

Imran S. Haque

Positions and Education

- 2016– **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*

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

Publications

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

- 2017 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*: Accepted. (2017)
Systematic Design and Comparison of Expanded Carrier Screening Panels
- DOI Artieri CG, Haverty C, Evans EA, Goldberg JD, **Haque IS**, Yaron Y, Muzzey D. *Prenat Diagn*: Published online AOP. (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 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 Amorim CE, Gao Z, Baker Z, Diesel JF, Simons YB, **Haque IS**, Pickrell J, Przeworski M. *bioRxiv*: 091579. (2016)
The population genetics of human disease: the case of recessive, lethal mutations
- 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
- DOI Ghioffi C, Goldberg JD, **Haque IS**, Lazarin GA, Wong KK. *bioRxiv*: 069393. (2016)
Clinical Utility of Expanded Carrier Screening: Reproductive Behaviors of At-Risk Couples
- 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 × 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

Invited Talks

- Jan 2017 **Society for Maternal-Fetal Medicine Annual Meeting**
1 in 550: Using 346,790 expanded carrier screens to estimate the risk of Mendelian conditions
- Aug 2016 **AGBT Precision Health Meeting**
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**
[video](#) 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)**
Folding@Everywhere: Computational Biochemistry in the New Era of HPC
- May 2010 **Resilience Workshop @ CCGrid 2010**
Hard Data on Soft Errors: A Global-Scale Assessment of GPGPU Memory Soft Error Rates
- Mar 2010 **OpenEye CUP XI**
LINGOs and GPUs

Open-source contributions

- 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