

Mehran Karimzadeh | CV

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Current position: Senior Scientist – Computational Biology at Exai Bio

Education

Academic Qualifications

- **UCSF and Vector Institute** **San Francisco, California and Toronto, Ontario**
Post-doctoral fellow with Hani Goodarzi and Bo Wang 2020–2022
- **University of Toronto** **Toronto, Ontario**
Ph.D. in Medical Biophysics 2016–2019
- **McGill University** **Montreal, Quebec**
M.Sc. in Human Genetics and Bioinformatics 2013–2015
- **University of Tehran** **Tehran, Iran**
B.Sc. in Biology 2008–2012

Research Projects

- **Post-doc project I:** 'Deconvolving the epigenome by learning from the transcriptome'. Supervisors: Hani Goodarzi and Bo Wang
- **Post-doc project II:** 'Epigenome and transcriptome encyclopedia of the trans-gender breast at the single-cell resolution'. Supervisors: Simon Knott, Hani Goodarzi, and Bo Wang
- **Post-doc project III:** 'Extracting context free grammar of RNA structure with fixed dilated convolutional layers to predict binding of RNA binding proteins'. Supervisor: Hani Goodarzi
- **Ph.D. project I:** 'Virtual ChIP-seq: predicting transcription factor binding sites by learning from the transcriptome'. Supervisor: Dr. Michael Hoffman
- **Ph.D. project II:** 'Epigenomics of HPV integration'. Supervisors: Dr. Michael Hoffman, Dr. Scott Bratman, and Dr. Mathieu Lupien
- **Ph.D. project III:** 'Methylome mappability'. Supervisors: Dr. Michael Hoffman
- **Master's project:** 'Aberration hub analysis for cancer genomics data'. Supervisor: Dr. Yasser Riazalhosseini
- **Undergraduate research project:** 'Downregulation of Wnt5a suppresses cell invasion in ovarian cancer cell line SkOv3'. Supervisor: Dr. Ghamartaj Hossein

Manuscripts — Peer reviewed

- Human papillomavirus integration transforms chromatin to drive oncogenesis.
Mehran Karimzadeh, Christopher Arlidge, Ariana Rostami, Mathieu Lupien, Scott V. Bratman, and Michael M. Hoffman.
bioRxiv. Accepted, Genome Biology 2023
- The molecular consequences of androgen activity in the human breast.
Raths F*, **Karimzadeh M.***, Ing N., Qu Y., Martinez A., Mulligan B., Lee T.Y., Devkota S., Wang B., Goodarzi H., Ray, E.Y., Cui X., Knott S.R.V. 2022.

Cell Genomics 2023.

* equal contribution.

- Single-cell profiling of healthy human kidney reveals features of sex-based transcriptional programs and tissue-specific immunity.
Caitriona M McEvoy, Julia M Murphy, Lin Zhang, Sergi Clotet-Freixas, Jessica A Mathews, James An, **Mehran Karimzadeh**, Delaram Pouyababar, Shenghui Su, Olga Zaslaver, Hannes Rost, Madhurangi Arambewela, Lewis Y Liu, Sally Zhang, Keith A Lawson, Antonio Finelli, Bo Wang, Sonya A MacParland, Gary D Bader, Ana Konvalinka, and Sarah Q Crome.
Nature Communications. 2022.
Contribution: collaborated on identifying the differentially expressed genes of cell types when comparing male and female renal tissues.
- Virtual ChIP-seq: Predicting transcription factor binding by learning from the transcriptome.
Mehran Karimzadeh and Michael M. Hoffman. *Genome biology* **23**, 126 (2022)
- Cell-Cell Contact Mediates Gene Expression and Fate Choice of Human Neural/Progenitor Stem Cells.
William B McIntyre, **Mehran Karimzadeh**, Yasser Riazalhosseini, Mohamad Khazaei, Michael G. Fehlings.
Volume 11, issue 11, article 1741, *Cells* 2022
Contribution: Analysis and interpretation of RNA-seq data.
- Multiscale interactome analysis coupled with off-target drug predictions reveals drug repurposing candidates for human coronavirus disease.
Michael Sugiyama, Haotian Cui, S Redka Dar'ya, **Mehran Karimzadeh**, Edurne Rujas, Hasaan Maan, Sikander Hayat, Kyle Cheung, Rahul Misra, Joseph B McPhee, Russell D Viirre, Andrew Haller, Roberto Botelho, Raffi Karshafian, Sarah A Sabatinos, Gregory D Fairn, Seyed Ali Madani Tonekaboni, Andreas Windemuth, Jean-Philippe Julien, Vijay Shahani, Stephen S MacKinnon, Bo Wang, Costin N Antonescu.
Volume 11, Article number 23315, 2021 *Scientific Reports*
Contribution: Proposed the collaboration with Cyclica for using graph convolutional layers in drug re-purposing, compiled necessary datasets, and co-supervised Haotian Cui.
- Early temporal dynamics of cellular responses to SARS-CoV-2
Arinjay Banerjee, Patrick Budykowski, Daniel Richard, Hassaan Maan, Jennifer Aguiar, Nader El-Sayes, Michael R. D'Agostino, Benjamin J-M Tremblay, Sam Afkhami, **Mehran Karimzadeh**, Lily Yip, Mario A Ostrowski, Jeremy A Hirota, Robert Kozak, Terence D Capellini, Matthew S Miller, Andrew G McArthur, Bo Wang, Andrew C Doxey, Samira Mubareka, Karen Mossman.
Volume 24, Issue 5, 102477, May 21, 2021 *iScience*.
Contribution: Statistical analysis and correcting for batch-effect.
- Massively multiplex single-molecule oligonucleosome footprinting.
Nour J. Abdulhay, Colin P. McNally, Laura J. Hsieh, Sivakanthan Kasinathan, Aidan Keith, Laurel S. Estes, **Mehran Karimzadeh**, Jason G Underwood, Hani Goodarzi, Geeta J. Narlikar, Vijay Ramani.
9:e59404 2020 *eLife*
Contribution: Assessing predictability of nucleosome footprints with residual convolutional networks.
- Umap and Bimap: tools for genome and methylome mappability.
Mehran Karimzadeh, Carl Ernst, Anshul Kundaje and Michael M. Hoffman.
Volume 46, Issue 20, 16 November 2018, Page e120, *Nucleic Acids Research* 2018. <https://doi.org/10.1093/nar/gky677>
- Top considerations for creating bioinformatics software documentation.
Mehran Karimzadeh, Michael M. Hoffman.
Volume 19, Issue 4, July 2018, Pages 693–699 *Briefings in Bioinformatics*
- A general framework for interrogation of mRNA stability programs identifies RNA-binding proteins that govern cancer transcriptomes.
Gabrielle Perron, Pouria Jandaghi, Shraddha Solanki, Maryam Safisamghabadi, Cristina Storoz, **Mehran Karimzadeh**, Andreas I. Papadakis, Madeleine Arseneault, Ghislaine Scelo, Rosamonde E. Banks, Jorg Tost, Mark Lathrop, Simon Tanguay, Alvis Brazma, Sidong Huang, Fadi Brimo, Hamed S. Najafabadi, and Yasser Riazalhosseini.
Volume 23, Issue 6, P1639-1650, May 08, 2018 *Cell Reports*. 2018. <https://doi.org/10.1016/j.>

celrep.2018.04.031.

Contribution: Statistical analysis and alternative splicing analysis of MBNL2 knockouts.

- Aberration hubs in protein interaction networks highlight actionable targets in cancer. **Mehran Karimzadeh**, Pouria Jandaghi, Hamed S. Najafabadi, Andreas Papadakis, Sebastian Trainor, Johan Rung, Mar González-Porta, Ghislaine Scelo, Nav Vasudev, Alvis Brazma, Sidong Huang, Rosamonde E. Banks, Mark Lathrop, Yasser Riazalhosseini. 9:25166-25180 2018 *Oncotarget* <https://doi.org/10.18632/oncotarget.25382>.
- Variation in genomic landscape of clear cell renal cell carcinoma across Europe. 2014 Oct 29;5:5135. doi: 10.1038/ncomms6135 *Nature Communications*. CAGEKID Consortium (11th author among 59 authors). 2014. Contribution: Pathway analysis, curation, and summarizing data in Figures 2 and 5, Supplementary Figures 5, 6, and 10, and Supplementary Tables.

Manuscripts — submitted

- Semi-automated genome annotation using epigenomic data and Segway. Eric G. Roberts, Mickaël Mendez, Coby Viner, **Mehran Karimzadeh**, Rachel Chan, Rachel Ancar, Davide Chicco, Jay R. Hesselberth, Anshul Kundaje, Michael M. Hoffman. *Revision requested from Nature Protocols*. 2016.

Manuscripts — in prep

- ATAC-seq deconvolution with CiberATAC identifies a prognostic regulon of HMG20B in metastatic colorectal adenocarcinoma. **Mehran Karimzadeh***, Johnny Yu*, Kristle Garcia, Tanvi Joshi, Norihiro Yamaguchi, Ethan Weinberg, Bo Wang, and Hani Goodarzi.
* equal contribution.
- Pythia uses fixed dilated convolutional layers to extract a context-free grammar of RNA structure and predict *in vivo* binding of RNA binding proteins. **Mehran Karimzadeh**, Bo Wang, and Hani Goodarzi.

Book Chapters

- Artificial intelligence in medicine. Xing et al. 2020. Elsevier. Chapter 7: Analytical methods and tools for integration of biomedical data in medicine. Lin Zhang, **Mehran Karimzadeh**, Matteo Welch, Chris McIntosh, and Bo Wang. ISBN: 978-0-12-821259-2

Funded Grants and Proposals

- MITACS grant for re-purposing combinations of existing drugs as a potential treatment against COVID-19. *Together with Bo Wang and Cyclica Inc.* April 2020
- CIHR fellowship grant for deconvolving the cistrome of colon cancer metastasis using deep learning. June 2021.

Presentations

- Blood-based early detection of non-small cell lung cancer using orphan noncoding RNAs. **Mehran Karimzadeh**, Jeffrey Wang, Aiden Sababi, Oluwadamilare I. Afolabi, Dung Ngoc Lam, Alice Huang, Diana R. Corti, Kristle C. Garcia, Seda Kilinc, Xuan Zhao, Jieyang Wang, Taylor B. Cavazos, Patrick Arensdorf, Kimberly H. Chau, Helen Li, Hani Goodarzi, Lisa Fish, Fereydoun Hormozdiari, Babak Alipanahi. AACR Annual Meeting 2023, Orlando, FL
- ATAC-seq deconvolution with CiberATAC identifies a prognostic regulon of HMG20B in metastatic colorectal adenocarcinoma. **Mehran Karimzadeh**, Johnny Yu, Kristle Garcia, Bo Wang, and Hani Goodarzi. Cedars-Sinai Medical Center. March 2022.

- Applications of deep learning in genomics. **Mehran Karimzadeh**. Invited speaker at Vector Institute Thursday seminar series. December 9th 2021.
- CiberATAC, A siamese residual convolutional neural network, deconvolves chromatin accessibility by learning from the transcriptome. **Mehran Karimzadeh**, Johnny Yu, Kristle Garcia, Bo Wang, and Hani Goodarzi. Oral presentation at Canadian Epigenetics Conference, November 2021.
- Pythia predicts binding of RNA binding proteins by learning the context free grammar of RNA structure. **Mehran Karimzadeh** and Hani Goodarzi. Invited speaker at the Broad Institute seminar series on Models, Inference, and algorithm. October 2021.
- * <https://youtu.be/-qmIL5IZ06g>
- Siamese ResNet is capable of deconvolving the epigenome by learning from the transcriptome. **Mehran Karimzadeh**, Johnny Yu, Kristle Garcia, Bo Wang*, and Hani Goodarzi*. Poster presentation at Vector Institute Research Symposium, February 2021.
- CiberATAC deconvolves chromatin accessibility by learning from the transcriptome. **Mehran Karimzadeh**, Johnny Yu, Kristle Garcia, Bo Wang*, and Hani Goodarzi*. Oral presentation at Vector Institute, September 2020.
- The ungracious guest; How integration of the human papilloma virus modifies the epigenome and transcriptome to promote tumourigenesis. **Mehran Karimzadeh**, Christopher Aldridge, Ariana Rostami, Scott Bratman, Mathieu Lupien, Michael M. Hoffman, poster presentation at The TFR1 Ontario Node Symposium, Toronto, Ontario, December 2019.
- The ungracious guest; How integration of the human papilloma virus modifies the epigenome and transcriptome to promote tumourigenesis. **Mehran Karimzadeh**, Christopher Aldridge, Ariana Rostami, Scott Bratman, Mathieu Lupien, Michael M. Hoffman, poster presentation at The Canadian Epigenetics Conference, Banff, Alberta, November 2019.
- The ungracious guest; How integration of the human papilloma virus modifies the epigenome and transcriptome to promote tumourigenesis. **Mehran Karimzadeh**, Christopher Aldridge, Ariana Rostami, Scott Bratman, Mathieu Lupien, Michael M. Hoffman, Invited speaker at James Leapock Memorial Symposium, Toronto, Ontario, May 2019.
- The ungracious guest; How integration of the human papilloma virus modifies the epigenome and transcriptome to promote tumourigenesis. **Mehran Karimzadeh**, Christopher Aldridge, Ariana Rostami, Scott Bratman, Mathieu Lupien, Michael M. Hoffman, speaker at TranCE Club, Toronto, Ontario, May 2019.
- Virtual ChIP-seq: Prediction of transcription factor binding by learning from the transcriptome, **Mehran Karimzadeh**, Michael M. Hoffman. **Lightning presentation and poster**. Genome Informatics, London, UK, Sep 2018
- Alternatively translated peptides in breast cancer. Yufang Liu, **Mehran Karimzadeh**, Michael Hoffman. Medical Biophysics summer undergraduate students poster day. August 2018. Toronto, Canada.
- Virtual ChIP-seq: Prediction of transcription factor binding by learning from the transcriptome, **Mehran Karimzadeh**, Michael M. Hoffman. **Oral presentation**. Great Lakes Genomics Conference, Toronto, Ontario, 17 May 2018
- Virtual ChIP-seq: Prediction of transcription factor binding by learning from the transcriptome, **Mehran Karimzadeh**, Michael M. Hoffman. **Oral presentation**. Vector Institute, Toronto, Ontario, 11 May 2018
- Virtual ChIP-seq: Prediction of transcription factor binding by learning from the transcriptome, **Mehran Karimzadeh**, Michael M. Hoffman. **Oral presentation**. Barbados workshop on cancer epigenomics, January 2018
- Virtual ChIP-seq: Prediction of transcription factor binding by learning from the transcriptome, **Mehran Karimzadeh**, Michael M. Hoffman. **Oral presentation**. Toronto Bioinformatics User Group Meeting, December 2017
- * https://youtu.be/SAvF-t_ksU8
- Virtual ChIP-seq: Prediction of transcription factor binding by learning from the transcriptome, **Mehran Karimzadeh**, Michael M. Hoffman. **Oral presentation**. Statistical methods for genetics and genomics, Dalla Lana school of public health, University of Toronto, 29 September 2017

- Virtual ChIP-seq: Prediction of transcription factor binding by learning from the transcriptome, **Mehran Karimzadeh**, Michael M. Hoffman. **Oral and poster presentation**. CHSGM, Quebec city, Quebec, Canada, 22–25 April 2017
- Transcription factor expression and its effects on binding site occupancy and motif preference, **Mehran Karimzadeh**, Michael M. Hoffman. GLBIO/CCBC, Toronto, Ontario, Canada, 16–19 May 2016
- Transcription factor expression and its effects on binding site occupancy and motif preference, **Mehran Karimzadeh**, Michael M. Hoffman. Cold Spring Harbor meeting on global regulation of gene expression, 15–19 March 2016
- A novel approach for cancer biomarker discovery based on integration of high-throughput genomics data into protein interaction subnetworks. **Mehran Karimzadeh**, Yasser Riazalhosseini. **Oral presentation**. Department of Human Genetics research day (June 2014), McGill University, Montreal, Quebec.
- A novel approach for cancer biomarker discovery based on integration of high-throughput genomics data into protein interaction subnetworks. **Mehran Karimzadeh**, Yasser Riazalhosseini. **Oral and poster presentation**. CHSGM, Victoria, British Columbia, 3–6 May 2014
- Analysis of clonal evolution in colorectal cancer, Donna M. Graham, Madeleine Arseneault, Mahadeo A. Sukhai, Louis Letourneau, **Mehran Karimzadeh**, Tong Zhang, Mariam Thomas, Michael H. A. Roehrl, Eric Xueyu Chen, Monika K. Krzyzanowska, Malcolm J. Moore, Amanda Giesler, Celeste Yu, Philippe L. Bedard, Suzanne Kamel-Reid, Lillian L. Siu, Yasser Riazalhosseini. 50th Annual meeting of American Society of Clinical Oncology (ASCO 2014) Chicago, US
- Wnt5a affects adhesion and migration of human ovarian cancer cell line SKOV-3. Heidarian Y., Hossein G., **Karimzadeh M.**. 5th international conference on Stem Cells and Cancer (ICSCC; 8–10 Nov 2014) New Delhi, India

Teaching experience

- Genomic Methodologies, Department of Molecular Genetics, University of Toronto, Spring 2022
- Dynamical systems modeling (BP205B), Department of Biophysics, UCSF, Winter 2022
- Cell biology, Department of Biology, University of Winnipeg, Fall 2021
- Genomic Methodologies, Department of Molecular Genetics, University of Toronto, Spring 2021
- Biostatistics, Department of Medical Biophysics, University of Toronto, Fall 2019
- Genomic Methodologies, Department of Molecular Genetics, University of Toronto, Spring 2020
- Biostatistics, Department of Medical Biophysics, University of Toronto, Fall 2018
- Genomic Methodologies, Department of Molecular Genetics, University of Toronto, Winter–Spring 2019
- R programming, McGill Centre for Bioinformatics, McGill University, Spring 2014
- Topics in biology, various high schools in Tehran, Ahwaz, Arak, Esfahan, and Mazandaran 2008–2012

Technical skills

- **Scripting Languages:** Proficient in R, Python, PyTorch, Scikit-learn, Keras, PyQT, bash, and high performance computing (SGE and Slurm). Basic skills in \LaTeX and HTML.
- **Bioinformatics skills:** Bulk and single-cell raw file processing, quality control, and data analysis (DNA-seq, RNA-seq, Bisulfite-seq, ChIP-seq, DNase-seq, ATAC-seq, scRNA-seq, and scATAC-seq). Methylation array and cDNA array data analysis. Networks and pathways bioinformatics. Statistical modelling, machine learning, and deep learning.
- **Laboratory skills:** Cell culture and invasion assay. Extraction and purification of DNA, RNA, and proteins (Western Blotting). Transfection and RNA interference.

Honors and Awards

- Bronze medal in National Biology Olympiad for high school students, *Tehran, Iran, Young Scholars' Club, Aug 2007*
- University of Tehran representative candidate for participation in the National Biology Olympiad for undergraduate students, *Tehran, Iran, April 2012*
- Bronze Medal Winner in National Biology Olympiad for undergraduate students, *Tehran, Iran, July 2012*
- Faculty of Medicine entrance award, McGill University, *Montreal, Quebec, January 2013*
- International travel award, Faculty of Medicine, McGill University, *Montreal, Quebec, April 2013*
- CIHR travel award to attend OICR cancer genomics bioinformatics Workshop, *Toronto, Ontario, May 2014*
- MBP excellence award, *Toronto, Ontario, September 2016*
- The Frank Fletcher Memorial Fund, Faculty of Medicine, University of Toronto, 2017-2018 Academic year
- The Ontario Graduate Scholarship, Ontario Ministry of Training, Colleges, and Universities, 2017-2018 Academic year
- MBP excellence award, *Toronto, Ontario, September 2017*
- The Frank Fletcher Memorial Fund, Faculty of Medicine, University of Toronto, 2018-2019 Academic year
- The Ontario Graduate Scholarship, Ontario Ministry of Training, Colleges, and Universities, 2018-2019 Academic year
- Genome Informatics 2018 conference bursary, September 2018, London, UK
- Arshia Tabrizi Memorial Scholarship by Mowfaghian Foundation, Parya Trillium Foundation, September 2018, Toronto, Canada
- Peterborough K.M. Hunter Charitable Foundation Graduate Awards, Faculty of Medicine, University of Toronto, 2018-2019 Academic year
- The Ontario Graduate Scholarship, Ontario Ministry of Training, Colleges, and Universities, 2019-2020 Academic year
- Parya Foundation Scholarship, Parya Trillium Foundation, September 2019, Toronto, Canada
- CIHR Post-doctoral Fellowship, Canadian Institute for Health Research, June 2021, Toronto, Canada

Internships and workshops

- Internship on Cell and Molecular Biology, *July-Sep 2010, Royan institute of biotechnology, Esfahan, Iran*
- Screening binding partners of DCC through SH2 domain in Netrin signaling pathway, *Feb-Apr 2012, McGill University, Prof. Nathalie Lamarche's lab, Montreal, QC*
- 5th Paris workshop on genomic epidemiology, *2-4 May 2013, Paris, France*
- Networks and pathways bioinformatics, *9-12 July 2013, EMBL-EBI, Hinxton, UK*
- Bioinformatics for cancer genomics, *26-30 May 2014, OICR, Toronto, ON*

Volunteer and extra-curricular activities

- Volunteer editor and writer in monthly journal of school of biology, University of Tehran[2009-2012]
- Volunteer Team guide in 3rd International Olympiad on Astronomy and Astrophysics, *Nov 2010, Tehran, Iran*
- Let's Talk Science Volunteer for first nation students science fair, *March 29-30, Wendake, QC*
- Journal club organizer, McGill University and Genome Quebec Innovation Centre, *September 2013 – May 2014, Montreal, Quebec.*
- Environmental Health and Safety committee member and student representative, McGill University and Genome Quebec Innovation Center, *January 2013 – December 2014, Montreal, Quebec.*
- Organizer of textbook club on machine learning, McGill University and Genome Quebec Innovation Center, *January 2013 – December 2014, Montreal, Quebec.*
- Organizer; Department of Medical Biophysics tech talks 2016–2019

- Lecturer at Department of Medical Biophysics March break camp for Grade 11 students, March 2018 and 2019
- Invited speaker for Genomic Methodologies (MMG3003Y) course, Department of Molecular Genetics, University of Toronto, Spring 2021
- Vector institute's delegate at Ontario Rising Stars in Cancer Research Program, OICR, since January 2020
- Reviewer for ISCB GLBIO/CCBC 2016 conference
- Reviewer for IJCAI 2016 conference
- Reviewer for PNAS journal 2017
- Reviewer for Oncotarget journal 2018
- Reviewer for CIBB 2018 conference
- Reviewer for Nucleic Acids Journal 2020
- Reviewer for PeerJ Computer Science Journal 2021
- Reviewer for BMC Supplements 2022
- Reviewer for Molecules (MDPI) 2022
- Reviewer for Nature Methods 2022

Work experience

- Part time biology Olympiad teacher for high school students. *Several schools affiliated with NODET (National organization for development of exceptional talents) in Tehran, Karaj, Ahwaz, Mazandaran, and Arak, Iran. [2009-2012]*
- Research assistant in bioinformatics. *Michael Hoffman lab, Princess Margaret Cancer Centre, Toronto, ON. [2015 — August 2016]*
- Part time bioinformatics consultant. *Collaboration with Janusz Rak and Yasser Riazalhosseini at the research institute of McGill University health centre. [July 2015 — November 2015]*
- Bioinformatics research clerk, Princess Margaret Cancer Centre. [January 2015 — August 2016]
- Post-doctoral fellow, UCSF and Vector Institute [January 2020 — present]
- Adjunct Professor, Department of Biology, University of Winnipeg, Fall 2021
- Deep learning consultant, Exai Bio Inc., Palo Alto, CA, Spring 2022

References

- **Babak Alipanahi**
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Exai Bio, Inc.
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- **Hani Goodarzi** Post-doctoral fellowship supervisor
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- **Bo Wang** Post-doctoral fellowship co-supervisor
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University of Toronto

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