

## CURRICULUM VITAE

### COLIN N. DEWEY

#### ADDRESS

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#### EDUCATION

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

#### PROFESSIONAL POSITIONS

- August 2006 – present Assistant Professor. Department of Biostatistics and Medical Informatics  
University of Wisconsin, Madison, WI
- June 2005 – August 2005 Scientific Visitor. National Center for Biotechnology Information  
National Library of Medicine, National Institutes of Health, Bethesda, MD

#### PROFESSIONAL APPOINTMENTS

- Faculty member. Genome Center of Wisconsin, University of Wisconsin, Madison, WI,  
August 2006 – present
- Faculty member. Genomics Cluster, University of Wisconsin, Madison, WI  
August 2006 – present
- Affiliate faculty member. Department of Computer Sciences, University of Wisconsin, Madison, WI  
August 2006 – present

Member. Cancer Genetics Program. Carbone Cancer Center, University of Wisconsin, Madison, WI  
September 2006 — present

Member. Biomedical Informatics Resource. Institute for Clinical and Translational Research. University of Wisconsin, Madison, WI  
2007 — present

Faculty trainer. Computation and Informatics in Biology and Medicine Training Program, University of Wisconsin, Madison, WI  
November 2006 — present

Faculty trainer. Genomic Sciences Training Program, University of Wisconsin, Madison, WI  
September 2006 — present

## **CONSORTIUM MEMBERSHIPS**

ENCODE Project Consortium (2004—2007)  
International Chicken Genome Sequencing Consortium (2004)  
Rat Genome Sequencing Project Consortium (2004)  
Mouse Genome Sequencing Consortium (2002)

## **PROFESSIONAL SOCIETY MEMBERSHIPS**

International Society for Computational Biology (2005—present)

## **HONORS AND AWARDS**

Howard Hughes Medical Institute Predoctoral Fellowship in Biological Sciences Honorable Mention (2003)  
National Science Foundation Graduate Research Fellowship Honorable Mention (2003)  
National Science Foundation Graduate Research Fellowship Honorable Mention (2001)  
Phi Beta Kappa Society (2001)  
Eta Kappa Nu Society (1999)  
University of California, Berkeley Edward Frank Kraft Scholarship Prize (1998)

## **EDUCATIONAL ACTIVITIES**

### **Classroom Instruction**

Introductory Bioinformatics, BMI/CS 576, Fall 2008, Fall 2009, Fall 2010  
Advanced Bioinformatics, BMI/CS 776, Spring 2007, Spring 2008

### **Short-courses and workshops**

Genetics, Natural Selection & Evolution. Science Masters Institute, Madison Metropolitan School District, Madison, WI (2007, 2008, 2009)

Computational Approaches to Analyzing Microarray Data Course. BioPharmaceutical Technology Center Institute, Madison, WI (2008)

Biological Sequence Alignment. PhD Program in Computational Biology. Instituto Gulbenkian de Ciência, Oeiras, Portugal (2008)

### **Postdocs supervised**

Jin Park, 2010—present (joint with Heidi Goodrich-Blair)

Eagu Kim, 2008—2009

### **PhD Advisees**

Laura LeGault, Computer Sciences, 2010—present

Bo Li, Computer Sciences, 2008—present

Farzad Rastegar, Computer Sciences, 2008—2010

### **Master's Advisees**

Kristopher Kosmatka, Computer Sciences, 2010—present

Jae Young Do, Computer Sciences, 2008—2009

### **Other Advisees**

Satish Kotha, Computer Sciences, 2009—2010 (joint with Cecile Ane)

Daniel Wong, Computer Sciences, short-term CIBM traineeship, 2007

### **Doctoral Thesis Defenses**

Yue Pan, Computer Sciences, 2009

Raman Arora, Electrical and Computer Engineering, 2009

Pei-Fen Kuan, Statistics, 2009

Keith Noto, Computer Sciences, 2007

Irene Ong, Computer Sciences, 2007

### **Doctoral Thesis Committees**

Ryan Haasl, Genetics 2010— present

Heejung Shim, Statistics 2008—2010

Raman Arora, Electrical and Computer Engineering, 2008—2009

### **Doctoral Advisory Committees**

Jessica Clarke, Genetics, 2007

Beth Dumont, Genetics, 2007

### **Masters Defenses**

Jessica Clarke, Genetics, 2008

## **EDITORIAL ACTIVITIES**

### **Journal review**

PLoS Computational Biology, Bioinformatics, BMC Bioinformatics, BMC Research Notes, Bulletin of Mathematical Biology, Genome Biology, Journal of Biomedicine and Biotechnology, Journal of Molecular Evolution

### **Conference review**

International Conference on Intelligent Systems for Molecular Biology (ISMB 2010), International Conference on Research in Computational Molecular Biology (RECOMB 2009,2010,2011), IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2007,2008,2009,2010), Brazilian Symposium on Bioinformatics (BSB 2008), International Conference on Genome Informatics (GIW 2008,2009), International Symposium on Bioinformatics Research and Applications (ISBRA 2008,2009).

### **Review panels**

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

### **Ad-hoc review of proposals**

National Science Foundation (2009)  
Swiss National Science Foundation (2007)

### **Book proposals**

Garland Science (2009)

## **SESSION CHAIR AT INTERNATIONAL MEETINGS**

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

## **RESEARCH INTERESTS**

My research focuses on algorithmic and statistical methodology for genomics and molecular evolution. I am particularly interested in methods for the analysis of next-generation sequencing data, the alignment of multiple whole genome sequences and the use of comparative genomics for discovery in molecular biology.

## **SERVICE ACTIVITIES**

### **University**

Faculty senate (alternate for Karl Broman), 2008—present

### **Biotechnology Center**

Faculty Advisory Committee for the Advanced Genome Analysis Resource (AGAR), 2010—present

### **Departmental**

Mentor for Computational Biology and Biostatistics Summer Research Program, 2009

Biostatistics and Medical Informatics Departmental Seminar Series Co-organizer, 2007—2009

Biostatistics and Medical Informatics Certificate Committee, 2008—present

Computer Science Graduate Advising Committee, 2008—present

Computer Science AI Qual Committee, 2007—present

Systems Biology Cluster Hiring Committee, 2007

## **GRANT SUPPORT**

### **Current Grant Support**

Title: Computational methods for the analysis of RNA-Seq data

Principal Investigator: Colin Dewey

Period: 07/01/10 — 03/30/13

Agency: National Institutes of Health, National Human Genome Research Institute

Role: PI (25%)

Title: Assembling a taxonomically balanced genome-scale reconstruction of the evolutionary history of the Enterobacteriaceae

Principal Investigator: Nicole Perna

Period: 09/01/09 — 08/31/14

Agency: National Science Foundation, Division of Environmental Biology

Role: Co-PI (5%)

Title: Small RNAs of the human intestinal microbiome

Principal Investigator: Heidi Goodrich-Blair

Period: 09/01/10 — 08/30/11

Agency: UW-Madison, Wisconsin Center for Infectious Disease (WisCID)

Role: Co-PI

# PUBLICATIONS

## Refereed Journal Articles

- 2010 B. Larget, S. Kotha, **C. Dewey**, C. Ane. (2010) BUCKy: Gene Tree / Species Tree Reconciliation with Bayesian Concordance Analysis. *Bioinformatics* 26(22):2910-2911.
- 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.
- 2009 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.
- 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.
- 2007 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.
- 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.
- 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.
- 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.
- 2006 **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.
- C. Dewey**, P. Huggins, K. Woods, B. Sturmfels, and L. Pachter (2006) Parametric alignment of *Drosophila* genomes. *PLoS Computational Biology* 2(6): e73.
- C. Dewey** and L. Pachter (2006) Evolution at the nucleotide level: the problem of multiple whole-genome alignment. *Human Molecular Genetics* 15:R51-R56.
- 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.

- 2004 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.
- The ENCODE Project Consortium (**one of 308 authors**) (2004) The ENCODE (ENCyclopedia of DNA Elements) Project. *Science* 306:636-640.
- 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.
- 2004 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.
- 2002 Mouse Genome Sequencing Consortium (**one of 222 authors**) (2002) Initial sequencing and comparative analysis of the mouse genome. *Nature* 420:520-562.

## Refereed Conference Articles

- 2009 R. Arora, **C. Dewey**, and W. Sethares. (2009) Reconstructing latent periods in genome sequences with insertions and deletions. *IEEE International Workshop on Genomic Signal Processing and Statistics (GENSiPS)*

## Book chapters

- 2007 **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.
- 2005 **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.

## INVITED PRESENTATIONS

### Scientific Meetings

- 2009 Critical Assessment of Massive Data Analysis (CAMDA), Chicago, IL, October 2009

### Seminars

- 2010 Department of Biosystems Science and Engineering, ETH Zürich, Switzerland
- 2009 Department of Computer Science Colloquium, Northern Illinois University, DeKalb, IL
- 2008 ECE 600 Seminar in Electrical and Computer Engineering, University of Wisconsin, Madison, WI
- 2007 Computation and Informatics in Biology and Medicine Seminar, University of Wisconsin, Madison, WI

Chaos and Complex Systems Seminar Series, University of Wisconsin, Madison, WI  
Genomic Sciences Training Program Retreat, University of Wisconsin, Madison, WI  
Evolution Seminar Series, University of Wisconsin, Madison, WI

2006 Computation and Informatics in Biology and Medicine Seminar, University of Wisconsin, Madison, WI  
Statistics and Genomics Seminar, University of California, Berkeley, CA

## **POSTER PRESENTATIONS**

2010 International Conference on Intelligent Systems for Molecular Biology, 2010, Boston, MA  
“Bacterial Whole-Genome Probabilistic Alignment”

2004 The Biology of Genomes, 2004, Cold Spring Harbor, NY  
“Construction of Orthology Maps for Multiple Whole Genomes”