

Curriculum Vitae
Colin N. Dewey
(Updated: February 16, 2021)

Address

Department of Biostatistics and Medical Informatics
School of Medicine and Public Health
University of Wisconsin-Madison
425 Henry Mall (2128 Genetics-Biotechnology Center)
Madison, Wisconsin 53706

Phone: (608) 263-7610

Email: colin.dewey@wisc.edu

Web: <http://www.biostat.wisc.edu/~cdewey>

ORCID ID: <https://orcid.org/0000-0003-1498-9254>

Education

- 2006 Ph.D. in Electrical Engineering and Computer Sciences with Computational and Genomic Biology Designated Emphasis, University of California, Berkeley, CA.
Dissertation title: Whole-genome alignments and polytopes for comparative genomics.
Advisor: Lior Pachter
- 2001 B.S. in Electrical Engineering and Computer Sciences, University of California, Berkeley, CA.

Positions held

- 2019 - Present Faculty Member, Center for Genomic Science Innovation, University of Wisconsin, Madison, WI.
- 2018 - Present Professor, Department of Biostatistics and Medical Informatics, University of Wisconsin, Madison, WI
- 2012 - 2018 Associate Professor, Department of Biostatistics and Medical Informatics, University of Wisconsin, Madison, WI.
- 2007 - Present Faculty Member, Biomedical Informatics Resource, Institute for Clinical and Translational Research, University of Wisconsin, Madison, WI.
- 2006 - Present Graduate Trainer, Computation and Informatics in Biology and Medicine Training Program, University of Wisconsin, Madison, WI.
- 2006 - Present Graduate Trainer, Genomic Sciences Training Program, University of Wisconsin, Madison, WI.
- 2006 - Present Faculty Member, Cancer Genetics Program, Carbone Cancer Center, University of Wisconsin, Madison, WI.
- 2006 - Present Affiliate Faculty Member, Department of Computer Sciences, University of Wisconsin, Madison, WI.
- 2006 - 2019 Faculty Member, Genome Center of Wisconsin, University of Wisconsin, Madison, WI.
- 2006 - Present Faculty Member, Genomics Cluster, University of Wisconsin, Madison, WI.

- 2006 - 2012 Assistant Professor, Department of Biostatistics and Medical Informatics, University of Wisconsin, Madison, WI.
- 2005 Scientific Visitor, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD. PI: Eugene Koonin.
- 2002 - 2006 Research Assistant, Department of Mathematics, University of California, Berkeley, CA. PI: Lior Pachter.

Honors and awards

- 2016 Vilas Associate, University of Wisconsin-Madison
- 2003 Howard Hughes Medical Institute Predoctoral Fellowship in Biological Sciences Honorable Mention.
- 2003 National Science Foundation Graduate Research Fellowship Honorable Mention.
- 2001 National Science Foundation Graduate Research Fellowship Honorable Mention.
- 2001 GAAAN Fellowship, University of California, Berkeley.
- 1998 University of California, Berkeley Edward Frank Kraft Scholarship Prize.

Society memberships

- 2005 - Present International Society for Computational Biology.
- 2001 - Present Phi Beta Kappa Society (national academic honor society).
- 1999 - Present Eta Kappa Nu Society (student honor society of IEEE: Institute of Electrical and Electronics Engineers).

Classroom teaching

Regular courses

1. Advanced Bioinformatics (BMI/CS 776)
Spring 2007, Spring 2008, Spring 2012, Spring 2013, Spring 2014, Spring 2015, Spring 2019
2. Introduction to Bioinformatics (BMI/CS 576)
Fall 2008, Fall 2009, Fall 2010, Fall 2015, Fall 2016, Fall 2018, Fall 2019, Fall 2020
3. Statistical Methods for Molecular Biology (STAT 877)
Spring 2012 (one lecture in jointly taught course), Spring 2014 (2 lectures), Spring 2017 (2 lectures), Fall 2020 (2 lectures)
4. Pathology Student Seminar (PATH 901)
Fall 2014 (one lecture), Fall 2015 (one lecture), Fall 2016 (one lecture)
5. Clinical Research Informatics (BMI 773)
Spring 2015 (one lecture)

Short Courses and Workshops

1. ISMB Tutorial: Computational methods for comparative regulatory genomics
Chicago, IL, July 6, 2018
Whole genome alignment
2. Workshop on Computational Approaches to Analyzing Microarray Data
Promega, Madison, WI. July 17, 2008.
One lecture on the topic of "Whole genome alignment"

3. Science Masters Institute Course on Genetics, Natural Selection, & Evolution
Madison Metropolitan School District, Madison, WI
20 hour course taught three times in 2007, 2008, and 2009.
4. Module on “Biological sequence alignment,” PhD Program in Computational Biology
Instituto Gulbenkian de Ciência, Oeiras, Portugal. December 4-10, 2007.
Developed and taught four lectures and two laboratory sections.

Mentor teaching

Postdoctoral Fellows

Department of Biostatistics and Medical Informatics, University of Wisconsin, Madison

1. Eagu Kim, Ph.D.: Fall 2008 - Summer 2009.
2. Jin Park, Ph.D.: Fall 2010 - Summer 2011 (co-advised with Prof. Heidi Goodrich-Blair, Department of Bacteriology).
3. Justin Lack, Ph.D.: Fall 2013 – present (NIH NRSA co-sponsor with sponsor Prof. John Pool, Department of Genetics).
4. Peng Liu, Ph.D.: Fall 2013 – Summer 2016 (co-advised with Prof. Sunduz Keles, Department of Biostatistics and Medical Informatics).
5. Nathanael Fillmore: Spring 2016 – Fall 2016.

Ph.D. Students

Department of Computer Sciences, University of Wisconsin, Madison.

1. Bo Li, Ph.D.: Fall 2008 – Summer 2013 (Ph.D. conferred August 2013)
Thesis title: Computational analysis of RNA-Seq data in the absence of a known genome.
2. Nathanael Fillmore, Ph.D.: Summer 2011 – Fall 2015 (Ph.D. conferred December 2015)
(joint with Prof. Michael Newton, Department of Biostatistics and Medical Informatics)
Thesis title: Generative models for transcriptome assembly and analysis.
3. Matthew Bernstein, Ph.D.: Fall 2014 – Summer 2019 (Ph.D. conferred August 2019)
Thesis title: Computational methods for transcriptome-based cellular phenotyping

M.S. Students

Department of Computer Sciences, University of Wisconsin, Madison.

1. Jae Young Do, M.S., Conferred May 2009.
M.S. project title: Parallel FSA: Improving the Performance of Multiple Sequence Alignment using a Workstation Cluster and Database.
2. Farzad Rastegar, M.S., Conferred August 2010.
Research area: Probabilistic whole-genome alignment.
3. Satish Kotha, M.S., Conferred August 2010 (co-advised with Prof. Cécile Ané, Department of Statistics).
Research area: Bayesian concordance analysis.
4. Kristopher Kosmatka, M.S., Conferred August 2011.
Research area: Automated inference of genomic rearrangements from optical maps.
5. Sid Kiblawi, RA, Spring 2014-Summer 2014
Research area: Large-scale gene orthology inference
6. Laura LeGault, RA, Fall 2010 – Fall 2014 (prelim passed April 2013)
Prelim title: Analysis of alternative splicing using probabilistic splice graphs and RNA-Seq.
7. Matthew Amodio, trainee, Fall 2016 – Summer 2017
Research area: Detection of RNA processing event dependencies
8. Steve Wang, RA, Fall 2018
Research area: Metadata-based sample type classification of public RNA-seq samples

9. Niveditha Hariharan, RA, Summer 2019 – Spring 2020
Research area: Active learning for biomedical metadata standardization
10. Matthew Crepea, RA, Spring 2019 - Fall 2019
Research area: Characterization of RNA processing event dependencies

Rotation Students

1. Norbert Binkiewicz, Spring 2013
Rotation project: SNP and allele specific expression inference from RNA-Seq data
2. Matthew Stone, BDS PhD student, Summer 2019 - Fall 2019
Rotation project: Alignment of Pacific Biosciences Iso-Seq data

Summer Students

Department of Computer Sciences, University of Wisconsin, Madison.

1. Daniel Wong, short-term CIBM traineeship, Summer 2007
Project title: Methods for online multiple sequence alignment.

Ph.D. Committees

1. Irene Ong, Ph.D., Computer Sciences, Conferred in August 2007.
Title: Computational techniques for inferring regulatory networks.
2. Keith Noto, Ph.D., Computer Sciences, Conferred in August 2007.
Title: Learning expressive computational models of gene regulatory sequences and responses.
3. Pei-Fen Kuan, Ph.D., Statistics, Conferred in May 2009.
Title: Statistical methods for the analysis of genomic data from tiling arrays and next generation sequencing technologies.
4. Raman Arora, Ph.D., Electrical and Computer Engineering, Conferred in August 2009.
Title: Group theoretical methods in signal processing: learning similarities, transformations & invariants.
5. Yue Pan, Ph.D., Computer Sciences, Conferred in August 2009.
Title: Inferring mechanism-based gene regulatory network models from expression and sequence data.
6. Heejung Shim, Ph.D., Statistics, Conferred in May 2010.
Title: BayesCAT: Bayesian Co-estimation of Alignment and Tree.
7. Dongjun Chung, Ph.D., Statistics, Conferred in August 2012.
Title: Statistical Methods and Software for Chip-Seq Data Analysis.
8. Ryan Haasl, Ph.D., Genetics, Conferred in May 2013.
Title: Consequential Repetition: Microsatellites As Targets of Selection.
9. Gloria Sheynkman, Ph.D., Chemistry, Conferred in May 2014
Title: Leveraging RNA-seq to detect novel protein variations via mass spectrometry
10. Ning Leng, Ph.D., Statistics, Conferred in August 2014
Title: Statistical methods for reliable inference in RNA-seq experiments to facilitate regenerative medicine.
11. Marijan Posavi, Ph.D., Zoology, Conferred in May 2015
Title: Evolutionary Mechanisms of Rapid Adaptation During Freshwater Invasions by the Saline Copepod *Eurytemora Affinis*
12. Kelly Pittman, Ph.D., Cellular and Molecular Biology, Conferred in August 2015
Title: Dual transcriptome analysis of *Toxoplasma gondii* infected mice leads to the investigation of Z- DNA binding protein-1 involvement during infection.
13. Tyler Harter, Ph.D., Computer Sciences, Conferred in August 2016
Title: Emergent Properties in Modular Storage: a Study of Apple Desktop Applications, Facebook Messages, and Docker Containers.

14. Tatum Mortimer, Ph.D., Microbiology, Conferred in August 2016
Title: Roles of recombination and selection in shaping pathogenic bacterial genomes
15. Rhonda Bacher, Ph.D., Statistics, Conferred in August 2017
Title: Statistical Methods for RNA-sequencing Data
16. Kailei Chen, Ph.D., Statistics, Conferred in August 2018
Title: Simultaneous Analysis Of Large Scale Datasets In Different Chip-Seq Problem Settings
17. Rene Welch, Ph.D., Statistics, Conferred in August 2018
Title: Statistical Methods For Chip-Exo/Nexus Quality Control, And Fine-Mapping Of Multi-Trait SNPs In High LD By Using Next-Generation Sequencing Data
18. Abigail Shockey, Ph.D., Microbiology, Conferred in August 2019
Title: Genomics of bacterial pathogens across evolutionary scales
19. Lindsey Bohr, Ph.D., Microbiology, Conferred in August 2020
Title: No Bacterium is an Island: The Role of Population Structure in Emergence and Maintenance of Pathogens
20. Kazuya Oikawa, Comparative Biomedical Science, Conferred in May 2021
Title: Optic Nerve Head Molecular and Cellular Pathology in a Spontaneous Large Animal Model of Glaucoma

Preliminary Exam Committees

1. Ryan Haasl, Genetics, June 2010.
Title: Microsatellites as targets of natural selection.
2. Dongjun Chung, Statistics, May 2011.
Title: Discovering transcription factor binding sites in highly repetitive regions of genomes with multi-read analysis of ChIP-seq data.
3. Kelly Pittman, Cellular and Molecular Biology, April 2012.
4. John Hvala, Genetics, April 2012.
Title: Searching for Syncopations in the Tempo and Mode of Junction Formation: How Rates of Ancestry Switching in Admixed Genomes Inform the Search for Speciation Genes.
5. Ning Leng, Statistics, January 2013.
Title: Statistical methods for reliable inference in RNA-seq experiments to facilitate regenerative medicine and personalized genomics medicine.
6. Xin Zeng, Statistics, November 2013.
Title: Supervising ChIP-seq Multi-read Allocation with DNase-seq for Annotating Repetitive Genomic Regions Through ENCODE-Derived Data
7. Erik Jessen, Genetics, February 2014.
Title: Nucleoid Associated Protein (NAP) dynamics, and influence on nucleoid structure and transcription
8. Tatum Mortimer, Microbiology, June 2014.
Title: Roles of recombination and selection in shaping pathogenic bacterial genomes
9. Rene Welch, Statistics, December 2015.
Title: Data exploration, quality control and statistical analysis of ChIP-exo experiments
21. Abigail Shockey, Microbiology, June 2016.
22. Lindsey Bohr, Microbiology, August 2016.
*Title: Characterizing HGT and Recombination in *Mycobacterium abscessus**
23. Rhonda Bacher, Statistics, December 2016.
Title: Statistical Methods for Single Cell RNA Sequencing Data
24. Megan Frayer, Genetics, March 2017.
Title: Genomic Analysis of Ancestry in House Mice Hybrid Zones
25. Kazuya Oikawa, Comparative Biomedical Science, May 2017.
26. Kazuya Oikawa, Comparative Biomedical Science, Prelim B, July 2018

- Title: Neuroinflammation in chronic glaucomatous optic neuropathy*
27. Emily Binversie, Comparative Biomedical Science, Prelim A, August 2019
 28. Madison Youngblom, Microbiology, May 2020
Title: Defining the niche of Staphylococcus saprophyticus
 29. Emily Binversie, Comparative Biomedical Science, Prelim B, August 2020
 30. Erika Lee, Biomedical Data Sciences, October 2020
Title: Structure-Driven Machine Learning for 3D Genome Organization

Thesis Background Oral Examination Committee

1. Anthony Cesnik, Chemistry, TBD

M.S. Committees

1. Jessica Clarke, M.S., Genetics, Conferred in August 2008.
Title: Evolution in regulation of the Environmental Stress Response in ascomycete fungi
2. Grace Shrader, M.S., Microbiology, Conferred in August 2016.
Title: A Computational Workflow for Quantifying Functional Potential of Microbial Communities from Metagenomic Time Series

Training Program Mentoring

1. Gloria Kreitinger, Chemistry, 2012-2013
Genomic Sciences Training Program (GSTP) secondary mentor (primary: Lloyd Smith)
2. Anthony Cesnik, Chemistry, 2014-Present
Computation and Informatics in Biology and Medicine Program (CIBM) secondary mentor (primary: Lloyd Smith)

Undergraduate Mentoring

1. Ali Al-Hanooti (University of Wisconsin, River Falls), Summer 2009.
Integrated Biological Sciences Summer Research Program - Computational Biology and Biostatistics Summer Research Program.
Project title: Breakage Models of Chromosomal Evolution
2. Kevin Liao (University of North Carolina, Chapel Hill), Summer 2016.
Integrated Biological Sciences Summer Research Program - Computational Biology and Biostatistics Summer Research Program.
Project title: Comparing similarity measures over RNA-seq derived gene expression profiles
3. Brett VanTassel (Ramapo College of New Jersey), Summer 2017.
Integrated Biological Sciences Summer Research Program – Biomedical Data Science Research Program.
Project title: Compression of RNA-seq alignments
4. Catherine Anderson (UW-Madison), Spring 2019 – Summer 2019.
Project title: Demultiplexing of Pacific Biosciences Iso-Seq data
5. Aparna Maddala (Georgia Tech), Summer 2019.
Integrated Biological Sciences Summer Research Program – Biomedical Data Science Research Program.
Project title: Cell type deconvolution of RNA-seq samples
6. Ana Arenas (UW–Madison), Undergraduate Research Scholar, Fall 2020 – present
Project title: Interpreting cell type classifications from single-cell RNA sequencing experiments with a data visualization app

Publications

*: indicates a student or postdoc under my supervision.

Papers published in or accepted by refereed journals

1. M. Bernstein*, Z. Ma, M. Gleicher, and **C. Dewey**. (2021) CellO: Comprehensive and hierarchical cell type classification of human cells with the Cell Ontology. *iScience*. 24:101913. doi:10.1016/j.isci.2020.101913
2. S. Su, G. Chhabra, M. Ndiaye, C. Singh, T. Ye, W. Huang, **C. Dewey**, V. Setaluri, and N. Ahmad (2021) PLK1 and NOTCH Positively Correlate in Melanoma and Their Combined Inhibition Results in Synergistic Modulations of Key Melanoma Pathways. *Molecular Cancer Therapeutics*. 20:161–172. doi:10.1158/1535-7163.MCT-20-0654
3. P. Liu*, A. Soukup, E. Bresnick, **C. Dewey**, and S. Keles. (2020) PRAM: a novel pooling approach for discovering intergenic transcripts from large-scale RNA sequencing experiments. *Genome Research*. 30:1655–1666. doi:10.1101/gr.252445.119
4. R. Houseright, E. Rosowski, P. Lam, S. Tauzin, O. Mulvaney, **C. Dewey**, and A. Huttenlocher. (2020) Cell type specific gene expression profiling reveals a role for complement component C3 in neutrophil responses to tissue damage. *Scientific Reports*. 10:15716. doi:10.1038/s41598-020-72750-9.
5. M. Nolte, P. Jing, **C. Dewey**, and B. Payseur. (2020) Giant Island Mice Exhibit Widespread Gene Expression Changes in Key Metabolic Organs. *Genome Biology and Evolution*. 12: 1277–1301. doi:10.1093/gbe/evaa118.
6. ENCODE Project Consortium. (2020) Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*. 2020;583: 699–710. doi:10.1038/s41586-020-2493-4.
7. P. Sanchez-Vazquez, **C. Dewey**, N. Kitten, W. Ross, and R. Gourse. (2019) Genome-wide effects on Escherichia coli transcription from ppGpp binding to its two sites on RNA polymerase. *Proc Natl Acad Sci USA*. 116: 8310-8319.
8. K. Hewitt, K. Katsumura, D. Matson, P. Devadas, N. Tanimura, A. Hebert, J. Coon, J.-S. Kim, **C. Dewey**, S. Keles, R. Paulson, and E. Bresnick. (2017) GATA Factor-Regulated Samd14 Enhancer Confers Red Blood Cell Regeneration and Survival in Severe Anemia. *Developmental Cell*. 42(3):213-225.e4.
9. I. Sedykh, B. Yoon, L. Roberson, O. Moskvina, **C. Dewey**, and Y. Grinblat. (2017) Zebrafish zic2 controls formation of periorbital neural crest and choroid fissure morphogenesis. *Developmental Biology*. 429(1):92-104.
10. M. Bernstein*, A. Doan, and **C. Dewey**. MetaSRA: normalized sample-specific metadata for the Sequence Read Archive. (2017) *Bioinformatics*. 33(18):2914-2923.
11. P. Liu*, R. Sanalkumar, E. Bresnick, S. Keleş and **C. Dewey**. (2016) Integrative analysis with RNA polymerase II ChIP-seq advances the limits of transcript quantification from RNA-seq. *Genome Research*. 26(8):1124-33.
12. P. Jiang, J. Nelson, N. Leng, M. Collins, S. Swanson, **C. Dewey**, J. Thomson, R. Stewart. (2016) Analysis of embryonic development in the unsequenced axolotl: Waves of transcriptomic upheaval and stability. *Developmental Biology*. 2016 Jul 27. pii: S0012-1606(15)30261-X.
13. N. Tanimura, E. Miller, K. Igarashi, D. Yang, J. Burstyn, **C. Dewey**, and E. Bresnick. (2016) Mechanism Governing Heme Synthesis Reveals a GATA Factor-Heme Circuit that Controls Differentiation. *EMBO Reports*. 17(2):249-65.
14. X. Zeng, B. Li*, R. Welch, C. Rojo, Y. Zheng, **C. Dewey**, and S. Keles. (2015) Perm-seq: Mapping protein-DNA interactions in segmental duplication and highly repetitive regions of genomes with prior-enhanced read mapping. *PLoS Computational Biology*. 11(10):e1004491.
15. K. Johnson, G. Kong, X. Gao, Y.-I. Chang, K. Hewitt, R. Sanalkumar, R. Prathibha, E. Ranheim, **C. Dewey**, J. Zhang, and E. Bresnick. (2015) Cis-regulatory mechanisms

- governing stem and progenitor cell transitions. *Science Advances*. 1(8):e1500503–e1500503.
16. K. Hewitt, D. Kim, P. Devadas, R. Prathibha, C. Zuo, R. Sanalkumar, K. Johnson, Y-A. Kang, J-S. Kim, **C. Dewey**, S. Keles, and E. Bresnick. (2015) Hematopoietic Signaling Mechanism Revealed From a Stem/Progenitor Cell Cistrome. *Molecular Cell*. 59(1):62-74.
 17. N. Leng, Y. Li, B. Mcintosh, B. Nguyen, B. Duffin, S. Tian, J. Thomson, **C. Dewey**, R. Stewart, and C. Kendzierski. (2015) EBSeq-HMM: A Bayesian approach for identifying gene-expression changes in ordered RNA-Seq experiments. *Bioinformatics*. 31(16):2614-2622.
 18. B. Li*, N. Fillmore*, Y. Bai, M. Collins, J. Thomson, R. Stewart, and **C. Dewey**. (2014) Evaluation of de novo transcriptome assemblies from RNA-Seq data. *Genome Biology*. 15(12):553.
 19. X. Gao, K. Johnson, Y. Chang, M. Boyer, **C. Dewey**, J. Zhang, and E. Bresnick. (2013) Gata2 cis-element is required for hematopoietic stem cell generation in the mammalian embryo. *Journal of Experimental Medicine*. 210(13):2833-42.
 20. Y. Zhang, A. Cooke, S. Park, **C. Dewey**, M. Wickens, and M. Sheets. (2013) Bicaudal-C spatially controls translation of vertebrate maternal mRNAs. *RNA*. 19(11):1575-82.
 21. L. LeGault* and **C. Dewey**. (2013) Inference of alternative splicing from RNA-Seq data with probabilistic splice graphs. *Bioinformatics*. 29(18):2300-2310.
 22. B. Haas, A. Papanicolaou, M. Yassour, M. Grabherr, P. Blood, J. Bowden, M. Couger, D. Eccles, B. Li*, M. Lieber, M. MacManes, M. Ott, J. Orvis, N. Pochet, F. Strozzi, N. Weeks, R. Westerman, T. William, **C. Dewey**, R. Henschel, R. LeDuc, N. Friedman and A. Regev. (2013) De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. *Nature Protocols*. 8(8):1494-1512.
 23. R. Stewart, C. Rascón, S. Tian, J. Nie, C. Barry, L. Chu, R. Wagner, M. Probasco, J. Bolin, N. Leng, S. Sengupta, M. Volkmer, B. Habermann, E. Tanaka, J. Thomson, and **C. Dewey**. (2013) Comparative RNA-seq analysis in the unsequenced axolotl: The oncogene burst highlights early gene expression in the blastema. *PLoS Computational Biology*. 9(3): e1002936.
 24. S. Li, W. Guo, **C. Dewey**, and M. Greaser. (2013) Rbm20 regulates titin alternative splicing as a splicing repressor. *Nucleic Acids Research*. 41(4): 2659-2672.
 25. C. Langley, K. Stevens, C. Cardeno, Y. Lee, D. Schrider, J. Pool, S. Langley, C. Suarez, R. Detig-Corbett, B. Kolaczowski, S. Fang, P. Nista, A. Holloway, A. Kern, **C. Dewey**, Y. Song, M. Hahn, and D. Begun. (2012) Genomic variation in natural populations of *Drosophila melanogaster*. *Genetics*. 192(2):533-98.
 26. B. Li* and **C. Dewey**. (2011) RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC Bioinformatics*. 12:323.
 27. **C. Dewey**. (2011) Positional orthology: putting genomic evolutionary relationships into context. *Briefings in Bioinformatics*. 12(5):401-412.
 28. D. Chung, P. F. Kuan, B. Li*, R. Sanalkumar, K. Liang, E. Bresnick, **C. Dewey**, and S. Keles. (2011) Discovering transcription factor binding sites in highly repetitive regions of genomes with multi-read analysis of ChIP-seq data. *PLoS Computational Biology*. 7:e1002111.
 29. B. Larget, S. Kotha*, **C. Dewey**, C. Ané. (2010) BUCKy: Gene Tree / Species Tree Reconciliation with Bayesian Concordance Analysis. *Bioinformatics* 26(22):2910-2911.
 30. B. Li*, V. Ruotti, R. Stewart, J. Thomson, **C. Dewey**. (2010) RNA-Seq gene expression estimation with read mapping uncertainty. *Bioinformatics* 26(4):493-500.
 31. M. White, C. Ané, **C. Dewey**, B. Larget, B. Payseur. (2009) Fine scale phylogenetic discordance across the house mouse genome. *PLoS Genetics* 5(11): e1000729.

32. R. Bradley, A. Roberts, M. Smoot, S. Juvekar, J. Do*, **C. Dewey**, I. Holmes, L. Pachter. (2009) Fast Statistical Alignment. *PLoS Computational Biology* 5(5): e1000392.
33. A. Stark, M. F. Lin, P. Kheradpour, J. S. Pedersen, L. Parts, J. W. Carlson, M. A. Crosby, M. D. Rasmussen, S. Roy, A. N. Deoras, J. G. Ruby, J. Brennecke, Harvard FlyBase curators, Berkeley Drosophila Genome Project, E. Hodges, A. S. Hinrichs, A. Caspi, B. Paten, S.-W. Park, M. V. Han, M. L. Maeder, B. J. Polansky, B. E. Robson, S. Aerts, J. van Helden, B. Hassan, D. G. Gilbert, D. A. Eastman, M. Rice, M. Weir, M. W. Hahn, Y. Park, **C. Dewey**, L. Pachter, W. J. Kent, D. Haussler, E. C. Lai, D. P. Bartel, G. J. Hannon, T. C. Kaufman, M. B. Eisen, A. G. Clark, D. Smith, S. E. Celniker, W. M. Gelbart, M. Kellis. (2007) Discovery of functional elements in 12 drosophila genomes using evolutionary signatures. *Nature* 450(7167):219-232.
34. D. Begun, A. Holloway, K. Stevens, L. Hillier, Y. Poh, M. Hahn, P. Nista, C. Jones, A. Kern, **C. Dewey**, L. Pachter, E. Myers, C. Langley (2007) Population genomics: whole-genome analysis of polymorphism and divergence in *Drosophila simulans*. *PLoS Biology* 5(11):e310.
35. E. Margulies, G. Cooper, G. Asimenos, D. Thomas, **C. Dewey** et al. (one of 78 authors, first five contributed equally) (2007) Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. *Genome Research* 17(6):760-774.
36. The ENCODE Project Consortium (**one** of 308 authors) (2007) Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature* 447:799-816.
37. **C. Dewey**, I. Rogozin, and E. Koonin (2006) Compensatory relationships between splice sites and exonic splicing signals depending on the length of vertebrate introns. *BMC Genomics* 7:311.
38. **C. Dewey**, P. Huggins, K. Woods, B. Sturmfels, and L. Pachter (2006) Parametric alignment of *Drosophila* genomes. *PLoS Computational Biology* 2(6): e73.
39. **C. Dewey** and L. Pachter (2006) Evolution at the nucleotide level: the problem of multiple whole-genome alignment. *Human Molecular Genetics* 15:R51-R56.
40. S. Lall, D. Grün, A. Krek, K. Chen, Y. Wang, **C. Dewey**, P. Sood, T. Colombo, N. Bray, P. MacMenamin, H. Kao, K. Gunsalus, L. Pachter, F. Piano and N. Rajewsky (2006) A genome-wide map of conserved microRNA targets in *C. elegans*. *Current Biology* 16:460–471.
41. International Chicken Genome Sequencing Consortium (**one** of 175 authors) (2004) Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* 432:695-716.
42. The ENCODE Project Consortium (**one** of 308 authors) (2004) The ENCODE (ENCyclopedia of DNA Elements) Project. *Science* 306:636-640.
43. **C. Dewey**, J.Q. Wu, S. Cawley, M. Alexandersson, R. Gibbs and L. Pachter (2004) Accurate identification of novel human genes through simultaneous gene prediction in human, mouse, and rat. *Genome Research* 14:661-664.
44. Rat Genome Sequencing Project Consortium (**one** of 230 authors) (2004) Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature* 428:493-521.
45. Mouse Genome Sequencing Consortium (**one** of 222 authors) (2002) Initial sequencing and comparative analysis of the mouse genome. *Nature* 420:520-562.

Papers submitted to refereed journals or in revision

Invited peer-reviewed papers published in conference proceedings

46. D. Albers, **C. Dewey** and M. Gleicher. (2011) Sequence Surveyor: Leveraging Overview for Scalable Genomic Alignment Visualization. *Proceedings of the IEEE Information Visualization Conference 2011 (InfoVis), Providence, RI, October 2011.*
47. **C. Dewey** and B. Li*. (2009) Transcriptome analysis methods for RNA-Seq data. *Proceedings of the Ninth International Conference for the Critical Assessment of Massive Data Analysis (CAMDA), Chicago, IL, October 2009.*
48. R. Arora, **C. Dewey**, and W. Sethares. (2009) Reconstructing latent periods in genome sequences with insertions and deletions. *Proceedings of the IEEE International Workshop on Genomic Signal Processing and Statistics (GENSiPS), Minneapolis, MN, May 2009.*

Chapters in books

49. **C. Dewey** (2019) Whole-genome alignment. In M. Anisimova, editor, *Evolutionary Genomics: Statistical and Computational Methods, Methods in Molecular Biology*, vol. 1910, Human Press.
50. **C. Dewey** (2012) Whole-genome alignment. In M. Anisimova, editor, *Evolutionary Genomics*, volume 855 of *Methods in Molecular Biology*. Humana Press.
51. **C. Dewey** (2007) Aligning multiple whole genomes with Mercator and MAVID. In N. Bergman, editor, *Comparative Genomics*, volume 395 of *Methods in Molecular Biology*. Humana Press.
52. **C. Dewey** and K. Woods (2005) Parametric Sequence Alignment. *Algebraic Statistics for Computational Biology*. Ed. L. Pachter and B. Sturmfels. Cambridge University Press, 193-205.

Research presentations

Invited conference or workshop presentations

1. Great Lakes Bioinformatics Conference (GLBIO)
Madison, WI, May 20, 2019
Teaching introductory bioinformatics with Jupyter notebook-based active learning
2. ISMB General Computational Biology track
Chicago, IL, July 7, 2018
MetaSRA: Normalized Human Sample-Specific Metadata for the Sequence Read Archive
(Presenter: M. Bernstein*)
3. ISMB BD2K track
Chicago, IL, July 7, 2018
MetaSRA: Normalized Human Sample-Specific Metadata for the Sequence Read Archive
(Presenter: M. Bernstein*)
4. Genome 10K and Genome Science Conference
Norwich, United Kingdom, August 29 - September 1, 2017.
Genome-wide characterization of RNA processing event dependencies
5. Fifth RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-SEQ),
Warsaw, Poland, April 10-11, 2015.
Evaluation of de novo transcriptome assemblies from RNA-Seq data
(Presenter: N. Fillmore*)

6. Molecular Medicine Tri-Conference, Genome and Transcriptome Analysis Program, San Francisco, CA, February 10-12, 2014.
Enabling transcript quantification in non-model organisms with RNA-Seq and generative probabilistic models
7. RNA-Seq 2013, Boston, MA June 19-20, 2013.
Inference of alternative splicing from RNA-Seq data with probabilistic splice graphs
8. University of Wisconsin-Madison Symposium on Integration of Mathematical and Biological Sciences (MathBio4: Scale), Madison, WI Oct 18-19, 2012.
Issues of scale in whole genome sequence alignment and visualization
9. Eighth International Purdue Symposium on Statistics, Purdue University, West Lafayette, IN June 20-24, 2012.
Inference of alternative splicing from RNA-Seq data with probabilistic splice graphs
10. Workshop on Transcriptomics and Epigenomics, Program in Mathematical and Computational Approaches in High-Throughput Genomics, Institute for Pure & Applied Mathematics, University of California, Los Angeles, October 25-28, 2011.
Enabling transcript quantification in non-model organisms with RNA-Seq and generative probabilistic models
11. International Biometric Society, Eastern North American Region (ENAR) Annual Meeting, Miami, FL, March 20-23, 2011.
Local alignments as approximations for RNA-Seq statistical models.
12. Ninth International Conference for the Critical Assessment of Massive Data Analysis (CAMDA), Chicago, IL, October 5-6, 2009.
Transcriptome analysis methods for RNA-Seq data.

Invited department seminars

1. Computation and Informatics in Biology and Medicine Seminar, University of Wisconsin, Madison, March 25, 2014
Bypassing genomics: the new era of transcriptomics with RNA-Seq and genome-free computational methods
2. Informatics Grand Rounds, Innovation Center for Biomedical Informatics, Georgetown University, Washington, DC (Webinar), October 21, 2013
Enabling transcriptomics in non-model organisms with RNA-Seq and generative probabilistic models
3. Department of Genetics Retreat, University of Wisconsin, Madison, Merrimac, WI, Sep 13, 2013.
Enabling transcriptomics in non-model organisms with RNA-Seq and generative probabilistic models
4. Department of Statistics Seminar, University of Wisconsin, Madison, Oct 3, 2012
Inference of alternative splicing from RNA-Seq data with probabilistic splice graphs
5. Combi seminar, Department of Genome Sciences, University of Washington, Seattle, October 5, 2011
Enabling transcript quantification in non-model organisms with RNA-Seq and generative probabilistic models
6. Center for Bioinformatics & Computational Biology Seminar, University of Maryland, College Park, April 5, 2011
Beyond counts: quantifying transcript expression with RNA-Seq and generative probabilistic models
7. Mathematical and Computational Biology Seminar, University of California, Berkeley, February 9, 2011
Beyond counts: quantifying transcript expression with RNA-Seq and generative probabilistic models

8. Bioinformatics Program Seminar, University of California, Los Angeles, February 7, 2011
Beyond counts: quantifying transcript expression with RNA-Seq and generative probabilistic models
9. Department of Biosystems Science and Engineering, ETH Zürich, Switzerland, April 13, 2010
Approximating statistical genomics models with local alignments: applications to gene expression estimation and whole-genome orthology prediction
10. Department of Computer Science Colloquium, Northern Illinois University, DeKalb, IL, March 9, 2009
Biological sequence alignment: a convergence of computer science and statistics
11. Department of Electrical and Computer Engineering, ECE 600 Seminar, University of Wisconsin, Madison, November 17, 2008
Bioinformatics: addressing the central dogma through computer science, statistics, and mathematics
12. Computation and Informatics in Biology and Medicine Seminar, University of Wisconsin, Madison, September 18, 2007
On the complexity of the human genome: insights from the ENCODE project
13. Chaos and Complex Systems Seminar Series, University of Wisconsin, Madison, September 4, 2007
On the complexity of the human genome: insights from the ENCODE project
14. Genomic Sciences Training Program Retreat, University of Wisconsin, Madison, June 8, 2007
Correlation of evolutionary constraint and biological function in the human genome: A report from the ENCODE project
15. Evolution Seminar Series, University of Wisconsin, Madison, May 3, 2007
Evolutionary analyses from vertebrate whole-genome alignments
16. Computation and Informatics in Biology and Medicine Seminar, University of Wisconsin, Madison, November 14, 2006
The genome alignment problem
17. Statistics and Genomics Seminar, University of California, Berkeley, April 6, 2006
Whole-genome alignments and polytopes for comparative genomics

Invited expert panels

1. Cambridge Healthtech Associates Webinar, November 12, 2013
The basics of RNA-Seq analysis in non-model organisms
2. NGS Leaders (<http://www.ngsleaders.org>) Webinar, November 15, 2012
Methods for RNA-Seq Data Analysis

Invited poster presentations

*: indicates the presenter

1. M. Amodio and **C. Dewey** (2017) Genome 10K and Genome Science Conference, Norwich, United Kingdom, August 29 - September 1, 2017.
Genome-wide characterization of RNA processing event dependencies
2. B. Li*, N. Fillmore and **C. Dewey** (2012) International Conference on Intelligent Systems for Molecular Biology, Long Beach, CA, July 15-17, 2012.
RSEM-EVAL: A Probabilistic Transcriptome Assembly Evaluator
3. F. Rastegar and **C. Dewey*** (2010) International Conference on Intelligent Systems for Molecular Biology, Boston, MA, July 11-13, 2010.
Bacterial Whole-Genome Probabilistic Alignment
4. **C. Dewey*** and L. Pachter (2004). The Biology of Genomes, Cold Spring Harbor Laboratory, NY, May 12-16, 2004.

Construction of Orthology Maps for Multiple Whole Genomes

Contributed poster presentations

*: *indicates the presenter*

1. N. Perna, B. Larget, C. Ané, **C. Dewey***, G. Plunkett III, L. Ho, J. Glasner, B. Ma, Y. Chung, F. Rastegar, M. Rusch, B. Biehl, P. Liss. (2011) NESCent challenges for large-scale phylogeny and alignment estimation workshop, Durham, NC, March 31-April 1, 2011.
Assembling the Tree of Life: Enterobacteriaceae

Research support

Current funding

Level of funding indicates total amount granted for the duration of the project.

1. Machine Learning Approaches For Metadata Standardization
American Family Data Science Institute, UW-Madison
PI: Colin Dewey, Department of Biostatistics and Medical Informatics, UW Madison
Level of funding: \$148,178.00
Dates: 10/01/2020-09/30/2022
2. Characterization and Statistical Modeling of RNA Processing Event Dependencies
UW-Madison Fall Competition Award
PI: Colin Dewey, Department of Biostatistics and Medical Informatics, UW Madison
Level of funding: \$57,962.00
Dates: 07/01/2018-06/30/2021
3. R01 EY027396-01A1 Therapeutic Inhibition of Optic Nerve Head Gliosis and Fibrosis in Glaucoma
National Institutes of Health
NEI
PI: Gillian McLellan
Role: Co-investigator (5%)
Support for CD: 5% salary in years four and five
Dates: 9/30/2017 - 6/30/2022
4. R01 HD091921 Regulation of cell fates by the Bicaudal-C translational repressor
National Institutes of Health
NICHD
PI: Michael Sheets, Department of Biomolecular Chemistry
Role: Co-Investigator (8.33%)
Support for CD: 8.33% salary and support for a half time pre-doctoral research assistant
Dates: 08/05/2018-05/31/23
5. P30 CA14520-42 UW Comprehensive Cancer Center Support
National Institutes of Health
NCI
PI: Howard Bailey
Role: Investigator (20%)
Support for CD: 20% salary

Dates: 4/01/07-3/31/18

Completed Research Grants

1. MetaRefine.bio
Alex's Lemonade Stand
PI: Colin Dewey, Department of Biostatistics and Medical Informatics, UW Madison
Level of funding: \$25,000.00
Dates: 10/15/2018-11/16/2020
2. HCA2-A-1708-02305 Computational tools for classification and human data interaction with cell-type labelled RNA-seq data
Chan Zuckerberg Initiative
PI: Colin Dewey, Department of Biostatistics and Medical Informatics, UW Madison
Level of funding: \$175,858.00
Dates: 04/01/2018-03/31/2020
3. U54 AI117924-01 The Center for Predictive Computational Phenotyping
National Institutes of Health
NIAID
PI: Mark Craven, Department of Biostatistics and Medical Informatics
Role: Project lead (20%)
Support for CD: 20% salary and support for a full time pre-doctoral research assistant.
Dates: 09/26/2014-08/31/2019
4. Vilas Associate Award
University of Wisconsin-Madison
PI: Colin Dewey, Department of Biostatistics and Medical Informatics
Support for CD: \$12,500 annually for research expenses
Dates: 07/01/2016-06/30/2018
5. R41 HG008566-01 Integrated biochemical and bioinformatic technologies for accurate transcriptome-wide full-length RNA assembly
National Institutes of Health, NHGRI
PIs: Michael Lodes (Lucigen Corporation), and Colin Dewey Department of Biostatistics and Medical Informatics, UW Madison
Support for CD: 17% salary and support for a full time pre-doctoral research assistant
Dates: 04/20/2015 - 12/31/2017
6. DEB 0936214 Assembling a taxonomically balanced genome-scale reconstruction of the evolutionary history of the Enterobacteriaceae
National Science Foundation
Division of Environmental Biology
PI: Nicole Perna, Department of Genetics, UW Madison
Role: Co-PI (5%)
Support for CD: A full time pre-doctoral research assistant.
Dates: 09/01/2009 - 08/31/2016
7. R01 GM100426-01A1 Genetics and Evolution of Extreme Body Size in Mice from Gough Island
National Institutes of Health
NIGMS

PI: Bret Payseur, Department of Genetics
Role: Co-Investigator (10% years 2 & 3)
Support for CD: 10% salary (years 2 & 3)
Dates: 07/01/2012-06/30/2016

8. U01 HG007019-01 Statistical Methods For Annotating Repetitive Genomic Regions Through ENCODE-derived data
National Institutes of Health
PI: Sunduz Keles
Role: Co-PI (15%)
Support for CD: 15% salary and salary for a postdoc
Dates: 09/17/2012- 6/30/2016
9. R21 HD076828-01 Defining the Xenopus translome
National Institutes of Health
NICHD
PI: Michael Sheets, Department of Biomolecular Chemistry
Role: Co-Investigator (10%)
Support for CD: 10% salary and support for a full time pre-doctoral research assistant
Dates: 07/05/2013-06/30/2016
10. R01 EY022098-01 Retinal Morphogenesis in Zebrafish
National Institutes of Health
PI: Yevgenya Grinblat, Departments of Zoology and Neuroscience, UW Madison
Role: Co-investigator (5% years 1-3)
Support for CD: 5% salary for years 1-2
Dates: 01/01/2012- 12/31/2014
11. R01 HG005232 Computational methods for the analysis of RNA-Seq data
National Institutes of Health
National Human Genome Research Institute
PI: Colin Dewey, Department of Biostatistics and Medical Informatics, UW Madison
Level of funding: \$553,623.00
Dates: 07/01/10 - 03/30/14
12. Small RNAs of the human intestinal microbiome
UW-Madison
Wisconsin Center for Infectious Disease (WisCID)
PI: Heidi Goodrich-Blair, Department of Bacteriology
Role: Co-PI
Support for CD: A full time postdoctoral researcher.
Dates: 09/01/2010 - 08/30/2011

Pending Research Grants

1. An integrative computational and experimental system for interpreting genomic variation
Research Forward, UW Madison
PIs: Audrey Gasch, Department of Medical Genetics, Mark Craven, Department of Biostatistics and Medical Informatics, UW Madison
Role: Collaborator

University service

University

1. Senator, Faculty senate, 2012 - 2017.
2. Alternate senator (for Karl Broman), Faculty senate, 2008 – 2012, 2019 – present

School of Medicine and Public Health

1. Chair, Bioinformatics Certificate Review Committee, 2014 – 2015.
2. Leader, Bioinformatics component of the ICTR Biomedical Informatics Core, 2014 – present.
3. Faculty Leader, Cancer Informatics Shared Resource (CISR), UW Carbone Cancer Center (UWCCC), 2019 - present

Biotechnology Center

1. Chair, Faculty Advisory Committee for the Bioinformatics Resource Center (BRC) 2012 - present.
2. Member, Faculty Advisory Committee for the Bioinformatics Resource Center (BRC) (formerly Advanced Genome Analysis Resource (AGAR)), 2010 - 2012.

Department of Biostatistics and Medical Informatics

1. Member, BMI Hiring Committee, 2016 - 2017.
2. Co-director, Bio-Data Science training program, 2016 - present.
3. Member, CIBM Training Program Management Committee, 2016 - present.
4. Member, BMI/MIR Hiring Committee, 2014 - 2015, 2018 - 2019.
5. Member, MS Program in Biomedical Data Science Steering Committee, 2014 - present.
6. Co-chair, BCG Scientific Advisory and Steering Committee, 2014 - present.
7. Member, BRC UWCCC Hiring Committee, 2014.
8. Member, Clinical Informatics Hiring Committee, 2013.
9. Member, Education and Curriculum Committee, 2010 - 2020.
10. Co-chair, Education and Curriculum Committee, 2020 - present.
11. Mentor, Computational Biology and Biostatistics Summer Research Program, 2009.
12. Member, Biostatistics and Medical Informatics Certificate Committee, 2008 - 2018.
13. Co-chair, Departmental Seminar Committee, 2007 - 2009.
14. Member, Systems Biology Cluster Hiring Committee, 2007.

Department of Computer Sciences

1. Member, Graduate Advising Committee, 2008 – 2017, 2018 – present
2. Member, Artificial Intelligence Qualifying Exam Committee, 2007 - 2020.

Professional service

Grant proposal review panels

1. National Institutes of Health, Biodata Management and Analysis (BDMA) study section, 2016.
2. National Institutes of Health, National Institute of Dental & Craniofacial Research, Special Emphasis Panel, 2014.
3. National Science Foundation, Information & Intelligent Systems Division (IIS), proposal panel, 2012.
4. National Institutes of Health, Center for Scientific Review Special Emphasis Panel, Topics in Bioengineering, Computation, and Biological Modeling #2 Proposal panel, 2011.

5. National Science Foundation, Computing and Communication Foundations (CCF), proposal panel, 2009.
6. National Science Foundation, Cyber-enabled Discovery and Innovation (CDI), Type I pre-proposal panel, 2008.
7. National Institutes of Health, National Cancer Institute, The Cancer Genome Atlas (TCGA), proposal panel, 2008.

Ad hoc review of proposals

1. Science Foundation Ireland (2017-1)
2. Research Grants Council of Hong Kong (2017-1, 2020-1)
3. University of Wisconsin Institute for Clinical and Translational Research (2014-1,2015-1,2017-1, 2019-1)
4. National Foundation for Prevention of Chemical Dependency Disease (2012-2)
5. National Science Foundation (2009-1, 2015-1)
6. Swiss National Science Foundation (2007-1)

Conference sessions chaired

1. Session on phylogeny, International Conference on Research in Computational Molecular Biology (RECOMB), Tucson, AZ, 2009.

Journal manuscript reviews

1. Algorithms for Molecular Biology (2010-1).
2. BMC Bioinformatics (2010-3, 2011-1, 2012-1, 2013-3, 2020-1).
3. BMC Genomics (2013-1)
4. BMC Research Notes (2010-1, 2012-1).
5. Bioinformatics (2006-1, 2007-2, 2008-1, 2009-1, 2010-4, 2011-5, 2012-6, 2013-1, 2014-1, 2015-2, 2016-4, 2017-3, 2018-2, 2019-1, 2020-5).
6. Biometrics (2014 - 1).
7. Briefings in Bioinformatics (2013-1).
8. Bulletin of Mathematical Biology (2009-2).
9. G3: Genes, Genomes, Genetics (2013-1).
10. Genetics (2012-1).
11. Genome Biology (2010-1, 2011-1, 2012-2, 2013-1, 2014-2, 2015-2, 2016-1, 2020-1).
12. Genome Biology and Evolution (2011-1).
13. Genome Research (2019-1, 2020-1).
14. GigaScience (2018-1).
15. IEEE/ACM Transactions on Computational Biology and Bioinformatics (2011-1).
16. International Journal of Approximate Reasoning (2016-1).
17. Journal of Biomedicine and Biotechnology (2010-1).
18. Journal of Molecular Evolution (2009-1).
19. Nature Biotechnology (2013-2, 2014-1, 2015-1, 2017-1, 2019-1, 2020-1).
20. Nature Communications (2013-1,2019-1, 2020-1).
21. Nature Methods (2012-1, 2015-1, 2016-1).
22. Nucleic Acids Research (2013-1, 2014-2, 2015-3, 2017-1).
23. PeerJ (2015-1, 2018-1).
24. PLoS Computational Biology (2009-1, 2013-1, 2014-2, 2020-1).
25. PLoS One (2011-1).
26. Proceedings of the National Academy of Sciences of the United States of America (2013-1, 2015-1).
27. RNA (2014-1, 2015-1, 2017-1).
28. Science (2014 - 1).

29. Scientific Reports (2016-1,2019-1).
30. Trends in Cancer (2020-1)
31. Trends in Genetics (2012-1).

Conference program committees or *ad hoc* reviews

1. ACM Conference on Bioinformatics, Computational Biology & Biomedicine (ACM-BCB) (2011-5, 2012-6).
2. Brazilian Symposium on Bioinformatics (BSB) (2008).
3. Great Lakes Bioinformatics Conference (GLBIO) (2017-1,2019-5).
4. IEEE International Conference on Bioinformatics and Biomedicine (BIBM) (2007-4, 2008-3, 2009-6, 2010-6).
5. International Conference on Algorithms for Computational Biology (AICoB) (2019-3, 2020-3, 2021-2).
6. International Conference on Genome Informatics (GIW) (2008-3, 2009-4).
7. International Conference on Intelligent Systems for Molecular Biology (ISMB) (2010-6, 2011-5, 2014-1).
8. International Conference on Research in Computational Molecular Biology (RECOMB) (2009-12, 2010-11, 2011-9, 2014-6, 2015-7, 2016-8).
9. International Conference on Research in Computational Molecular Biology, Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq) (2011-2).
10. International Symposium on Bioinformatics Research and Applications (ISBRA) (2008-5, 2009-4).
11. Workshop on Algorithms in Bioinformatics (WABI) (2020-1)

Book proposal reviews

1. Garland Science (2009-1).