Asif Javed

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Research Interests

Computational Genomics, Translational and Clinical Genetics, Next Generation Sequencing

Work Experience

Research Scientist   August 2014 - present
Genome Institute of Singapore, A*STAR   Singapore

Research Associate   December 2011 - July 2014
Genome Institute of Singapore, A*STAR   Singapore

Design and application of analysis methods which combine clinical reports with sequencing data to predict disease causal variant(s) in rare disorders (http://phen-gen.org/)
Published in **Nature Methods**, first and co-corresponding author.

- Investigator for **2M SGD BMRC** grant for industrial collaboration with **Appistry Inc.** (USA) to study and compare NGS pipelines
- Principal investigator for **160k SGD** research collaborative agreement with **Ramathibodi hospital**, (Mahidol University, Thailand) analyzing rare familial disorders
- Principal investigator for GIS team participating international genomic interpretation competition **CLARITY** challenge (**Genome Biology**)
- Conducted multiple 2-day Next Generation Sequencing Bioinformatics workshops UITM Malaysia (Apr 12), GIS A*STAR (May 12), AIT Biotech (Nov 12)
- Funded and supervised one research officer (2 years), trained 4 interns

Postdoctoral Researcher   December 2008 - December 2011
Computational Biology Center, IBM T. J. Watson Research   Yorktown, NY, USA

Designed computational tool to identify historic recombinations from their evidence in SNP data from current individuals. Frequency and sharing of recombination elucidate ancient human migration paths

- Received **IBM Research Accomplishment** for *Results from Genographic*
- Received **IBM First Invention Filing Award**, for US patent *Sampling the space of Ancestral Recombination Graphs*

Research Intern   May 2008 - August 2008
Computational Biology Center, IBM T. J. Watson Research   Yorktown, NY, USA

Teaching / Research Assistant   August 2004 - December 2008
Rensselaer Polytechnic Institute   Troy, NY, USA

Designed linear algebraic algorithms to select a small panel of representative markers (tagging SNPs) which can be to used to predict the remaining from SNP-chip data
Courses assisted: Computer Science 1, Models of Computation, Randomized Algorithms

Teaching / Research Assistant   August 2001 - May 2004
University of Illinois at Chicago   Chicago, IL, USA

Designed and implemented distributed data mining algorithms
Courses assisted: Random Signal Processing, Analog Communication Circuits, Computer Architecture, Digital Logic

Teaching Assistant   August 2000 - August 2001
Lahore University of Management and Sciences   Lahore, Pakistan
Courses assisted: Discrete Mathematics, Algorithm Design, Advanced Algorithm Design, Circuits and Systems 1, Algorithms in Computational Biology

Clinical Collaborations
Studying the following disorders in clinical collaborations within and outside Singapore

- Leukemia progression
- Intellectual disability
- Novel Ophthalmologic condition
- Muscular dystrophies
- Cardiac disorders
- Neuro-developmental disorders

Education

Rensselaer Polytechnic Institute   Troy, NY, USA
Ph.D., Computer Science, (CGPA 4.0), December 2008
thesis: *A computational analysis of human genetic variation*

University of Illinois at Chicago   Chicago, IL, USA
M.S., Computer Engg., (CGPA 3.9, C.S. GPA 4.0), May 2004
thesis: *Scalable parallel algorithm for mining frequent patterns on message passing systems*

University of Engineering and Technology, Lahore   Lahore, Pakistan
B.S. in Electrical Engineering (with honors) 2000

Publications

- B. Pupacdi, **A. Javed**, M.J. Zaki and M. Ruchirawat, *NSIT: Novel Sequence Identification Tool*, **PLoS One**, Sep 2014. (**IF=3.53**)

- **A. Javed***, S. Agrawal, and P.C. Ng*, *Phen-Gen: combining Phenotype and Genotype to analyze rare disorders*, **Nature Methods**, Sep 2014. (* *corresponding authors*) (**IF=23.56**)

- C.A. Brownstein, ..., **A. Javed**, et al., *An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results inthe CLARITY Challenge*, **Genome Biology**, Mar 2014. (**IF=10.50**)

- **A. Javed**, M. Mele, M. Pybus, et. al, and The Genographic Consortium, *Recombination networks as genetic markers: a human variation study of the Old World*, **Hum Genet**, Apr 2012. (**IF=4.63**)

- M. Mele, **A. Javed**, M. Pybus, et. al, and The Genographic Consortium, *The footprint of recombination gives a new insight in the effective population size and the history of the Old World human populations*, **Mol Biol Evol**, Jan 2012. (**IF=14.31**)

- **A. Javed**, P. Paschou, M.W. Mahoney, and P. Drineas, *Efficient genomewide selection of PCA-correlated tSNPs for genotype imputation.*, **Ann Hum Genet**, Nov 2011. (**IF=1.93**)

- **A. Javed**, M. Pybus, M. Mele, et. al, *IRiS: Construction of ARG networks at genomic scales*, **Bioinformatics**, Sep 2011. (**IF=5.32**)

- L. Parida, P.F. Palamara, **A. Javed**, *A Minimal Descriptor of an Ancestral Recombinations Graph*, **BMC Bioinformatics**, APBC, Feb 2011. (**IF=2.67**)

- P. Paschou, J. Lewis, **A. Javed**, P. Drineas, *Ancestry informative markers for fine-scale individual assignment to worldwide populations*, **J Med Genet.** Dec 2010. (**IF=5.64**)
- M. Mele, **A. Javed**, F. Calafell, et. al, and The Genographic Consortium, *A New Method to Reconstruct Recombination Events at a Genomic Scale*, **PLOS Comput Biol.** Nov 2010. (**IF=4.87**)
- **A. Javed** and L. Parida, *Recombinomics: Population Genomics from a Recombination Perspective*, **Proceedings of C3S2E**, May, 2010. (**Acceptance=23%**)
- L. Parida, **A. Javed**, M. Mele, F. Calafell, J. Bertranpetit and The Genographic Consortium, *Minimizing recombinations in consensus networks for phylogeographic studies*, **BMC Bioinformatics**, Jan 2009. (**IF=2.67**)
- L. Parida, **A. Javed**, M. Mele, and J. Bertranpetit, *A case for Recombinomics*, IBM Technical Report RC24677, Aug 2008.
- **A. Javed** and P. Paschou, *Extracting tagging SNPs from genome-wide datasets*, DMBI, workshop held in conjunction with SDM, Apr 2007.
- P. Paschou, M.W. Mahoney, **A. Javed**, et. al, *Intra- and inter-population genotype reconstruction from tagging SNPs*, **Genome Research**, Jan 2007. (**IF=14.4**)
- P. Drineas, **A. Javed**, M. Magdon-Ismail, G. Pandurangan, R.Virrankoski, and A. Savvides, *Distance matrix reconstruction from incomplete distance information for sensor network localization*, (**SECON**), Sep 2006. (**Acceptance=26%**)
- **A. Javed** and A. Khokhar, *Frequent pattern mining on message passing multiprocessor systems*, (**Distributed and Parallel Databases**), Nov 2004. (**IF=0.81**)
- **A. Javed** and A. Khokhar, *Scalable parallel algorithm for mining frequent patterns on message passing parallel systems*, ISCA (**PDCS**), Aug 2003.

Consortium publications

- G. Brandt et al., and **The Genographic Consortium***, *Ancient DNA reveals key stages in the formation of central European mitochondrial genetic diversity*, **Science**, Oct 13. (**IF=31.48**)
- P. Brotherton et al., and **The Genographic Consortium***, *Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans*, **Nat Commun**, Apr 2013. (**IF=10.02**)
- D.A. Badro et al., and **The Genographic Consortium***, *Y-chromosome and mtDNA genetics reveal significant contrasts in affinities of modern Middle Eastern populations with European and African populations*, **PLoS One**, Jan 2013. (**IF=3.53**)
- G. Arunkumar et al., and **The Genographic Consortium***, *Population differentiation of southern Indian male lineages correlates with agricultural expansions predating the caste system*, **PLoS One**, Nov 2012. (**IF=3.53**)
- B. Martnez-Cruz et al., and **The Genographic Consortium***, *Evidence of pre-roman tribal genetic structure in basques from uniparentally inherited markers*, **Mol Biol Evol**, Sep 2012. (**IF=14.31**)
- B. Martnez-Cruz et al., and **The Genographic Consortium***, *Y-chromosome analysis in individuals bearing the Basarab name of the first dynasty of Wallachian kings*, **PLoS One**, Jul 2012. (**IF=3.53**)

- T.G. Schurr et al., and **The Genographic Consortium***, *Clan, language, and migration history has shaped genetic diversity in Haida and Tlingit populations from Southeast Alaska*, **Am J Phys Anthropol**, Jul 2012. (**IF=2.51**)

- M.C. Dulik et al., and **The Genographic Consortium***, *Y-chromosome analysis reveals genetic divergence and new founding native lineages in Athapaskan- and Eskimoan-speaking populations*, **Proc Natl Acad Sci**, May 2012. (**IF=9.81**)

- M. Haber et al., and **The Genographic Consortium***, *Afghanistan's ethnic groups share a Y-chromosomal heritage structured by historical events*, **PLoS One**, Mar 2012. (**IF=3.53**)

- Y. Lu et al., and **The Genographic Consortium***, *Mitochondrial origin of the matrilocal Mosuo people in China*, **Mitochondrial DNA**, Feb 2012. (**IF=1.27**)

- L. Kang et al., and **The Genographic Consortium**, *Y-chromosome O3 haplogroup diversity in Sino-Tibetan populations reveals two migration routes into the eastern Himalayas*, **Ann Hum Genet**, Jan 2012. (**IF=1.93**)

- J.B. Gaieski et al., and **The Genographic Consortium***, *Genetic ancestry and indigenous heritage in a Native American descendant community in Bermuda*, **Am J Phys Anthropol**, Nov 2011. (**IF=2.51**)

- M.S. Jota et al., and **The Genographic Consortium***, *A new subhaplogroup of native American Y-Chromosomes from the Andes*, **Am J Phys Anthropol**, Sep 2011. (**IF=2.51**)

- S. Yan et al., and **The Genographic Consortium***, *An updated tree of Y-chromosome Haplogroup O and revised phylogenetic positions of mutations P164 and PK4*, **Eur J Hum Genet**, Sep 2011. (**IF=4.32**)

- X. Cai et al., and **The Genographic Consortium***, *Human Migration through Bottlenecks from Southeast Asia into East Asia during Last Glacial Maximum Revealed by Y Chromosomes*, **PLoS One**, Aug 2011. (**IF=3.53**)

- B. Martnez-Cruz et al., and **The Genographic Consortium***, *Multiplex single-nucleotide polymorphism typing of the human Y chromosome using TaqMan probes*, **Investig Genet**, May 2011. (**IF=5.8**)

- O. Balanovsky et al., and **The Genographic Consortium***, *Parallel Evolution of Genes and Languages in the Caucasus Region*, **Mol Biol Evol**, May 2011. (**IF=14.31**)

- C.J. Adler et al., and **The Genographic Consortium***, *Survival and recovery of DNA from ancient teeth and bones*, **Journal of Archaeological Science**, May 2011. (**IF=2.14**)

- K. Yang et al., and **The Genographic Consortium***, *Positive selection on mitochondrial M7 lineages among the Gelong people in Hainan*, **Journal of Human Genetics** March 2011. (**IF=2.36**)

- M. Haber et al., and **The Genographic Consortium***, *Influences of history, geography, and religion on genetic structure: the Maronites in Lebanon*, **Eur J Hum Genet** Dec 2010. (**IF=4.32**)

- Z. Qin et al., and **The Genographic Consortium***, *A mitochondrial revelation of early human migrations to the Tibetan Plateau before and after the last glacial maximum*, **Am J Phys Anthropol** Dec 2010. (**IF=2.51**)

- W. Haak et al., and **The Genographic Consortium***, *Ancient DNA from European early neolithic farmers reveals their near eastern affinities*, **PLOS Biol.** Nov 2010. (**IF=12.69**)

Patents

- *Sampling the space of Ancestral Recombination Graphs* (**US 20120331008 A1**).

Selected Presentations

- *Incorporating phenotypic information to improve Mendelian disease-gene predictions*, poster presented at **63rd Annual Meeting of ASHG**, Oct 2013.
- *Leveraging phenotypic priors for disease-gene implication in rare disorders*, poster presented at HGM ICG joint conference April 2013.
- *Two roads both taken: walking the phenotypic and genotypic paths to disease gene implication*, poster presented at the **62th Annual Meeting of ASHG**, Nov. 2012.
- *Leveraging phenotypic priors for disease-gene implication in rare disorders*, invited talk at **National University Health System**, Singapore Oct. 2012.
- *Recombinomics*, oral presentation at Structure Discovery in Biology: Motifs, Networks & Phylogenies seminar at **Schloss Dagstuhl**, Jun. 2010.
- *Recombinomics*, invited talk at **Genome Biology and Bioinformatics Annual Retreat** at University of Toronto, May 2010.
- *RECO project*, oral presentation at Genographic Consortium annual meeting, Feb. 2010.
- **A. Javed**, *Recombinomics: recombination-based population genomics*, accepted tutorial at **APBC 2010**, Jan. 2010.
- *IRiS-detecting recombinations for phylogenetics and more*, oral presentation at Genome Informatics meeting at **CSHL**, Oct. 2009.
- *Recombinations-based population genomics*, oral presentation at Workshop on Algorithms in Human Population Genomics at **DIMACS**, Rutgers University, Apr. 2009.
- *Novel matrix decomposition for knowledge discovery in genomic data*, white paper presentation at **Cyber-Enabled Discovery and Innovation**, NSF symposium held at Rensselaer Polytechnic Institute, Sep. 2007.
- *Parallel frequent pattern mining*, poster presentation in **Midwest Database Symposium**, Chicago April 2004.

Computer Skills

Operating Systems: Microsoft Windows, Unix, Linux

Programming Languages: C/C++, Assembly (x86 architecture), Perl

Parallel Programming: MPI 1 & 2, OpenMP

Tools: Matlab, bash shell scripting, LaTeX

Bioinformatics: BWA, Bowtie, SAMtools, GATK, IGV, Picard, VCFtools, bedtools, ANNOVAR, VAAST, PLINK, arlequin, Beagle, LDHat, fastPHASE, IMPUTE2

Professional Activities

- Program Committee Member, RECOMB-CG 14, ISMB 13, BICoB 13, AIMM 12, BIOKDD (KDD 12), BICoB 12, BIOKDD (KDD 11), BIODM (ICDM 10), DMBI (SDM 08)
- Reviewer for Bioinformatics, Human Genetics, PloS Genetics, Nature Methods.

References

Available on request.