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| Michael M. Hoffman | | 101 College St TMDT 11-311  Toronto, ON M5G 1L7 |
| Work +1 416 581 7481  E-mail michael.hoffman@utoronto.ca |
| Current positions | 2013–present Princess Margaret Cancer Centre *Toronto, ON*  Scientist  2014–present University of Toronto *Toronto, ON*  Assistant Professor**, Department of Medical Biophysics**  Assistant Professor**, Department of Computer Science** | |
| Education | 2008–2013 University of Washington *Seattle, WA*  Senior Fellow   * 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   * Adviser: Dr. Ewan Birney, Associate Director, European Bioinformatics Institute * 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   * 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 | |
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| Publications (journal) | J1716. **Viner C**, **Hoffman MM**. “Determining the epigenome using DNA alone.” *Nat Methods.* 2015 Mar; 12:191–2.  J15. Libbrecht MW, Ay F, **Hoffman MM**, Gilbert DM, Bilmes JA, Noble WS. “Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell type-specific expression.” *Genome Res*. 2015; 25:544–57.  J14. Church DM, Schneider VA, Steinberg KM, Schatz MC, Quinlan AR, Chin CS, Kitts PA, Aken B, Marth GT, **Hoffman MM**, Herrero J, Mendoza LZ, Durbin R, Flicek P. “Extending reference assembly models.” *Genome Biol*. 2015; 16:13.  J13. Ho JWK, Jung YL, Liu T, Alver BH, Lee S, Ikegami K, Sohn K, Minoda A, Tolstorukov MY, Appert A, Parker SCJ, Gu T, Kundaje A, Riddle NC, Bishop E, Egelhofer TA, Hu SS, Alekseyenko AA, Rechtsteiner A, Asker D, Belsky JA, Bowman SK, Chen QB, Chen RA, Day DS, Dong Y, Dose AC, Duan X, Epstein CB, Ercan S, Feingold EA, Ferrari F, Garrigues JM, Gehlenborg N, Good PJ, Haseley P, He D, Herrmann M, **Hoffman MM**, Jeffers TE, Kharchenko PV, Kolasinska-Zwierz P, Kotwaliwale CV, Kumar N, Langley SA, Larschan EN, Latorre I, Libbrecht MW, Lin X, Park R, Pazin MJ, Pham HN, Plachetka A, Qin B, Schwartz YB, Shoresh N, Stempor P, Vielle A, Wang C, Whittle CM, Xue H, Kingston RE, Kim JH, Bernstein BE, Dernburg AF, Pirrotta V, Kuroda MI, Noble WS, Tullius TD, Kellis M, MacAlpine DM, Strome S, Elgin SCR, Liu XS, Lieb JD, Ahringer J, Karpen GH, Park PJ. “Comparative analysis of metazoan chromatin organization.” *Nature*. 2014 Aug 28; 512:449–52.   * News and Views: Muerdter F, Stark A. *Nature*. 2014 Aug 28; 512:374–5.   J12. **Hoffman MM**\*, Ernst J\*, Wilder SP, Kundaje A, Harris RS, Libbrecht M, Giardine B, **Ellenbogen PM**, Bilmes JA, Birney E, Hardison RC, Dunham I, Kellis M, Noble WS. “Integrative annotation of chromatin elements from ENCODE data.” *Nucleic Acids Res.* 2013 Jan; 41:827–41.   * Featured Article in *Nucleic Acids Research*. * Cited 103 times.   J11. **ENCODE Project Consortium**. “An integrated Encyclopedia of DNA Elements in the human genome.” *Nature*. 2012 Sep 6; 489:57–74.   * Author contribution: “Lead analyst”. * Featured on cover of *Nature*. * Recommended by Faculty of 1000. * News and Views: Ecker JR et al. *Nature.* 2012 Sep 6; 489:52–55. * Cited 2,809 times.   J10. Landt SG, Marinov GK, Kundaje A, Kheradpour P, Pauli F, Batzoglou S, Bernstein B, Bickel P, Brown B, Cayting P, Chen Y, Desalvo G, Epstein C, Fisher-Aylor KI, Euskirchen G, Gerstein M, Gertz J, Hartemink AJ, **Hoffman MM**, Iyer VR, Jung YL, Karmakar S, Kellis M, Kharchenko PV, Li Q, Liu T, Liu XS, Ma L, Milosavljevic A, Myers RM, Park PJ, Pazin MJ, Perry MD, Raha D, Reddy TE, Rozowsky J, Shoresh N, Sidow A, Slattery M, Stamatoyonnopoulous JA, Tolstorukov MY, White KP, Xi S, Farnham PJ, Lieb JF, Wold BJ, Snyder M. “ChIP-seq guidelines and practices used by the ENCODE and modENCODE consortia.” *Genome Res*. 2012 Sep; 22:1813–31.   * Recommended by Faculty of 1000. * Cited 296 times.   J9. **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.   * Cited 129 times.   J8. **ENCODE Project Consortium**. “A user’s guide to the Encyclopedia of DNA Elements (ENCODE) functional genomic data.” *PLOS Biol*. 2011 Apr; 9:e1001046.   * Recommended by Faculty of 1000. * Cited 648 times.   J7. **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.  J6. **Hoffman MM**, **Buske OJ**, Noble WS. “The Genomedata format for storing large-scale functional genomics data.” *Bioinformatics.* 2010 Jun 1; 26:1458–9.  J5. 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.  J4. **Hoffman MM**, Birney E. “An effective model for natural selection in promoters.” *Genome Res*. 2010 May; 20:685–92.  J3. **Hoffman MM**, Birney E. “Estimating the neutral rate of nucleotide substitution using introns.” *Mol Biol Evol*. 2007 Feb; 24:522–31.  J2. **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.   * Featured on cover of *Nature*. * News and Views: Schmutz J, Grimwood J. *Nature*. 2004 Dec 9; 432:679–80. * Cited 1,552 times.   J1. **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; 32:D174–81.   * Cited 96 times.   *Boldface indicates Michael Hoffman or one of his trainees is an author or a consortium member. Underline indicates Michael Hoffman is an author or a consortium member.* | |
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| Publications (conference proceedings) | C1. 2Libbrecht MW, **Hoffman MM**, Noble WS, Bilmes JA. “Entropic graph-based posterior regularization.” International Conference on Machine Learning. 2015. Lille, France. | |
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| Publications (submitted) | S1. 2Lundberg SM, Tu WB, Raught B, Penn LZ, **Hoffman MM**, Lee SI. “Learning the human chromatin network from all ENCODE ChIP-seq data.” 2015. Submitted. Preprint: <http://dx.doi.org/10.1101/023911> | |
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| Other scholarships and awards | Canadian Cancer Society Research Institute Junior Investigator Grant Panel Travel Award, 2014.   * Trinity College Moore, Beale Sargent and Mitchell Fund, 2005 * The University of Texas at Austin Junior Fellows Research Grant, 2003. * The University of Texas at Austin Undergraduate Research Fellowship, 1999-2000, 2000-2001, 2002-2003. * NSF Research Experience for Undergraduates supplement, 1999. * Dedman Merit Scholarship, 1998-2002. * Dorothy B. Banks Charitable Trust Scholarship, 1999-2000. * IBM Thomas J. Watson Memorial Scholarship, 1998-2002. * National Merit Scholarship, 1998-2002. | |
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| Honors | Bioinformatics.ca Bioinformatics Expert, 2014.   * *Genome Technology* Young Investigator, 2011. * Phi Beta Kappa Award of Distinction, 2003. * Phi Beta Kappa Induction, 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. | |
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| Invited/keynote presentations | Semi-automated human genome annotation using chromatin data. Institute for Operations Research and the Management Sciences Annual Meeting. Philadelphia, PA. 1–4 November 2015.   * Cold Spring Harbor Laboratory Meeting on Genome Informatics. Cold Spring Harbor, NY. October 2015. * Transcription factor binding motifs in an expanded epigenetic alphabet. Taiwan-Canada Joint Workshop on Epigenetics. Canadian Human and Statistical Genetics Meeting. Vancouver, BC. 21 April 2015. * Semi-automated genome annotation and an expanded epigenetic alphabet. Program in Genetic Networks Workshop. Canadian Institute for Advanced Research. Toronto, ON. 10 April 2015. * Semi-automated genome annotation and an expanded epigenetic alphabet. Department of Biochemistry and Molecular Genetics. University of Colorado Anschutz Medical Campus. Denver, CO. 3 April 2015. * Semi-automated genome annotation and an expanded epigenetic alphabet. Bioinformatics Club. University of Waterloo. Waterloo, ON. 24 March 2015. * Semi-automated human genome annotation. Signals and Intelligence Chapter/Signal Processing Chapter/Engineering in Medicine and Biology Chapter. Toronto Section. Institute of Electrical and Electronics Engineers. Toronto, ON. 9 March 2015. * Transcription factor binding prediction. Biohackathon. University of Toronto Internationally Genetically Engineered Machine. University of Toronto. Toronto, ON. 22 January 2015. * Semi-automated genome annotation and an expanded epigenetic alphabet. Understanding non-coding DNA through intra and inter-species epigenomic variation. Bellairs Research Institute. Holetown, Barbados. 9 January 2015. * Semi-automated genome annotation and an expanded epigenetic alphabet. McGill University. Montreal, QC. 21 November 2014. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Major Discoveries in Biology. Undergraduate Program in Genomic Sciences. National Autonomous University of Mexico. Mexico City, Mexico (videoconference). 5 March 2014. * Semi-automated Genome Annotation with Segway. Institute of Electrical and Electronics Engineers International Workshop on Genomic Signal Processing and Statistics 2013. Houston, TX. 17 November 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Toronto Bioinformatics Users Group. Toronto, ON. 27 November 2013. * Unsupervised pattern discovery in human chromatin structure through genomic segmentation. Workshop on Epigenomics and Cell Function 2013. Association for Computing Machinery Conference on Bioinformatics, Computational Biology and Biomedicine. Washington, DC. 22 September 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Genentech. South San Francisco, CA. 12 November 2012. * 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. * Predicting Selection in Promoters by Simulating the Effects of Mutations. Waterman Seminar, Leibniz Institute of Plant Genetics and Crop Plant Research. Gatersleben, Germany. Autumn 2007. * Student address, The University of Texas at Austin 120th Spring Commencement, College of Natural Sciences Convocation. Austin, TX. 17 May 2003. * Student address, The University of Texas at Austin 55th Honors Day Convocation. Austin, TX. 12 April 2003. | |
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| Session chair | Big data analytics in genomics. Institute for Operations Research and the Management Sciences Annual Meeting. Philadelphia, PA. November 2015.   * Epigenomics and non-coding genome. Cold Spring Harbor Laboratory Meeting on Genome Informatics. Cold Spring Harbor, NY. October 2015. * Genomes and big data – data integration. Fourth Annual Canadian Human and Statistical Genetics Meeting. Vancouver, BC. 19 April 2015. * Genomic and epigenomic signatures in cancer. Epigenetic Mechanisms in Cancer. Structural Genomics Consortium. Toronto, ON. 4 June 2014. * Genome organization and variant detection. Association for Computing Machinery Conference on Bioinformatics, Computational Biology and Biomedicine. Washington, DC. 24 September 2013. | |
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| Invited panelist | Informatics, Annotation, and Computing. Applied Cancer Genomics Symposium, Toronto, ON. 3 October 2014.   * The job search process: postdoctoral, faculty, and industry jobs. Toronto Bioinformatics Users Group. Toronto, ON. 27 November 2013. * Networking. Women in Genome Sciences Discussion. University of Washington. 23 February 2012. | |
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| Selected conference presentations | Segway: semi-automated genome annotation. Bioinformatics Open Source Conference. Dublin, Ireland. 10 July 2015.   * Transcription factor binding in an expanded epigenetic alphabet. World Congress on Medical Physics. International Union for Physical and Engineering Sciences. Toronto, ON. 11 June 2015. * Transcription factor binding in an expanded epigenetic alphabet. Keystone Symposium on DNA Methylation. Keystone Symposia on Molecular and Cellular Biology. Keystone, CO. 1 April 2015. * Transcription factor motif discovery and prediction in an expanded epigenetic alphabet. Cold Spring Harbor Laboratory/Wellcome Trust Conference on Genome Informatics. Cambridge, United Kingdom. 22 September 2014. * One genome, many epigenomes, machine learning. Workshop on Big Data for Health, University of Toronto. Toronto, ON. 4 July 2014. * Semi-automated annotation of functional elements with whole genome RNA-seq. Machine Learning in Computational Biology 2012. Neural Information Processing Systems Conference 2012. Stateline, NV. 7 December 2012. * Semi-automated annotation of the human genome using chromatin data. University of Washington Postdoctoral Association Research Symposium. Seattle, WA. 27 November 2012. * Functional genomics and machine learning. SynBioCon 2012. Austin, TX. 26 May 2012. * Semi-automated annotation of the human genome using whole-genome RNA-seq. ENCODE and modENCODE AWG/PI Meeting. Cambridge, MA. 22 May 2012. * Discovery of functional elements using whole-genome RNA-seq. The Biology of Genomes. Cold Spring Harbor, NY. 9 May 2012. * Chromosomal features: large-scale integration. ENCODE AWG Workshop. Stanford, CA. 7 March 2011. * Large-scale integration group update. ENCODE AWG Workshop. Barcelona, Spain. 20 July 2010. * Large-scale behavior task group. ENCODE AWG Workshop. Rockville, MD. 8 March 2010. * Segway: a dynamic Bayesian network for genomic segmentation. ENCODE and modENCODE Consortia Meeting. Bethesda, MD. Spring 2009. * ENCODE and Segway. ENCODE AWG Workshop. Rockville, MD. December 2008. * Properties of natural selection in mammalian promoters. Sanger-Cambridge PhD Symposium. Hinxton, England. Spring 2008. * Sunflower: a model of transcription factor binding. EMBL Predoctoral Fellow Retreat. Barcelona, Spain. Summer 2007. * Measurements of evolution and natural selection. Trinity College Science Society Symposium. Cambridge, England. Spring 2007. * Poly: rapid development of embarrassingly parallelizable applications. Bioinformatics Open Source Conference. Glasgow, Scotland. Summer 2004. * Visualizing protein–DNA and protein–RNA interactions with AANT. Trinity College Science Society Symposium. Cambridge, England. 13 March 2004. | |
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| Other teaching | “Epigenomics.” Summer Student Program. Department of Medical Biophysics. University of Toronto. 8 June 2015.   * “Gene Regulation Network Analysis.” Pathway and Network Analysis of –omic Data. 3 June 2015. * MBP 1015Y: Biophysics Seminar. Department of Medical Biophysics. University of Toronto. 15 October 2014–13 May 2015. * “Gene Regulation Network Analysis.” High-throughput Biology: From Sequence to Networks. Canadian Bioinformatics Workshop. 3 May 2015. * "Transcription Factor Regulatory Analysis." Pathway and Network Analysis of ‑omics Data. Canadian Bioinformatics Workshop, 4 June 2014. * “Introduction to ENCODE” and “The Segway annotation of the ENCODE Data.” Iowa Institute of Human Genetics Bioinformatics Short Course. Taught two one-hour lectures. University of Iowa. 30–31 July 2013. * “Genes and gambling: using probability to make sense of biology.” Guest lecture for undergraduate computer science course, Bellevue College. Winter 2010. * “Introduction to Python.” Taught two-day seminar. European Molecular Biology Laboratory. Autumn 2005. * EMBL Predoctoral Bioinformatics Workshop. Organizing committee member and teaching assistant for three-day course. European Molecular Biology Laboratory. Autumn 2004. * “Biological sequence analysis.” Discussion leader for eight-week seminar. The University of Texas at Austin Society for Computational Biology. Summer 2003. | |
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| Other seminars | Epigenetics. Princess Margaret Cancer Foundation Board Retreat. Toronto, ON. 8 November 2014.   * Machine Learning and Epigenomics. Princess Margaret Cancer Centre Research Retreat. Huntsville, ON. 15 May 2014. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Department of Genetics. University of Pennsylvania. Philadelphia, PA. 25 July 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Ontario Cancer Institute. Toronto, ON. 4 July 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Institute for Human Genetics. University of California, San Francisco. San Francisco, CA. 21 March 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Analytical and Translational Genetics Unit. Massachusetts General Hospital. 24 April 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Department of Electrical and Computer Engineering. University of Texas at Austin. 22 April 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. The Jackson Laboratory. Bar Harbor, ME. 11 March 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. McKusick-Nathans Institute of Genetic Medicine. Johns Hopkins University. Baltimore, MD. 7 March 2013. * Semi-automated annotation of the human genome using chromatin data. Biomedical Postdoc Seminar. University of Washington. Seattle, WA. 4 March 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Department of Human Genetics. University of Utah. Salt Lake City, UT. 25 February 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. National Eye Institute. National Institutes of Health. Bethesda, MD. 30 January 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Department of Molecular and Medical Genetics. Oregon Health and Science University. Portland, OR. 23 January 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Department of Human Genetics. Emory University. Atlanta, GA. 14 January 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. McDermott Center for Human Growth and Development/Center for Human Genetics. University of Texas Southwestern Medical Center. Dallas, TX. 7 January 2013. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Earl Stadtman Symposium on Genetics, Genomics, and Systems Biology. Division of Intramural Research. National Institutes of Health. Bethesda, MD. 17 December 2012. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Computational Biology Group Meeting/CSE 591C. Department of Computer Science. Seattle, WA. 14 December 2012. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Program in Bioinformatics and Integrative Biology. University of Massachusetts Medical School. Worcester, MA. 10 December 2012. * Semi-automated annotation of the human genome using chromatin and RNA-seq data. Department of Pediatrics. University of California, San Diego. 4 June 2012. * Unsupervised and semi-supervised pattern discovery in human chromatin structure. Section of Genetic Medicine. University of Chicago. Chicago, IL. 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, CO. 10 April 2012. * Semi-automated annotation of the human genome using whole-genome RNA-seq. Postdoctoral Research Talk. Department of Genome Sciences. University of Washington. 16 May 2012. * Segway: pattern discovery in multitrack functional genomics data. Research Reports. Department of Genome Sciences. University of Washington. 13 November 2009. * Segway: a dynamic Bayesian network for genomic segmentation. Reading and Research in Computational Biology. CSE 590C. 4 May 2009. * Properties of natural selection in mammalian promoters. Seminar, Broad Institute of MIT and Harvard. Cambridge, MA. Spring 2008. * Properties of natural selection in mammalian promoters. Seminar, Program in Bioinformatics and Integrative Biology, University of Massachusetts Medical School. Worcester, MA. Spring 2008. | |
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| Prior positions | **Senior Fellow**, Department of Genome Sciences, University of Washington, 2008–2013.   * **Predoctoral Fellow**, EMBL–European Bioinformatics Institute, 2003–2008. * **Research Assistant**, Department of Chemistry and Biochemistry, The University of Texas at Austin, 1999–2003. * **Undergraduate Research Program Participant**, Cold Spring Harbor Laboratory, 2001. * **Undergraduate Research Fellow**, Plant Biochemistry Research Training Center, Washington State University, 2000. | |
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| Trainees and staff supervised | T14. **Madani Tonekaboni, S. Ali.** MSc Student, Department of Medical Biophysics, University of Toronto. 2015.  T13. **Sood, Ankur Jai.** BESc (Honors) Student, Summer Student Program, Department of Medical Biophysics, University of Toronto. 2015–present.  T12. **Zeng, Xing.** BSc (Honors) Student, Undergraduate Toronto Research Experience in Computer Science, Department of Computer Science, University of Toronto. 2015–present.  T11. **Karimzadeh, Mehran R.** Research Assistant, University Health Network, 2015–present.  T10. **Chicco, Davide.** Postdoctoral Fellow, University Health Network, 2014–present.  T9. **Viner, Coby.** MSc Student, Department of Computer Science, University of Toronto, 2014–present.  T8. **Roberts, Eric.** Bioinformatics Programmer, University Health Network, 2014–present.  T7. **Shaw, Adam J.** Student, Google Summer of Code, 2014. Present position: Software Engineer, Google, San Bruno, California, USA.  T6. **Petwe, Harshad S.** BS Student, Department of Computer Science and Engineering, University of Washington, 2012.  T5. **Ellenbogen, Paul.** BS Student, Department of Computer Science and Engineering, University of Washington, 2011–2013. Present position: PhD Student, Department of Computer Science, Princeton University, Princeton, USA.  T4. **Sahu, Avinash D.** MS Student, School of Communication and Computer Science, École Polytechnic Fédérale de Lausanne, 2011. Present position: PhD Student, Department of Computer Science, University of Maryland, College Park, Maryland, USA.  T3. **Staples, Jeffrey.** PhD Student, Department of Genome Sciences, University of Washington, 2011. Present position: Bioinformatics R&D Developer, Regeneron Genetics, Tarrytown, NY, USA.  T2. **Lemus Vergara, Tzitziki J.** PhD Student, Department of Genome Sciences, University of Washington, 2009. Present position: PhD Student, Department of Genome Sciences, University of Washington, Seattle, Washington, USA.  T1. **Buske, Orion J.** BS (Honors) Student, Department of Computer Science and Engineering, University of Washington, 2009–2010. Present position: PhD Student, Department of Computer Science, University of Toronto, Toronto, Ontario, Canada. | |
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| Software | Segway: a dynamic Bayesian network method for segmenting genomic data. <http://pmgenomics.ca/hoffmanlab/proj/segway/>.   * Segtools: exploratory data analysis of genomic segmentations. <http://pmgenomics.ca/hoffmanlab/proj/segtools/>. * Genomedata: a format for storing large-scale functional genomics data. <http://pmgenomics.ca/hoffmanlab/proj/genomedata/>. * Sunflower: a model of transcription factor binding and evolution. | |
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| Databases | AANT: the Amino Acid-Nucleotide Interaction Database.   * FIAT: Factors in *Arabidopsis* Translation. <http://browning.cm.utexas.edu/arabidopsis/fiat/>. * AtProbe: *Arabidopsis thaliana* Promoter Binding Element Database. <http://exon.cshl.org/cgi-bin/atprobe/atprobe.pl>. | |
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| Leadership and committee positions | **Member**, Graduate Admissions Committee, Department of Computer Science, University of Toronto, 2014–2015.   * **Member**, Program Committee, Research in Computational Molecular Biology (RECOMB), 2014–present. * **Teleconference member,** Genomics Peer Review Committee, Canadian Institutes for Health Research, 2015. * **Member**, Review Committee, Collaborative Personalized Cancer Medicine Team Grant, Princess Margaret Cancer Centre, 2015. * **Judge**, Summer Student Poster Day, Department of Medical Biophysics, University of Toronto, 2014–2015. * **Mentor**, National Resource for Network Biology, Google Summer of Code, 2014. * **Co-chair**, University Health Network Cancer Genomics Program Bioinformatics Subcommittee, 2013–present. * **Member**, Princess Margaret Genomics Centre Advisory Board, 2013–present. * **Chair**, Large-scale Integration Task Group, ENCODE Analysis Working Group, 2010–2012. * **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**, University of Texas at Austin Barbecue Club, 1999–2003. * **Chair**, Texas Student Publications Handbook Revision Committee, 2002. * **Chair**, Texas Student Publications Election Committee, 2001–2002. * **Member**, University of Texas at Austin Information Technology Coordinating Council, 1999–2002. * **Member**, University of Texas at Austin General Faculty Admissions and Registration Committee, 1999–2000. | |
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| Professional activities | **Organizer**, Early Career Investigators Meeting on Quantitative Problems in Human Genetics and Health. Banff International Research Station. Banff, AB, Canada. 10 January 2016–15 January 2016.   * **Reviewer** for journals: Nature Methods, Genome Biology, PLOS Computational Biology, Nucleic Acids Research, Scientific Reports, Bioinformatics, PLoS ONE, BMC Genomics, BMC Bioinformatics, Journal of Machine Learning Research, IEEE Transactions on Computational Biology and Bioinformatics, Artificial Intelligence in Medicine, Computational and Structural Biotechnology Journal. * **Reviewer** for conferences: Intelligent Systems in Molecular Biology/European Conferences on Computational Biology (ISMB/ECCB), Research in Computational Molecular Biology (RECOMB). * **Reviewer** for funders: United Kingdom Medical Research Council. * **Reviewer** for research theses: Department of Computer Science, University of Toronto (Aryan Arbabi). * **Invited Participant**, National Human Genome Research Institute planning workshop: Planning the future of genomics: foundational research and applications in genomic medicine. | |
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| Other organizations | **Member**, Global Alliance for Genomics and Health, 2014–present.   * **Member**, Association for Computing Machinery Special Interest Group on Bioinformatics, 2013–present. * **Member**, National Postdoctoral Association, 2011–2013. * **Member**, Northwest Institute of Genetic Medicine, 2009–2013. * **Member**, University of Washington Postdoctoral Association, 2008–2013. * **Member**, Phi Beta Kappa, 2003–present. * **Member**, International Society for Computational Biology, 2003–2004, 2010–2011, 2015–2016. * **Junior Member**, Isaac Newton Institute for Mathematical Sciences, 2006–2013. * **Member**, American Association for the Advancement of Science, 2007–2008. * **Member**, Genetics Society, 2006–2007. * **Member**, Society of Computational Biology, 2002–2003. * **Member**, Microbiology and Molecular Biology Student Society, 1998–1999. | |
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| Interviews | “Strength In Numbers: Finding And Developing Bioinformaticians.” *Front Line Genomics*. 13 October 2014.   * “Kelso: For barbecue, this Texan-turned-Canadian goes to great lengths.” *Austin American-Statesman*. 27 July 2014. * “As Biomedical Researchers Face Tough Job Market, Experts Offer Advice and Propose Changes.” GenomeWeb Daily News. 5 June 2014. * “101 questions with a bioinformatician #4: Michael Hoffman.” ACGT. 20 April 2014. * “Meet Michael Hoffman.” Princess Margaret Cancer Foundation Blog. 16 January 2014. | |
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| Citizenship and immigration | United States of America: citizen.   * Canada: permanent resident. | |