

Michael M. Hoffman

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Education 2008–present University of Washington *Seattle, WA*

Senior Fellow

- Research mentor: Dr. William Stafford Noble, Professor
- National Human Genome Research Institute K99/R00 Pathway to Independence Award

2003–2008 University of Cambridge (Trinity College) *Cambridge, UK*

Doctor of Philosophy, Bioinformatics

- Thesis adviser: Dr. Ewan Birney, Senior Scientist
- Marshall Scholar
- National Science Foundation Graduate Research Fellow

1998–2003 The University of Texas at Austin *Austin, TX*

Bachelor of Science, Biochemistry, with Highest Honors, Special Honors

Bachelor of Arts, Plan II Honors Liberal Arts, with Highest Honors

- Thesis adviser: Dr. Andrew D. Ellington, Professor
- College of Natural Sciences Commencement Speaker, Dean's Honored Graduate
- College of Liberal Arts Dean's Distinguished Graduate
- GPA: 3.965/4.000—University Honors Major GPA: 4.000/4.000

Publications
(refereed)

1. Landt SG, Marinov GK, Kheradpour P, Kundaje A, Pauli F, Batzoglou S, Bernstein B, Bickel P, Brown B, Cayting P, Chen Y, Epstein C, Fisher-Aylor K, Euskirchen G, Gerstein M, Gertz J, Guigo R, Hartemink AJ, **Hoffman MM**, Iyer V, Jung YL, Karmakar S, Kellis M, Kharchenko P, Liu T, Liu XS, Ma L, Milosavljevic A, Myers RM, Park P, Pazin MJ, Perry MD, Raha D, Reddy TE, Rozowsky J, Shores N, Sidow A, Slattery M, Stamatoyonopoulos J, Tolstorukov M, White K, Xi S, Farnham P, Lieb J, Wold B, Snyder M. ChIP-seq guidelines and practices used by the ENCODE and modENCODE consortia. *Genome Res.* In press.
2. **Hoffman MM**, Buske OJ, Wang J, Weng Z, Bilmes JA, Noble WS. Unsupervised pattern discovery in human chromatin structure through genomic segmentation. *Nat Methods.* 2012 Mar 18; 9:473-6.
3. Buske OJ, **Hoffman MM**, Ponts N, Le Roch KG, Noble WS. Exploratory analysis of genomic segmentations with Segtools. *BMC Bioinformatics.* 2011 Oct 26; 12:415.
4. ENCODE Project Consortium. A user's guide to the Encyclopedia of DNA Elements (ENCODE) functional genomic data. *PLoS Biol.* 2011 Apr; 9:e1001046.
5. Chen X, **Hoffman MM**, Bilmes JA, Hesselberth JR, Noble WS. A dynamic Bayesian network for identifying protein-binding footprints from single molecule-based sequencing data. *Bioinformatics.* 2010 Jun 15; 26:i334-42.
6. **Hoffman MM**, Buske OJ, Noble WS. The Genomdata format for storing large-scale functional genomics data. *Bioinformatics.* 2010 Jun 1; 26:1458-9.
7. **Hoffman MM**, Birney E. An effective model for natural selection in promoters. *Genome Res.* 2010 May; 20:685-92.
8. **Hoffman MM**, Birney E. Estimating the neutral rate of nucleotide substitution using introns. *Mol Biol Evol.* 2007 Feb; 24:522-31.
9. International Chicken Genome Sequencing Consortium. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* 2004 Dec 9; 432:695-716.
10. **Hoffman MM**, Khrapov MA, Cox JC, Yao J, Tong L, Ellington AD. AANT: the Amino Acid-Nucleotide Interaction Database. *Nucleic Acids Res.* 2004 Jan 1;

**Publications
(submitted)**

1. **Hoffman MM***, Ernst J*, Wilder SP, Kundaje A, Harris RS, Libbrecht M, Giardine B, Bilmes JA, Birney E, Hardison RC, Dunham I, Kellis M, Noble WS. Integrative annotation of chromatin elements from ENCODE data. Submitted.
2. ENCODE Project Consortium. An integrated Encyclopedia of DNA Elements in the human genome. Submitted.

**Grants
(principal
investigator)**

- Pattern discovery for comparative epigenomics. NIH/NHGRI K99HG006259. 5 years, direct costs \$671,913, total costs \$947,929.
- Graduate research fellowship. NSF/DGE DGE-0435785. 3 years, total costs \$122,500.

**Other
scholarships
and awards**

- National Merit Scholarship, 1998–2002.
- IBM Thomas J. Watson Memorial Scholarship, 1998–2002.
- Dorothy B. Banks Charitable Trust Scholarship, 1999–2000.
- Dedman Merit Scholarship, 1998–2002.
- NSF Research Experience for Undergraduates supplement, 1999.
- The University of Texas at Austin Undergraduate Research Fellowship, 1999–2000, 2000–2001, 2002–2003.
- The University of Texas at Austin Junior Fellows Research Grant, 2003.
- Trinity College Moore, Beale Sargent and Mitchell Fund, 2005

Honors

- *Genome Technology* Young Investigator (nominator: Francis Collins), 2011.
- Phi Beta Kappa Award of Distinction, 2003.
- Inducted into Phi Beta Kappa, 2003.
- Cambridge Overseas Trust Honorary Scholar, 2003.
- College of Liberal Arts Junior Fellow, 2000–2003.
- College of Natural Sciences Dean's Scholar, 1998–2003.
- College of Liberal Arts Plan II Honors Program (2% of university), 1998–2003.
- College of Natural Sciences College Scholar 2000, 2001, 2002, 2003.

**Invited/keynote
presentations**

- Unsupervised and semi-supervised pattern discovery in human chromatin structure. Section of Genetic Medicine. University of Chicago. 23 April 2012.
- Simultaneous segmentation of multiple functional genomics data sets with heterogeneous patterns of missing data. Department of Computer Science. Colorado State University. Fort Collins, Colorado. 10 April 2012.
- Unsupervised pattern discovery in ENCODE chromatin data. Department of Genome Sciences Seminar. University of Washington. Seattle, Washington. 7 September 2011.
- Unsupervised pattern discovery in human chromatin data. Computational Biology Center Guest Seminar. Memorial Sloan-Kettering Cancer Center. New York, New York. 18 May 2011.
- Segway: finding patterns in chromatin data. Center for Bioinformatics Research Special Talk, Indiana University. Bloomington, Indiana. 18 November 2010.
- Finding the patterns in chromatin data. Fifth Barbados Workshop on Gene Regulation: The role of chromatin in 3D structure. Holetown, Barbados. 21 April 2010.
- Properties of natural selection in mammalian promoters. Weizmann UK Symposium: Biological complexity: from models to systems. London, England. Summer 2008.
- Properties of natural selection in mammalian promoters. Seminar, Broad Institute of MIT and Harvard. Cambridge, MA. Spring 2008.

2003–2008 EMBL–European Bioinformatics Institute Cambridge, UK

Predoctoral Fellow

- Research Supervisor: Dr. Ewan Birney, Senior Scientist
- Developed bioinformatics methods for studying the binding of transcription factors and the evolution of noncoding DNA in vertebrates.

2002–2003 Department of Chemistry and Biochemistry
The University of Texas at Austin Austin, TX

Research Assistant

- Research Supervisor: Dr. Andrew D. Ellington, Professor
- Developed database of protein-nucleic acid interactions and bioinformatics methods for elucidating microRNA targets.

2001 Cold Spring Harbor Laboratory Cold Spring Harbor, NY

Undergraduate Research Program Participant

- Research Supervisor: Dr. Michael Q. Zhang, Associate Professor
- Created a database of promoter binding elements in *Arabidopsis thaliana*.

1999–2001 Department of Chemistry and Biochemistry
The University of Texas at Austin Austin, TX

Research Assistant

- Research Supervisor: Dr. Karen S. Browning, Associate Professor
- Designed and executed immunocytochemical experiments to determine cellular locations of specific proteins in *Arabidopsis* and wheat.

2000 Plant Biochemistry Research Training Center
Washington State University Pullman, WA

Undergraduate Research Fellow

- Research Supervisor: Dr. Vincent R. Franceschi, Professor
- Performed immunocytochemical experiments to localize specific proteins in *Arabidopsis* using a transmission electron microscope and a laser scanning confocal microscope.

Software

- Segway: a dynamic Bayesian network method for segmenting genomic data.
<<http://noble.gs.washington.edu/proj/segway/>>.
- Segtools: exploratory data analysis of genomic segmentations.
<<http://noble.gs.washington.edu/proj/segtools/>>.
- Genomedata: a format for storing large-scale functional genomics data.
<<http://noble.gs.washington.edu/proj/genomedata/>>.
- Sunflower: a model of transcription factor binding and evolution.
<<http://www.ebi.ac.uk/~hoffman/software/sunflower/>>.
- Textinput: streamlined version of stdlib fileinput.
<<http://pypi.python.org/pypi/textinput/>>.
- Optbuild: build command lines for external programs.
<<http://pypi.python.org/pypi/optbuild/>>.
- Metascript: a model of gene evolution incorporating alternative transcripts.
<<http://pypi.python.org/pypi/metascript/>>.
- Xyddplot: dot-dash-density plots for R.
<<http://www.ebi.ac.uk/~hoffman/software/xyddplot/>>.
- GALAXI: Global and Local Alignment eXcel Implementation.

- <<http://www.ebi.ac.uk/~hoffman/software/galaxi/>>.
 - Renamer: rename files according to a ruleset.
<<http://www.ebi.ac.uk/~hoffman/software/renamer/>>.
 - Ensclip: unique identifiers for Ensembl features.
<<http://www.ebi.ac.uk/~hoffman/software/ensclip/>>.
 - Poly: rapid development of embarrassingly parallelizable applications.
<<http://www.ebi.ac.uk/~hoffman/software/poly/>>.
 - Ensembl/Jython.
<<http://oct2006.archive.ensembl.org/info/software/java/jython.html>>.
 - Genematrix. <<http://research.cm.utexas.edu/kbrowning/flat/genematrix.tar.gz>>.
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Databases

- AANT: the Amino Acid-Nucleotide Interaction Database.
<<http://aant.icmb.utexas.edu/>>.
 - FIAT: Factors in *Arabidopsis* Translation. <<http://www.cm.utexas.edu/flat/>>.
 - AtProbe: *Arabidopsis thaliana* Promoter Binding Element Database.
<<http://exon.cshl.org/cgi-bin/atprobe/atprobe.pl>>.
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Leadership and committee positions

- **Chair**, Large-scale Integration Task Group, ENCODE Analysis Working Group, 2010–present.
 - **Chair**, Cambridge University Student Pugwash Society, 2006–2007. **Secretary**, 2007–2008. *Organized seminar series on science and society topics.*
 - **Representative**, EMBL–European Bioinformatics Institute Predoctoral Fellow Association, 2004–2005.
 - **Secretary/Treasurer**, International Society for Computational Biology Student Council, 2004. **Member**, 2003–2004.
 - **President**, Texas Student Publications Board of Operating Trustees, 2002–2003. **Vice President**, 2001–2002. **Member**, 2000–2003. *Managed finances, personnel, and policy of daily newspaper, radio station, television station, and other media. \$2.9 million annual budget.*
 - **Member**, College of Natural Sciences Dean’s Scholars Committee, 2000–2003.
 - **Founder and Co-President**, Barbecue Club, 1999–2003.
 - **Chair**, Texas Student Publications Handbook Revision Committee, 2002.
 - **Chair**, Texas Student Publications Election Committee, 2001–2002.
 - **Member**, Information Technology Coordinating Council, 1999–2002.
 - **Member**, General Faculty Admissions and Registration Committee, 1999–2000.
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Professional activities

- **Reviewer** for journals: *Nucleic Acids Research*, *Bioinformatics*, *BMC Bioinformatics*
 - **Reviewer** for conferences: Intelligent Systems in Molecular Biology/European Conferences on Computational Biology (ISMB/ECCB), Research in Computational Molecular Biology (RECOMB)
 - **Participant**, Planning the future of genomics: foundational research and applications in genomic medicine, National Human Genome Research Institute.
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Other organizations

- **Member**, International Society for Computational Biology, 2003–2004, 2010–2011.
 - **Member**, Northwest Institute of Genetic Medicine, 2009–present.
 - **Member**, University of Washington Postdoctoral Association, 2008–present.
 - **Member**, National Postdoctoral Association, 2011–present.
 - **Member**, American Association for the Advancement of Science, 2007–2008.
 - **Member**, Genetics Society, 2006–2007.
 - **Junior Member**, Isaac Newton Institute for Mathematical Sciences, 2006–present.
 - **Member**, Society of Computational Biology, 2002–2003.
 - **Member**, Microbiology and Molecular Biology Student Society, 1998–1999.
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Languages

- **Computer** Python, R, LaTeX, SQL, Perl, C, Bash, Emacs LISP, HTML, CSS
 - **Human** English, Spanish
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References

- Dr. William Stafford Noble, Professor, Department of Genome Sciences, University of Washington.
+1 206 543 8930 william-noble@uw.edu
 - Dr. Jeff A. Bilmes, Professor, Department of Electrical Engineering, University of Washington.
+1 206 221 5236 bilmes@ee.washington.edu
 - Dr. Ewan Birney, Associate Director, EMBL–European Bioinformatics Institute.
+44 1223 494 420 birney@ebi.ac.uk
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Citizenship

- United States of America. Proof available upon request.