Pouya Kheradpour

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Qualification summary

- Over ten years experience with large-scale biological data (genome sequence, population variation, epigenetic and TF ChIP-chip/seq, gene expression RNA-seq/microarrays)
- Expertise in machine learning, statistics, computational modeling, high-throughput computing, experiment design
- Experience with C/C++, Java, R, MATLAB, Python, HTML, Bash
- Member of several NIH consortia (12 Drosophila, 29 Mammals, ENCODE, modENCODE, Epigenomics Roadmap, GTEx)

Education

- **Massachusetts Institute of Technology** at Cambridge, MA   August 2005–February 2012
  Ph.D. in Computer Science
  Advisor: Manolis Kellis
  Thesis title: Computational Regulatory Genomics: Motifs, Networks, and Dynamics
- **University of Illinois at Urbana-Champaign**   August 2001–May 2005
  B.S. in Computer Science
  M.S. in Computer Science
  Advisors: ChengXiang Zhai, Gene Robinson, and Charles Whitfield
  Thesis title: Computational Methods for Modeling Eukaryotic Gene Regulation

Research Experience

- **Verily Life Sciences**—Senior Scientist   April 2016–Present
  Verily Life Sciences—Scientist   November 2015–April 2016
  Google[x]—Quantitative Analyst   July 2015–November 2015
  Computational biology research and development
- **MIT CSAIL**—Postdoctoral Associate   February 2012–July 2015
  Designed and analyzed high-throughput enhancer experiments; characterized RNA edited sites across hundreds of individuals and dozens of tissues; predicted links between enhancers and genes; developed model to distinguish individuals from NGS data
- **MIT CSAIL**—Graduate Research Assistant   August 2005–February 2012
  Developed and applied computational algorithms for understanding regulatory dynamics using regulatory motifs and epigenetic data
- **UIUC Entomology**—Research Assistant   February 2003–August 2005
  Applied computational methods for microarray and sequence analysis of honey bee and related organisms
- **Argonne National Laboratory**—Research Intern   Summer 2003
  Designed genetic and statistical algorithms for identifying functional sites in BRCA1 proteins

Teaching Experience

- **Linguam Connect LLC**—Instructor   Summer 2014
  CCP11/CCP13: Designed and taught online course on JavaScript programming
- **MIT Electrical Engineering and Computer Science**—Graduate Teaching Assistant   Fall 2005, Fall 2008
  6.095/6.047: Undergraduate/graduate computational biology course; wrote and graded homework and exam problems; led recitation sessions; delivered five guest lectures between 2008-2012
- **UIUC Computer Science**—Graduate Teaching Assistant   Spring 2004, Fall 2004, Spring 2005
  CS101: Undergraduate introductory computer science course in MATLAB and C; taught two laboratory sections weekly and helped write and grade exam and laboratory problems

Publications

- **Evidence of reduced recombination rate in human regulatory domains**
  Yaping Liu, Abhishek Sarkar, Pouya Kheradpour, Jason Ernst, and Manolis Kellis

Genome Biology, 2017 October 20, doi:10.1186/s13059-017-1308-x

○ **The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans**
GTEx Consortium
Science, 2015 May 8, doi:10.1126/science.1262110

○ **Integrative analysis of 111 reference human epigenomes**
Roadmap Epigenomics Consortium, Anshul Kundaje*, Wouter Meuleman*, Jason Ernst*, Misha Bilenky*, Angela Yen, Alireza Heravi-Moussavi, Pouya Kheradpour, Zhizhuo Zhang, Jianrong Wang, Michael J. Ziller, Viren Amin, John W. Whitaker, Matthew D. Schultz, Lucas D. Ward, Abhishek Sarkar, Gerald Quon, Richard S. Sandstrom, Matthew L. Eaton, Yi-Chieh Wu, Andreas R. Pfenning, Xinchen Wang, Melina Claussnitzer, Yaping Liu, Cristian Coarfa, R. Alan Harris, Noam Shoresh, Charles B. Epstein, Elizabeta Gjoneska, Danny Leung, Wei Xie, R. David Hawkins, Ryan Lister, Chibo Hong, Philippe Gascard, Andrew J. Mungall, Richard Moore, Eric Chuah, Angela Tam, Theresa K. Canfield, R. Scott Hansen, Rajinder Kaul, Peter J. Sabo, Mukul S. Bansal, Annaick Carles, Jesse R. Dixon, Kai-How Farh, Soheil Feizi, Rosa Karlic, Ah-Ram Kim, Ashwinikumar Kulkarni, Daofeng Li, Rebecca Lowdon, GiNell Elliott, Tim R. Mercer, Shane J. Neph, Vitor Onuchic, Paz Polak, Nisha Rajagopal, Pradipta Ray, Richard C. Sallari, Kyle T. Siebenthall, Nicholas A. Sinnott-Armstrong, Michael Stevens, Robert E. Thurman, Jie Wu, Bo Zhang, Xin Zhou, Arthur E. Beaudet, Laurie A. Boyer, Philip L. De Jager, Peggy J. Farnham, Susan J. Fisher, David Haussler, Steven J. M. Jones, Wei Li, Marco A. Marra, Michael T. McManus, Shamil Sunyaev, James A. Thomson, Thea D. Tlsty, Li-Huei Tsai, Wei Wang, Robert A. Waterland, Michael Q. Zhang, Lisa H. Chadwick, Bradley E. Bernstein, Joseph F. Costello, Joseph R. Ecker, Martin Hirst, Alexander Meissner, Aleksandar Milosavljevic, Bing Ren, John A. Stamatoyannopoulos, Ting Wang, and Manolis Kellis
Nature, 2015 February 18, doi:10.1038/nature14248

○ **Comparative analysis of regulatory information and circuits across distant species**
Alan P. Boyle*, Carlos L. Araya*, Cathleen Brdlik, Philip Cayting, Chao Cheng, Yong Cheng, Kathryn Gardner, LaDeana W. Hillier, Judith Janette, Lixia Jiang, Dionna Kasper, Trupti Kawli, Pouya Kheradpour, Anshul Kundaje, Jingyi Jessica Li, Lijia Ma, Wei Niu, E. Jay Rehm, Joel Rozowsky, Matthew Slattery, Rebecca Spokony, Robert Terrell, Dionne Vafeados, Daifeng Wang, Peter Weisdepp, Yi-Chieh Wu, Dan Xie, Koon-Kiu Yan, Elise A. Feingold, Peter J. Good, Michael J. Pazin, Haiyan Huang, Peter J. Bickel, Steven E. Brenner, Valerie Reinke, Robert H. Waterston, Mark Gerstein, Kevin P. White, Manolis Kellis, and Michael Snyder
Nature, 2014 August 27, doi:10.1038/nature13668

○ **Diverse patterns of genomic targeting by transcriptional regulators in *Drosophila melanogaster***
Matthew Slattery*, Lijia Ma*, Rebecca F. Spokony*, Robert K. Arthur, Pouya Kheradpour, Anshul Kundaje, Nicolas Nègre, Alex Crofts, Ryan Ptashkin, Jennifer Zieba, Alexander Ostapenko, Sarah Suchy, Alec Victorsen, Nader Jameel, A. Jason Grundstad, Wenxuan Gao, Jennifer R. Moran, E. Jay Rehm, Robert L. Grossman, Manolis Kellis, and Kevin P. White
Genome Research, 2014 July 1, doi:10.1101/gr.168807.113

○ **Systematic discovery and characterization of regulatory motifs in ENCODE TF binding experiments**
Pouya Kheradpour and Manolis Kellis
Nucleic Acids Research, 2013 December 13, doi:10.1093/nar/gkt1249

○ **Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay**
Pouya Kheradpour, Jason Ernst, Alexandre Melnikov, Peter Rogov, Li Wang, Xiaolan Zhang, Jessica Alston, Tarjei S. Mikkelsen, and Manolis Kellis
Genome Research, 2013 March 19, doi:10.1101/gr.144899.112

○ **Analysis of variation at transcription factor binding sites in *Drosophila* and humans**
Mikhail Spivakov, Junaid Akhtar, Pouya Kheradpour, Kathryn Beal, Charles Girardot, Gautier Koscielny, Javier Herrero, Manolis Kellis, Eileen EM Furlong, and Ewan Birney
Genome Biology, 2012 September 5, doi:10.1186/gb-2012-13-9-r49

○ **An integrated encyclopedia of DNA elements in the human genome**
The ENCODE Project Consortium
Nature, 2012 September 6, doi:10.1038/nature11247

○ **ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia**
Stephen G. Landt*, Georgi K. Marinov*, Anshul Kundaje*, Pouya Kheradpour, Florencia Pauli, Serafim Batzoglou, Bradley E. Bernstein, Peter Bickel, James B. Brown, Philip Cayting, Yiwen Chen, Gilberto DeSalvo, Charles Epstein, Katherine I. Fisher-Aylor, Ghia Euskirchen, Mark Gerstein, Jason Gertz, Alexander J. Hartemink, Michael M. Hoffman, Vishwanath R. Iyer, Youngsook L. Jung, Subhradip Karmakar, Manolis Kellis, Peter V. Kharchenko, Qunhua Li, Tao Liu, X. Shirley Liu, Lijia Ma, Aleksandar Milosavljevic, Richard M. Myers, Peter J. Park, Michael J. Pazin, Marc D. Perry, Debasish Raha, Timothy E. Reddy, Joel Rozowsky, Noam Shoresh, Arend Sidow, Matthew Slattery, John A. Stamatoyannopoulos, Michael Y. Tolstorukov, Kevin P. White, Simon Xi, Peggy J. Farnham, Jason D. Lieb, Barbara J. Wold, and, Michael

Snyder
Genome Research, 2012 September 5, doi:10.1101/gr.136184.111

- **Computational Regulatory Genomics: Motifs, Networks, and Dynamics**
  Pouya Kheradpour
  Ph.D. Thesis, MIT, 2012 February 3, doi:1721.1/70871

- **A high-resolution map of human evolutionary constraint using 29 mammals**
  Kerstin Lindblad-Toh, Manuel Garber*, Or Zuk*, Michael F. Lin*, Brian J. Parker*, Stefan Washietl*, Pouya Kheradpour*, Jason Ernst*, Gregory Jordan*, Evan Mauceli*, Lucas D. Ward*, Craig B. Lowe*, Alisha K. Holloway*, Michele Clamp*, Sante Gnerre*, Jessica Alföldi, Kathryn Beal, Jean Chang, Hiram Clawson, James Cuff, Federica Di Palma, Stephen Fitzgerald, Paul Flicek, Mitchell Guttman, Melissa J. Hubisz, David B. Jaffe, Irwin Jungreis, W. James Kent, Dennis Kostka, Marcia Lara, Andre L. Martins, Tim Massingham, Ida Moltke, Brian J. Raney, Matthew D. Rasmussen, Jim Robinson, Alexander Stark, Albert J. Vilella, Jiayu Wen, Xiaohui Xie, Michael C. Zody, Broad Institute Sequencing Platform Whole Genome Assembly Team, Kim C. Worley, Christie L. Kovar, Donna M. Muzny, Richard A. Gibbs, Baylor College of Medicine Human Genome Sequencing Center Sequencing Team, Wesley C. Warren, Elaine R. Mardis, George M. Weinstock, Richard K. Wilson, Genome Institute at Washington University, Ewan Birney, Elliott H. Margulies, Javier Herrero, Eric D. Green, David Haussler, Adam Siepel, Nick Goldman, Katherine S. Pollard, Jakob S. Pedersen, Eric S. Lander, and Manolis Kellis
  Nature, 2011 October 27, doi:10.1038/nature10530

- **Locating protein-coding sequences under selection for additional, overlapping functions in 29 mammalian genomes**
  Michael F. Lin, Pouya Kheradpour, Stefan Washietl, Brian J. Parker, Jakob S. Pedersen, and Manolis Kellis
  Genome Research, 2011 October 12, doi:10.1101/gr.108753.110

- **An Epigenetic Signature for Monoallelic Olfactory Receptor Expression**
  Angeliki Magklara, Angela Yen*, Bradley M. Colquitt*, E. Josephine Clowney*, William Allen, Eirene Markenscoff-Papadimitriou, Zoe A. Evans, Pouya Kheradpour, George Mountoufaris, Catriona Carey, Gilad Barnea, Manolis Kellis, and Stavros Lomvardas
  Cell, 2011 May 13, doi:10.1016/j.cell.2011.03.040

- **A User's Guide to the Encyclopedia of DNA Elements (ENCODE)**
  The ENCODE Project Consortium
  PLoS Biology, 2011 April 19, doi:10.1371/journal.pbio.1001046

- **Mapping and analysis of chromatin state dynamics in nine human cell types**
  Jason Ernst, Pouya Kheradpour, Tarjei S. Mikkelsen, Noam Shoresh, Lucas D. Ward, Charles B. Epstein, Xiaolan Zhang, Li Wang, Robbyn Issner, Michael Coyne, Manching Ku, Timothy Durham, Manolis Kellis*, and Bradley E. Bernstein*
  Nature, 2011 May 5, doi:10.1038/nature09906

- **A cis-regulatory map of the *Drosophila* genome**
  Nicolas Nègre*, Christopher D. Brown*, Lijia Ma*, Christopher Aaron Bristow*, Steven W. Miller*, Ulrich Wagner*, Pouya Kheradpour, Matthew L. Eaton, Paul Loriaux, Rachel Sealfon, Zirong Li, Haruhiko Ishii, Rebecca F. Spokony, Jia Chen, Lindsay Hwang, Chao Cheng, Richard P. Auburn, Melissa B. Davis, Marc Domanus, Parantu K. Shah, Carolyn A. Morrison, Jennifer Zieba, Sarah Suchy, Lionel Senderowicz, Alec Victorsen, Nicholas A. Bild, A. Jason Grundstad, David Hanley, David M. MacAlpine, Mattias Mannervik, Koen Venken, Hugo Bellen, Robert White, Mark Gerstein, Steven Russell, Robert L. Grossman, Bing Ren, James W. Posakony, Manolis Kellis, and Kevin P. White
  Nature, 2011 March 24, doi:10.1038/nature09990

- **Identification of functional elements and regulatory circuits by *Drosophila* modENCODE**
  The modENCODE Consortium, Sushmita Roy*, Jason Ernst*, Peter V. Kharchenko*, Pouya Kheradpour*, Nicolas Nègre*, Matthew L. Eaton*, Jane M. Landolin*, Christopher A. Bristow*, Lijia Ma*, Michael F. Lin*, Stefan Washietl*, Bradley I. Arshinoff*, Ferhat Ay*, Patrick E. Meyer*, Nicolas Robine*, Nicole L. Washington*, Luisa Di Stefano*, Eugene Berezikov, Christopher D. Brown, Rogerio Candeias, Joseph W. Carlson, Adrian Carr, Irwin Jungreis, Daniel Marbach, Rachel Sealfon, Michael Y. Tolstorukov, Sebastian Will, Artyom A. Alekseyenko, Carlo Artieri, Benjamin W. Booth, Angela N. Brooks, Qi Dai, Carrie A. Davis, Michael O. Duff, Xin Feng, Andrey A. Gorchakov, Tingting Gu, Jorja G. Henikoff, Philipp Kapranov, Renhua Li, Heather K. MacAlpine, John Malone, Aki Minoda, Jared Nordman, Katsutomo Okamura, Marc Perry, Sara K. Powell, Nicole C. Riddle, Akiko Sakai, Anastasia Samsonova, Jeremy E. Sandler, Yuri B. Schwartz, Noa Sher, Rebecca Spokony, David Sturgill, Marijke van Baren, Kenneth H. Wan, Li Yang, Charles Yu, Elise Feingold, Peter Good, Mark Guyer, Rebecca Lowdon, Kami Ahmad, Justen Andrews, Bonnie Berger, Steven E. Brenner, Michael R. Brent, Lucy Cherbas, Sarah C. R. Elgin, Thomas R. Gingeras, Robert Grossman, Roger A. Hoskins, Thomas C. Kaufman, William Kent, Mitzi I. Kuroda, Terry Orr-Weaver, Norbert Perrimon, Vincenzo Pirrotta, James W. Posakony, Bing Ren, Steven Russell, Peter Cherbas, Brenton R. Graveley, Suzanna Lewis, Gos Micklem, Brian Oliver, Peter J. Park, Susan E. Celniker, Steven Henikoff, Gary H. Karpen, Eric C. Lai, David M. MacAlpine, Lincoln D. Stein, Kevin P. White, and

Manolis Kellis
Science, 2010 December 24, doi:10.1126/science.1198374

○ **A comprehensive map of insulator elements for the *Drosophila* genome**
Nicolas Nègre*, Christopher D. Brown*, Parantu K. Shah, Pouya Kheradpour, Carolyn A. Morrison, Jorja G. Henikoff, Xin Feng, Kami Ahmad, Steven Russell, Robert A. H. White, Lincoln Stein, Steven Henikoff, Manolis Kellis, and Kevin P. White
PLoS Genetics, 2010 January 15, doi:10.1371/journal.pgen.1000814

○ **The Tasmanian devil transcriptome reveals Schwann cell origins of a clonally transmissible cancer**
Elizabeth P. Murchison, Cesar Tovar, Arthur Hsu, Hannah S. Bender, Pouya Kheradpour, Clare A. Rebbeck, David Obendorf, Carly Conlan, Melanie Bahlo, Catherine A. Blizzard, Stephen Pyecroft, Alexandre Kreiss, Manolis Kellis, Alexander Stark, Timothy T. Harkins, Jennifer A. Marshall Graves, Gregory M. Woods, Gregory J. Hannon, and Anthony T. Papenfuss *Science*, 2010 January 1, doi:10.1126/science.1180616

○ **Histone modifications at human enhancers reflect global cell-type-specific gene expression**
Nathaniel D. Heintzman*, Gary C. Hon*, R. David Hawkins*, Pouya Kheradpour, Alexander Stark, Lindsey F. Harp, Zhen Ye, Leonard K. Lee, Rhona K. Stuart, Christina W. Ching, Keith A. Ching, Jessica E. Antosiewicz-Bourget, Hui Liu, Xinmin Zhang, Roland D. Green, Victor V. Lobanenkov, Ron Stewart, James A. Thomson, Gregory E. Crawford, Manolis Kellis, and Bing Ren *Nature*, 2009 March 18, doi:10.1038/nature07829

○ **Genome analysis of the platypus reveals unique signatures of evolution**
Nature, 2008 May 8, doi:10.1038/nature06936

○ **Conservation of small RNA pathways in platypus**
Elizabeth P. Murchison, Pouya Kheradpour, Ravi Sachidanandam, Carly Smith, Emily Hodges, Zhenyu Xuan, Manolis Kellis, Frank Grützner, Alexander Stark, and Gregory J. Hannon
Genome Research, 2008 May 7, doi:10.1101/gr.073056.107

○ **A single Hox locus in *Drosophila* produces functional microRNAs from opposite DNA strands**
Alexander Stark*, Natascha Bushati*, Calvin H. Jan, Pouya Kheradpour, Emily Hodges, Julius Brennecke, David P. Bartel, Stephen M. Cohen, and Manolis Kellis
Genes and Development, 2008 January 1, doi:10.1101/gad.1613108

○ **Discovery of functional elements in 12 *Drosophila* genomes using evolutionary signatures**
Alexander Stark*, Michael F. Lin*, Pouya Kheradpour*, Jakob S. Pedersen*, Leopold Parts, Joseph W. Carlson, Madeline A. Crosby, Matthew D. Rasmussen, Sushmita Roy, Ameya N. Deoras, J. Graham Ruby, Julius Brennecke, Harvard FlyBase curators, Berkeley Drosophila Genome Project, Emily Hodges, Angie S. Hinrichs, Anat Caspi, Benedict Paten, Seung-Won Park, Mira V. Han, Morgan L. Maeder, Benjamin J. Polansky, Bryanne E. Robson, Stein Aerts, Jacques van Helden, Bassem Hassan, Donald G. Gilbert, Deborah A. Eastman, Michael Rice, Michael Weir, Matthew W. Hahn, Yongkyu Park, Colin N. Dewey, Lior Pachter, W. James Kent, David Haussler, Eric C. Lai, David P. Bartel, Gregory J. Hannon, Thomas C. Kaufman, Michael B. Eisen, Andrew G. Clark, Douglas Smith, Susan E. Celniker, William M. Gelbart, and Manolis Kellis
Nature, 2007 November 8, doi:10.1038/nature06340

○ **Evolution of genes and genomes on the *Drosophila* phylogeny**
Drosophila 12 Genomes Consortium
Nature, 2007 November 8, doi:10.1038/nature06341

○ **Reliable prediction of regulator targets using 12 *Drosophila* genomes**
Pouya Kheradpour*, Alexander Stark*, Sushmita Roy, and Manolis Kellis
Genome Research, 2007 November 7, doi:10.1101/gr.7090407

○ **Systematic discovery and characterization of fly microRNAs using 12 *Drosophila* genomes**
Alexander Stark*, Pouya Kheradpour*, Leopold Parts, Julius Brennecke, Emily Hodges, Gregory J. Hannon, and Manolis Kellis
Genome Research, 2007 November 7, doi:10.1101/gr.6593807

○ **Beyond the Bits: Cooperative Packet Recovery Using Physical Layer Information**
Grace R. Woo, Pouya Kheradpour, Dawei Shen, and Dina Katabi
ACM MobiCom, 2007 September 9, doi:10.1145/1287853.1287871

○ **Fold-specific substitution matrices for protein classification**
Richard B. Vilim, R. M. Cunningham, Bo Lu, Pouya Kheradpour, and F. J. Stevens
Bioinformatics, 2004 February 5, doi:10.1093/bioinformatics/btg492

Selected presentations

- **Regulatory motif centric validation, dissection, and construction of transcriptional enhancers** — May 2013
  Selected talk, ENCODE Consortium Meeting, Stanford, CA
- **Systematic prediction and validation of enhancer regulatory motifs in ENCODE cell lines** — November 2012
  Selected talk, RECOMB Satellite on Regulatory Genomics, San Francisco, CA
- **Computational Regulatory Genomics: Motifs, Networks, and Dynamics** — May 2011
  Invited talk, UIUC Institute for Genomic Biology, Urbana, IL
- **Regulatory motifs associated with TF binding and chromatin dynamics** — December 2009
  Selected talk, RECOMB Satellite on Regulatory Genomics, Cambridge, MA
- **Target identification in flies and mammals using comparative genomics** — March 2008
  Selected talk, Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY
- **Systematic discovery and characterization of *Drosophila* miRNAs** — October 2007
  Selected talk, RECOMB Satellite on Regulatory Genomics, Cambridge, MA

Awards & Honors

- 2005 National Science Foundation Graduate Research Fellowship Recipient
- 2005 Hertz Fellowship Finalist
- 2005 Outstanding Teaching Assistant, Department of Computer Science, UIUC
- 2004 Excellent Teaching Assistant, Department of Computer Science, UIUC