

**Curriculum Vitae**  
Colin N. Dewey  
(Updated: October 17, 2017)

**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>

**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**

- 2012 - Present 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 - Present 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
2. Introduction to Bioinformatics (BMI/CS 576)  
Fall 2008, Fall 2009, Fall 2010, Fall 2015, Fall 2016
3. Statistical Methods for Molecular Biology (STAT 877)  
Spring 2012 (one lecture in jointly taught course), Spring 2014 (2 lectures), Spring 2017 (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. Workshop on Computational Approaches to Analyzing Microarray Data  
Promega, Madison, WI. July 17, 2008.  
One lecture on the topic of "Whole genome alignment"
2. 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.
3. 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: 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, trainee, Fall 2014 – present (qualifying exam passed September 2015)  
*Research area:* 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

### Rotation Students

1. Norbert Binkiewicz, Spring 2013  
*Rotation project:* SNP and allele specific expression inference from RNA-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, To be conferred in August 2017  
*Title:* Statistical Methods for RNA-sequencing Data

### 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*
10. Abigail Shockey, Microbiology, June 2016.
11. Lindsey Bohr, Microbiology, August 2016.  
*Title: Characterizing HGT and Recombination in *Mycobacterium abscessus**
12. Rhonda Bacher, Statistics, December 2016.  
*Title: Statistical Methods for Single Cell RNA Sequencing Data*
13. Megan Frayer, Genetics, March 2017.  
*Title: Genomic Analysis of Ancestry in House Mice Hybrid Zones*
14. Kazuya Oikawa, Comparative Biomedical Science, May 2017.

#### 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

## Publications

\*: indicates a student or postdoc under my supervision.

### Papers published in or accepted by refereed journals

1. 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.
2. 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.
3. M. Bernstein\*, A. Doan, and **C. Dewey**. MetaSRA: normalized sample-specific metadata for the Sequence Read Archive. (2017) *Bioinformatics*. 33(18):2914-2923.
4. 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.
5. 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.
6. 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.
7. 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.
8. 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.
9. 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.

10. 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.
11. 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.
12. 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.
13. 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.
14. L. LeGault\* and **C. Dewey**. (2013) Inference of alternative splicing from RNA-Seq data with probabilistic splice graphs. *Bioinformatics*. 29(18):2300-2310.
15. 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.
16. 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.
17. 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.
18. 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.
19. B. Li\* and **C. Dewey**. (2011) RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC Bioinformatics*. 12:323.
20. **C. Dewey**. (2011) Positional orthology: putting genomic evolutionary relationships into context. *Briefings in Bioinformatics*. 12(5):401-412.
21. 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.
22. B. Larget, S. Kotha\*, **C. Dewey**, C. Ané. (2010) BUCKy: Gene Tree / Species Tree Reconciliation with Bayesian Concordance Analysis. *Bioinformatics* 26(22):2910-2911.
23. 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.
24. 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.
25. 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.
26. 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.
27. 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.
  28. 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.
  29. 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.
  30. **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.
  31. **C. Dewey**, P. Huggins, K. Woods, B. Sturmfels, and L. Pachter (2006) Parametric alignment of *Drosophila* genomes. *PLoS Computational Biology* 2(6): e73.
  32. **C. Dewey** and L. Pachter (2006) Evolution at the nucleotide level: the problem of multiple whole-genome alignment. *Human Molecular Genetics* 15:R51-R56.
  33. 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.
  34. 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.
  35. The ENCODE Project Consortium (**one** of 308 authors) (2004) The ENCODE (ENCyclopedia of DNA Elements) Project. *Science* 306:636-640.
  36. **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.
  37. 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.
  38. 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

39. 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.



40. **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.*
41. 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

42. **C. Dewey** (2012) Whole-genome alignment. In M. Anisimova, editor, *Evolutionary Genomics*, volume 855 of *Methods in Molecular Biology*. Humana Press.
43. **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.
44. **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. Genome 10K and Genome Science Conference  
Norwich, United Kingdom, August 29 - September 1, 2017.  
*Genome-wide characterization of RNA processing event dependencies*
2. 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\*)
3. 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*
4. RNA-Seq 2013, Boston, MA June 19-20, 2013.  
*Inference of alternative splicing from RNA-Seq data with probabilistic splice graphs*
5. 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*
6. 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*
7. 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*
8. 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.*

9. 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. 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*
2. 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*
3. **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. 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

2. 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: 09/26/2014-08/31/2018
3. 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 - 09/30/2017
4. UL1 TR000427-10 Institutional Clinical and Translational Science Award (UW-Madison)  
National Institutes of Health, NCATS  
PI: Marc Drezner  
Role: Investigator (20%)  
Support for CD: 20% salary  
Dates: 09/17/07-5/31/18
5. P30 CA14520-42 UW Comprehensive Cancer Center Support  
National Institutes of Health  
NCI  
PI: Howard Bailey  
Role: Investigator (10%)  
Support for CD: 10% salary  
Dates: 4/01/07-3/31/18

#### Completed Research Grants

1. 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
2. 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

3. 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
4. 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
5. 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
6. 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
7. 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. 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: 04/01/2018-03/31/23
2. OT3 Multi-Component Research Project - An End to End System for Linking Genotypes to Complex Phenotypes  
National Institutes of Health  
NHLBI  
PI: Mark Craven, Department of Biostatistics and Medical Informatics, UW Madison  
Role: Co-Investigator (10%)  
Dates: 09/29/2017 - 03/29/2017

## **University service**

### University

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

### 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.

### 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 - present.
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.
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 - present.
10. Mentor, Computational Biology and Biostatistics Summer Research Program, 2009.
11. Member, Biostatistics and Medical Informatics Certificate Committee, 2008 - present.
12. Co-chair, Departmental Seminar Committee, 2007 - 2009.
13. Member, Systems Biology Cluster Hiring Committee, 2007.

### Department of Computer Sciences

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

## **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)
3. University of Wisconsin Institute for Clinical and Translational Research (2014-1,2015-1,2017-1)
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).
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).
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).
12. Genome Biology and Evolution (2011-1).
13. IEEE/ACM Transactions on Computational Biology and Bioinformatics (2011-1).
14. International Journal of Approximate Reasoning (2016-1).
15. Journal of Biomedicine and Biotechnology (2010-1).
16. Journal of Molecular Evolution (2009-1).

17. Nature Biotechnology (2013-2, 2014-1, 2015-1, 2017-1).
18. Nature Communications (2013-1).
19. Nature Methods (2012-1, 2015-1, 2016-1).
20. Nucleic Acids Research (2013-1, 2014-2, 2015-3, 2017-1).
21. PeerJ (2015-1).
22. PLoS Computational Biology (2009-1, 2013-1, 2014-2).
23. PLoS One (2011-1).
24. Proceedings of the National Academy of Sciences of the United States of America (2013-1, 2015-1).
25. RNA (2014-1, 2015-1, 2017-1).
26. Science (2014 - 1).
27. Scientific Reports (2016-1).
28. Trends in Genetics (2012-1).

#### Conference program committees

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).
4. IEEE International Conference on Bioinformatics and Biomedicine (BIBM) (2007-4, 2008-3, 2009-6, 2010-6).
5. International Conference on Genome Informatics (GIW) (2008-3, 2009-4).
6. International Conference on Intelligent Systems for Molecular Biology (ISMB) (2010-6, 2011-5, 2014-1).
7. International Conference on Research in Computational Molecular Biology (RECOMB) (2009-12, 2010-11, 2011-9, 2014-6, 2015-7, 2016-8).
8. International Conference on Research in Computational Molecular Biology, Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq) (2011-2).
9. International Symposium on Bioinformatics Research and Applications (ISBRA) (2008-5, 2009-4).

#### Book proposal reviews

1. Garland Science (2009-1).