

Colin N. Dewey

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- EDUCATION**
- Ph.D. **University of California, Berkeley**
Electrical Engineering and Computer Sciences
Computational and Genomic Biology Designated Emphasis
December 2006
- B.S. **University of California, Berkeley**
Electrical Engineering and Computer Sciences, High Honors
May 2001

- POSITIONS**
- 2006-present **University of Wisconsin-Madison**
Department of Biostatistics and Medical Informatics
Department of Computer Sciences
Genome Center of Wisconsin
Assistant Professor
- 2005 (Summer) **National Center for Biotechnology Information (NCBI),
National Library of Medicine,
National Institutes of Health (NIH), Bethesda, MD**
Scientific Visitor

RESEARCH INTERESTS

Algorithms for problems in comparative genomics.
Alignment algorithms for multiple whole genome sequences.
Applications of computational geometry and machine learning to genomics.

CONSORTIUM MEMBERSHIPS 2004-2007 **ENCODE Project Consortium**

- 2004 **International Chicken Genome Sequencing Consortium**
- 2004 **Rat Genome Sequencing Project Consortium**
- 2002 **Mouse Genome Sequencing Consortium**

- HONORS/AWARDS**
- 2003 **Howard Hughes Medical Institute (HHMI)**
Predoctoral Fellowship in Biological Sciences Honorable Mention
 - 2003 **National Science Foundation (NSF)**
Graduate Research Fellowship Honorable Mention
 - 2001 **National Science Foundation (NSF)**
Graduate Research Fellowship Honorable Mention
 - 2001-present **Phi Beta Kappa**
 - 1999-present **Eta Kappa Nu**
Electrical and Computer Engineering Honor Society
 - 1998 **University of California, Berkeley**
Edward Frank Kraft Scholarship Prize
- PUBLICATIONS**
- 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. N. 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.
 - The ENCODE Project Consortium (2007) *Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project*. Nature 447:799-816.
 - E. Margulies, G. Cooper, G. Asimenos, D. Thomas, C. Dewey et al. (2007) *Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome*. Genome Research.17(6):760-774.

- 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.
- 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.
- 2006 C. Dewey (2006) *Whole-genome alignments and polytopes for comparative genomics*. Ph.D. dissertation. University of California, Berkeley.
- 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.
- 2005 C. Dewey and K. Woods “Parametric Sequence Alignment.” *Algebraic Statistics for Computational Biology*. Ed. L. Pachter and B. Sturmfels. Cambridge University Press, November 2005. 193-205.
- 2004 International Chicken Genome Sequencing Consortium (2004) *Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution*. *Nature* 432:695-716.
- The ENCODE Project Consortium (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.
- Rat Genome Sequencing Project Consortium (2004) *Genome sequence of the Brown Norway rat yields insights into mammalian evolution*. *Nature* 428:493-521.

- 2002 Mouse Genome Sequencing Consortium (2002) *Initial sequencing and comparative analysis of the mouse genome*. Nature 420:520-562.
- CONFERENCES ATTENDED**
- 2005 **ENCODE Workshop, Hinxton, UK**
Multiple-species alignment analysis group
- Clay Mathematics Institute Workshop, Cambridge, MA**
Algebraic Statistics for Computational Biology
- ENCODE Consortium Meeting, Gaithersburg, MD**
- ENCODE Data Analysis Workshop, Rockville, MD**
Multiple-species alignment analysis group.
- 2004 **Cold Spring Harbor Laboratory Meeting, Cold Spring Harbor, NY**
The Biology of Genomes
Poster: *Construction of orthology maps for multiple whole genomes*
- TALKS**
- 2008 **Computational Approaches to Analyzing Microarray Data Course, BioPharmaceutical Technology Center Institute (BTCI), Madison, WI (07/17/2008)**
Whole genome alignments
- 2007 **Computation and Informatics in Biology and Medicine Seminar, UW-Madison, (9/18/2007)**
On the complexity of the human genome: insights from the ENCODE project
- Chaos and Complex Systems Seminar Series, UW-Madison, (9/4/2007)**
On the complexity of the human genome: insights from the ENCODE project
- Genomic Sciences Training Program retreat, UW-Madison, (6/8/2007)**
Correlation of evolutionary constraint and biological function in the human genome: A report from the ENCODE project
- Evolution Seminar Series, UW-Madison, (5/03/2007)**
Evolutionary analyses from vertebrate whole-genome alignments
- 2006 **Computation and Informatics in Biology and Medicine Seminar, UW-Madison, (11/14/2006)**
The genome alignment problem
- Statistics and Genomics Seminar, UC Berkeley, (4/6/2006)**
Whole-genome alignments and polytopes for comparative genomics

**PROFESSIONAL
AFFILIATIONS**

International Society for Computational Biology (ISCB)