# John D. Kececioglu

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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

Professor, University of Arizona, Department of Computer Science, August 2018–present.

Associate Head, Department of Computer Science, University of Arizona, January–August 2012.

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

Associate Professor, University of Arizona, Department of Computer Science, August 2000–July 2018.

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, awards, and recognitions

Senior Member, International Society for Computational Biology, 2017–present.

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

Design, analysis, and implementation of algorithms; bioinformatics and computational biology; astroinformatics and computational astronomy; combinatorial optimization.

## Teaching interests

Bioinformatics; design and analysis of algorithms; data structures; theory of computation; discrete mathematics.

## Conference papers

Krieger, S. and J. Kececioglu. "Computing robust optimal factories in metabolic reaction networks." Proceedings of the 28th *Conference on Research in Computational Molecular Biology* (RECOMB), Springer Lecture Notes in Computer Science 14758, 253–269, 2024.

Krieger, S. and J. Kececioglu. "Computing shortest hyperpaths for pathway inference in cellular reaction networks." Proceedings of the 27th *Conference on Research in Computational Molecular Biology* (RECOMB), Springer Lecture Notes in Bioinformatics 13976, 155–173, 2023.

Krieger, S. and J. Kececioglu. "Computing optimal factories in metabolic networks with negative regulation." *Bioinformatics* 38, Special Issue on Proceedings of the 30th ISCB *Conference on Intelligent Systems for Molecular Biology* (ISMB), i369–i377, 2022.

Krieger, S. and J. Kececioglu. "Fast approximate shortest hyperpaths for inferring pathways in cell signaling hypergraphs." Proceedings of the 21st ISCB/EATCS *Workshop on Algorithms in Bioinformatics* (WABI), Leibniz International Proceedings in Informatics 201, 20:1–20, 2021.

Krieger, S. and J. Kececioglu. "Predicting protein secondary structure by an ensemble through feature-based accuracy estimation." Proceedings of the 11th ACM *Conference on Bioinformatics, Computational Biology, and Health Informatics* (ACM-BCB), 29:1–10, 2020.

Krieger, S. and J. Kececioglu. "Boosting the accuracy of protein secondary structure prediction through nearest neighbor search and method hybridization." *Bioinformatics* 36, Special Issue on Proceedings of the 28th ISCB *Conference on Intelligent Systems for Molecular Biology* (ISMB), i317–i325, 2020.

DeBlasio, D. and J. Kececioglu. "Boosting alignment accuracy by adaptive local realignment." Proceedings of the 21st *Conference on Research in Computational Molecular Biology* (RECOMB), Springer Lecture Notes in Bioinformatics 10229, 1–17, 2017.

DeBlasio, D. and J. Kececioglu. "Predicting core columns of protein multiple sequence alignments for improved parameter advising." Proceedings of the 16th ISCB/EATCS *Workshop on Algorithms in Bioinformatics* (WABI), Springer Lecture Notes in Bioinformatics 9838, 77–89, 2016.

DeBlasio, D. and J. Kececioglu. "Ensemble multiple sequence alignment via advising." Proceedings of the 6th ACM *Conference on Bioinformatics, Computational Biology, and Health Informatics* (ACM-BCB), 452–461, 2015.

DeBlasio, D. and J. Kececioglu. "Learning parameter sets for alignment advising." Proceedings of the 5th ACM *Conference on Bioinformatics, Computational Biology, and Health Informatics* (ACM-BCB), 230–239, 2014.

DeBlasio, D., T. Wheeler and J. Kececioglu. "Estimating the accuracy of multiple alignments and its use in parameter advising." Proceedings of the 16th *Conference on Research in Computational Molecular Biology* (RECOMB), Springer Lecture Notes in Bioinformatics 7262, 45–59, 2012.

Kim, E., T. Wheeler and J. Kececioglu. "Learning models for aligning protein sequences with predicted secondary structure." Proceedings of the 13th *Conference on Research in Computational Molecular Biology* (RECOMB), Springer Lecture Notes in Bioinformatics 5541, 512–531, 2009.

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

Wheeler, T. and J. Kececioglu. "Multiple alignment by aligning alignments." *Bioinformatics* 23, Special Issue on Proceedings of the 15th ISCB *Conference on Intelligent Systems for Molecular Biology* (ISMB), i559–i568, 2007.

Kececioglu, J. and E. Kim. "Simple and fast inverse alignment." Proceedings of the 10th *Conference on Research in Computational Molecular Biology* (RECOMB), Springer 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 Programmming 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 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 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 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 Lecture Notes in Computer Science 807, 307–325, 1994.

Kececioglu, 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 Lecture Notes in Computer Science 684, 87–105, 1993.

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

## Journal papers

Krieger, S. and J. Kececioglu. "Robust optimal metabolic factories." *Journal of Computational Biology* 31:10, 1045–1086, 2024. `doi:10.1089/cmb.2024.0748`

Krieger, S. and J. Kececioglu. "Shortest hyperpaths in directed hypergraphs for reaction pathway inference." *Journal of Computational Biology* 30:11, 1198–1225, 2023. `doi:10.1089/cmb.2023.0242`

Trilling, D.E., M. Gowanlock, D. Kramer, A. McNeill, B. Donnelly, N. Butler and J. Kececioglu. "The Solar System Notification Alert Processing System (`SNAPS`): design, architecture, and first data release (`SNAPShot1`)." *The Astronomical Journal* 165:111, 17 pages, 2023. `doi:10.3847/1538-3881/acac7f`

Krieger, S. and J. Kececioglu. "Heuristic shortest hyperpaths in cell signaling hypergraphs." *Algorithms for Molecular Biology* 17:12, 26 pages, 2022. `doi:10.1186/s13015-022-00217-9`

Matheson, T., C. Stubens, N. Wolf, C.-H. Lee, G. Narayan, A. Saha, A. Scott, M. Soraisam, A.S. Bolton, B. Hauger, D.R. Silva, J. Kececioglu, C. Scheidegger, R. Snodgrass, P.D. Aleo, E. Evans-Jacquez, N. Singh, Z. Wang, S. Yang and Z. Zhao. "The `ANTARES` astronomical time-domain event broker." *The Astronomical Journal* 161:107, 16 pages, 2021. `doi:10.3847/1538-3881/abd703`

DeBlasio, D. and J. Kececioglu. "Adaptive local realignment of protein sequences." *Journal of Computational Biology* 25:7, 780–793, 2018.

Narayan, G., T. Zaidi, M.D. Soraisam, Z. Wang, M. Lochner, T. Matheson, A. Saha, S. Yang, Z. Zhao, J. Kececioglu, C. Scheidegger, R.T. Snodgrass, T. Axelrod, T. Jenness, R.S. Maier, S.T. Ridgway, R.L. Seaman, E.M. Evans, N. Singh, C. Taylor, J. Toeniskoetter, E. Welch and S. Zhu. "Machine-learning-based brokers for real-time classification of the LSST alert stream." *The Astrophysical Journal Supplement Series* 236:9, 26 pages, 2018. `doi:10.3847/1538-4365/aab781`

DeBlasio, D. and J. Kececioglu. "Learning parameter-advising sets for multiple sequence alignment." IEEE/ACM *Transactions on Computational Biology and Bioinformatics* 14:5, 1028–1041, 2017.

DeBlasio, D. and J. Kececioglu. "Core column prediction for protein multiple sequence alignments." *Algorithms for Molecular Biology* 12:11, 16 pages, 2017. `doi:10.1186/s13015-017-0102-3`

Suh, Y.-K., R. Snodgrass, J. Kececioglu, P. Downey, R. Maier and C. Yi. "`EMP`: execution time measurement protocol for compute-bound programs." *Software – Practice and Experience* 47:4, 559–597, 2017.

Kececioglu, J. and D. DeBlasio. “Accuracy estimation and parameter advising for protein multiple sequence alignment.” *Journal of Computational Biology* 20:4, 259–279, 2013.

Huynh, L., J. Kececioglu, M. Köppe and I. Tagkopoulos. “Automatic design of synthetic gene circuits through mixed integer non-linear programming.” *Public Library of Science ONE* 7:4, e35529, 9 pages, 2012. `doi:10.1371/journal.pone.0035529`

Kececioglu, J., E. Kim and T. Wheeler. “Aligning protein sequences with predicted secondary structure.” *Journal of Computational Biology* 17:3, 561–580, 2010.
(Selected for Faculty of 1000 Biology, `http://f1000biology.com/article/id/3324957`)

Kim, E. and J. Kececioglu. “Learning scoring schemes for sequence alignment from partial examples.” IEEE/ACM *Transactions on Computational Biology and Bioinformatics* 5:4, 546–556, 2008.

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.

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 Sciences USA* 86, 4412–4415, 1989.

## Other publications

Saha, A., Z. Wang, T. Matheson, G. Narayan, R. Snodgrass, J. Kececioglu, C. Scheidegger, T. Axelrod, T. Jenness, S. Ridgway, R. Seaman, C. Taylor, J. Toeniskoetter, E. Welch, S. Yang and T. Zaidi. “`ANTARES`: progress towards building a broker of time-domain alerts.” Proceedings of *SPIE* 9910 (Observatory Operations: Strategies, Processes, and Systems VI), 8 pages, 2016.
`doi:10.1117/12.2232095`

DeBlasio, D. and J. Kececioglu. “Parameter advising for multiple sequence alignment.” *BMC Bioinformatics* 16(S2):A3, 3 pages, 2015. `doi:10.1186/1471-2105-16-s2-a3`

Saha, A., T. Matheson, R. Snodgrass, J. Kececioglu, G. Narayan, R. Seaman, T. Jenness and T. Axelrod. "`ANTARES`: a prototype transient broker system." Proceedings of *SPIE* 9149 (Observatory Operations: Strategies, Processes, and Systems V), 8 pages, 2014. `doi:10.1117/12.2056988`

Matheson, T., A. Saha, R. Snodgrass and J. Kececioglu. "`ANTARES`: the Arizona-NOAO temporal analysis and response to events system." Proceedings of the 3rd *Hot-Wiring the Transient Universe Workshop*, 145–150, 2014.

Huynh, L., J. Kececioglu and I. Tagkopoulos. "Automated design of synthetic gene circuits through linear approximation and mixed integer optimization." Proceedings of the 3rd *International Workshop on Bio-Design Automation* (IWBDA), 48–49, 2011.
`http://wiki.bu.edu/ece-cidar/index.php/IWBDA_2011#Proceedings`

Linn, C., S. Debray and J. Kececioglu. "Enhancing software tamper-resistance via stealthy address computations." Proceedings of the 19th *Computer Security Applications Conference* (ACSAC), 3 pages, 2003.

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.

Nadimpalli, R.G., W. Zhang, J. Kececioglu and E.W. Taylor. "The HIV-1 `nef` transframe protein has significant sequence and structural similarity to chemokines, as assessed by threading (inverse folding), sequence analysis, and molecular modeling." *Antiviral Research* 34:2, A57, 1997.

Kececioglu, J. and D. Kececioglu. "Quantified software reliability techniques." Proceedings of the 2nd IASTED *Symposium on Quality Control and Reliability*, 15–18, 1987.

## Books

DeBlasio, D. and J. Kececioglu. *Parameter Advising for Multiple Sequence Alignment.* Springer, New York, Computational Biology Series Volume 26, xiv+152 pages, 2017.
`isbn:978-3-319-64917-7`

## Edited proceedings and journal issues

IEEE/ACM *Transactions on Computational Biology and Bioinformatics*, Special Issue on Invited Papers from ACM-BCB 2016 (7th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics), J. Kececioglu, guest editor (10 papers), to appear 2018.

*Proceedings of the 7th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics* (ACM-BCB 2016), J. Kececioglu and A. Wilcox (Program Chairs), U. Catalyürek and G. Melton-Meaux (General Chairs), X. Shi and Y. Shen (Publication Chairs), Association for Computing Machinery, New York, 675 pages, 2016. `isbn:978-1-4503-4225-4`

## Book reviews

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

## Dissertation

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

## Software

Krieger, S. and J. Kececioglu. `Freeia`: robust optimal factories in metabolic reaction networks. Version 1.0, 2023. `http://freeia.cs.arizona.edu`

Krieger, S. and J. Kececioglu. `Mmunin`: integer-linear-programming-based cutting-plane algorithm for shortest source-sink hyperpaths. Version 1.0, 2022. `http://mmunin.cs.arizona.edu`

Krieger, S. and J. Kececioglu. `Odinn`: optimal minimum-hyperedge factories in metabolic networks with negative regulation. Version 1.0, 2022. `http://odinn.cs.arizona.edu`

Krieger, S. and J. Kececioglu. `Hhugin`: hypergraph heuristic for general shortest source-sink hyperpaths. Version 1.0, 2021. `http://hhugin.cs.arizona.edu`

Krieger, S. and J. Kececioglu. `Ssylla`: protein secondary structure prediction by an ensemble leveraging accuracy estimation. Version 1.1, 2021. `http://ssylla.cs.arizona.edu`

Krieger, S. and J. Kececioglu. `Nnessy`: nearest-neighbor-based prediction of protein secondary structure without searching for homology. Version 1.0.2, 2020. `http://nnessy.cs.arizona.edu`

DeBlasio, D. and J. Kececioglu. `Facet`: feature-based accuracy estimator for protein multiple sequence alignments. Version 1.4, 2015. `http://facet.cs.arizona.edu`

Desai, S., L. Peairs and J. Kececioglu. `InverseOpt`: general linear inverse parametric optimization from partial examples. Version 0.1, 2015. `http://inverseopt.cs.arizona.edu`

Wheeler, T. and J. Kececioglu. `Opal`: forming and polishing multiple sequence alignments by optimally aligning alignments. Version 2.1.3, 2013. `http://opal.cs.arizona.edu`

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

Starrett, D., T. Wheeler and J. Kececioglu. `AlignAlign`: optimal alignment of alignments. Version 0.9.7, 2005. `http://alignalign.cs.arizona.edu`

Kececioglu, J., A. Schäffer, S. Gupta, S. Altschul and D. Lipman. `MSA`: sum-of-pairs multiple sequence alignment. Version 2.1, 1996. `ftp://fastlink.nih.gov/pub/msa`

## Grants

US National Science Foundation, CISE/IIS Information Integration and Informatics Program, "EAGER: Breaking the Speed and Accuracy Barrier for Protein Property Prediction," J. Kececioglu (PI), Grant 2041613, August 2020–July 2023, $199,853.

Arizona Board of Regents (ABOR), Regents' Innovation Fund (RIF) Program, "An Outlier Detection and Alert Processing System for Time-Domain Astronomy," M. Gowanlock (PI); J. Kececioglu, N. Butler, and D. Trilling (co-PIs); September 2019–August 2021, $299,995.

US National Science Foundation, CISE/CCF Transdisciplinary Research in Principles of Data Science (TRIPODS) Program, "UA-TRIPODS – Building Theoretical Foundations for Data Sciences," H. Zhang (PI); D. Glickenstein, S. Kobourov and J. Watkins (co-PIs); M. Brio, J. Kececioglu, W. Piegorsch and S. Sethuraman (Senior Personnel); Grant 1740858, September 2017–August 2020, $1,368,498.

US National Science Foundation, CISE/CCF Algorithmic Foundations Program, "Collaborative: Cell Signaling Hypergraphs: Algorithms and Applications," J. Kececioglu (PI), T.M. Murali (collaborator), Grant 1617192, August 2016–July 2019, $212,007.

US National Science Foundation, OIA Integrated NSF Support Promoting Interdisciplinary Research and Education (INSPIRE) Program, "Arizona-NOAO Temporal Analysis and Response to Events System (ANTARES)," R. Snodgrass (PI); J. Kececioglu, T. Matheson and A. Saha (co-PIs); Grant 1344024, September 2013–August 2017, $733,334.

US National Science Foundation, CISE/IIS Information Integration and Informatics Program, "Parameter Inference and Parameter Advising in Computational Biology," J. Kececioglu (PI), Grant 1217886, October 2012–September 2017, $496,575.

US National Science Foundation, CISE/IIS Information Integration and Informatics Program, REU Supplement to "Parameter Inference and Parameter Advising in Computational Biology," J. Kececioglu (PI), Grant 1340379, May 2013–September 2017, $16,000.

US National Science Foundation, CISE/CCF Algorithmic Foundations Program, "Collaborative: EAGER: A Model Based System for the Automated Design of Synthetic Genetic Circuits by Mathematical Optimization," J. Kececioglu (PI); I. Tagkopoulos and M. Köppe (collaborators); Grant 1147844, September 2011–August 2013, $28,902.

US National Science Foundation, CISE/IIS Information Integration and Informatics Program, "EAGER: An Exploratory System for Inverse Parametric Optimization," J. Kececioglu (PI), Grant 1050293, September 2010–August 2012, $59,996.

US Department of Education, Graduate Assistance in Areas of National Need (GAANN) Program, "Graduate Assistance in Computer Science: An Area of National Need," J. Kececioglu (PI); A. Efrat, R. Gupta and S. Westbrook (co-PIs); Grant P200A070545, August 2007–July 2012, $383,643.

US National Science Foundation, Integrative Graduate Education and Research Traineeship (IGERT) Program, "IGERT Program in Comparative Genomics," M. Nachman (PI); V. Chandler, J. Kececioglu, N. Moran and D. Vercelli (co-PIs); Grant 0654435, July 2007–June 2013, $2,999,835.

US National Science Foundation, BIO/DBI Biological Databases and Informatics Program, "Robust Tools for Biological Sequence Analysis," J. Kececioglu (PI), Grant 0317498, August 2003–July 2008, $500,498.

US National Science Foundation, BIO/DBI 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. Kececioglu (co-PIs); Grant 9872649, September 1998–August 2001, $3,246,755.

US National Science Foundation, BIO/DBI Computational Biology Activities Program, "CAREER: Applied Algorithms for Computational Molecular Biology," J. Kececioglu (PI), Grant 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" organized by J. Kececioglu 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" organized by J. Kececioglu at the SIAM Annual Meeting, October 1995, $4,000.

## Selected professional activities

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

Associate Editor, IEEE/ACM *Transactions on Computational Biology and Bioinformatics*, 2008–2019. `http://www.computer.org/tcbb/`

Scientific Advisory Board, Max Planck Institute for Informatics, Saarbrücken, Germany, 2003–2006. `http://mpi-sb.de`

Program Committee Co-Chair, ACM-BCB 2016 (7th ACM *Conference on Bioinformatics, Computational Biology, and Health Informatics*), October 2–5, 2016, Seattle, Washington.

Program Committee Track Co-Chair for Sequence Analysis, ACM-BCB 2012 (3rd ACM *Conference on Bioinformatics, Computational Biology, and Biomedicine*), October 7–10, 2012, Orlando, Florida.

Program Committee Track Co-Chair for Sequence Analysis, ISMB 2011 (19th ISCB *Conference on Intelligent Systems for Molecular Biology*), July 17–19, 2011, Vienna, Austria.

Conference Chair, RECOMB 2009 (13th *Conference on Research in Computational Molecular Biology*), May 18–21, 2009, Tucson, Arizona.

Program Committee Member, ISMB 2022, 2021, 2020, 2019, 2018, 2016, 2015, 2014, 2013, 2012, 2011, 2010, 2009, 2008 (ISCB *Conference on Intelligent Systems for Molecular Biology*); RECOMB 2019, 2018, 2017, 2009, 2008, 2002, 1999 (*Conference on Research in Computational Molecular Biology*); ACM-BCB 2022, 2021, 2020, 2019, 2018, 2016, 2015, 2012 (ACM *Conference on Bioinformatics, Computational Biology, and Health Informatics*); WABI 2008, 2001 (ISCB *Workshop on Algorithms in Bioinformatics*); ISBRA 2008, 2007 (*International Symposium on Bioinformatics Research and Applications*); APBC 2006 (*Asia-Pacific Bioinformatics Conference*); CPM 2009, 2000 (*Symposium on Combinatorial Pattern Matching*); ALENEX 2000 (*Workshop on Algorithm Engineering and Experiments*); SPIRE 2001, 2000 (*Symposium on String Processing and Information Retrieval*).

National Science Foundation Review Panelist, Small III Bioinformatics Panel, 2018; 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.

National Institutes of Health Review Panelist, Biological Data Management and Analysis Panel, 2013; 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.

Faculty Member, Faculty of 1000 (F1000Prime), Bioinformatics, Biomedical Informatics, and Computational Biology Faculty, Sequence Analysis Section, 2017–2019. `http://f1000.com`

Member, ISCB Conferences Committee, 2011–present; ISCB Publications Committee, 2011–present.

Member of ACM (Association for Computing Machinery), 1985–present; ISCB (International Society for Computational Biology), 2000–present.

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

## Students and mentees

## Postdoctoral

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

## PhD

Spencer Krieger. *Algorithmic Inference of Cellular Reaction Pathways and Protein Secondary Structure.* PhD dissertation, Department of Computer Science, The University of Arizona, July 2022.
(Lane Postdoctoral Fellow, Carnegie Mellon University, Department of Computational Biology; Jian Ma, mentor)

August Woerner. *On the Neutralome of Great Apes and Nearest Neighbor Search in Metric Spaces.* PhD dissertation, Graduate Interdisciplinary Program in Genetics, The University of Arizona, August 2016.
(Co-advisor: Michael Hammer, Department of Ecology and Evolutionary Biology)
(Postdoctoral Fellow, University of North Texas, Department of Molecular and Medical Genetics; Bruce Budowle, mentor)

Dan DeBlasio. *Parameter Advising for Multiple Sequence Alignment.* PhD dissertation, Department of Computer Science, The University of Arizona, May 2016.
(Currently: Assistant Teaching Professor, Computational Biology Department, Carnegie Mellon University)
(Formerly: Assistant Professor, Department of Computer Science, University of Texas at El Paso)
(Formerly: Lane Postdoctoral Fellow, Carnegie Mellon University, Department of Computational Biology; Carl Kingsford, mentor)

Travis Wheeler. *Efficient Construction of Accurate Multiple Alignments and Large-Scale Phylogenies.* PhD dissertation, Department of Computer Science, The University of Arizona, August 2009.
(Co-advisor: Michael Sanderson, Department of Ecology and Evolutionary Biology)
(Currently: Associate Professor, College of Pharmacy, University of Arizona)
(Formerly: Associate Professor, Department of Computer Science, University of Montana)
(Formerly: Postdoctoral Fellow, Howard Hughes Medical Institute Janelia Research Campus; Sean Eddy, mentor)

Eagu Kim. *Inverse Parametric Alignment for Accurate Biological Sequence Comparison.* PhD dissertation, Department of Computer Science, The University of Arizona, August 2008.
(Postdoctoral Fellow, University of Wisconsin-Madison, Department of Biostatistics and Medical Informatics; Colin Dewey, mentor)

Dean Starrett. *Optimal Alignment of Multiple Sequence Alignments.* PhD dissertation, Department of Computer Science, The University of Arizona, August 2008.
(Postdoctoral Fellow, University of California at Berkeley, Department of Bioengineering; Kimmen Sjölander, mentor)

## MS

David Perkins. *Predicting Protein Secondary Structure by Linear and Dynamic Programming.* MS thesis, Department of Computer Science, The University of Arizona, May 2009.

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

Jun Yu. *Separating Repeats in DNA Sequence Assembly.* MS thesis, Department of Computer Science, University of Georgia, August 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, May 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, December 1997.

### BS

Nathaniel Holle. *A Subquadratic-Time Heuristic for K-Medians in a Metric Space that Leverages Fast Nearest-Neighbor Search.* BS honors thesis, Department of Computer Science, The University of Arizona, May 2018.

David Porfirio. *Single-Sequence Protein Secondary Structure Prediction by Nearest-Neighbor Classification of Protein Words.* BS honors thesis, Department of Computer Science, The University of Arizona, May 2016.
(PhD student, Department of Computer Science, University of Wisconsin-Madison)

Joseph Thomas. *An Adaptive Data Structure for Nearest Neighbor Search in a General Metric Space.* BS honors thesis, Department of Computer Science, The University of Arizona, May 2010.
(PhD, Department of Mathematics, The University of Arizona, May 2015)

## Outreach

### News articles

"How to find the rarest of the rare in Southern skies." *UANews*, December 17, 2013.
`http://uanews.org/story/how-to-find-the-rarest-of-the-rare-in-southern-skies`

"Anything you can imagine happening in our vast universe already has." *Arizona Daily Star*, October 18, 2013.
`http://tucson.com/news/science/anything-you-can-imagine-happening-in-our-vast-universe-already/article_ee32f7d4-e8d2-5363-99ad-fdf8472484ef.html`

"A boost for analyzing biological sequences." *UANews*, February 1, 2013.
`http://uanews.org/story/a-boost-for-analyzing-biological-sequences`

### Lay talks

"`ANTARES`: finding a needle in a stack of needles." T. Matheson, A. Saha, R. Snodgrass and J. Kececioglu (speakers). *UA Science Café*: Lecture Series on Big Data, Tucson, Arizona, February 9, 2017. `http://www.youtube.com/watch?v=_NSCR__Seaw`

## Selected invited presentations

"Inferring pathways in metabolic networks via optimal factories and hyperpaths" (keynote). 4th *Workshop on Metabolism and Mathematical Models*: Two for a Tango, INRIA (French National Institute for Research in Digital Science and Technology), Lyon, France, November 20, 2024.

"Parameter inference and parameter advising for multiple sequence alignment." *Symposium on Mastering Genomes* (honoring the 65th birthday of Gene Myers), Max Planck Institute for Molecular Cell Biology and Genetics, Dresden, Germany, November 25, 2019.

"Parameter inference and parameter advising in computational biology." College of Engineering Invited Lecture Series, Gianforte School of Computing, Montana State University, Bozeman, April 15, 2019.

“Parameter inference and parameter advising in computational biology.” *Workshop on the Future of Algorithms in Biology* (FAB), Carnegie Mellon University, Pittsburgh, Pennsylvania, September 28, 2018.

“Parameter advising for multiple sequence alignment.” *Conference on Models and Algorithms for Genome Evolution* (MAGE) (honoring 50 years of research by David Sankoff), Bromont, Quebec, Canada, August 24, 2013.

“Learning to align protein sequences with predicted secondary structure.” Department of Computer Science, University of California at Davis, October 22, 2009.

“Learning models for aligning protein sequences with predicted secondary structure.” Department of Mathematics, University of California at Berkeley, September 23, 2009.

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

“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.

“Multiple sequence alignment: exact algorithms, approximation algorithms, and complexity.” 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.” 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.” Department of Applied Mathematics, University of Heidelberg, Germany, June 26, 1997.

“Discrete algorithms on sequences.” *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.

“Computing optimal multiple sequence alignments.” Max-Planck-Institut für Informatik, Saarbrücken, Germany, November 22, 1995.

“A tour of multiple sequence alignment theory.” *Computational Genomics* ’95, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, November 2, 1995.

"Computing optimal multiple sequence alignments." *Minisymposium on Discrete Algorithms in Computational Biology*, SIAM Annual Meeting, Charlotte, North Carolina, October 24, 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." 6th *Symposium on Combinatorial Pattern Matching* (CPM), 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.

"Chromosome inversions and algorithms for sorting by reversals." 3rd International *Conference on Bioinformatics and Genome Research*, Florida State University, Tallahassee, June 1, 1994.

"Efficient bounds for oriented chromosome-inversion distance." *Minisymposium on Combinatorial Methods for Genome Rearrangements*, University of Southern California, Los Angeles, March 18, 1994.

"Chromosome inversions and algorithms for genome rearrangements." Department of Biomathematical Sciences, Mount Sinai School of Medicine, New York, March 8, 1994.

"Reconstructing a history of recombinations from a set of sequences." Department of Computer Science, Pennsylvania State University, University Park, January 20, 1994.

"Pattern matching on strings." *Future Directions in Computer Misuse and Anomaly Detection* II, University of California at Davis, September 27, 1993.

"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 the inversion distance between two chromosomes." *Mathematics and Molecular Biology* III: Computational Approaches to Nucleic Acid Structure and Function, Santa Fe, November 9, 1992.

"Maximum weight trace: A new problem in multiple sequence alignment." *Workshop on Molecular Sequence Analysis*, University of New Mexico, Albuquerque, November 6, 1992.

"Exact and approximation algorithms for the inversion distance between two chromosomes." Department of Computer Science, University of California at Berkeley, September 24, 1992.

"Exact and approximation algorithms for DNA sequence reconstruction." Department of Computer Science, University of California at Berkeley, January 30, 1992.