Fereydoun Hormozdiari, Ph.D.

Contact Information

UC Davis Genome Center
451 Health Science Drive
Davis, CA, 95616

(206) 779-8406
http://www.HormozdiariLab.org
fhormozd@ucdavis.edu
Associate Professor at UC-Davis

Affiliations

Associate Professor at University of California at Davis
UC Davis Genome Center, Davis, CA, USA
Biochemistry and Molecular Medicine, Sacramento, CA, USA
MIND Institute, Sacramento, CA, USA

Research Interests

Computational biology and bioinformatics
Machine learning in biology and medicine
Genomics of neurodevelopmental disorders
Cancer genomics
Algorithms

Education

Simon Fraser University (SFU), Burnaby, BC, Canada

Ph.D. in Computing Science **Jan 2007 – Sep 2011**

- Thesis title: Structural Variation Discovery: The easy, the hard and the ugly

M.Sc. in Computing Science **Sep 2004 – Dec 2006**

- Thesis title: Protein-protein interaction network comparison and emulation

Sharif University of Technology, Tehran, Iran

B.Sc. in Computer Engineering **Sep 1999 – Jul 2004**

Honours and Awards

◇ US - Israel Binational Science Foundation - **BSF Research Grant** 2022-2026
◇ **NSF CAREER Award 2021-2026**
◇ **Sloan Research Fellowship 2017-2019**
◇ Governor General Gold Medal - Winner of SFU's **Best PhD Thesis 2012**
◇ NSERC Alexander Graham Bell Canada Graduate Scholarship, 2009–2011
◇ **Best Paper Award**, HitSeq 2011: Conference on High Throughput Sequencing Analysis and Algorithms (Special interest group of ISMB 2011: July 15-16, 2011, Vienna, Austria)
◇ Simon Fraser University Graduate Fellowship, 2005, 2007 and 2008
◇ Various travel and minor research awards to attend: ISMB'08, RECOMB'09, ISMB'10
◇ H-index: 41 and Erdős Number: 2

Academic Research Positions

Associate Professor **July 2022 – Now**
University of California at Davis
UC Davis Genome Center, Davis, CA, USA
Biochemistry and Molecular Medicine, Sacramento, CA, USA
MIND Institute, Sacramento, CA, USA
Computational biology and machine learning approaches with focus on diseases

Assistant Professor **Sep 2015 – June 2022**
UC Davis Genome Center, Davis, CA, USA
Biochemistry and Molecular Medicine, Sacramento, CA, USA
MIND Institute, Sacramento, CA, USA
Computational biology and bioinformatics with focus on human genomics of diseases

Postdoctoral Fellow **Oct 2011 – July 2015**
Genome Sciences Department, University of Washington (UW), Seattle, WA, USA
*Development of computational biology algorithms under supervision of **Prof. Evan E. Eichler***

Graduate student (MSc and PhD) and Research Assistant **Sep 2006 – Sep 2011**
School of Computing Science, Simon Fraser University, Burnaby, BC, Canada
*Development of computational biology algorithms under supervision of **Prof. Cenk Sahinalp**.*

Industry Positions

Director of Computational Biology and Algorithms **Aug 2022 – Now**
Exai Bio, Palo Alto, CA, USA (Exai Bio)
Leading the computational biology and algorithms team in developing a new liquid bioposy approach

Consultant **Jan 2022 – July 2022**
Exai Bio, Palo Alto, CA, USA (Exai Bio)
Consulting on development of novel computational biology methods for liquid bioposy

Peer-Reviewed Journal Publications

Citations are according to Google Scholar as of August 2022.
Total papers: 75
H-index: 41
Total citation: 35254
Erdős Number : 2
Full list of publication : Google Scholar

——————Publications After Joining UC-Davis——————

JC Chow, **F Hormozdiari** †. (†: corresponding authors)
Prediction of Neurodevelopmental Disorders Based on De Novo Coding Variation
Journal of Autism and Developmental Disorders 2022; 1-14

JC Chow, R Zhou, **F Hormozdiari** †
MAGI-MS: Multiple seed-centric module discovery
Bioinfromatics Advances 2022; Vol 2 (1), vbac025

P Khorsand, L Denti, P Bonizzoni†, R Chikhi†, **F Hormozdiari** †.
Comparative genome analysis using sample-specific string detection in accurate long reads
Bioinformatics Advances 2021; Volume 1, Issue 1, 2021, vbab005
Source Code - GitHub

P Khorsand, **F Hormozdiari** †.
Nebula: ultra-efficient mapping-free structural variant genotyper.
Nucleic Acids Research 2021; gkab025, https://doi.org/10.1093/nar/gkab025.
Source Code - GitHub

C Ricketts, D Seidman, V Popic, **F Hormozdiari**, S Batzoglou, I Hajirasouliha.
Meltos: Multi-Sample Tumor Phylogeny Reconstruction for Structural Variants.
Bioinformatics 2020 Oct 4. pii: btz737. doi: 10.1093/bioinformatics/btz737.

J Chow, M Jensen, H Amini, F Hormozdiari, O Penn, S Shifman, S Girirajan, **F Hormozdiari** †.
Dissecting the genetic basis of comorbid epilepsy phenotypes in neurodevelopmental disorders.
Genome Med. 2019; Oct 25;11(1):65. doi: 10.1186/s13073-019-0678-y.
Source Code - GitHub

F Hormozdiari, B van de Geijn, J Nasser, O Weissbrod, S Gazal, CJ Ju, LO Connor, MLA Hujoel, J Engreitz, **F Hormozdiari**, AL Price.
Functional disease architectures reveal unique biological role of transposable elements.
Nat Commun. 2019 Sep 6;10(1):4054. doi: 10.1038/s41467-019-11957-5.

DS Standage, CT Brown, **F Hormozdiari** †.
Kevlar: A Mapping-Free Framework for Accurate Discovery of De Novo Variants.
iScience 2019; Special issue: RECOMB-Seq. DOI: https://doi.org/10.1016/j.isci.2019.07.032.
Source Code - GitHub

L Huynh, **F hormozdiari**†.
TAD fusion score: discovery and ranking the contribution of deletions to genome structure.
Genome Biology 2019; 20(1), 60. DOI: 10.1186/s13059-019-1666-7.
Source Code - GitHub

MJP Chaisson, et al.
Multi-platform discovery of haplotype-resolved structural variation in human genomes.
Nature Communication 2019;10(1):1784. doi: 10.1038/s41467-018-08148-z. [cited by **273**]

S Mangul, LS Martin, B Langmead, JE Sanchez-Galan, I Toma, **F Hormozdiari**, et al.
How bioinformatics and open data can boost basic science in countries and universities with limited resources.
Nature Biotechnology 2019; 37 (3), 334. DOI: 10.1038/s41587-019-0053-y.

A Soylev, T Le, H Amini, C Alkan†, **F Hormozdiari**†. (joint corresponding authors)
Discovery of tandem and interspersed segmental duplications using high throughput sequencing.
Bioinformatics. 2019; pii: btz237. doi: 10.1093/bioinformatics/btz237
Source Code - GitHub

B Coe, et al.
Neurodevelopmental disease genes implicated by de novo mutation and copy number variation morbidity.
Nature Genetics. 2018; 51(1):106-116. doi: 10.1038/s41588-018-0288-4

L Huynh , **F. Hormozdiari**†.
Combinatorial Approach for Complex Disorder Prediction: Case Study of Neurodevelopmental Disorders.
Genetics. 2018; 210(4):1483-1495. doi: 10.1534/genetics.118.301280.
Source Code - GitHub

BJ Main, A Everitt, AJ Cornel, **F Hormozdiari**, GC Lanzaro.
Genetic variation associated with increased insecticide resistance in the malaria mosquito, Anopheles coluzzii.
Parasites and vectors 2018; 11(1), 225.

ZN Kronenberg, et al.
High-resolution comparative analysis of great ape genomes
Science 2018; 360 (6393), eaar6343

TN Turner, et al.
Genomic patterns of de novo mutation in simplex autism
Cell 2017; 171 (3), 710-722. e12

A Soylev, C Kockan, **F Hormozdiari**†, C Alkan† (joint corresponding authors)
Toolkit for automated and rapid discovery of structural variants
Methods 2017; 129, 3-7.

HAF Stessman, et al.
Targeted sequencing identifies 91 neurodevelopmental-disorder risk genes with autism and developmental-disability biases
Nature genetics 2017; 49 (4), 515 [cited by 135].

Jayne Y Hehir-Kwa, et al.
A high-quality human reference panel reveals the complexity and distribution of genomic structural variants
Nature communications 2016; 7, 12989

TN Turner, **F Hormozdiari**, MH Duyzend, SA McClymont, PW Hook, et al.
Genome sequencing of autism-affected families reveals disruption of putative noncoding regulatory DNA
The American Journal of Human Genetics 2016; 98 (1), 58-74 [cited by 147]

The 1000 Genomes Project consortium.
A global reference for human genetic variation
Nature 2015; 526(7571), p.68 [cited by **7529**].

PH Sudmant, et al.
An integrated map of structural variation in 2,504 human genomes
Nature 2015; 526(7571), p.75 [cited by **855**].

P Sudmant, S Mallick, BJ Nelson, **F Hormozdiari**, Krumm N, et al.
Global diversity, population stratification, and selection of human copy-number variation
Science 2015; 349(6253), p.aab3761 [cited by **269**].

————————Publications before Joining UC-Davis————————

WP. Kloosterman, LC. Francioli, **F. Hormozdiari**, T. Marschall, et al.
Characteristics of de novo structural changes in the human genome.
Genome Research 2015; Apr 16. pii: gr.185041.114.

F. Hormozdiari, O. Penn, E. Borenstein and EE. Eichler.
The discovery of integrated gene networks for autism and related disorders.
Genome Research 2015; 25(1):142-54 [cited by **201**].

M. Chaisson, J. Huddleston, MY. Dennis, PH. Sudmant, M. Malig, **F. Hormozdiari**, et al.
Resolving the complexity of the human genome using single-molecule sequencing.
Nature 2014; Nov 10; 10.1038/nature13907 [cited by **588**].

Genome of the Netherlands Consortium.
Whole-genome sequence variation, population structure and demographic history of the Dutch population.
Nature Genetics 2014; 46(8):818-25.

CD. Campbell, K. Mohajeri, M. Malig , **F. Hormozdiari**, et al.
Whole-genome sequencing of individuals from a founder population identifies candidate genes for asthma.
PLoS One 2014; Aug 12;9(8).]

F. Hormozdiari, MK. Konkel, J. Prado-Martinez, G. Chiatante, IH. Herraez, et al.
Rates and patterns of great ape retrotransposition.
Proc Natl Acad Sci (PNAS) 2013; 110(33):13457-62. doi: 10.1073/pnas.1310914110.

J. Prado-Martinez, et al.
Great ape genetic diversity and population history.
Nature 2013; 7548(499): 471-475 [cited by **485**].

J. Prado-Martinez, et al.
The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild.
BMC Genomics 2013; 14:363.

C. Wu, et al.
Integrated genome and transcriptome sequencing identifies a novel form of hybrid and aggressive prostate cancer.
The Journal of Pathology 2012; 227(1):53-61.

AV. Lapuk, et al.
From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer.
The Journal of Pathology 2012; 227(3):286-97.

The 1000 genome Project Consortium.
A integrated map of genetic variation from 1,092 human genomes
Nature 2012; 491: 56-65 [Cited by **6828**].

F. Hormozdiari*, I. Hajirasouliha, A. McPherson, EE. Eichler and SC. Sahinalp.
Simultaneous structural variation discovery in multiple paired-end sequenced genomes.
Genome Research 2011; 21(12):2203-12
◇ Featured on the cover of the journal.
◇ Highlighted in: Nature Biotechnology, 29, 1101 (2011).

F. Hormozdiari, et al.
Alu repeat discovery and characterization within human genomes.
Genome Research 2011; 21: 840-849.

A. McPherson, **F. Hormozdiari**, A. Zayed, R. Giuliany, et al.
deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data.
PLoS Computational Biology 2011; 7(5): e1001138. doi:10.1371/journal.pcbi.1001138 [cited by **502**].

M. Ventura, et al.
Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee.
Genome Research 2011; 21:1640-9.

RE. Mills, et al.
Mapping copy number variation at fine-scale by population-scale genome sequencing.
Nature 2011; 470: 59-65 [cited by **936**].

A. McPherson*, C. Wu*, I. Hajirasouliha*, **F. Hormozdiari***, et al.
Comrad: a novel algorithmic framework for the integrated analysis of RNA-Seq and WGSS data.
Bioinformatics, 2011; 27(11):1481-8. Epub 2011 Apr 9).

A. Schonhuth, R. Salari, **F. Hormozdiari**, A. Cherkasov and SC. Sahinalp.
Towards improved assessment of functional similarity in large-scale screens:an indel study.
Journal of Computational Biology 2010; 17(1): 1-20.

F. Hach, **F. Hormozdiari**, C. Alkan, F. Hormozdiari, I. Birol, EE. Eichler and SC. Sahinalp.
mrsFAST : a cache-oblivious algorithm for short-read mapping.
Nature Methods 2010; 7(8): 576–577 [cited by 264].

F. Hormozdiari*, R. Salari*, V. Bafna and SC. Sahinalp.
Protein protein interaction network evaluation for identifying potential drug targets.
Journal of Computational Biology 2010; 17(5): 669-684.

I. Hajirasouliha*, **F. Hormozdiari***, C. Alkan*, JM. Kidd, I. Birol, EE. Eichler and SC. Sahinalp.
Detection of locus and content of novel sequence insertions using paired-end next-generation sequencing.
Bioinformatics 2010; 26(10):1277-83. Epub 2010 Apr 12) [cited by 111].

The 1000 genome Project Consortium.
A map of human genome variation from population-scale sequencing.
Nature 2010; 467: 1061-1073 [cited by **7257**].

F. Hormozdiari, et al.
Next Generation VariationHunter: Combinatorial Algorithms for Transposon Insertion Discovery.
Bioinformatics 2010; 26(12):i350-i357 [cited by **249**].

F. Hormozdiari*, R. Salari*, M. Hsing, A. Schonuth and SC. Sahinalp.
The effect of insertion and deletions (indels) on wirings in protein interaction networks: a large scale study.
Journal of Computational Biology 2009; 16(2):159-167.

F. Hormozdiari*, C. Alkan, EE. Eichler and SC. Sahinalp.
Combinatorial Algorithms for Structural Variation Detection in High Throughput Sequenced Genomes.
Genome Research, 2009; 19:1270-1278 [cited by **367**].

S. Lee, **F. Hormozdiari**, C. Alkan and M. Brudno.
MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions.
Nature Methods, 2009; 6:473-474 [cited by 102].

C. Alkan, et al.
Personalized copy number and segmental duplication maps using next-generation sequencing.
Nature Genetics 2009; 41: 1061-1067 [cited by 381].

N. Alon, P. Dao, I. Hajirasouliha, **F. Hormozdiari** and SC. Sahinalp
Biomolecular Network Motif Counting and Discovery by Color Coding.
Bioinformatics 2008; 24 (13):i241-9 [cited by 62].

I. Hajirasouliha*, **F. Hormozdiari***, SC. Sahinalp and I. Birol.
Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies.
Bioinformatics 2008; 24 (13):i32-40.

SK. Chan, M. Hsing, **F. Hormozdiari** and A. Cherkasov.
Relationship between insertion/deletion (indel) frequency of proteins and essentiality.
BMC Bioinformatics 2007; 8: 227.

F. Hormozdiari, P. Berenbrink, N. Przulj and SC. Sahinalp.
Not all scale-free networks are born equal: the role of the seed graph in PPI network evolution.
PLoS Computational Biology 2007; 3(7): e118. doi:10.1371/journal.pcbi.0030118.

Selected Presentations

ASHG'20, San Diego, USA, October 2020 (Virtual)
Computational algorithms for prediction of structural variant impact on 3D genome structure
RECOMB'18, Paris, France, April 2018.
Contribution of structural variation to genome structure: TAD fusion discovery and ranking
RECOMB'17, Hong-Kong, China, April 2017.
Ultra-Accurate Complex Disorder Prediction: Case Study of Neurodevelopmental Disorders
IMFAR'15, San Francisco, USA, May 2015.
The Discovery of Gene Modules for Autism Utilizing Co-Expression and PPI Networks
ISMB'10 , Boston, USA, July 2010.
Next Generation VariationHunter: Combinatorial Algorithms for Transposon Insertion Discovery.
RECOMB'09, Tucson, AZ, USA, May 2009.
Combinatorial Algorithms for Structural Variation Detection in High Throughput Sequenced Genomes.
ISMB'08, Toronto, Canada, July 2008.
Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies.

Teaching Experience

Instructor, UC-Davis
- GGG201B: Genomics (Winter 2017, 2018, 2019, 2020)
- ECS 289N: Bioinformatics and Comp Biology (Winter 2018)

Instructor, Summer School at UCLA
CGSI (Computational Genomics Summer Ins.) at 2016, 2017, 2018 and 2019
lecture 2016 - Video; lecture 2017 - Video; lecture 2018 - Video; lecture 2019 - Video

Mentoring at UC-Davis

Hormozdiari Lab Members
Marketa Tomkova. Postdoctoral fellow, UC-Davis *from 2021- Now*
Parsoa Khorsand. PhD Graduate Student, UC-Davis *From 2017- Now*
Julie Chow. PhD Graduate Student, UC-Davis *From 2017- Now*
Ashleigh Thomas. MSc Graduate Student, *From 2019 - Now*
Thong Minh Le. PhD Graduate Student *From 2017-2019 (graduated)*
Jason Driver. MSc Graduate Student, UC-Davis *From 2017-2018 (graduated)*
Songyu Li. MSc Graduate Student, UC-Davis *From 2017-2019 (graduated)*
Linh Huynh. Postdoctoral fellow, UC-Davis *from 2016-2019*
Carlos Rojas. Postdoctoral fellow, UC-Davis *from 2018-2019*

Mentoring before UC-Davis

Pinar Kavak. Visiting undergraduate student, SFU.
Reza Shahidi-Nejad. Project based graduate student, SFU.
Michael Duyzend. PhD student, UW.
Joseph Marcus. Visiting undergraduate student, UW.
Ahmed Mahfouz. Visiting graduate student, UW.

Conference Program Committee

PSB'11, Organizing and Co-chair of Personal Genomics session.
RECOMB-SEQ2017, Program Chair
ISMB'13-18, 21, Program Committee.
ACM-BCB'15-21, Program Committee.
RECOMB'15-22, Program Committee.

Memberships

The 1000 Genomes Project, Analysis Group
The 1000 Genomes Project, Structural Variation Group
The Genome of Netherlands (GoNL) Consortium
The great ape genome project
ISCB - International Society for Computational Biology
ASHG - The American Society of Human Genetics

Funding

US-Israel Binational Science Foundation Research Grant
Hormozdiari, Fereydoun (co-PI)
09/01/2022-08/30/2026
Amount: $228,000
Unraveling cellular and genotypic heterogeneity of ASD using systems genetics
Role: co-PI

NSF CAREER Award
Hormozdiari, Fereydoun (PI)
03/01/2021- 03/31/2026
Amount: $503,744
Computational methods to improve our understanding of the diversity of genomic structural variation
Role: PI

Sloan Research Fellowship
Hormozdiari, Fereydoun (PI)
09/15/17-09/14/19
Amount: $60,000
Discovery of complex genetic variation and its contribution to human disease and evolution
Role:PI