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Education

PhD in Computer Science, University of Arizona, December 1991. Gene Myers, thesis advisor.

MS in Computer Science, University of Arizona, December 1986.

BS in Mechanical Engineering, University of Arizona, May 1985.

Professional experience

Associate Professor, University of Arizona, BIO5 Institute, August 2005–present.

Associate Professor, University of Arizona, Department of Computer Science, August 2000–present.

Associate Professor, University of Georgia, Department of Computer Science, August 1999–July 2000.

Assistant Professor, University of Georgia, Department of Computer Science, January 1995–July 1999.

Visiting Fellow, Max-Planck-Institut für Informatik, Saarbrücken, Germany, June–July 1996, June–July 1997.

Visiting Fellow, DIMACS Center for Discrete Mathematics and Theoretical Computer Science, Rutgers University, October–December 1994.

Postdoctoral Fellow, University of California at Davis, Department of Computer Science, January 1992–September 1994. Dan Gusfield, postdoctoral advisor.

Postdoctoral Fellow, Université de Montréal, Centre de Recherches Mathématiques, Montréal, Canada, January–December 1991. David Sankoff, postdoctoral advisor.

Honors and awards

National Science Foundation CAREER Award, 1997–2001.

Lilly Teaching Fellow, University of Georgia, 1997–98.

Department of Energy Human Genome Distinguished Postdoctoral Fellowship, 1993–94.

National Science Foundation Postdoctoral Fellowship, Program in Mathematics and Molecular Biology, 1992–93.

Centre de Recherches Mathématiques Postdoctoral Fellowship, Université de Montréal, 1991.

Research interests

Computational biology, design and analysis of algorithms, algorithm implementation, combinatorial optimization.

Teaching interests

Design and analysis of algorithms, data structures, theory of computation, algorithms for computational biology, bioinformatics.

Journal papers

- Kim, E. and J. Kececioglu. “Learning scoring schemes for sequence alignment from partial examples.” To appear in *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 5:4, 2008.
- Wheeler, T.J. and J.D. Kececioglu. “Multiple alignment by aligning alignments.” *Bioinformatics* 23, Proceedings of the 15th ISCB Conference on Intelligent Systems for Molecular Biology (ISMB), i559–i568, 2007.
- Kececioglu, J., H.-P. Lenhof, K. Mehlhorn, P. Mutzel, K. Reinert and M. Vingron. “A polyhedral approach to sequence alignment problems.” *Discrete Applied Mathematics* 104, 143–186, 2000.
- Kececioglu, J. and D. Gusfield. “Reconstructing a history of recombinations from a set of sequences.” *Discrete Applied Mathematics* 88, 239–260, 1998.
- Ravi, R. and J. Kececioglu. “Approximation algorithms for multiple sequence alignment under a fixed evolutionary tree.” *Discrete Applied Mathematics* 88, 355–366, 1998.
- Taylor, E.W., A. Bhat, R.G. Nadimpalli, W. Zhang and J. Kececioglu. “HIV-1 encodes a sequence overlapping *env* gp41 with highly significant similarity to selenium-dependent glutathione peroxidases.” *Journal of Acquired Immune Deficiency Syndromes and Human Retrovirology* 15:5, 393–394, 1997.
- Christof, T., M. Jünger, J. Kececioglu, P. Mutzel, and G. Reinelt. “A branch-and-cut approach to physical mapping of chromosomes by unique end-probes.” *Journal of Computational Biology* 4:4, 433–447, 1997.
- Kececioglu, J., M. Li, and J. Tromp. “Inferring a DNA sequence from erroneous copies.” *Theoretical Computer Science* 185:1, 3–13, 1997.
- Sankoff, D., G. Sundaram, and J. Kececioglu. “Steiner points in the space of genome rearrangements.” *International Journal of Foundations of Computer Science* 7:1, 1–9, 1996.
- Gupta, S., J. Kececioglu, and A. Schäffer. “Improving the practical space and time efficiency of the shortest-paths approach to sum-of-pairs multiple sequence alignment.” *Journal of Computational Biology* 2:3, 459–472, 1995.
- Kececioglu, J. and E. Myers. “Combinatorial algorithms for DNA sequence assembly.” *Algorithmica* 13:1/2, 7–51, 1995.
- Kececioglu, J. and D. Sankoff. “Exact and approximation algorithms for sorting by reversals, with application to genome rearrangement.” *Algorithmica* 13:1/2, 180–210, 1995.
- Lipman, D., S. Altschul, and J. Kececioglu. “A tool for multiple sequence alignment.” *Proceedings of the National Academy of Science USA* 86, 4412–4415, 1989.

Conference papers

- Kim, E. and J. Kececioglu. “Inverse sequence alignment from partial examples.” Proceedings of the 7th EATCS/ISCB Workshop on Algorithms in Bioinformatics (WABI), Springer-Verlag Lecture Notes in Bioinformatics 4645, 359–370, 2007.

- Kececioglu, J. and E. Kim. “Simple and fast inverse alignment.” Proceedings of the 10th *Conference on Research in Computational Molecular Biology* (RECOMB), Springer-Verlag Lecture Notes in Bioinformatics 3909, 441–455, 2006.
- Collberg, C., E. Carter, S. Debray, A. Huntwork, J. Kececioglu, C. Linn and M. Stepp. “Dynamic path-based software watermarking.” Proceedings of the 25th *ACM Conference on Programming Language Design and Implementation* (PLDI), 107–118, 2004.
- Kececioglu, J. and D. Starrett. “Aligning alignments exactly.” Proceedings of the 8th *ACM Conference on Research in Computational Molecular Biology* (RECOMB), 85–96, 2004.
- Kececioglu, J. and J. Yu. “Separating repeats in DNA sequence assembly.” Proceedings of the 5th *ACM Conference on Research in Computational Molecular Biology* (RECOMB), 176–183, 2001.
- Kececioglu, J., S. Shete and J. Arnold. “Reconstructing distances in physical maps of chromosomes with nonoverlapping probes.” Proceedings of the 4th *ACM Conference on Research in Computational Molecular Biology* (RECOMB), 183–192, 2000.
- Christof, T. and J. Kececioglu. “Computing physical maps of chromosomes with nonoverlapping probes by branch-and-cut.” Proceedings of the 3rd *ACM Conference on Research in Computational Molecular Biology* (RECOMB), 115–123, 1999.
- Kececioglu, J. and J. Pecqueur. “Computing maximum-cardinality matchings in sparse general graphs.” Proceedings of the 2nd *Workshop on Algorithm Engineering* (WAE), 121–132, 1998. <http://www.mpi-sb.mpg.de/~wae98/PROCEEDINGS>
- Kececioglu, J. and W. Zhang. “Aligning alignments.” Proceedings of the 9th *Symposium on Combinatorial Pattern Matching* (CPM), Springer-Verlag Lecture Notes in Computer Science 1448, 189–208, 1998.
- Reinert, K., H.-P. Lenhof, P. Mutzel, K. Mehlhorn, and J. Kececioglu. “A branch-and-cut algorithm for multiple sequence alignment.” Proceedings of the 1st *ACM Conference on Research in Computational Molecular Biology* (RECOMB), 241–249, 1997.
- Christof, T., M. Jünger, J. Kececioglu, P. Mutzel, and G. Reinelt. “A branch-and-cut approach to physical mapping with end-probes.” Proceedings of the 1st *ACM Conference on Research in Computational Molecular Biology* (RECOMB), 84–92, 1997.
- Ravi, R. and J. Kececioglu. “Approximation algorithms for multiple sequence alignment under a fixed evolutionary tree.” Proceedings of the 6th *Symposium on Combinatorial Pattern Matching* (CPM), Springer-Verlag Lecture Notes in Computer Science 937, 330–339, 1995.
- Gupta, S., J. Kececioglu and A. Schäffer. “Making the shortest-paths approach to sum-of-pairs multiple sequence alignment more space efficient in practice.” Proceedings of the 6th *Symposium on Combinatorial Pattern Matching* (CPM), Springer-Verlag Lecture Notes in Computer Science 937, 128–143, 1995.
- Kececioglu, J. and R. Ravi. “Of mice and men: Algorithms for evolutionary distances between genomes with translocation.” Proceedings of the 6th *ACM-SIAM Symposium on Discrete Algorithms* (SODA), 604–613, 1995.
- Kececioglu, J. and D. Gusfield. “Reconstructing a history of recombinations from a set of sequences.” Proceedings of the 5th *ACM-SIAM Symposium on Discrete Algorithms* (SODA), 471–480, 1994.
- Kececioglu, J. and D. Sankoff. “Efficient bounds for oriented chromosome-inversion distance.” Proceedings of the 5th *Symposium on Combinatorial Pattern Matching* (CPM), Springer-Verlag Lecture Notes in Computer Science 807, 307–325, 1994.

Kececioğlu, J. and D. Sankoff. “Exact and approximation algorithms for the inversion distance between two chromosomes.” Proceedings of the 4th *Symposium on Combinatorial Pattern Matching* (CPM), Springer-Verlag Lecture Notes in Computer Science 684, 87–105, 1993.

Kececioğlu, J. “The maximum trace problem in multiple sequence alignment.” Proceedings of the 4th *Symposium on Combinatorial Pattern Matching* (CPM), Springer-Verlag Lecture Notes in Computer Science 684, 106–119, 1993.

Technical reports

Zhang, W., J. Kececioğlu and E.W. Taylor. “Assessing the relatedness of an aligned family and a proposed member through accurate sequence alignment.” Technical Report 97-3, Department of Computer Science, The University of Georgia, August 1997.

Dissertation

Kececioğlu, J. *Exact and Approximation Algorithms for DNA Sequence Reconstruction*. Technical Report 91-26, Department of Computer Science, The University of Arizona, December 1991.

Book reviews

Review of *Sequence Analysis Primer*, Michael Gribskov and John Devereux, editors, Stockton Press, New York, 1991. In *Journal of Classification* 10, 144–148, 1993.

Software

Wheeler, T. and J. Kececioğlu. **Opal**: forming and polishing multiple sequence alignments by optimally aligning alignments. Version 0.3.7, 2007. <http://opal.cs.arizona.edu>

Kim, E. and J. Kececioğlu. **Ipa**: inverse parametric sequence alignment via linear programming. Version 1.0, 2007. <http://inversealign.cs.arizona.edu>

Starrett, D., T. Wheeler and J. Kececioğlu. **AlignAlign**: optimal alignment of alignments. Version 0.9.7, 2005. <http://alignalign.cs.arizona.edu>

Kececioğlu, J., A. Schäffer, S. Gupta, S. Altschul and D. Lipman. **MSA**: sum-of-pairs multiple sequence alignment. Version 2.0, 1995. <ftp://fastlink.nih.gov/pub/msa>

Grants

US Department of Education, Graduate Assistance in Areas of National Need (GAANN) Program, “Graduate Assistance in Computer Science: An Area of National Need,” J. Kececioğlu (PI), A. Efrat, R. Gupta and S. Westbrook (co-PIs), Grant P200A070545, August 2007–July 2010, \$383,643.

US National Science Foundation, Integrative Graduate Education and Research Traineeship (IGERT) Program, “IGERT Program in Comparative Genomics,” M. Nachman (PI), D. Vercelli, J. Kececioğlu, N. Moran and V. Chandler (co-PIs), Grant 0654435, July 2007–June 2012, \$2,999,835.

US National Science Foundation, Biological Databases and Informatics Program, “Robust Tools for Biological Sequence Analysis,” J. Kececioğlu (PI), Grant DBI-0317498, August 2003–July 2008, \$500,498.

US National Science Foundation, Plant Genome Research Program, “Cross-linked Sorghum and Rice Physical Maps as a Foundation for Analyzing Genome Structure, Function and Variation in C_4 Grasses,” A. Paterson (PI), L. Pratt, M.-M. Cordonnier-Pratt, S. Bhandarkar, and J. Kececioğlu (co-PIs), Grant DBI-9872649, September 1998–August 2001, \$3,246,755.

US National Science Foundation, CAREER Award, Computational Biology Activities Program, “Applied Algorithms for Computational Molecular Biology,” J. Kececioğlu (PI), Grant DBI-0196202, September 1997–August 2002, \$241,111.

US National Science Foundation, Program in Mathematics and Molecular Biology, Travel support for minisymposium “Discrete Algorithms in Computational Biology II” at the SIAM Conference on Discrete Mathematics, June 1996, \$5,000.

US National Science Foundation, Program in Mathematics and Molecular Biology, Travel support for minisymposium “Discrete Algorithms in Computational Biology I” at the SIAM Annual Meeting, October 1995, \$4,000.

Selected professional activities

Associate Editor, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2008–present. <http://www.computer.org/tcbb/>

Editorial Board, *Algorithms for Molecular Biology*, 2005–present. <http://almob.org>

Scientific Advisory Board, Max-Planck-Institut für Informatik, Saarbrücken, Germany, 2003–06.

Conference Chair, RECOMB 2009 (13th *Conference on Research in Computational Molecular Biology*), Tucson, Arizona. <http://www.bio5.org/recomb2009>

Program Committees of RECOMB 2008, 2002, 1999 (*Conference on Research in Computational Molecular Biology*); ISMB 2008 (*Conference on Intelligent Systems for Molecular Biology*); WABI 2008, 2001 (*Workshop on Algorithms in Bioinformatics*); ISBRA 2008, 2007 (*International Symposium on Bioinformatics Research and Applications*); APBC 2006 (*Asia-Pacific Bioinformatics Conference*); CPM 2000 (*Symposium on Combinatorial Pattern Matching*); ALENEX 2000 (*Workshop on Algorithm Engineering and Experiments*); SPIRE 2001, 2000 (*Symposium on String Processing and Information Retrieval*).

NSF Review Panelist, Biological Databases and Informatics Panel, 2005; Theory of Computing Panel, 2005; Medium ITR Bioinformatics Panel, 2004; Small ITR Bioinformatics Panel, 2003; Computational Biology Activities Panel, 1996.

NIH Review Panelist, Software Development and Maintenance Panel, 2006.

Organizing Committee, 4th DIMACS *Algorithm Implementation Challenge* on Sequence Assembly and Genome Rearrangements, Center for Discrete Mathematics and Theoretical Computer Science, Piscataway, New Jersey, 1995.

Organizing Committee, DIMACS Workshop on Sequence Alignment, Special Year on Mathematical Support for Molecular Biology, Center for Discrete Mathematics and Theoretical Computer Science, Piscataway, New Jersey, 1994.

Referee for the *Journal of the ACM*, *ACM Computing Surveys*, *SIAM Journal on Computing*, *Algorithmica*, *Journal of Algorithms*, *Discrete Applied Mathematics*, *Information Processing Letters*, *Journal of Computational Biology*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, and *Bioinformatics*.

Students

Postdoctoral

Thomas Christof. *Branch-and-Cut Algorithms for Physical Mapping of Chromosomes*. Department of Computer Science, University of Georgia, 1998.

PhD

Eagu Kim. *Inverse Parametric Alignment for Accurate Biological Sequence Comparison*. PhD dissertation, Department of Computer Science, The University of Arizona, August 2008.

Dean Starrett. *Optimal Alignment of Multiple Sequence Alignments*. PhD dissertation, Department of Computer Science, The University of Arizona, August 2008.

MS

Jonathan Myers. *Inferring Fragment Overlaps in DNA Sequence Assembly*. MS thesis, Department of Computer Science, University of Georgia, 2001.

Jun Yu. *Separating Repeats in DNA Sequence Assembly*. MS thesis, Department of Computer Science, University of Georgia, 2000.

Justin Pecqueur. *An Experimental Study of Edmonds' Algorithm for Maximum-Cardinality Matching in Sparse General Graphs*. MS thesis, Department of Computer Science, University of Georgia, 1998.

Yuhua Liu. *An Implementation of the Suffix-Tree Data Structure and its Application to String Matching*. MS thesis, Department of Computer Science, University of Georgia, 1997.

Selected invited presentations

“Learning scoring schemes for sequence alignment from partial examples.” INFORMS Annual Meeting, Session on Sequence Analysis in Computational Biology, Washington, DC, October 13, 2008.

“How to find optimal alignment parameters.” Department of Microbiology, Montana State University, Bozeman, November 4, 2005.

“Multiple sequence alignment: complexity, approximation, and exact solution.” CRM Summer School on the Mathematics of Bioinformatics, Centre de Recherches Mathématiques, Université de Montréal, Canada, August 29, 2003.

“Reconstructing a history of recombinations from a set of sequences.” Max-Planck-Institut für Informatik, Saarbrücken, Germany, June 18, 2003.

“Computing maps of chromosomes that are provably good.” Minisymposium on Computational Challenges in Computational Biology, University of Tennessee, Knoxville, August 17, 2001.

“Separating repeats in DNA sequence assembly.” RECOMB Satellite Meeting on DNA Sequence Assembly, University of Southern California, Los Angeles, May 20, 2001.

“Computing optimal maps of chromosomes by branch-and-cut.” Minisymposium on Computational Genetics, Case Western Reserve University, Cleveland, Ohio, October 20, 2000.

“Physical mapping of chromosomes with nonoverlapping probes” (2 hour tutorial). PIMS Workshop on Mathematical Genomics, Pacific Institute for the Mathematical Sciences, University of British Columbia, Vancouver, Canada, June 2, 1999.

- “Computing physical maps of chromosomes with nonoverlapping probes by branch-and-cut.” Institute for Biomedical Computing, Washington University, St. Louis, Missouri, May 4, 1999.
- “A survey of multiple sequence alignment” (3 hour tutorial). CISM Summer School on Computational Biology, International Center for Mechanical Sciences, Udine, Italy, June 12, 1998.
- “A new approach to maximum-likelihood physical-mapping by clone-clone hybridization.” Max-Planck-Institut für Informatik, Saarbrücken, Germany, July 2, 1997.
- “A new approach to maximum-likelihood physical-mapping by clone-clone hybridization.” Institute for Algorithms and Scientific Computing, German National Research Center for Information Technology, Sankt Augustin, Germany, June 27, 1997.
- “A new approach to maximum-likelihood physical-mapping by clone-clone hybridization.” Department of Applied Mathematics, University of Heidelberg, Germany, June 26, 1997.
- “Discrete algorithms on sequences” (1 hour tutorial). Mathematics and Molecular Biology V: Statistics and Inference in Molecular Biology, Santa Fe, New Mexico, January 14, 1997.
- “Computing optimal multiple sequence alignments.” 2nd Sandia Workshop on Computational Molecular Biology, DIMACS Special Year on Mathematical Support for Molecular Biology, Albuquerque, New Mexico, March 6, 1996.
- “A tour of multiple sequence alignment theory” (3 hour tutorial). Computational Genomics '95, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, November 2, 1995.
- “Computing optimal multiple sequence alignments.” Max-Planck-Institut für Informatik, Saarbrücken, Germany, November 22, 1995.
- “Algorithms for evolutionary distances between genomes with translocations.” Dagstuhl Seminar on Molecular Bioinformatics, Schloss Dagstuhl, Wadern, Germany, July 10, 1995.
- “Combinatorial algorithms for DNA sequencing and mapping” (4 hour tutorial). 6th Symposium on Combinatorial Pattern Matching, Helsinki, Finland, July 4, 1995.
- “A tour of multiple sequence alignment theory.” DIMACS Workshop on Sequence Alignment, Center for Discrete Mathematics and Theoretical Computer Science, Rutgers University, Piscataway, New Jersey, November 11, 1994.
- “DNA sequencing in the presence of errors.” IMA Summer Program on Molecular Biology, Institute for Mathematics and its Applications, University of Minnesota, Minneapolis, July 6, 1994.
- “Efficient bounds for oriented chromosome-inversion distance.” Minisymposium on Combinatorial Methods for Genome Rearrangements, University of Southern California, Los Angeles, March 18, 1994.
- “Reconstructing a history of recombinations from a set of sequences.” Department of Computer Science, Pennsylvania State University, University Park, January 20, 1994.
- “The maximum trace problem in multiple sequence alignment.” Department of Mathematics, University of Southern California, Los Angeles, March 11, 1993.
- “Exact and approximation algorithms for DNA sequence reconstruction.” Department of Computer Science, University of California, Berkeley, January 30, 1992.

References

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David Sankoff, Fellow of the Canadian Institute for Advanced Research; Centre de Recherches Mathématiques; Université de Montréal; C.P. 6128, succ. A; Montréal, Québec H3C 3J7; Canada. Tel: (514) 343-7574. Fax: (514) 343-2254. Email: sankoff@ere.umontreal.ca

Dan Gusfield, Professor, Department of Computer Science, University of California, Davis, CA 95616. Tel: (916) 752-7131. Fax: (916) 752-4767. Email: gusfield@cs.ucdavis.edu

Richard Karp, Professor, Department of Computer Science and Engineering, University of Washington, Seattle, WA 98195-2350. Tel: (206) 543-4226. Email: karp@cs.washington.edu