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Imran S. Haque

Positions **Publications** **Patents**
Invited Talks **Awards** **Open-Source** **Teaching**

Positions and Education

2016–2018 **Freenome**, *Chief Scientific Officer*
2016 **Counsyl**, *VP, Scientific Affairs*
2013–2016 **Counsyl**, *Director, Research*
2011–2013 **Counsyl**, *Sr. Software Engineer/Sr. Research Scientist*

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2006–2011 **PhD, Computer Science**, *Stanford University*
Dissertation: Accelerating Chemical Similarity Search with GPUs and Metric Embeddings
Committee: Vijay Pande, Daphne Koller, Russ Altman
2002–2006 **BS, Hons., Electrical Engineering and Computer Science**, *UC Berkeley*

Publications

Google Scholar statistics: https://scholar.google.com/citations?user=Cp_wDj4AAAAJ

2018 In sub. Cecchi A, Vengoechea ES, Kaseniit KE, Hardy MW, Kiger LA, Mehta N, **Haque IS**, Moyer K, Page PZ, Muzzey D, Grinzaid KA. In submission to *Am J Hum Genet*.
Screening for Tay-Sachs disease carriers by full-exon sequencing with novel variant interpretation outperforms enzyme testing in a pan-ethnic cohort

In press Heitzer E, **Haque IS**, Roberts CE, Speicher MR. In press at *Nat Rev Genet*. (2018)
Current and future perspectives of liquid biopsies in genomics-driven oncology

DOI Hogan GJ, Vysotskaia VS, Beauchamp KA, Seisenberger S, Grauman PV, Haas KR, Hong SH, Jeon D, Kash S, Lai HH, Melroy LM, Theilmann MR, Chu CS, Iori K, Maguire JR, Evans EA, **Haque IS**, Mar-Heyming R, Kang HP, Muzzey D. *Clin Chem* 64(7):AOP. (2018)
Validation of an Expanded Carrier Screen that Optimizes Sensitivity via Full-Exon Sequencing and Panel-wide Copy Number Variant Identification

DOI Beauchamp KA, Muzzey D, Wong KK, Hogan GJ, Karimi K, Candille SI, Mehta N, Kaseniit KE, Mar-Heyming R, Kang HP, Evans EA, Goldberg JD, Lazarin GA, **Haque IS**. *Genet Med* 20(1):55–63. (2018)
Systematic Design and Comparison of Expanded Carrier Screening Panels

DOI Ghiossi C, Goldberg JD, **Haque IS**, Lazarin GA, Wong KK. *J Genet Counsel* 27:616–625. (2018)
Clinical Utility of Expanded Carrier Screening: Reproductive Behaviors of At-Risk Couples

2017 DOI **Haque IS**, Elemento O. *bioRxiv*: 237578. (2017)
Challenges in Using ctDNA to Achieve Early Detection of Cancer

DOI Artieri CG, Haverty C, Evans EA, Goldberg JD, **Haque IS**, Yaron Y, Muzzey D. *Prenat Diagn* 37(5):482–490. (2017)
Noninvasive Prenatal Screening at Low Fetal Fraction: Comparing Whole-Genome Sequencing and Single-Nucleotide Polymorphism Methods

DOI Vysotskaia VS, Hogan GJ, Gould GM, Wang X, Robertson AD, Haas KR, Theilmann MR, Spurka L, Grauman PV, Lai HH, Jeon D, Haliburton G, Leggett M, Chu CS, Iori K, Maguire JR, Ready K, Evans EA, Kang HP, **Haque IS**. *PeerJ* 5:e3046. (2017)
Development and validation of a 36-gene sequencing assay for hereditary cancer risk assessment

DOI Amorim CE, Gao Z, Baker Z, Diesel JF, Simons YB, **Haque IS**, Pickrell J, Przeworski M. *PLoS Genetics* 13(9):e1006915. (2017)
The population genetics of human disease: the case of recessive, lethal mutations

DOI Lazarin GA, **Haque IS**, Evans EA, Goldberg JD. *Prenat Diagn* 37(4):350–355. (2017)
Smith-Lemli-Opitz syndrome carrier frequency and estimates of in utero mortality rates

2016 DOI **Haque IS**, Lazarin GA, Kang HP, Evans EA, Goldberg JD, Wapner RJ. *JAMA* 316(7):734–742. (2016)
Modeled Fetal Risk of Genetic Diseases Identified by Expanded Carrier Screening

DOI Kang HP, Maguire JR, Chu CS, **Haque IS**, Lai H, Mar-Heyming R, Ready K, Vysotskaia VS, Evans EA. *PeerJ* 4:e2162. (2016)
Design and validation of a next generation sequencing assay for hereditary *BRCA1* and *BRCA2* mutation testing

DOI Mehta N, Lazarin GA, Spiegel E, Berentsen K, Brennan K, Giordano J, **Haque IS**, Wapner R. *Genet Test Molec Biomarker* 20(9):504–509. (2016)
Tay-Sachs Carrier Screening by Enzyme and Molecular Analyses in the New York City Minority Population

DOI Kaseniit KE, Theilmann MR, Robertson A, Evans EA, **Haque IS**. *Clin Chem* 62(10):1401–1408. (2016)
Group Testing Approach for Trinucleotide Repeat Expansion Disorder Screening

DOI Lazarin GA, **Haque IS**. *Semin Perinatol* 40(1):29–34. (2016)
Expanded carrier screening: A review of early implementation and literature

2015 DOI Vikram S, Rasmussen MD, Evans EA, **Haque IS**. *bioRxiv*: 021527. (2015)
SSCM: A method to analyze and predict the pathogenicity of sequence variants

2014 DOI Lazarin GA, Hawthorne F, Collins NS, Platt EA, Evans EA, **Haque IS**. *PLoS One*: e114391. (2014)
Systematic Classification of Disease Severity for Evaluation of Expanded Carrier Screening Panels

DOI **Haque IS**, Beauchamp KA, Pande VS. *bioRxiv*: 008631. (2014)
A Fast 3 x N Matrix Multiply Routine for Calculation of Protein RMSD

2013 DOI Kearnes SM, **Haque IS**, Pande VS. *J Chem Inf Model* 54(1):5–15. (2013)
SCISSORS: Practical Considerations

DOI Lazarin GA, **Haque IS**, Nazareth S, Iori K, Patterson AS, Jacobson JL, Marshall JR, Seltzer WK, Patrizio P, Evans EA, et al.. *Genet Med* 15(3):178–186. (2013)
An empirical estimate of carrier frequencies for 400+ causal Mendelian variants: results from an ethnically diverse clinical sample of 23,453 individuals

2011 DOI Ready K, **Haque IS**, Srinivasan BS, Marshall JR. *Fertil Steril*: 407–413. (2011)
Knowledge and attitudes regarding expanded genetic carrier screening among women's healthcare providers

DOI **Haque IS**, Pande VS, Walters WP. *J Chem Inf Model* 51(9):2345–2351. (2011)
Anatomy of high-performance 2D similarity calculations

DOI **Haque IS**, Pande VS. *J Chem Inf Model* 51(9):2248–2253. (2011)
Error bounds on the SCISSORS approximation method

Haque IS, Pande VS. In *GPU Computing Gems: Emerald Edition (Ed: W.-M. W. Hwu)*. (2011)
Large-Scale Chemical Informatics on GPUs

DOI Beauchamp KA, Bowman GR, Lane TJ, Maibaum L, **Haque IS**, Pande VS. *J Chem Theor Comput*: 3412–3419. (2011)
MSMBuilder2: Modeling Conformational Dynamics at the Picosecond to Millisecond Scale

DOI Pronk S, Larsson P, Pouya I, Bowman GR, **Haque IS**, Beauchamp K, Hess B, Pande VS, Kasson PM, Lindahl E. In proceedings of *SC11: 2011 Intl Conf High Perf Comput, Network, Storage and Analysis*. 60. (2011)
Copernicus: A new paradigm for parallel adaptive molecular dynamics

2010 DOI **Haque IS**, Pande VS. In proceedings of *CCGrid 2010: 10th IEEE/ACM International Conference on Cluster, Cloud and Grid Computing*. 691–696. (2010)
Hard data on soft errors: A large-scale assessment of real-world error rates in GPGPU

DOI **Haque IS**, Pande VS, Walters WP. *J Chem Inf Model* 50(4):560–564. (2010)
SIML: a fast SIMD algorithm for calculating LINGO chemical similarities on GPUs and CPUs

DOI **Haque IS**, Pande VS. *J Chem Inf Model* 50(6):1075–1088. (2010)
SCISSORS: a linear-algebraical technique to rapidly approximate chemical similarities

DOI **Haque IS**, Pande VS. *J Comput Chem* 31(1):117–132. (2010)
PAPER—accelerating parallel evaluations of ROCS

DOI Ponder JW, Wu C, Ren P, Pande VS, Chodera JD, Schnieders MJ, **Haque I**, Mobley DL, Lambrecht DS, DiStasio Jr RA, et al.. *J Phys Chem B* 114(8):2549–2564. (2010)
Current status of the AMOEBA polarizable force field

2006 DOI Pitera JW, **Haque I**, Swope WC. *J Chem Phys* 124:141102. (2006)
Absence of reptation in the high-temperature folding of the trpzip2 β-hairpin peptide

Patents and Published Patent Applications

2017 URL Evans EA, **Haque IS**, Beauchamp K, Chu C, Artieri CG, Welker N. *US Patent App*: 15/619,078. (2017)
Nucleic acid sequencing adapters and uses thereof

URL **Haque IS**, Maguire JR, Chu C, Evans EA. *US Patent App*: 15/587,811. (2017)
Noninvasive prenatal diagnostic methods

URL Kaseniit KE, Theilmann MR, Robertson AD, Evans EA, **Haque IS**. *US Patent App*: 15/488,129. (2017)
Group testing approach for a genetic screening assay

2016 URL **Haque IS**, Evans EA, Vikram SM, Rasmussen MD. *US Patent App*: 15/189,957. (2016)
Methods of predicting pathogenicity of genetic sequence variants

URL Gibiansky AL, **Haque IS**, Maguire JR, Robertson AD. *US Patent App*: 14/884,656. (2016)
Variant caller

2015 URL Patterson AS, **Haque IS**, Evans EA, Chu C. *US Patent App*: 14/540,334. (2015)
Automated nucleic acid repeat count calling methods

2011 URL **Haque I**, Pande V. *US Patent* (granted 2014):8,706,427. (2011)
Method for rapidly approximating similarities

Invited Talks

Mar 2019 **Molecular Medicine Tri-Con**
(How to fix) the very reasonable ineffectiveness of machine learning in biomarker discovery

Oct 2018 **AACR Special Conf. on Convergence: AI, Big Data, and Prediction in Cancer**
Making hay of needles: Connecting clinical and physical parameters in the search for early cancer

Oct 2018 **Early Detection of Cancer**
slides The Reasonable Ineffectiveness of Biological Data

Jul 2018 **DeepChem User Group Meeting**
slides (What to do) when gradient descent digs too deep, and too greedily

Oct 2017 **Cancer Crosslinks (Keynote Presentation)**
slides Embracing heterogeneity: The freenome, information, and early disease detection

Jan 2017 **Society for Maternal-Fetal Medicine Annual Meeting**
slides 1 in 550: Using 346,790 expanded carrier screens to estimate the risk of Mendelian conditions

Aug 2016 **AGBT Precision Health Meeting**
slides Overcoming artificial selection to achieve the promise of inherited cancer screening

Sep 2015 **American Society for Reproductive Medicine Annual Meeting**
"Rare" disease is common: results from 388,994 expanded carrier screens of up to 108 genes

Apr 2015 **ChildX 2015**
Can/Do: the disconnect between what we can do and what we do in perinatal precision medicine

Nov 2013 **PyData 2013**
slides+code Beyond the dict: Python tools for data wrangling

Nov 2010 **Hyperience: 5th National Dutch Informatics Congress (Keynote Presentation)**
slides Folding@Everywhere: Computational Biochemistry in the New Era of HPC

May 2010 **Resilience Workshop @ CCGrid 2010**
slides Hard Data on Soft Errors: A Global-Scale Assessment of GPGPU Memory Soft Error Rates

Mar 2010 **OpenEye CUP XI**
slides LINGOs and GPUs

Fellowships and Awards

2006–2009 National Science Foundation Graduate Research Fellowship

2005–2006 UC Berkeley Alumni Scholarship

2004–2006 SRCEA Undergraduate Research Assistant Scholarship

2002–2006 UC Berkeley Chancellor's Scholarship

2002–2006 Robert Byrd Honors Scholarship

Open-source contributions

Primary author **xorshift**
High-performance vectorized RNGs for Python

Primary author **MemtestG80/MemtestCL**
Tools to check GPU memory for errors

Primary author **SIML**
High-performance LINGO similarity library for GPU and CPU

Primary author **PAPER**
GPU-based 3-D shape comparison for chemical similarity

Primary author **IRMSD**
Optimal SSE2/SSE3-based code for structural RMSD computation

Contributor **scikit-learn**
Python machine learning toolkit

Teaching experience

Winter 2011 Teaching Assistant, Stanford CS 109, Introduction to Probability for Computer Scientists, Mehran Sahami

Fall 2010 Teaching Assistant, Stanford CS 148, Introduction to Computer Graphics and Imaging, Pat Hanrahan

Spring 2010 Teaching Assistant, Stanford BMI214/CS 274, Representations and Algorithms for Computational Molecular Biology, Russ Altman