conf. WSC'95*, 1200–1206.
- Boroujerdi, A., and Moret, B.M.E., "Persistence in computational geometry," *Proc. 7th Canadian Conf. Comput. Geometry CCCG'95*, 1995, 241–246.
- Kooshesh, A.A., and Moret, B.M.E., "Folding a simple polygon: a paradigm for computational geometry," *Proc. ACM Comput. Science Conf.*, ACM Press (1995), 114–118.
- Moret, B.M.E., and Shapiro, H.D., "An empirical assessment of algorithms for constructing a minimum spanning tree," *DIMACS Monographs* **15** (1994), 99–117.
- Boroujerdi, A., and Moret, B.M.E., "Spatial data structures in simulation and planning," *Proc. 11th Ann. Conf. Command & Control Decision Aids*, 1994, 719–723.
- Helman, P., Moret, B.M.E., and Shapiro, H.D., "An exact characterization of greedy structures," *SIAM J. Discrete Math.* **6**, 2 (1993), 274–283.
- Moret, B.M.E., Boroujerdi, A., Dong, C., and Ma, Q., "Joint routing in networks," *Proc. Workshop on Network Optimization Theory & Practice*, Centro Studi Cappuccini, Italy (1993), 175–180.
- Kooshesh, A.A., and Moret, B.M.E., "Three-coloring the vertices of a triangulated simple polygon," *Pattern Recognition* **25**, 4 (1992), 443.

Refereed Publications (since 1990), cont'd:

- Helman, P., Moret, B.M.E., and Shapiro, H.D., "An exact characterization of greedy structures," *Proc. 2nd Conf. on Integer Prog. & Combin. Optimization IPCO-92* (1992), 287–297.
- Abrahamson, K., Fellows, M.R., Langston, M.A., and Moret, B.M.E., "Constructive complexity," *Discrete Applied Math.* **34** (1991), 3–16.
- Moret, B.M.E., and Shapiro, H.D., "How to find a minimum spanning tree in practice," *Proc. Conf. New Results & New Trends in Comput. Sci.*, in *LNCS 555*, 192–203, Springer Verlag, 1991.
- Moret, B.M.E., and Shapiro, H.D., "An empirical analysis of algorithms for constructing a minimum spanning tree," *Proc. 2nd Int'l Workshop on Data Structures & Algs. WADS'91*, in *LNCS 519*, 400–411, Springer Verlag, 1991.
- Kooshesh, A.A., and Moret, B.M.E., "Folding triangulated simple polygons: structural and algorithmic results," *Proc. 3rd Int'l Conf. Inf. & Comput. ICCI'91*, in *LNCS 497*, 102–110, Springer Verlag, 1991.
- Kooshesh, A.A., Moret, B.M.E., and Székely, L.L., "Improved bounds for the prison yard problem," *Congressus Numerantium* **76** (1990), 145–149.
- Tseng, C.T., and Moret, B.M.E., "A method for the choice of smoothing parameters," *Mathematical & Computer Modelling* **13**, 9 (1990), 1–16.
- Tseng, C.T., and Moret, B.M.E., "A new method for one-dimensional linear feature transformations," *Pattern Recognition* **23**, 7 (1990), 745–752.
- Tseng, C.T., and Moret, B.M.E., "The design of a non-parametric classifier," *Proc. 10th Int'l Conf. on Pattern Recognition ICPR-90*, Atlantic City (1990), Vol. I, 428–432.

Keynote Addresses, Major Invited Lectures, and Major Tutorials (since 2000):

- "Computational challenges in comparative genomics," tutorial, *14th Pacific Symp. on Bioinformatics PSB'09* (2009).
- "Beyond gap models: Reconstructing alignments and phylogenies under genomic-scale events," tutorial, *13th Pacific Symp. on Bioinformatics PSB'08* (2008).
- "Large-scale phylogenetic reconstruction, the tree of life, and the CIPRES project," keynote, Workshop on Bioalgorithms, Singapore National University, July 2006.
- "Phylogenetic reconstruction: Handling large scale and complex data," *Frontiers of Science* lecture series, U. California at San Diego, Jan. 2006.
- "Large-scale phylogenetic reconstruction, the Tree of Life, and CIPRES," invited lecture, *The Problems of Phylogenetic Analysis of Large Datasets*, Mathematical Biosciences Institute, OSU, Dec 2005.
- "Large-scale phylogenetic reconstruction and the Tree of Life," keynote, *Robert Cedergren Bioinformatics Symp.*, U. de Montréal, Nov. 2005.
- "Phylogenetic reconstruction: Handling large scale and complex data," invited lecture, *24th Summer Symp. on Molecular Biology*, Penn State, July 2005
- "Phylogenetic methods for building the Tree of Life," invited lecture, *Gordon Conf. on Structural, Functional, and Evolutionary Genomics*, Bates College, June 2005.
- "Algorithm engineering challenges from the Tree of Life," keynote, *7th Workshop on Alg. Engin. & Experiments ALENEX'05* (2005).
- "Network (reticulated) evolution: Biology, models, and algorithms," tutorial, *9th Pacific Symp. on Bioinformatics PSB'04* (2004).
- "Phylogenetic reconstruction based on gene-rearrangement data", invited lecture, *Mathematics of Evolution and Phylogeny*, Institut Henri Poincaré, Paris, June 2003.
- "Algorithmic engineering: It's all about speed," invited lectures, *School on Algorithmic Engineering*, Rome, Sep. 2001.

Postdocs Supervised:

- Wei Xu, 2008–present (EPFL).
Alexandros Stamatakis, 2006–2008 (EPFL); Asst. Prof. of Computer Science, Tech. U. Munich (Germany).
Tiffani Williams, Sloan Postdoctoral Fellow in Comput. Molecular Biol., 2002–2004; Radcliffe Fellow, 2004–2005; Asst. Prof. of Computer Science, Texas A&M.
Tanya Berger-Wolf, NSF Postdoctoral Associate, 2002–2004; DIMACS Fellow, 2004–2005; Asst. Prof. of Computer Science, U. Illinois at Chicago.

Ph.D. Students Supervised:

- Cristina Ghiurcuta, 2009-present (EPFL).
Nishanth Nair, 2009-present (EPFL).
Vaibhav Rajan, 2008–present (EPFL).
Yu Lin, 2007–present (EPFL).
Yann Christinat, 2007–present (EPFL).
Nicholas Pattengale, 2007–present (UNM).
Xiuwei Zhang, 2006–present (EPFL).
Krister Swenson: “Genomic distances in the presence of arbitrary deletions, insertions, duplications, and inversions,” Ph.D. (EPFL), November 2009. Postdoctoral fellow, U. of Ottawa.
Monique Morin: “Network Evolution: Models, Evaluation, and Reconstruction,” Ph.D. (UNM), August 2007, Adjunct Assistant Professor, U. New Mexico at Los Alamos.
Michael Collins: “Two Studies in Combinatorial Optimization: Minimum-Link Tours and Contact Map Alignments,” Ph.D. (UNM), May 2005, Member of the Technical Staff, Sandia National Laboratories, New Mexico.
Jijun Tang: “Phylogeny Reconstruction from Gene-Order Data,” Ph.D. (UNM), August 2004, Assoc. Prof. of Computer Science & Engineering, U. South Carolina.
Srinivas Doddi: “Approximation Algorithms for Some Packing and Covering Problems,” Ph.D. (UNM), December 2000. Staff scientist, Timbre Technologies, San Jose, CA.
Ali Boroujerdi: “Joint Routing and Persistency,” Ph.D. (UNM), December 1994. Staff scientist, Naval Research Laboratory, Washington DC.
Ali Kooshesh: “Structuring Techniques for Path and Visibility Problems,” Ph.D. (UNM), December 1992. Prof. of Computer Science, Sonoma State College, CA.
Mark Hoover: “Complexity, Structure and Algorithms for Edge-Partition Problems,” Ph.D. (UNM), December 1990. Educational Testing Service, Princeton, NJ.
Chea-Tin (Tim) Tseng: “The Design of a Non-Parametric Classification System,” Ph.D. (UNM, in EE), May 1989. Import-export, California and Taiwan.

M.S. Students Supervised (since 2000):

- Alisa Yurovsky: “A phylogenetic investigation of flu strains,” MS (EPFL) in progress.
Kremena Diatchka: “Phylogenetic boosting for regulatory network inference with continuous parameters,” MS (EPFL), February 2009.
Thomas Turnherr: “Population estimation and analysis of human embryonic stem cell cultures,” MS (EPFL), December 2007.
Maryam Zaheri: “Using phylogenetic information to improve the inference of regulatory networks,” MS (EPFL), December 2007; PhD student in Biology, U. Lausanne.
Masoud Alipour: “Impact of alignment size and sampling proportion on bootstrap support values for phylogenetic trees,” MS (EPFL), December 2007; PhD student, EPFL.

M.S. Students Supervised (since 2000, cont'd):

- Eric Gottlieb: "Comparing large sets of phylogenetic trees," MS (UNM), May 2007; staff member, Sandia National Laboratories.
- Moulik Kothari: "Using transpositions distances in phylogenetic reconstruction from gene-order data," MS (UNM), May 2006.
- James Tanzola: "Point labeling for geographic information systems," MS, December 2005; manager, Electronic Clearing House, Albuquerque.
- Ashish Agarwal: "DistPlot: Web-based graphical tool for sequence distance analysis," MS, August 2005; MBA student, Carnegie-Mellon U.
- Sung-Hee Lee: "Approximate bottom-line dead-end elimination," MS, August 2005.
- Ning Tao: "FindModel: Identifying an evolutionary model from a set of sequences," MS, August 2005; staff developer, Los Alamos National Laboratory.
- Ke Ye: "A comparison of EST clustering algorithms," MS, August 2005.
- Chunai Cai: "Modeling and filtering for large-array radioastronomy data," MS, May 2005; staff programmer, Very Large Array radio observatory, New Mexico.
- Nicholas Pattengale: "Mathematical structures in the space of phylogenetic trees," MS, May 2005; staff member, Sandia National Laboratories.
- Mahesh Kulkarni: "Database organization and querying for phylogenetic applications," MS, December 2004; bioinformatics consultant, Glaxo-Smith-Kline.
- Zachariah Betz: "Clustering for phylogenetic reconstruction," MS, December 2004.
- Joel Earnest-DeYoung: "Massive gene loss among closely related bacteria: a phylogenetic investigation," MS, August 2004; staff member, Foss Analytical A/S (Denmark).
- Tao Liu: "Quartet-based methods in phylogenetic reconstruction from gene-order data," MS, August 2004; developer, Access Solutions Inc., Albuquerque.
- Anna Tholse: "Identifying and reconstructing hybridization events," MS, August 2003; software designer, Microsoft Inc., Dublin (Ireland).
- John Kitlinger: "Visibility graph among polygonal obstacles: an experimental comparison of algorithms," MS, August 2003; high-school teacher, NM.
- Matthew Fricke: "Phylogeny reconstruction with neural networks," MS, August 2003; staff programmer, biophysics research program, UNM.
- Zhan Li: "Shared-memory parallel implementations," MS, May 2003; research programmer, Penn. State U.
- Jingkun Yu: "An experimental comparison of data structures and algorithms for multidimensional rectilinear geometric queries," MS, August 2002; Beijing (China).
- Jijun Tang: "Algorithms for phylogeny reconstruction from gene-order data," MS, May 2002; Asst. Prof., U. South Carolina.
- Yan Xu: "A comparison of convex hull algorithms," MS, May 2002; staff member, Los Alamos National Laboratory.
- Adam Siepel: "The inversion median in computational biology," MS, December 2001; Asst. Prof., Cornell U.
- Cara Slutter: MS December 2001; staff developer, NM State Court, NM.
- Russell Waymire: MS May 2001; staff member, Sandia National Laboratories.
- Rongkun Zhao: "Learning in Bayesian networks," MS, December 2000; staff developer, Houston school district, Houston.

Courses Taught:

Freshman: discrete mathematics, computer literacy.

Sophomore: programming techniques, data structures.

Junior-Senior: data structures and algorithms, operating systems.

Senior-Graduate: algorithms, data structures, computer architecture, image and pattern analysis.

Graduate: computational biology, computational geometry, computability theory, complexity theory, optimization and approximation algorithms, parallel algorithms, pattern recognition, randomized and on-line algorithms, machine learning.

Courses Introduced (EPFL):

Topics in Bioinformatics I (introduced 2006, with P. Bücher and F. Naef).

Topics in Bioinformatics II (introduced 2007, with P. Bücher and F. Naef).

Computational Molecular Biology (introduced 2007).

Theory of Computation (introduced 2010).

Courses Introduced (UNM):

CS 303: design and analysis of algorithms (introduced 1984).

CS 461: data structures and algorithms (introduced 1982, redesigned 1990, 1998).

CS 401: preparation for theory (introduced 1998).

CS 432: image and pattern analysis (introduced 1983, with E. Angel & J. Brayer).

CS 442: parallel processing (introduced 1991, with S. Forrest & A.B. Maccabe).

CS 500: introduction to the theory of computation (introduced 1994).

CS 502: complexity theory (introduced 1981, redesigned 1988).

CS 503: computability theory (introduced 1982).

CS 506: computational geometry (introduced 1990, redesigned 1996).

CS 509: parallel algorithms (introduced 1992).

CS 531: pattern recognition (introduced 1981).

CS 561: data structures and algorithms (introduced 2003).

CS 591: machine learning (introduced 1991, with S. Forrest).

CS 591: randomized and on-line algorithms (introduced 1996).

CS 591: computational molecular biology (introduced 2001, with D. Sankoff).

CS 602: advanced complexity theory (introduced 1996).

Teaching Awards (UNM):

Students' Faculty Recognition Award (secret ballot vote of graduating seniors and graduate students for the professor who had the most impact on their education), 1993, 1994, 1995, 1996.

Selected as one of 14 UNM faculty members to serve as mentor for the Regents' Scholars program in its inaugural year.

Teaching Excellence Award, School of Engineering, 1991.

Graduate Teacher of the Year Award, The University of New Mexico, 1990.

Curriculum Development (UNM):

As chair of the graduate committee (1981–1995), graduate advisor (1984–1991), and graduate unit chair (2003–2006), I was responsible for developing and updating the M.S. and Ph.D. curricula, including course requirements and examinations as well as general directions. As a member of the UNM core curriculum task force, I helped develop a university-wide interdisciplinary curriculum.