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**Personal Data:**

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

**Languages:**

English, French, German, elements of Chinese and 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*, School of Computer and Communication Sciences, EPFL (Swiss Federal Institute of Technology). Holder of the Chair of Bioinformatics, teaching and research in algorithms, theory of computation, and computational biology.
- 2006– *Group Leader*, Swiss Institute of Bioinformatics.
- 2009–2013 *Director*, BS & MS programs in CS, EPFL.
- 2003–2006 *Director*, CIPRES ([www.phylo.org](http://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        *NIH College of Reviewers:* charter member, 2010–present.  
*Steering Committee:* ALENEX (Workshop on Alg. Engin. & Experiments): 2002–present.  
*Program Committees:* 13th Workshop on Alg. Eng. & Experiments ALENEX’12, 5th IEEE Conf. Bioinformatics & Biomedicine BIBM’12, 10th RECOMB Workshop on Compar. Genomics RECOMB-CG’12, 12th Workshop on Algs. in Bioinformatics WABI’12.

**Recent Professional Activities:**

- Editor-in-Chief    ACM Journal of Experimental Algorithmics 1995–2003 (founding editor).
- Assoc. Editor      IEEE/ACM Trans. on Computational Biology and Bioinformatics 2003–2008.
- Chair            *NIH Panel*, National Centers for Biomedical Computing (June 2010).  
*NIH Study Section:* Biodata Mgt. 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. Engin. & Experiments ALENEX’00.
- Member        *NIH Study Section:* Biodata Mgt. and Analysis (BDMA), charter member, 2004–2008.  
*Steering Committee:* ESA (European Symp. on Algs.) 1999–2002.  
*Program Committees (international confs.):* BIBE (Conf. Bioinformatics & Bioeng.) 2009; ALENEX (SIAM Workshop on Alg. Eng. & Experiments) 1999–2004, 2007, 2011–2012; BIBM (IEEE Conf. on Bioinformatics & Biomedicine) 2007–2009, 2011–2012; COCOON (Computing & Combinatorics Conf.) 2003, 2006; CSB (Comput. Systems Bioinformatics Conf.) 2009–2010; ECCB (European Conf. on Comput. Biol.) 2005, 2008–2010; GIW (Int’l Conf. on Genome Informatics) 2007–2009; ISBRA (Int’l Symp. on Bioinformatics Res. & Appls.) 2008–2010; ISMB (Conf. on Intelligent Systems for Mol. Bio.) 2006–2009; PRIB (IAPR Conf. on Pattern Recognition in Bioinformatics) 2007–2008; RECOMB (Conf. Research on Comput. Mol. Bio.) 2010–2011; RECOMB-CG (RECOMB Workshop on Compar. Genomics) 2005–2006, 2008–2012; SODA (SIAM Symp. on Discrete Algs.) 1999; WABI (Workshop on Algs. in Bioinformatics) 2001–2012; 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 15th Pacific Symp. on Biocomputing PSB’10 and 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 2000):**

- PI on "Models and algorithms for genome evolution," funded by the Swiss National Science Foundation, 2008–2011, CHF 150K.
- PI on "Models and algorithms for noncoding genes," an IPhD project sponsored by SystemsX.ch, 2008–2011, CHF 150K.
- 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).

**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  $\mathcal{NCP}$ . 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 2000):**

- Lin, Y., Rajan, V., and Moret, B.M.E., “A metric for phylogenetic trees based on matching,” *IEEE/ACM Trans. Comput. Biology & Biocomp.*, accepted, to appear (2012). (*special issue on ISBRA'11*).
- Christinat, Y., and Moret, B.M.E., “Inferring transcript phylogenies,” *Proc. 5th IEEE Conf. Bioinformatics & Biomedicine BIBM'11*, 208–215, IEEE Press (2011).
- Lin, Y., and Moret, B.M.E., “A new genomic evolutionary model for rearrangements, duplications, and losses that applies across eukaryotes and prokaryotes,” *J. Computational Biology* **18**, 9, 1055–1064 (2011). (*special issue on RECOMB-CG'10*).
- Lin, Y., Rajan, V., and Moret, B.M.E., “Fast and accurate phylogenetic reconstruction from high-resolution whole-genome data and a novel robustness estimator,” *J. Computational Biology* **18**, 9, 1131–1139 (2011). (*special issue on RECOMB-CG'10*).
- Lin, Y., Rajan, V., and Moret, B.M.E., “Bootstrapping phylogenies inferred from rearrangement data,” in *Proc. 11th Workshop on Algs. in Bioinformatics WABI'11*, in *LNCS 6833*, 175–187, Springer Verlag (2011).
- Xu, A.W., and Moret, B.M.E., “GASTS: parsimony scoring under rearrangements,” in *Proc. 11th Workshop on Algs. in Bioinformatics WABI'11*, in *LNCS 6833*, 351–363, Springer Verlag (2011).
- Yurovsky, A., and Moret, B.M.E., “FluReF: an automated flu virus reassortment finder based on phylogenetic trees,” *BMC Genomics* **12**, Suppl. 2, S3 (2011). (*special issue on BIBM'10*).
- Lin, Y., Rajan, V., and Moret, B.M.E., “A metric for phylogenetic trees based on matching,” *Proc. 7th Int'l Symp. Bioinformatics Research & Appls. ISBRA'11*, in *LNCS 6398*, 197–208 (2011).
- Zhang, X., and Moret, B.M.E., “ProPhyC: a probabilistic phylogenetic model for refining regulatory networks,” *Proc. 7th Int'l Symp. Bioinformatics Research & Appls. ISBRA'11*, in *LNCS 6398*, 228–239 (2011).
- Pattengale, N.D., Aberer, A.A., Swenson, K.M., Stamatakis, A., and Moret, B.M.E., “Uncovering hidden phylogenetic consensus in large datasets,” *IEEE/ACM Trans. Comput. Biology & Biocomp.* **8**, 4 (2011), 902–911. (*special issue on ISBRA'10*).
- Yurovsky, A., and Moret, B.M.E., “FluRF: an automated flu virus reassortment finder based on phylogenetic trees,” *Proc. 4th IEEE Conf. Bioinformatics & Biomedicine BIBM'10*, 579–584, IEEE Press, 2010.
- Lin, Y., and Moret, B.M.E., “A new genomic evolutionary model for rearrangements, duplications, and losses that applies across eukaryotes and prokaryotes,” *Proc. 8th RECOMB Workshop on Comparative Genomics RECOMB-CG'10*, in *LNCS 6398*, 228–239 (2010).
- Lin, Y., Rajan, V., and Moret, B.M.E., “Fast and accurate phylogenetic reconstruction from high-resolution whole-genome data and a novel robustness estimator,” *Proc. 8th RECOMB Workshop on Comparative Genomics RECOMB-CG'10*, in *LNCS 6398*, 137–148 (2010).
- Pattengale, N.D., Swenson, K.M., and Moret, B.M.E., “Uncovering hidden phylogenetic consensus,” *Proc. 6th Int'l Symp. Bioinformatics Research & Appls. ISBRA'10*, in *LNCS 6053*, 128–139 (2010).
- Pattengale, N.D., Alipour, M., Bininda-Emonds, O.R.P., Moret, B.M.E., and Stamatakis, A., “How many bootstrap replicates are necessary?” *J. Comput. Biol.* **17**, 3 (2010), 337–354 (*special issue on RECOMB'09*).
- Swenson, K.M., Rajan, V., Lin, Y., and Moret, B.M.E., “Sorting signed permutations by inversions in  $O(n \log n)$  time,” *J. Comput. Biol.* **17**, 3 (2010), 489–501 (*special issue on RECOMB'09*).
- Zhang, X., and Moret, B.M.E., “Refining transcriptional regulatory networks using network evolutionary models and gene histories,” *BMC Algorithms in Mol. Biol.* 2010, 5(1):1 (2010). (*special issue on best papers from WABI'09*).
- 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*, in *BMC Bioinformatics* 2010, 11 (Suppl. 1):S30.

**Refereed Publications (since 2000), cont'd:**

- 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*, in *BMC Bioinformatics* 2010, 11 (Suppl. 1):S54.
- 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. (*special issue on RECOMB-CG'08*).
- 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 RECOMB'06*).
- 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.

**Refereed Publications (since 2000), cont'd:**

- 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).
- Pattengale, N.D., and Moret, B.M.E., "Phylogenetic postprocessing," *Proc. IEEE Comput. Systems Bioinf. Conf. Workshops (CSBW'05)*, 57–58, 2005.
- Swenson, K.M., Pattengale, N.D., Moret, B.M.E., "Identifying orthologs: cycle splitting on the breakpoint graph," *Proc. IEEE Comput. Systems Bioinf. Conf. Workshops (CSBW'05)*, 65–68, 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).

**Refereed Publications (since 2000), cont'd:**

- 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.
- 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.
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- 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).
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**Refereed Publications (since 2000), cont'd:**

- 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.
- 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.

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

- “Defining and computing syntenic blocks,” invited address, *1st RECOMB Workshop on Open Problems in Algorithmic Biology RECOMB-AB’12* (2012).
- “Phylogenetic analysis: the Tree of Life, whole genomes, and beyond,” invited address, *5th IEEE Conference on Bioinformatics and Biomedicine BIBM’11* (2011).
- “How can we compare and summarize trees?,” invited address, *3rd RECOMB Workshop on Bioinformatics Education RECOMB-BE’11* (2011).
- “Phylogenetic analysis of whole genomes,” keynote, *7th Int’l Symposium on Bioinformatics Research and Applications ISBRA’11* (2011).
- “Computational challenges in comparative genomics,” tutorial, *15th Pacific Symp. on Bioinformatics PSB’10* (2010).
- “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 and the Tree of Life,” keynote, *Robert Cedergren Bioinformatics Symp.*, U. de Montréal, Nov. 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).
- “Algorithmic engineering: It’s all about speed,” invited lectures, *School on Algorithmic Engineering*, Rome, Sep. 2001.

**Postdocs Supervised:**

Xiuwei Zhang, 2011–current (EPFL).

Wei Xu, 2008–2010 (EPFL). Postdoctoral fellow, Harvard Medical School.

Alexandros Stamatakis, 2006–2008 (EPFL). Senior group leader, Heidelberg Research Institute, Germany.

Tanya Berger-Wolf, NSF Postdoctoral Associate, 2002–2004. Assoc. Prof. of Computer Science, U. Illinois at Chicago.

Tiffani Williams, Sloan Postdoctoral Fellow in Comput. Molecular Biol., 2002–2004. Asst. Prof. of Computer Science, Texas A&M.

**Ph.D. Students Supervised (EPFL):**

Mingfu Shao, 2012–present.

Min Ye, 2011–present.

Cristina Ghiurcuta, 2009–present.

Nishanth Nair, 2009–present.

Vaibhav Rajan, 2008–2012.

Yu Lin, 2007–2012.

Yann Christinat, 2007–2012.

Xiuwei Zhang: “Transcriptional regulatory networks across species: evolution, inference, and refinement,” Ph.D., August 2011. Postdoctoral Fellow, EPFL.

Krister Swenson: “Genomic distances in the presence of arbitrary deletions, insertions, duplications, and inversions,” Ph.D., November 2009. Postdoctoral Fellow, McGill U.

**Ph.D. Students Supervised (UNM):**

Nicholas Pattengale: “Efficient Algorithms for Phylogenetic Post-Analysis,” Ph.D., March 2010. Senior Member of the Technical Staff, Sandia Nat'l Labs, Albuquerque.

Monique Morin: “Network Evolution: Models, Evaluation, and Reconstruction,” Ph.D., 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., May 2005. Member of the Technical Staff, Sandia Nat'l Labs, Albuquerque.

Jijun Tang: “Phylogeny Reconstruction from Gene-Order Data,” Ph.D., August 2004. Assoc. Prof. of Computer Science & Engineering, U. South Carolina.

Srinivas Doddi: “Approximation Algorithms for Some Packing and Covering Problems,” Ph.D., December 2000. Staff Scientist, Timbre Technologies, San Jose, CA.

Ali Boroujerdi: “Joint Routing and Persistency,” Ph.D., December 1994. Staff Scientist, Naval Research Laboratory, Washington DC.

Ali Kooshesh: “Structuring Techniques for Path and Visibility Problems,” Ph.D., December 1992. Prof. of Computer Science, Sonoma State College, CA.

Mark Hoover: “Complexity, Structure and Algorithms for Edge-Partition Problems,” Ph.D., December 1990.

Chea-Tin (Tim) Tseng: “The Design of a Non-Parametric Classification System,” Ph.D. (in EE), May 1989.

**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.