

**BIOGRAPHICAL SKETCH**

Brendan J. Frey, PhD, FRSC  
*CEO & Founder*, Deep Genomics Inc.  
*Professor*, Electrical and Computer Engineering and the Donnelly Centre, University of Toronto  
*Senior Research Scientist*, Vector Institute for Artificial Intelligence  
*Senior Fellow*, Canadian Institute for Advanced Research

**Academic and Training Background**

INSTITUTION AND LOCATION	DEGREE (if applicable)	MM/YY	FIELD OF STUDY
University of Calgary	B.Sc	1986-1990	Elec & Comp Eng
University of Manitoba	M.Sc.	1991-1993	Physics, Engineering
University of Toronto	Ph.D.	1993-1997	Machine Learning
University of Illinois at Urbana-Champaign	Postdoc	1997-1999	Machine Learning

**Statement of Research**

Over a decade after the human genome was sequenced and after billions of dollars have been spent on its annotation, the pivotal question that my lab seeks to answer remains: **How are the instructions for making and maintaining diverse human cells encoded in the genome?** To answer this question, we must understand the 'regulatory code' that governs gene expression in different cellular contexts. Deciphering the code will transform biomedical science and will revolutionize medicine by enabling us to predict and control the impact of genetic variation on human biology. There are already petabytes of publicly available genomics data, and much more will be released soon. But data generation alone will not solve the problem: the more data we acquire, the more complex and mysterious the genome appears. **My lab is leading a high profile, international effort to reverse-engineer the regulatory code, brining biologists, computer scientists, engineers, statisticians, medical researchers and clinicians.** We recently used our computational model of splicing regulation to identify tens of thousands of non-coding disease mutations that act by altering splicing regulation (Xiong et al, Science 2015; Alipanahi et al, Nature Biotechnology 2015).

**Work Experience**

2017-current *Senior Research Scientist*, Vector Institute for Artificial Intelligence, Canada  
2015-current *CEO & Founder*, Deep Genomics Inc., Toronto  
2004-current *Professor*, Electrical & Computer Engineering, University of Toronto, Canada  
2004-current *Professor*, Donnelly Centre, University of Toronto, Canada  
2004-current *Professor*, Computer Science, University of Toronto, Canada  
2008-2009 *Visiting Professor*, University of Cambridge, Cavendish Laboratories, UK  
2000-2008 *Research Management Consultant*, Microsoft Research Redmond, USA  
2001-2004 *Assistant Professor*, Electrical & Computer Engineering, University of Toronto, Canada  
1998-2001 *Assistant Professor*, Computer Science, University of Waterloo, Canada  
1998-2006 *Adjunct Professor*, University of Illinois at Urbana-Champaign, USA  
1997-1999 *Beckman Fellow*, University of Illinois at Urbana-Champaign, USA  
1990-1991 *Junior Research Scientist*, Bell-Northern Research, Ottawa, Canada

**Selected Accomplishments and Honors**

2015 Fellow of the Royal Society of Canada  
2012 John C. Polanyi Award, NSERC  
2009 Fellow of the AAAS  
2009 EWR Steacie Fellow, NSERC  
2008 Fellow of the IEEE  
2006-2016 Fellow of the Canadian Institute for Advanced Research  
2007-2017 Canada Research Chair in Biological Computation (Tier 1)

Apple v. Caltech  
IPR2017-00210

Apple 1066

**Selected Peer-reviewed Publications** (selected from 150 total peer-reviewed publications)

\* indicates corresponding authors, members of Frey's lab are indicated in bold

1. **B. Alipanahi, A. Delong**, M. T. Weirauch, **B. J. Frey\***. Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning. *Nature Biotechnology* 33, 831-838 | doi:10.1038/nbt.3300, July 2015.
2. **H. Y. Xiong, B. Alipanahi, L. J. Lee, H. Bretschneider**, D. Merico, R. K. C. Yuen, Y. Hua, S. Gueroussov, **H. S. Najafabadi**, T. R. Hughes, Q. D. Morris, Y. Barash, A. R. Krainer, N. Jojic, S. W. Scherer, B. J. Blencowe and **B. J. Frey\***. The human splicing code reveals new insights into the genetic determinants of disease. *Science Express*, December 18, 2014, *Science* 347, DOI:10.1126/science.1254806, January 9, 2015.
3. M. Uddin, K. Tammimies, G. Pellecchia, **B. Alipanahi**, P. Hu, Z. Wang, B. J. Blencowe, **B. J. Frey**, D. Merico, R.K.C. Yuen, S. W. Scherer\*. Brain-expressed exons under purifying selection are enriched for de novo mutations in autism spectrum disorder. *Nature Genetics* 46, 742-747, 2014.
4. **M. K. K. Leung, H. Y. Xiong, L. J. Lee, B. J. Frey\***. Deep learning of the tissue-regulated splicing code. Proceedings of the 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), and *Bioinformatics* 30:12, i121-i129, 2014.
5. D. Ray et al (2013). A compendium of RNA binding motifs for decoding gene regulation. *Nature* 499:172-7.
6. H. Han, M. Irimia, P. J. Ross, H.-K. Sung, **B. Alipanahi**, L. David, A. Golipour, M. Gabut, P. M. Lacovos, E. N. Nachman, E. Wang, D. Trcka, T. Thompson, D. O'Hanlon, V. Slobodeniuc, N. L. Barbosa-Morais, C. B. Burge, J. Moffat, **B. J. Frey**, A. Nagy, J. Ellis, J. L. Wrana, B. J. Blencowe\*. MBNL proteins repress embryonic stem cell-specific alternative splicing and reprogramming. *Nature* 498:7453, June 2013.
7. **B. Alipanahi, B. J. Frey\***. Network cleanup. *Nature Biotechnology* 31, 714-715, August 2013.
8. **C. Chung**, A. Emili, **B.J. Frey\***. A non-parametric Bayesian approach to post-translational modification refinement of predictions from tandem mass spectrometry. *Bioinformatics* 29:7, 821-829, 2013.
9. N.L. Barbosa-Morais, M. Irimia, Q. Pan, **H.Y. Xiong**, S. Gueroussov, **L.J. Lee**, V. Slobodeniuc, C. Kutter, S. Watt, R. Olak, T.-H. Kim, C. M. Misquitta-Ali, M. D. Wilson, P. M. Kim, D. T. Odom, **B. J. Frey**, B.J. Blencowe\*. The evolutionary landscape of alternative splicing. *Science* 338:6114, 1587-1593, December 2012.
10. **H. Xiong, Y. Barash, B. J. Frey\***. Bayesian Prediction of Tissue-Regulated Splicing from RNA Sequence and Cellular Context. *Bioinformatics* 27:18, 2554-2562, September 2011.
11. **J. C. Huang and B. J. Frey\***. Cumulative Distribution Networks and the Derivative-sum-product Algorithm: Models and Inference for Cumulative Distribution Functions on Graphs. *Journal of Machine Learning Research* 12 301-348, 2011.
12. **Y. Barash, J. Calarco, W. Gao**, Q. Pan, **X. Wang, O. Shai**, B. J. Blencowe\*, **B. J. Frey\***. Deciphering the splicing code. *Nature* 465:6, 53-60, May 6, 2010.

**Research Support**

1. Canadian Institute for Advanced Research (CIFAR) (PI: B. J. Frey), CIFAR Grant; Project period: 2006-2016, "Program in Genetic Networks" & "Program in Neural Computation"
2. Canadian Institutes of Health Research (PI: B. J. Frey), CIHR Operating Grant, 2010-2014, "Genome-wide analysis of the regulation of alternative splicing"
3. Natural Sciences and Engineering Research Council of Canada (PI: B. J. Frey), NSERC Discovery Grant and Accelerator Grant, 2013-2017, "A Unified Model of Gene Regulation"
4. Natural Sciences and Engineering Research Council of Canada (PI: B. J. Frey), John Polanyi Award, 2012-2015, "Using Regulatory Models to Identify Genetic Mutations That Cause Disease"